Supplementary Table S1. All proteins detected in EGFP+ cells from the kidney.

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
Na+/K+ -ATPase alpha 1 subunit	Atp1a1	NP_659149	113	1172	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
aconitase 2, mitochondrial	Aco2	NP_542364	85	998	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
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	Atp5b	NP_058054	56	804	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	NP_848492	112	715	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
actin, alpha 2, smooth muscle, aorta	Acta2	NP_031418	42	691	actin cytoskeleton, cytoplasm, cytoskeleton, smooth muscle contractile fiber	ATP binding, nucleotide binding, protein binding	regulation of blood pressure, vascular smooth muscle contraction
spectrin alpha 2	Spna2	NP_001070022	285	673	cortical cytoskeleton, cytoplasm, cytoskeleton, fascia adherens, membrane, Z disc	actin binding, calcium ion binding, calmodulin binding	actin filament capping
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	NP_031531	60	653	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
solute carrier family 25, member 5	Slc25a5	NP_031477	33	485	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
hemoglobin, beta adult major chain	Hbb-b1	NP_032246	16	461	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
spectrin beta 2 isoform 2	Spnb2	NP_033286	251	417	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

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	394	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
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	NP_766599	51	375	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
malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	NP_032643	36	374	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
actin, gamma, cytoplasmic 1	Actg1	NP_033739	42	363	actin cytoskeleton, costamere, cytoplasm, cytoskeleton, myofibril	ATP binding, nucleotide binding, protein binding, structural constituent of cytoskeleton	sarcomere organization
ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	NP_031534	68	337	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
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	Slc25a3	NP_598429	40	337	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, symporter activity	transport
histone cluster 1, H4a	Hist1h4a	NP_835499	11	335	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly

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	314	hemoglobin complex	heme binding, iron ion binding, metal ion binding, oxygen binding, oxygen transporter activity	erythrocyte development, in utero embryonic development, oxygen transport, transport
heat shock protein 9	Hspa9	NP_034611	73	294	cytoplasm, mitochondrion	ATP binding, enzyme binding, nucleotide binding, protein binding, unfolded protein binding	protein export from nucleus, protein folding, response to stress
mitochondrial trifunctional protein, alpha subunit	Hadha	NP_849209	83	287	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
oxoglutarate dehydrogenase (lipoamide)	Ogdh	NP_035086	116	276	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
clathrin, heavy polypeptide (Hc)	Cltc	NP_001003908	192	248	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
acyl-CoA synthetase medium-chain family member 2	Acsm2	NP_666309	64	245	cellular_component, mitochondrion	ATP binding, butyrate-CoA ligase activity, catalytic activity, ligase activity, magnesium ion binding, metal ion binding, molecular_function, nucleotide binding	biological_process, fatty acid metabolic process, lipid metabolic process, metabolic process
filamin B, beta	Flnb	NP_598841	277	240	cytoplasm, cytoskeleton, focal adhesion, stress fiber	actin binding, protein binding	skeletal muscle tissue development
succinate dehydrogenase Fp subunit	Sdha	NP_075770	73	237	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
aldehyde dehydrogenase 1 family, member L1	Aldh1l1	NP_081682	99	233	cytoplasm	acyl carrier activity, formyltetrahydrofolate dehydrogenase activity, hydroxymethyl-, formyl- and related transferase activity, methyltransferase activity, oxidoreductase activity, phosphopantetheine binding	10-formyltetrahydrofolate catabolic process, biosynthetic process, metabolic process, one-carbon metabolic process, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
nicotinamide nucleotide transhydrogenase	Nnt	NP_032736	114	231	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
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	Slc25a31	NP_848473	35	228	cell projection, cilium, flagellum, integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	NP_613063	23	202	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
acetyl-CoA synthetase 2-like	Acss1	NP_542142	75	192	mitochondrial matrix, mitochondrion	acetate-CoA ligase activity, AMP binding, ATP binding, catalytic activity, ligase activity, nucleotide binding	acetyl-CoA biosynthetic process, metabolic process
peroxiredoxin 5 precursor	Prdx5	NP_036151	22	179	cytoplasm, mitochondrion, peroxisome	antioxidant activity, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	cell redox homeostasis, oxidation reduction
acetyl-Coenzyme A acetyltransferase 1 precursor	Acat1	NP_659033	45	179	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
glutamate oxaloacetate transaminase 2, mitochondrial	Got2	NP_034455	47	173	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
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	NP_663493	80	171	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
heat shock protein 8	Hspa8	NP_112442	71	168	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
PREDICTED: hypothetical protein isoform 2	LOC100039281	XP_001472561	19	159	not classified	not classified	not classified
dihydrolipoamide dehydrogenase	Dld	NP_031887	54	149	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
Na+/K+ -ATPase beta 1 subunit	Atp1b1	NP_033851	35	149	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
ubiquinol cytochrome c reductase core protein 2	Uqcrc2	NP_080175	48	149	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding	electron transport chain, proteolysis, transport
aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	NP_598803	58	147	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
heat shock protein 1, beta	Hsp90ab1	NP_032328	83	146	cytoplasm, intracellular, mitochondrion	ATP binding, nucleotide binding, protein binding, unfolded protein binding	placenta development, protein folding, response to stress
cytochrome c oxidase subunit IV isoform 1	Cox4i1	NP_034071	20	141	membrane, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, protein binding	not classified
inner membrane protein, mitochondrial	Immt	NP_083949	84	132	integral to membrane, integral to mitochondrial inner membrane, membrane, mitochondrial inner membrane, mitochondrion	molecular_function	biological_process
peroxiredoxin 1	Prdx1	NP_035164	22	130	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
3-oxoacid CoA transferase 1	Oxct1	NP_077150	56	127	mitochondrion	3-oxoacid CoA-transferase activity, CoA-transferase activity, transferase activity	cellular ketone body metabolic process, ketone body catabolic process, metabolic process
histone cluster 2, H2be	Hist2h2be	NP_835586	14	125	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly
IQ motif containing GTPase activating protein 1	Iqgap1	NP_057930	189	123	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
actinin, alpha 1	Actn1	NP_598917	103	120	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
heat shock protein 2	Hspa2	NP_001002012	70	118	mitochondrion	ATP binding, nucleotide binding, protein binding	response to stress
triosephosphate isomerase 1	Tpi1	NP_033441	27	117	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
cytochrome c oxidase subunit II	COX2	NP_904331	26	117	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
heat shock protein 1 (chaperonin)	Hspd1	NP_034607	61	115	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
ATPase, H+ transporting, lysosomal V1 subunit B1	Atp6v1b1	NP_598918	57	114	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
hemoglobin, beta adult minor chain	Hbb-b2	NP_058652	16	112	hemoglobin complex	heme binding, iron ion binding, metal ion binding, oxygen binding, oxygen transporter activity	oxygen transport, transport
glutamate dehydrogenase 1	Glud1	NP_032159	61	110	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
lactate dehydrogenase B	Ldhb	NP_032518	37	109	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
hexokinase 1	Hk1	NP_034568	106	109	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
histone cluster 2, H2bb	Hist2h2bb	NP_783597	14	108	chromosome, nucleosome, nucleus	DNA binding	not classified

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	107	mitochondrion	ATP binding, biotin binding, catalytic activity, ligase activity, nucleotide binding, propionyl-CoA carboxylase activity	metabolic process
malate dehydrogenase 1, NAD (soluble)	Mdh1	NP_032644	36	106	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
predicted gene, OTTMUSG00000007855	OTTMUSG00000007855	NP_001074488	15	103	not classified	not classified	not classified
ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	NP_079683	53	102	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
electron transferring flavoprotein, alpha polypeptide	Etfa	NP_663590	35	102	mitochondrial electron transfer flavoprotein complex, mitochondrion	electron carrier activity, FAD binding	electron transport chain, transport
glyceraldehyde-3-phosphate dehydrogenase	Gapdh	NP_032110	36	101	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
leucine-rich PPR motif-containing protein	Lrpprc	NP_082509	157	101	cytoplasm, membrane, mitochondrion, nucleus	DNA binding, protein binding, RNA binding, single-stranded DNA binding	mRNA transport, regulation of transcription, transcription, transport
aldolase A, fructose-bisphosphate	Aldoa	NP_031464	39	99	extracellular region, flagellum, platelet alpha granule lumen	catalytic activity, fructose-bisphosphate aldolase activity, lyase activity	glycolysis, metabolic process
pyruvate kinase, muscle	Pkm2	NP_035229	58	99	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
tubulin, alpha 4	Tuba4a	NP_033473	50	98	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	NP_033855	29	98	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
superoxide dismutase 2, mitochondrial	Sod2	NP_038699	25	98	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
voltage-dependent anion channel 1	Vdac1	NP_035824	31	95	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
acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	NP_059062	71	94	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
pyruvate dehydrogenase (lipoamide) beta	Pdhb	NP_077183	39	94	mitochondrion	catalytic activity, oxidoreductase activity, pyruvate dehydrogenase (acetyl-transferring) activity	glycolysis, metabolic process, oxidation reduction
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	NP_083849	40	94	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
apoptosis-inducing factor, mitochondrion-associated 1	Aifm1	NP_036149	67	91	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
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	Slc25a4	NP_031476	33	89	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	binding, transporter activity	transport
tubulin, beta 3	Tubb3	NP_075768	50	89	axon, intracellular, microtubule, microtubule cytoskeleton, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
aldehyde dehydrogenase 2, mitochondrial	Aldh2	NP_033786	57	88	mitochondrion	aldehyde dehydrogenase (NAD) activity, oxidoreductase activity	metabolic process, oxidation reduction
H2A histone family, member X	H2afx	NP_034566	15	88	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
citrate synthase	Cs	NP_080720	52	87	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
histone cluster 1, H1c	Hist1h1c	NP_056601	21	86	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly, nucleosome positioning
enolase 1, alpha non-neuron	Eno1	NP_075608	47	86	not classified	lyase activity, magnesium ion binding, phosphopyruvate hydratase activity, protein binding	glycolysis
ubiquitin B	Ubb	NP_035794	34	85	cytoplasm, nucleus	protein binding	not classified
vacuolar H+ATPase B2	Atp6v1b2	NP_031535	57	84	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
pyruvate carboxylase	Pcx	NP_032823	130	82	cytoplasm, mitochondrial inner membrane, mitochondrion	ATP binding, biotin binding, catalytic activity, ligase activity, manganese ion binding, metal ion binding, nucleotide binding, pyruvate carboxylase activity	gluconeogenesis, lipid biosynthetic process, metabolic process
protein disulfide isomerase associated 3	Pdia3	NP_031978	57	81	endoplasmic reticulum	isomerase activity, protein disulfide isomerase activity	cell redox homeostasis, positive regulation of apoptosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
L-3-hydroxyacyl-Coenzyme A dehydrogenase	Hadh	NP_032238	34	80	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
dynein, cytoplasmic, heavy chain 1	Dync1h1	NP_084514	532	80	cytoplasm, dynein complex, microtubule	ATP binding, ATPase activity, microtubule motor activity, motor activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	microtubule-based movement
peptidylprolyl isomerase A	Ppia	NP_032933	18	79	cytoplasm, cytosol	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity, protein binding	neuron differentiation, protein folding
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	NP_080979	20	79	mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
calnexin	Canx	NP_001103970	67	78	endoplasmic reticulum, integral to membrane, membrane	calcium ion binding, protein binding, sugar binding, unfolded protein binding	protein folding
carbonic anhydrase 2	Car2	NP_033931	29	76	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
carnitine palmitoyltransferase 1a, liver	Cpt1a	NP_038523	88	76	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	acyltransferase activity, carnitine O-palmitoyltransferase activity, transferase activity	fatty acid metabolic process, lipid metabolic process, transport
eukaryotic translation elongation factor 1 alpha 1	Eef1a1	NP_034236	50	75	cytoplasm	GTP binding, nucleotide binding, translation elongation factor activity	not classified
solute carrier family 25 (mitochondrial carrier, Aralar), member 12	Slc25a12	NP_766024	75	75	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, calcium ion binding, transporter activity	malate-aspartate shuttle, transport
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	NP_663589	68	73	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
creatine kinase, mitochondrial 1, ubiquitous	Ckmt1	NP_034027	47	72	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
mitochondrial trifunctional protein, beta subunit	Hadhb	NP_663533	51	71	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
calbindin-28K	Calb1	NP_033918	30	70	cytoplasm, cytosol, nucleus	calcium ion binding, vitamin D binding	locomotory behavior

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutaminase isoform 2	Gls	NP_001106854	66	68	not classified	glutaminase activity	behavior, glutamine catabolic process, regulation of respiratory gaseous exchange by neurological system process, synaptic transmission
ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	NP_598587	56	68	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
aldehyde dehydrogenase 4 family, member A1	Aldh4a1	NP_780647	62	68	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
ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	Atp5k	NP_031533	8	67	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
solute carrier family 12, member 3	Slc12a3	NP_062288	111	67	apical plasma membrane, cytosol, integral to membrane, membrane, plasma membrane	cation:chloride symporter activity, sodium ion binding, symporter activity, transporter activity	chloride transport, ion transport, sodium ion transport, transport
heat shock protein 5	Hspa5	NP_071705	72	65	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, response to stress
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	NP_056644	74	63	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, calcium ion binding, L-glutamate transmembrane transporter activity	aspartate transport, malate-aspartate shuttle, transport
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor	Atp5d	NP_079589	18	63	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
plectin 1 isoform 2	Plec1	NP_958787	516	63	contractile fiber, cytoplasm, cytoskeleton, insoluble fraction	actin binding	not classified
keratin 7	Krt7	NP_149064	51	62	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified
fumarate hydratase 1	Fh1	NP_034339	54	61	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
pyruvate dehydrogenase E1 alpha 1	Pdha1	NP_032836	43	60	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
actinin alpha 4	Actn4	NP_068695	105	60	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
tubulin, beta 4	Tubb4	NP_033477	50	59	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
valosin containing protein	Vcp	NP_033529	89	58	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
ATPase, H+ transporting, lysosomal V0 subunit A isoform 4	Atp6v0a4	NP_536715	96	58	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
methylenetetrahydrofolate dehydrogenase 1	Mthfd1	NP_620084	101	58	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
NADH dehydrogenase (ubiquinone) Fe-S protein 3	Ndufs3	NP_080964	30	57	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
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	Ndufb10	NP_080960	21	56	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
solute carrier family 12, member 1 isoform F	Slc12a1	NP_001073158	120	55	apical plasma membrane, integral to membrane, membrane	cation:chloride symporter activity, potassium ion binding, protein binding, sodium ion binding, symporter activity, transporter activity	chloride transport, ion transport, potassium ion transport, sodium ion transport, transport
peroxiredoxin 2	Prdx2	NP_035693	22	55	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
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mccc1	NP_076133	79	55	mitochondrial inner membrane, mitochondrion	ATP binding, biotin binding, catalytic activity, ligase activity, methylcrotonoyl-CoA carboxylase activity, nucleotide binding	metabolic process
heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1	Hnrnpa2b1	NP_058086	36	54	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
propionyl Coenzyme A carboxylase, beta polypeptide	Pccb	NP_080111	58	54	mitochondrion	ATP binding, ligase activity, nucleotide binding, propionyl-CoA carboxylase activity	not classified

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	54	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
histone cluster 1, H2ab	Hist1h2ab	NP_783591	14	54	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform b	Atp5c1	NP_001106209	30	53	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
spectrin beta 3	Spnb3	NP_067262	271	53	not classified	actin binding	not classified
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	Ndufb9	NP_075661	22	53	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10	NP_077159	41	53	mitochondrion, respiratory chain	ATP binding, phosphotransferase activity, alcohol group as acceptor	electron transport chain, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, transport
cytochrome c-1	Cyc1	NP_079843	35	53	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
phosphoglycerate kinase 1	Pgk1	NP_032854	45	52	cytoplasm	ATP binding, kinase activity, nucleotide binding, phosphoglycerate kinase activity, transferase activity	glycolysis
keratin complex 1, acidic, gene 10	Krt10	NP_034790	57	52	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	NP_035637	47	52	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
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	NP_079634	43	52	mitochondrial inner membrane, mitochondrion, respiratory chain	binding, catalytic activity, coenzyme binding	cellular metabolic process, electron transport chain, metabolic process, transport
IQ motif containing GTPase activating protein 2	Iqgap2	NP_081987	181	52	intracellular	calmodulin binding, GTPase activator activity, protein binding	regulation of small GTPase mediated signal transduction
heterogeneous nuclear ribonucleoprotein L	Hnrnpl	NP_796275	60	52	nucleus, pronucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing
lamin A isoform A	Lmna	NP_001002011	74	51	intermediate filament, lamin filament, nucleus	protein binding, structural molecule activity	nuclear envelope organization
calbindin 2	Calb2	NP_031612	31	51	gap junction	calcium ion binding	not classified
heat shock protein 1, alpha	Hsp90aa1	NP_034610	85	51	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
glucose phosphate isomerase 1	Gpi1	NP_032181	63	50	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
solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	Slc25a11	NP_077173	34	50	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
13kDa differentiation-associated protein	Ndufa12	NP_079827	18	50	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	electron carrier activity, NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Echs1	NP_444349	31	50	mitochondrion	catalytic activity, enoyl-CoA hydratase activity, lyase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
solute carrier family 8 (sodium/calcium exchanger), member 1 isoform B	Slc8a1	NP_001106269	107	49	integral to membrane, membrane, membrane fraction, plasma membrane, sarcolemma, T-tubule	antiporter activity, calcium ion binding, calcium:sodium antiporter activity, calmodulin binding, protein binding, sodium ion binding	calcium ion transport, cell communication, ion transport, regulation of the force of heart contraction, sodium ion transport, transport
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	NP_803421	42	49	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
albumin	Alb	NP_033784	69	48	cytoplasm, extracellular region, extracellular space	copper ion binding, lipid binding, metal ion binding	transport
brain protein 44	Brp44	NP_081706	14	48	mitochondrion	not classified	not classified
tubulin, alpha 1	Tuba1a	NP_035783	50	47	cytoplasmic microtubule, 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
keratin complex 2, basic, gene 8	Krt8	NP_112447	55	46	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
NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	NP_598427	51	46	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
ankyrin 3, epithelial isoform h	Ank3	NP_733925	210	46	axon, membrane fraction, synapse	protein binding	axon guidance, synapse organization
similar to Tu translation elongation factor, mitochondrial	LOC100041265	NP_001104813	50	45	not classified	not classified	not classified
hydroxysteroid 11-beta dehydrogenase 2	Hsd11b2	NP_032315	42	45	endoplasmic reticulum, microsome	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
voltage-dependent anion channel 2	Vdac2	NP_035825	32	45	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
electron transferring flavoprotein, dehydrogenase	Etfdh	NP_080070	68	45	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
PREDICTED: similar to Electron transferring flavoprotein, beta polypeptide isoform 2	LOC100045699	XP_001474234	28	45	not classified	not classified	not classified
myosin IC isoform b	Myo1c	NP_001074243	118	44	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
peroxiredoxin 3	Prdx3	NP_031478	28	44	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
isocitrate dehydrogenase 3 (NAD+), gamma	Idh3g	NP_032349	43	44	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
villin 2	Ezr	NP_033536	69	44	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
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	Ndufb7	NP_080119	16	44	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity	electron transport chain, transport
succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	Sdhb	NP_075863	32	43	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
myosin VI	Myo6	NP_001034635	146	41	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
keratin 18	Krt18	NP_034794	48	41	intermediate filament	protein binding, structural molecule activity	apoptosis, tumor necrosis factor-mediated signaling pathway
tubulin, beta 5	Tubb5	NP_035785	50	41	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
adenylate kinase 3	Ak3	NP_067274	25	41	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
gelsolin	Gsn	NP_666232	86	41	cytoplasm, cytoskeleton, extracellular region, lamellipodium	actin binding, calcium ion binding	actin filament capping, vesicle-mediated transport
acyl-Coenzyme A dehydrogenase, medium chain	Acadm	NP_031408	46	40	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
cytochrome c, somatic	Cycs	NP_031834	12	40	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
choline dehydrogenase	Chdh	NP_780552	66	40	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
transketolase	Tkt	NP_033414	68	39	not classified	calcium ion binding, catalytic activity, metal ion binding, transferase activity, transketolase activity	metabolic process, regulation of growth
heterogeneous nuclear ribonucleoprotein U	Hnrnpu	NP_058085	88	39	ribonucleoprotein complex	nucleic acid binding	not classified
protease, serine, 15	Lonp1	NP_083058	106	39	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

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	NP_694704	53	39	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
PREDICTED: hypothetical protein	LOC100046199	XP_001475883	21	39	not classified	not classified	not classified
phosphoglycerate mutase 2	Pgam2	NP_061358	29	38	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
phosphoglycerate mutase 1	Pgam1	NP_075907	29	38	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
PREDICTED: hypothetical protein	EG626058	XP_895712	22	38	not classified	not classified	not classified
PREDICTED: similar to ubiquitin A-52 residue ribosomal protein fusion product 1 isoform 2	LOC629750	XP_899768	15	38	not classified	not classified	not classified
keratin complex 2, basic, gene 1	Krt1	NP_032499	66	37	intermediate filament, keratin filament, membrane, plasma membrane	structural molecule activity	not classified
annexin A5	Anxa5	NP_033803	36	37	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
hydroxyacyl-Coenzyme A dehydrogenase type II	Hsd17b10	NP_058043	27	37	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	NP_083548	25	37	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
methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	NP_084302	61	37	mitochondrion	ATP binding, ligase activity, methylcrotonoyl-CoA carboxylase activity, nucleotide binding	not classified
low density lipoprotein receptor-related protein 2	Lrp2	NP_001074557	519	36	apical part of cell, apical plasma membrane, brush border, coated pit, endocytic vesicle, endoplasmic reticulum, endosome, Golgi apparatus, integral to membrane, membrane, membrane fraction	calcium ion binding, protein binding, receptor activity, SH3 domain binding	cell proliferation, endocytosis, forebrain development, receptor-mediated endocytosis, vitamin metabolic process
H1 histone family, member 0	H1f0	NP_032223	21	36	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	Ndufa13	NP_075801	17	36	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, nucleus, respiratory chain	ATP binding	apoptosis, electron transport chain, transport
serum deprivation response	Sdpr	NP_620080	47	36	cytoplasm, membrane	lipid binding, protein binding	positive regulation of transcription from RNA polymerase II promoter
cadherin 16	Cdh16	NP_031689	90	35	integral to membrane, membrane, plasma membrane	calcium ion binding, protein binding	cell adhesion, homophilic cell adhesion
carnitine acetyltransferase	Crat	NP_031786	71	35	endoplasmic reticulum, membrane, mitochondrial inner membrane, mitochondrion, peroxisome	acyltransferase activity, carnitine O-acetyltransferase activity, transferase activity	fatty acid metabolic process, lipid metabolic process, transport
eukaryotic translation elongation factor 2	Eef2	NP_031933	95	35	cytoplasm, ribonucleoprotein complex	GTP binding, GTPase activity, nucleotide binding, translation elongation factor activity	translation
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	Ndufa4	NP_035016	9	35	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
calreticulin	Calr	NP_031617	48	34	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
glutamate oxaloacetate transaminase 1, soluble	Got1	NP_034454	46	34	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
lactate dehydrogenase A	Ldha	NP_034829	36	34	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
tumor rejection antigen gp96	Hsp90b1	NP_035761	92	34	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
destrin	Dstn	NP_062745	19	34	cortical actin cytoskeleton, cytoplasm, intracellular	actin binding	cell motion, cytokinesis, positive regulation of actin filament depolymerization
vacuolar H+ ATPase E1	Atp6v1e1	NP_031536	26	33	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
B-cell receptor-associated protein 37	Phb2	NP_031557	33	33	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
cytochrome c oxidase, subunit Va	Cox5a	NP_031773	16	33	membrane, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, iron ion binding, metal ion binding	not classified
prothymosin alpha	Ptma	NP_032998	12	33	nucleus	not classified	not classified
microsomal glutathione S-transferase 3	Mgst3	NP_079845	17	33	cellular_component, endoplasmic reticulum, integral to membrane, membrane, microsome	glutathione transferase activity, molecular_function, transferase activity	biological_process
acyl-Coenzyme A dehydrogenase, long-chain	Acadl	NP_031407	48	32	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
RAB1, member RAS oncogene family	Rab1	NP_033022	23	32	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
ubiquitin-activating enzyme E1	Uba1	NP_033483	118	32	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
prolyl 4-hydroxylase, beta polypeptide	P4hb	NP_035162	57	32	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
Rhesus blood group-associated B glycoprotein	Rhbg	NP_067350	50	32	basolateral plasma membrane, cytoplasmic vesicle, integral to membrane, integral to plasma membrane, membrane, plasma membrane	ammonia transporter activity, ammonium transmembrane transporter activity	ammonium transport, transport
LPS-responsive beige-like anchor isoform alpha	Lrba	NP_109620	317	32	cytoplasmic membrane-bounded vesicle	protein kinase A binding	endosome transport, protein localization, signal transduction
es1 protein	D10Jhu81e	NP_613067	28	32	centriole, mitochondrion	molecular_function	biological_process
keratin 86	Krt86	NP_034797	53	31	intermediate filament, keratin filament	structural molecule activity	not classified
proline dehydrogenase	Prodh	NP_035302	68	31	mitochondrial inner membrane, mitochondrion	oxidoreductase activity, proline dehydrogenase activity	glutamate biosynthetic process, oxidation reduction, proline catabolic process, proline metabolic process
cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	NP_079904	10	31	mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity	not classified
sorting and assembly machinery component 50 homolog	Samm50	NP_848729	52	31	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, outer membrane	not classified	not classified
dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	Dci	NP_034153	32	30	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
isovaleryl coenzyme A dehydrogenase	Ivd	NP_062800	46	30	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 K	Hnrnpk	NP_079555	51	30	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	DNA binding, nucleic acid binding, protein binding, RNA binding	mRNA processing, RNA splicing
heat shock protein 4	Hspa4	NP_032326	94	29	cytoplasm	ATP binding, nucleotide binding	response to stress
branched chain aminotransferase 2, mitochondrial	Bcat2	NP_033867	44	29	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
filamin, alpha	Flna	NP_034357	281	29	cytoplasm, cytoskeleton, trans-Golgi network	actin binding, protein binding, protein kinase C binding	early endosome to late endosome transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
upregulated during skeletal muscle growth 5	Usmg5	NP_075700	6	29	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	not classified
ribophorin I	Rpn1	NP_598694	69	29	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, transferase activity	protein amino acid glycosylation
succinate dehydrogenase complex, subunit C, integral membrane protein	Sdhc	NP_079597	18	28	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
nucleoside-diphosphate kinase 2	Nme2	NP_001070997	17	27	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
DEAH (Asp-Glu-Ala-His) box polypeptide 9	Dhx9	NP_031868	150	27	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
heat shock 70kDa protein 1B	Hspa1b	NP_034608	70	27	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
peptidylprolyl isomerase B	Ppib	NP_035279	24	27	endoplasmic reticulum	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity	protein folding
succinate-Coenzyme A ligase, ADP-forming, beta subunit	Sucla2	NP_035636	50	27	mitochondrion	ATP binding, catalytic activity, ligase activity, nucleotide binding, succinate-CoA ligase (ADP-forming) activity, succinate-CoA ligase activity	metabolic process, tricarboxylic acid cycle
histone cluster 1, H1e	Hist1h1e	NP_056602	22	27	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
ras homolog gene family, member A	Rhoa	NP_058082	22	27	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
leucine zipper-EF-hand containing transmembrane protein 1	Letm1	NP_062668	83	27	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	calcium ion binding	not classified
vinculin	Vcl	NP_033528	117	26	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
voltage-dependent anion channel 3	Vdac3	NP_035826	31	26	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
RAB5C, member RAS oncogene family	Rab5c	NP_077776	23	26	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
TNF receptor-associated protein 1	Trap1	NP_080784	80	26	mitochondrion	ATP binding, nucleotide binding, unfolded protein binding	protein folding, response to stress
transgelin 2	Tagln2	NP_848713	22	26	not classified	not classified	muscle organ development
cytochrome c oxidase subunit I	COX1	NP_904330	57	26	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	copper ion binding, cytochrome-c oxidase activity, electron carrier activity, heme binding, iron ion binding, metal ion binding, oxidoreductase activity	aerobic respiration, electron transport chain, oxidation reduction, transport
PREDICTED: similar to 3-methylcrotonyl-CoA carboxylase alpha subunit	LOC677576	XP_001005025	28	26	not classified	not classified	not classified
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	Ndufb6	NP_001028477	16	25	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	Myl6	NP_034990	17	25	myosin complex, unconventional myosin complex	calcium ion binding, motor activity, structural constituent of muscle	muscle filament sliding, skeletal muscle tissue development
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	NP_035870	28	25	cytoplasm, mitochondrion, nucleus	not classified	protein targeting
annexin A4	Anxa4	NP_038499	36	25	apical plasma membrane	calcium ion binding, calcium-dependent phospholipid binding	kidney development
keratin 14	Krt14	NP_058654	53	25	cytoplasm, intermediate filament, keratin filament, nucleus	protein binding, structural molecule activity	not classified
RAB11a, member RAS oncogene family	Rab11a	NP_059078	24	25	endosome, membrane, plasma membrane, trans-Golgi network	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
selenium binding protein 2	Selenbp2	NP_062287	53	25	cytoplasm, membrane, nucleus	selenium binding	protein transport, transport
succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	NP_063932	35	25	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
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	Atp5j2	NP_065607	10	25	membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	not classified	ATP biosynthetic process, ion transport, proton transport, transport
ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	NP_079986	29	25	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
myosin ID	Myo1d	NP_796364	116	25	myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	not classified
annexin A6 isoform b	Anxa6	NP_001103681	75	24	cytoplasm, perinuclear region of cytoplasm	calcium ion binding, calcium-dependent phospholipid binding	calcium ion transport, regulation of muscle contraction
alpha glucosidase 2 alpha neutral subunit	Ganab	NP_032086	109	24	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
dihydrolipoamide branched chain transacylase E2	Dbt	NP_034152	53	24	mitochondrion	acyltransferase activity, cofactor binding, dihydrolipoyllysine-residue (2-methylpropanoyl)transferase activity, lipoic acid binding, protein binding, transferase activity	acyl-CoA biosynthetic process, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	NP_056544	75	24	cytoplasm, mitochondrion, peroxisomal membrane, 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	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction, spermatogenesis
abhydrolase domain containing 14b	Abhd14b	NP_083907	22	24	cytoplasm, nucleus	hydrolase activity	not classified
NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	NP_659119	24	24	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
PREDICTED: hypothetical protein	LOC100042503	XP_001478493	15	24	not classified	not classified	not classified
ribosomal protein L18	Rpl18	NP_033103	22	23	cellular_component, cytoplasm, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
S100 calcium binding protein G	S100g	NP_033919	9	23	apical plasma membrane, basolateral plasma membrane	calcium ion binding, vitamin D binding	not classified
cytochrome c oxidase, subunit Vb	Cox5b	NP_034072	14	23	membrane, mitochondrial envelope, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, metal ion binding, zinc ion binding	not classified
WD repeat domain 1	Wdr1	NP_035845	66	23	actin cytoskeleton, cytoplasm, cytoskeleton	actin binding	sensory perception of sound
ATPase, H+ transporting, V1 subunit D	Atp6v1d	NP_076210	28	23	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
RAB14, member RAS oncogene family	Rab14	NP_080973	24	23	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
glutathione S-transferase kappa 1	Gstk1	NP_083831	26	23	mitochondrial inner membrane, mitochondrion, outer membrane-bounded periplasmic space	glutathione peroxidase activity, glutathione transferase activity, protein disulfide oxidoreductase activity, transferase activity	glutathione metabolic process
carboxylesterase 3	Ces3	NP_444430	62	23	endoplasmic reticulum	carboxylesterase activity, fatty-acyl-ethyl-ester synthase activity, hydrolase activity	acyl-CoA metabolic process, response to toxin
aldolase B, fructose-bisphosphate	Aldob	NP_659152	40	23	not classified	catalytic activity, fructose-bisphosphate aldolase activity, lyase activity	glycolysis, metabolic process
spectrin beta 2 isoform 1	Spnb2	NP_787030	274	23	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATP synthase F0 subunit 8	ATP8	NP_904332	8	23	not classified	not classified	not classified
adaptor-related protein complex 2, beta 1 subunit isoform a	Ap2b1	NP_001030931	106	22	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
catalase	Cat	NP_033934	60	22	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
coatomer protein complex subunit alpha	Copa	NP_034068	139	22	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
superoxide dismutase 1, soluble	Sod1	NP_035564	16	22	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 maintenance, 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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
acyl-Coenzyme A dehydrogenase, short/branched chain	Acadsb	NP_080102	48	22	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
biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	NP_080788	33	22	cytoplasm, mitochondrion	hydrolase activity	not classified
PREDICTED: hypothetical protein LOC219189	1300010F03Rik	XP_920456	213	22	extracellular region, mitochondrion	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	not classified
glutathione peroxidase 1	Gpx1	NP_032186	22	21	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
phosphoglycerate kinase 2	Pgk2	NP_112467	45	21	cytoplasm	ATP binding, kinase activity, nucleotide binding, phosphoglycerate kinase activity, transferase activity	glycolysis
3-hydroxybutyrate dehydrogenase, type 1	Bdh1	NP_780386	38	21	mitochondrial inner membrane, mitochondrion	3-hydroxybutyrate dehydrogenase activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
PREDICTED: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11 isoform 6	Ndufa11	XP_930081	15	21	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	protein transporter activity	electron transport chain, protein transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cofilin 1, non-muscle	Cfl1	NP_031713	19	20	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
aldo-keto reductase family 1, member B3 (aldose reductase)	Akr1b3	NP_033788	36	20	cytoplasm	aldehyde reductase activity, oxidoreductase activity	oxidation reduction
cell division cycle 42	Cdc42	NP_033991	21	20	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
ribosomal protein L7	Rpl7	NP_035421	31	20	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
ATPase, H+/K+ exchanging, gastric, alpha polypeptide	Atp4a	NP_061201	113	20	integral to membrane, membrane, plasma 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, protein heterodimerization activity	ATP biosynthetic process, ATP hydrolysis coupled proton transport, cation transport, ion transport, metabolic process, monovalent inorganic cation transport, pH reduction, potassium ion transport, proton transport, regulation of proton transport, response to drug, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
stomatin-like protein 2	Stoml2	NP_075720	38	20	cytoplasm, cytoskeleton, membrane, mitochondrial inner membrane, mitochondrion	not classified	not classified
ubiquinol-cytochrome c reductase, complex III subunit VII	Uqcrq	NP_079628	10	20	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, transport
apolipoprotein O	Apoo	NP_080949	23	20	integral to membrane, membrane	not classified	not classified
NADH dehydrogenase subunit 1	ND1	NP_904328	36	20	integral to membrane, mitochondrion	NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity	oxidation reduction
ADP-ribosylation factor 3	Arf3	NP_031504	21	19	Golgi apparatus, intracellular	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
carnitine palmitoyltransferase 2	Cpt2	NP_034079	74	19	membrane, mitochondrial inner membrane, mitochondrion	acyltransferase activity, carnitine O-palmitoyltransferase activity, transferase activity	fatty acid metabolic process, lipid metabolic process, transport
talin 1	Tln1	NP_035732	270	19	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
enolase 2, gamma neuronal	Eno2	NP_038537	47	19	cytoplasm, intracellular, membrane, perikaryon, phosphopyruvate hydratase complex, plasma membrane	lyase activity, magnesium ion binding, metal ion binding, phosphopyruvate hydratase activity	glycolysis
tubulin, beta	Tubb2b	NP_076205	50	19	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst	NP_084501	49	19	mitochondrion, oxoglutarate dehydrogenase complex	acyltransferase activity, dihydrolipoyllysine-residue succinyltransferase activity, lipoic acid binding, transferase activity	metabolic process, tricarboxylic acid cycle
3-hydroxyisobutyrate dehydrogenase precursor	Hibadh	NP_663542	35	19	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
peroxiredoxin 6	Prdx6	NP_031479	25	18	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
ADP-ribosylation factor 5	Arf5	NP_031506	21	18	cytoplasm, Golgi apparatus, intracellular, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
enolase 3, beta muscle	Eno3	NP_031959	47	18	cytoplasm, phosphopyruvate hydratase complex	lyase activity, magnesium ion binding, metal ion binding, phosphopyruvate hydratase activity	glycolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
catenin alpha 1	Ctnna1	NP_033948	100	18	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
matrin 3	Matr3	NP_034901	95	18	intracellular, nucleus	metal ion binding, nucleic acid binding, nucleotide binding, RNA binding, zinc ion binding	not classified
ribosomal protein S18	Rps18	NP_035426	18	18	cytoplasm, intracellular, ribonucleoprotein complex, ribosome	RNA binding, rRNA binding, structural constituent of ribosome	translation
erythrocyte protein band 4.1-like 3	Epb4.1l3	NP_038841	103	18	cytoplasm, cytoskeleton, extrinsic to membrane	actin binding, binding, cytoskeletal protein binding, structural molecule activity	cortical actin cytoskeleton organization
Parkinson disease protein 7	Park7	NP_065594	20	18	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
vacuolar protein sorting 35	Vps35	NP_075373	92	18	cytoplasm, integral to membrane, membrane	not classified	protein transport, transport, vacuolar protein processing
cytochrome b-5	Cyb5	NP_080073	15	18	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
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	Ndufa5	NP_080890	13	18	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	oxidoreductase activity, acting on NADH or NADPH	electron transport chain, respiratory electron transport chain, transport
FXYD domain-containing ion transport regulator 2 isoform b	Fxyd2	NP_439888	7	18	integral to membrane, membrane	ion channel activity, potassium ion binding, sodium ion binding	ion transport, potassium ion transport, sodium ion transport, transport
isocitrate dehydrogenase 3, beta subunit	Idh3b	NP_570954	42	18	mitochondrion	oxidoreductase activity	oxidation reduction
ladinin	Lad1	NP_598425	59	18	basement membrane, extracellular region, proteinaceous extracellular matrix	not classified	not classified
MOCO sulphurase C-terminal domain containing 2	Mosc2	NP_598445	38	18	membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	catalytic activity, molybdenum ion binding, oxidoreductase activity, pyridoxal phosphate binding	oxidation reduction
very-long-chain acyl-CoA dehydrogenase VLCAD homolog	Acad9	NP_766266	69	18	mitochondrion	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
malic enzyme 3, NADP(+)-dependent, mitochondrial	Me3	NP_852072	67	18	mitochondrion	binding, catalytic activity, malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity, malic enzyme activity, metal ion binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	malate metabolic process, metabolic process, oxidation reduction
cytochrome b	CYTB	NP_904340	43	18	integral to membrane, membrane, membrane fraction, mitochondrial inner membrane, mitochondrion, respiratory chain	electron carrier activity, iron ion binding, metal ion binding, oxidoreductase activity	electron transport chain, oxidation reduction, respiratory electron transport chain, transport
keratin 76	Krt76	NP_001028349	63	17	intermediate filament, keratin filament	structural molecule activity	not classified
glutathione S-transferase, mu 2	Gstm2	NP_032209	26	17	cytoplasm	glutathione transferase activity, protein binding, transferase activity	metabolic process
Wiskott-Aldrich syndrome homolog	Was	NP_033541	54	17	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
nucleolin	Ncl	NP_035010	77	17	nucleolus, nucleoplasm, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	not classified
pendrin	Slc26a4	NP_035997	86	17	apical plasma membrane, integral to membrane, membrane	anion transmembrane transporter activity, chloride ion binding, secondary active sulfate transmembrane transporter activity, transporter activity	organ morphogenesis, regulation of pH, regulation of protein localization, sulfate transport, transport
ribosomal protein S9-like	Rps9	NP_084043	23	17	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, rRNA binding, structural constituent of ribosome	translation
RAS-related protein-1a	Rap1a	NP_663516	21	17	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
RAB35, member RAS oncogene family	Rab35	NP_937806	23	17	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
PREDICTED: similar to mKIAA0829 protein isoform 4	Cand1	XP_909201	159	17	nucleus	binding	modification-dependent protein catabolic process, regulation of transcription, transcription
hypothetical protein LOC237880	1700071K01 Rik	NP_001028937	29	16	not classified	not classified	not classified
basigin isoform 2	Bsg	NP_001070652	30	16	integral to membrane, membrane, plasma membrane	mannose binding, sugar binding	not classified
talin 2	Tln2	NP_001074711	272	16	cell junction, cytoplasm, cytoskeleton, focal adhesion, membrane, plasma membrane, ruffle, synapse	actin binding, binding, protein binding, structural constituent of cytoskeleton	cytoskeletal anchoring at plasma membrane
glioblastoma amplified	Gbas	NP_032121	33	16	mitochondrion	molecular_function	biological_process
prohibitin	Phb	NP_032857	30	16	membrane, mitochondrial inner membrane, mitochondrion	not classified	DNA replication

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	NP_033562	29	16	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
kallikrein 1	Klk1	NP_034769	29	16	not classified	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	proteolysis
t-complex protein 10b	Tcp10b	NP_035683	49	16	not classified	not classified	not classified
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	NP_035869	28	16	cellular_component, cytoplasm	monooxygenase activity, protein domain specific binding	protein targeting, signal transduction, small GTPase mediated signal transduction
RAB10, member RAS oncogene family	Rab10	NP_057885	23	16	Golgi apparatus, membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport
progesterone receptor membrane component	Pgrmc1	NP_058063	22	16	endoplasmic reticulum, integral to membrane, membrane, microsome	heme binding, lipid binding, receptor activity, steroid binding	not classified
hypoxia up-regulated 1	Hyou1	NP_067370	111	16	endoplasmic reticulum	ATP binding, nucleotide binding	response to stress
LIM domain and actin binding 1 isoform b	Lima1	NP_075550	66	16	actin cytoskeleton, cytoplasm, cytoskeleton	actin binding, metal ion binding, molecular_function, zinc ion binding	biological_process
tetratricopeptide repeat domain 11	Fis1	NP_079838	17	16	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion, peroxisome	binding	apoptosis
fumarylacetoacetate hydrolase domain containing 2A	Fahd2a	NP_083905	35	16	not classified	calcium ion binding, catalytic activity, hydrolase activity, magnesium ion binding, metal ion binding	metabolic process
coatomer protein complex, subunit beta 1	Copb1	NP_203534	107	16	COPI vesicle coat, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat	binding, structural molecule activity	intracellular protein transport, protein transport, transport, vesicle-mediated transport
nodal modulator 1	Nomo1	NP_694697	133	16	not classified	not classified	not classified
isoleucine-tRNA synthetase 2, mitochondrial	Iars2	NP_941055	113	16	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
plasma membrane calcium ATPase 4	Atp2b4	NP_998781	133	16	integral to membrane, integral to plasma membrane, membrane	ATP binding, hydrolase activity, nucleotide binding	calcium ion transport, ion transport, transport
PREDICTED: hypothetical protein	EG621837	XP_001473932	9	16	not classified	not classified	not classified
hepatocellular carcinoma-associated antigen 112	Tmem176a	NP_001091741	27	15	integral to membrane, membrane	not classified	not classified
myoferlin	Fer1l3	NP_001093104	233	15	cytoplasmic vesicle, integral to membrane, membrane, nucleus, plasma membrane	protein binding	cellular response to heat
calmodulin 1	Calm1	NP_033920	17	15	not classified	calcium ion binding	cell cycle, positive regulation of DNA binding
ornithine aminotransferase	Oat	NP_058674	48	15	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
myosin, heavy polypeptide 14	Myh14	NP_082297	228	15	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
NADH-ubiquinone oxidoreductase flavoprotein 3 isoform 1	1500032D16 Rik	NP_084363	50	15	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	molecular_function	electron transport chain, transport
glycine-N-acyltransferase	Glyat	NP_666047	34	15	mitochondrion	acyltransferase activity, glycine N-acyltransferase activity, transferase activity	not classified
AAA-ATPase TOB3	Atad3a	NP_849534	67	15	mitochondrial inner membrane, mitochondrion	ATP binding, nucleoside-triphosphatase activity, nucleotide binding	not classified
reticulon 3 isoform 1	Rtn3	NP_001003934	104	14	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane	molecular_function, protein binding	apoptosis, transport, vesicle-mediated transport
N-myc downstream regulated gene 1	Ndrg1	NP_032707	43	14	not classified	not classified	not classified
protein kinase C and casein kinase substrate in neurons 2	Pacsin2	NP_035992	56	14	cytoplasm, cytoplasmic vesicle, cytosol, trans-Golgi network	cytoskeletal protein binding, kinase activity, protein binding	endocytosis, negative regulation of endocytosis, signal transduction
glutathione S-transferase, pi 1	Gstp1	NP_038569	24	14	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	NP_080448	36	14	mitochondrion	2,4-dienoyl-CoA reductase (NADPH) activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
glutathione S-transferase, mu 4	Gstm4	NP_081040	26	14	cytosol	glutathione transferase activity, transferase activity	nitrobenzene metabolic process, xenobiotic catabolic process
NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	Ndufab1	NP_082453	17	14	mitochondrion, respiratory chain	acyl carrier activity, cofactor binding, phosphopantetheine binding	electron transport chain, fatty acid biosynthetic process, lipid biosynthetic process, transport
CDGSH iron sulfur domain 1	Cisd1	NP_598768	12	14	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
PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U-like 2	LOC100046 594	XP_001477737	85	14	nucleus	nucleic acid binding, protein binding	not classified
complement component 1, q subcomponent binding protein	C1qbp	NP_031599	31	13	mitochondrial matrix, mitochondrion	protein binding	not classified
cytochrome c oxidase, subunit VI a, polypeptide 1	Cox6a1	NP_031774	12	13	membrane, mitochondrial inner membrane, mitochondrial respiratory chain complex IV, mitochondrion	cytochrome-c oxidase activity	not classified
guanosine diphosphate (GDP) dissociation inhibitor 2	Gdi2	NP_032138	51	13	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
kinesin family member 5B	Kif5b	NP_032474	110	13	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

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	13	apical plasma membrane, basolateral plasma membrane, integral to membrane, membrane	not classified	not classified
H2A histone family, member Y	H2afy	NP_036145	40	13	Barr body, centrosome, chromosome, condensed chromosome, nucleosome, nucleus	chromatin binding, DNA binding	chromatin modification, dosage compensation, nucleosome assembly
malonyl-CoA decarboxylase	Mlycd	NP_064350	55	13	cytoplasm, mitochondrion, peroxisome	carboxy-lyase activity, lyase activity, malonyl-CoA decarboxylase activity	fatty acid biosynthetic process, lipid biosynthetic process
ARP3 actin-related protein 3 homolog	Actr3	NP_076224	47	13	cell projection, cytoplasm, cytoskeleton, lamellipodium	actin binding, ATP binding, nucleotide binding, protein binding	regulation of actin filament polymerization
leucine aminopeptidase 3	Lap3	NP_077754	56	13	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
SERPINE1 mRNA binding protein 1	Serbp1	NP_080090	45	13	cytoplasm, nucleus	RNA binding	not classified
SA hypertension-associated homolog	Acsm3	NP_997606	66	13	mitochondrial matrix, mitochondrion	ATP binding, butyrate-CoA ligase activity, catalytic activity, fatty-acid ligase activity, ligase activity, magnesium ion binding, metal ion binding, nucleotide binding	fatty acid biosynthetic process, fatty acid metabolic process, lipid metabolic process, metabolic process
PREDICTED: hypothetical protein	LOC674419	XP_982574	30	13	not classified	not classified	not classified
early endosome antigen 1	Eea1	NP_001001932	161	12	cytoplasm, early endosome, endosome, intracellular, membrane, serine-pyruvate aminotransferase complex	metal ion binding, zinc ion binding	not classified
heterogeneous nuclear ribonucleoprotein A1 isoform b	Hnrnpa1	NP_001034218	39	12	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
adducin 1 (alpha) isoform 3	Add1	NP_001095914	73	12	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
isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	NP_001104790	47	12	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
adaptor protein complex AP-1, beta 1 subunit	Ap1b1	NP_031480	104	12	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
acidic ribosomal phosphoprotein P0	Rplp0	NP_031501	34	12	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	ribosome biogenesis, translational elongation
cytochrome P450, family 4, subfamily b, polypeptide 1	Cyp4b1	NP_031849	59	12	endoplasmic reticulum, membrane, microsome	aromatase activity, electron carrier activity, heme binding, iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity	oxidation reduction
discs large homolog 1	Dlg1	NP_031888	103	12	basolateral plasma membrane, cell junction, cell projection membrane, cell-cell adherens junction, endoplasmic reticulum, immunological synapse, lateral plasma membrane, membrane, membrane raft, neuromuscular junction, plasma membrane, postsynaptic density, postsynaptic membrane, synapse	protein binding, protein complex scaffold	activation of protein kinase activity, amyloid precursor protein metabolic process, branching involved in ureteric bud morphogenesis, embryonic skeletal system morphogenesis, formation of immunological synapse, hard palate development, lens development in camera-type eye, membrane raft organization, negative regulation of epithelial cell proliferation, negative regulation of T cell proliferation, peristalsis, positive regulation of actin filament polymerization, positive regulation of cell proliferation, positive regulation of developmental growth, positive regulation of multicellular organism growth, protein localization, regulation of membrane potential, reproductive structure development, smooth muscle tissue development, T cell activation, T cell cytokine production, tissue morphogenesis, ureteric bud development
acyl-CoA synthetase long-chain family member 1	Acsl1	NP_032007	78	12	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, nucleotide binding	fatty acid metabolic process, lipid metabolic process, metabolic process
leukotriene A4 hydrolase	Lta4h	NP_032543	69	12	cytoplasm	catalytic activity, hydrolase activity, leukotriene-A4 hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	leukotriene biosynthetic process, proteolysis

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	12	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
SAR1a gene homolog	Sar1a	NP_033146	22	12	endoplasmic reticulum, Golgi apparatus, intracellular, sarcoplasmic reticulum	GTP binding, nucleotide binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport
AHNAK nucleoprotein isoform 1	Ahnak	NP_033773	604	12	cell-cell junction	not classified	not classified
chaperonin containing Tcp1, subunit 3 (gamma)	Cct3	NP_033966	61	12	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	NP_034158	73	12	cytoplasm, nucleus	ATP binding, ATP-dependent helicase activity, DNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	not classified
profilin 1	Pfn1	NP_035202	15	12	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
ubiquitin specific protease 5 (isopeptidase T)	Usp5	NP_038728	96	12	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
aquaporin 3	Aqp3	NP_057898	32	12	basolateral plasma membrane, integral to membrane, integral to plasma membrane, membrane, pore complex	transporter activity, water channel activity	transport, water transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
stratifin	Sfn	NP_061224	28	12	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
hydroxysteroid dehydrogenase like 2	Hsdl2	NP_077217	54	12	mitochondrion	binding, catalytic activity, oxidoreductase activity, sterol carrier activity	metabolic process, oxidation reduction
ribosome binding protein 1 isoform a	Rrbp1	NP_077243	158	12	endoplasmic reticulum, integral to endoplasmic reticulum membrane, integral to membrane, membrane	not classified	protein transport, transmembrane transport, transport
GrpE-like 1, mitochondrial	Grpel1	NP_077798	24	12	mitochondrion	adenyl-nucleotide exchange factor activity, chaperone binding, protein binding, protein homodimerization activity	protein folding, protein import into mitochondrial matrix
coiled-coil-helix-coiled-coil-helix domain containing 3	Chchd3	NP_079612	26	12	mitochondrial inner membrane, mitochondrion	not classified	not classified
sorcin isoform 2	Sri	NP_079894	20	12	cytoplasm, intracellular, plasma membrane, vesicle, Z disc	calcium ion binding, protein binding	calcium ion transport
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	Ndufa6	NP_080263	15	12	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
glyoxalase domain containing 4	Glod4	NP_080305	33	12	mitochondrion	not classified	not classified
vacuolar H+ ATPase C2	Atp6v1c2	NP_598460	48	12	proton-transporting V-type ATPase, V1 domain	hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, protein binding	ATP synthesis coupled proton transport, ion transport, proton transport, transport
sarcosine dehydrogenase	Sardh	NP_619606	102	12	cytoplasm, mitochondrion	aminomethyltransferase activity, oxidoreductase activity, sarcosine dehydrogenase activity	glycine catabolic process, oxidation reduction
cytochrome c oxidase subunit III	COX3	NP_904334	30	12	integral to membrane, membrane, mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	hydrolase activity, oxidoreductase activity	ATP biosynthetic process, ion transport, oxidation reduction, proton transport, transport
PREDICTED: proline-rich polypeptide 6 isoform 4	Prr6	XP_921840	28	12	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
aldo-keto reductase family 1, member C19	Akr1c19	NP_001013807	37	11	cellular_component	molecular_function	biological_process
predicted gene, OTTMUSG00000002778	OTTMUSG00000002778	NP_001104805	12	11	not classified	not classified	not classified
cysteine and glycine-rich protein 2	Csrp2	NP_031818	21	11	nucleus	metal ion binding, molecular_function, zinc ion binding	cell differentiation, multicellular organismal development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATP-binding cassette, sub-family D, member 3	Abcd3	NP_033017	75	11	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, peroxisomal membrane, peroxisome	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	transport
golgi apparatus protein 1	Glg1	NP_033175	134	11	Golgi apparatus, Golgi membrane, integral to membrane, membrane, plasma membrane	sugar binding	not classified
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	Ndufa2	NP_035015	11	11	membrane, mitochondrial inner membrane, mitochondrial respiratory chain complex I, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
ribosomal protein L6	Rpl6	NP_035420	34	11	cytoplasm, intracellular, nucleolus, nucleus, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
nuclease sensitive element binding protein 1	Ybx1	NP_035862	36	11	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
annexin A11	Anxa11	NP_038497	54	11	nucleus	calcium ion binding, calcium-dependent phospholipid binding, phosphatidylethanolamine binding	not classified
metaxin 1	Mtx1	NP_038632	36	11	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	not classified	protein targeting to mitochondrion, protein transport, transport
esterase D/formylglutathione hydrolase	Esd	NP_058599	31	11	cytoplasm, cytoplasmic membrane-bounded vesicle, cytoplasmic vesicle	carboxylesterase activity, hydrolase activity, hydrolase activity, acting on ester bonds, S-formylglutathione hydrolase activity	not classified
aldehyde dehydrogenase 9, subfamily A1	Aldh9a1	NP_064377	56	11	cytoplasm, cytosol	4-trimethylammoniobutyraldehyde dehydrogenase activity, aldehyde dehydrogenase (NAD) activity, oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	carnitine metabolic process, metabolic process, oxidation reduction
L-specific multifunctional beta-oxdiation protein	Ehhadh	NP_076226	78	11	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
ribosomal protein L4	Rpl4	NP_077174	47	11	intracellular, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	biological_process, translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glyoxalase 1	Glo1	NP_079650	21	11	not classified	lactoylglutathione lyase activity, lyase activity, metal ion binding, zinc ion binding	not classified
L-arginine:glycine amidinotransferase	Gatm	NP_080237	48	11	cytoplasm, membrane, mitochondrial inner membrane, mitochondrial intermembrane space, mitochondrion	glycine amidinotransferase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines, transferase activity	creatine biosynthetic process
apolipoprotein O-like	Apool	NP_080841	29	11	extracellular region, mitochondrial inner membrane, mitochondrion	not classified	not classified
phosphoglucomutase 2	Pgm2	NP_082408	62	11	not classified	magnesium ion binding, metal ion binding, phosphoglucomutase activity	glucose metabolic process
hypothetical protein LOC64697	Keg1	NP_083826	34	11	microtubule, mitochondrion	acyltransferase activity, glycine N-acyltransferase activity, transferase activity	not classified
glutamyl-prolyl-tRNA synthetase	Eprs	NP_084011	170	11	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
acyl-CoA synthetase medium-chain family member 1	Acsm1	NP_473435	65	11	mitochondrial matrix, mitochondrion	acyl-CoA ligase activity, ATP binding, butyrate-CoA ligase activity, catalytic activity, fatty-acid ligase activity, GTP binding, ligase activity, magnesium ion binding, metal ion binding, nucleotide binding	fatty acid biosynthetic process, fatty acid metabolic process, lipid metabolic process, metabolic process
Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	NP_598557	23	11	cytoplasm, immunological synapse	GTPase activator activity, protein binding, Rho GDP dissociation inhibitor activity	regulation of protein localization, Rho protein signal transduction
high density lipoprotein binding protein	Hdlbp	NP_598569	142	11	cytoplasm, high-density lipoprotein particle, nucleus	RNA binding	cholesterol metabolic process, lipid metabolic process, lipid transport, steroid metabolic process, transport
transmembrane protein 109	Tmem109	NP_598903	26	11	cellular_component, endoplasmic reticulum, integral to membrane, membrane, nucleus, sarcoplasmic reticulum	molecular_function	biological_process
eukaryotic translation initiation factor 4B	Eif4b	NP_663600	41	11	not classified	nucleic acid binding, nucleotide binding, RNA binding, translation initiation factor activity	translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
aldhehyde dehydrogenase family 5, subfamily A1	Aldh5a1	NP_766120	56	11	mitochondrion	oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor, succinate-semialdehyde dehydrogenase activity	acetate metabolic process, galactosylceramide metabolic process, gamma-aminobutyric acid catabolic process, gamma-aminobutyric acid metabolic process, glucose metabolic process, glucosylceramide metabolic process, glutamate metabolic process, glutamine metabolic process, glutathione metabolic process, glycerophospholipid metabolic process, metabolic process, neurotransmitter catabolic process, oxidation reduction, post-embryonic development, respiratory electron transport chain, short-chain fatty acid metabolic process, succinate metabolic process
DnaJ (Hsp40) homolog, subfamily C, member 11	Dnajc11	NP_766292	63	11	mitochondrial inner membrane	heat shock protein binding, molecular_function	biological_process
peptidase M20 domain containing 1	Pm20d1	NP_835180	56	11	extracellular region	hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, protein dimerization activity, zinc ion binding	proteolysis
glycyl-tRNA synthetase	Gars	NP_851009	82	11	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
PREDICTED: similar to aldehyde reductase	LOC100044692	XP_001472913	33	11	not classified	not classified	not classified
PREDICTED: similar to nuclear pore complex-associated intranuclear coiled-coil protein TPR	LOC100043998	XP_001474187	149	11	not classified	not classified	not classified
PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	LOC675851	XP_990709	14	11	not classified	not classified	not classified
tubulin, alpha-like 3	Tubal3	NP_001029051	50	10	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
glutaminase isoform 1	Gls	NP_001074550	74	10	not classified	glutaminase activity	behavior, glutamine catabolic process, regulation of respiratory gaseous exchange by neurological system process, synaptic transmission
adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	NP_031485	104	10	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
CAP, adenylate cyclase-associated protein 1	Cap1	NP_031624	52	10	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
heat-responsive protein 12	Hrsp12	NP_032313	14	10	not classified	endonuclease activity, hydrolase activity, nuclease activity	not classified
heat shock protein 1 (chaperonin 10)	Hspe1	NP_032329	11	10	cytoplasm, mitochondrion	ATP binding	protein folding, response to stress
methylmalonyl-Coenzyme A mutase	Mut	NP_032676	83	10	mitochondrion	cobalamin binding, cobalt ion binding, intramolecular transferase activity, isomerase activity, metal ion binding, methylmalonyl-CoA mutase activity	metabolic process, post-embryonic development
RAB7, member RAS oncogene family	Rab7	NP_033031	23	10	cytoplasmic vesicle, endosome, Golgi apparatus, late endosome, lysosome	GTP binding, nucleotide binding	intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport
ribosomal protein L26	Rpl26	NP_033106	17	10	cellular_component, ribosome	molecular_function	biological_process
ataxin 2	Atxn2	NP_033151	136	10	cytoplasm, perinuclear region of cytoplasm	DBD domain binding	negative regulation of multicellular organism growth
cathepsin D	Ctsd	NP_034113	45	10	lysosome, mitochondrion	aspartic-type endopeptidase activity, hydrolase activity, peptidase activity	autophagic vacuole formation, proteolysis
glutamate-cysteine ligase, catalytic subunit	Gclc	NP_034425	73	10	cytosol, glutamate-cysteine ligase complex	ATP binding, glutamate-cysteine ligase activity, ligase activity, nucleotide binding, protein heterodimerization activity	glutathione biosynthetic process, glutathione metabolic process, L-ascorbic acid metabolic process, negative regulation of apoptosis, negative regulation of protein ubiquitination, positive regulation of proteasomal ubiquitin-dependent protein catabolic process, regulation of mitochondrial depolarization, response to arsenic, response to xenobiotic stimulus
glutathione S-transferase, mu 1	Gstm1	NP_034488	26	10	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
prosaposin	Psap	NP_035309	61	10	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
coatomer protein complex, subunit beta 2 (beta prime)	Copb2	NP_056642	102	10	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
N-acylsphingosine amidohydrolase 1	Asah1	NP_062708	45	10	lysosome	ceramidase activity, hydrolase activity	lipid metabolic process
mitochondrial carrier homolog 2	Mtch2	NP_062732	33	10	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
RAB2A, member RAS oncogene family	Rab2a	NP_067493	24	10	endoplasmic reticulum, Golgi apparatus, membrane	GTP binding, nucleotide binding	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
tropomyosin 3, gamma	Tpm3	NP_071709	33	10	cleavage furrow, cortical cytoskeleton, cytoplasm, cytoskeleton, filamentous actin, growth cone, neuron projection, podosome	actin binding	not classified
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	NP_076092	75	10	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
coenzyme Q9 homolog	Coq9	NP_080728	35	10	mitochondrion	not classified	ubiquinone biosynthetic process
histidine triad nucleotide binding protein 2	Hint2	NP_081147	17	10	extracellular region, mitochondrion	catalytic activity, hydrolase activity	not classified
NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	NP_082664	27	10	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
ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	NP_083296	78	10	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	ATP binding, ATPase activity, ATPase activity, coupled to transmembrane movement of substances, nucleoside-triphosphatase activity, nucleotide binding	transport
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
ubiquitin-conjugating enzyme E2N	Ube2n	NP_542127	17	10	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
eukaryotic translation initiation factor 3, subunit H	Eif3h	NP_542366	40	10	cytoplasm, eukaryotic translation initiation factor 3 complex	translation initiation factor activity	translation, translational initiation
huntingtin interacting protein 1 related	Hip1r	NP_659507	119	10	coated pit, cytoplasm, cytoplasmic vesicle, cytoskeleton, membrane	actin binding, phospholipid binding	endocytosis, receptor-mediated endocytosis
hypothetical protein LOC217830	9030617O03Rik	NP_663423	66	10	mitochondrion	not classified	not classified
Cobl-like 1 isoform 1	Cobll1	NP_795999	133	10	cellular_component	molecular_function	biological_process
ATP synthase F0 subunit 6	ATP6	NP_904333	25	10	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	hydrogen ion transmembrane transporter activity, hydrolase activity	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
PREDICTED: similar to Eukaryotic translation elongation factor 2	LOC433776	XP_001475612	46	10	not classified	not classified	not classified
acyl-Coenzyme A dehydrogenase, short chain	Acads	NP_031409	45	9	mitochondrion	acyl-CoA dehydrogenase activity, butyryl-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
branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	NP_031559	50	9	mitochondrion	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity, cyclin-dependent protein kinase 5 activator regulator activity, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, potassium ion binding	metabolic process, oxidation reduction, positive regulation of transcription, DNA-dependent
annexin A2	Anxa2	NP_031611	39	9	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
guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	Gnb2l1	NP_032169	35	9	cell soma, cytoplasm, membrane, plasma membrane	protein kinase C binding, receptor activity	intracellular signaling cascade, protein localization
glutathione S-transferase, theta 1	Gstt1	NP_032211	27	9	cytoplasm, nucleus	glutathione transferase activity, transferase activity	glutathione metabolic process
ribosomal protein S2	Rps2	NP_032529	31	9	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation
lymphocyte cytosolic protein 1	Lcp1	NP_032905	70	9	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
protease (prosome, macropain) 26S subunit, ATPase 5	Psmc5	NP_032976	46	9	cytoplasm, holo TFIIH complex, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, peptidase activity, protein binding, transcription factor binding	negative regulation of transcription, protein catabolic process
ribosomal protein L29	Rpl29	NP_033108	18	9	cytosolic ribosome, intracellular, peripheral to membrane of membrane fraction, polysomal ribosome, ribonucleoprotein complex, ribosome	heparin binding, structural constituent of ribosome	cell proliferation, cell-substrate adhesion, multicellular organism growth, translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
RAN, member RAS oncogene family	Ran	NP_033417	24	9	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
cytochrome c oxidase, subunit VIIa 2	Cox7a2	NP_034075	9	9	membrane, mitochondrial inner membrane, mitochondrial respiratory chain, mitochondrion	cytochrome-c oxidase activity, electron carrier activity	not classified
crystallin, zeta	Cryz	NP_034098	35	9	cytoplasm	NADP or NADPH binding, NADPH:quinone reductase activity, oxidoreductase activity, zinc ion binding	oxidation reduction
integrin beta 1 (fibronectin receptor beta)	Itgb1	NP_034708	88	9	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
chapsyn-110	Dlg2	NP_035937	95	9	cell junction, membrane, plasma membrane, postsynaptic membrane, synapse	protein binding	sensory perception of pain, synaptic transmission
tubulointerstitial nephritis antigen	Tinag	NP_036163	54	9	not classified	not classified	not classified
hexokinase 2	Hk2	NP_038848	103	9	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
stress-induced phosphoprotein 1	Stip1	NP_058017	63	9	cytoplasm, nucleus	binding	not classified
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
phosphatidylethanolamine binding protein 1	Pebp1	NP_061346	21	9	cell surface, cytoplasm	ATP binding, lipid binding, nucleotide binding, peptidase inhibitor activity, serine-type endopeptidase inhibitor activity	sperm capacitation
neuronal protein 15.6	Ndufb11	NP_062308	17	9	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
cardiotrophin-like cytokine factor 1	Clcf1	NP_064336	25	9	extracellular region, extracellular space	cytokine activity	B cell differentiation, cell surface receptor linked signal transduction, JAK-STAT cascade
ribosomal protein S14	Rps14	NP_065625	16	9	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cell cycle exit and neuronal differentiation 1	Cend1	NP_067291	15	9	integral to membrane, membrane	molecular_function	biological_process
non-POU-domain-containing, octamer binding protein	Nono	NP_075633	55	9	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
small glutamine-rich tetratricopeptide repeat (TPR) containing protein	Sgta	NP_078775	34	9	cellular_component	binding, protein binding, protein heterodimerization activity, protein homodimerization activity	biological_process
ribosomal protein, large P2	Rplp2	NP_080296	12	9	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translational elongation
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	Ndufb8	NP_080337	22	9	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial respiratory chain complex I, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity	electron transport chain, mitochondrial electron transport, NADH to ubiquinone, transport
ribosomal protein S20	Rps20	NP_080423	13	9	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation
dephospho-CoA kinase domain containing	Dcakd	NP_080827	26	9	not classified	ATP binding, dephospho-CoA kinase activity, kinase activity, nucleotide binding	coenzyme A biosynthetic process
sideroflexin 1	Sfxn1	NP_081600	36	9	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
growth and transformation-dependent protein	2310056P07 Rik	NP_081618	18	9	integral to membrane, membrane	not classified	not classified
acyl-Coenzyme A dehydrogenase family, member 10	Acad10	NP_082313	119	9	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
zinc finger protein 142	Zfp142	NP_084164	195	9	not classified	not classified	not classified
sideroflexin 3	Sfxn3	NP_444427	35	9	integral to membrane, membrane, mitochondrion	cation transmembrane transporter activity, iron ion binding	cation transport, ion transport, iron ion transport, transport
heterogeneous nuclear ribonucleoprotein A3 isoform c	Hnrnpa3	NP_444493	37	9	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
splicing factor 3b, subunit 3	Sf3b3	NP_598714	136	9	nucleus, spliceosomal complex	nucleic acid binding	mRNA processing, RNA splicing
glutathione S-transferase, theta 3	Gstt3	NP_598755	27	9	cellular_component	glutathione transferase activity, transferase activity	glutathione metabolic process
ionized calcium binding adapter molecule 2	2810003C17 Rik	NP_660126	17	9	not classified	calcium ion binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	NP_766295	37	9	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
hyaluronoglucosaminidase 3	Hyal3	NP_821139	46	9	extracellular region, lysosome	catalytic activity, hyaluronoglucosaminidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds	carbohydrate metabolic process, metabolic process
PREDICTED: similar to 60S ribosomal protein L9 isoform 1	LOC100048162	XP_001480029	22	9	not classified	not classified	not classified
PREDICTED: similar to vesicle associated protein	Sec31a	XP_912694	144	9	cytoplasm, cytoplasmic vesicle, endoplasmic reticulum, endosome, membrane	not classified	protein transport, transport, vesicle-mediated transport
xylulokinase homolog (H. influenzae)	Xylb	NP_001028381	60	8	not classified	ATP binding, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity, xylulokinase activity	carbohydrate metabolic process, D-xylose metabolic process
integrin alpha 1	Itga1	NP_001028400	131	8	external side of plasma membrane, integral to membrane, integrin complex, membrane	calcium ion binding, magnesium ion binding, protein binding, receptor activity	cell adhesion, cellular extravasation, integrin-mediated signaling pathway, neutrophil chemotaxis
NADPH-dependent retinol dehydrogenase/reductase isoform 1	Dhrs4	NP_001033027	30	8	mitochondrion, peroxisome	binding, carbonyl reductase (NADPH) activity, catalytic activity, oxidoreductase activity, retinal dehydrogenase activity	metabolic process, oxidation reduction, retinal metabolic process
thioredoxin reductase 1 isoform 1	Txnrd1	NP_001035988	67	8	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
predicted gene, EG668668	EG668668	NP_001074505	30	8	not classified	not classified	not classified
ribosomal protein S16-like	LOC100039355	NP_001103687	16	8	not classified	not classified	not classified
aconitase 1	Aco1	NP_031412	98	8	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
mannosidase 2, alpha 1	Man2a1	NP_032575	132	8	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cytochrome c oxidase subunit VIIa polypeptide 2-like	Cox7a2l	NP_033213	12	8	membrane, mitochondrial inner membrane, mitochondrial respiratory chain, mitochondrion	cytochrome-c oxidase activity, electron carrier activity	not classified
trans-golgi network protein	Tgoln1	NP_033469	38	8	Golgi apparatus, integral to membrane, membrane, plasma membrane, trans-Golgi network	not classified	not classified
chaperonin containing Tcp1, subunit 4 (delta)	Cct4	NP_033967	58	8	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
chaperonin containing Tcp1, subunit 6a (zeta)	Cct6a	NP_033968	58	8	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
fatty acid binding protein 3, muscle and heart	Fabp3	NP_034304	15	8	cytoplasm	binding, lipid binding, transporter activity	phosphatidylcholine biosynthetic process, transport
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	NP_035017	18	8	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
ribosomal protein S7	Rps7	NP_035430	22	8	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
transaldolase 1	Taldo1	NP_035658	37	8	cytoplasm	catalytic activity, transaldolase activity, transferase activity	carbohydrate metabolic process, metabolic process, pentose-phosphate shunt
myosin, heavy polypeptide 11, smooth muscle	Myh11	NP_038635	223	8	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
solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	NP_038798	32	8	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, secondary active transmembrane transporter activity	mitochondrial transport, transport
ERO1-like	Ero1l	NP_056589	54	8	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
keratin complex 2, basic gene 18	Krt85	NP_058575	56	8	intermediate filament, keratin filament	structural molecule activity	not classified
USO1 homolog, vesicle docking protein	Uso1	NP_062363	107	8	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
chloride channel Kb	Clcnkb	NP_062675	75	8	cellular_component, chloride channel complex, integral to membrane, membrane	chloride channel activity, chloride ion binding, ion channel activity, molecular_function, protein binding, voltage-gated chloride channel activity, voltage-gated ion channel activity	biological_process, chloride transport, ion transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
non-metastatic cells 3, protein expressed in	Nme3	NP_062704	19	8	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
acyl-CoA thioesterase 9	Acot9	NP_062710	51	8	mitochondrion	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity, palmitoyl-CoA hydrolase activity	not classified
fumarylacetoacetate hydrolase domain containing 1	Fahd1	NP_075969	25	8	mitochondrial inner membrane, mitochondrion	calcium ion binding, catalytic activity, hydrolase activity, magnesium ion binding, metal ion binding	metabolic process
Sec61 beta subunit	Sec61b	NP_077133	10	8	cellular_component, endoplasmic reticulum, integral to membrane, membrane	ribosome binding	biological_process, protein transport, transmembrane transport, transport
vacuolar H+ ATPase G1	Atp6v1g1	NP_077135	14	8	cytosol, intracellular, lysosomal membrane, plasma membrane, synaptic vesicle, vacuolar proton-transporting V-type ATPase complex	ATPase activity, hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, protein binding	ion transport, proton transport, transport
chloride channel Ka	Clcnka	NP_077723	76	8	chloride channel complex, integral to membrane, 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, regulation of body fluid levels, transport
brain protein 17 isoform 2	Pnkd	NP_079856	16	8	cytoplasm, membrane, mitochondrion, nucleus	hydrolase activity, hydroxyacylglutathione hydrolase activity, metal ion binding, molecular_function, zinc ion binding	biological_process
ribosomal protein S13	Rps13	NP_080809	17	8	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
transmembrane emp24 domain-containing protein 10	Tmed10	NP_081051	25	8	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
protein disulfide isomerase-associated 6	Pdia6	NP_082235	49	8	endoplasmic reticulum	isomerase activity, protein disulfide isomerase activity	cell redox homeostasis
citrate lyase beta like	Clybl	NP_083832	38	8	cellular_component, citrate lyase complex, mitochondrion	carbon-carbon lyase activity, catalytic activity, citrate (pro-3S)-lyase activity, lyase activity, magnesium ion binding, metal ion binding, molecular_function	biological_process, cellular aromatic compound metabolic process
mitochondrial ribosomal protein S2	Mrps2	NP_536700	32	8	intracellular, mitochondrion, ribonucleoprotein complex, ribosome, small ribosomal subunit	structural constituent of ribosome	translation
apolipoprotein A-I binding protein	Apoa1bp	NP_659146	31	8	cellular_component, extracellular region	protein binding	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
archain 1	Arcn1	NP_666097	57	8	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
pyridoxal (pyridoxine, vitamin B6) kinase	Pdxk	NP_742146	35	8	cytoplasm	ATP binding, kinase activity, metal ion binding, nucleotide binding, pyridoxal kinase activity, transferase activity, zinc ion binding	pyridoxine biosynthetic process
4-aminobutyrate aminotransferase	Abat	NP_766549	56	8	mitochondrion	(S)-3-amino-2-methylpropionate transaminase activity, 4-aminobutyrate transaminase activity, catalytic activity, pyridoxal phosphate binding, transaminase activity, transferase activity	behavioral response to cocaine, gamma-aminobutyric acid metabolic process, neurotransmitter catabolic process
hypothetical protein LOC223665	C030006K11Rik	NP_789798	24	8	not classified	not classified	not classified
UDP glucuronosyltransferase 1 family, polypeptide A7C	Ugt1a7c	NP_964004	60	8	endoplasmic reticulum, integral to membrane, membrane, microsome	glucuronosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	metabolic process
PREDICTED: similar to serine beta lactamase-like protein LACT-1 isoform 2	LOC677144	XP_001004138	61	8	not classified	not classified	not classified
PREDICTED: similar to Nedd4 binding protein 2	LOC100044124	XP_001474752	137	8	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC634990	XP_914990	16	8	not classified	not classified	not classified
NADH dehydrogenase (ubiquinone) Fe-S protein 5	Ndufs5	NP_001025445	13	7	mitochondrion	not classified	not classified
hypothetical protein LOC67809	1200015F23Rik	NP_001028308	52	7	cytoplasm, integral to membrane, membrane, microtubule, mitochondrion, nucleus	binding	apoptosis, cell differentiation
adenylate kinase 2 isoform a	Ak2	NP_001029138	26	7	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
argininosuccinate synthetase	Ass1	NP_031520	47	7	mitochondrion	argininosuccinate synthase activity, ATP binding, ligase activity, nucleotide binding	arginine biosynthetic process, cellular amino acid biosynthetic process, urea cycle
dynactin 1	Dctn1	NP_031861	142	7	cell leading edge, cytoplasm, cytoskeleton, dynein complex, microtubule	motor activity, protein binding	not classified
selenium binding protein 1	Selenbp1	NP_033176	53	7	cytoplasm, membrane, nucleus	selenium binding	brown fat cell differentiation, protein transport, transport
dihydropyrimidinase-like 2	Dpysl2	NP_034085	62	7	axon, cell soma, cytoplasm, dendrite, mitochondrion	hydrolase activity	cell differentiation, multicellular organismal development, nervous system development
D-dopachrome tautomerase	Ddt	NP_034157	13	7	cytoplasm	D-dopachrome decarboxylase activity, lyase activity	melanin biosynthetic process
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	NP_034194	68	7	dynein complex, microtubule	motor activity	not classified
eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3s10	NP_034253	162	7	cytoplasm, eukaryotic translation initiation factor 3 complex, nucleus	protein binding, translation initiation factor activity	formation of translation initiation complex, translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
keratin complex 2, basic, gene 17	Krt2	NP_034798	71	7	intermediate filament, keratin filament	structural molecule activity	not classified
macrophage migration inhibitory factor	Mif	NP_034928	13	7	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) 28 subunit, alpha	Psme1	NP_035319	29	7	proteasome activator complex, proteasome complex	proteasome activator activity, protein binding	antigen processing and presentation of exogenous antigen
cytoplasmic FMR1 interacting protein 1	Cyfip1	NP_035500	145	7	cell junction, cell projection, cytoplasm, lamellipodium, perinuclear region of cytoplasm, synapse, synaptosome	actin binding, profilin binding	cell differentiation, lamellipodium assembly, multicellular organismal development, nervous system development, regulation of cell shape
solute carrier family 4 (anion exchanger), member 1	Slc4a1	NP_035533	103	7	basolateral plasma membrane, cortical cytoskeleton, integral to membrane, membrane	anion exchanger activity, anion transmembrane transporter activity, inorganic anion exchanger activity, protein binding	anion transport, chloride transport, ion transport, transport
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	NP_035868	28	7	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
brain protein 44-like	Brp44l	NP_061289	12	7	mitochondrial inner membrane, mitochondrion	molecular_function	biological_process
staphylococcal nuclease domain containing 1	Snd1	NP_062750	102	7	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
nucleoporin 160	Nup160	NP_067487	158	7	nuclear pore, nucleus	nucleocytoplasmic transporter activity	mRNA export from nucleus, mRNA transport, protein transport, transmembrane transport, transport
nicotinamide phosphoribosyltransferase	Nampt	NP_067499	55	7	cytoplasm	nicotinamide phosphoribosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups	NAD biosynthetic process, pyridine nucleotide biosynthetic process
ribosomal protein L23	Rpl23	NP_075029	15	7	cytosolic ribosome, intracellular, nucleolus, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
cell line NK14 derived transforming oncogene	Rab8a	NP_075615	24	7	membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	protein transport, small GTPase mediated signal transduction, transport
blood vessel epicardial substance	Bves	NP_077247	41	7	integral to membrane, membrane	not classified	not classified
coiled-coil-helix-coiled-coil-helix domain containing 6	Chchd6	NP_079627	30	7	cellular_component	molecular_function	biological_process
ubiquinol-cytochrome c reductase hinge protein	Uqcrh	NP_079917	10	7	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
UMP-CMP kinase	Cmpk	NP_079923	26	7	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
thioesterase superfamily member 2	Them2	NP_080066	15	7	cytoplasm, mitochondrion	hydrolase activity	not classified
actin related protein 2/3 complex, subunit 4	Arpc4	NP_080828	20	7	Arp2/3 protein complex, cell projection, cytoplasm, cytoskeleton	actin binding, molecular_function	actin filament polymerization, biological_process
cingulin-like 1	Cgnl1	NP_080875	148	7	actin cytoskeleton, apical junction complex, cell junction, myosin complex, tight junction	molecular_function, motor activity	biological_process
keratin 33A	Krt33a	NP_082259	46	7	cellular_component, intermediate filament	protein binding, structural molecule activity	biological_process
SAC1 (supressor of actin mutations 1, homolog)-like	Sacm1l	NP_109617	67	7	cellular_component, endoplasmic reticulum, integral to membrane, membrane	hydrolase activity, molecular_function	biological_process
keratin 82	Krt82	NP_444479	57	7	intermediate filament, keratin filament	structural molecule activity	not classified
argininosuccinate lyase	Asl	NP_598529	52	7	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
nuclear mitotic apparatus protein 1	Numa1	NP_598708	236	7	nucleus	tubulin binding	not classified
LRP16 protein	Macrod1	NP_598908	27	7	mitochondrion	not classified	not classified
malic enzyme 2, NAD(+)-dependent, mitochondrial	Me2	NP_663469	66	7	mitochondrion	binding, catalytic activity, malate dehydrogenase (oxaloacetate-decarboxylating) activity, malic enzyme activity, metal ion binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	malate metabolic process, metabolic process, oxidation reduction
plastin 3 precursor	Pls3	NP_663604	71	7	cytoplasm	actin binding, calcium ion binding, molecular_function	biological_process
leucyl/cystinyl aminopeptidase	Lnpep	NP_766415	117	7	integral to membrane, membrane, membrane fraction, microsome, perinuclear region of cytoplasm, plasma membrane	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, protein binding, zinc ion binding	protein catabolic process, proteolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
sulfite oxidase	Suox	NP_776094	61	7	mitochondrion	electron carrier activity, heme binding, iron ion binding, metal ion binding, molybdenum ion binding, oxidoreductase activity, sulfite oxidase activity	oxidation reduction
eukaryotic translation initiation factor 5A	Eif5a	NP_853613	17	7	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
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
UDP glucuronosyltransferase 1 family, polypeptide A1	Ugt1a1	NP_964007	60	7	endoplasmic reticulum, integral to membrane, integral to plasma membrane, membrane, microsome	glucuronosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	metabolic process
PREDICTED: similar to ribosomal protein L28	LOC100039731	XP_001473974	16	7	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047156	XP_001477347	24	7	not classified	not classified	not classified
UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Uap1l1	NP_001028465	57	6	not classified	nucleotidyltransferase activity, transferase activity	metabolic process
tetratricopeptide repeat domain 38	Ttc38	NP_001028509	52	6	not classified	binding	not classified
hypothetical protein LOC654795	2310014G06Rik	NP_001076444	31	6	not classified	binding, catalytic activity, coenzyme binding	cellular metabolic process, metabolic process
radixin isoform a	Rdx	NP_001098086	69	6	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
ribosomal protein L18A family member	OTTMUSG00000021609	NP_001104586	22	6	not classified	not classified	not classified
alcohol dehydrogenase 1 (class I)	Adh1	NP_031435	40	6	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
chondroitin sulfate proteoglycan 6	Smc3	NP_031816	142	6	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
ferredoxin reductase	Fdxr	NP_032023	54	6	mitochondrial inner membrane, mitochondrion	electron carrier activity, ferredoxin-NADP+ reductase activity, oxidoreductase activity	cholesterol metabolic process, electron transport chain, lipid metabolic process, oxidation reduction, steroid metabolic process, transport
karyopherin (importin) beta 1	Kpnb1	NP_032405	97	6	cytoplasm, nucleus	binding, protein binding, protein transporter activity	intracellular protein transport, protein import into nucleus, protein transport, ribosomal protein import into nucleus, transport
alanyl (membrane) aminopeptidase	Anpep	NP_032512	110	6	integral to membrane, membrane	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	angiogenesis, cell differentiation, multicellular organismal development, proteolysis
lysophospholipase 1	Lypla1	NP_032892	25	6	cytoplasm, mitochondrion	hydrolase activity	fatty acid metabolic process, lipid metabolic process
ribosomal protein L12	Rpl12	NP_033102	18	6	cytoplasm, nucleolus, nucleus, ribonucleoprotein complex, ribosome	protein binding, RNA binding, structural constituent of ribosome	biological_process, translation
indolethylamine N-methyltransferase	Inmt	NP_033375	29	6	cytoplasm	amine N-methyltransferase activity, methyltransferase activity, transferase activity	not classified
ATPase, H+ transporting, lysosomal V0 subunit C	Atp6v0c	NP_033859	16	6	integral to membrane, membrane, proton-transporting two-sector ATPase complex, proton-transporting domain, proton-transporting V-type ATPase, V0 domain, vacuolar proton-transporting V-type ATPase complex, vacuole	hydrogen ion transmembrane transporter activity, hydrogen-exporting ATPase activity, phosphorylative mechanism, protein binding	ATP synthesis coupled proton transport, ion transport, lysosomal lumen acidification, proton transport, transport, vacuolar acidification
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
glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	NP_034404	81	6	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
high mobility group box 1	Hmgb1	NP_034569	25	6	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
heterochromatin protein 1, binding protein 3	Hp1bp3	NP_034600	61	6	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
lamin B2	Lmnb2	NP_034852	67	6	intermediate filament, lamin filament, membrane, nucleus	structural molecule activity	not classified
KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	NP_035447	48	6	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
myosin XVIIIa	Myo18a	NP_035716	231	6	cytoplasm, cytoskeleton, myosin complex	ATP binding, molecular_function, motor activity, nucleotide binding, protein binding	biological_process
thioredoxin 1	Txn1	NP_035790	12	6	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-activating enzyme E1, Chr Y 1	Ube1y1	NP_035797	118	6	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
caseinolytic protease X isoform 1	Clpx	NP_035932	69	6	mitochondrial inner membrane, mitochondrion	ATP binding, ATPase activity, metal ion binding, nucleoside-triphosphatase activity, nucleotide binding, protein binding, unfolded protein binding, zinc ion binding	protein folding
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	NP_036095	30	6	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
guanine nucleotide-binding protein, beta-4 subunit	Gnb4	NP_038559	37	6	heterotrimeric G-protein complex	GTPase activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
estradiol 17 beta-dehydrogenase 8	H2-Ke6	NP_038571	27	6	membrane fraction, mitochondrial envelope, mitochondrion, plasma membrane	binding, catalytic activity, estradiol 17-beta-dehydrogenase activity, oxidoreductase activity, testosterone 17-beta-dehydrogenase activity	androgen metabolic process, estrogen metabolic process, lipid biosynthetic process, metabolic process, oxidation reduction, steroid biosynthetic process
myxovirus (influenza virus) resistance 2	Mx2	NP_038634	74	6	cytoplasm	GTP binding, GTPase activity, nucleotide binding	innate immune response, response to virus
ribosomal protein L13	Rpl13	NP_058018	24	6	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
peroxiredoxin 4	Prdx4	NP_058044	31	6	cytoplasm, mitochondrion	antioxidant activity, molecular_function, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	biological_process, cell redox homeostasis, oxidation reduction
metaxin 2	Mtx2	NP_058084	30	6	membrane, mitochondrial outer membrane, mitochondrion	not classified	protein targeting to mitochondrion, protein transport, transport
coatomer protein complex, subunit gamma isoform 1	Copg	NP_059505	98	6	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
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
proteolipid protein 2	Plp2	NP_062729	17	6	integral to membrane, membrane	not classified	not classified
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	NP_075691	13	6	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	ATP synthesis coupled electron transport, electron transport chain, transport
peroxisomal trans 2-enoyl CoA reductase	Pecr	NP_076012	32	6	mitochondrion, peroxisome	binding, catalytic activity, oxidoreductase activity, trans-2-enoyl-CoA reductase (NADPH) activity	fatty acid biosynthetic process, fatty acid elongation, lipid biosynthetic process, metabolic process, oxidation reduction
hydroxyacyl glutathione hydrolase	Hagh	NP_077246	29	6	not classified	hydrolase activity, hydroxyacylglutathione hydrolase activity, metal ion binding, zinc ion binding	not classified
cytochrome b5 type B precursor	Cyb5b	NP_079834	16	6	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	heme binding, iron ion binding, metal ion binding	electron transport chain, transport
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	Ndufb3	NP_079873	12	6	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
ubiquinol-cytochrome c reductase binding protein	Uqcrb	NP_080495	14	6	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
lectin, mannose-binding, 1	Lman1	NP_081676	58	6	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
diaphorase 1	Cyb5r3	NP_084063	34	6	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
eukaryotic translation initiation factor 3, subunit 9	Eif3b	NP_598677	91	6	cytoplasm	nucleic acid binding, nucleotide binding, RNA binding	translation
aldehyde dehydrogenase family 7, member A1	Aldh7a1	NP_613066	56	6	mitochondrion	L-aminoadipate-semialdehyde dehydrogenase activity, oxidoreductase activity	metabolic process, oxidation reduction
eukaryotic translation initiation factor 4A1	Eif4a1	NP_659207	46	6	not classified	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding, translation initiation factor activity	translation
pitrilysin metallepetidase 1	Pitrm1	NP_660113	117	6	mitochondrion	catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
carbonic reductase 4	Cbr4	NP_663570	25	6	cytoplasm	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
phosphatidylinositol-binding clathrin assembly protein	Picalm	NP_666306	72	6	clathrin coat, coated pit, cytoplasmic vesicle, Golgi apparatus, membrane	clathrin binding, phosphatidylinositol binding, phospholipid binding	clathrin coat assembly, endocytosis, hemopoiesis, multicellular organismal development, receptor-mediated endocytosis
solute carrier family 43, member 2	Slc43a2	NP_775564	62	6	integral to membrane, membrane, plasma membrane	L-amino acid transmembrane transporter activity	L-amino acid transport
pyruvate dehydrogenase complex, component X	Pdhx	NP_780303	54	6	mitochondrion	acyltransferase activity, lipoic acid binding, protein binding, transferase activity	metabolic process
aspartyl-tRNA synthetase	Dars	NP_803228	57	6	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
ROD1 regulator of differentiation 1 isoform 2	Rod1	NP_835458	57	6	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing
NADH dehydrogenase subunit 5	ND5	NP_904338	68	6	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity	electron transport chain, oxidation reduction, transport
acyl-CoA synthetase short-chain family member 3	Acss3	NP_941038	54	6	mitochondrion	acetate-CoA ligase activity, ATP binding, catalytic activity, ligase activity, nucleotide binding	metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
pantophysin isoform 2	Sypl	NP_942003	27	6	cytoplasmic vesicle, integral to membrane, membrane, secretory granule, synaptic vesicle	transporter activity	transport
branched chain ketoacid dehydrogenase E1, beta polypeptide	Bckdhb	NP_954665	36	6	mitochondrial inner membrane, mitochondrion	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity, alpha-ketoacid dehydrogenase activity, catalytic activity, oxidoreductase activity	cellular amino acid catabolic process, metabolic process, oxidation reduction
PREDICTED: cingulin	Cgn	XP_001001375	150	6	apical junction complex, cell junction, myosin complex, tight junction	molecular_function, motor activity	biological_process
PREDICTED: similar to hCG1640785	LOC100045659	XP_001474736	12	6	not classified	not classified	not classified
proteasome activator subunit 2 isoform 2	Psme2	NP_001025026	26	5	proteasome activator complex, proteasome complex	proteasome activator activity, protein binding	antigen processing and presentation of exogenous antigen
potassium inwardly-rectifying channel J10	Kcnj10	NP_001034573	42	5	integral to membrane, integral to plasma membrane, membrane	ATP binding, inward rectifier potassium channel activity, ion channel activity, nucleotide binding, potassium channel activity, potassium ion binding, protein binding, voltage-gated ion channel activity	ion transport, potassium ion transport, transport
dynamin 2	Dnm2	NP_001034609	98	5	cell junction, cytoplasm, cytoskeleton, membrane, microtubule, plasma membrane, postsynaptic membrane, synapse	GTP binding, GTPase activity, hydrolase activity, motor activity, nucleotide binding, protein binding	endocytosis
carbonic anhydrase 1	Car1	NP_001077426	28	5	cytoplasm	carbonate dehydratase activity, lyase activity, metal ion binding, zinc ion binding	one-carbon metabolic process
sorting nexin 12 isoform 2	Snx12	NP_001103781	20	5	not classified	phosphoinositide binding, protein binding	cell communication, protein transport, transport
annexin A7	Anxa7	NP_001104264	50	5	cytosol, insoluble fraction, nuclear envelope, nucleus, plasma membrane, soluble fraction, vesicle	calcium ion binding, calcium-dependent phospholipid binding, protein binding	cell proliferation, cellular calcium ion homeostasis, cellular water homeostasis, hemostasis, regulation of cell shape, response to salt stress
nascent polypeptide-associated complex alpha subunit isoform a	Naca	NP_001106670	220	5	cytoplasm, nucleus	DNA binding, TATA-binding protein binding, transcription coactivator activity	protein transport, regulation of transcription, transcription, transport
ADP-ribosylation factor 6	Arf6	NP_031507	20	5	cytoplasm, endosome, Golgi apparatus, intracellular, plasma membrane	GTP binding, nucleotide binding, protein binding	apoptosis, liver development, protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
carbonyl reductase 1	Cbr1	NP_031646	31	5	cellular_component, cytoplasm	binding, carbonyl reductase (NADPH) activity, catalytic activity, oxidoreductase activity	biological_process, metabolic process, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	Ppm1g	NP_032040	59	5	nucleus, protein serine/threonine phosphatase complex	catalytic activity, hydrolase activity, magnesium ion binding, manganese ion binding, metal ion binding, phosphoprotein phosphatase activity, protein serine/threonine phosphatase activity	cell cycle, cell cycle arrest, protein amino acid dephosphorylation
interferon activated gene 204	Ifi204	NP_032355	69	5	cytoplasm, nucleolus, nucleoplasm, nucleus	protein binding, transcription cofactor activity	DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis, multicellular organismal development, positive regulation of osteoblast differentiation, regulation of transcription, regulation of transcription from RNA polymerase II promoter, transcription
integrin alpha V	Itgav	NP_032428	115	5	external side of plasma membrane, integral to membrane, integrin complex, membrane, plasma membrane	calcium ion binding, protein binding, receptor activity	angiogenesis, apoptotic cell clearance, blood vessel development, cell adhesion, cell differentiation, integrin-mediated signaling pathway, multicellular organismal development
4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	Nipsnap1	NP_032724	33	5	mitochondrial inner membrane, mitochondrion	molecular_function	biological_process
phosphatidylinositol transfer protein, alpha	Pitpna	NP_032876	32	5	cytoplasm, integral to membrane, intracellular	lipid binding, phospholipid binding	transport
protease (prosome, macropain) 26S subunit, ATPase 1	Psmc1	NP_032973	49	5	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding	protein catabolic process
scinderin	Scin	NP_033158	69	5	cytoplasm, cytoskeleton	actin binding, calcium ion binding	actin filament capping
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	NP_033802	29	5	cytoplasm, nuclear matrix, nucleus	protein binding	regulation of transcription, transcription
calcium/calmodulin-dependent serine protein kinase	Cask	NP_033936	102	5	basolateral plasma membrane, cytoplasm, cytosol, membrane, nucleus, plasma membrane, synapse, synaptosome	ATP binding, calmodulin binding, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	positive regulation of transcription from RNA polymerase II promoter, protein amino acid phosphorylation
phosphoribosylglycinamide formyltransferase	Gart	NP_034386	108	5	cytoplasm	ATP binding, catalytic activity, hydroxymethyl-, formyl- and related transferase activity, ligase activity, manganese ion binding, metal ion binding, methyltransferase activity, nucleotide binding, phosphoribosylamine-glycine ligase activity, phosphoribosylformylglycinamidine cyclo-ligase activity, phosphoribosylglycinamide formyltransferase activity, transferase activity	biosynthetic process, 'de novo' IMP biosynthetic process, purine base biosynthetic process, purine nucleotide biosynthetic 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	5	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
ribosomal protein L10A	Rpl10a	NP_035417	25	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, RNA binding, structural constituent of ribosome	biological_process, RNA processing, translation
valyl-tRNA synthetase	Vars	NP_035820	140	5	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
ribosomal protein S3	Rps3	NP_036182	27	5	cytoplasm, intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation
ribosomal protein L8	Rpl8	NP_036183	28	5	cellular_component, cytoplasm, intracellular, ribonucleoprotein complex, ribosome	molecular_function, RNA binding, rRNA binding, structural constituent of ribosome	biological_process, translation
drebrin-like	Dbnl	NP_038838	48	5	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
aminoadipate-semialdehyde synthase precursor	Aass	NP_038958	103	5	mitochondrion	catalytic activity, electron carrier activity, oxidoreductase activity, saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity, saccharopine dehydrogenase (NADP+, L-lysine-forming) activity	generation of precursor metabolites and energy, L-lysine catabolic process, oxidation reduction
damage specific DNA binding protein 1	Ddb1	NP_056550	127	5	cytoplasm, nucleus	DNA binding, nucleic acid binding	DNA repair, modification-dependent protein catabolic process, response to DNA damage stimulus
ATP-binding cassette, subfamily E, member 1	Abce1	NP_056566	67	5	cytoplasm, mitochondrion	ATP binding, ATPase activity, electron carrier activity, iron-sulfur cluster binding, nucleoside-triphosphatase activity, nucleotide binding	not classified
alpha isoform of regulatory subunit A, protein phosphatase 2	Ppp2r1a	NP_058587	65	5	cytosol, protein phosphatase type 2A complex	binding, protein binding	not classified
ribosomal protein S3a	Rps3a	NP_058655	30	5	cytosol, intracellular, nucleus, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	translation
ribosomal protein, large, P1	Rplp1	NP_061341	11	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translational elongation
soc-2 (suppressor of clear) homolog	Shoc2	NP_062632	65	5	not classified	protein binding	not classified
heterogeneous nuclear ribonucleoprotein H2	Hnrnph2	NP_063921	49	5	nucleus, ribonucleoprotein complex	molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process
acid sphingomyelinase-like phosphodiesterase 3a	Smpdl3a	NP_065586	50	5	extracellular region, extracellular space	hydrolase activity, hydrolase activity, acting on glycosyl bonds, sphingomyelin phosphodiesterase activity	metabolic process, sphingomyelin catabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
adenylate kinase 1	Ak1	NP_067490	23	5	cytoplasm, mitochondrion, plasma membrane	adenylate kinase activity, ATP binding, kinase activity, nucleobase, nucleoside, nucleotide kinase activity, nucleotide binding, transferase activity	ATP metabolic process, cell cycle arrest, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
eukaryotic translation elongation factor 1 delta isoform b	Eef1d	NP_075729	31	5	eukaryotic translation elongation factor 1 complex	translation elongation factor activity	translation, translational elongation
ribosomal protein L35	Rpl35	NP_079868	15	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
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
eukaryotic translation elongation factor 1 gamma	Eef1g	NP_080283	50	5	eukaryotic translation elongation factor 1 complex	translation elongation factor activity	translation, translational elongation
endoplasmic reticulum protein ERp29 precursor	Erp29	NP_080405	29	5	endoplasmic reticulum, endoplasmic reticulum lumen	not classified	protein secretion
enoyl Coenzyme A hydratase domain containing 2	Echdc2	NP_081004	26	5	mitochondrion	catalytic activity, lyase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
dehydrogenase/reductase (SDR family) member 1	Dhrs1	NP_081095	34	5	mitochondrial inner membrane	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
histidine triad protein member 5	Dcps	NP_081306	39	5	cytoplasm, nucleus	hydrolase activity, protein binding	deadenylation-dependent decapping of nuclear-transcribed mRNA, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
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
asparaginyl-tRNA synthetase	Nars	NP_081626	63	5	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
proteasome 26S non-ATPase subunit 1	Psmd1	NP_081633	106	5	proteasome complex	binding, enzyme regulator activity	regulation of protein catabolic process
katanin p60 subunit A-like 2	Katnal2	NP_081997	46	5	microtubule	ATP binding, hydrolase activity, microtubule-severing ATPase activity, nucleotide binding	not classified
Coenzyme A synthase	Coasy	NP_082172	62	5	not classified	ATP binding, catalytic activity, dephospho-CoA kinase activity, kinase activity, nucleotide binding, nucleotidyltransferase activity, pantetheine-phosphate adenylyltransferase activity, transferase activity	biosynthetic process, coenzyme A biosynthetic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	NP_082506	56	5	mitochondrial inner membrane, mitochondrion	glycine hydroxymethyltransferase activity, methyltransferase activity, transferase activity	one-carbon metabolic process
thioredoxin domain containing 4	Txndc4	NP_083848	47	5	endoplasmic reticulum, endoplasmic reticulum lumen	not classified	cell redox homeostasis, response to unfolded protein
carbonic anhydrase 15	Car15	NP_085035	35	5	extracellular region	carbonate dehydratase activity, lyase activity, metal ion binding, zinc ion binding	one-carbon metabolic process
chloride intracellular channel 1	Clic1	NP_254279	27	5	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
Bartter syndrome, infantile, with sensorineural deafness (Barttin)	Bsnd	NP_536706	34	5	basolateral plasma membrane, integral to membrane, integral to plasma membrane, membrane, plasma membrane, protein complex	chloride channel activity, protein binding	cellular chloride ion homeostasis, cellular ion homeostasis, cellular potassium ion homeostasis, sensory perception of sound
U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	U2af2	NP_598432	53	5	nucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
hypothetical protein LOC70984	4931406C07 Rik	NP_598493	35	5	nucleus	hydrolase activity, hydrolase activity, acting on ester bonds, metal ion binding, zinc ion binding	not classified
ribonuclease/angiogenin inhibitor 1	Rnh1	NP_660117	50	5	cytoplasm	protein binding	not classified
hexokinase domain containing 1	Hkdc1	NP_663394	102	5	not classified	ATP binding, hexokinase activity, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity	carbohydrate metabolic process, glycolysis
tetraspanin 8	Tspan8	NP_666122	26	5	integral to membrane, membrane	not classified	not classified
splicing factor, arginine/serine-rich 7	Sfrs7	NP_666195	27	5	nucleus	metal ion binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding, zinc ion binding	mRNA processing, RNA splicing
sorbitol dehydrogenase	Sord	NP_666238	38	5	soluble fraction	L-iditol 2-dehydrogenase activity, metal ion binding, oxidoreductase activity, zinc ion binding	oxidation reduction, sorbitol metabolic process
inorganic pyrophosphatase 2	Ppa2	NP_666253	38	5	cytoplasm, mitochondrion	hydrolase activity, inorganic diphosphatase activity, magnesium ion binding, metal ion binding	phosphate metabolic process
monoamine oxidase A	Maoa	NP_776101	60	5	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion	amine oxidase activity, electron carrier activity, oxidoreductase activity	catecholamine metabolic process, dopamine catabolic process, neurotransmitter catabolic process, oxidation reduction
Fe-containing alcohol dehydrogenase 1	Adhfe1	NP_780445	50	5	cellular_component, mitochondrion	hydroxyacid-oxoacid transhydrogenase activity, metal ion binding, oxidoreductase activity	oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cytoskeleton-associated protein 4	Ckap4	NP_780660	64	5	cell surface, endoplasmic reticulum, integral to membrane, membrane	protein binding	biological_process
ATPase, H+ transporting, lysosomal V1 subunit G3	Atp6v1g3	NP_796371	14	5	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
NADH dehydrogenase subunit 4	ND4	NP_904337	52	5	integral to membrane, membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity	electron transport chain, oxidation reduction, transport
UDP-glucose ceramide glucosyltransferase-like 1	Ugcgl1	NP_942602	176	5	endoplasmic reticulum	transferase activity, transferase activity, transferring glycosyl groups, UDP-glucose:glycoprotein glucosyltransferase activity	protein amino acid glycosylation
PREDICTED: similar to Isochorismatase domain-containing protein 2A, mitochondrial	Isoc2a	XP_001475311	22	5	not classified	not classified	not classified
PREDICTED: similar to novel C2, FerI (NUC094) and FerB (NUC096) domain containing protein	Fer1l4	XP_001481330	194	5	integral to membrane, membrane	not classified	not classified
translocase of inner mitochondrial membrane 10 homolog	Timm9	NP_001020024	10	4	membrane, mitochondrial inner membrane, mitochondrial intermembrane space protein transporter complex, mitochondrion	metal ion binding, protein binding, zinc ion binding	protein import into mitochondrial inner membrane, protein targeting to mitochondrion, protein transport, transmembrane transport, transport
cytochrome b5 domain containing 2	Cyb5d2	NP_001020097	12	4	integral to membrane, membrane	heme binding	not classified
calcium activated chloride channel	AI747448	NP_001028371	102	4	not classified	not classified	not classified
hypothetical protein LOC218236	BC010304	NP_001028440	122	4	cytoplasm, membrane, plasma membrane	RNA binding	not classified
heterogeneous nuclear ribonucleoprotein D isoform b	Hnrnpd	NP_001070734	36	4	chromosome, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	regulation of mRNA stability, regulation of transcription, transcription
hypothetical protein LOC74148	1300001I01Rik	NP_001074627	152	4	not classified	binding	not classified
NADH-ubiquinone oxidoreductase flavoprotein 3 isoform 2	1500032D16Rik	NP_001077360	12	4	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	molecular_function	electron transport chain, transport
catenin, delta 1 isoform 2	Ctnnd1	NP_001078917	103	4	cytoplasm, lamellipodium, membrane, membrane fraction, nucleus, plasma membrane	protein binding, protein phosphatase binding, RPTP-like protein binding	cell adhesion, cell-cell adhesion, epithelial cell differentiation involved in salivary gland development, morphogenesis of a polarized epithelium, regulation of transcription, salivary gland morphogenesis, transcription, Wnt receptor signaling pathway
CD151 antigen	Cd151	NP_001104520	28	4	integral to membrane, membrane	not classified	not classified
hypothetical protein LOC666274	EG666274	NP_001104748	19	4	not classified	not classified	not classified
macrophage migration inhibitory factor-like	LOC100040259	NP_001104800	12	4	not classified	not classified	not classified
erythrocyte protein band 4.1-like 5 isoform 2	Epb4.1l5	NP_001106887	58	4	cell junction, cytoplasm, cytoskeleton, extrinsic to membrane	binding, cytoskeletal protein binding	axial mesoderm development, paraxial mesoderm development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
catenin (cadherin associated protein), beta 1, 88kDa	Ctnnb1	NP_031640	85	4	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
cathepsin B preproprotein	Ctsb	NP_031824	37	4	lysosome, mitochondrion	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis, regulation of catalytic activity
fatty acid synthase	Fasn	NP_032014	272	4	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	NP_032318	79	4	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
peptidase D	Pepd	NP_032846	55	4	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
protein kinase C substrate 80K-H	Prkcsh	NP_032951	59	4	alpha-glucosidase II complex, endoplasmic reticulum	alpha-glucosidase activity, calcium ion binding, kinase activity, protein binding, RNA binding	N-glycan processing
polypyrimidine tract binding protein 1 isoform 2	Ptbp1	NP_032982	57	4	nucleus	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
SEC8	Exoc4	NP_033174	111	4	exocyst	PDZ domain binding	exocytosis, protein transport, transport, vesicle docking during exocytosis
serine hydroxymethyltransferase 1 (soluble)	Shmt1	NP_033197	53	4	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
thiosulfate sulfurtransferase, mitochondrial	Tst	NP_033463	33	4	mitochondrial inner membrane, mitochondrion	thiosulfate sulfurtransferase activity, transferase activity	sulfate transport
proteasome 26S non-ATPase subunit 3	Psmd3	NP_033465	61	4	proteasome complex	enzyme regulator activity	regulation of protein catabolic process
tubulin, beta 2	Tubb2a	NP_033476	50	4	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
cadherin 1	Cdh1	NP_033994	98	4	adherens junction, apical part of cell, basolateral plasma membrane, cell junction, cell-cell adherens junction, cell-cell junction, integral to membrane, membrane, plasma membrane	beta-catenin binding, calcium ion binding, protein binding, protein phosphatase binding, RPTP-like protein binding	cell adhesion, cell-cell adhesion, homophilic cell adhesion, protein homooligomerization, protein metabolic process, regulation of branching involved in salivary gland morphogenesis, regulation of caspase activity, salivary gland cavitation, trophectodermal cell differentiation
ferritin heavy chain 1	Fth1	NP_034369	21	4	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 nucleotide-binding protein, beta-2 subunit	Gnb2	NP_034442	37	4	heterotrimeric G-protein complex	GTPase activity, protein binding, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
galectin 3	Lgals3	NP_034835	27	4	cytoplasm, nucleus, proteinaceous extracellular matrix	IgE binding, protein binding, sugar binding	cell differentiation, extracellular matrix organization, skeletal system development
RNA binding motif protein, X-linked	Rbmx	NP_035382	42	4	ribonucleoprotein complex	nucleic acid binding	not classified
bisphosphate 3'-nucleotidase 1	Bpnt1	NP_035924	33	4	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
solute carrier family 27 (fatty acid transporter), member 2	Slc27a2	NP_036108	70	4	endoplasmic reticulum, integral to membrane, membrane, mitochondrion, peroxisome	ATP binding, catalytic activity, ligase activity, long-chain-fatty-acid-CoA ligase activity, nucleotide binding	fatty acid metabolic process, lipid metabolic process, long-chain fatty acid metabolic process, metabolic process
heat shock protein 105	Hsph1	NP_038587	96	4	cytoplasm, nucleus	ATP binding, nucleotide binding, protein binding	chaperone mediated protein folding requiring cofactor, response to stress
splicing factor 3a, subunit 2	Sf3a2	NP_038679	51	4	nucleus	metal ion binding, RNA splicing factor activity, transesterification mechanism, zinc ion binding	nuclear mRNA splicing, via spliceosome
vacuolar protein sorting 45	Vps45	NP_038869	65	4	endosome, Golgi apparatus, membrane	protein binding	protein transport, transport, vesicle docking during exocytosis, vesicle-mediated transport
translocase of inner mitochondrial membrane 9 homolog	Timm13	NP_038923	10	4	mitochondrion	not classified	not classified
AU RNA-binding enoyl-coenzyme A hydratase	Auh	NP_057918	33	4	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	4	mitochondrion, peroxisome	catalytic activity, isomerase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
thioredoxin-like 1	Txnl1	NP_058072	32	4	cytoplasm	not classified	cell redox homeostasis, electron transport chain, transport
ribosomal protein L5	Rpl5	NP_058676	34	4	cytoplasm, intracellular, nucleus, ribonucleoprotein complex, ribosome	5S rRNA binding, protein binding, RNA binding, rRNA binding, structural constituent of ribosome	biological_process, translation
3-monooxgenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	NP_061359	28	4	cellular_component, cytoplasm	protein domain specific binding	protein targeting
ribophorin II	Rpn2	NP_062616	69	4	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
ADP-ribosylation factor-like 3	Arl3	NP_062692	20	4	Golgi apparatus, intracellular, membrane, nucleus	GTP binding, magnesium ion binding, metal ion binding, nucleotide binding	cell cycle, cell division, small GTPase mediated signal transduction
DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	NP_062768	46	4	membrane	heat shock protein binding, metal ion binding, unfolded protein binding, zinc ion binding	protein folding
DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	NP_062769	56	4	not classified	binding, heat shock protein binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
actin related protein 2/3 complex, subunit 3	Arpc3	NP_062798	21	4	Arp2/3 protein complex, cell projection, cytoplasm, cytoskeleton, lamellipodium	actin binding	regulation of actin filament polymerization
mitochondrial carrier homolog 1	Mtch1	NP_063933	42	4	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	apoptosis, transport
DnaJ (Hsp40) homolog, subfamily B, member 12	Dnajb12	NP_064349	42	4	integral to membrane, membrane	heat shock protein binding, unfolded protein binding	protein folding
aspartyl beta-hydroxylase isoform 1	Asph	NP_075553	83	4	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
ribosomal protein S19	Rps19	NP_075622	16	4	intracellular, nucleolus, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	translation
chromosome segregation 1-like	Cse1l	NP_076054	110	4	cytoplasm, nucleus	binding, importin-alpha export receptor activity, protein transporter activity	cell proliferation, intracellular protein transport, protein transport, transport
importin 5	Ipo5	NP_076068	124	4	cytoplasm, nucleus	binding, protein binding, protein transporter activity	intracellular protein transport, protein transport, transport
ribosomal protein L24	Rpl24	NP_077180	18	4	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
transmembrane protein 14C	Tmem14c	NP_079663	12	4	integral to membrane, membrane, mitochondrion	not classified	not classified
mitochondrial ribosomal protein S28	Mrps28	NP_079710	21	4	mitochondrion, ribonucleoprotein complex, ribosome	not classified	not classified
hypothetical protein LOC66302	2410005O16 Rik	NP_079752	35	4	cytoplasm, microtubule	binding	not classified
DC2 protein	2310008M10 Rik	NP_079785	17	4	integral to membrane, membrane	not classified	not classified
ribosomal protein L15	Rpl15	NP_079862	24	4	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
translocase of inner mitochondrial membrane 50 homolog	Timm50	NP_079892	40	4	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
cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	Chordc1	NP_080120	37	4	not classified	calcium ion binding, metal ion binding, zinc ion binding	not classified
succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	NP_080124	17	4	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	NP_080174	33	4	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
ribosomal protein L14	Rpl14	NP_080250	24	4	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
hypothetical protein LOC67432	0610010D20 Rik	NP_080428	35	4	mitochondrion	catalytic activity, lyase activity, molecular_function	biological_process, metabolic process
CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Cdipt	NP_080914	24	4	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
dimethylarginine dimethylaminohydrolase 1	Ddah1	NP_081269	31	4	cytoplasm	dimethylargininase activity, hydrolase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines, metal ion binding, zinc ion binding	nitric oxide biosynthetic process, protein amino acid nitrosylation
hypothetical protein LOC69225	0710008K08 Rik	NP_081271	37	4	cellular_component	molecular_function	biological_process
ribosomal protein S27	Rps27	NP_081291	9	4	intracellular, ribonucleoprotein complex, ribosome	metal ion binding, protein binding, structural constituent of ribosome, zinc ion binding	translation
aspartoacylase-3	Acy3	NP_082133	35	4	apical plasma membrane, cytoplasm, membrane fraction	aminoacylase activity, aspartoacylase activity, hydrolase activity, hydrolase activity, acting on ester bonds, identical protein binding, metal ion binding, zinc ion binding	metabolic process
acyl-CoA synthetase long-chain family member 5	Acsl5	NP_082252	76	4	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
methylmalonyl CoA epimerase	Mcee	NP_082902	19	4	mitochondrion	isomerase activity, methylmalonyl-CoA epimerase activity	not classified
EF hand domain containing 1	Efhd1	NP_083165	27	4	mitochondrial inner membrane	calcium ion binding	neuron projection development
RAB1B, member RAS oncogene family	Rab1b	NP_083852	22	4	cytoplasm, membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
actin related protein 2/3 complex, subunit 2	Arpc2	NP_083987	34	4	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
splicing factor 3b, subunit 2	Sf3b2	NP_084385	98	4	not classified	protein binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
regulator of nonsense transcripts 1	Upf1	NP_109605	123	4	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
nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	NP_149071	40	4	mitochondrion, peroxisome	hydrolase activity, magnesium ion binding, manganese ion binding, metal ion binding	not classified
glyoxylate reductase/hydroxypyruvate reductase	Grhpr	NP_525028	35	4	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
rhotekin isoform 3	Rtkn	NP_598396	61	4	intracellular	GTP binding, GTPase inhibitor activity, GTP-Rho binding, nucleotide binding, Rho GTPase binding	apoptosis, signal transduction
cytoplasmic FMR1 interacting protein 2	Cyfip2	NP_598530	146	4	cell junction, cytoplasm, synapse, synaptosome	molecular_function, protein binding	apoptosis, biological_process, cell adhesion
heterogeneous nuclear ribonucleoprotein F	Hnrnpf	NP_598595	46	4	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	NP_598801	83	4	ribonucleoprotein complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process
glycoprotein, synaptic 2	Gpsn2	NP_598879	36	4	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
otubain 1	Otub1	NP_598911	31	4	not classified	cysteine-type peptidase activity, hydrolase activity, peptidase activity	immune response, modification-dependent protein catabolic process
virus-induced signaling adapter	D430028G21Rik	NP_659137	53	4	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion	not classified	immune response, innate immune response, response to virus
hypothetical protein LOC109168	5730596K20Rik	NP_666203	61	4	integral to membrane, membrane	GTP binding, GTPase activity, nucleotide binding	not classified
5-oxoprolinase (ATP-hydrolysing)	Oplah	NP_694762	138	4	not classified	5-oxoprolinase (ATP-hydrolyzing) activity, ATP binding, catalytic activity, hydrolase activity, nucleotide binding	not classified
solute carrier family 25, member 1	Slc25a1	NP_694790	34	4	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
acyl-CoA synthetase family member 2	Acsf2	NP_722502	68	4	mitochondrion	ATP binding, catalytic activity, ligase activity, nucleotide binding	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
phospholipase C, gamma 2	Plcg2	NP_758489	148	4	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
splicing factor, arginine/serine-rich 1 isoform 1	Sfrs1	NP_775550	28	4	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
ilvB (bacterial acetolactate synthase)-like	Ilvbl	NP_776112	68	4	integral to membrane, membrane	catalytic activity, magnesium ion binding, metal ion binding, thiamin pyrophosphate binding, transferase activity	not classified
transmembrane protein 65	Tmem65	NP_780421	25	4	integral to membrane, membrane	not classified	not classified
hypothetical protein LOC109154	2410014A08Rik	NP_780612	32	4	endoplasmic reticulum, integral to membrane, membrane	not classified	carbohydrate metabolic process
U5 snRNP-specific protein, 200 kDa	Ascc3l1	NP_796188	245	4	ribonucleoprotein complex	ATP binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	not classified
MAL2 proteolipid protein	Mal2	NP_849251	19	4	integral to membrane, membrane, plasma membrane	not classified	not classified
glutathione S-transferase, pi 2	Gstp2	NP_861461	24	4	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
pleckstrin homology domain containing, family A member 6	Plekha6	NP_891846	131	4	not classified	not classified	not classified
erythrocyte protein band 4.1	Epb4.1	NP_906273	96	4	actin cytoskeleton, cortical cytoskeleton, cytoplasm, cytoskeleton, extrinsic to membrane, membrane, nucleus	actin binding, cytoskeletal protein binding, spectrin binding, structural molecule activity	actin cytoskeleton organization, cortical actin cytoskeleton organization, regulation of cell shape
ubiquinol-cytochrome c reductase complex protein	1110020P15Rik	NP_932096	7	4	membrane, mitochondrial envelope, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, transport
tyrosyl-tRNA synthetase 2, mitochondrial	Yars2	NP_937889	53	4	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, tyrosine-tRNA ligase activity	translation, tRNA aminoacylation for protein translation, tyrosyl-tRNA aminoacylation
PREDICTED: similar to Rab6-interacting protein 2	LOC100048600	XP_001480600	128	4	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG665562	XP_915749	14	4	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG629116	XP_916411	15	4	cellular_component	molecular_function	biological_process
enhanced green fluorescent protein	egfp	AAB02572	27	3	not classified	not classified	not classified
reticulon 1 isoform RTN1-C	Rtn1	NP_001007597	24	3	endoplasmic reticulum, integral to membrane, membrane	molecular_function	biological_process
pleckstrin homology domain containing, family N member 1	Plekhn1	NP_001008234	39	3	not classified	protein binding	not classified
hypothetical protein LOC228715	Gm561	NP_001028469	12	3	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
exportin 1, CRM1 homolog	Xpo1	NP_001030303	123	3	cytoplasm, nucleus, ribonucleoprotein complex	binding, protein binding, protein transporter activity, RNA binding	intracellular protein transport, mRNA transport, protein export from nucleus, protein localization in nucleus, protein transport, regulation of centrosome duplication, regulation of protein catabolic process, transport
haloacid dehalogenase-like hydrolase domain containing 2 isoform 1	Hdhd2	NP_001034290	29	3	not classified	catalytic activity, hydrolase activity	metabolic process
SCO cytochrome oxidase deficient homolog 1	Sco1	NP_001035115	32	3	mitochondrial inner membrane, mitochondrion	copper ion binding, metal ion binding	cell redox homeostasis, cellular copper ion homeostasis, copper ion transport, respiratory chain complex IV assembly
hypothetical protein LOC68646 isoform 2	1110020G09Rik	NP_001035485	48	3	mitochondrion	NAD+ kinase activity	metabolic process
limkain b1	4921513D23Rik	NP_001074623	193	3	peroxisome	nucleic acid binding, nucleotide binding, RNA binding	not classified
phosphogluconate dehydrogenase	Pgd	NP_001074743	53	3	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
methyl CpG binding protein 2 isoform 1	Mecp2	NP_001075448	54	3	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
Bcl-2 inhibitor of transcription isoform b	Ptrh2	NP_001092280	20	3	mitochondrion	aminoacyl-tRNA hydrolase activity, hydrolase activity	translation
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	Arfgef1	NP_001095900	208	3	cellular_component	molecular_function	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
catenin (cadherin associated protein), alpha 2 isoform 2	Ctnna2	NP_001103234	105	3	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
heterogeneous nuclear ribonucleoprotein M isoform b	Hnrnpm	NP_001103383	74	3	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
peptidylprolyl isomerase H isoform 1	Ppih	NP_001103599	19	3	cytoplasm, nucleus, spliceosomal complex	isomerase activity, peptidyl-prolyl cis-trans isomerase activity	mRNA processing, protein folding, RNA splicing
acid phosphatase 1, soluble isoform 1	Acp1	NP_001103709	18	3	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
ribosomal protein L27-like	EG621100	NP_001103809	16	3	not classified	not classified	not classified
aspartyl aminopeptidase isoform a	Dnpep	NP_001104301	52	3	cytoplasm, vacuole	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
ribosomal protein L21-like	EG668319	NP_001104783	19	3	not classified	not classified	not classified
adenylosuccinate synthetase 1	Adssl1	NP_031447	50	3	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
adenylosuccinate synthetase, non muscle	Adss	NP_031448	50	3	cytoplasm	adenylosuccinate synthase activity, GTP binding, ligase activity, magnesium ion binding, metal ion binding, nucleotide binding	AMP biosynthetic process, purine nucleotide biosynthetic process
ADP-ribosylation factor 4	Arf4	NP_031505	20	3	cytoplasm, Golgi apparatus, intracellular, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
chaperonin containing Tcp1, subunit 5 (epsilon)	Cct5	NP_031663	60	3	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	NP_031866	69	3	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
diaphanous homolog 1	Diap1	NP_031884	139	3	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
Ddx19-like protein	Ddx19a	NP_031942	54	3	cytoplasm, membrane, nuclear pore, nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA transport, protein transport, transmembrane transport, transport
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	NP_032324	45	3	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
eukaryotic translation initiation factor 3, subunit 6	Eif3e	NP_032414	52	3	cytoplasm, eukaryotic translation initiation factor 3 complex, nucleus	translation initiation factor activity	translation, translational initiation
aminolevulinate, delta-, dehydratase	Alad	NP_032551	36	3	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
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	NP_032603	58	3	integral to membrane, membrane, plasma membrane	catalytic activity, cation binding, protein binding	amino acid transport, carbohydrate metabolic process, transport
nucleoside-diphosphate kinase 1	Nme1	NP_032730	17	3	cytoplasm, microsome, nucleus, soluble fraction	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleoside diphosphate kinase activity, nucleotide binding, transferase activity	cell differentiation, CTP biosynthetic process, endocytosis, GTP biosynthetic process, lactation, mammary gland development, nervous system development, nucleotide metabolic process, UTP biosynthetic process
nucleobindin 1	Nucb1	NP_032775	53	3	cytoplasm, Golgi apparatus, membrane	calcium ion binding, DNA binding	not classified
palmitoyl-protein thioesterase 1	Ppt1	NP_032943	34	3	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
aminopeptidase puromycin sensitive	Npepps	NP_032968	103	3	cytoplasm, nucleus	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	NP_032970	26	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
polymerase I and transcript release factor	Ptrf	NP_033012	44	3	caveola, cytoplasm, endoplasmic reticulum, membrane, microsome, mitochondrion, nucleus, plasma membrane	protein binding, RNA binding, RNA polymerase I transcription termination factor activity, rRNA binding, rRNA primary transcript binding	regulation of transcription, transcription, transcription initiation from RNA polymerase I promoter, transcription termination
Rho-associated coiled-coil forming kinase 1	Rock1	NP_033097	158	3	cytoplasm, Golgi apparatus, intracellular, membrane	ATP binding, diacylglycerol binding, kinase activity, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, zinc ion binding	actin cytoskeleton organization, apoptosis, bleb formation, cytokinesis, intracellular signaling cascade, negative regulation of neuron apoptosis, protein amino acid phosphorylation, Rho protein signal transduction, signal transduction
ribosomal protein S5	Rps5	NP_033121	23	3	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	structural constituent of ribosome	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
solute carrier family 3, member 1	Slc3a1	NP_033231	78	3	mitochondrial inner membrane	not classified	not classified
signal sequence receptor, delta	Ssr4	NP_033305	19	3	endoplasmic reticulum, integral to membrane, membrane	receptor activity	not classified
syntaxin 4A (placental)	Stx4a	NP_033320	34	3	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
tripeptidyl peptidase II	Tpp2	NP_033444	140	3	cytoplasm	aminopeptidase activity, hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	proteolysis
ribosomal protein L13a	Rpl13a	NP_033464	23	3	intracellular, large ribosomal subunit, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
adaptor protein complex AP-1, mu 2 subunit isoform 2	Ap1m2	NP_033808	48	3	clathrin adaptor complex, cytoplasmic vesicle, Golgi apparatus, membrane, trans-Golgi network	protein binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
calpain 2	Capn2	NP_033924	80	3	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
cell division cycle 10 homolog	Sept7	NP_033989	51	3	cytoplasm, septin complex, synaptosome	GTP binding, nucleotide binding, protein binding	cell cycle, cell division, mitosis
COP9 (constitutive photomorphogenic) homolog, subunit 2	Cops2	NP_034069	52	3	cytoplasm, nucleus, signalosome	protein binding, transcription corepressor activity	cell proliferation, negative regulation of transcription
carnitine palmitoyltransferase 1b, muscle	Cpt1b	NP_034078	88	3	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion	acyltransferase activity, carnitine O-palmitoyltransferase activity, kinase activity, transferase activity	fatty acid metabolic process, lipid metabolic process, long-chain fatty acid transport, transport
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
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	NP_034401	38	3	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
guanosine diphosphate (GDP) dissociation inhibitor 1	Gdi1	NP_034403	51	3	cytoplasm	GTPase activator activity, Rab GDP-dissociation inhibitor activity	protein transport, regulation of GTPase activity
guanine nucleotide binding protein, alpha 11	Gna11	NP_034431	42	3	heterotrimeric G-protein complex	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding, signal transducer activity	activation of phospholipase C activity by dopamine receptor signaling pathway, glutamate signaling pathway, G-protein coupled receptor protein signaling pathway, heart development, pigmentation during development, protein amino acid ADP-ribosylation, regulation of action potential, regulation of melanocyte differentiation, signal transduction, skeletal system development
glutathione S-transferase omega 1	Gsto1	NP_034492	27	3	cytoplasm	glutathione transferase activity, transferase activity	metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
lysosomal membrane glycoprotein 2 isoform 2	Lamp2	NP_034815	46	3	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
protein phosphatase 5, catalytic subunit	Ppp5c	NP_035285	57	3	cytoplasm, cytosol, nucleus	binding, hydrolase activity, iron ion binding, manganese ion binding, metal ion binding, phosphoprotein phosphatase activity, protein binding, protein serine/threonine phosphatase activity	protein amino acid dephosphorylation, response to morphine
prolyl endopeptidase	Prep	NP_035286	81	3	cytoplasm, nucleus	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	protein metabolic process, proteolysis
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	NP_035318	53	3	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	protein catabolic process
sterol carrier protein 2, liver	Scp2	NP_035457	59	3	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
sepiapterin reductase	Spr	NP_035597	28	3	cytoplasm	binding, catalytic activity, oxidoreductase activity, sepiapterin reductase activity	cell morphogenesis involved in neuron differentiation, death, dopamine metabolic process, L-phenylalanine metabolic process, metabolic process, norepinephrine metabolic process, oxidation reduction, pteridine metabolic process, regulation of multicellular organism growth, serotonin metabolic process, tetrahydrobiopterin biosynthetic process, tetrahydrobiopterin metabolic process, voluntary musculoskeletal movement
surfeit gene 4	Surf4	NP_035642	30	3	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
vimentin	Vim	NP_035831	54	3	cell leading edge, cytoplasm, cytoskeleton, intermediate filament, type III intermediate filament	protein binding, structural molecule activity	intermediate filament-based process
coronin, actin binding protein 1B	Coro1b	NP_035908	54	3	cellular_component, cytoplasm, cytoskeleton	actin binding, protein binding	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
COP9 (constitutive photomorphogenic), subunit 3	Cops3	NP_036121	48	3	cytoplasm, nucleus, signalosome	protein binding	in utero embryonic development
solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Slc9a3r1	NP_036160	39	3	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 31	Bcap31	NP_036190	28	3	endoplasmic reticulum, Golgi membrane, integral to membrane, membrane, plasma membrane	receptor activity	apoptosis, immune response, intracellular protein transport, protein transport, spermatogenesis, transport, vesicle-mediated transport
ATPase, H+ transporting, V0 subunit D isoform 1	Atp6v0d1	NP_038505	40	3	early endosome, proton-transporting two-sector ATPase complex, proton-transporting domain, proton-transporting V-type ATPase, V0 domain	hydrogen ion transmembrane transporter activity, hydrogen-exporting ATPase activity, phosphorylative mechanism	ATP synthesis coupled proton transport, ion transport, proton transport, transport
heme binding protein 1	Hebp1	NP_038574	21	3	cytoplasm, cytosol, mitochondrion	heme binding	heme metabolic process
hypoxanthine guanine phosphoribosyl transferase 1	Hprt1	NP_038584	25	3	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
purine-nucleoside phosphorylase 1	Pnp1	NP_038660	32	3	cytosol	catalytic activity, purine-nucleoside phosphorylase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring pentosyl groups	deoxyguanosine catabolic process, deoxyinosine catabolic process, dGTP metabolic process, GTP biosynthetic process, guanosine catabolic process, inosine catabolic process, negative regulation of apoptosis, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, nucleoside metabolic process, positive regulation of alpha-beta T cell differentiation, positive regulation of B cell differentiation, positive regulation of DNA repair, positive regulation of T cell mediated cytotoxicity, positive regulation of T cell proliferation, purine nucleoside metabolic process, response to gamma radiation, urate biosynthetic process
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
nucleosome binding protein 1	Nsbp1	NP_057919	45	3	chromatin, nucleoplasm, nucleus	chromatin binding, DNA binding	regulation of transcription, regulation of transcription from RNA polymerase I promoter, transcription
ubiquitin carboxyl-terminal esterase L3	Uchl3	NP_057932	26	3	cytoplasm, intracellular	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	adult walking behavior, eating behavior, modification-dependent protein catabolic process, protein deubiquitination, ubiquitin-dependent protein catabolic process
ATPase, Ca++ transporting, ubiquitous	Atp2a3	NP_058025	114	3	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
caveolin 2	Cav2	NP_058596	18	3	caveola, Golgi apparatus, integral to membrane, integral to plasma membrane, membrane, perinuclear region of cytoplasm, plasma membrane	protein homodimerization activity	endocytosis, endoplasmic reticulum organization, mitochondrion organization, negative regulation of cell proliferation, negative regulation of endothelial cell proliferation, protein oligomerization, skeletal muscle fiber development
inositol (myo)-1(or 4)-monophosphatase 1	Impa1	NP_061352	30	3	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
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
RNA and export factor binding protein 2	Refbp2	NP_062357	24	3	cytoplasm, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding, single-stranded DNA binding	mRNA processing, mRNA transport, RNA splicing, transport
NS1-associated protein 1 isoform 1	Syncrip	NP_062640	70	3	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, poly(A) RNA binding, RNA binding	mRNA processing, RNA splicing
actin-like 6A	Actl6a	NP_062647	47	3	chromatin remodeling complex, nucleus	ATP binding, chromatin binding, protein binding	chromatin modification, chromatin remodeling, regulation of growth, regulation of transcription, transcription
thioredoxin 2	Txn2	NP_064297	18	3	mitochondrion	electron carrier activity, protein disulfide oxidoreductase activity	cell redox homeostasis, electron transport chain, glycerol ether metabolic process, transport
inositol 1,4,5-triphosphate receptor 2 isoform 1	Itpr2	NP_064307	307	3	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
Sec11-like 1	Sec11a	NP_064335	21	3	endoplasmic reticulum, integral to membrane, membrane, microsome	hydrolase activity, peptidase activity, serine-type peptidase activity	proteolysis, signal peptide processing
carnitine/acylcarnitine translocase	Slc25a20	NP_065266	33	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
EH-domain containing 3	Ehd3	NP_065603	61	3	endocytic vesicle, endosome, membrane, plasma membrane	ATP binding, calcium ion binding, GTP binding, GTPase activity, nucleotide binding, protein binding	not classified
flightless I homolog	Flii	NP_071292	145	3	cytoplasm, cytoskeleton, nucleus	actin binding, protein binding	actin cytoskeleton organization, actin filament severing, multicellular organismal development, regulation of transcription, transcription
OCIA domain containing 1	Ociad1	NP_075918	28	3	cellular_component, endosome	molecular_function	biological_process
pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	NP_079549	12	3	cytoplasm, nucleus	4-alpha-hydroxytetrahydrobiopterin dehydratase activity, lyase activity, phenylalanine 4-monooxygenase activity, protein binding, transcription coactivator activity	positive regulation of transcription, protein heterooligomerization, protein homotetramerization, regulation of protein homodimerization activity, tetrahydrobiopterin biosynthetic process
guanine nucleotide binding protein (G protein), gamma 12	Gng12	NP_079554	8	3	heterotrimeric G-protein complex, membrane, plasma membrane	signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
mitochondrial ribosomal protein S7	Mrps7	NP_079581	28	3	intracellular, mitochondrial small ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
NADH-ubiquinone oxidoreductase B9 subunit	Ndufa3	NP_079624	9	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
Ts translation elongation factor, mitochondrial	Tsfm	NP_079813	35	3	intracellular, mitochondrion	translation elongation factor activity	translation, translational elongation
mitochondrial ribosomal protein S25	Mrps25	NP_079854	20	3	mitochondrial small ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	not classified
ankyrin repeat and SOCS box-containing 17	Asb17	NP_080034	34	3	not classified	not classified	intracellular signaling cascade, modification-dependent protein catabolic process
prenylcysteine oxidase 1	Pcyox1	NP_080099	56	3	lysosome	oxidoreductase activity, oxidoreductase activity, acting on sulfur group of donors, oxygen as acceptor, prenylcysteine oxidase activity	oxidation reduction, prenylcysteine catabolic process
thioredoxin-related transmembrane protein 2	Txndc14	NP_080144	34	3	integral to membrane, membrane	not classified	cell redox homeostasis
RAB5A, member RAS oncogene family	Rab5a	NP_080163	24	3	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
ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	Atp5e	NP_080259	6	3	membrane, mitochondrial inner membrane, mitochondrial proton-transporting ATP synthase complex, mitochondrial proton-transporting ATP synthase complex, catalytic core F(1), mitochondrion, proton-transporting ATP synthase complex, catalytic core F(1)	hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, proton-transporting ATPase activity, rotational mechanism	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin light chain, regulatory B-like	2900073G15 Rik	NP_080340	20	3	not classified	calcium ion binding	not classified
coenzyme Q5 homolog, methyltransferase	Coq5	NP_080780	37	3	mitochondrion	methyltransferase activity, transferase activity	ubiquinone biosynthetic process
parathymosin	Ptms	NP_081264	11	3	not classified	not classified	immune response
keratin 5	Krt5	NP_081287	62	3	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified
6.8 kDa mitochondrial proteolipid	2010107E04 Rik	NP_081636	7	3	mitochondrion	not classified	not classified
hypothetical protein LOC70564	5730469M10 Rik	NP_081740	24	3	extracellular region	not classified	not classified
3-oxoacyl-ACP synthase, mitochondrial	Oxsm	NP_081971	49	3	mitochondrion	3-oxoacyl-[acyl-carrier-protein] synthase activity, acyltransferase activity, catalytic activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	biosynthetic process, fatty acid biosynthetic process, lipid biosynthetic process, metabolic process
protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	NP_082168	112	3	cytoplasm	phosphoprotein phosphatase activity	protein amino acid dephosphorylation, regulation of nucleocytoplasmic transport
RAN binding protein 3	Ranbp3	NP_082209	53	3	cytoplasm, nucleus	not classified	intracellular transport, protein transport, transport
solute carrier family 25, member 35	Slc25a35	NP_082324	33	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
aarF domain containing kinase 1	Adck1	NP_082381	60	3	extracellular region	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	NP_083051	56	3	endoplasmic reticulum, membrane, microsome	aromatase activity, electron carrier activity, heme binding, iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	oxidation reduction
glucan (1,4-alpha-), branching enzyme 1	Gbe1	NP_083079	80	3	cellular_component	1,4-alpha-glucan branching enzyme activity, catalytic activity, cation binding, hydrolase activity, hydrolyzing O-glycosyl compounds, transferase activity, transferase activity, transferring glycosyl groups	carbohydrate metabolic process, glycogen biosynthetic process
actin related protein 2/3 complex, subunit 5-like	Arpc5l	NP_083085	17	3	cellular_component, cytoplasm, cytoskeleton	actin binding, molecular_function	biological_process, regulation of actin filament polymerization

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
zinc finger transcription factor TRPS1	Trps1	NP_114389	141	3	intracellular, nucleus	DNA binding, metal ion binding, protein binding, sequence-specific DNA binding, transcription factor activity, transcription repressor activity, zinc ion binding	negative regulation of transcription, DNA-dependent, regulation of transcription, regulation of transcription, DNA-dependent, transcription
spectrin beta 4	Spnb4	NP_115999	289	3	axon, axon hillock, cytoplasm, nuclear matrix, PML body, spectrin	actin binding, ankyrin binding	adult behavior, adult walking behavior, axonogenesis, fertilization, positive regulation of multicellular organism growth, sensory perception of sound, transmission of nerve impulse
actinin alpha 2	Actn2	NP_150371	104	3	cytoplasm, striated muscle thin filament, Z disc	actin binding, actin filament binding, calcium ion binding, ligand-dependent nuclear receptor transcription coactivator activity, protein binding, protein binding, bridging, protein homodimerization activity, thyroid hormone receptor coactivator activity, ZASP binding	muscle contraction
ribosomal protein 10	Rpl10	NP_443067	25	3	cytoplasm, cytosolic large ribosomal subunit, intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
major vault protein	Mvp	NP_542369	96	3	cytoplasm, ribonucleoprotein complex	not classified	not classified
solute carrier family 5 (sodium/glucose cotransporter), member 2	Slc5a2	NP_573517	73	3	integral to membrane, membrane	sodium ion binding, symporter activity, transporter activity	carbohydrate transport, ion transport, sodium ion transport, transport
optic atrophy 1 homolog	Opa1	NP_598513	111	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	GTP binding, nucleotide binding	apoptosis, response to stimulus, visual perception
calcium binding protein 39	Cab39	NP_598542	40	3	cytoplasm	calcium ion binding	not classified
prostaglandin E synthase 2	Ptges2	NP_598544	43	3	cytoplasm, cytosol, Golgi apparatus, integral to membrane, membrane, nucleus	DNA binding, electron carrier activity, isomerase activity, prostaglandin-E synthase activity, protein disulfide oxidoreductase activity, transcription activator activity	cell redox homeostasis, fatty acid biosynthetic process, lipid biosynthetic process, prostaglandin biosynthetic process, regulation of transcription, secretion
golgi autoantigen, golgin subfamily a, 2 isoform a	Golga2	NP_598613	116	3	cis-Golgi network, Golgi apparatus, membrane	not classified	not classified
oxidative-stress responsive 1	Oxsr1	NP_598746	52	3	not classified	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation, response to oxidative stress

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATP citrate lyase	Acly	NP_598798	120	3	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
PDZ-domain protein scribble	Scrib	NP_598850	180	3	basolateral plasma membrane, cytoplasm, membrane	protein binding	asymmetric protein localization, cell migration, mammary gland duct morphogenesis, morphogenesis of embryonic epithelium, positive chemotaxis
ATPase, H+/K+ transporting, nongastric, alpha polypeptide	Atp12a	NP_619593	115	3	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
pre-mRNA processing factor 8	Prpf8	NP_619600	274	3	nucleus, ribonucleoprotein complex, spliceosomal complex, U5 snRNP	protein binding, RNA binding	mRNA processing, nuclear mRNA splicing, via spliceosome, RNA splicing
3-mercaptopyruvate sulfurtransferase	Mpst	NP_619611	33	3	cytoplasm, mitochondrial inner membrane, mitochondrion	3-mercaptopyruvate sulfurtransferase activity, thiosulfate sulfurtransferase activity, transferase activity	sulfate transport
biliverdin reductase B (flavin reductase (NADPH))	Blvrb	NP_659172	22	3	cytoplasm	biliverdin reductase activity, binding, catalytic activity, coenzyme binding, flavin reductase activity, oxidoreductase activity	cellular metabolic process, metabolic process, oxidation reduction
dihydroxyacetone kinase 2 homolog	Dak	NP_663471	60	3	not classified	ATP binding, catalytic activity, cobalt ion binding, FAD-AMP lyase (cyclizing) activity, glycerone kinase activity, kinase activity, lyase activity, magnesium ion binding, manganese ion binding, metal ion binding, nucleotide binding, transferase activity	glycerol metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
signal recognition particle 68	Srp68	NP_666144	71	3	cytoplasm, nucleolus, nucleus, ribonucleoprotein complex, signal recognition particle, endoplasmic reticulum targeting	RNA binding	not classified
nardilysin, N-arginine dibasic convertase, NRD convertase 1	Nrd1	NP_666262	133	3	not classified	catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, protein binding, zinc ion binding	proteolysis
thyroid hormone receptor associated protein 3	Thrap3	NP_666265	108	3	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
ER lipid raft associated 2	Erlin2	NP_705820	38	3	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
hypothetical protein LOC108654	4933403F05 Rik	NP_722489	32	3	integral to membrane, membrane	not classified	not classified
ribosomal protein L32	Rpl32	NP_742083	16	3	cytosolic large ribosomal subunit, intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
GRAM domain containing 1B	Gramd1b	NP_766356	101	3	integral to membrane, membrane	not classified	not classified
PDS5, regulator of cohesion maintenance, homolog B	Pds5b	NP_780519	164	3	cellular_component, nucleus	DNA binding, molecular_function	cell cycle, cell division, mitosis, regulation of cell proliferation
glycerol-3-phosphate dehydrogenase 1-like	Gpd1l	NP_780589	38	3	cytoplasm, glycerol-3-phosphate dehydrogenase complex	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, glycerol-3-phosphate catabolic process, glycerol-3-phosphate metabolic process, oxidation reduction
potassium channel tetramerization domain containing 12	Kctd12	NP_808383	36	3	membrane, voltage-gated potassium channel complex	protein binding, voltage-gated potassium channel activity	potassium ion transport
carbonic anyhydrase 12	Car12	NP_848483	40	3	integral to membrane, membrane	carbonate dehydratase activity, lyase activity, metal ion binding, zinc ion binding	one-carbon metabolic process
golgi-specific brefeldin A-resistance factor 1	Gbf1	NP_849261	207	3	cellular_component	molecular_function, protein binding	biological_process
RAB18, member RAS oncogene family	Rab18	NP_851415	23	3	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
arginyl-tRNA synthetase-like	Rars2	NP_852071	65	3	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, arginine-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding	arginyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hypothetical protein LOC109359	C430003P19Rik	NP_932134	47	3	not classified	not classified	not classified
OPA3 protein	Opa3	NP_997408	20	3	cellular_component, mitochondrion	molecular_function	biological_process
PREDICTED: similar to AFG3(ATPase family gene 3)-like 2 (yeast)	LOC100048880	XP_001472434	33	3	not classified	not classified	not classified
PREDICTED: microtubule-actin crosslinking factor 1	Macf1	XP_001472773	608	3	actin cytoskeleton, cell cortex, cytoplasm, cytoskeleton, microtubule cytoskeleton	actin binding, calcium ion binding, microtubule binding, protein binding	cell cycle arrest, cell motion, establishment or maintenance of cell polarity, mesoderm formation, posttranslational protein targeting to membrane, protein localization, Wnt receptor signaling pathway
PREDICTED: similar to FERMRhoGEF (Arhgef) and pleckstrin domain protein 1	LOC100045542	XP_001473991	119	3	not classified	not classified	not classified
PREDICTED: similar to Eif2s2 protein	LOC100040220	XP_001474301	38	3	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L23a	LOC100046437	XP_001475762	18	3	not classified	not classified	not classified
PREDICTED: similar to Mus musculus ribosomal protein L19	LOC100046041	XP_001475785	23	3	not classified	not classified	not classified
PREDICTED: similar to PH domain leucine-rich repeat-containing protein phosphatase (PH domain leucine-rich repeat protein phosphatase) (Pleckstrin homology domain-containing family E protein 1) (Suprachiasmatic nucleus circadian oscillatory protein)...	Phlpp	XP_001475889	183	3	cytoplasm, membrane, nucleus	catalytic activity, hydrolase activity, manganese ion binding, metal ion binding, phosphoprotein phosphatase activity, protein binding	apoptosis
PREDICTED: similar to Tubulin, beta 4	LOC100042651	XP_001479082	50	3	not classified	not classified	not classified
PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6	LOC631040	XP_909811	13	3	not classified	not classified	not classified
PREDICTED: similar to mKIAA1116 protein isoform 8	Rbm16	XP_923871	139	3	not classified	not classified	not classified
PREDICTED: similar to endothelial monocyte-activating polypeptide	EG665509	XP_988080	11	3	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA 2610301G19 gene	2610301G19Rik	XP_990438	103	3	not classified	not classified	not classified
PREDICTED: similar to zeta proteasome chain; PSMA5	LOC676113	XP_992657	26	3	not classified	not classified	not classified
G protein-coupled receptor 126	Gpr126	NP_001002268	130	2	cell surface, cytoplasm, integral to membrane, membrane, plasma membrane	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
ubiquitin specific peptidase 7	Usp7	NP_001003918	128	2	cytoplasm, nucleus	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process
synaptic nuclear envelope 2	Syne2	NP_001005510	783	2	myofibril, nuclear envelope, Z disc	actin binding, molecular_function	establishment or maintenance of cell polarity, fibroblast migration, nuclear envelope organization, protein localization in nucleus
erythrocyte protein band 4.1-like 1 isoform a	Epb4.1l1	NP_001006665	98	2	cytoplasm, cytoskeleton, extrinsic to membrane	actin binding, binding, cytoskeletal protein binding, protein binding, structural molecule activity	cortical actin cytoskeleton organization
a disintegrin and metalloprotease domain 22 isoform b	Adam22	NP_001007222	91	2	integral to membrane, membrane	metalloendopeptidase activity, metallopeptidase activity, zinc ion binding	proteolysis
unc-13 homolog D	Unc13d	NP_001009573	123	2	not classified	protein binding	defense response to virus, 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
dynein, cytoplasmic 1 light intermediate chain 2	Dync1li2	NP_001013398	54	2	cellular_component, dynein complex, microtubule	ATP binding, molecular_function, motor activity, nucleotide binding	biological_process
UbiE-YGHL1 fusion protein	LOC554292	NP_001019843	30	2	not classified	not classified	not classified
phosphodiesterase 1C isoform b	Pde1c	NP_001020739	72	2	not classified	3',5'-cyclic-nucleotide phosphodiesterase activity, calcium- and calmodulin-regulated 3',5'-cyclic-GMP phosphodiesterase activity, calmodulin binding, calmodulin-dependent cyclic-nucleotide phosphodiesterase activity, catalytic activity, hydrolase activity	response to calcium ion, signal transduction
glutaminase 2 (liver, mitochondrial)	Gls2	NP_001028436	66	2	mitochondrion	glutaminase activity, hydrolase activity	glutamine metabolic process
hypothetical protein LOC226527	BC026585	NP_001028456	38	2	not classified	binding, catalytic activity, oxidoreductase activity, zinc ion binding	metabolic process, oxidation reduction
PDGFA associated protein 1	Pdap1	NP_001028485	21	2	extracellular space	platelet-derived growth factor binding	platelet-derived growth factor receptor signaling pathway
IQ motif containing GTPase activating protein 3	Iqgap3	NP_001028656	185	2	not classified	not classified	not classified
coiled-coil domain containing 139	Pus10	NP_001028826	60	2	not classified	isomerase activity	tRNA processing
ubiquitin protein ligase E3A isoform 3	Ube3a	NP_001029134	98	2	cytoplasm, cytosol, intracellular, nucleus, proteasome complex	acid-amino acid ligase activity, ligase activity, protein binding, transcription coactivator activity, ubiquitin-protein ligase activity	androgen receptor signaling pathway, modification-dependent protein catabolic process, ovarian follicle development, positive regulation of phosphoinositide 3-kinase cascade, positive regulation of transcription from RNA polymerase II promoter, prostate gland growth, protein modification process, protein ubiquitination, sperm entry, ubiquitin-dependent protein catabolic process
hypothetical protein LOC328099	AU021838	NP_001032835	28	2	not classified	not classified	not classified
zinc finger homeobox 2	Zfhx2	NP_001034287	273	2	cellular_component, nucleus	DNA binding, metal ion binding, molecular_function, zinc ion binding	biological_process
hypothetical protein LOC230866 isoform 2	C230096C10Rik	NP_001034289	111	2	integral to membrane, membrane	not classified	not classified
Cd63 antigen	Cd63	NP_001036045	26	2	endosome, endosome membrane, integral to membrane, late endosome, lysosome, membrane, plasma membrane	not classified	not classified
heterogeneous nuclear ribonucleoprotein H3	Hnrnph3	NP_001073293	37	2	not classified	not classified	not classified
thymopoietin isoform delta	Tmpo	NP_001073599	46	2	chromatin, chromosome, integral to membrane, membrane, nuclear envelope, nucleus	DNA binding, protein binding	regulation of transcription
cell division cycle 2-like 5 (cholinesterase-related cell division controller) isoform 1	Cdc2l5	NP_001074527	165	2	not classified	ATP binding, cyclin-dependent protein kinase activity, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
hypothetical protein LOC69885	2610002D18Rik	NP_001074568	38	2	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
kinesin family member 13B	Kif13b	NP_001074646	205	2	microtubule	ATP binding, motor activity, nucleotide binding	not classified
breakpoint cluster region homolog	Bcr	NP_001074881	143	2	intracellular	ATP binding, GTPase activator activity, guanyl-nucleotide exchange factor activity, kinase activity, nucleotide binding, protein serine/threonine kinase activity, Rho guanyl-nucleotide exchange factor activity, transferase activity	brain development, intracellular signaling cascade, protein amino acid phosphorylation, regulation of cell cycle, regulation of Rho protein signal transduction, signal transduction
vomeronasal receptor Vmn2r3	Vmn2r3	NP_001098084	101	2	not classified	not classified	not classified
arsenate resistance protein 2 isoform 3	Ars2	NP_001103380	99	2	cellular_component	molecular_function	not classified
Sjogren syndrome antigen B	Ssb	NP_001103615	48	2	nucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	RNA processing
SPEG complex locus isoform 1	Speg	NP_031489	354	2	nucleus	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cell differentiation, protein amino acid phosphorylation
FXYD domain-containing ion transport regulator 2 isoform a	Fxyd2	NP_031529	8	2	integral to membrane, membrane	ion channel activity, potassium ion binding, sodium ion binding	ion transport, potassium ion transport, sodium ion transport, 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
chaperonin containing Tcp1, subunit 7 (eta)	Cct7	NP_031664	60	2	chaperonin-containing T-complex, cytoplasm	ATP binding, identical protein binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
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
cathepsin H	Ctsh	NP_031827	37	2	lysosome	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis
cortactin	Cttn	NP_031829	61	2	cell cortex, cell projection, cytoplasm, cytoskeleton, lamellipodium, ruffle	protein binding	not classified
Ewing sarcoma breakpoint region 1	Ewsr1	NP_031994	68	2	cytoplasm, intracellular, membrane, nucleus, plasma membrane	calmodulin binding, metal ion binding, nucleic acid binding, nucleotide binding, RNA binding, zinc ion binding	regulation of transcription, transcription
frataxin	Fxn	NP_032070	23	2	mitochondrion	not classified	adult walking behavior, aerobic respiration, cellular iron ion homeostasis, embryonic development ending in birth or egg hatching, iron-sulfur cluster assembly, mitochondrion organization, negative regulation of multicellular organism growth, negative regulation of organ growth, oxidative phosphorylation, proprioception

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
insulin-like growth factor binding protein 7	Igfbp7	NP_032074	29	2	extracellular region	growth factor binding, insulin-like growth factor binding, protein binding	cell adhesion, regulation of cell growth
myotrophin	Mtpn	NP_032124	13	2	cytoplasm	not classified	not classified
gamma-glutamyltransferase 1	Ggt1	NP_032142	62	2	integral to membrane, integral to plasma membrane, membrane	acyltransferase activity, gamma-glutamyltransferase activity, transferase activity	glutathione biosynthetic process, glutathione metabolic process, spermatogenesis
guanine nucleotide binding protein, alpha q polypeptide	Gnaq	NP_032165	42	2	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
guanine nucleotide-binding protein, beta-1 subunit	Gnb1	NP_032168	37	2	heterotrimeric G-protein complex, photoreceptor outer segment	GTPase activity, signal transducer activity	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger, cell proliferation, G-protein coupled receptor protein signaling pathway, phototransduction, visible light, sensory perception of taste, signal transduction
glutathione peroxidase 4 isoform 2 precursor	Gpx4	NP_032188	22	2	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
histone deacetylase 1	Hdac1	NP_032254	55	2	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
3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	NP_032280	34	2	mitochondrial inner membrane, mitochondrion	catalytic activity, hydroxymethylglutaryl-CoA lyase activity, lyase activity, metal ion binding	metabolic process
homeobox A4	Hoxa4	NP_032291	30	2	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
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
intergral membrane protein 1	Stt3a	NP_032434	81	2	endoplasmic reticulum, integral to membrane, membrane, membrane fraction	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, oligosaccharyl transferase activity, transferase activity	protein amino acid glycosylation
laminin, gamma 2	Lamc2	NP_032511	130	2	basement membrane, extracellular matrix, extracellular region, proteinaceous extracellular matrix	heparin binding, protein binding	cell adhesion
leukotriene C4 synthase	Ltc4s	NP_032547	17	2	endoplasmic reticulum, integral to membrane, membrane, nucleus	enzyme activator activity, leukotriene-C4 synthase activity, lipid binding, lyase activity	leukotriene biosynthetic process, leukotriene metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
nucleophosmin 1	Npm1	NP_032748	33	2	centrosome, cytoplasm, cytosol, granular component, large ribosomal subunit, nuclear speck, nucleolus, nucleoplasm, nucleus, ribonucleoprotein complex, small ribosomal subunit	DNA binding, nucleic acid binding, protein binding, ribosomal large subunit binding, ribosomal small subunit binding, RNA binding, rRNA binding	cell growth, cell volume homeostasis, negative regulation of nuclear mRNA splicing, via spliceosome, nucleocytoplasmic transport, positive regulation of cell proliferation, positive regulation of cellular biosynthetic process, positive regulation of centrosome duplication, positive regulation of protein kinase activity, protein localization, protein oligomerization, regulation of cell cycle, regulation of centrosome duplication, regulation of DNA damage response, signal transduction by p53 class mediator, ribosomal large subunit biogenesis, ribosomal large subunit export from nucleus, ribosomal small subunit biogenesis, ribosomal small subunit export from nucleus, rRNA export from nucleus
platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	NP_032801	26	2	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
protein kinase, cGMP-dependent, type II	Prkg2	NP_032952	87	2	not classified	ATP binding, cGMP binding, cGMP-dependent protein kinase activity, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
RAD21 homolog	Rad21	NP_033035	72	2	nuclear chromosome, nucleus	calcium ion binding	apoptosis, cell cycle, cell division, chromosome segregation, DNA repair, mitosis, response to DNA damage stimulus
ribosomal protein S4, X-linked	Rps4x	NP_033120	30	2	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, rRNA binding, structural constituent of ribosome	translation
neuroplastin	Nptn	NP_033171	31	2	integral to membrane, membrane, plasma membrane	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
stimulated by retinoic acid gene 8	Stra8	NP_033318	45	2	cytoplasm	not classified	DNA replication, female meiosis sister chromatid cohesion, fertilization, meiosis, meiotic cell cycle DNA replication checkpoint, meiotic chromosome condensation, meiotic DNA double-strand break formation, oocyte development, ovarian follicle development, reciprocal meiotic recombination, regulation of organ growth, spermatogenesis, synapsis
topoisomerase (DNA) II beta	Top2b	NP_033435	182	2	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
ubiquitin-conjugating enzyme E2L 3	Ube2l3	NP_033482	18	2	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, regulation of protein metabolic process
uromodulin	Umod	NP_033496	71	2	anchored to membrane, apical plasma membrane, extracellular region, membrane, plasma membrane	calcium ion binding	not classified
ubiquitin specific protease 9, X chromosome	Usp9x	NP_033507	290	2	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
viral oncogene yes homolog	Yes1	NP_033561	61	2	cytoplasm	ATP binding, kinase activity, non-membrane spanning protein tyrosine kinase activity, nucleotide binding, protein binding, protein kinase activity, protein tyrosine kinase activity, transferase activity	glucose transport, protein amino acid phosphorylation
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	Adamts1	NP_033751	106	2	basement membrane, cytoplasmic vesicle, extracellular matrix, extracellular region, proteinaceous extracellular matrix	heparin binding, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, protein binding, zinc ion binding	heart trabecula formation, kidney development, negative regulation of angiogenesis, ovulation from ovarian follicle, proteolysis
calpain, small subunit 1	Capns1	NP_033925	28	2	cytoplasm, membrane, plasma membrane	calcium ion binding, calcium-dependent cysteine-type endopeptidase activity	not classified
capping protein (actin filament) muscle Z-line, beta isoform b	Capzb	NP_033928	31	2	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cytochrome c oxidase, subunit VIIa 1	Cox7a1	NP_034074	9	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial respiratory chain, mitochondrion	cytochrome-c oxidase activity, electron carrier activity	not classified
DNA methyltransferase (cytosine-5) 1	Dnmt1	NP_034196	183	2	centromeric heterochromatin, cytoplasm, heterochromatin, nucleus, replication fork	DNA (cytosine-5-)-methyltransferase activity, DNA binding, metal ion binding, methyltransferase activity, protein binding, transcription factor binding, transcription repressor activity, transferase activity, zinc ion binding	DNA methylation, gene silencing, maintenance of DNA methylation, negative regulation of transcription, DNA-dependent, regulation of cell proliferation, regulation of gene expression, regulation of transcription, transcription
epidermal growth factor	Egf	NP_034243	133	2	extracellular region, extracellular space, integral to membrane, membrane, plasma membrane	calcium ion binding, epidermal growth factor receptor binding, growth factor activity	activation of MAPKK activity, branching morphogenesis of a tube, epidermal growth factor receptor signaling pathway, mammary gland alveolus development, peptidyl-tyrosine phosphorylation, positive regulation of cell proliferation, positive regulation of granule cell precursor proliferation, regulation of peptidyl-tyrosine phosphorylation
flavin containing monooxygenase 1	Fmo1	NP_034361	60	2	endoplasmic reticulum, integral to membrane, intrinsic to endoplasmic reticulum membrane, membrane, microsome	FAD binding, flavin-containing monooxygenase activity, monooxygenase activity, NADP or NADPH binding, oxidoreductase activity	oxidation reduction
glutathione S-transferase, alpha 4	Gsta4	NP_034487	26	2	cellular_component, cytoplasm	glutathione transferase activity, transferase activity	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
heterogeneous nuclear ribonucleoprotein A/B isoform 2	Hnrnpab	NP_034578	31	2	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
laminin, gamma 1	Lamc1	NP_034813	177	2	basal lamina, basement membrane, extracellular matrix, extracellular region, laminin-10 complex, proteinaceous extracellular matrix	protein binding	cell adhesion
myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog	Mllt4	NP_034936	206	2	adherens junction, cell junction, cell-cell adherens junction, cytoplasm	cell adhesion molecule binding, protein binding	cell adhesion, signal transduction
mitochondrial ribosomal protein L40	Mrpl40	NP_035052	24	2	mitochondrion, ribonucleoprotein complex, ribosome	molecular_function	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	NP_035174	69	2	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
phosphoprotein enriched in astrocytes 15 isoform 2	Pea15a	NP_035193	15	2	cytoplasm, membrane fraction, microtubule associated complex	protein binding, protein kinase C binding	apoptosis, carbohydrate transport, intracellular signaling cascade, regulation of apoptosis, transport
signal-induced proliferation associated gene 1	Sipa1	NP_035509	112	2	intracellular, nucleus	GTPase activator activity, protein binding	regulation of cell cycle, regulation of small GTPase mediated signal transduction
superoxide dismutase 3, extracellular	Sod3	NP_035565	27	2	extracellular region, extracellular space, trans-Golgi network	antioxidant activity, copper ion binding, metal ion binding, oxidoreductase activity, protein binding, superoxide dismutase activity, zinc ion binding	oxidation reduction, response to hypoxia, superoxide metabolic process
timeless homolog	Timeless	NP_035719	138	2	nucleus	protein binding, protein heterodimerization activity, protein homodimerization activity	branching involved in ureteric bud morphogenesis, branching morphogenesis of a tube, cell cycle, cell division, circadian rhythm, embryonic development, lung development, mitosis, morphogenesis of an epithelium, multicellular organismal development, negative regulation of gene-specific transcription from RNA polymerase II promoter, regulation of transcription, response to DNA damage stimulus, rhythmic process, transcription
tight junction protein 2	Tjp2	NP_035727	131	2	cell junction, gap junction, membrane, nucleus, plasma membrane, tight junction	protein binding	not classified
translin	Tsn	NP_035780	26	2	cytoplasm, nucleus	DNA binding, mRNA binding, protein binding, RNA binding, sequence-specific DNA binding	not classified
lin 7 homolog c	Lin7c	NP_035829	22	2	cell junction, membrane, plasma membrane, postsynaptic membrane, synapse, synaptosome, tight junction	protein binding	exocytosis, neurotransmitter secretion, protein transport, transport
tryptophanyl-tRNA synthetase	Wars	NP_035840	54	2	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, tryptophan-tRNA ligase activity	translation, tRNA aminoacylation for protein translation, tryptophanyl-tRNA aminoacylation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
G protein-coupled receptor 34	Gpr34	NP_035953	43	2	integral to membrane, membrane, plasma membrane	G-protein coupled receptor activity, purinergic nucleotide receptor activity, G-protein coupled, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
HCLS1 associated X-1	Hax1	NP_035956	32	2	endoplasmic reticulum, membrane, mitochondrion, nucleus	protein binding	cell surface receptor linked signal transduction
membrane bound C2 domain containing protein	Mbc2	NP_035973	122	2	integral to membrane, membrane	not classified	not classified
poly(rC) binding protein 1	Pcbp1	NP_035995	37	2	nucleus, ribonucleoprotein complex	DNA binding, protein binding, RNA binding, translation activator activity	mRNA processing
evolutionarily conserved signaling intermediate in Toll pathway	Ecsit	NP_036159	50	2	cytoplasm, mitochondrion, nucleus, transcription factor complex	protein binding, RNA polymerase II transcription factor activity, signal transducer activity, transcription factor activity	BMP signaling pathway, immune response, innate immune response, mesoderm formation, regulation of transcription from RNA polymerase II promoter, transmembrane receptor protein serine/threonine kinase signaling pathway
nitrilase 1	Nit1	NP_036179	36	2	cellular_component	hydrolase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	nitrogen compound metabolic process
ATP-binding cassette 1, sub-family A, member 1	Abca1	NP_038482	254	2	Golgi apparatus, integral to membrane, integral to plasma membrane, intracellular membrane-bounded organelle, membrane, plasma membrane	anion transmembrane transporter activity, ATP binding, ATPase activity, cholesterol transporter activity, nucleoside-triphosphatase activity, nucleotide binding, phospholipid transporter activity, protein binding	cholesterol efflux, cholesterol metabolic process, cholesterol transport, lipoprotein biosynthetic process, lipoprotein metabolic process, peptide secretion, phagocytosis, engulfment, phospholipid efflux, phospholipid translocation, protein amino acid lipidation, reverse cholesterol transport, transport
synaptotagmin-like 4	Sytl4	NP_038785	76	2	cytoplasmic vesicle, extrinsic to membrane, membrane, secretory granule	metal ion binding, neurexin binding, phospholipid binding, protein binding, Rab GTPase binding, zinc ion binding	exocytosis, intracellular protein transport
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	Atp5l	NP_038823	11	2	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
klotho	Kl	NP_038851	116	2	extracellular region, integral to membrane, membrane, plasma membrane	beta-glucuronidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds, protein binding	aging, carbohydrate metabolic process, energy reserve metabolic process, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
TROVE domain family, member 2	Trove2	NP_038863	60	2	cytoplasm, ribonucleoprotein complex	nucleic acid binding, protein binding, RNA binding	not classified
glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	NP_038875	45	2	mitochondrial inner membrane, mitochondrion	acyltransferase activity, catalytic activity, glycine C-acetyltransferase activity, pyridoxal phosphate binding, transferase activity, transferase activity, transferring nitrogenous groups	biosynthetic process, metabolic 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
ATPas, class II, type 9B	Atp9b	NP_056620	128	2	integral to membrane, membrane	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, nucleotide binding, phospholipid-translocating ATPase activity, receptor activity	ATP biosynthetic process, metabolic process, phospholipid transport
S-adenosylhomocysteine hydrolase	Ahcy	NP_057870	48	2	cytoplasm, cytosol	adenosylhomocysteinase activity, copper ion binding, hydrolase activity, protein self-association	one-carbon metabolic process, S-adenosylhomocysteine catabolic process
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
vesicle-associated membrane protein 8	Vamp8	NP_058074	11	2	early endosome, integral to membrane, membrane	protein binding	vesicle-mediated transport
squamous cell carcinoma antigen recognized by T-cells 3	Sart3	NP_058622	110	2	cytoplasm, intracellular, nucleus	nucleic acid binding, nucleotide binding, RNA binding	RNA processing
osteoclast stimulating factor 1	Ostf1	NP_059071	24	2	cellular_component, cytoplasm	protein binding	not classified
solute carrier family 5 (inositol transporters), member 3	Slc5a3	NP_059087	80	2	integral to membrane, membrane	sodium ion binding, symporter activity, transporter activity	inositol metabolic process, ion transport, myo-inositol transport, peripheral nervous system development, regulation of respiratory gaseous exchange, sodium ion transport, transport
sorting nexin 3	Snx3	NP_059500	19	2	cellular_component	molecular_function, phosphoinositide binding, protein binding	biological_process, cell communication, protein transport, transport

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
eukaryotic translation initiation factor 3, subunit 7 (zeta)	Eif3d	NP_061219	64	2	cytoplasm, eukaryotic translation initiation factor 3 complex	translation initiation factor activity	formation of translation initiation complex, translation, translational initiation
solute carrier family 4 (anion exchanger), member 4	Slc4a4	NP_061230	121	2	integral to membrane, integral to plasma membrane, membrane, plasma membrane	anion exchanger activity, anion transmembrane transporter activity, inorganic anion exchanger activity, sodium ion binding, sodium:bicarbonate symporter activity, symporter activity	anion transport, bicarbonate transport, ion transport, regulation of pH, sodium ion transport, transport
claudin 8	Cldn8	NP_061248	25	2	cell junction, integral to membrane, membrane, plasma membrane, tight junction	structural molecule activity	not classified
formin binding protein 3	Prpf40a	NP_061255	108	2	nucleus	protein binding	mRNA processing, RNA splicing
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
eukaryotic translation initiation factor 3, subunit I	Eif3i	NP_061269	36	2	cellular_component, cytoplasm, eukaryotic translation initiation factor 3 complex	molecular_function, translation initiation factor activity	biological_process, translation, translational initiation
aldo-keto reductase family 1, member E1	Akr1e1	NP_061347	34	2	cytoplasm	1,5-anhydro-D-fructose reductase activity, oxidoreductase activity	oxidation reduction
nucleolar protein 5	Nol5	NP_061356	60	2	nucleolus, nucleus	snoRNP binding	ribosome biogenesis
fructose bisphosphatase 1	Fbp1	NP_062268	37	2	not classified	fructose 1,6-bisphosphate 1-phosphatase activity, hydrolase activity, magnesium ion binding, metal ion binding, phosphoric ester hydrolase activity	carbohydrate metabolic process, gluconeogenesis
glucosamine-phosphate N-acetyltransferase 1	Gnpnat1	NP_062298	21	2	endosome, ER-Golgi intermediate compartment, Golgi apparatus, late endosome, membrane	acyltransferase activity, glucosamine 6-phosphate N-acetyltransferase activity, N-acetyltransferase activity, transferase activity	metabolic process, UDP-N-acetylglucosamine biosynthetic process
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	Ndufa1	NP_062316	8	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
polypyrimidine tract binding protein 2	Ptbp2	NP_062423	58	2	nucleus, spliceosomal complex	mRNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, mRNA splice site selection, RNA splicing
methionine aminopeptidase 2	Metap2	NP_062622	53	2	not classified	aminopeptidase activity, cobalt ion binding, hydrolase activity, metal ion binding, metalloexopeptidase activity, peptidase activity, protein binding	cellular process, proteolysis
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
HLA-B-associated transcript 1A	Bat1a	NP_062667	49	2	nucleus, spliceosomal complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
SMC1 structural maintenance of chromosomes 1-like 1	Smc1a	NP_062684	143	2	chromosome, nucleus	ATP binding, nucleotide binding, protein binding	cell cycle, cell division, chromosome organization, DNA repair, meiosis, mitosis, response to DNA damage stimulus
APAF1 interacting protein	Apip	NP_062709	27	2	cellular_component, cytoplasm	metal ion binding, molecular_function, zinc ion binding	apoptosis, negative regulation of apoptosis
adhesion regulating molecule 1	Adrm1	NP_062796	42	2	cytoplasm, nucleus, proteasome complex	not classified	not classified
X-linked myotubular myopathy gene 1	Mtm1	NP_064310	70	2	not classified	hydrolase activity, phosphatase activity, phosphoprotein phosphatase activity, protein tyrosine phosphatase activity	dephosphorylation, muscle maintenance
keratin 71	Krt71	NP_064340	57	2	intermediate filament, keratin filament	structural constituent of cytoskeleton, structural molecule activity	cytoskeleton organization, hair follicle morphogenesis
histone cell cycle regulation defective interacting protein 5	Nfu1	NP_064429	22	2	cytoplasm, cytosol, mitochondrion	iron ion binding, iron-sulfur cluster binding, protein binding	biological_process, iron-sulfur cluster assembly
U2 small nuclear ribonucleoprotein B	Snrpb2	NP_067310	25	2	cellular_component, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, protein binding, RNA binding	biological_process, mRNA processing, RNA splicing
protein phosphatase 1, regulatory (inhibitor) subunit 1A	Ppp1r1a	NP_067366	19	2	not classified	phosphoprotein phosphatase inhibitor activity, protein binding	carbohydrate metabolic process, glycogen metabolic process, signal transduction
carboxylesterase 1	Ces1	NP_067431	63	2	endoplasmic reticulum	carboxylesterase activity, hydrolase activity	not classified
heterogeneous nuclear ribonucleoprotein H1	Hnrnph1	NP_067485	49	2	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
nicastrin	Ncstn	NP_067620	78	2	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane, membrane fraction, plasma membrane	protein binding	Notch signaling pathway, protein processing
protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	NP_068680	43	2	cAMP-dependent protein kinase complex, cytoplasm, neuromuscular junction	cAMP binding, cAMP-dependent protein kinase regulator activity, kinase activity, nucleotide binding, protein binding	cell proliferation, mesoderm formation, organ morphogenesis, protein amino acid phosphorylation, regulation of protein amino acid phosphorylation, signal transduction
acyl-CoA thioesterase 10	Acot10	NP_073727	51	2	mitochondrion	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity	acyl-CoA metabolic process
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
mitochondrial ribosomal protein S34	Mrps34	NP_075749	26	2	cellular_component, mitochondrion, ribonucleoprotein complex, ribosome	molecular_function	biological_process
mitochondrial ribosomal protein L46	Mrpl46	NP_075820	32	2	mitochondrion, ribonucleoprotein complex, ribosome	not classified	not classified
elaC homolog 2	Elac2	NP_075968	93	2	nucleus	endonuclease activity, hydrolase activity, metal ion binding, nuclease activity, zinc ion binding	tRNA processing

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
seryl-aminoacyl-tRNA synthetase 2	Sars2	NP_076126	58	2	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, serine-tRNA ligase activity	seryl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
carnitine O-octanoyltransferase	Crot	NP_076222	70	2	peroxisome	acyltransferase activity, carnitine O-octanoyltransferase activity, transferase activity	fatty acid metabolic process, fatty acid transport, lipid metabolic process, transport
toll interacting protein	Tollip	NP_076253	30	2	cytoplasm	protein binding	immune response, inflammatory response
coiled-coil-helix-coiled-coil-helix domain containing 2	Chchd2	NP_077128	16	2	mitochondrion	molecular_function	biological_process
mitochondrial ribosomal protein S23	Mrps23	NP_077136	20	2	mitochondrial small ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	not classified
ribosomal protein S23	Rps23	NP_077137	16	2	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	structural constituent of ribosome	translation
hypothetical protein LOC76916	4930455C21Rik	NP_077235	32	2	integral to membrane, membrane	not classified	not classified
aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	Akr7a5	NP_079613	41	2	Golgi apparatus, mitochondrion	oxidoreductase activity	oxidation reduction
ATPase, H+ transporting, lysosomal V1 subunit F	Atp6v1f	NP_079657	13	2	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
acylphosphatase 1, erythrocyte (common) type	Acyp1	NP_079697	11	2	not classified	acylphosphatase activity, hydrolase activity	not classified
serologically defined colon cancer antigen 1	Sdccag1	NP_079717	121	2	nucleus	not classified	not classified
mitochondrial ribosomal protein S15	Mrps15	NP_079820	29	2	intracellular, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
nipsnap homolog 3A	Nipsnap3a	NP_079899	28	2	cytoplasm, mitochondrion	not classified	not classified
ubiquinol-cytochrome c reductase subunit	Uqcr	NP_079926	7	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial membrane, mitochondrion, respiratory chain	electron carrier activity, ubiquinol-cytochrome-c reductase activity	biological_process, electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, transport
tetratricopeptide repeat domain 35	Ttc35	NP_080012	35	2	nucleus	binding	not classified
mannose-6-phosphate receptor binding protein 1	M6prbp1	NP_080112	47	2	cytoplasm, endosome, lipid particle, membrane	not classified	transport
CDGSH iron sulfur domain 2	Cisd2	NP_080178	15	2	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
mitochondrial ribosomal protein L10	Mrpl10	NP_080430	29	2	mitochondrial large ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	ribosome biogenesis
all-trans-13,14-dihydroretinol saturase	Retsat	NP_080435	67	2	endoplasmic reticulum, endoplasmic reticulum membrane, membrane, nuclear outer membrane	all-trans-retinol 13,14-reductase activity, electron carrier activity, oxidoreductase activity	oxidation reduction, retinol metabolic process
solute carrier family 25, member 46	Slc25a46	NP_080441	46	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
transcription elongation factor B (SIII), polypeptide 2	Tceb2	NP_080581	13	2	nucleus	protein binding	modification-dependent protein catabolic process, regulation of transcription, transcription
methionine sulfoxide reductase A	Msra	NP_080598	26	2	cellular_component	oxidoreductase activity, oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor, peptide-methionine-(S)-S-oxide reductase activity	oxidation reduction, protein metabolic process
U2-associated SR140 protein	2610101N10 Rik	NP_080752	113	2	not classified	nucleic acid binding, nucleotide binding, RNA binding	RNA processing
thioredoxin domain containing 17	Txndc17	NP_080835	14	2	cellular_component, cytoplasm	not classified	biological_process, cell redox homeostasis
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	Ndufb2	NP_080888	12	2	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
TOE1 homolog	Toe1	NP_080930	57	2	nucleus	metal ion binding, nucleic acid binding, zinc ion binding	not classified
phosphoribosyl pyrophosphate synthetase 2	Prps2	NP_080938	35	2	not classified	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, ribose phosphate diphosphokinase activity, transferase activity	cellular biosynthetic process, nucleoside metabolic process, nucleotide biosynthetic process, ribonucleoside monophosphate biosynthetic process
vacuolar protein sorting 53	Vps53	NP_080940	94	2	endosome, Golgi apparatus, membrane	not classified	protein transport, transport
biliverdin reductase A	Blvra	NP_080954	34	2	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
RIKEN cDNA 1110007C09	1110007C09 Rik	NP_081014	21	2	intracellular, nucleus	protein binding	regulation of apoptosis
RIKEN cDNA 1110007M04	1110007M04 Rik	NP_081018	20	2	mitochondrion	calmodulin binding	not classified
Ssu72 RNA polymerase II CTD phosphatase homolog	Ssu72	NP_081175	23	2	cytoplasm, nucleus	hydrolase activity, phosphoprotein phosphatase activity	mRNA processing
hypothetical protein LOC69064	1810014F10 Rik	NP_081204	17	2	not classified	fucose binding	carbohydrate transport
OCIA domain containing 2	Ociad2	NP_081226	17	2	endosome, mitochondrial inner membrane, mitochondrion	not classified	not classified
hypothetical protein LOC69186	1810027O10 Rik	NP_081258	12	2	integral to membrane, membrane, mitochondrial inner membrane	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
glyoxalase domain containing 5	Glod5	NP_081503	17	2	not classified	not classified	not classified
transcription factor MEL1	Prdm16	NP_081780	141	2	nucleus, transcriptional repressor complex	sequence-specific DNA binding, SMAD binding, transcription coactivator activity, transcription repressor activity	brown fat cell differentiation, neurogenesis, regulation of cellular respiration, white fat cell differentiation
D-lactate dehydrogenase	Ldhd	NP_081846	52	2	mitochondrion	catalytic activity, D-lactate dehydrogenase (cytochrome) activity, D-lactate dehydrogenase activity, FAD binding, oxidoreductase activity, protein binding	ATP biosynthetic process, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
threonine aldolase 1	Tha1	NP_082195	21	2	cellular_component	not classified	biological_process
Mak3p homolog	Nat13	NP_082384	19	2	cytoplasm	acyltransferase activity, N-acetyltransferase activity, protein binding, transferase activity	metabolic process, N-terminal protein amino acid acetylation
furry homolog-like isoform 1	Fryl	NP_082470	338	2	cellular_component	protein binding	biological_process
phosphoglucomutase 3	Pgm3	NP_082628	59	2	not classified	intramolecular transferase activity, phosphotransferases, isomerase activity, magnesium ion binding, metal ion binding, phosphoacetylglucosamine mutase activity, phosphoglucomutase activity	carbohydrate metabolic process, embryonic development, glucose 1-phosphate metabolic process, hemopoiesis, spermatogenesis, UDP-N-acetylglucosamine biosynthetic process
glutaredoxin 5	Glrx5	NP_082695	16	2	mitochondrion	electron carrier activity, protein disulfide oxidoreductase activity	cell redox homeostasis
transmembrane 9 superfamily member 1	Tm9sf1	NP_083056	69	2	integral to membrane, membrane	not classified	not classified
raptor	4932417H02 Rik	NP_083174	149	2	TORC1 complex	binding, protein binding	not classified
HEAT-like repeat-containing protein	8430415E04 Rik	NP_083256	99	2	cytoplasm	binding	not classified
mitochondrial phosphoenolpyruvate carboxykinase 2	Pck2	NP_083270	73	2	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
proline-, glutamic acid-, leucine-rich protein 1	Pelp1	NP_083507	118	2	cytoplasm, nucleus	not classified	transcription
phosphohistidine phosphatase	Phpt1	NP_083569	14	2	cytoplasm	hydrolase activity, phosphoprotein phosphatase activity	not classified
phosphoribosyl pyrophosphate synthetase 1-like 1	Prps1l1	NP_083570	35	2	not classified	kinase activity, magnesium ion binding, metal ion binding, ribose phosphate diphosphokinase activity	nucleotide biosynthetic process
signal peptidase complex subunit 3	Spcs3	NP_083977	20	2	not classified	not classified	not classified
dynein cytoplasmic 2 heavy chain 1	Dync2h1	NP_084127	492	2	cell projection, cilium, cytoplasm, dynein complex, membrane, microtubule, plasma membrane	ATP binding, ATPase activity, microtubule motor activity, motor activity, nucleoside-triphosphatase activity, nucleotide binding	asymmetric protein localization, cell projection organization, cilium assembly, determination of left/right symmetry, dorsal/ventral pattern formation, embryonic limb morphogenesis, forebrain development, microtubule-based movement, multicellular organismal development, protein processing
aldo-keto reductase family 1, member C21	Akr1c21	NP_084177	37	2	cellular_component, cytoplasm	aldo-keto reductase activity, oxidoreductase activity	lipid metabolic process, oxidation reduction, steroid biosynthetic process, steroid metabolic process
apurinic/apyrimidinic endonuclease 2	Apex2	NP_084219	57	2	intracellular, mitochondrial inner membrane, mitochondrion, nucleus	DNA binding, DNA-(apurinic or apyrimidinic site) lyase activity, endonuclease activity, lyase activity, nuclease activity, zinc ion binding	DNA repair, response to DNA damage stimulus
coiled-coil domain containing 93 isoform c	Ccdc93	NP_084231	72	2	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
crystallin, lambda 1	Cryl1	NP_084280	35	2	not classified	binding, catalytic activity, L-gulonate 3-dehydrogenase activity, oxidoreductase activity	fatty acid metabolic process, metabolic process, oxidation reduction
neurobeachin	Nbea	NP_085098	327	2	cell junction, cytosol, endomembrane system, membrane, plasma membrane, postsynaptic membrane, synapse, trans-Golgi network	protein kinase A binding, protein kinase binding	post-Golgi vesicle-mediated transport, protein localization, protein targeting
ankycorbin	Rai14	NP_109615	109	2	cytoplasm, cytoskeleton, mitochondrion	not classified	not classified
endoplasmic reticulum aminopeptidase 1	Erap1	NP_109636	107	2	cytoplasm, endoplasmic reticulum, integral to membrane, membrane	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, receptor activity, zinc ion binding	immune response, positive regulation of angiogenesis, proteolysis
insulin degrading enzyme	Ide	NP_112419	118	2	cytoplasm	ATP binding, catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, nucleotide binding, peptidase activity, zinc ion binding	proteolysis
testis specific gene A14	Tsga14	NP_114387	41	2	not classified	not classified	not classified
D-glucuronyl C5-epimerase	Glce	NP_201577	70	2	Golgi apparatus, integral to membrane, membrane	isomerase activity, racemase and epimerase activity, acting on carbohydrates and derivatives, UDP-glucuronate 5'-epimerase activity	glycosaminoglycan biosynthetic process, heparan sulfate proteoglycan biosynthetic process, heparin biosynthetic process
AF4/FMR2 family, member 4	Aff4	NP_291043	127	2	nucleus	molecular_function	regulation of transcription, spermatid development, transcription
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
dehydrogenase/reductase (SDR family) member 8	Hsd17b11	NP_444492	33	2	cytoplasm, extracellular region	binding, catalytic activity, estradiol 17-beta-dehydrogenase activity, oxidoreductase activity	lipid biosynthetic process, metabolic process, oxidation reduction, steroid biosynthetic process
PRKC, apoptosis, WT1, regulator	Pawr	NP_473397	36	2	cytoplasm, nucleus	protein binding	apoptosis, interleukin-2 biosynthetic process, negative regulation of B cell proliferation, negative regulation of T cell proliferation, negative regulation of T cell receptor signaling pathway, positive regulation of amyloid precursor protein biosynthetic process, regulation of transcription, transcription
proline synthetase co-transcribed isoform a	Prosc	NP_473398	30	2	cellular_component	molecular_function	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
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
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
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
nucleoporin 155	Nup155	NP_573490	155	2	membrane, nuclear pore, nucleus	structural constituent of nuclear pore	mRNA transport, nucleocytoplasmic transport, protein transport, transmembrane transport, transport
RNA binding motif protein 39	Rbm39	NP_573505	59	2	nucleus	nucleic acid binding, nucleotide binding, protein binding, RNA binding, transcription coactivator activity	mRNA processing, regulation of transcription, RNA splicing, transcription
leucine rich repeat containing 59	Lrrc59	NP_598568	35	2	endoplasmic reticulum, integral to membrane, membrane, microsome	protein binding	not classified
dystonin isoform a	Dst	NP_598594	615	2	actin cytoskeleton, cytoplasm, cytoplasmic membrane-bounded vesicle, cytoskeleton, hemidesmosome, microtubule cytoskeleton, neurofilament cytoskeleton	actin binding, calcium ion binding, microtubule binding, protein binding	axonogenesis, cell adhesion, cell cycle arrest, cytoplasmic microtubule organization, regulation of microtubule polymerization or depolymerization, retrograde axon cargo transport
hypothetical protein LOC75007	4930504E06 Rik	NP_598619	50	2	cellular_component	molecular_function	biological_process
syntaxin 12	Stx12	NP_598648	31	2	Golgi apparatus, integral to membrane, membrane	protein binding, SNAP receptor activity	intracellular protein transport, protein transport, transport
nicalin homolog	Ncln	NP_598770	63	2	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
pelota homolog	Pelo	NP_598819	43	2	cellular_component, cytoplasm, nucleus	endonuclease activity, hydrolase activity, metal ion binding, molecular_function, nuclease activity	cell cycle, cell division, cell proliferation, chromosome organization, translation
adenosine kinase	Adk	NP_598840	40	2	cytosol, nucleus	adenosine kinase activity, ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, transferase activity	dATP biosynthetic process, purine ribonucleoside salvage
peptidylprolyl isomerase F	Ppif	NP_598845	22	2	mitochondrion	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity	protein folding
tyrosyl-tRNA synthetase	Yars	NP_598912	59	2	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, RNA binding, tRNA binding, tyrosine-tRNA ligase activity	translation, tRNA aminoacylation for protein translation, tyrosyl-tRNA aminoacylation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
pyrroline-5-carboxylate reductase 1	Pycr1	NP_659044	32	2	mitochondrion	binding, catalytic activity, oxidoreductase activity, pyrroline-5-carboxylate reductase activity	cellular amino acid biosynthetic process, metabolic process, oxidation reduction, proline biosynthetic process
TAO kinase 1	Taok1	NP_659074	116	2	cytoplasm	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	NP_659088	22	2	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, regulation of protein metabolic process
COX15 homolog	Cox15	NP_659123	46	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	molecular_function	protein complex assembly
acyl-CoA synthetase family member 3	Acsf3	NP_659181	65	2	mitochondrion	ATP binding, catalytic activity, ligase activity, nucleotide binding	fatty acid metabolic process, lipid metabolic process, metabolic process
abhydrolase domain containing 11	Abhd11	NP_660250	34	2	cellular_component	catalytic activity, hydrolase activity	biological_process
thioredoxin domain containing 5	Txndc5	NP_663342	46	2	endoplasmic reticulum, endoplasmic reticulum lumen	isomerase activity	cell redox homeostasis
S-adenosylhomocysteine hydrolase-like 1	Ahcyl1	NP_663517	59	2	cellular_component, endoplasmic reticulum	adenosylhomocysteinase activity, hydrolase activity	one-carbon metabolic process
ubiquitin-conjugating enzyme E2M	Ube2m	NP_663553	21	2	not classified	acid-amino acid ligase activity, ATP binding, ligase activity, nucleotide binding, small conjugating protein ligase activity	modification-dependent protein catabolic process, post-translational protein modification, protein modification process, regulation of protein metabolic process
pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	NP_663605	48	2	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
TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf6l	NP_666204	67	2	nucleus	DNA binding, RNA polymerase II transcription factor activity, transcription initiation factor activity	regulation of transcription, regulation of transcription factor activity, transcription, transcription initiation
ARP1 actin-related protein 1 homolog B	Actr1b	NP_666219	42	2	cytoplasm, cytoskeleton	ATP binding, nucleotide binding, protein binding	not classified
Rho GTPase activating protein 1	Arhgap1	NP_666236	50	2	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
alanyl-tRNA synthetase	Aars	NP_666329	107	2	cellular_component, cytoplasm	alanine-tRNA ligase activity, aminoacyl-tRNA ligase activity, ATP binding, ligase activity, ligase activity, forming aminoacyl-tRNA and related compounds, nucleic acid binding, nucleotide binding	alanyl-tRNA aminoacylation, cellular response to unfolded protein, cerebellar Purkinje cell layer development, endoplasmic reticulum unfolded protein response, hair follicle development, negative regulation of neuron apoptosis, neuromuscular process, neuromuscular process controlling balance, protein folding, response to amino acid stimulus, skin development, translation, tRNA aminoacylation, tRNA modification
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
isoleucyl-tRNA synthetase	Iars	NP_742012	144	2	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
Parkinson disease 7 domain containing 1	Pddc1	NP_742114	23	2	extracellular region	not classified	not classified
ciliary rootlet coiled-coil, rootletin	Crocc	NP_742120	227	2	centriole, ciliary rootlet	kinesin binding, structural molecule activity	cell cycle, cell projection organization
coenzyme Q6 homolog	Coq6	NP_766170	51	2	not classified	FAD binding, monooxygenase activity, oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	metabolic process, oxidation reduction, ubiquinone biosynthetic process
pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	NP_766253	49	2	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 finger, C3HC type 1	Zc3hc1	NP_766323	53	2	nucleus	metal ion binding, protein binding, zinc ion binding	anti-apoptosis, cell cycle, cell division, mitosis, modification-dependent protein catabolic process
amine oxidase (flavin-containing)	Maob	NP_766366	59	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	amine oxidase activity, electron carrier activity, oxidoreductase activity	oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
inositol hexaphosphate kinase 3	Ihpk3	NP_766615	44	2	cytoplasm, nucleus	ATP binding, inositol trisphosphate 3-kinase activity, kinase activity, nucleotide binding, transferase activity	not classified
3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	Hmgcll1	NP_776092	37	2	not classified	catalytic activity, hydroxymethylglutaryl-CoA lyase activity, lyase activity, metal ion binding	metabolic process
valyl-tRNA synthetase 2-like	Vars2	NP_780346	118	2	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
centlein isoform 1	Cntln	NP_780484	161	2	not classified	not classified	not classified
retinol dehydrogenase 13 (all-trans and 9-cis)	Rdh13	NP_780581	36	2	not classified	oxidoreductase activity	metabolic process, oxidation reduction
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
RAB5B, member RAS oncogene family	Rab5b	NP_803130	24	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
transmembrane protein 16J	Tmem16j	NP_848468	87	2	not classified	not classified	not classified
arylacetamide deacetylase-like 1	Aadacl1	NP_848887	46	2	endoplasmic reticulum, integral to membrane, membrane, microsome	carboxylesterase activity, hydrolase activity, phosphate binding, serine hydrolase activity	lipid catabolic process, metabolic process, protein amino acid dephosphorylation, xenobiotic metabolic process
tetratricopeptide repeat domain 15	Ttc15	NP_848926	88	2	not classified	binding	not classified
sirtuin 5 (silent mating type information regulation 2 homolog) 5	Sirt5	NP_849179	34	2	not classified	hydrolase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, metal ion binding, NAD binding, protein binding, zinc ion binding	chromatin silencing, protein amino acid deacetylation, regulation of transcription
myosin IE	Myo1e	NP_851417	127	2	cellular_component, myosin complex	ATP binding, molecular_function, motor activity, nucleotide binding	hemopoiesis, in utero embryonic development, kidney development, nitrogen compound metabolic process, platelet-derived growth factor receptor signaling pathway, post-embryonic hemopoiesis, vasculogenesis
hypothetical protein LOC231293	C130090K23Rik	NP_851840	78	2	integral to membrane, membrane	not classified	GPI anchor biosynthetic process
NADH dehydrogenase subunit 2	ND2	NP_904329	39	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity	electron transport chain, oxidation reduction, oxygen and reactive oxygen species metabolic process, transport
strawberry notch homolog	Sbno2	NP_906271	149	2	not classified	transcription repressor activity	macrophage activation during immune response, negative regulation of transcription, DNA-dependent, regulation of inflammatory response, regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cyclin-dependent kinase (CDC2-like) 11	Cdc2l6	NP_937807	52	2	not classified	ATP binding, cyclin-dependent protein kinase activity, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cell division, protein amino acid phosphorylation
tripartite motif-containing 56	Trim56	NP_958761	80	2	intracellular	metal ion binding, protein binding, zinc ion binding	not classified
LIM domain only 7	Lmo7	NP_963287	193	2	apical plasma membrane, cell-cell adherens junction	actinin binding, metal ion binding, zinc ion binding	cell-cell adhesion
H2A histone family, member Y2	H2afy2	NP_996883	40	2	Barr body, chromosome, nucleosome, nucleus	DNA binding	chromatin modification, dosage compensation, nucleosome assembly
mitochondrial ribosomal protein S26	Mrps26	NP_997090	23	2	mitochondrion, ribonucleoprotein complex, ribosome	not classified	not classified
pam, highwire, rpm 1	Mycbp2	NP_997098	521	2	anaphase-promoting complex, axon, microtubule cytoskeleton, nucleus	ligase activity, metal ion binding, protein binding, protein homodimerization activity, zinc ion binding	branchiomotor neuron axon guidance, cell morphogenesis involved in neuron differentiation, central nervous system projection neuron axonogenesis, modification-dependent protein catabolic process, motor axon guidance, regulation of cytoskeleton organization, regulation of mitotic metaphase/anaphase transition, regulation of protein localization, regulation of transcription, transcription
signal transducer and activator of transcription 3 isoform 2	Stat3	NP_998825	88	2	cytoplasm, nucleus, plasma membrane	calcium ion binding, DNA binding, protein binding, protein dimerization activity, protein kinase binding, sequence-specific DNA binding, signal transducer activity, transcription activator activity, transcription factor activity	acute-phase response, cytokine-mediated signaling pathway, eating behavior, eye photoreceptor cell differentiation, glucose homeostasis, JAK-STAT cascade involved in growth hormone signaling pathway, positive regulation of transcription from RNA polymerase II promoter, regulation of multicellular organism growth, regulation of transcription, regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent, sexual reproduction, signal transduction, temperature homeostasis, transcription, transcription from RNA polymerase II promoter
PREDICTED: hypothetical protein	LOC668408	XP_001001317	22	2	not classified	not classified	not classified
PREDICTED: similar to S-adenosylhomocysteine hydrolase	LOC677344	XP_001002625	23	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG665937	XP_001471658	21	2	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L19	LOC100045367	XP_001472655	15	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039525	XP_001473106	18	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 ribosomal protein L3 isoform 3	LOC100045885	XP_001474762	40	2	not classified	not classified	not classified
PREDICTED: similar to NTAK alpha2 isoform 4	LOC100045947	XP_001475441	92	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100040891	XP_001475496	17	2	not classified	not classified	not classified
PREDICTED: similar to hCG1994130	LOC100045504	XP_001475615	14	2	not classified	not classified	not classified
PREDICTED: similar to Nme6 protein	LOC100046163	XP_001475760	21	2	not classified	not classified	not classified
PREDICTED: similar to Protein disulfide isomerase associated 6	LOC100046302	XP_001476035	43	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC433745	XP_001476854	21	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046994	XP_001477245	72	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047450	XP_001478226	7	2	not classified	not classified	not classified
PREDICTED: similar to Uncharacterized protein KIAA0423	A430041B07Rik	XP_001478588	201	2	not classified	binding	not classified
PREDICTED: similar to zinc finger, UBR1 type 1 isoform 2	Zubr1	XP_001479796	573	2	cytoplasm, cytoskeleton, integral to membrane, membrane, nucleus	calmodulin binding, ligase activity, metal ion binding, ubiquitin-protein ligase activity, zinc ion binding	modification-dependent protein catabolic process
PREDICTED: similar to ribosomal protein S3a	LOC100043780	XP_001480995	30	2	not classified	not classified	not classified
PREDICTED: golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	XP_001481110	369	2	Golgi apparatus	not classified	not classified
PREDICTED: progesterone receptor membrane component 2 isoform 1	Pgrmc2	XP_130859	23	2	cellular_component, integral to membrane, membrane	heme binding, lipid binding, protein binding, receptor activity, steroid binding	biological_process
PREDICTED: similar to ribosomal protein L27A	EG432798	XP_484309	17	2	not classified	not classified	not classified
PREDICTED: tensin 1	Tns1	XP_619639	201	2	cell-substrate junction, focal adhesion	actin binding	cell migration, cell-substrate junction assembly
PREDICTED: similar to RIKEN cDNA 1110020P15 gene	EG622178	XP_891680	7	2	not classified	not classified	not classified
PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6	EG623286	XP_894909	13	2	not classified	not classified	not classified
PREDICTED: similar to S100 calcium-binding protein A11	EG546623	XP_910351	17	2	not classified	not classified	not classified
PREDICTED: leucine-rich repeats and guanylate kinase domain containing isoform 3	Lrguk	XP_915918	93	2	not classified	ATP binding, kinase activity, nucleotide binding, protein binding, transferase activity	not classified
PREDICTED: similar to FLJ00341 protein isoform 3	Nbeal2	XP_916280	310	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG433073	XP_918674	21	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: similar to glucocorticoid induced transcript 1	EG545216	XP_919798	48	2	not classified	not classified	not classified
PREDICTED: similar to Small subunit processome component 20 homolog (Down-regulated in metastasis protein) isoform 4	Utp20	XP_922382	318	2	nucleus	not classified	not classified
PREDICTED: similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	4930408G06Rik	XP_984875	162	2	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L27a-like	EG666648	XP_990276	16	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG638833	XP_995982	38	2	not classified	not classified	not classified
F-box protein 41	Fbxo41	NP_001001160	94	1	intracellular	zinc ion binding	modification-dependent protein catabolic process
Leber congenital amaurosis 5-like	Lca5l	NP_001001492	82	1	not classified	not classified	not classified
LIM and calponin homology domains 1	Limch1	NP_001001980	118	1	not classified	actin binding, metal ion binding, zinc ion binding	actomyosin structure organization
F-box and leucine-rich repeat protein 11	Fbxl11	NP_001001984	133	1	nucleus	DNA binding, histone demethylase activity (H3-K36 specific), 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, protein binding, zinc ion binding	chromatin modification, modification-dependent protein catabolic process, oxidation reduction, regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ribosomal protein L17	Rpl17	NP_001002239	21	1	cellular_component, intracellular, large ribosomal subunit, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
TAR DNA binding protein isoform 5	Tardbp	NP_001003898	34	1	nucleus	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, regulation of transcription, RNA splicing, transcription
contactin associated protein-like 2 isoform a	Cntnap2	NP_001004357	148	1	integral to membrane, membrane	protein binding, receptor binding	cell adhesion, signal transduction
phospholipase A2, group IVC (cytosolic, calcium-independent)	Pla2g4c	NP_001004762	68	1	cellular_component	molecular_function	biological_process
Erbb2 interacting protein isoform 1	Erbb2ip	NP_001005868	162	1	basolateral plasma membrane, cell junction	protein binding	protein targeting
solute carrier family 25, member 42	Slc25a42	NP_001007571	35	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding	transport
development and differentiation enhancing factor-like 1	Ddefl1	NP_001008233	99	1	cytoplasm	ARF GTPase activator activity, metal ion binding, zinc ion binding	regulation of ARF GTPase activity
SR-related CTD-associated factor 1	Scaf1	NP_001008422	134	1	nucleus	protein domain specific binding, RNA binding	mRNA processing, RNA splicing, transcription from RNA polymerase II promoter
WD repeat domain 91	Wdr91	NP_001013384	83	1	not classified	not classified	not classified
protein kinase, AMP-activated, alpha 1 catalytic subunit	Prkaa1	NP_001013385	64	1	cytoplasm	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cholesterol biosynthetic process, fatty acid biosynthetic process, fatty acid oxidation, glucose metabolic process, lipid biosynthetic process, protein amino acid phosphorylation, steroid biosynthetic process, sterol biosynthetic process
killer cell lectin-like receptor subfamily H, member 1	Gm156	NP_001014997	26	1	not classified	receptor activity, sugar binding	not classified
radical S-adenosyl methionine and flavodoxin domains 1 isoform 1	Tyw1	NP_001015876	82	1	not classified	4 iron, 4 sulfur cluster binding, catalytic activity, electron carrier activity, FMN binding, iron ion binding, iron-sulfur cluster binding, metal ion binding, nucleotide binding, oxidoreductase activity	oxidation reduction, tRNA processing
jumonji domain containing 3	Jmjd3	NP_001017426	176	1	nucleus	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, sequence-specific DNA binding	chromatin modification, histone demethylation, inflammatory response, negative regulation of transcription from RNA polymerase II promoter, oxidation reduction
cytochrome c oxidase subunit XVII assembly protein homolog	Cox17	NP_001017429	7	1	mitochondrial intermembrane space, mitochondrion	copper chaperone activity, copper ion binding, enzyme activator activity, metal ion binding	copper ion transport
UDP glucuronosyltransferase 2 family, polypeptide A2	Ugt2a2	NP_001019319	60	1	integral to membrane, membrane	glucuronosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	Ddx49	NP_001020093	54	1	cellular_component	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process
testase 6	EG384813	NP_001020411	83	1	not classified	not classified	not classified
WD repeat domain 61 isoform a	Wdr61	NP_001020546	34	1	not classified	not classified	not classified
hypothetical protein LOC545428	2610301F02 Rik	NP_001020747	84	1	not classified	not classified	not classified
SEC14-like 3	Sec14l3	NP_001025108	46	1	not classified	not classified	not classified
Sec23 interacting protein	Sec23ip	NP_001025153	111	1	cytoplasmic vesicle, endoplasmic reticulum, membrane	metal ion binding	not classified
FAT tumor suppressor homolog 2	Fat2	NP_001025159	480	1	not classified	calcium ion binding	not classified
conserved nuclear protein Nhn1 isoform a	Zc3h18	NP_001025164	108	1	nucleus	metal ion binding, nucleic acid binding, zinc ion binding	not classified
peripheral myelin protein 2	Pmp2	NP_001025476	15	1	not classified	binding, lipid binding, transporter activity	transport
syntaxin-binding protein 3B	Stxbp3b	NP_001025488	31	1	cellular_component	molecular_function	biological_process
hypothetical protein LOC97130	C77080	NP_001028361	111	1	not classified	not classified	not classified
hypothetical protein LOC102502	AI427122	NP_001028382	70	1	cytoplasm	actin binding, calcium ion binding, molecular_function	biological_process
zinc finger and BTB domain containing 16	Zbtb16	NP_001028496	74	1	nuclear speck, nucleus, transcriptional repressor complex	DNA binding, metal ion binding, protein binding, specific transcriptional repressor activity, zinc ion binding	anterior/posterior pattern formation, central nervous system development, embryonic hindlimb morphogenesis, embryonic limb morphogenesis, embryonic pattern specification, forelimb morphogenesis, hemopoiesis, leg morphogenesis, male germ-line stem cell division, mesonephros development, negative regulation of cell proliferation, negative regulation of myeloid cell differentiation, negative regulation of transcription, DNA-dependent, positive regulation of apoptosis, regulation of transcription, skeletal system development
NLR family, CARD domain containing 4	Nlrc4	NP_001028539	117	1	not classified	not classified	inflammatory response, regulation of apoptosis, regulation of caspase activity
hypothetical protein LOC319277	A230046K03 Rik	NP_001028547	136	1	not classified	not classified	not classified
expressed sequence AU045404	Alg10b	NP_001028613	55	1	integral to membrane, membrane, plasma membrane	transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	not classified
hypothetical protein LOC381126	Gm944	NP_001028617	97	1	not classified	not classified	not classified
F-box and WD-40 domain protein 10	Fbxw10	NP_001028841	117	1	cellular_component	molecular_function	biological_process
zinc fingr protein 551	Zfp551	NP_001028992	80	1	intracellular, nucleus	metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, DNA-dependent
hypothetical protein LOC66270 isoform 1	1810015C04 Rik	NP_001030023	53	1	integral to membrane, membrane	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
NIMA (never in mitosis gene a)- related kinase 10	Nek10	NP_001030037	42	1	not classified	ATP binding, 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	protein amino acid phosphorylation
zinc finger CCCH-type containing 12B	Zc3h12b	NP_001030079	94	1	not classified	not classified	not classified
transient receptor potential cation channel, subfamily M, member 3 isoform i	Trpm3	NP_001030323	28	1	integral to membrane	cation channel activity, ion channel activity, receptor activity	cation transport, ion transport, transport
plasma membrane calcium ATPase 2 isoform 2	Atp2b2	NP_001031761	133	1	apical plasma membrane, cell soma, cilium, endoplasmic reticulum, integral to membrane, membrane, microsome, plasma membrane	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium ion binding, calcium ion transmembrane transporter activity, calcium-dependent ATPase activity, calcium-transporting ATPase activity, calmodulin binding, 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, auditory receptor cell stereocilium organization, calcium ion transport, cation transport, cell morphogenesis, cellular calcium ion homeostasis, cerebellar granule cell differentiation, cerebellar Purkinje cell differentiation, cerebellar Purkinje cell layer morphogenesis, cerebellum development, cGMP metabolic process, detection of mechanical stimulus involved in sensory perception of sound, inner ear development, inner ear morphogenesis, inner ear receptor cell differentiation, ion transport, lactation, locomotion, locomotory behavior, metabolic process, neuromuscular process controlling balance, organelle organization, otolith mineralization, positive regulation of calcium ion transport, regulation of cell size, regulation of synaptic plasticity, sensory perception of sound, serotonin metabolic process, synapse organization
RUN and SH3 domain containing 2	Rusc2	NP_001032798	162	1	cytoplasm	not classified	not classified
brain-specific angiogenesis inhibitor 1-associated protein 2 isoform c	Baiap2	NP_001032843	53	1	cell projection, cytoplasm, membrane	cytoskeletal adaptor activity, protein binding, SH3 domain binding	filopodium assembly, Rho protein signal transduction, signal transduction
beta-transducin repeat containing protein isoform a	Btrc	NP_001032847	69	1	not classified	ligase activity, protein binding	branching involved in mammary gland duct morphogenesis, mammary gland epithelial cell proliferation, protein catabolic process, regulation of cell cycle, regulation of I-kappaB kinase/NF-kappaB cascade
ubiquitin specific protease 14 isoform 2	Usp14	NP_001033678	52	1	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
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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
mitochondrial ribosomal protein L1 isoform 2	Mrpl1	NP_001034173	31	1	intracellular, large ribosomal subunit, mitochondrial large ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	RNA binding, structural constituent of ribosome	RNA processing, translation
defensin beta 26	Defb26	NP_001034209	20	1	not classified	not classified	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
transcription elongation regulator 1	Tcerg1	NP_001034563	124	1	nuclear matrix, nucleus	protein binding, transcription factor activity	regulation of transcription, transcription
solute carrier organic anion transporter family, member 6b1	Slco6b1	NP_001034564	79	1	integral to plasma membrane	organic anion transmembrane transporter activity	organic anion transport
poly (ADP-ribose) polymerase family, member 14	Parp14	NP_001034619	204	1	cytoplasm, nucleus	NAD+ ADP-ribosyltransferase activity, nucleic acid binding, protein binding, transferase activity, transferase activity, transferring glycosyl groups	regulation of transcription, transcription
ecotropic viral integration site 5 like	Evi5l	NP_001034667	93	1	not classified	Rab GTPase activator activity	not classified
paternally expressed 10 isoform RF1	Peg10	NP_001035701	42	1	cytoplasm, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	apoptosis, cell differentiation, placenta development
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
Opa interacting protein 5	Oip5	NP_001036118	27	1	Cajal body, chromatin, chromocenter, chromosome, centromeric region, nucleus	protein binding	cell cycle, cell division, mitosis
neogenin isoform 2	Neo1	NP_001036217	160	1	integral to membrane, membrane, plasma membrane	cadherin binding, protein binding, receptor activity, transcription regulator activity	cell adhesion, myoblast fusion, regulation of transcription
hedgehog interacting protein-like 1	Hhipl1	NP_001037845	88	1	extracellular region, membrane	scavenger receptor activity	not classified
adaptor protein complex AP-2, alpha 1 subunit isoform b	Ap2a1	NP_001070732	105	1	clathrin adaptor complex, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat, secretory granule	protein binding, protein transporter activity	endocytosis, intracellular protein transport, protein transport, transport, vesicle-mediated transport
glutathione S-transferase, alpha 3	Gsta3	NP_001070821	25	1	cytoplasm	glutathione transferase activity, transferase activity	metabolic process

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
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
cerebellar degeneration-related protein 2-like	Cdr2l	NP_001074398	53	1	not classified	not classified	not classified
breast cancer 2	Brca2	NP_001074470	371	1	cytoplasm, nucleus	protein binding, single-stranded DNA binding	brain development, cell aging, cell proliferation, chordate embryonic development, chromosome organization, cytokinesis during cell cycle, DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis, DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator, DNA damage response, signal transduction resulting in induction of apoptosis, DNA recombination, DNA repair, double-strand break repair, double-strand break repair via homologous recombination, female gonad development, hemocyte proliferation, hemopoiesis, inner cell mass cell proliferation, male meiosis I, oocyte maturation, positive regulation of mitotic cell cycle, regulation of S phase of mitotic cell cycle, replication fork protection, response to DNA damage stimulus, response to gamma radiation, response to UV
signal-induced proliferation-associated 1 like 3	Sipa1l3	NP_001074497	195	1	not classified	not classified	not classified
hypothetical protein LOC68505	1110014N23 Rik	NP_001074510	86	1	Golgi apparatus	not classified	lipid transport, protein transport, transport
coiled-coil domain containing 90A	Ccdc90a	NP_001074528	38	1	integral to membrane, membrane, mitochondrion	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
lactase	Lct	NP_001074547	218	1	not classified	hydrolase activity, hydrolase activity, acting on glycosyl bonds	metabolic process
cytokine like 1	Cytl1	NP_001074575	16	1	not classified	transcription activator activity	chondrocyte differentiation, chondroitin sulfate proteoglycan biosynthetic process, positive regulation of transcription factor activity, positive regulation of transcription from RNA polymerase II promoter
TATA element modulatory factor 1	Tmf1	NP_001074580	122	1	cytoplasm, Golgi apparatus, membrane, nucleus	DNA binding	regulation of transcription, transcription
hypothetical protein LOC75404	1100001E04 Rik	NP_001074592	67	1	not classified	not classified	not classified
oxoglutarate dehydrogenase-like	Ogdhl	NP_001074599	117	1	not classified	not classified	not classified
prickle-like 2	Prickle2	NP_001074615	102	1	apicolateral plasma membrane, lateral plasma membrane, membrane, nucleus	metal ion binding, zinc ion binding	establishment or maintenance of epithelial cell apical/basal polarity
LON peptidase N-terminal domain and ring finger 1	Lonrf1	NP_001074619	93	1	not classified	not classified	not classified
unc13 homolog 3	Unc13c	NP_001074622	250	1	cell junction, cellular_component, cytoplasm, membrane, plasma membrane, synapse	diacylglycerol binding, metal ion binding, non-kinase phorbol ester receptor activity, zinc ion binding	exocytosis, intracellular signaling cascade, synaptic transmission
HEAT repeat containing 5B	Heatr5b	NP_001074648	224	1	not classified	not classified	not classified
Atpase, class I, type 8B, member 2	Atp8b2	NP_001074651	137	1	integral to membrane, membrane	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, nucleotide binding, phospholipid-translocating ATPase activity, protein binding	ATP biosynthetic process, phospholipid transport
LEM domain containing 3	Lemd3	NP_001074662	100	1	integral to membrane, integral to nuclear inner membrane, membrane, nuclear envelope, nucleus	DNA binding, nucleotide binding	not classified
endoplasmic reticulum metallopeptidase 1	Ermp1	NP_001074682	100	1	endoplasmic reticulum, integral to membrane, membrane	hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
host cell factor 2	Hcfc2	NP_001074687	79	1	not classified	not classified	not classified
myosin IA	Myo1a	NP_001074688	119	1	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

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
excision repair cross-complementing rodent repair deficiency, complementation group 6	Ercc6	NP_001074690	166	1	not classified	not classified	activation of JNKK activity, activation of JUN kinase activity, DNA damage response, signal transduction resulting in induction of apoptosis, DNA repair, photoreceptor cell maintenance, pyrimidine dimer repair, response to DNA damage stimulus, response to gamma radiation, response to oxidative stress, response to superoxide, response to toxin, response to UV, response to UV-B, response to X-ray, transcription-coupled nucleotide-excision repair
hypothetical protein LOC69549	2310009B15 Rik	NP_001074695	15	1	not classified	not classified	not classified
hypothetical protein LOC75687	2310066E14 Rik	NP_001074710	132	1	not classified	binding	not classified
versican	Vcan	NP_001074718	367	1	extracellular region, proteinaceous extracellular matrix	binding, calcium ion binding, hyaluronic acid binding, sugar binding	cell adhesion, heart development
leucine-rich repeats and calponin homology (CH) domain containing 3	Lrch3	NP_001074724	86	1	extracellular region	protein binding	not classified
BAT2 domain containing 1	Bat2d	NP_001074759	311	1	cellular_component	molecular_function	biological_process
PDS5, regulator of cohesion maintenance, homolog A	Pds5a	NP_001074790	150	1	nucleus	not classified	cell cycle, cell division, mitosis
chondroitin sulfate synthase 3	Chsy3	NP_001074797	100	1	Golgi apparatus, Golgi cisterna membrane, integral to membrane, membrane	glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase activity, metal ion binding, N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase activity, transferase activity, transferase activity, transferring hexosyl groups	not classified
dynein, axonemal, heavy chain 2	Dnahc2	NP_001074799	512	1	cell projection, cilium, dynein complex, microtubule	ATP binding, ATPase activity, microtubule motor activity, motor activity, nucleoside-triphosphatase activity, nucleotide binding	microtubule-based movement
tetratricopeptide repeat domain 37	Ttc37	NP_001074821	174	1	not classified	not classified	not classified
vacuolar protein sorting 8 homolog	Vps8	NP_001074835	161	1	not classified	metal ion binding, protein binding, zinc ion binding	not classified
hypothetical protein LOC270150	BC038167	NP_001074838	14	1	not classified	not classified	not classified
SH3/ankyrin domain gene 2 isoform a	Shank2	NP_001074839	135	1	cell junction, cell projection, cytoplasm, membrane, plasma membrane, postsynaptic membrane, synapse	protein binding, SH3 domain binding	not classified
myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	NP_001074852	540	1	histone methyltransferase complex, nucleus	DNA binding, histone methyltransferase activity (H3-K4 specific), histone-lysine N-methyltransferase activity, metal ion binding, methyltransferase activity, protein binding, transferase activity, zinc ion binding	chromatin modification, histone methylation, intracellular signaling cascade, regulation of transcription, regulation of transcription, DNA-dependent, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
midasin	Mdn1	NP_001074861	630	1	not classified	ATP binding, nucleotide binding	not classified
armadillo repeat containing 4	Armc4	NP_001074862	115	1	cellular_component	molecular_function	biological_process
myosin XVI	Myo16	NP_001074866	208	1	cytoplasm, myosin complex	actin binding, ATP binding, motor activity, nucleotide binding	not classified
hypothetical protein LOC665775	A230054D04 Rik	NP_001074891	327	1	not classified	not classified	not classified
tubulin tyrosine ligase-like family, member 5	Ttll5	NP_001074892	151	1	cell projection, cilium, cytoplasm, nucleus	ligase activity, tubulin-tyrosine ligase activity	protein modification process, transcription
hypothetical protein LOC75906	4930589M24 Rik	NP_001074897	133	1	not classified	not classified	not classified
prolyl-tRNA synthetase (mitochondrial)(putative) isoform 2	Pars2	NP_001077356	58	1	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, proline-tRNA ligase activity	prolyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
glutathione peroxidase 3 isoform 1	Gpx3	NP_001077398	28	1	extracellular region	glutathione peroxidase activity, oxidoreductase activity, peroxidase activity, selenium binding	hydrogen peroxide catabolic process, oxidation reduction, response to oxidative stress
apoptotic chromatin condensation inducer 1 isoform 4	Acin1	NP_001078942	65	1	nucleolus, nucleus	nucleic acid binding, nucleotide binding	apoptosis
hypothetical protein LOC268498	E030025P04 Rik	NP_001078981	21	1	not classified	not classified	not classified
myelin transcription factor 1-like isoform 3	Myt1l	NP_001087247	133	1	nucleus	DNA binding, metal ion binding, protein binding, transcription factor activity, zinc ion binding	cell differentiation, multicellular organismal development, nervous system development, regulation of transcription, regulation of transcription, DNA-dependent, transcription
hypothetical protein LOC69126	1810022K09 Rik	NP_001093144	11	1	not classified	not classified	not classified
cytochrome P450, family 2, subfamily j, polypeptide 12	Cyp2j12	NP_001093652	58	1	not classified	not classified	not classified
SREBF chaperone	Scap	NP_001096632	140	1	cytoplasmic vesicle, endoplasmic reticulum, endoplasmic reticulum membrane, Golgi apparatus, integral to membrane, membrane	cholesterol binding, protein binding	cholesterol metabolic process, lipid metabolic process, regulation of cholesterol biosynthetic process, regulation of fatty acid biosynthetic process, regulation of fatty acid metabolic process, response to hypoxia, response to insulin stimulus, steroid metabolic process
hypothetical protein LOC105351	AW209491	NP_001098116	47	1	not classified	not classified	not classified
vomeronasal receptor Vmn2r68	Vmn2r68	NP_001098651	98	1	not classified	not classified	not classified
vomeronasal 2, receptor 78	Vmn2r78	NP_001098659	98	1	not classified	not classified	not classified
PHD finger protein 21A isoform 3	Phf21a	NP_001103161	67	1	histone deacetylase complex, nucleus	chromatin binding, DNA binding, metal ion binding, protein binding, zinc ion binding	chromatin modification, negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, suckling behavior, transcription
post-synaptic density protein 95 isoform 2	Dlg4	NP_001103222	80	1	alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid selective glutamate receptor complex, cell junction, cytoplasm, extrinsic to internal side of plasma membrane, membrane, membrane fraction, plasma membrane, postsynaptic density, postsynaptic membrane, synapse, synaptosome	neurexin binding, protein binding, structural molecule activity	locomotory behavior, regulation of long-term neuronal synaptic plasticity, response to cocaine, synaptic vesicle maturation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATPase, Cu++ transporting, alpha polypeptide isoform 1	Atp7a	NP_001103227	162	1	cell soma, cytoplasmic vesicle, Golgi apparatus, integral to membrane, integral to membrane of membrane fraction, membrane, membrane fraction, neuron projection, plasma membrane, trans-Golgi network	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic activity, copper ion binding, copper ion transmembrane transporter activity, copper-exporting ATPase activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, metal ion transmembrane transporter activity, nucleotide binding, protein binding, superoxide dismutase copper chaperone activity	ATP biosynthetic process, ATP metabolic process, blood vessel development, blood vessel remodeling, cartilage development, catecholamine metabolic process, cellular copper ion homeostasis, central nervous system neuron development, cerebellar Purkinje cell differentiation, collagen fibril organization, copper ion export, copper ion import, copper ion transport, dendrite morphogenesis, detoxification of copper ion, dopamine metabolic process, elastic fiber assembly, elastin biosynthetic process, epinephrine metabolic process, extracellular matrix organization, hair follicle morphogenesis, hindlimb morphogenesis, ion transport, locomotory behavior, lung alveolus development, metabolic process, metal ion transport, mitochondrion organization, negative regulation of metalloenzyme activity, neuron projection morphogenesis, neuroprotection, norepinephrine
calpain 3 isoform b	Capn3	NP_001103231	82	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
procollagen, type XVIII, alpha 1 isoform 1	Col18a1	NP_001103461	156	1	basement membrane, extracellular matrix, extracellular region, proteinaceous extracellular matrix	binding, extracellular matrix structural constituent, metal ion binding, protein binding, structural molecule activity, zinc ion binding	angiogenesis, cell adhesion, endothelial cell morphogenesis, extracellular matrix organization, positive regulation of apoptosis, positive regulation of cell migration, positive regulation of cell proliferation
elongation factor Tu GTP binding domain containing 2 isoform b	Eftud2	NP_001103465	109	1	nucleus, spliceosomal complex	GTP binding, GTPase activity, nucleotide binding, protein binding, translation elongation factor activity	mRNA processing, RNA splicing
WD repeat domain 36 isoform 2	Wdr36	NP_001103486	98	1	cellular_component	molecular_function	biological_process
capicua homolog isoform c	Cic	NP_001103602	164	1	nucleus	DNA binding	regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform a	Atp2a2	NP_001103610	115	1	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
GRB10 interacting GYF protein 2 isoform b	Gigyf2	NP_001103682	149	1	not classified	not classified	not classified
protein phosphatase 1H (PP2C domain containing) isoform 1	Ppm1h	NP_001103688	56	1	protein serine/threonine phosphatase complex	catalytic activity, hydrolase activity, phosphoprotein phosphatase activity, protein serine/threonine phosphatase activity	protein amino acid dephosphorylation
calpain 1, large subunit	Capn1	NP_001103974	82	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	proteolysis
predicted gene, EG665615	EG665615	NP_001104249	14	1	not classified	not classified	not classified
zinc finger protein 661	Zfp661	NP_001104499	49	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, regulation of transcription, DNA-dependent, transcription
serine (or cysteine) proteinase inhibitor, clade H, member 1	Serpinh1	NP_001104514	47	1	cytoplasm, endoplasmic reticulum	protein binding, serine-type endopeptidase inhibitor activity, unfolded protein binding	collagen biosynthetic process, collagen fibril organization, protein maturation, response to stress
autophagy related 16 like 2	Atg16l2	NP_001104581	69	1	cytoplasm	not classified	autophagy, protein transport, transport
hypothetical protein LOC209550	EG209550	NP_001104588	112	1	not classified	not classified	not classified
eukaryotic translation initiation factor 2B, subunit 3 gamma isoform 1	Eif2b3	NP_001104747	50	1	eukaryotic translation initiation factor 2B complex	guanyl-nucleotide exchange factor activity, protein binding, translation initiation factor activity	biological_process
predicted gene, ENSMUSG00000059775	ENSMUSG00000059775	NP_001104770	13	1	not classified	not classified	not classified
leucine rich repeat (in FLII) interacting protein 1 isoform 1	Lrrfip1	NP_001104781	79	1	cytoplasm, nucleus	DNA binding, protein binding	regulation of transcription, transcription
neural precursor cell expressed, developmentally down-regulated gene 9 isoform 1	Nedd9	NP_001104794	93	1	cytoplasm, cytoskeleton, nucleus	protein binding	cell adhesion, cell cycle, cell division, mitosis, regulation of growth
predicted gene, ENSMUSG00000044330	ENSMUSG00000044330	NP_001106138	10	1	not classified	not classified	not classified
a disintegrin and metalloprotease domain 12	Adam12	NP_031426	99	1	integral to membrane, membrane, plasma membrane, proteinaceous extracellular matrix	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, protein binding, SH3 domain binding, zinc ion binding	cell adhesion, proteolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
poly (ADP-ribose) polymerase family, member 1	Parp1	NP_031441	113	1	intracellular, nucleolus, nucleoplasm, nucleus	DNA binding, metal ion binding, NAD or NADH binding, NAD+ ADP-ribosyltransferase activity, protein binding, transferase activity, transferase activity, transferring glycosyl groups, zinc ion binding	base-excision repair, DNA metabolic process, DNA repair, protein amino acid ADP-ribosylation, regulation of growth rate, response to DNA damage stimulus, telomere maintenance
adenomatosis polyposis coli	Apc	NP_031488	311	1	axon part, cell projection, cell projection membrane, cytoplasm, cytoplasmic microtubule, growth cone, lateral plasma membrane, nucleus	beta-catenin binding, binding, microtubule binding, protein binding	anterior/posterior pattern formation, axis specification, axonogenesis, cell migration, chromosome organization, cytokinesis after mitosis, dorsal/ventral pattern formation, hair follicle development, kidney development, mitotic cell cycle spindle assembly checkpoint, mitotic metaphase/anaphase transition, muscle maintenance, negative regulation of apoptosis, negative regulation of cell proliferation, negative regulation of epithelial cell proliferation, negative regulation of epithelial cell proliferation involved in prostate gland development, negative regulation of MAPKKK cascade, negative regulation of microtubule depolymerization, negative regulation of odontogenesis, negative regulation of Wnt receptor signaling pathway, pattern specification process, positive regulation of apoptosis, positive regulation of cell adhesion, positive regulation of cell
aquaporin 1	Aqp1	NP_031498	29	1	integral to membrane, integral to plasma membrane, membrane	transporter activity, water channel activity	transport, water transport
asialoglycoprotein receptor 2	Asgr2	NP_031519	35	1	integral to membrane, membrane	binding, calcium ion binding, receptor activity, sugar binding	endocytosis, glycoprotein metabolic process, lipid homeostasis, regulation of protein stability
ataxia telangiectasia mutated homolog	Atm	NP_031525	349	1	cytoplasmic vesicle, nucleoplasm, nucleus, spindle	ATP binding, DNA binding, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, protein kinase activity, protein serine/threonine kinase activity, transferase activity	brain development, cell cycle, DNA damage checkpoint, DNA damage response, signal transduction resulting in induction of apoptosis, DNA repair, female gamete generation, heart development, lipoprotein catabolic process, negative regulation of apoptosis, neuron apoptosis, positive regulation of neuron apoptosis, protein amino acid phosphorylation, response to DNA damage stimulus, response to ionizing radiation, somitogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
baculoviral IAP repeat-containing 6	Birc6	NP_031592	529	1	membrane fraction	protein binding, ubiquitin-protein ligase activity	anti-apoptosis, labyrinthine layer development, positive regulation of cell proliferation, protein ubiquitination, regulation of cell proliferation, spongiotrophoblast layer development
caspase 11	Casp4	NP_031635	43	1	intracellular	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity, protein binding	apoptosis, induction of apoptosis, negative regulation of apoptosis, proteolysis, regulation of apoptosis
cadherin 15	Cdh15	NP_031688	86	1	integral to membrane, membrane, neuromuscular junction, plasma membrane	calcium ion binding, protein binding	cell adhesion, homophilic cell adhesion
cofilin 2, muscle	Cfl2	NP_031714	19	1	cytoplasm, cytoskeleton, intracellular, nucleus	actin binding	not classified
procollagen, type IV, alpha 4	Col4a4	NP_031761	164	1	basement membrane, collagen, collagen type IV, extracellular region, proteinaceous extracellular matrix	extracellular matrix structural constituent	not classified
cryptochrome 1 (photolyase-like)	Cry1	NP_031797	68	1	cytoplasm, nucleus	DNA photolyase activity, nucleotide binding, photoreceptor activity, protein binding, receptor activity	circadian rhythm, DNA repair, protein-chromophore linkage, regulation of transcription, response to stimulus, rhythmic process, transcription
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
cytochrome P450, family 2, subfamily b, polypeptide 13	Cyp2b13	NP_031839	56	1	not classified	iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity	oxidation reduction
receptor accessory protein 5	Reep5	NP_031900	21	1	integral to membrane, membrane	protein binding, receptor activity	not classified
eukaryotic elongation factor-2 kinase	Eef2k	NP_031934	82	1	not classified	ATP binding, binding, calcium ion binding, calmodulin binding, elongation factor-2 kinase activity, kinase activity, nucleotide binding, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
eukaryotic translation initiation factor 4E	Eif4e	NP_031943	25	1	cytoplasm	protein binding, RNA binding, translation initiation factor activity	regulation of translation, translation, translational initiation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO 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
endonuclease G	Endog	NP_031957	32	1	mitochondrion	endonuclease activity, hydrolase activity, magnesium ion binding, manganese ion binding, metal ion binding, nuclease activity, nucleic acid binding	DNA fragmentation involved in apoptosis, in utero embryonic development, positive regulation of apoptosis, response to antibiotic, response to tumor necrosis factor
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
enhancer of rudimentary homolog	Erh	NP_031977	12	1	not classified	molecular_function	cell cycle
ecotropic viral integration site 5	Evi5	NP_031990	93	1	intracellular, nucleus	Rab GTPase activator activity	cell cycle, cell division, regulation of Rab GTPase activity
coagulation factor V	F5	NP_032002	247	1	extracellular region, extracellular space, platelet alpha granule	calcium ion binding, copper ion binding, metal ion binding, molecular_function, oxidoreductase activity	blood circulation, blood coagulation, cell adhesion, oxidation reduction
fibulin 2 isoform a	Fbln2	NP_032018	132	1	extracellular region, proteinaceous extracellular matrix	calcium ion binding, extracellular matrix binding, protein binding	positive regulation of cell-substrate adhesion
fibroblast growth factor 17	Fgf17	NP_032030	25	1	extracellular region	growth factor activity	fibroblast growth factor receptor signaling pathway, positive regulation of cell proliferation
structural maintenance of chromosomes 2-like 1	Smc2	NP_032043	134	1	chromosome, cytoplasm, nucleus	ATP binding, nucleotide binding, protein binding	cell cycle, cell division, chromosome condensation, chromosome organization, mitosis
flotillin 1	Flot1	NP_032053	48	1	flotillin complex, membrane, membrane raft, plasma membrane	molecular_function, protein binding	biological_process
acid alpha-glucosidase	Gaa	NP_032090	106	1	lysosome	alpha-glucosidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, diaphragm contraction, glycogen catabolic process, glycogen metabolic process, heart morphogenesis, locomotory behavior, lysosome organization, metabolic process, muscle maintenance, neuromuscular process controlling balance, neuromuscular process controlling posture, regulation of the force of heart contraction, striated muscle contraction, tissue development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
gamma-aminobutyric acid (GABA) receptor, rho 1	Gabrr1	NP_032101	55	1	cell junction, chloride channel complex, integral to membrane, membrane, plasma membrane, postsynaptic membrane, synapse	chloride channel activity, chloride ion binding, extracellular ligand-gated ion channel activity, GABA-A receptor activity, ion channel activity	ion transport, transport
glutamic acid decarboxylase 1	Gad1	NP_032103	67	1	axon, cytoplasm, mitochondrion, synapse	carboxy-lyase activity, catalytic activity, glutamate decarboxylase activity, lyase activity, pyridoxal phosphate binding	carboxylic acid metabolic process, neurotransmitter biosynthetic process
Golgi autoantigen, golgin subfamily a, 3	Golga3	NP_032172	163	1	cytoplasm, ER-Golgi intermediate compartment, Golgi apparatus, Golgi membrane, membrane	protein binding	cell differentiation, multicellular organismal development, spermatogenesis
glutamate receptor, ionotropic, delta 1	Grid1	NP_032192	112	1	cell junction, integral to membrane, membrane, plasma membrane, postsynaptic membrane, synapse	extracellular-glutamate-gated ion channel activity, ion channel activity, ionotropic glutamate receptor activity, protein binding, receptor activity	ion transport, transport
glutathione S-transferase, alpha 1 (Ya)	Gsta1	NP_032207	26	1	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
host cell factor C1	Hcfc1	NP_032250	210	1	cytoplasm, nucleus	transcription coactivator activity	cell cycle, reactivation of latent virus
hyperpolarization-activated, cyclic nucleotide-gated K+ 2	Hcn2	NP_032252	95	1	integral to membrane, membrane	cAMP binding, ion channel activity, nucleotide binding, potassium channel activity, potassium ion binding, protein binding, sodium channel activity, sodium ion binding, voltage-gated ion channel activity, voltage-gated potassium channel activity	ion transport, potassium ion transport, regulation of membrane potential, sodium ion transport, transport
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
histidine triad nucleotide binding protein 1	Hint1	NP_032274	14	1	cytoplasm, nucleus	hydrolase activity	not classified
high mobility group box 2	Hmgb2	NP_032278	24	1	chromosome, nucleus	DNA binding	male gonad development, positive regulation of gene-specific transcription from RNA polymerase II promoter, response to steroid hormone stimulus, spermatogenesis
lipase, hepatic	Lipc	NP_032306	57	1	extracellular region, extracellular space, high-density lipoprotein particle	catalytic activity, heparin binding, hydrolase activity, lipase activity, triacylglycerol lipase activity	cholesterol homeostasis, cholesterol metabolic process, cholesterol transport, lipid catabolic process, lipid metabolic process
histamine receptor H1	Hrh1	NP_032311	56	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, rhythmic process, signal transduction
histamine receptor H 2 isoform 2	Hrh2	NP_032312	40	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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
interferon alpha 11 precursor	Ifna11	NP_032359	22	1	extracellular region, extracellular space	cytokine activity, cytokine receptor binding	defense response, response to virus
interleukin 12 receptor, beta 1	Il12rb1	NP_032379	82	1	external side of plasma membrane, integral to membrane, membrane	cytokine receptor activity, receptor activity	peptidyl-tyrosine phosphorylation
integrin alpha 6	Itga6	NP_032423	120	1	basolateral plasma membrane, cell surface, external side of plasma membrane, integral to membrane, integrin complex, membrane, plasma membrane	calcium ion binding, integrin binding, protein binding, receptor activity	brown fat cell differentiation, cell adhesion, cell adhesion mediated by integrin, cell-matrix adhesion, cellular response to extracellular stimulus, filopodium assembly, integrin-mediated signaling pathway, leukocyte migration, odontogenesis of dentine-containing tooth, positive regulation of cell-cell adhesion
ketohexokinase	Khk	NP_032465	33	1	not classified	ATP binding, ketohexokinase activity, kinase activity, nucleotide binding, transferase activity	carbohydrate metabolic process
kinesin family member 1B isoform a	Kif1b	NP_032467	130	1	cytoplasm, cytoplasmic vesicle, cytoplasmic vesicle membrane, cytoskeleton, microtubule, microtubule associated complex, mitochondrion	ATP binding, ATPase activity, microtubule binding, microtubule motor activity, motor activity, nucleotide binding, protein binding	anterograde axon cargo transport, cytoskeleton-dependent intracellular transport, embryonic development, microtubule-based movement, mitochondrion transport along microtubule, nerve-nerve synaptic transmission, neuromuscular synaptic transmission
kinesin family member 4	Kif4	NP_032472	140	1	microtubule, nucleus	ATP binding, DNA binding, microtubule motor activity, motor activity, nucleotide binding	microtubule-based movement
karyopherin (importin) alpha 1	Kpna1	NP_032491	60	1	cytoplasm, nuclear pore, nucleus	binding, protein transporter activity	intracellular protein transport, protein import into nucleus, protein transport, transport
kinectin 1	Ktn1	NP_032503	153	1	endoplasmic reticulum, integral to membrane, membrane	kinesin binding	microtubule-based movement
laminin, alpha 1 precursor	Lama1	NP_032506	338	1	basal lamina, basement membrane, extracellular matrix, extracellular region, laminin-1 complex, proteinaceous extracellular matrix	extracellular matrix structural constituent, protein binding, receptor binding	branching involved in lung morphogenesis, branching involved in salivary gland morphogenesis, cell adhesion, cell surface receptor linked signal transduction, establishment of epithelial cell apical/basal polarity, morphogenesis of an epithelial sheet, regulation of cell adhesion, regulation of cell migration, regulation of embryonic development, tissue development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
low density lipoprotein receptor-related protein 1	Lrp1	NP_032538	505	1	coated pit, cytoplasm, integral to membrane, membrane, membrane fraction, nucleus, plasma membrane	calcium ion binding, metal ion binding, receptor activity	apoptotic cell clearance, endocytosis, multicellular organismal development, negative regulation of Wnt receptor signaling pathway
lumican	Lum	NP_032550	38	1	extracellular region, proteinaceous extracellular matrix	protein binding	not classified
killer cell lectin-like receptor subfamily B member 1C	Klrb1c	NP_032553	25	1	external side of plasma membrane, integral to membrane, integral to plasma membrane, membrane	binding, protein homodimerization activity, receptor activity, sugar binding	positive regulation of natural killer cell mediated cytotoxicity
minichromosome maintenance deficient 2 mitotin	Mcm2	NP_032590	102	1	nuclear origin of replication recognition complex, nucleus	ATP binding, DNA binding, DNA replication origin binding, metal ion binding, nucleotide binding, protein binding, zinc ion binding	cell cycle, DNA replication, DNA replication initiation, DNA unwinding during replication, nucleosome assembly, regulation of transcription, transcription
minichromosome maintenance deficient 5, cell division cycle 46	Mcm5	NP_032592	82	1	nucleus	ATP binding, DNA binding, nucleotide binding	cell division, DNA replication, DNA replication initiation, regulation of transcription, transcription
transformed mouse 3T3 cell double minute 4	Mdm4	NP_032601	55	1	intracellular, nucleus	metal ion binding, protein binding, zinc ion binding	positive regulation of cell proliferation
ATP-binding cassette, sub-family C, member 1	Abcc1	NP_032602	171	1	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
matrix metallopeptidase 15	Mmp15	NP_032635	75	1	integral to membrane, membrane, proteinaceous extracellular matrix	calcium ion binding, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	metabolic process, proteolysis
meiosis-specific nuclear structural protein 1	Mns1	NP_032639	60	1	intermediate filament, nuclear envelope, nucleus	not classified	meiosis
membrane protein, palmitoylated	Mpp1	NP_032647	52	1	cell projection, cortical cytoskeleton, membrane	protein binding	not classified
mannose receptor, C type 1	Mrc1	NP_032651	165	1	cell surface, integral to membrane, membrane	binding, calcium ion binding, mannose binding, receptor activity, sugar binding, transmembrane receptor activity	endocytosis
murinoglobulin 2	Mug2	NP_032672	162	1	extracellular region, extracellular space	endopeptidase inhibitor activity, peptidase inhibitor activity, protein binding, serine-type endopeptidase inhibitor activity	not classified
kallikrein 1-related peptidase b3	Klk1b3	NP_032719	29	1	not classified	growth factor activity, hydrolase activity, metal ion binding, peptidase activity, receptor signaling protein activity, serine-type endopeptidase activity, serine-type peptidase activity, zinc ion binding	proteolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
nidogen 2	Nid2	NP_032721	154	1	basement membrane, extracellular region, membrane, proteinaceous extracellular matrix	calcium ion binding, protein binding	cell adhesion, cell-matrix adhesion
nemo like kinase	Nlk	NP_032728	58	1	cytoplasm, nucleus	kinase activity, metal ion binding, nucleotide binding, protein kinase activity, transferase activity	protein amino acid autophosphorylation, protein amino acid phosphorylation, transcription, Wnt receptor signaling pathway
noggin	Nog	NP_032737	26	1	extracellular region, extracellular space	not classified	anatomical structure formation involved in morphogenesis, BMP signaling pathway, brain development, cartilage development, cell differentiation, central nervous system development, in utero embryonic development, mesenchymal cell differentiation, multicellular organismal development, negative regulation of cell differentiation, notochord morphogenesis, pattern specification process, pituitary gland development, positive regulation of epithelial cell proliferation, prostatic bud formation, regulation of BMP signaling pathway, skeletal system development, ureteric bud development, urogenital system development
Niemann Pick type C1	Npc1	NP_032746	143	1	endosome, integral to membrane, lysosome, membrane	hedgehog receptor activity, protein binding	bile acid metabolic process, cholesterol efflux, cholesterol homeostasis, cholesterol transport, endocytosis, lysosomal transport, negative regulation of macroautophagy
catenin (cadherin associated protein), delta 2	Ctnnd2	NP_032755	135	1	cell junction, nucleus	binding, protein binding	cell adhesion, learning, morphogenesis of a branching structure, multicellular organismal development, regulation of synaptic plasticity, regulation of transcription, transcription
outer dense fiber of sperm tails 1	Odf1	NP_032783	28	1	outer dense fiber	not classified	cell differentiation, multicellular organismal development, spermatogenesis
immunoglobulin (CD79A) binding protein 1	Igbp1	NP_032810	39	1	cytoplasm	not classified	B cell activation, regulation of signal transduction, response to biotic stimulus
phospholipase A2 receptor 1	Pla2r1	NP_032893	171	1	extracellular region, integral to membrane, membrane, plasma membrane	binding, receptor activity, sugar binding	endocytosis
cytosolic phospholipase A2, group IVA	Pla2g4a	NP_032895	85	1	cytoplasm, cytoplasmic vesicle	calcium ion binding, hydrolase activity, lysophospholipase activity, phospholipase A2 activity, phospholipase activity	lipid catabolic process, phospholipid catabolic process, regulation of cell proliferation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
phospholipase C, beta 3	Plcb3	NP_032900	139	1	nucleus	calcium ion binding, hydrolase activity, phosphoinositide phospholipase C activity, phospholipase C activity, phosphoric diester hydrolase activity, signal transducer activity	intracellular signaling cascade, lipid catabolic process, lipid metabolic process, signal transduction
cathepsin A isoform a	Ctsa	NP_032932	56	1	lysosome, mitochondrion	carboxypeptidase activity, hydrolase activity, peptidase activity, protein binding, serine-type carboxypeptidase activity	proteolysis
periplakin	Ppl	NP_032935	204	1	cell junction, cytoplasm, cytoskeleton, extrinsic to plasma membrane, membrane, mitochondrion, nucleus, plasma membrane	protein binding	keratinization
protein kinase, cAMP dependent regulatory, type II alpha	Prkar2a	NP_032950	46	1	cAMP-dependent protein kinase complex	cAMP binding, cAMP-dependent protein kinase regulator activity, kinase activity, nucleotide binding, protein binding	regulation of protein amino acid phosphorylation, signal transduction
DnaJ (Hsp40) homolog, subfamily C, member 3B	Dnajc3	NP_032955	57	1	not classified	not classified	not classified
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
prostaglandin-endoperoxide synthase 1	Ptgs1	NP_032995	69	1	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
RAB4A, member RAS oncogene family	Rab4a	NP_033029	24	1	cytoplasm, endosome, membrane	GTP binding, nucleotide binding, protein binding, protein transporter activity	protein transport, regulation of endocytosis, small GTPase mediated signal transduction, transport
recombination activating gene 2	Rag2	NP_033046	59	1	nucleus	DNA binding, endonuclease activity, hydrolase activity, nuclease activity	B cell differentiation, B cell homeostatic proliferation, B cell lineage commitment, DNA recombination, positive regulation of organ growth, T cell differentiation, T cell differentiation in the thymus, T cell lineage commitment, V(D)J recombination
RAS protein-specific guanine nucleotide-releasing factor 2	Rasgrf2	NP_033053	136	1	cytoplasm, endoplasmic reticulum, intracellular, membrane, plasma membrane	calcium ion binding, guanyl-nucleotide exchange factor activity, Rho guanyl-nucleotide exchange factor activity	intracellular signaling cascade, regulation of Rho protein signal transduction, regulation of small GTPase mediated signal transduction, small GTPase mediated signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
retinoblastoma binding protein 4	Rbbp4	NP_033056	48	1	nucleus, NuRD complex	protein binding	cell cycle, chromatin modification, chromatin remodeling, DNA replication, regulation of transcription, transcription
retinoblastoma binding protein 7	Rbbp7	NP_033057	48	1	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
ribosomal protein L22	Rpl22	NP_033105	15	1	cytoplasm, intracellular, ribonucleoprotein complex, ribosome	heparin binding, RNA binding, structural constituent of ribosome	alpha-beta T cell differentiation, translation
ribosomal protein L30	Rpl30	NP_033109	13	1	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
RNA polymerase 1-4	Rpo1-4	NP_033114	194	1	DNA-directed RNA polymerase I complex, nucleus	DNA binding, DNA-directed RNA polymerase activity, magnesium ion binding, metal ion binding, nucleotidyltransferase activity, protein binding, transferase activity, zinc ion binding	transcription
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
polymerase (RNA) II (DNA directed) polypeptide C	Polr2c	NP_033116	31	1	cytoplasm, nucleus	DNA binding, DNA-directed RNA polymerase activity, protein binding, protein dimerization activity	transcription
Ras suppressor protein 1	Rsu1	NP_033131	31	1	cellular_component	molecular_function, protein binding	Ras protein signal transduction
retinoid X receptor gamma	Rxrg	NP_033133	51	1	nucleus	DNA binding, ligand-dependent nuclear receptor activity, metal ion binding, receptor activity, retinoid-X receptor activity, sequence-specific DNA binding, steroid binding, steroid hormone receptor activity, transcription factor activity, zinc ion binding	positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription, DNA-dependent, retinoic acid receptor signaling pathway, transcription
ryanodine receptor 1, skeletal muscle	Ryr1	NP_033135	565	1	integral to membrane, junctional membrane complex, membrane fraction, sarcoplasmic reticulum, sarcoplasmic reticulum membrane, T-tubule	ion channel activity, protein binding, receptor activity, voltage-gated calcium channel activity	calcium ion transport, ion transport, muscle contraction, regulation of muscle contraction, release of sequestered calcium ion into cytosol, transport
S100 calcium binding protein A13	S100a13	NP_033139	11	1	not classified	calcium ion binding	not classified
sodium channel, voltage-gated, type VII, alpha polypeptide	Scn7a	NP_033161	192	1	integral to membrane	ion channel activity, sodium channel activity, voltage-gated ion channel activity	ion transport, sodium ion transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
sphingosine phosphate lyase 1	Sgpl1	NP_033189	64	1	endoplasmic reticulum, integral to membrane, membrane	carboxy-lyase activity, catalytic activity, lyase activity, pyridoxal phosphate binding, sphinganine-1-phosphate aldolase activity	apoptosis, carboxylic acid metabolic process, face morphogenesis, fibroblast migration, hemopoiesis, kidney development, lipid metabolic process, nitrogen compound metabolic process, palate development, platelet-derived growth factor receptor signaling pathway, post-embryonic development, regulation of multicellular organism growth, skeletal system morphogenesis, vasculogenesis
solute carrier family 4 (anion exchanger), member 1, adaptor protein	Slc4a1ap	NP_033232	80	1	not classified	not classified	not classified
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 isoform 1	Hltf	NP_033236	113	1	nucleus	ATP binding, ATPase activity, 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, RNA polymerase II transcription factor activity, transcription activator activity, zinc ion binding	chromatin modification, regulation of transcription from RNA polymerase II promoter, transcription
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
U1 small nuclear ribonucleoprotein 70 kDa	Snrp70	NP_033250	52	1	nucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	not classified
small nuclear ribonucleoprotein D1	Snrpd1	NP_033252	13	1	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	not classified	mRNA processing, RNA splicing
small nuclear ribonucleoprotein E	Snrpe	NP_033253	11	1	nucleus, ribonucleoprotein complex, spliceosomal complex	RNA binding	mRNA processing, RNA splicing
serine (or cysteine) proteinase inhibitor, clade B, member 9	Serpinb9	NP_033282	42	1	not classified	protein binding	anti-apoptosis
signal recognition particle receptor, B subunit	Srprb	NP_033301	30	1	endoplasmic reticulum, integral to membrane, membrane, ribonucleoprotein complex	GTP binding, nucleotide binding, receptor activity	not classified
stanniocalcin 1	Stc1	NP_033311	27	1	extracellular region, extracellular space	hormone activity	cellular calcium ion homeostasis, cellular monovalent inorganic anion homeostasis
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
synaptotagmin 4	Syt4	NP_033334	48	1	cell junction, cytoplasmic vesicle, integral to membrane, membrane, neuron projection, perinuclear region of cytoplasm, synapse, synaptic vesicle	calcium ion binding, metal ion binding, transporter activity	neurotransmitter secretion, regulation of calcium ion-dependent exocytosis, synaptic vesicle transport, transport
transcription elongation factor A protein 2	Tcea2	NP_033352	34	1	nucleus	DNA binding, metal ion binding, nucleic acid binding, protein binding, RNA polymerase II transcription factor activity, transcription elongation regulator activity, transcription regulator activity, translation elongation factor activity, zinc ion binding	regulation of transcription, regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent, RNA elongation, transcription
tight junction protein 1	Tjp1	NP_033412	195	1	adherens junction, apical junction complex, basolateral plasma membrane, cell junction, cell-cell adherens junction, cell-cell junction, cytoplasm, intercellular canaliculus, membrane, nucleus, plasma membrane, tight junction	protein binding, protein domain specific binding	blastocyst formation
topoisomerase (DNA) I	Top1	NP_033434	91	1	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
tumor necrosis factor (ligand) superfamily, member 10	Tnfsf10	NP_033451	33	1	extracellular space, integral to membrane, membrane	cytokine activity, protein binding, tumor necrosis factor receptor binding	apoptosis, immune response
villin 1	Vil1	NP_033535	93	1	brush border, cytoplasm, cytoskeleton	actin binding, calcium ion binding	actin filament capping, cytoskeleton organization
neurensin 1	Nrsn1	NP_033539	22	1	cell soma, cytoplasmic membrane-bounded vesicle, growth cone, integral to membrane, membrane	not classified	nervous system development
alpha thalassemia/mental retardation syndrome X-linked homolog	Atrx	NP_033556	279	1	heterochromatin, nuclear chromosome, nucleus	ATP binding, chromatin binding, DNA binding, helicase activity, hydrolase activity, metal ion binding, nucleic acid binding, nucleotide binding, protein binding, sequence-specific DNA binding, transcription factor activity, zinc ion binding	DNA repair, forebrain development, regulation of transcription, DNA-dependent, response to DNA damage stimulus
zinc finger protein of the cerebellum 2	Zic2	NP_033600	55	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, protein binding, zinc ion binding	cell differentiation, central nervous system development, multicellular organismal development, nervous system development, neural tube closure, pigmentation during development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
mitogen-activated protein kinase kinase kinase 12	Map3k12	NP_033608	96	1	axon part, cytoplasm, cytosol, growth cone, membrane, plasma membrane	ATP binding, kinase activity, magnesium ion binding, MAP kinase kinase kinase activity, nucleotide binding, protein homodimerization activity, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity, transferase activity	histone phosphorylation, peptidyl-serine phosphorylation, peptidyl-threonine phosphorylation, protein amino acid autophosphorylation, protein amino acid phosphorylation
actin-like 7a	Actl7a	NP_033741	49	1	cytoplasm, cytoskeleton, male germ cell nucleus, microtubule-based flagellum	protein binding	not classified
a disintegrin and metalloprotease domain 2 (fertilin beta)	Adam2	NP_033748	82	1	integral to membrane, membrane	metalloendopeptidase activity, protein binding, zinc ion binding	adult behavior, cell adhesion, proteolysis, visual learning
adenylosuccinate lyase	Adsl	NP_033764	55	1	not classified	(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate AMP-lyase (fumarate-forming) activity, catalytic activity, lyase activity, N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity	purine nucleotide biosynthetic process, purine ribonucleotide biosynthetic process
activated leukocyte cell adhesion molecule	Alcam	NP_033785	65	1	axon, cell soma, external side of plasma membrane, integral to membrane, membrane	protein binding	axon guidance, cell adhesion, motor axon guidance
ankyrin repeat and FYVE domain containing 1	Ankfy1	NP_033801	129	1	cytoplasm, endosome, endosome membrane, membrane	metal ion binding, protein binding, zinc ion binding	endocytosis
adaptor protein complex AP-2, mu1	Ap2m1	NP_033809	50	1	clathrin adaptor complex, clathrin coat of coated pit, coated pit, membrane, mitochondrion, plasma membrane, secretory granule	lipid binding, protein binding	intracellular protein transport, vesicle-mediated transport
apurinic/apyrimidinic endonuclease 1	Apex1	NP_033817	35	1	cytoplasm, intracellular, nucleus	DNA binding, DNA-(apurinic or apyrimidinic site) lyase activity, endonuclease activity, lyase activity, magnesium ion binding, metal ion binding, nuclease activity	cell redox homeostasis, DNA repair, response to DNA damage stimulus
adenine phosphoribosyl transferase	Aprt	NP_033828	20	1	cytoplasm	adenine binding, adenine phosphoribosyltransferase activity, AMP binding, transferase activity, transferase activity, transferring glycosyl groups	adenine metabolic process, adenine salvage, grooming behavior, nucleoside metabolic process, purine ribonucleoside salvage
aquaporin 2	Aqp2	NP_033829	29	1	apical plasma membrane, cytoplasmic vesicle, integral to endosome membrane, integral to membrane, integral to plasma membrane, membrane, membrane fraction, plasma membrane, recycling endosome, recycling endosome membrane	transporter activity, water channel activity	cellular response to water deprivation, renal water transport, transport, water transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
v-raf murine sarcoma 3611 viral oncogene homolog	Araf	NP_033833	68	1	mitochondrion	ATP binding, diacylglycerol binding, kinase activity, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, receptor signaling protein activity, transferase activity, zinc ion binding	intracellular signaling cascade, protein amino acid phosphorylation, signal transduction
antioxidant protein 1	Atox1	NP_033850	7	1	not classified	copper ion binding, metal ion binding	cellular copper ion homeostasis, copper ion transport, ion transport, metal ion transport, transport
axin 1	Axin1	NP_033863	96	1	cytoplasm, cytoplasmic membrane-bounded vesicle, intracellular, lateral plasma membrane, nucleus	protein binding, protein homodimerization activity, signal transducer activity	multicellular organismal development, negative regulation of Wnt receptor signaling pathway, positive regulation of JNK cascade, protein catabolic process, sensory perception of sound, Wnt receptor signaling pathway
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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
breast cancer 1	Brca1	NP_033894	199	1	centrosome, condensed chromosome, cytoplasm, intracellular, nucleus, ribonucleoprotein complex	damaged DNA binding, DNA binding, ligase activity, metal ion binding, protein binding, RNA binding, zinc ion binding	cell cycle, centrosome cycle, centrosome duplication, chordate embryonic development, DNA damage response, signal transduction resulting in induction of apoptosis, DNA repair, DNA replication, dosage compensation, by inactivation of X chromosome, fatty acid biosynthetic process, lipid biosynthetic process, modification-dependent protein catabolic process, response to DNA damage stimulus
peripheral benzodiazepine receptor	Tspo	NP_033905	19	1	integral to membrane, membrane, mitochondrion	receptor activity	not classified
protein disulfide isomerase associated 4	Pdia4	NP_033917	72	1	endoplasmic reticulum, endoplasmic reticulum lumen	isomerase activity, protein binding, protein disulfide isomerase activity	cell redox homeostasis
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
calpastatin	Cast	NP_033947	81	1	cellular_component	calcium-dependent cysteine-type endopeptidase inhibitor activity, cysteine-type endopeptidase inhibitor activity, peptidase inhibitor activity	protein catabolic process
chaperonin containing Tcp1, subunit 6b (zeta)	Cct6b	NP_033969	58	1	cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
cyclin-dependent kinase 4	Cdk4	NP_034000	34	1	cyclin-dependent protein kinase holoenzyme complex, nucleoplasm, nucleus, transcription factor complex	ATP binding, cyclin-dependent protein kinase activity, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cell cycle, cell division, protein amino acid phosphorylation, regulation of cell cycle, regulation of cell proliferation, signal transduction
tripeptidyl-peptidase I	Tpp1	NP_034036	61	1	mitochondrion	hydrolase activity, serine-type endopeptidase activity, serine-type peptidase activity	lysosome organization, neuromuscular process controlling balance
copine VI	Cpne6	NP_034077	62	1	axon, dendrite, membrane fraction	phosphatidylserine binding	biological_process
cathepsin W preproprotein	Ctsw	NP_034115	42	1	not classified	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis
D-amino acid oxidase 1	Dao1	NP_034148	39	1	peroxisome	D-amino-acid oxidase activity, oxidoreductase activity	leucine metabolic process, oxidation reduction
DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	Ddx4	NP_034159	76	1	cell part, cytoplasm, nucleus, ribonucleoprotein complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, protein binding	multicellular organismal development, regulation of protein localization
dynamin	Dnm1	NP_034195	97	1	cytoplasm, cytoskeleton, membrane coat, microtubule	GTP binding, GTPase activity, hydrolase activity, identical protein binding, motor activity, nucleotide binding, protein binding	endocytosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
dystrophin related protein 2	Drp2	NP_034208	108	1	cytoplasm, cytoskeleton, plasma membrane	calcium ion binding, metal ion binding, protein binding, zinc ion binding	not classified
EH-domain containing 1	Ehd1	NP_034249	61	1	early endosome, endocytic vesicle, endosome, membrane, plasma membrane	ATP binding, calcium ion binding, GTP binding, GTPase activity, nucleotide binding, protein binding	endocytosis, endosome transport
eukaryotic translation initiation factor 1A	Eif1a	NP_034250	17	1	not classified	RNA binding, translation initiation factor activity	translation, translational initiation
eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	NP_034251	125	1	cytoplasm, endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	ATP binding, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, translation initiation factor activity	activation of caspase activity, apoptosis, bone mineralization, calcium-mediated signaling, chondrocyte development, endoplasmic reticulum organization, endoplasmic reticulum unfolded protein response, fat cell differentiation, insulin secretion, insulin-like growth factor receptor signaling pathway, lactation, negative regulation of myelination, negative regulation of translation, pancreas development, positive regulation of protein binding, positive regulation of signal transduction, protein amino acid autophosphorylation, protein amino acid phosphorylation, regulation of fatty acid metabolic process, regulation of translation, response to stress, response to unfolded protein, skeletal system development, SREBP-mediated signaling pathway, translation, virus-infected cell apoptosis
Ets2 repressor factor	Erf	NP_034285	59	1	nucleus	DNA binding, sequence-specific DNA binding, transcription factor activity	regulation of transcription, regulation of transcription, DNA-dependent, transcription
fumarylacetoacetate hydrolase	Fah	NP_034306	46	1	not classified	calcium ion binding, catalytic activity, fumarylacetoacetase activity, hydrolase activity, magnesium ion binding, metal ion binding	arginine catabolic process, aromatic amino acid family metabolic process, L-phenylalanine catabolic process, metabolic process, tyrosine catabolic process
fibrillin 2	Fbn2	NP_034311	314	1	extracellular region, microfibril, proteinaceous extracellular matrix	binding, calcium ion binding, extracellular matrix structural constituent	embryonic limb morphogenesis, limb morphogenesis
fibroblast growth factor 5	Fgf5	NP_034333	29	1	extracellular region	growth factor activity	glial cell differentiation, positive regulation of cell division

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
FK506 binding protein 4	Fkbp4	NP_034349	52	1	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
folylpolyglutamyl synthetase	Fpgs	NP_034366	65	1	cytoplasm, mitochondrion	ATP binding, ligase activity, nucleotide binding, tetrahydrofolylpolyglutamate synthase activity	biosynthetic process, folic acid and derivative biosynthetic process, one-carbon metabolic process
mitochondrial ribosomal protein S33 isoform 1	Mrps33	NP_034400	12	1	cellular_component, mitochondrion, ribonucleoprotein complex, ribosome	molecular_function	biological_process
guanine nucleotide binding protein (G protein), alpha inhibiting 3	Gnai3	NP_034436	41	1	cytoplasm, Golgi apparatus, heterotrimeric G-protein complex	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding, protein binding, signal transducer activity	G-protein coupled receptor protein signaling pathway, regulation of heart contraction, signal transduction
G-protein-coupled receptor 50	Gpr50	NP_034470	65	1	integral to membrane, membrane, plasma membrane	G-protein coupled receptor activity, melatonin receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
granzyme A	Gzma	NP_034500	29	1	extracellular region	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	apoptosis, cytolysis, proteolysis
hexosaminidase B	Hexb	NP_034552	61	1	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
histidine rich calcium binding protein	Hrc	NP_034603	85	1	sarcoplasmic reticulum membrane	not classified	calcium ion homeostasis, regulation of heart contraction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
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
insulin-like growth factor 2 receptor	Igf2r	NP_034645	274	1	cytoplasm, endosome, integral to membrane, lysosome, membrane, membrane fraction, nuclear envelope lumen, nucleus, trans-Golgi network transport vesicle	glycoprotein binding, insulin-like growth factor binding, mannose binding, receptor activity, transporter activity	transport
interleukin 16	Il16	NP_034681	141	1	cytoplasm, extracellular region, extracellular space, intracellular, nucleus	cytokine activity, protein binding	chemotaxis, induction of positive chemotaxis, leukocyte chemotaxis, regulation of transcription, transcription
integrin linked kinase	Ilk	NP_034692	51	1	cell junction, focal adhesion, membrane, plasma membrane	ATP binding, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity, transferase activity	branching involved in ureteric bud morphogenesis, establishment or maintenance of epithelial cell apical/basal polarity, integrin-mediated signaling pathway, positive regulation of cell proliferation, protein amino acid phosphorylation, regulation of signal transduction
integrin alpha 5	Itga5	NP_034707	115	1	external side of plasma membrane, integral to membrane, integrin complex, membrane, synaptosome	calcium ion binding, integrin binding, protein binding, receptor activity	cell adhesion, cell-cell adhesion mediated by integrin, cell-substrate junction assembly, heterophilic cell adhesion, integrin-mediated signaling pathway, leukocyte adhesion, memory
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
lysosomal membrane glycoprotein 1	Lamp1	NP_034814	44	1	endosome, external side of plasma membrane, integral to membrane, late endosome, lysosome, melanosome, membrane, multivesicular body, plasma membrane, sarcolemma	protein binding	not classified
like-glycosyltransferase	Large	NP_034817	88	1	Golgi apparatus, integral to membrane, membrane	transferase activity, transferase activity, transferring glycosyl groups	glycoprotein biosynthetic process, muscle maintenance
lamin B1	Lmnb1	NP_034851	67	1	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
lysyl oxidase-like 1	Loxl1	NP_034859	66	1	extracellular matrix, extracellular region, proteinaceous extracellular matrix	copper ion binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor, protein binding	oxidation reduction
lysosomal trafficking regulator	Lyst	NP_034878	425	1	cytoplasm, cytosol	not classified	blood coagulation, defense response to bacterium, defense response to protozoan, defense response to virus, leukocyte chemotaxis, lysosome organization, mast cell secretory granule organization, melanosome organization, microtubule-based process, neutrophil mediated immunity, phospholipid homeostasis, phospholipid metabolic process, pigment granule organization, pigmentation, positive regulation of natural killer cell activation, protein transport, response to drug, secretion of lysosomal enzymes, T cell mediated immunity, transport
mutS homolog 3	Msh3	NP_034959	123	1	not classified	ATP binding, centromeric DNA binding, damaged DNA binding, DNA binding, mismatched DNA binding, nucleotide binding	DNA repair, mismatch repair, response to DNA damage stimulus, somatic hypermutation of immunoglobulin genes, somatic recombination of immunoglobulin gene segments
myelin basic protein expression factor 2, repressor	Myef2	NP_034982	57	1	nucleus	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	transcription
myosin IB	Myo1b	NP_034993	129	1	myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	not classified
neuronal apoptosis inhibitory protein 5	Naip5	NP_035000	160	1	intracellular	metal ion binding, zinc ion binding	apoptosis
neutrophil cytosolic factor 2	Ncf2	NP_035007	59	1	acrosomal vesicle, cytoplasm, cytosol	binding, protein binding, Rac GTPase binding, superoxide-generating NADPH oxidase activity	NADP catabolic process, superoxide anion generation, superoxide metabolic process
neurofilament, heavy polypeptide	Nefh	NP_035034	117	1	intermediate filament, mitochondrion, neurofilament	not classified	intermediate filament bundle assembly, intermediate filament cytoskeleton organization, microtubule cytoskeleton organization, neurofilament cytoskeleton organization
nitrogen fixation gene, yeast homolog 1	Nfs1	NP_035041	51	1	cytoplasm, mitochondrial matrix, mitochondrion, nucleus	catalytic activity, cysteine desulfurase activity, pyridoxal phosphate binding, transferase activity	cysteine metabolic process, iron incorporation into metallo-sulfur cluster, metabolic process, Mo-molybdopterin cofactor biosynthetic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
natural killer tumor recognition	Nktr	NP_035048	163	1	not classified	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity	protein folding
orthodenticle 1	Otx1	NP_035153	38	1	nucleus	DNA binding, protein binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity	anterior/posterior pattern formation, forebrain development, inner ear morphogenesis, midbrain development, multicellular organismal development, regulation of transcription, regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent
programmed cell death 6	Pdcd6	NP_035181	22	1	cytoplasm, endoplasmic reticulum, membrane, microsome, nucleus, soluble fraction	calcium ion binding, calcium-dependent protein binding, protein binding	activation of caspase activity, apoptosis, response to calcium ion
phosphodiesterase 4D, cAMP specific	Pde4d	NP_035186	85	1	cytoplasm, cytoskeleton, membrane	3',5'-cyclic-nucleotide phosphodiesterase activity, catalytic activity, hydrolase activity, metal ion binding	cAMP catabolic process, signal transduction, smooth muscle contraction
ErbB3-binding protein 1	Pa2g4	NP_035249	44	1	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
polymerase (DNA directed), delta 1, catalytic subunit	Pold1	NP_035261	124	1	nucleus	3'-5' exonuclease activity, DNA binding, DNA-directed DNA polymerase activity, exonuclease activity, hydrolase activity, metal ion binding, nuclease activity, nucleic acid binding, nucleotide binding, nucleotidyltransferase activity, transferase activity, zinc ion binding	base-excision repair, gap-filling, DNA replication, DNA replication proofreading, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
proteasome activator subunit 3	Psme3	NP_035322	30	1	cytoplasm, nucleus, proteasome activator complex, proteasome complex	peptidase activity, proteasome activator activity	apoptosis, cell cycle
RAD1 homolog	Rad1	NP_035362	32	1	nucleus	damaged DNA binding, exodeoxyribonuclease III activity, exonuclease activity, hydrolase activity, nuclease activity	DNA repair, response to DNA damage stimulus
RAD52 homolog	Rad52	NP_035366	47	1	nucleus	protein binding	DNA recombination, DNA repair, double-strand break repair via homologous recombination, response to DNA damage stimulus
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

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
SH3 domain protein 1B	Itsn2	NP_035495	189	1	cytoplasm, intracellular	calcium ion binding, protein binding, Rho guanyl-nucleotide exchange factor activity	endocytosis, regulation of Rho protein signal transduction
solute carrier family 16, member 7	Slc16a7	NP_035521	53	1	integral to membrane, membrane, plasma membrane	secondary active monocarboxylate transmembrane transporter activity, symporter activity	organic anion transport, transport
solute carrier family 34 (sodium phosphate), member 1	Slc34a1	NP_035522	69	1	integral to membrane, membrane, plasma membrane	protein binding, sodium ion binding, sodium-dependent phosphate transmembrane transporter activity, symporter activity	bone remodeling, ion transport, phosphate transport, sodium ion transport, transport
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4	Smarca4	NP_035547	182	1	heterochromatin, nuclear euchromatin, nucleolus, nucleus, perichromatin fibrils, SWI/SNF complex	ATPase activity, chromatin binding, protein binding, transcription factor binding	blastocyst growth, blastocyst hatching, embryonic hindlimb morphogenesis, epidermis morphogenesis, extracellular matrix organization, forebrain development, glial cell fate determination, heart development, heart trabecula formation, hindbrain development, keratinocyte differentiation, methylation-dependent chromatin silencing, negative regulation of transcription from RNA polymerase II promoter, nucleosome assembly, vasculogenesis
sortilin-related receptor, LDLR class A repeats-containing	Sorl1	NP_035566	247	1	integral to membrane, low-density lipoprotein particle, membrane	receptor activity	cholesterol metabolic process, endocytosis, lipid metabolic process, lipid transport, multicellular organismal development, steroid metabolic process, transport
spectrin alpha 1	Spna1	NP_035595	280	1	cortical cytoskeleton, cytoplasm, cytoskeleton, membrane, spectrin	actin binding, calcium ion binding	actin filament capping, hemopoiesis, porphyrin biosynthetic process, regulation of cell shape
striatin, calmodulin binding protein	Strn	NP_035630	86	1	cellular_component, cytoplasm, membrane	calmodulin binding, molecular_function	biological_process
syntaxin binding protein 2	Stxbp2	NP_035633	66	1	not classified	syntaxin binding	protein transport, transport, vesicle docking during exocytosis, vesicle-mediated transport
upstream binding transcription factor, RNA polymerase I isoform 1	Ubtf	NP_035681	89	1	nucleolus, nucleus	DNA binding, protein binding	regulation of transcription, transcription
sex determining region Y	Sry	NP_035694	49	1	cytoplasm, nucleus	DNA bending activity, DNA binding, protein binding	cell differentiation, male sex determination, regulation of transcription, sex determination, sex differentiation, transcription
THO complex 4	Thoc4	NP_035698	27	1	cytoplasm, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding, single-stranded DNA binding	mRNA processing, mRNA transport, RNA splicing, transport
testis expressed gene 264	Tex264	NP_035703	34	1	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
nuclear receptor subfamily 2, group C, member 1	Nr2c1	NP_035759	65	1	cellular_component, nucleus	DNA binding, histone deacetylase binding, ligand-dependent nuclear receptor activity, metal ion binding, protein binding, protein homodimerization activity, receptor activity, sequence-specific DNA binding, steroid hormone receptor activity, transcription factor activity, transcription repressor activity, zinc ion binding	negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription, DNA-dependent, transcription
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
uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	NP_035801	33	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding	mitochondrial transport, transport
utrophin	Utrn	NP_035812	393	1	cell junction, dystrophin-associated glycoprotein complex, neuromuscular junction, synapse	actin binding, protein binding	adult somatic muscle development
villin-like	Vill	NP_035830	87	1	not classified	actin binding, calcium ion binding	actin filament capping, cytoskeleton organization
xanthine dehydrogenase	Xdh	NP_035853	147	1	peroxisome	2 iron, 2 sulfur cluster binding, catalytic activity, electron carrier activity, FAD binding, iron ion binding, iron-sulfur cluster binding, metal ion binding, molybdenum ion binding, oxidoreductase activity, xanthine dehydrogenase activity, xanthine oxidase activity	lactation, oxidation reduction, regulation of epithelial cell differentiation
cyclin D binding myb-like transcription factor 1 isoform 1	Dmtf1	NP_035936	85	1	nucleus	DNA binding	cell cycle, regulation of transcription, transcription
germ cell-less	Gmcl1	NP_035948	60	1	nuclear envelope, nuclear matrix, nucleus	protein binding	cell differentiation, multicellular organismal development, regulation of transcription, spermatogenesis
phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	NP_035952	66	1	integral to membrane, membrane	phosphatidylinositol N-acetylglucosaminyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups	GPI anchor biosynthetic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
monoglyceride lipase	Mgll	NP_035974	33	1	not classified	acylglycerol lipase activity, carboxylesterase activity, hydrolase activity	not classified
3'-phosphoadenosine 5'-phosphosulfate synthase 1	Papss1	NP_035993	71	1	sulfate adenylyltransferase complex (ATP)	adenylylsulfate kinase activity, ATP binding, catalytic activity, kinase activity, nucleotide binding, nucleotidyltransferase activity, sulfate adenylyltransferase (ATP) activity, transferase activity, transferase activity, transferring phosphorus-containing groups	3'-phosphoadenosine 5'-phosphosulfate biosynthetic process, sulfate assimilation
proteasome 26S ATPase subunit 4	Psmc4	NP_036004	47	1	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding	blastocyst development, protein catabolic process
protein tyrosine phosphatase, non-receptor type 21	Ptpn21	NP_036007	133	1	cytoplasm, cytoskeleton	binding, hydrolase activity, phosphatase activity, phosphoprotein phosphatase activity, protein tyrosine phosphatase activity	dephosphorylation, protein amino acid dephosphorylation
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
annexin A10	Anxa10	NP_036052	35	1	mitochondrion	calcium ion binding, calcium-dependent phospholipid binding	not classified
mitogen-activated protein kinase binding protein 1	Mapkbp1	NP_036071	163	1	cellular_component	protein binding	activation of JNKK activity
lysophospholipase 2	Lypla2	NP_036072	25	1	cytoplasm	hydrolase activity	fatty acid metabolic process, lipid metabolic process
mitogen activated protein kinase kinase kinase 4	Map3k4	NP_036078	180	1	cytoplasm	ATP binding, kinase activity, magnesium ion binding, MAP kinase kinase kinase activity, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
proteasome (prosome, macropain) subunit, alpha type 6	Psma6	NP_036098	27	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
COP9 signalosome subunit 4	Cops4	NP_036131	46	1	cytoplasm, nucleus, signalosome	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
polymerase (DNA directed), kappa	Polk	NP_036178	96	1	nucleus	damaged DNA binding, DNA binding, DNA-directed DNA polymerase activity, magnesium ion binding, metal ion binding, nucleotidyltransferase activity, transferase activity, zinc ion binding	DNA repair, DNA replication, response to DNA damage stimulus
adducin 2 (beta)	Add2	NP_038486	81	1	cytoplasm, cytoskeleton, membrane, plasma membrane	actin binding, calmodulin binding, metal ion binding, structural molecule activity	hemopoiesis
adrenergic receptor, beta 3	Adrb3	NP_038490	43	1	integral to membrane, membrane, membrane fraction, plasma membrane	adrenoceptor activity, beta-3 adrenergic receptor binding, beta-adrenergic receptor activity, G-protein coupled receptor activity, receptor activity, signal transducer activity	activation of adenylate cyclase activity by G-protein signaling pathway, brown fat cell differentiation, diet induced thermogenesis, G-protein coupled receptor protein signaling pathway, heat generation, negative regulation of multicellular organism growth, response to cold, signal transduction, vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure
clusterin	Clu	NP_038520	52	1	extracellular region	not classified	cell death
eukaryotic translation initiation factor 4A2	Eif4a2	NP_038534	46	1	not classified	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding, translation initiation factor activity	response to protein stimulus, translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
fibroblast growth factor 9	Fgf9	NP_038546	23	1	extracellular region, extracellular space	growth factor activity, heparin binding	angiogenesis, cell differentiation, cell-cell signaling, chondrocyte differentiation, embryonic gut development, embryonic limb morphogenesis, embryonic skeletal system development, fibroblast growth factor receptor signaling pathway, inner ear morphogenesis, lung development, male gonad development, male sex determination, multicellular organismal development, negative regulation of Wnt receptor signaling pathway, osteoblast differentiation, positive regulation of cardiac muscle cell proliferation, positive regulation of cell division, positive regulation of cell proliferation, positive regulation of epithelial cell proliferation, positive regulation of fibroblast growth factor receptor signaling pathway, positive regulation of MAPKKK cascade, positive regulation of mesenchymal cell proliferation, positive regulation of smoothened signaling pathway
platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	Pafah1b1	NP_038653	47	1	cell leading edge, centrosome, cytoplasm, cytoskeleton, membrane, microtubule, microtubule associated complex, microtubule cytoskeleton, motile primary cilium, nonmotile primary cilium, nuclear envelope, nucleus, perinuclear region of cytoplasm	hydrolase activity, microtubule binding, phosphoprotein binding, protein binding, protein homodimerization activity	acrosome assembly, actin cytoskeleton organization, adult locomotory behavior, cell cycle, cell differentiation, cell division, cell migration, cerebral cortex development, hippocampus development, layer formation in the cerebral cortex, learning or memory, lipid catabolic process, microtubule cytoskeleton organization, mitosis, multicellular organismal development, nervous system development, neuroblast proliferation, neuromuscular process controlling balance, neuron migration, nuclear envelope disassembly, regulation of Rho GTPase activity, retrograde axon cargo transport, synaptic transmission, transmission of nerve impulse, transport, vesicle transport along microtubule
solute carrier family 22 member 2	Slc22a2	NP_038695	62	1	integral to membrane, integral to plasma membrane, membrane	ion transmembrane transporter activity, organic cation transmembrane transporter activity, transporter activity	cation transport, ion transport, organic cation transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
spectrin beta 1	Spnb1	NP_038703	268	1	cortical cytoskeleton, cytoplasm, cytoskeleton, membrane, plasma membrane, spectrin	actin binding, structural constituent of cytoskeleton	actin filament capping, porphyrin biosynthetic process
suppressor of Ty 5 homolog	Supt5h	NP_038704	121	1	nucleus	transcription elongation regulator activity	positive regulation of RNA elongation from RNA polymerase II promoter, regulation of transcription, regulation of transcription from RNA polymerase II promoter, transcription
t-complex protein 1	Tcp1	NP_038714	60	1	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
nuclear receptor subfamily 2, group E, member 3	Nr2e3	NP_038736	43	1	nucleus, transcription factor complex	DNA binding, ligand-dependent nuclear receptor activity, metal ion binding, protein binding, receptor activity, sequence-specific DNA binding, steroid binding, steroid hormone receptor activity, transcription factor activity, zinc ion binding	negative regulation of cell proliferation, negative regulation of transcription from RNA polymerase II promoter, positive regulation of rhodopsin gene expression, positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription, DNA-dependent, retina development in camera-type eye, transcription
thioredoxin reductase 2 precursor	Txnrd2	NP_038739	57	1	cytoplasm, mitochondrion	FAD binding, NADP or NADPH binding, oxidoreductase activity, protein binding, selenium binding, thioredoxin-disulfide reductase activity	cell redox homeostasis, heart development, hemopoiesis, oxidation reduction, response to oxygen radical
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
eukaryotic translation initiation factor 2 alpha kinase 4	Eif2ak4	NP_038747	187	1	cytoplasm, cytosolic ribosome	aminoacyl-tRNA ligase activity, ATP binding, eukaryotic translation initiation factor 2alpha kinase activity, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity, translation initiation factor activity	cellular response to starvation, endoplasmic reticulum unfolded protein response, negative regulation of translation, protein amino acid phosphorylation, regulation of translational initiation, regulation of translational initiation in response to stress, translation, tRNA aminoacylation for protein translation
MAX-interacting protein	Mga	NP_038748	333	1	nucleus, transcription factor complex	DNA binding, transcription factor activity, transcription regulator activity	regulation of transcription, regulation of transcription, DNA-dependent, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
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
phospholipase A2, group VII	Pla2g7	NP_038765	49	1	extracellular region	1-alkyl-2-acetylglycerophosphocholine esterase activity, hydrolase activity	inflammatory response, lipid catabolic process
nibrin	Nbn	NP_038780	84	1	chromosome, chromosome, telomeric region, intracellular, nucleus, replication fork	damaged DNA binding	cell cycle, cell proliferation, DNA damage checkpoint, DNA repair, meiosis, neuromuscular process controlling balance, response to DNA damage stimulus
SH2 domain containing 3C	Sh2d3c	NP_038809	94	1	cytoplasm, intracellular, membrane	guanyl-nucleotide exchange factor activity, protein binding, transmembrane receptor protein tyrosine kinase adaptor protein activity	signal transduction, small GTPase mediated signal transduction
polo-like kinase 3	Plk3	NP_038835	72	1	membrane	ATP binding, kinase activity, nucleotide binding, polo kinase kinase activity, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cell cycle, protein amino acid phosphorylation
GTP binding protein 1	Gtpbp1	NP_038846	72	1	not classified	GTP binding, GTPase activity, nucleotide binding	not classified
RAB GTPase activating protein 1-like isoform a	Rabgap1l	NP_038890	92	1	early endosome, Golgi apparatus, intracellular, nucleus	GTPase activator activity, Rab GTPase activator activity	regulation of protein localization, regulation of Rab GTPase activity
phospholipase C-like 2	Plcl2	NP_038908	126	1	cytoplasm	calcium ion binding, phosphoinositide phospholipase C activity, phospholipase C activity, phosphoric diester hydrolase activity, signal transducer activity	intracellular signaling cascade, lipid metabolic process, signal transduction
sex comb on midleg homolog 1	Scmh1	NP_038911	74	1	nucleus	protein binding, transcription repressor activity	multicellular organismal development, negative regulation of transcription, regulation of transcription, transcription
translocase of inner mitochondrial membrane 8 homolog a	Timm8a1	NP_038926	11	1	membrane, mitochondrial inner membrane, mitochondrial intermembrane space protein transporter complex, mitochondrion	metal ion binding, zinc ion binding	protein import into mitochondrial inner membrane, protein targeting to mitochondrion, protein transport, transmembrane transport, transport
vesicle-associated membrane protein, associated protein A	Vapa	NP_038961	28	1	endoplasmic reticulum, integral to membrane, membrane, microtubule, plasma membrane	molecular_function, structural molecule activity	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ATPase, class II, type 9A	Atp9a	NP_056546	119	1	integral to membrane, membrane	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic activity, hydrolase activity, magnesium ion binding, metal ion binding, nucleotide binding, phospholipid-translocating ATPase activity	ATP biosynthetic process, metabolic process, phospholipid transport
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
patatin-like phospholipase domain containing 6	Pnpla6	NP_056616	147	1	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane, membrane fraction	carboxylesterase activity, hydrolase activity, lysophospholipase activity	angiogenesis, lipid catabolic process, lipid metabolic process, organ morphogenesis, phosphatidylcholine metabolic process
chloride channel 5	Clcn5	NP_057900	83	1	endosome, Golgi apparatus, integral to membrane, membrane, plasma membrane	antiporter activity, ATP binding, chloride ion binding, ion channel activity, nucleotide binding, voltage-gated chloride channel activity	chloride transport, endocytosis, ion transport, transport
H2A histone family, member Z	H2afz	NP_058030	14	1	Barr body, chromosome, nucleosome, nucleus	DNA binding	multicellular organismal development, nucleosome assembly
C-type lectin, superfamily member 13	Clec4f	NP_058031	61	1	integral to membrane, membrane	binding, receptor activity, sugar binding	endocytosis
serine/arginine-rich protein specific kinase 1	Srpk1	NP_058075	73	1	cytoplasm, nucleus	ATP binding, kinase activity, magnesium ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cell differentiation, chromosome segregation, mRNA processing, protein amino acid phosphorylation, protein kinase cascade, regulation of mRNA processing, RNA splicing
Y box protein 2	Ybx2	NP_058571	38	1	cytoplasm, nucleus, polysome, ribonucleoprotein complex	chromatin binding, DNA binding, lipid binding, mRNA 3'-UTR binding, mRNA binding, nucleic acid binding, ribonucleoprotein binding, RNA binding, translation regulator activity	mRNA stabilization, negative regulation of binding, negative regulation of translation, oogenesis, regulation of transcription, DNA-dependent, spermatid development
keratin 35	Krt35	NP_058576	48	1	intermediate filament	structural molecule activity	not classified
heterogeneous nuclear ribonucleoprotein C	Hnrnpc	NP_058580	34	1	nucleus, pronucleus, ribonucleoprotein complex, spliceosomal complex	mRNA binding, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
claudin 7	Cldn7	NP_058583	22	1	cell junction, integral to membrane, membrane, plasma membrane, tight junction	structural molecule activity	not classified
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	B3gnt2	NP_058584	46	1	Golgi apparatus, integral to membrane, membrane	galactosyltransferase activity, manganese ion binding, transferase activity, transferase activity, transferring glycosyl groups	axon guidance, protein amino acid glycosylation, sensory perception of smell
tropomodulin 3	Tmod3	NP_058659	40	1	cytoplasm, cytoskeleton, filamentous actin, lamellipodium, ruffle	actin binding, microtubule minus-end binding, tropomyosin binding	negative regulation of cell motion, pointed-end actin filament capping

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
3-phosphoglycerate dehydrogenase	Phgdh	NP_058662	57	1	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
caseinolytic protease, ATP-dependent, proteolytic subunit homolog	Clpp	NP_059089	30	1	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
PAK-interacting exchange factor beta isoform c	Arhgef7	NP_059098	73	1	intracellular	guanyl-nucleotide exchange factor activity, protein binding, Rho guanyl-nucleotide exchange factor activity	intracellular signaling cascade, regulation of Rho protein signal transduction
golgi autoantigen, golgin subfamily a, 4	Golga4	NP_061218	258	1	cytoplasm, Golgi apparatus, membrane	not classified	not classified
GIPC PDZ domain containing family, member 1	Gipc1	NP_061241	36	1	cytoplasm, cytosol, dendritic shaft, dendritic spine, membrane, synaptic vesicle, vesicle membrane	actin binding, GTPase activator activity, myosin binding, protein binding, protein homodimerization activity	endothelial cell migration, glutamate secretion, G-protein coupled receptor protein signaling pathway, negative regulation of proteasomal ubiquitin-dependent protein catabolic process, positive regulation of transforming growth factor beta receptor signaling pathway, protein targeting, regulation of protein stability, regulation of synaptic plasticity, synaptic transmission
nuclear factor of activated T-cells 5 isoform b	Nfat5	NP_061293	168	1	cytoplasm, nucleus	DNA binding, protein binding, transcription factor activity	cytokine production, positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription, DNA-dependent, transcription, transcription, DNA-dependent

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
SH2B adaptor protein 2	Sh2b2	NP_061295	67	1	actin filament, cytoplasm, membrane, plasma membrane, ruffle, stress fiber	protein binding, SH3/SH2 adaptor activity, signal transducer activity, transmembrane receptor protein tyrosine kinase adaptor protein activity	actin cytoskeleton organization, antigen receptor-mediated signaling pathway, B-1 B cell homeostasis, brown fat cell differentiation, cytokine-mediated signaling pathway, glucose homeostasis, insulin receptor signaling pathway, intracellular signaling cascade, negative regulation of glucose import, regulation of immune response, regulation of metabolic process
basic FGF repressed, zinc binding protein	Uqcc	NP_061376	24	1	cytoplasmic membrane-bounded vesicle, cytoplasmic vesicle	protein binding	biological_process
roundabout homolog 1	Robo1	NP_062286	176	1	axolemma, integral to membrane, membrane	protein binding, protein heterodimerization activity, receptor activity	axon guidance, cell differentiation, chemotaxis, multicellular organismal development, nervous system development
unc93 homolog B	Unc93b1	NP_062322	67	1	endoplasmic reticulum, integral to membrane, membrane	molecular_function	antigen processing and presentation of exogenous peptide antigen via MHC class II, toll-like receptor signaling pathway
amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	Apbb1ip	NP_062329	74	1	cell junction, cell projection, cytoplasm, cytoskeleton, membrane, plasma membrane	not classified	signal transduction
glucose-6-phosphate dehydrogenase 2	G6pd2	NP_062341	59	1	not classified	binding, catalytic activity, glucose-6-phosphate dehydrogenase activity, oxidoreductase activity	carbohydrate metabolic process, glucose metabolic process, metabolic process, oxidation reduction
acyl-CoA synthetase long-chain family member 4 isoform 2	Acsl4	NP_062350	74	1	endoplasmic reticulum, integral to membrane, membrane, microsome, mitochondrial outer membrane, mitochondrion, peroxisome	ATP binding, catalytic activity, ligase activity, long-chain-fatty-acid-CoA ligase activity, magnesium ion binding, nucleotide binding	fatty acid metabolic process, lipid metabolic process, metabolic process, regulation of fatty acid metabolic process
ubiquitin carboxyl-terminal esterase L5	Uchl5	NP_062508	38	1	intracellular, proteasome complex	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process
REV1-like	Rev1	NP_062516	137	1	intracellular, nucleus	damaged DNA binding, deoxycytidyl transferase activity, DNA binding, DNA-directed DNA polymerase activity, magnesium ion binding, metal ion binding, nucleotidyltransferase activity, transferase activity	DNA repair, DNA replication, error-prone postreplication DNA repair, response to DNA damage stimulus
calcium channel, voltage-dependent, alpha 1F subunit	Cacna1f	NP_062528	222	1	cell soma, integral to membrane, integral to membrane of membrane fraction, membrane, voltage-gated calcium channel complex	calcium channel activity, calcium ion binding, ion channel activity, voltage-gated calcium channel activity, voltage-gated ion channel activity	axonogenesis, calcium ion transport, cellular calcium ion homeostasis, dendrite morphogenesis, ion transport, response to stimulus, transport, visual perception

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
phosphofructokinase, platelet	Pfkp	NP_062677	85	1	6-phosphofructokinase complex, cytoplasm, cytosol	6-phosphofructokinase activity, ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, transferase activity	glycolysis
sorting nexin 1	Snx1	NP_062701	59	1	endosome, Golgi apparatus, membrane	phosphoinositide binding, protein binding, protein transporter activity	cell communication, intracellular protein transport, protein transport, transport
SPEN homolog, transcriptional regulator	Spen	NP_062737	399	1	nucleus	binding, DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding, single-stranded DNA binding, transcription activator activity, transcription corepressor activity, transcription factor activity, transcription repressor activity	negative regulation of transcription, DNA-dependent, Notch signaling pathway, regulation of transcription, regulation of transcription from RNA polymerase II promoter, transcription
prostaglandin E synthase 3 (cytosolic)	Ptges3	NP_062740	19	1	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
A kinase anchor protein 8	Akap8	NP_062748	76	1	condensed chromosome, female pronucleus, intracellular, nuclear chromatin, nucleus	chromatin binding, DNA binding, kinase activity, metal ion binding, zinc ion binding	mitotic chromosome condensation
vacuolar protein sorting 29	Vps29	NP_062754	20	1	cytoplasm, endosome, membrane	hydrolase activity, metal ion binding, phosphoserine phosphatase activity, zinc ion binding	Golgi to vacuole transport, protein transport, transport
peroxisomal biogenesis factor 14	Pex14	NP_062755	41	1	membrane, peroxisomal membrane, peroxisome	not classified	protein transport, transmembrane transport, transport
SEC23B	Sec23b	NP_062761	86	1	COPII vesicle coat, endoplasmic reticulum, Golgi apparatus, 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
acid phosphatase 6, lysophosphatidic	Acp6	NP_062774	48	1	extracellular region, mitochondrion	acid phosphatase activity, hydrolase activity	biological_process
drebrin 1	Dbn1	NP_062787	72	1	actin cytoskeleton, cytoplasm, intracellular	actin binding	actin filament organization, cell differentiation, multicellular organismal development, nervous system development
membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 6)	Mpp6	NP_064323	61	1	integral to membrane, membrane, plasma membrane	guanylate kinase activity, protein binding	not classified
zinc finger protein 111	Zfp111	NP_064324	80	1	nucleus	metal ion binding, zinc ion binding	transcription
canopy 2 homolog	Cnpy2	NP_064337	21	1	endoplasmic reticulum	molecular_function	biological_process
2-hydroxyacyl-CoA lyase 1	Hacl1	NP_064359	64	1	peroxisome	catalytic activity, lyase activity, magnesium ion binding, metal ion binding, thiamin pyrophosphate binding, transferase activity	lipid metabolic process

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	1	cellular_component, cytoplasm	protein binding, SH3/SH2 adaptor activity	myeloid cell differentiation, transmembrane receptor protein tyrosine kinase signaling pathway
HLA-B associated transcript 2	Bat2	NP_064411	229	1	cellular_component, cytoplasm, nucleus	molecular_function	biological_process
calcium channel, voltage-dependent, alpha 2/delta subunit 2	Cacna2d2	NP_064659	130	1	integral to membrane, membrane, voltage-gated calcium channel complex	calcium channel activity, calcium ion binding, ion channel activity, metal ion binding, voltage-gated calcium channel activity, voltage-gated ion channel activity	calcium ion transport, ion transport, muscle fiber development, neuromuscular junction development, positive regulation of organ growth, regulation of multicellular organism growth, rhythmic synaptic transmission, transport
WD repeat domain 46	Wdr46	NP_065628	69	1	cellular_component	not classified	not classified
junctophilin 1	Jph1	NP_065629	72	1	endoplasmic reticulum, integral to membrane, membrane, microsome, plasma membrane, sarcoplasmic reticulum, Z disc	structural constituent of muscle	muscle organ development
c-K-ras2 protein	Kras	NP_067259	21	1	intracellular, membrane, membrane fraction, plasma membrane	GTP binding, GTPase activity, nucleotide binding, protein binding	actin cytoskeleton organization, negative regulation of neuron apoptosis, positive regulation of cell proliferation, positive regulation of Rac protein signal transduction, Ras protein signal transduction, regulation of long-term neuronal synaptic plasticity, regulation of synaptic transmission, GABAergic, small GTPase mediated signal transduction, striated muscle cell differentiation, visual learning
solute carrier family 7, member 9	Slc7a9	NP_067266	54	1	integral to membrane, membrane	amino acid transmembrane transporter activity	amino acid transport, transport
Ellis van Creveld gene homolog	Evc	NP_067267	113	1	integral to membrane, membrane	not classified	not classified
junction-mediating and regulatory protein	Jmy	NP_067285	111	1	cellular_component, nucleus	actin binding, protein binding, transcription coactivator activity	cell cycle arrest, DNA repair, induction of apoptosis, positive regulation of transcription factor activity, regulation of transcription from RNA polymerase II promoter, regulation of transcription in response to stress, response to DNA damage stimulus
piwi like homolog 1	Piwil1	NP_067286	99	1	chromatoid body, cytoplasm, mRNA cap binding complex, polysome	mRNA binding, piRNA binding, protein binding, RNA binding, single-stranded RNA binding	cell differentiation, gene silencing by RNA, meiosis, multicellular organismal development, piRNA metabolic process, regulation of translation, spermatid development, spermatogenesis
integrin beta 6	Itgb6	NP_067334	86	1	integral to membrane, integrin complex, membrane	binding, integrin binding, protein binding, receptor activity	cell adhesion, cell-matrix adhesion, inflammatory response, integrin-mediated signaling pathway

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
amiloride-sensitive cation channel 5, intestinal	Accn5	NP_067345	57	1	integral to membrane, membrane, plasma membrane	amiloride-sensitive sodium channel activity, ion channel activity, sodium channel activity, sodium ion binding	ion transport, sodium ion transport, transport
cofactor of BRCA1	A730008L03 Rik	NP_067368	54	1	nucleus	not classified	negative regulation of transcription, regulation of transcription, transcription
hypothetical protein LOC58227	9630031F12 Rik	NP_067391	108	1	not classified	not classified	not classified
heat shock protein, DNAJ-like 4	Dnaja4	NP_067397	45	1	membrane	heat shock protein binding, metal ion binding, unfolded protein binding, zinc ion binding	protein folding
solute carrier family 35, member B4	Slc35b4	NP_067410	38	1	Golgi apparatus, integral to membrane, membrane	not classified	carbohydrate transport, transport
aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	NP_067448	37	1	apical plasma membrane, cytosol	alcohol dehydrogenase (NADP+) activity, aldehyde reductase activity, L-glucuronate reductase activity, oxidoreductase activity	aldehyde catabolic process, biological_process, D-glucuronate catabolic process, L-ascorbic acid biosynthetic process, oxidation reduction
epsilon subunit of coatomer protein complex	Cope	NP_067513	35	1	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
mitochondrial ribosomal protein S30	Mrps30	NP_067531	50	1	cellular_component, mitochondrion, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
fidgetin-like 1	Fignl1	NP_068691	75	1	not classified	ATP binding, hydrolase activity, magnesium ion binding, metal ion binding, nucleoside-triphosphatase activity, nucleotide binding	not classified
transient receptor potential cation channel, subfamily V, member 4	Trpv4	NP_071300	98	1	cilium, integral to membrane, membrane, plasma membrane	calcium channel activity, calcium ion binding, calmodulin binding, ion channel activity, osmosensor activity, protein binding, receptor activity	calcium ion transport, hyperosmotic salinity response, ion transport, osmosensory signaling pathway, regulation of response to osmotic stress, response to osmotic stress, transport, vasopressin secretion
niban protein	Niban	NP_071301	80	1	cellular_component, cytoplasm	molecular_function	biological_process, negative regulation of protein amino acid phosphorylation, positive regulation of protein amino acid phosphorylation, positive regulation of translation, regulation of translation, response to endoplasmic reticulum stress, response to stress
sirtuin 2 (silent mating type information regulation 2, homolog) 2	Sirt2	NP_071877	43	1	cytoplasm, cytoskeleton, microtubule	hydrolase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, metal ion binding, NAD binding, NAD or NADH binding, zinc ion binding	cell cycle, cell division, chromatin silencing, mitosis, protein amino acid deacetylation, regulation of transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
equilibrative nucleoside transporter 1	Slc29a1	NP_075018	50	1	integral to membrane, integral to plasma membrane, membrane	nucleoside transmembrane transporter activity	nucleoside transport, transport
calsyntenin 1	Clstn1	NP_075538	109	1	cell junction, cell projection, endoplasmic reticulum, extracellular region, Golgi apparatus, integral to membrane, membrane, nucleus, plasma membrane, postsynaptic membrane, synapse	calcium ion binding, protein binding	cell adhesion, cellular calcium ion homeostasis, homophilic cell adhesion, synaptic transmission
CNDP dipeptidase 2	Cndp2	NP_075638	53	1	cytosol	carboxypeptidase activity, dipeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, protein dimerization activity, zinc ion binding	proteolysis
ETHE1 protein	Ethe1	NP_075643	28	1	cytoplasm, mitochondrion, nucleus	hydrolase activity, metal ion binding, zinc ion binding	not classified
Nit protein 2	Nit2	NP_075664	31	1	cytoplasm, mitochondrion	hydrolase activity, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	nitrogen compound metabolic process
protein phosphatase-1 regulatory subunit 7	Ppp1r7	NP_075689	41	1	nucleus	protein binding	not classified
chaperone, ABC1 activity of bc1 complex like	Cabc1	NP_075830	72	1	mitochondrion	ATP binding, kinase activity, nucleotide binding, transferase activity	not classified
myosin light chain, regulatory B	Mylc2b	NP_075891	20	1	apical part of cell, myosin complex	calcium ion binding, motor activity	not classified
syncoilin	Sync	NP_075974	54	1	cytoplasm, cytosol, intermediate filament, sarcolemma, synapse, Z disc	protein binding, structural molecule activity	intermediate filament-based process
myo-inositol 1-phosphate synthase A1	Isyna1	NP_076116	61	1	cytoplasm	binding, catalytic activity, inositol-3-phosphate synthase activity, isomerase activity	inositol biosynthetic process, metabolic process, phospholipid biosynthetic process
RAB27A protein	Rab27a	NP_076124	25	1	Golgi apparatus, intracellular, membrane, secretory granule	GTP binding, GTPase activity, myosin V binding, nucleotide binding	blood coagulation, cytotoxic T cell degranulation, melanocyte differentiation, melanosome localization, melanosome transport, natural killer cell degranulation, pigment granule localization, pigment granule transport, pigmentation, protein targeting, protein transport, small GTPase mediated signal transduction, vesicle-mediated transport
alcohol dehydrogenase PAN2	Rdh14	NP_076186	36	1	not classified	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
M-phase phosphoprotein, mpp8	Mphosph8	NP_076262	96	1	nucleus	not classified	not classified
ryanodine receptor 2, cardiac	Ryr2	NP_076357	565	1	integral to membrane, sarcoplasmic reticulum membrane, Z disc	ion channel activity, protein binding, receptor activity, ryanodine-sensitive calcium-release channel activity	calcium ion transport, ion transport, response to caffeine, transport

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	U2af1	NP_077149	28	1	nucleus, ribonucleoprotein complex, spliceosomal complex	metal ion binding, nucleic acid binding, nucleotide binding, RNA binding, RS domain binding, zinc ion binding	mRNA processing, RNA splicing
Der1-like domain family, member 1	Derl1	NP_077169	29	1	endoplasmic reticulum, integral to membrane, membrane	not classified	protein transport, response to unfolded protein, transport
LIM only protein HLP	Crip2	NP_077185	23	1	cellular_component	metal ion binding, molecular_function, zinc ion binding	hemopoiesis, positive regulation of cell proliferation
quinoid dihydropteridine reductase	Qdpr	NP_077198	26	1	not classified	6,7-dihydropteridine reductase activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction, tetrahydrobiopterin biosynthetic process
cytochrome P450 CYP4F18	Cyp4f18	NP_077764	60	1	endoplasmic reticulum, integral to membrane, membrane, microsome	electron carrier activity, heme binding, iron ion binding, leukotriene-B4 20-monooxygenase activity, metal ion binding, monooxygenase activity, oxidoreductase activity	oxidation reduction
leucine zipper protein 1	Luzp1	NP_077772	119	1	nucleus	molecular_function	biological_process
RAB21, member RAS oncogene family	Rab21	NP_077774	24	1	cytoplasmic vesicle, endoplasmic reticulum, endosome, Golgi apparatus, membrane	GTP binding, nucleotide binding, protein binding	protein transport, small GTPase mediated signal transduction, transport
radial spoke head 1 homolog	Rsph1	NP_079566	34	1	cytoplasm	not classified	meiosis
required for meiotic nuclear division 1 homolog	Rmnd1	NP_079619	52	1	cellular_component	molecular_function	biological_process
required for meiotic nuclear division 5 homolog B	Rmnd5b	NP_079622	44	1	not classified	not classified	not classified
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
6-phosphogluconolactonase	Pgls	NP_079672	27	1	not classified	6-phosphogluconolactonase activity, hydrolase activity	carbohydrate metabolic process, pentose-phosphate shunt
pyrroline-5-carboxylate reductase-like	Pycrl	NP_079688	29	1	cellular_component	binding, catalytic activity, cytidine deaminase activity, identical protein binding, oxidoreductase activity, protein binding, pyrroline-5-carboxylate reductase activity	cellular amino acid biosynthetic process, cytidine deamination, metabolic process, oxidation reduction, proline biosynthetic process
ribosomal protein L7-like 1	Rpl7l1	NP_079709	29	1	cellular_component, intracellular, large ribosomal subunit, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome, transcription regulator activity	biological_process, translation
transmembrane protein 126A	Tmem126a	NP_079736	22	1	cellular_component, integral to membrane, membrane	molecular_function	biological_process
ATPase, H+ transporting, lysosomal V1 subunit C1	Atp6v1c1	NP_079770	44	1	plasma membrane, proton-transporting V-type ATPase, V1 domain	hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, protein binding	ATP synthesis coupled proton transport, ion transport, proton transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
mitochondrial ribosomal protein L37	Mrpl37	NP_079776	48	1	mitochondrial ribosome, mitochondrion, ribonucleoprotein complex, ribosome	not classified	not classified
ERGIC and golgi 3	Ergic3	NP_079792	43	1	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane	not classified	transport, vesicle-mediated transport
hypothetical protein LOC66508	2400001E08 Rik	NP_079881	18	1	not classified	not classified	not classified
signal recognition particle 72	Srp72	NP_079967	75	1	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	1	endoplasmic reticulum, Golgi apparatus, TRAPP complex	protein binding	transport, vesicle-mediated transport
cysteine-rich perinuclear theca 5	Cypt6	NP_080014	20	1	not classified	not classified	not classified
peroxisomal lon protease	Lonp2	NP_080103	95	1	cytoplasm, nucleus, peroxisomal matrix, peroxisome	ATP binding, ATP-dependent peptidase activity, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, peptidase activity, protein binding, serine-type endopeptidase activity, serine-type peptidase activity	peroxisome organization, proteolysis
mannose phosphate isomerase	Mpi	NP_080113	47	1	cytoplasm	isomerase activity, mannose-6-phosphate isomerase activity, metal ion binding, zinc ion binding	carbohydrate metabolic process, mannose metabolic process
vacuolar protein sorting 28	Vps28	NP_080118	25	1	cytosol, endosome, membrane, plasma membrane	protein binding	protein transport, transport
acyl-Coenzyme A dehydrogenase family, member 8	Acad8	NP_080138	45	1	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
mitochondrial ribosomal protein S18B	Mrps18b	NP_080154	29	1	intracellular, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
DEK oncogene (DNA binding)	Dek	NP_080176	43	1	cellular_component, nucleus	DNA binding, molecular_function, nucleic acid binding	response to protein stimulus
myc induced nuclear antigen	Mina	NP_080186	54	1	nucleolus, nucleus	not classified	regulation of cell proliferation, ribosome biogenesis
phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Paics	NP_080215	47	1	not classified	ATP binding, carboxy-lyase activity, catalytic activity, ligase activity, lyase activity, nucleotide binding, phosphoribosylaminoimidazole carboxylase activity, phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	'de novo' IMP biosynthetic process, purine nucleotide biosynthetic process
hypothetical protein LOC67105	1700034H14 Rik	NP_080245	28	1	integral to membrane, membrane, mitochondrion	not classified	protein transport, transmembrane transport, transport
SVH protein	Armc10	NP_080310	33	1	endoplasmic reticulum, integral to membrane, membrane	binding	regulation of growth
proline racemase-like	2810055F11 Rik	NP_080314	38	1	not classified	isomerase activity, proline racemase activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
serum response factor binding protein 1	Srfbp1	NP_080316	49	1	cytoplasm, nucleus	protein binding	biological_process, regulation of transcription, transcription
CAP, adenylate cyclase-associated protein, 2	Cap2	NP_080332	53	1	membrane, plasma membrane	actin binding, binding	cytoskeleton organization
inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	Ikbkap	NP_080355	150	1	cellular_component, cytoplasm, nucleus	protein binding	biological_process, regulation of transcription, transcription
MAWD binding protein homolog 2	3110049J23 Rik	NP_080361	32	1	not classified	catalytic activity, isomerase activity	biosynthetic process
dishevelled associated activator of morphogenesis 1	Daam1	NP_080378	123	1	cytoplasm	actin binding, Rho GTPase binding	actin cytoskeleton organization, cellular component organization
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
high mobility group nucleosomal binding domain 3 isoform HMGN3a	Hmgn3	NP_080398	11	1	chromatin, nucleus	chromatin binding, DNA binding	biological_process
hypothetical protein LOC67392	4833420G17 Rik	NP_080403	72	1	not classified	not classified	not classified
splicing factor 3a, subunit 1	Sf3a1	NP_080451	89	1	nucleus, spliceosomal complex	RNA binding	mRNA processing, RNA processing, RNA splicing
phosducin-like	Pdcl	NP_080452	34	1	not classified	not classified	response to stimulus, visual perception
5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	NP_080471	64	1	not classified	catalytic activity, hydrolase activity, IMP cyclohydrolase activity, phosphoribosylaminoimidazolecarboxamide formyltransferase activity, transferase activity	IMP biosynthetic process, purine nucleotide biosynthetic process
cell division cycle and apoptosis regulator 1	Ccar1	NP_080477	132	1	cytoplasm, nuclear envelope lumen	molecular_function, nucleic acid binding	apoptosis, cell cycle, positive regulation of apoptosis, regulation of transcription, transcription
ring finger protein 151	Rnf151	NP_080481	27	1	nucleus	metal ion binding, protein binding, zinc ion binding	not classified
1-acylglycerol-3-phosphate O-acyltransferase 2	Agpat2	NP_080488	31	1	endoplasmic reticulum, integral to membrane, membrane	1-acylglycerol-3-phosphate O-acyltransferase activity, acyltransferase activity, transferase activity	metabolic process, phospholipid biosynthetic process
PTPRF interacting protein, binding protein 1 (liprin beta 1)	Ppfibp1	NP_080497	109	1	cellular_component	DNA binding, integrase activity, molecular_function	biological_process, DNA integration
mitochondrial ribosomal protein L49	Mrpl49	NP_080522	19	1	intracellular, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
TRM112-like	0610038D11 Rik	NP_080582	14	1	protein complex	protein binding, protein methyltransferase activity	not classified
RER1 homolog	Rer1	NP_080671	23	1	Golgi apparatus, integral to membrane, membrane	not classified	not classified
RNA (guanine-7-) methyltransferase	Rnmt	NP_080716	53	1	mRNA cap binding complex, nucleus	methyltransferase activity, mRNA (guanine-N7-)-methyltransferase activity, protein binding, RNA binding, transferase activity	mRNA capping, mRNA processing
SGT1, suppressor of G2 allele of SKP1	Sugt1	NP_080750	38	1	not classified	binding	modification-dependent protein catabolic process
centrosome and spindle pole associated protein 1	Cspp1	NP_080769	137	1	not classified	not classified	not classified

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
phosphopantothenoylcysteine synthetase	Ppcs	NP_080770	34	1	not classified	ligase activity, phosphopantothenate--cysteine ligase activity	not classified
mitochondrial ribosomal protein S11	Mrps11	NP_080774	20	1	intracellular, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	Atp5s	NP_080812	23	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
nucleolar RNA helicase homolog	Ddx56	NP_080814	61	1	nucleolus, nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	ribosome biogenesis, rRNA processing
proteasome 26S non-ATPase subunit 8	Psmd8	NP_080821	40	1	proteasome complex, proteasome regulatory particle	not classified	proteolysis
hypothetical protein LOC68073	A930016P21 Rik	NP_080822	27	1	integral to membrane, membrane	not classified	not classified
glycine cleavage system protein H (aminomethyl carrier)	Gcsh	NP_080848	19	1	glycine cleavage complex, mitochondrion	lipoic acid binding	glycine catabolic process
nucleolar protein family A, member 1	Nola1	NP_080854	23	1	dense fibrillar component, nucleus, ribonucleoprotein complex, small nucleolar ribonucleoprotein complex	RNA binding, rRNA binding, snoRNA binding	biological_process, ribosome biogenesis, rRNA processing
syntaxin 19	Stx19	NP_080864	34	1	membrane	SNAP receptor activity	intracellular protein transport
coiled-coil domain containing 34	Ccdc34	NP_080889	23	1	not classified	not classified	not classified
family with sequence similarity 98, member B	2610510H03 Rik	NP_080896	45	1	not classified	not classified	not classified
hypothetical protein LOC68241	9530058B02 Rik	NP_080909	18	1	cellular_component	protein binding	biological_process
solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	NP_080922	35	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, symporter activity, transporter activity	transport
replication protein A1	Rpa1	NP_080929	69	1	condensed chromosome, condensed nuclear chromosome, DNA replication factor A complex, male germ cell nucleus, nucleus, PML body	chromatin binding, DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	chromosome organization, DNA replication, double-strand break repair via homologous recombination, hemopoiesis, homeostasis of number of cells within a tissue, in utero embryonic development, meiosis, positive regulation of cell proliferation
mitochondrial ribosomal protein L14	Mrpl14	NP_081008	16	1	intracellular, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
hypothetical protein LOC68544	2310036O22 Rik	NP_081036	18	1	not classified	not classified	not classified
collagen type VI alpha 4	1110001D15 Rik	NP_081039	160	1	extracellular region, proteinaceous extracellular matrix	protein binding	cell adhesion
vacuolar protein sorting 25	Vps25	NP_081052	21	1	cytoplasm, mitochondrion, nucleus	not classified	protein transport, regulation of transcription, transcription, transport
ADP-ribosylation factor-like 8A	Arl8a	NP_081099	21	1	cellular_component, endosome, intracellular, lysosome, membrane	GTP binding, molecular_function, nucleotide binding	biological_process, small GTPase mediated signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ras responsive element binding protein 1 isoform 2	Rreb1	NP_081106	140	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, transcription
calcium binding protein 39-like	Cab39l	NP_081184	39	1	cellular_component	molecular_function	biological_process
mannosidase, beta A, lysosomal-like	Manbal	NP_081244	9	1	integral to membrane, membrane	not classified	not classified
GTP binding protein 4	Gtpbp4	NP_081276	74	1	nucleus	GTP binding, nucleotide binding	ribosome biogenesis
RWD domain containing 2A	Rwdd2a	NP_081376	34	1	not classified	not classified	not classified
differentially expressed in FDCP 6	Def6	NP_081461	73	1	cytoplasm, membrane, nucleus, plasma membrane	protein binding	not classified
castor homolog 1, zinc finger	Casz1	NP_081471	126	1	intracellular, nucleus	DNA binding, metal ion binding, zinc ion binding	regulation of transcription, transcription
forty-two-three domain containing 1	Fyttd1	NP_081502	36	1	not classified	not classified	not classified
hypothetical protein LOC69894	2010107G23 Rik	NP_081527	13	1	cellular_component, integral to membrane, membrane	protein binding	biological_process
mannosidase, beta A, lysosomal	Manba	NP_081564	101	1	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
membrane-associated ring finger (C3HC4) 5	5-Mar	NP_081590	31	1	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion	ligase activity, metal ion binding, zinc ion binding	modification-dependent protein catabolic process
PRP31	Prpf31	NP_081604	55	1	Cajal body, nuclear speck, nucleus, ribonucleoprotein complex, spliceosomal complex, U4/U6 x U5 tri-snRNP complex	protein binding, ribonucleoprotein binding, RNA binding	assembly of spliceosomal tri-snRNP, mRNA processing, nuclear mRNA splicing, via spliceosome, RNA splicing
hypothetical protein LOC70363	1700010C24 Rik	NP_081677	36	1	not classified	not classified	not classified
ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	NP_081715	39	1	cellular_component, integral to membrane, membrane	molecular_function, receptor activity	biological_process
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
keratin 34	Krt34	NP_081839	45	1	intermediate filament	structural molecule activity	not classified
mesoderm induction early response 1 isoform a	Mier1	NP_081972	60	1	nucleus	DNA binding	regulation of transcription, transcription
gamma-glutamyltransferase 6	Ggt6	NP_082095	51	1	integral to membrane, membrane	acyltransferase activity, gamma-glutamyltransferase activity, transferase activity	glutathione biosynthetic process
interferon induced with helicase C domain 1	Ifih1	NP_082111	116	1	cytoplasm, intracellular, nucleus	ATP binding, DNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, protein binding, RNA binding	immune response, innate immune response, regulation of apoptosis, response to virus
retinoic acid receptor responder (tazarotene induced) 2	Rarres2	NP_082128	18	1	extracellular region	not classified	brown fat cell differentiation, defense response
zinc finger protein 297B isoform a	Zbtb43	NP_082223	57	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, protein binding, zinc ion binding	regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
dihydrouridine synthase 4-like	Dus4l	NP_082278	37	1	not classified	catalytic activity, FAD binding, oxidoreductase activity, tRNA dihydrouridine synthase activity	metabolic process, oxidation reduction, tRNA processing
NFKB inhibitor interacting Ras-like protein 2	Nkiras2	NP_082300	21	1	cytoplasm, intracellular	GTP binding, nucleotide binding	small GTPase mediated signal transduction
sulfatase 2	Sulf2	NP_082348	100	1	cell surface, endoplasmic reticulum, extracellular space, Golgi apparatus	arylsulfatase activity, calcium ion binding, catalytic activity, hydrolase activity, metal ion binding, N-acetylglucosamine-6-sulfatase activity, sulfuric ester hydrolase activity	metabolic process, sulfur metabolic process
coiled-coil domain containing 123	Ccdc123	NP_082396	90	1	cellular_component, mitochondrion	protein binding	biological_process
DEAH (Asp-Glu-Ala-His) box polypeptide 36	Dhx36	NP_082412	114	1	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	not classified
splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	NP_082424	162	1	not classified	metal ion binding, zinc ion binding	not classified
cytidine deaminase	Cda	NP_082452	16	1	not classified	cytidine deaminase activity, hydrolase activity, identical protein binding, metal ion binding, zinc ion binding	cytidine metabolic process
SET domain containing 3	Setd3	NP_082538	67	1	not classified	not classified	not classified
phosphoglycerate mutase family member 5	Pgam5	NP_082549	32	1	cytoplasm, nucleus	catalytic activity	metabolic process
PDZ domain containing 11	Pdzd11	NP_082579	16	1	not classified	protein binding	not classified
proline-rich coiled-coil 1	Prrc1	NP_082723	46	1	cellular_component, Golgi apparatus	identical protein binding	biological_process
coiled-coil domain containing 103	Ccdc103	NP_082768	27	1	not classified	not classified	not classified
mannosidase, alpha, class 2C, member 1	Man2c1	NP_082912	116	1	not classified	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, mannose metabolic process, metabolic process
golgi associated, gamma adaptin ear containing, ARF binding protein 2	Gga2	NP_083034	66	1	clathrin adaptor complex, endosome, Golgi apparatus, Golgi apparatus part, intracellular, membrane, trans-Golgi network	ADP-ribosylation factor binding, protein binding	biological_process, intracellular protein transport, protein transport, transport, vesicle-mediated transport
clathrin, light polypeptide (Lcb)	Cltb	NP_083146	23	1	clathrin coat of coated pit, clathrin coat of trans-Golgi network vesicle, coated pit, cytoplasmic vesicle, membrane	calcium ion binding, protein binding, structural molecule activity	biological_process, intracellular protein transport, vesicle-mediated transport
scavenger receptor class A, member 5	Scara5	NP_083179	54	1	cell surface, integral to membrane, integral to plasma membrane, membrane, plasma membrane	ferritin receptor activity, iron ion binding, protein binding, receptor activity, scavenger receptor activity	cellular iron ion homeostasis, cellular response to heat, endocytosis, ion transport, iron ion transmembrane transport, iron ion transport, protein homotrimerization, transport
leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	NP_083191	115	1	not classified	protein binding	cell cycle, cell division, mitosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hypoxia-inducible factor prolyl 4-hydroxylase	4933406E20Rik	NP_083220	57	1	endoplasmic reticulum, integral to membrane, membrane	calcium ion 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, zinc ion binding	oxidation reduction
leucine rich repeat containing 17	Lrrc17	NP_083253	52	1	not classified	protein binding	not classified
mitochondrial ribosomal protein L47	Mrpl47	NP_083293	30	1	mitochondrial ribosome, mitochondrion, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
coiled-coil domain containing 7	Ccdc7	NP_083337	43	1	cellular_component	molecular_function	biological_process
pre-mRNA cleavage complex II protein Pcf11	Pcf11	NP_083354	173	1	not classified	not classified	not classified
hedgehog acyltransferase-like	Hhatl	NP_083371	56	1	endoplasmic reticulum, integral to membrane, membrane	protein binding	negative regulation of N-terminal protein palmitoylation
hypothetical protein LOC75425	2610036D13Rik	NP_083558	121	1	not classified	binding	not classified
progesterone-induced blocking factor 1 isoform a	Pibf1	NP_083596	90	1	not classified	not classified	not classified
acylphosphatase 2, muscle type	Acyp2	NP_083620	12	1	not classified	acylphosphatase activity, hydrolase activity	not classified
cullin 2	Cul2	NP_083678	82	1	cullin-RING ubiquitin ligase complex	protein binding, ubiquitin protein ligase binding	modification-dependent protein catabolic process, protein catabolic process, ubiquitin-dependent protein catabolic process
ATPase, class VI, type 11B	Atp11b	NP_083846	134	1	integral to membrane, membrane	ATP binding, hydrolase activity, magnesium ion binding, nucleotide binding	not classified
thioredoxin domain containing 11 isoform 1	Txndc11	NP_083858	106	1	endoplasmic reticulum, integral to membrane, membrane	not classified	cell redox homeostasis
hypothetical protein LOC76416	1700022C21Rik	NP_083878	35	1	not classified	not classified	not classified
ADP-ribosylation factor related protein 1	Arfrp1	NP_083978	23	1	Golgi apparatus, intracellular, membrane fraction	GTP binding, GTPase activity, nucleotide binding	gastrulation, small GTPase mediated signal transduction
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	Ppfia3	NP_084017	133	1	cytoplasm	not classified	not classified
docking protein 5	Dok5	NP_084037	35	1	cellular_component	insulin receptor binding, transmembrane receptor protein tyrosine kinase signaling protein activity	MAPKKK cascade, nervous system development, transmembrane receptor protein tyrosine kinase signaling pathway
hypothetical protein LOC76886	6430514L14Rik	NP_084060	42	1	not classified	not classified	not classified
golgi autoantigen, golgin subfamily a, 1	Golga1	NP_084069	87	1	Golgi apparatus, membrane, perinuclear region of cytoplasm, trans-Golgi network	protein binding	not classified
sec1 family domain containing 1	Scfd1	NP_084101	72	1	cellular_component, cytoplasm, endoplasmic reticulum, Golgi apparatus, membrane	molecular_function	biological_process, protein transport, transport, vesicle docking during exocytosis, vesicle-mediated transport
GC-rich promoter binding protein 1-like 1	Gpbp1l1	NP_084144	52	1	nucleus	DNA binding	regulation of transcription, transcription
tubulin-specific chaperone d	Tbcd	NP_084154	133	1	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
PRELI domain containing 2	Prelid2	NP_084218	20	1	not classified	not classified	not classified
CDKN2A interacting protein N-terminal like	Cdkn2aipnl	NP_084252	13	1	not classified	not classified	not classified
DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	NP_084372	67	1	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	not classified
transmembrane protein 33 isoform 2	Tmem33	NP_084384	28	1	cellular_component, integral to membrane, membrane	protein binding	biological_process
LSM6 homolog, U6 small nuclear RNA associated	Lsm6	NP_084421	9	1	cytoplasm, nucleus, ribonucleoprotein complex	protein heterodimerization activity, RNA binding	mRNA catabolic process, mRNA processing, RNA splicing, rRNA processing, tRNA processing
GINS complex subunit 3	Gins3	NP_084474	25	1	nucleus	not classified	DNA replication
coronin 7	Coro7	NP_084481	101	1	cytoplasm, cytoplasmic vesicle, Golgi apparatus, integral to membrane of membrane fraction, membrane, soluble fraction	not classified	not classified
vacuolar protein sorting 16	Vps16	NP_085036	95	1	actin filament, cytoplasm, early endosome, endosome, lysosome, membrane	actin binding, protein binding	biological_process, intracellular protein transport, protein transport, transport
histone cluster 1, H1a	Hist1h1a	NP_085112	22	1	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly, spermatogenesis
aldo-keto reductase family 1, member C6	Akr1c6	NP_085114	37	1	cellular_component	estradiol 17-beta-dehydrogenase activity, oxidoreductase activity	lipid biosynthetic process, oxidation reduction, steroid biosynthetic process, steroid metabolic process
protein kinase C and casein kinase substrate in neurons 3	Pacsin3	NP_112019	49	1	cytoplasm, membrane, plasma membrane, trans-Golgi network	cytoskeletal protein binding, kinase activity, protein binding	endocytosis, negative regulation of endocytosis
WD repeat domain 10	Ift122	NP_112454	135	1	cytoplasm, flagellum	not classified	not classified
solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	NP_112473	58	1	integral to membrane, membrane	folic acid binding, reduced folate carrier activity	transport
solute carrier family 2 (facilitated glucose transporter), member 2	Slc2a2	NP_112474	57	1	brush border, integral to membrane, membrane, plasma membrane	glucose transmembrane transporter activity, substrate-specific transmembrane transporter activity, transporter activity	carbohydrate transport, transmembrane transport, transport
pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	NP_112546	33	1	cytoplasm, membrane	lipid binding, phosphatidylinositol binding	not classified
testis expressed gene 14	Tex14	NP_113563	163	1	cytoplasm	ATP binding, nucleotide binding, protein kinase activity, protein tyrosine kinase activity	protein amino acid phosphorylation
ectonucleotide pyrophosphatase/phosphodiesterase 5	Enpp5	NP_114392	54	1	extracellular region, integral to membrane, integral to plasma membrane, membrane	catalytic activity, hydrolase activity, nucleotide diphosphatase activity	metabolic process, nucleotide catabolic process
ring finger protein 123	Rnf123	NP_115932	149	1	cellular_component, cytoplasm	ligase activity, metal ion binding, molecular_function, protein binding, zinc ion binding	biological_process, modification-dependent protein catabolic process
threonyl-tRNA synthetase	Tars	NP_149065	83	1	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, ligase activity, forming aminoacyl-tRNA and related compounds, nucleotide binding, threonine-tRNA ligase activity	threonyl-tRNA aminoacylation, translation, tRNA aminoacylation, tRNA aminoacylation for protein translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cholinergic receptor, muscarinic 3, cardiac	Chrm3	NP_150372	66	1	cell junction, integral to membrane, integral to plasma membrane, membrane, plasma membrane, postsynaptic membrane, synapse	acetylcholine receptor activity, G-protein coupled receptor activity, muscarinic acetylcholine receptor activity, receptor activity, signal transducer activity	activation of phospholipase C activity by muscarinic acetylcholine receptor signaling pathway, digestion, G-protein coupled receptor protein signaling pathway, muscarinic acetylcholine receptor signaling pathway, positive regulation of smooth muscle contraction, signal transduction, smooth muscle contraction, synaptic transmission, cholinergic
sprouty-related protein 1 with EVH-1 domain	Spred1	NP_277059	51	1	membrane, nucleus, plasma membrane	protein binding, stem cell factor receptor binding	inactivation of MAPK activity, multicellular organismal development, regulation of signal transduction
dachshund 2	Dach2	NP_291083	69	1	nucleus	DNA binding, protein binding	multicellular organismal development, regulation of transcription, transcription
component of Sp100-rs	Csprs	NP_291094	33	1	nucleus	receptor activity	not classified
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
cytochrome c oxidase, subunit VIc	Cox6c	NP_444301	8	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity	biological_process
RAS-homolog enriched in brain	Rheb	NP_444305	20	1	intracellular, membrane, plasma membrane, spliceosomal complex	GTP binding, magnesium ion binding, metal ion binding, nucleotide binding	small GTPase mediated signal transduction
reticulon 3 isoform 4	Rtn3	NP_444306	25	1	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane	molecular_function, protein binding	apoptosis, transport, vesicle-mediated transport
aldehyde dehydrogenase family 1, subfamily A3	Aldh1a3	NP_444310	56	1	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
15 kDa selenoprotein precursor	15-Sep	NP_444332	18	1	endoplasmic reticulum, endoplasmic reticulum lumen	protein binding, selenium binding	'de novo' posttranslational protein folding
poly A binding protein, cytoplasmic 5	Pabpc5	NP_444344	43	1	cellular_component	molecular_function	biological_process
wingless-related MMTV integration site 16	Wnt16	NP_444346	41	1	extracellular region, proteinaceous extracellular matrix	signal transducer activity	multicellular organismal development, Wnt receptor signaling pathway, Wnt receptor signaling pathway, calcium modulating pathway

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	Smarca5	NP_444354	122	1	chromatin remodeling complex, nucleus	ATP binding, ATP-dependent helicase activity, DNA binding, helicase activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides, nucleic acid binding, nucleosome binding, nucleotide binding, transcription activator activity, transcription regulator activity	ATP-dependent chromatin remodeling, chromatin assembly or disassembly, chromatin modification, chromatin remodeling, embryonic development, regulation of transcription, DNA-dependent
protocadherin beta 14	Pcdhb14	NP_444369	87	1	integral to membrane, membrane, plasma membrane	calcium ion binding, protein binding	cell adhesion, homophilic cell adhesion
protocadherin beta 17	Pcdhb17	NP_444372	88	1	integral to membrane, membrane	calcium ion binding, protein binding	cell adhesion
mitochondrial ribosomal protein L43	Mrpl43	NP_444394	18	1	mitochondrial large ribosomal subunit, mitochondrion, ribonucleoprotein complex, ribosome	molecular_function	translation
cortactin binding protein 2	Cttnbp2	NP_525024	179	1	actin cytoskeleton	cytoskeletal regulatory protein binding	actin cytoskeleton organization
SMC (structural maintenace of chromosomes 1)-like 2	Smc1b	NP_536718	145	1	chromosome, chromosome, centromeric region, lateral element, nucleus, synaptonemal complex	ATP binding, DNA binding, nucleotide binding, protein binding	cell cycle, chromosome organization, meiosis, sister chromatid cohesion
histidyl-tRNA synthetase-like	Hars2	NP_542367	57	1	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, histidine-tRNA ligase activity, ligase activity, nucleotide binding	histidyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
PAS domain containing serine/threonine kinase	Pask	NP_543126	151	1	cytoplasm, intracellular	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, signal transducer activity, transferase activity	protein amino acid phosphorylation, regulation of transcription, DNA-dependent, signal transduction
toll-like receptor 7	Tlr7	NP_573474	122	1	integral to membrane, intrinsic to membrane, membrane	protein binding, receptor activity, transmembrane receptor activity	immune response, inflammatory response, innate immune response, positive regulation of interleukin-6 production, signal transduction
zinc finger protein 704	Zfp704	NP_573481	61	1	intracellular	metal ion binding, zinc ion binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
GS homeobox 2	Gsx2	NP_573555	32	1	nucleus	DNA binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity	brain development, central nervous system development, forebrain dorsal/ventral pattern formation, forebrain morphogenesis, hindbrain morphogenesis, multicellular organismal development, neuron fate commitment, neuron fate specification, olfactory bulb interneuron differentiation, pattern specification process, regulation of respiratory gaseous exchange by neurological system process, regulation of transcription, regulation of transcription, DNA-dependent, spinal cord association neuron differentiation, subpallium neuron fate commitment, transcription
v-crk sarcoma virus CT10 oncogene homolog	Crk	NP_598417	34	1	cytoplasm, membrane, plasma membrane	kinase activity, protein binding, protein phosphorylated amino acid binding, SH3/SH2 adaptor activity	not classified
avian erythroblastosis virus E-26 (v-ets) oncogene related	Erg	NP_598420	55	1	nucleus	DNA binding, protein binding, sequence-specific DNA binding, transcription factor activity	regulation of transcription, regulation of transcription, DNA-dependent, transcription
Rab31-like	Rab31	NP_598446	21	1	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction
poly-U binding splicing factor 60 isoform b	Puf60	NP_598452	59	1	nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	apoptosis, mRNA processing, regulation of transcription, RNA splicing, transcription
pyrroline-5-carboxylate reductase family, member 2	Pycr2	NP_598466	34	1	not classified	binding, catalytic activity, oxidoreductase activity, pyrroline-5-carboxylate reductase activity	cellular amino acid biosynthetic process, metabolic process, oxidation reduction, proline biosynthetic process
suppression of tumorigenicity 13	St13	NP_598487	42	1	cytoplasm	binding	not classified
WD repeat domain 23	Wdr23	NP_598495	62	1	not classified	not classified	not classified
hypothetical protein LOC72722	2810405J04Rik	NP_598508	55	1	not classified	not classified	not classified
nuclear pore complex-associated protein Tpr	Tpr	NP_598541	267	1	nuclear envelope	molecular_function	biological_process
lamin B receptor	Lbr	NP_598576	71	1	integral to membrane, membrane, nuclear inner membrane, nuclear lamina, nucleus	DNA binding, nucleic acid binding, receptor activity	not classified
EH-domain containing 4	Ehd4	NP_598599	61	1	endosome, membrane	ATP binding, calcium ion binding, GTP binding, GTPase activity, nucleotide binding, protein binding	not classified
olfactomedin-like 3	Olfml3	NP_598620	46	1	extracellular region	not classified	multicellular organismal development
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
CUB domain-containing protein 1	Cdcp1	NP_598735	93	1	integral to membrane, membrane, plasma membrane	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
thyroid hormone receptor interactor 12	Trip12	NP_598736	224	1	not classified	ligase activity	modification-dependent protein catabolic process
methionine adenosyltransferase II, beta	Mat2b	NP_598778	37	1	not classified	binding, catalytic activity, dTDP-4-dehydrorhamnose reductase activity	extracellular polysaccharide biosynthetic process, metabolic process, one-carbon metabolic process
transmembrane emp24 protein transport domain containing 4	Tmed4	NP_598781	26	1	endoplasmic reticulum, integral to membrane, membrane	not classified	transport
5',3'-nucleotidase, mitochondrial	Nt5m	NP_598790	26	1	mitochondrion	5'-nucleotidase activity, hydrolase activity, magnesium ion binding, metal ion binding, nucleotide binding, phosphatase activity	dUMP catabolic process, nucleotide metabolic process
FERMRhoGEF (Arhgef) and pleckstrin domain protein 1	Farp1	NP_598843	119	1	cellular_component, cytoplasm	molecular_function	biological_process
neurocalcin delta	Ncald	NP_598855	22	1	not classified	calcium ion binding	not classified
immunoglobulin-like domain containing receptor 1	Ildr1	NP_598870	59	1	integral to membrane, membrane, plasma membrane	receptor activity	not classified
acyl-CoA thioesterase 2	Acot2	NP_598949	50	1	mitochondrion	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity, palmitoyl-CoA hydrolase activity, thiolester hydrolase activity	acyl-CoA metabolic process, lipid metabolic process
Yip1 domain family, member 2	Yipf2	NP_612176	35	1	integral to membrane, membrane	not classified	not classified
G7c protein	D17H6S56E-3	NP_613048	96	1	extracellular region	not classified	not classified
D6Wsu176e protein	D6Wsu176e	NP_613053	25	1	extracellular region	not classified	not classified
phosphatidate cytidylyltransferase 2	Cds2	NP_619592	51	1	endoplasmic reticulum, integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	nucleotidyltransferase activity, phosphatidate cytidylyltransferase activity, transferase activity, transferase activity, transferring phosphorus-containing groups	phospholipid biosynthetic process
leucine rich repeat containing 4	Lrrc4	NP_619623	73	1	integral to membrane, membrane	protein binding	not classified
O-linked N-acetylglucosamine transferase	Ogt	NP_631883	117	1	cytoplasm, intracellular, nucleus	binding, N-acetyltransferase activity, protein binding, protein N-acetylglucosaminyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups	protein amino acid O-linked glycosylation
developmental pluripotency-associated 3	Dppa3	NP_631964	18	1	cytoplasm, female pronucleus, male pronucleus, nucleus	not classified	embryonic cleavage
UDP-glucose pyrophosphorylase 2	Ugp2	NP_647458	57	1	cytoplasm	nucleotidyltransferase activity, transferase activity, UTP:glucose-1-phosphate uridylyltransferase activity	metabolic process
interleukin 31 receptor A	Il31ra	NP_647460	81	1	integral to membrane, membrane, plasma membrane	cytokine receptor activity, receptor activity	immune response
kinesin family member 18A	Kif18a	NP_647464	101	1	microtubule	ATP binding, microtubule motor activity, motor activity, nucleotide binding	microtubule-based movement, protein transport, transport
basic, immunoglobulin-like variable motif containing	Bivm	NP_653141	57	1	cellular_component, cytoplasm, nucleus	molecular_function	biological_process
sushi domain containing 4	Susd4	NP_659045	54	1	integral to membrane, membrane	not classified	not classified
transmembrane protein 40	Tmem40	NP_659054	25	1	integral to membrane, membrane	not classified	not classified

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO 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
hypothetical protein LOC215929	AI317395	NP_659070	41	1	integral to membrane, membrane, plasma membrane	sodium ion binding, symporter activity	carbohydrate transport, ion transport, sodium ion transport, transport
protein phosphatase 1, regulatory (inhibitor) subunit 1B	Ppp1r1b	NP_659077	22	1	cytoplasm, nucleus	phosphoprotein phosphatase inhibitor activity, protein serine/threonine phosphatase inhibitor activity	negative regulation of female receptivity, signal transduction, transcription
alanyl-tRNA synthetase domain containing 1	Aarsd1	NP_659078	45	1	cytoplasm	alanine-tRNA ligase activity, aminoacyl-tRNA ligase activity, ATP binding, ligase activity, forming aminoacyl-tRNA and related compounds, nucleic acid binding, nucleotide binding, protein binding	alanyl-tRNA aminoacylation, translation, tRNA aminoacylation
BAP28 protein	Heatr1	NP_659084	242	1	not classified	not classified	not classified
hypothetical protein LOC234564	AU018778	NP_659179	62	1	not classified	carboxylesterase activity, hydrolase activity	not classified
eukaryotic translation initiation factor 3 subunit 6 interacting protein	Eif3eip	NP_660121	67	1	cytoplasm, eukaryotic translation initiation factor 3 complex, fibrillar center, nucleolus, nucleoplasm	protein binding, translation initiation factor activity	translation, translational initiation
carbohydrate sulfotransferase 10	Chst10	NP_660124	44	1	cellular_component, Golgi apparatus, integral to membrane, membrane	sulfotransferase activity, transferase activity	carbohydrate biosynthetic process, carbohydrate metabolic process, learning, long-term memory
GRP1-binding protein GRSP1	Frmd4b	NP_660130	112	1	cytoplasm, cytoskeleton	binding	not classified
NOL1/NOP2/Sun domain family member 2	Nsun2	NP_663329	78	1	cytoplasm, nucleus	methyltransferase activity, RNA binding, transferase activity, tRNA (cytosine-5-)-methyltransferase activity, tRNA binding	tRNA processing
G protein pathway suppressor 1	Gps1	NP_663345	53	1	cytoplasm, nucleus, signalosome	protein binding	not classified
lactamase, beta 2	Lactb2	NP_663356	33	1	mitochondrion	hydrolase activity, metal ion binding, zinc ion binding	not classified
hypothetical protein LOC28088	D10Wsu52e	NP_663397	55	1	cellular_component	molecular_function	biological_process
lethal giant larvae homolog 2	Llgl2	NP_663413	114	1	cellular_component, cytoplasm	molecular_function	biological_process, cell cycle, cell division, exocytosis
peroxisomal biogenesis factor 6	Pex6	NP_663463	105	1	cytoplasm, membrane, peroxisome	ATP binding, nucleoside-triphosphatase activity, nucleotide binding, protein binding	peroxisome organization
hypothetical protein LOC224893	BC011426	NP_663465	63	1	nucleus	metal ion binding, zinc ion binding	transcription
solute carrier family 5 (sodium/glucose cotransporter), member 9	Slc5a9	NP_663526	75	1	integral to membrane, membrane	sodium ion binding, transporter activity	ion transport, sodium ion transport, transport
tetratricopeptide repeat domain 13	Ttc13	NP_663582	85	1	not classified	not classified	not classified
leucine rich repeat containing 49	Lrrc49	NP_663591	86	1	cytoplasm, cytoskeleton, microtubule	protein binding	not classified
hypothetical protein LOC106064	AW549877	NP_666042	33	1	not classified	not classified	not classified
zinc finger CCCH type containing 7	Zc3h7a	NP_666043	99	1	not classified	metal ion binding, zinc ion binding	not classified
spectrin SH3 domain binding protein 1 isoform 2	Abi1	NP_666106	52	1	cell junction, cell leading edge, cell projection, cytoplasm, cytoskeleton, intracellular, lamellipodium, nucleus, synapse, synaptosome	protein binding, protein tyrosine kinase activator activity	cellular process, peptidyl-tyrosine phosphorylation, somitogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hypothetical protein LOC237711	C230094A16 Rik	NP_666128	218	1	cytoplasm, microtubule	not classified	not classified
glycolipid transfer protein domain containing 2	Gltpd2	NP_666132	34	1	cytoplasm	glycolipid binding, glycolipid transporter activity	glycolipid transport
potassium channel, subfamily K, member 13	Kcnk13	NP_666149	45	1	integral to membrane, membrane	ion channel activity, potassium channel activity, potassium ion binding, voltage-gated ion channel activity	ion transport, potassium ion transport, transport
proline rich protein 5	Prr5	NP_666173	43	1	not classified	GTPase activator activity	actin cytoskeleton organization, cell cycle, positive regulation of cell migration
keratin 6L	Krt79	NP_666175	58	1	intermediate filament, keratin filament	structural molecule activity	not classified
hypothetical protein LOC227737	9130404D14 Rik	NP_666231	85	1	not classified	not classified	not classified
PDX1 C-terminal inhibiting factor 1	Pcif1	NP_666241	81	1	nucleus	protein binding	not classified
Rho GTPase activating protein 24 isoform 2	Arhgap24	NP_666273	73	1	cell junction, cell projection, cellular_component, cytoplasm, cytoskeleton, intracellular	GTPase activator activity, molecular_function	angiogenesis, biological_process, cell differentiation, multicellular organismal development, signal transduction
putative DNA glycosylase	Neil3	NP_666320	67	1	intracellular, nucleus	damaged DNA binding, DNA binding, DNA-(apurinic or apyrimidinic site) lyase activity, hydrolase activity, hydrolyzing N-glycosyl compounds, metal ion binding, zinc ion binding	base-excision repair, DNA repair, nucleotide-excision repair, response to DNA damage stimulus
Vac14 homolog	Vac14	NP_666328	88	1	endoplasmic reticulum, endosome, membrane, microsome, vacuolar membrane	binding, kinase activator activity	cell death, response to osmotic stress
gem (nuclear organelle) associated protein 8	Gemin8	NP_666350	28	1	cytoplasm, nucleus, spliceosomal complex	not classified	mRNA processing, RNA splicing
olfactory receptor 727	Olfr727	NP_666431	37	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
olfactory receptor 883	Olfr883	NP_666531	35	1	integral to membrane	olfactory receptor activity, receptor activity	G-protein coupled receptor protein signaling pathway, sensory perception of smell
olfactory receptor 868	Olfr868	NP_666770	34	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
olfactory receptor 146	Olfr146	NP_666958	34	1	integral to membrane, membrane, plasma membrane	G-protein coupled receptor activity, olfactory receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, response to stimulus, sensory perception of smell, signal transduction
solute carrier family 8 (sodium/calcium exchanger), member 2	Slc8a2	NP_683748	101	1	integral to membrane, membrane	not classified	not classified
cell division cycle 5-like	Cdc5l	NP_690023	92	1	cytoplasm, nucleus, spliceosomal complex	DNA binding, RNA binding	cell cycle, mRNA processing, regulation of transcription, RNA splicing, transcription
matrix metallopeptidase 21	Mmp21	NP_694423	65	1	cellular_component, extracellular region, proteinaceous extracellular matrix	calcium ion binding, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	biological_process, metabolic process, proteolysis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	NP_694705	86	1	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	not classified
hypothetical protein LOC224904	2410015M20 Rik	NP_694792	13	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
pleckstrin homology-like domain, family B, member 2	Phldb2	NP_700461	141	1	cytoplasm, membrane	not classified	not classified
coiled-coil domain containing 65	Ccdc65	NP_705738	58	1	not classified	not classified	not classified
aldehyde dehydrogenase 1 family, member L2	Aldh1l2	NP_705771	102	1	cytoplasm	acyl carrier activity, formyltetrahydrofolate dehydrogenase activity, hydroxymethyl-, formyl- and related transferase activity, methyltransferase activity, oxidoreductase activity, phosphopantetheine binding	10-formyltetrahydrofolate catabolic process, biosynthetic process, metabolic process, one-carbon metabolic process, oxidation reduction
pyrroline-5-carboxylate synthetase isoform 2	Aldh18a1	NP_705782	87	1	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
centaurin, beta 1	Centb1	NP_722483	82	1	cellular_component	ARF GTPase activator activity, ATP binding, hydrolase activity, kinase activity, metal ion binding, molecular_function, nucleotide binding, phospholipase C activity, protein tyrosine kinase activity, receptor activity, signal transducer activity, zinc ion binding	biological_process, intracellular signaling cascade, lipid catabolic process, lipid metabolic process, regulation of ARF GTPase activity, signal transduction
protein kinase N3	Pkn3	NP_722500	98	1	cytoplasm, intracellular, nucleus	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein kinase C activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation, signal transduction
Myc-binding protein-associated protein	Mycbpap	NP_733771	82	1	cytoplasm, membrane	protein binding	cell differentiation, multicellular organismal development, spermatogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 16	Adamts16	NP_742050	136	1	cellular_component, extracellular matrix, extracellular region, proteinaceous extracellular matrix	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, molecular_function, peptidase activity, zinc ion binding	biological_process, proteolysis
vacuolar protein sorting 18	Vps18	NP_758473	110	1	actin filament, early endosome, endosome, lysosome, membrane	actin binding, metal ion binding, protein binding, zinc ion binding	endosome organization, protein transport, transport
fucokinase isoform 1	Fuk	NP_758487	119	1	not classified	ATP binding, fucokinase activity, kinase activity, nucleotide binding, transferase activity	not classified
doublesex and mab-3 related transcription factor like family A2	Dmrta2	NP_758500	53	1	cellular_component, nucleus	DNA binding, metal ion binding, molecular_function, transcription factor activity, zinc ion binding	biological_process, regulation of transcription, DNA-dependent, sex differentiation
FAST kinase domains 2	Fastkd2	NP_766010	79	1	not classified	ATP binding, protein kinase activity	apoptosis
shroom family member 2	Shroom2	NP_766029	165	1	apical junction complex, apical plasma membrane, cell cortex, cell junction, cell soma, cell-cell adherens junction, cell-cell junction, cortical actin cytoskeleton, cytoplasm, cytoskeleton, filamentous actin, membrane, microtubule, plasma membrane, tight junction	actin binding, actin filament binding, beta-catenin binding, protein binding, protein domain specific binding	actin filament bundle formation, apical protein localization, brain development, cell migration, cell morphogenesis, cell-cell junction maintenance, cellular pigment accumulation, ear development, establishment of melanosome localization, eye pigment granule organization, lens morphogenesis in camera-type eye, melanosome organization, multicellular organismal development, negative regulation of actin filament depolymerization
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 18	Adamts18	NP_766054	135	1	extracellular matrix, extracellular region, proteinaceous extracellular matrix	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
nuclear receptor coactivator 7 isoform 1	Ncoa7	NP_766083	106	1	nucleus	not classified	cell wall macromolecule catabolic process, regulation of transcription, transcription
Rho GTPase activating protein 29	Arhgap29	NP_766113	142	1	intracellular	diacylglycerol binding, GTPase activator activity, metal ion binding, zinc ion binding	intracellular signaling cascade, signal transduction
RUN domain containing 1	Rundc1	NP_766154	68	1	not classified	not classified	not classified
signal-induced proliferation-associated 1 like 1	Sipa1l1	NP_766167	197	1	intracellular	GTPase activator activity, protein binding	regulation of small GTPase mediated signal transduction
DEAH (Asp-Glu-Ala-His) box polypeptide 29	Dhx29	NP_766182	154	1	cytoplasm	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, translation initiation factor activity	translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
SEC24 related gene family, member C	Sec24c	NP_766184	119	1	not classified	not classified	protein transport, transport
translocase of outer mitochondrial membrane 22 homolog	Tomm22	NP_766197	16	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	receptor activity	protein transport, transmembrane transport, transport
geranylgeranyltransferase type I	Pggt1b	NP_766215	42	1	not classified	CAAX-protein geranylgeranyltransferase activity, catalytic activity, metal ion binding, prenyltransferase activity, transferase activity, zinc ion binding	not classified
alkyldihydroxyacetone phosphate synthase	Agps	NP_766254	72	1	peroxisome	alkylglycerone-phosphate synthase activity, catalytic activity, FAD binding, oxidoreductase activity, transferase activity	lipid biosynthetic process
glucosidase, alpha; neutral C	Ganc	NP_766260	104	1	cellular_component	alpha-glucosidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, glucose metabolic process, metabolic process
coenzyme Q3 homolog, methyltransferase	Coq3	NP_766275	41	1	mitochondrion	2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity, hexaprenyldihydroxybenzoate methyltransferase activity, methyltransferase activity, transferase activity	metabolic process, ubiquinone biosynthetic process
InaD-like isoform 1	Inadl	NP_766284	199	1	apical part of cell, cell junction, cytoplasm, membrane, plasma membrane, tight junction	protein binding	not classified
leukocyte receptor cluster (LRC) member 8	Leng8	NP_766324	87	1	not classified	not classified	not classified
pleckstrin homology domain containing, family A member 7	Plekha7	NP_766331	117	1	not classified	protein binding	not classified
guanylate binding protein family, member 6	BC057170	NP_766365	71	1	not classified	not classified	not classified
contactin associated protein-like 5	C230078M14Rik	NP_766439	144	1	integral to membrane, membrane	protein binding, receptor binding	cell adhesion, signal transduction
WD repeat and FYVE domain containing 3	Wdfy3	NP_766470	392	1	autophagic vacuole, cytoplasm, cytoplasmic part, extrinsic to membrane, membrane, nuclear envelope	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity, metal ion binding, phosphatidylinositol binding, transferase activity, transferase activity, transferring glycosyl groups, zinc ion binding	not classified
SNF2 histone linker PHD RING helicase isoform b	Shprh	NP_766525	185	1	nucleosome, nucleus	ATP binding, DNA binding, helicase activity, hydrolase activity, ligase activity, metal ion binding, nucleic acid binding, nucleotide binding, protein binding, zinc ion binding	DNA repair, modification-dependent protein catabolic process, nucleosome assembly, response to DNA damage stimulus
serine (or cysteine) proteinase inhibitor, clade B, member 1b	Serpinb1b	NP_766640	43	1	cellular_component, cytoplasm	peptidase inhibitor activity, serine-type endopeptidase inhibitor activity	regulation of protein catabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
peptidase (mitochondrial processing) alpha	Pmpca	NP_775272	58	1	mitochondrion	catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
hypothetical protein LOC67306	3110050N22 Rik	NP_775273	35	1	not classified	not classified	not classified
hypothetical protein LOC227446	2310035C23 Rik	NP_775279	135	1	not classified	binding	not classified
PRUNEM1	Prune	NP_775482	50	1	cell junction, cytoplasm, nucleus	hydrolase activity, inorganic diphosphatase activity, manganese ion binding, metal ion binding, pyrophosphatase activity	not classified
zinc finger protein 445	Zfp445	NP_775540	115	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, transcription factor activity, zinc ion binding	regulation of transcription, regulation of transcription, DNA-dependent, transcription
zinc finger, FYVE domain containing 16	Zfyve16	NP_775568	167	1	cytoplasm, endosome, membrane	metal ion binding, zinc ion binding	not classified
X Kell blood group precursor related family member 6 homolog	Xkr6	NP_775569	42	1	not classified	not classified	not classified
RAB8B, member RAS oncogene family	Rab8b	NP_775589	24	1	membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	protein transport, small GTPase mediated signal transduction, transport
Rpgrip1-like	Rpgrip1l	NP_775607	145	1	cell projection, centrosome, cilium, cilium axoneme, cytoplasm, microtubule basal body	not classified	brain development, camera-type eye development, cerebellum development, cilium assembly, corpus callosum development, determination of left/right symmetry, embryonic forelimb morphogenesis, embryonic hindlimb morphogenesis, in utero embryonic development, kidney development, lateral ventricle development, limb morphogenesis, liver development, neural tube patterning, nose development, olfactory bulb development, pericardium development, regulation of smoothened signaling pathway, specification of segmental identity, mandibular segment, specification of segmental identity, maxillary segment, telencephalon development
neurobeachin like 1	Nbeal1	NP_775620	306	1	not classified	not classified	not classified
ubiquitin specific protease 43	Usp43	NP_776115	124	1	not classified	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
histidine acid phosphatase domain containing 1	Hisppd1	NP_776121	128	1	cytoplasm	acid phosphatase activity, ATP binding, diphosphoinositol-pentakisphosphate kinase activity, kinase activity, nucleotide binding, transferase activity	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
cysteine conjugate-beta lyase 2	Ccbl2	NP_776124	47	1	not classified	1-aminocyclopropane-1-carboxylate synthase activity, catalytic activity, cysteine-S-conjugate beta-lyase activity, kynurenine-oxoglutarate transaminase activity, lyase activity, pyridoxal phosphate binding, transaminase activity, transferase activity, transferase activity, transferring nitrogenous groups	biosynthetic process
hypothetical protein LOC207781	5830404H04Rik	NP_777272	77	1	not classified	not classified	not classified
phosphoglucomutase 5	Pgm5	NP_778178	62	1	cell junction, cell-cell adherens junction, cell-substrate junction, dystrophin-associated glycoprotein complex, Z disc	intramolecular transferase activity, phosphotransferases, magnesium ion binding, metal ion binding, phosphoglucomutase activity, protein binding, serine-type endopeptidase activity	carbohydrate metabolic process, cell adhesion, glucose metabolic process, proteolysis
solute carrier family 38, member 2	Slc38a2	NP_780330	56	1	integral to membrane, membrane, plasma membrane	amino acid transmembrane transporter activity, sodium ion binding, symporter activity	amino acid transport, ion transport, sodium ion transport, transport
transient receptor potential cation channel, subfamily M, member 4	Trpm4	NP_780339	136	1	integral to membrane, membrane, plasma membrane	ATP binding, calcium activated cation channel activity, calcium channel activity, calcium ion binding, calmodulin binding, ion channel activity, nucleotide binding, voltage-gated ion channel activity	calcium ion transport, immune response, ion transport, regulation of membrane potential, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
galactokinase 2	Galk2	NP_780363	49	1	cytoplasm	ATP binding, galactokinase activity, kinase activity, N-acetylgalactosamine kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity	carbohydrate phosphorylation, galactose metabolic process, metabolic process, phosphorylation
hypothetical protein LOC71653 isoform 2	4930506M07Rik	NP_780381	53	1	cell projection, growth cone	molecular_function	membrane depolarization, multicellular organismal development
serine/arginine repetitive matrix 2	Srrm2	NP_780438	284	1	nucleus, spliceosomal complex	not classified	mRNA processing, RNA splicing
formin homology 2 domain containing 3	Fhod3	NP_780485	176	1	cytoplasm, cytoskeleton	actin binding	actin cytoskeleton organization, cellular component organization
solute carrier family 25, member 41	Slc25a41	NP_780542	35	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
myosin binding protein C, slow type	8030451F13Rik	NP_780627	126	1	cytoskeleton	structural constituent of cytoskeleton	muscle contraction
ARP5 actin-related protein 5 homolog	Actr5	NP_780628	68	1	cellular_component	ATP binding, molecular_function, protein binding	biological_process, regulation of transcription, transcription
plakophilin 4 isoform 2	Pkp4	NP_780673	127	1	cell junction	binding, protein binding	cell adhesion
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
actin, beta-like 2	Actbl2	NP_780706	42	1	cytoplasm, cytoskeleton	ATP binding, nucleotide binding, protein binding	not classified
PDZ domain containing 6	Intu	NP_780724	105	1	not classified	not classified	not classified
F-box protein 46	Fbxo46	NP_780739	65	1	not classified	not classified	modification-dependent protein catabolic process
FCH and double SH3 domains 1	Fchsd1	NP_783615	76	1	not classified	not classified	not classified
hypothetical protein LOC319352	C530028O21Rik	NP_783627	30	1	integral to membrane, membrane	not classified	not classified
RNA binding motif protein 35b	Rbm35b	NP_789808	77	1	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
coiled coil domain containing 88A	Ccdc88a	NP_789811	212	1	cell projection, cytoplasm, cytoplasmic vesicle, membrane, plasma membrane	microtubule binding, protein kinase B binding	activation of protein kinase B activity, DNA replication, regulation of cell proliferation, regulation of DNA replication, regulation of protein amino acid phosphorylation
5'-nucleotidase, cytosolic II-like 1 protein	Nt5dc1	NP_795942	53	1	not classified	hydrolase activity, magnesium ion binding, metal ion binding	not classified
centromere protein T	Cenpt	NP_796124	56	1	chromosome, chromosome, centromeric region, nucleus	not classified	not classified
serine protease Desc4	9930032O22Rik	NP_796136	47	1	extracellular region, integral to membrane, integral to plasma membrane, membrane	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	proteolysis
synaptonemal complex protein 2	Sycp2	NP_796165	172	1	lateral element, nucleus, synaptonemal complex	DNA binding, protein binding, protein heterodimerization activity	apoptosis, cell cycle, cell division, female meiosis, fertilization, male genitalia morphogenesis, male meiosis, meiosis, organ morphogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
testis flippase	4930417M19 Rik	NP_796169	136	1	integral to membrane, membrane	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, nucleotide binding, phospholipid-translocating ATPase activity	ATP biosynthetic process, phospholipid transport
leucine rich repeat neuronal 4	Lrrn4	NP_796277	80	1	integral to membrane, membrane	protein binding	not classified
phosphoinositide-3-kinase, regulatory subunit 5, p101	Pik3r5	NP_796294	97	1	cytoplasm, membrane, nucleus	kinase activity	not classified
myotubularin related protein 9	Mtmr9	NP_808262	63	1	cytoplasm	enzyme regulator activity, phosphatase activity, protein binding	dephosphorylation
dual oxidase 2	Duox2	NP_808278	172	1	integral to membrane, membrane	calcium ion binding, oxidoreductase activity	adenohypophysis morphogenesis, bone mineralization, fertilization, hormone metabolic process, inner ear development, multicellular organism growth, oxidation reduction, thyroid gland development, thyroid hormone metabolic process
hypothetical protein LOC228850	B230339M05 Rik	NP_808326	166	1	intracellular	GTPase activator activity	regulation of small GTPase mediated signal transduction
tumor suppressor candidate 5	Tusc5	NP_808377	19	1	integral to membrane, membrane	not classified	response to biotic stimulus
killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	Kir3dl1	NP_808417	46	1	integral to membrane, membrane, plasma membrane	receptor activity	not classified
dedicator of cytokinesis 5	Dock5	NP_808448	214	1	cellular_component, cytoplasm	guanyl-nucleotide exchange factor activity, molecular_function	biological_process
transmembrane protein 67	Tmem67	NP_808529	112	1	integral to membrane, membrane, plasma membrane	not classified	not classified
Fras1 related extracellular matrix protein 1	Frem1	NP_808531	245	1	basement membrane, extracellular region, proteinaceous extracellular matrix	binding, calcium ion binding, metal ion binding, protein binding, sugar binding	cell adhesion, cell-matrix adhesion, multicellular organismal development
hypothetical protein LOC330361	AW146020	NP_808552	87	1	nucleus	DNA binding, transcription factor activity	regulation of transcription, transcription
piwi-like 4	Piwil4	NP_808573	99	1	cytoplasm, nucleus, P granule	piRNA binding, protein binding, RNA binding	cell differentiation, DNA methylation during gametogenesis, gene silencing by RNA, meiosis, multicellular organismal development, piRNA metabolic process, regulation of translation, spermatogenesis
prominin 2 isoform 2	Prom2	NP_835148	55	1	cell projection, cilium, integral to membrane, membrane, plasma membrane	not classified	not classified
ADP-ribosylation factor-like 6 interacting protein 2 isoform 2	Arl6ip2	NP_835151	47	1	integral to membrane, membrane	GTP binding, GTPase activity, nucleotide binding, protein binding	not classified
phosphodiesterase 4D interacting protein isoform 2	Pde4dip	NP_835181	127	1	cytoplasm, Golgi apparatus, nucleus	protein binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
AMP-activated protein kinase alpha 2 catalytic subunit	Prkaa2	NP_835279	62	1	nucleus	AMP-activated protein kinase activity, ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cholesterol biosynthetic process, fatty acid biosynthetic process, lipid biosynthetic process, protein amino acid phosphorylation, response to stress, steroid biosynthetic process, sterol biosynthetic process
sorting nexin 26	Snx26	NP_839983	140	1	cytoplasm, intracellular, membrane, plasma membrane	GTPase activator activity, protein binding, Rac GTPase activator activity, Rho GTPase activator activity	protein transport, signal transduction, transport
DEAH (Asp-Glu-Ala-His) box polypeptide 33	Dhx33	NP_848144	78	1	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	not classified
myosin IG	Myo1g	NP_848534	117	1	myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	not classified
proteasome 26S non-ATPase subunit 11	Psmd11	NP_848731	47	1	proteasome complex	not classified	not classified
solute carrier family 30 (zinc transporter), member 9	Slc30a9	NP_848766	63	1	cytoplasm, integral to membrane, membrane, nucleus	cation transmembrane transporter activity, molecular_function, zinc ion binding	biological_process, cation transport, ion transport, regulation of transcription, transcription, transport, zinc ion transport
ataxia, cerebellar, Cayman type homolog	Atcay	NP_848777	42	1	not classified	not classified	transport
coiled-coil domain containing 100	Ccdc100	NP_848801	113	1	centrosome	protein binding, protein C-terminus binding	cell proliferation, cerebral cortex development, interkinetic nuclear migration, microtubule cytoskeleton organization, neurogenesis, regulation of microtubule-based process, regulation of protein localization, spindle astral microtubule organization
RAB3 GTPase activating protein subunit 1	Rab3gap1	NP_848805	110	1	cytoplasm	GTPase activator activity, Rab GTPase activator activity	not classified
zinc finger protein 592	Zfp592	NP_848822	133	1	intracellular, nucleus	DNA binding, metal ion binding, protein binding, zinc ion binding	regulation of transcription, transcription
aldehyde dehydrogenase 8 family, member A1	Aldh8a1	NP_848828	54	1	cellular_component, cytoplasm	oxidoreductase activity, retinal dehydrogenase activity	9-cis-retinoic acid biosynthetic process, metabolic process, oxidation reduction, retinal metabolic process
kelch-like 8	Klhl8	NP_848856	70	1	not classified	protein binding	not classified
EGF-like, fibronectin type III and laminin G domains	Egflam	NP_848863	110	1	basement membrane, cell junction, extracellular matrix, extracellular region, interstitial matrix, proteinaceous extracellular matrix, synapse	glycosaminoglycan binding	extracellular matrix organization, peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan, positive regulation of cell-substrate adhesion

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
ATP/GTP binding protein-like 2	Agbl2	NP_848870	99	1	cytoplasm	carboxypeptidase activity, hydrolase activity, metal ion binding, metallocarboxypeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
expressed sequence AI790205	Gpr107	NP_848875	62	1	integral to membrane, membrane	receptor activity	not classified
BCL6 co-repressor-like 1	Bcorl1	NP_848897	190	1	nucleus	not classified	chromatin modification, regulation of transcription, transcription
hypothetical protein LOC320484	A430107D22 Rik	NP_848900	115	1	intracellular	GTPase activator activity	regulation of small GTPase mediated signal transduction
Fanconi anemia, complementation group M	Fancm	NP_849243	226	1	nucleus	ATP binding, ATP-dependent helicase activity, DNA binding, helicase activity, hydrolase activity, nuclease activity, nucleic acid binding, nucleotide binding, protein binding	DNA metabolic process, DNA repair, response to DNA damage stimulus
Kazal-type serine peptidase inhibitor domain 1	Kazald1	NP_849260	34	1	extracellular matrix, extracellular region, interstitial matrix, proteinaceous extracellular matrix	insulin-like growth factor binding	cell differentiation, extracellular matrix organization, multicellular organismal development, ossification, regulation of cell growth
solute carrier family 25, member 29	Slc25a29	NP_851845	33	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	acyl carnitine transporter activity, binding, transporter activity	acyl carnitine transport, transport
DENN/MADD domain containing 1B isoform 1	Dennd1b	NP_851992	77	1	not classified	not classified	not classified
coiled-coil-helix-coiled-coil-helix domain containing 7	Chchd7	NP_852056	10	1	cellular_component	molecular_function	biological_process
fructosamine 3-kinase-related protein	BC032265	NP_852085	34	1	not classified	kinase activity, transferase activity	not classified
cDNA sequence BC022641	Edc4	NP_853625	151	1	cytoplasm, nucleus	not classified	not classified
R3H domain (binds single-stranded nucleic acids)	R3hdm1	NP_861415	124	1	not classified	not classified	not classified
hypothetical protein LOC75216	4930534B04 Rik	NP_861536	129	1	not classified	not classified	not classified
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
ring finger protein 20	Rnf20	NP_892044	114	1	cellular_component, chromosome, nucleus	ligase activity, metal ion binding, molecular_function, protein binding, zinc ion binding	biological_process, chromatin modification, modification-dependent protein catabolic process
Cdc42 binding protein kinase beta	Cdc42bpb	NP_898837	195	1	cytoplasm	ATP binding, diacylglycerol binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, small GTPase regulator activity, transferase activity, zinc ion binding	intracellular signaling cascade, protein amino acid phosphorylation
zinc finger protein 598	Zfp598	NP_898972	99	1	cellular_component, intracellular	metal ion binding, molecular_function, protein binding, zinc ion binding	biological_process
hypothetical protein LOC242602	BC055111	NP_899005	46	1	not classified	not classified	not classified
schlafen 5	Slfn5	NP_899024	101	1	nucleus	ATP binding, nucleotide binding	cell differentiation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
FAT tumor suppressor homolog 4	Fat4	NP_899044	540	1	integral to membrane, membrane	calcium ion binding, protein binding	cell adhesion, homophilic cell adhesion
hypothetical protein LOC68550	1110002N22 Rik	NP_899098	42	1	not classified	not classified	not classified
phosphodiesterase 4A, cAMP specific isoform 5	Pde4a	NP_899668	94	1	not classified	3',5'-cyclic-AMP phosphodiesterase activity, 3',5'-cyclic-nucleotide phosphodiesterase activity, catalytic activity, hydrolase activity	signal transduction
NACHT, LRR and PYD containing protein 9b	Nlrp9b	NP_918947	115	1	cytoplasm	ATP binding, nucleotide binding, protein binding	not classified
A kinase (PRKA) anchor protein (yotiao) 9	Akap9	NP_919444	434	1	cytoplasm, pericentriolar material	kinase activity, protein binding	not classified
alcohol dehydrogenase PAN1B-like	Hsd17b13	NP_932147	34	1	extracellular region	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
periaxin isoform L	Prx	NP_932165	148	1	cytoplasm, membrane, nucleus, plasma membrane	protein binding	not classified
hypothetical protein LOC207375	ORF34	NP_932773	120	1	not classified	not classified	not classified
nucleoporin 188	Nup188	NP_938046	197	1	nuclear pore, nucleus	not classified	mRNA transport, protein transport, transmembrane transport, transport
alanyl-tRNA synthetase 2, mitochondrial	Aars2	NP_941010	107	1	cellular_component, cytoplasm, mitochondrion	alanine-tRNA ligase activity, aminoacyl-tRNA ligase activity, ATP binding, ligase activity, ligase activity, forming aminoacyl-tRNA and related compounds, molecular_function, nucleic acid binding, nucleotide binding	alanyl-tRNA aminoacylation, biological_process, translation, tRNA aminoacylation
H1 histone family, member X	H1fx	NP_941024	20	1	chromosome, nucleus	DNA binding	not classified
hypothetical protein LOC279029	Gm711	NP_941030	75	1	not classified	ATP binding, nucleotide binding, protein kinase activity	protein amino acid phosphorylation
actin binding LIM protein family, member 3	Ablim3	NP_941051	78	1	cytoplasm	actin binding, metal ion binding, zinc ion binding	cytoskeleton organization, positive regulation of transcription from RNA polymerase II promoter
outer dense fiber of sperm tails 3-like 1	Odf3l1	NP_941075	31	1	not classified	not classified	not classified
neuroligin 2	Nlgn2	NP_942562	91	1	integral to membrane, membrane, synapse	protein binding	cell adhesion, regulation of respiratory gaseous exchange by neurological system process, regulation of synaptic transmission, synapse organization
PHD finger protein 15	Phf15	NP_955003	92	1	not classified	metal ion binding, protein binding, zinc ion binding	not classified
endothelin converting enzyme 1	Ece1	NP_955011	85	1	cell surface, Golgi apparatus, integral to membrane, membrane, plasma membrane	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	peptide hormone processing, pharyngeal system development, proteolysis
WEE1 homolog 2	Wee2	NP_958758	62	1	nucleus	ATP binding, kinase activity, magnesium ion binding, non-membrane spanning protein tyrosine kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	mitosis, protein amino acid phosphorylation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
plectin 1 isoform 6	Plec1	NP_958791	534	1	contractile fiber, cytoplasm, cytoskeleton, insoluble fraction	actin binding	not classified
UDP glucuronosyltransferase 1 family, polypeptide A9	Ugt1a9	NP_964006	60	1	endoplasmic reticulum, integral to membrane, membrane, microsome	glucuronosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	metabolic process
interferon alpha 6T	OTTMUSG00000011275	NP_996750	22	1	extracellular space	cytokine activity	response to virus
taste receptor, type 2, member 129	Tas2r129	NP_996912	37	1	integral to membrane, membrane	G-protein coupled receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, response to stimulus, sensory perception of taste, signal transduction
transmembrane protein 16g	Tmem16g	NP_996914	97	1	chloride channel complex, integral to membrane, membrane, plasma membrane	calcium ion binding, chloride channel activity, chloride ion binding, ion channel activity	ion transport, transport
hypothetical protein LOC73072	BC068157	NP_997086	111	1	not classified	not classified	not classified
lysophosphatidylcholine acyltransferase 4	Lpcat4	NP_997089	57	1	endoplasmic reticulum, integral to membrane, membrane	acyltransferase activity, transferase activity	metabolic process, phospholipid biosynthetic process
hypothetical protein LOC240066	BC066107	NP_997128	64	1	nucleus	metal ion binding, zinc ion binding	transcription
olfactory receptor 1051	Olfr1051	NP_997445	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
dystrobrevin alpha isoform 1	Dtna	NP_997533	77	1	cell junction, cytoplasm, dystrobrevin complex, microsome, sarcolemma, synapse	calcium ion binding, metal ion binding, protein binding, zinc ion binding	not classified
PREDICTED: similar to Ki-67	Mki67	XP_001000692	351	1	chromosome, centromeric region, condensed chromosome, cytoplasm, intracellular, nucleolus, nucleus	not classified	cell proliferation, meiosis
PREDICTED: hypothetical protein	Gm536	XP_001001008	17	1	not classified	not classified	not classified
PREDICTED: thyroid hormone receptor interactor 11 isoform 3	Trip11	XP_001001171	226	1	not classified	receptor activity	not classified
PREDICTED: heterogeneous nuclear ribonucleoprotein A0	Hnrpa0	XP_001001311	31	1	not classified	not classified	not classified
PREDICTED: similar to KIAA1858 protein	Gm22	XP_001001798	335	1	not classified	not classified	not classified
PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	EG629557	XP_001002772	36	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC66808	9030624G23Rik	XP_001003228	18	1	not classified	not classified	not classified
PREDICTED: plexin B2 isoform 14	Plxnb2	XP_001003435	206	1	integral to membrane, membrane	protein binding	positive regulation of axonogenesis
PREDICTED: START domain containing 9	Stard9	XP_001004201	504	1	microtubule	ATP binding, motor activity, nucleotide binding	not classified
PREDICTED: hypothetical protein isoform 1	LOC100044330	XP_001472000	28	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC320625	9330101J02Rik	XP_001472215	214	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039079	XP_001472265	11	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC78167	4930439D14Rik	XP_001472326	37	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	LOC100039184	XP_001472463	4	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100044506	XP_001472509	17	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039211	XP_001472511	15	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG245516	XP_001472556	94	1	not classified	not classified	not classified

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
PREDICTED: hypothetical protein LOC75255	4930562F07Rik	XP_001472732	14	1	not classified	not classified	not classified
PREDICTED: similar to SMC4 protein	LOC100044651	XP_001472819	148	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100045035	XP_001472867	26	1	not classified	not classified	not classified
PREDICTED: similar to Copine V	LOC100048828	XP_001472874	59	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC70941	4921539E11Rik	XP_001473247	40	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039707	XP_001473323	23	1	not classified	not classified	not classified
PREDICTED: similar to TTF-2 protein	LOC100044984	XP_001473497	42	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039772	XP_001473532	15	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC78244	4930461P20Rik	XP_001473693	62	1	not classified	not classified	not classified
PREDICTED: similar to Ankrd12 protein	LOC100043992	XP_001473831	33	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100045557	XP_001474006	22	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100040172	XP_001474258	19	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: hypothetical protein	LOC100040405	XP_001474680	39	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100045662	XP_001474747	51	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC677427	XP_001474950	11	1	not classified	not classified	not classified
PREDICTED: similar to Traf2 and NCK interacting kinase, splice isoform 2	Tnik	XP_001474959	125	1	not classified	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, small GTPase regulator activity, transferase activity	protein amino acid phosphorylation
PREDICTED: hypothetical protein	LOC667147	XP_001475011	30	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100045882	XP_001475133	16	1	not classified	not classified	not classified
PREDICTED: similar to L23 mitochondrial-related protein isoform 2	LOC100040519	XP_001475261	17	1	ribosome	not classified	not classified
PREDICTED: similar to Gapdh protein	LOC100040480	XP_001475428	15	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046043	XP_001475508	28	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	ENSMUSG00000056391	XP_001475572	43	1	not classified	not classified	not classified
PREDICTED: similar to Translocase of outer mitochondrial membrane 20 homolog (yeast)	LOC546321	XP_001475586	14	1	not classified	not classified	not classified
PREDICTED: similar to 40S ribosomal protein S29	EG632013	XP_001476064	7	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC673968	XP_001476092	23	1	not classified	not classified	not classified
PREDICTED: similar to STAT3-interacting protein as a repressor	LOC434799	XP_001476131	28	1	not classified	not classified	not classified
PREDICTED: similar to Selenoprotein K	LOC100046282	XP_001476445	10	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046662	XP_001476788	13	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046760	XP_001476811	9	1	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L39	LOC100046220	XP_001476878	8	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG633285	XP_001477109	60	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC78147	8430439B09Rik	XP_001477185	8	1	not classified	not classified	not classified
PREDICTED: OTU domain containing 3	Otud3	XP_001477778	50	1	not classified	not classified	not classified
PREDICTED: similar to CDNA sequence BC018101	EG382161	XP_001477881	70	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100042323	XP_001477991	11	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047366	XP_001478045	12	1	not classified	not classified	not classified
PREDICTED: similar to THO complex 2	LOC100042165	XP_001478330	183	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100042273	XP_001478355	17	1	not classified	not classified	not classified
PREDICTED: similar to olfactory receptor MOR264-3	LOC100047739	XP_001478839	36	1	not classified	not classified	not classified
PREDICTED: hypothetical protein isoform 2	LOC634257	XP_001478882	22	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 Ezh1 protein	LOC100044129	XP_001478998	85	1	nucleus	DNA binding, histone-lysine N-methyltransferase activity, methyltransferase activity, protein binding, transferase activity	chromatin modification, regulation of transcription, transcription
PREDICTED: hypothetical protein	LOC100047609	XP_001479061	70	1	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA 1700022C21 gene	LOC100047902	XP_001479145	33	1	not classified	not classified	not classified
PREDICTED: similar to ADIR1	LOC100047963	XP_001479288	35	1	not classified	not classified	not classified
PREDICTED: similar to olfactory receptor MOR183-2	LOC100048042	XP_001479447	40	1	not classified	not classified	not classified
PREDICTED: similar to Ran-binding protein 16 isoform 3	LOC100048165	XP_001479590	124	1	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA B230315N10 gene	B230315N10Rik	XP_001479610	70	1	nucleus	metal ion binding, zinc ion binding	transcription
PREDICTED: similar to Eukaryotic translation initiation factor 5 isoform 2	LOC100047658	XP_001479649	49	1	not classified	not classified	not classified
PREDICTED: similar to Cytochrome P450, family 2, subfamily a, polypeptide 12 isoform 3	EG233005	XP_001479661	50	1	not classified	iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity	oxidation reduction
PREDICTED: similar to Mannose-P-dolichol utilization defect 1	LOC100048170	XP_001479721	19	1	not classified	not classified	not classified
PREDICTED: similar to UGT1.6	LOC100048293	XP_001480001	33	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC672884	XP_001480393	136	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100048424	XP_001480537	7	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	ENSMUSG00000075265	XP_001481037	13	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100048769	XP_001481256	41	1	not classified	not classified	not classified
PREDICTED: similar to ubiquitin specific protease 24	Usp24	XP_001481331	332	1	not classified	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process
PREDICTED: similar to SH3 domain binding protein	Wipf3	XP_001481334	49	1	cytoplasm	actin binding	cell differentiation, multicellular organismal development, spermatogenesis
PREDICTED: similar to novel KRAB box and zinc finger, C2H2 type domain containing protein	LOC436100	XP_001481343	72	1	not classified	not classified	not classified
PREDICTED: similar to FERM and PDZ domain containing 2	Frmpd2	XP_001481344	142	1	not classified	not classified	not classified
PREDICTED: similar to hCG1813078	Dnahc17	XP_001481351	512	1	cell projection, cilium, dynein complex, microtubule	ATP binding, ATPase activity, microtubule motor activity, motor activity, nucleotide binding	microtubule-based movement
PREDICTED: similar to very large inducible GTPase 1	Gm1966	XP_001481361	279	1	not classified	not classified	not classified
PREDICTED: gene model 969, (NCBI)	Gm969	XP_001481372	103	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC625662	XP_127483	85	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC236874	XP_135951	19	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Gm221	XP_136914	82	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Hephl1	XP_146812	128	1	integral to membrane, membrane	copper ion binding, metal ion binding, oxidoreductase activity	copper ion transport, ion transport, oxidation reduction, transport
PREDICTED: hypothetical protein LOC320827 isoform 1	C530008M17Rik	XP_287460	140	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Gm1043	XP_355598	111	1	not classified	not classified	not classified
PREDICTED: similar to Rab5B	LOC433464	XP_485050	22	1	not classified	not classified	not classified
PREDICTED: zinc finger and BTB domain containing 10 isoform 1	Zbtb10	XP_485202	117	1	cellular_component	molecular_function	biological_process
PREDICTED: similar to 2410089E03Rik protein	EG546032	XP_486078	47	1	not classified	not classified	not classified
PREDICTED: similar to 40S ribosomal protein S14 isoform 1	EG545121	XP_619341	16	1	not classified	not classified	not classified
PREDICTED: similar to 60S ribosomal protein L38	EG547172	XP_622034	9	1	not classified	not classified	not classified
PREDICTED: similar to TL antigen isoform 1	H2-T3-like	XP_622848	43	1	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L23a	EG619734	XP_889280	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: microtubule-actin crosslinking factor 1 isoform 2	Macf1	XP_890015	839	1	actin cytoskeleton, cell cortex, cytoplasm, cytoskeleton, microtubule cytoskeleton	actin binding, calcium ion binding, microtubule binding, protein binding	cell cycle arrest, cell motion, establishment or maintenance of cell polarity, mesoderm formation, posttranslational protein targeting to membrane, protein localization, Wnt receptor signaling pathway
PREDICTED: hypothetical protein LOC77522	D630002J15 Rik	XP_890528	12	1	integral to membrane, membrane	not classified	not classified
PREDICTED: hypothetical protein	EG621697	XP_892477	16	1	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L22	LOC623483	XP_893035	35	1	not classified	not classified	not classified
PREDICTED: microtubule associated serine/threonine kinase 3 isoform 2	Mast3	XP_893383	144	1	not classified	ATP binding, kinase activity, magnesium ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
PREDICTED: similar to CDNA sequence BC061237	EG624966	XP_894601	40	1	not classified	not classified	not classified
PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase	EG626358	XP_896039	41	1	not classified	not classified	not classified
PREDICTED: similar to Histone H1	EG629389	XP_899364	33	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC319887 isoform 3	E030030I06 Rik	XP_903028	20	1	not classified	not classified	not classified
PREDICTED: similar to Histone H1	LOC630555	XP_909191	25	1	not classified	not classified	not classified
PREDICTED: similar to hCG401196	4921511H13 Rik	XP_909489	264	1	nucleus	not classified	not classified
PREDICTED: hypothetical protein LOC68075	1520402A15 Rik	XP_910167	26	1	not classified	not classified	not classified
PREDICTED: similar to Chromosome 4 open reading frame 26	Gm1045	XP_910708	14	1	not classified	not classified	not classified
PREDICTED: similar to acidic ribosomal phosphoprotein P1	LOC270362	XP_910749	12	1	not classified	not classified	not classified
PREDICTED: similar to Serine/threonine-protein kinase MRCK gamma (CDC42-binding protein kinase gamma) (Myotonic dystrophy kinase-related CDC42-binding kinase gamma) (Myotonic dystrophy protein kinase-like alpha) (MRCK gamma) (DMPK-like gamma)	Cdc42bpg	XP_911542	172	1	cytoplasm	ATP binding, diacylglycerol binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, small GTPase regulator activity, transferase activity, zinc ion binding	intracellular signaling cascade, protein amino acid phosphorylation
PREDICTED: similar to CXXC finger 6 isoform 2	Cxxc6	XP_912173	219	1	cellular_component, nucleus	DNA binding, iron ion binding, metal ion binding, molecular_function, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, zinc ion binding	biological_process, oxidation reduction
PREDICTED: hypothetical protein LOC70980	4931431F19 Rik	XP_912873	55	1	mitochondrion	molecular_function	biological_process
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 Glyceraldehyde-3-phosphate dehydrogenase	EG215974	XP_915137	54	1	not classified	not classified	not classified
PREDICTED: similar to vomeronasal receptor V1RC13	EG546903	XP_915275	36	1	not classified	not classified	not classified
PREDICTED: similar to Regulator of G-protein signalling 22	LOC635821	XP_916087	129	1	not classified	not classified	not classified
PREDICTED: similar to spermatogenesis associated glutamate (E)-rich protein 2	LOC635905	XP_916210	29	1	not classified	not classified	not classified
PREDICTED: similar to mitochondrial ribosomal protein S21	EG626573	XP_916948	10	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG269105	XP_918900	15	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 CCR4-NOT transcription complex, subunit 1 isoform 16	Cnot1	XP_919363	267	1	cellular_component	molecular_function, protein binding	biological_process, regulation of transcription, transcription
PREDICTED: hypothetical protein	1700024P16 Rik	XP_920737	89	1	not classified	not classified	not classified
PREDICTED: similar to Murinoglobulin 1	EG640530	XP_922625	165	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG243642	XP_922857	33	1	not classified	not classified	not classified
PREDICTED: similar to Bardet-Biedl syndrome 10 protein homolog isoform 3	Bbs10	XP_922897	79	1	not classified	ATP binding, nucleotide binding, protein binding	cellular protein metabolic process
PREDICTED: macrophage antigen h	4933425B16 Rik	XP_922940	31	1	integral to membrane, membrane, plasma membrane	binding, receptor activity, sugar binding	not classified
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 60S ribosomal protein L7 isoform 4	EG268809	XP_924795	29	1	not classified	not classified	not classified
PREDICTED: similar to ATP-binding cassette, sub-family B (MDR/TAP), member 7 isoform 7	Abcb7	XP_925448	83	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	ATP binding, ATPase activity, ATPase activity, coupled to transmembrane movement of substances, nucleoside-triphosphatase activity, nucleotide binding	cellular iron ion homeostasis, transport
PREDICTED: hypothetical protein LOC71996 isoform 4	1600014K23 Rik	XP_926394	21	1	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA 2310028O11 gene isoform 6	2310028O11 Rik	XP_929663	9	1	integral to membrane, membrane	molecular_function	biological_process
PREDICTED: hypothetical protein	LOC674274	XP_978458	21	1	not classified	not classified	not classified
PREDICTED: similar to Aldehyde dehydrogenase 3 family, member B1	Aldh3b2	XP_979234	65	1	not classified	not classified	not classified
PREDICTED: similar to MHC class I antigen isoform 7	ENSMUSG00000073403	XP_979787	42	1	not classified	not classified	not classified
PREDICTED: HECT domain containing 1	Hectd1	XP_979999	289	1	not classified	ligase activity	modification-dependent protein catabolic process, neural tube closure
PREDICTED: similar to fragile site-associated protein	4932438A13 Rik	XP_980288	555	1	integral to membrane, membrane	not classified	not classified
PREDICTED: mucin 2	Muc2	XP_980706	91	1	extracellular region, inner mucus layer, outer mucus layer, proteinaceous extracellular matrix	protein binding	apoptosis, induction of apoptosis, negative regulation of cell migration, negative regulation of cell proliferation
PREDICTED: hypothetical protein	LOC674771	XP_982053	31	1	not classified	not classified	not classified
PREDICTED: similar to Rmi1 protein	LOC665550	XP_982784	69	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG665756	XP_984329	145	1	not classified	not classified	not classified
PREDICTED: similar to KIAA1683 protein	2410018E23 Rik	XP_984456	141	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC675231	XP_985436	17	1	not classified	not classified	not classified
PREDICTED: similar to mFLJ00251 protein	Dnhd1	XP_988314	264	1	not classified	not classified	not classified
PREDICTED: similar to TNS1 protein	Tns1	XP_989880	186	1	cell-substrate junction, focal adhesion	actin binding	cell migration, cell-substrate junction assembly
PREDICTED: similar to hCG2011852	EG666713	XP_990666	394	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC74471	4933440N22 Rik	XP_991148	29	1	not classified	not classified	not classified
PREDICTED: similar to mKIAA0897 protein	Ppfia4	XP_993485	130	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG667503	XP_996026	122	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC676542	XP_996040	57	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG667682	XP_996461	14	1	not classified	not classified	not classified
PREDICTED: similar to myeloid/lymphoid or mixed-lineage leukemia 2	Mll2	XP_999353	566	1	histone methyltransferase complex, nucleus	metal ion binding, methyltransferase activity, protein binding, transferase activity, zinc ion binding	in utero embryonic development
PREDICTED: similar to 17,000 dalton myosin light chain	LOC676975	XP_999583	17	1	not classified	not classified	not classified