Chemical Proteomics of Reactive Cysteine Residues in Two Disease Models:

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Chemical Proteomics of Reactive Cysteine Residues in Two Disease Models

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Chemical Proteomics of Reactive Cysteine Residues in Two Disease Models

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Cysteine residues perform many essential cellular functions, including nucleophilic and redox catalysis, metal coordination, structural stabilization and cellular protection. Cysteine-related mutations are oftentimes related to diseases due to the amino acid's functional importance. This has led cysteine to become a focus of small molecule drug discovery. A comparison of the cysteine proteome of diseased cells versus healthy cells can elucidate novel cysteine residues that play an important role in progressing the disease state. Two disease models were chosen to be the focus of this proteomic study; breast cancer through the human epithelial MCF10 progression series and immunoactivation through the Raw 246.7 mouse macrophage cell line. Comparative proteomics with mass spectrometry revealed several changes within the cysteine proteome when the cells were diseased. Some cysteines had changes in reactivity, most likely indicating a loss or gain of a modification or disulfide bond. Other cysteines showed increased labeling due to an increase in the overall expression of the protein encompassing the cysteine residue. Further follow-up of an interesting hit from the Raw cell comparison, immune responsive gene 1 (IRG1), was conducted. IRG1 produces itaconate from cis-aconitate under inflammatory conditions, disrupting the citric acid cycle. IRG1 was confirmed to have increased expression following activation of the macrophage cells by lipopolysaccharides. It was also successfully recombinantly expressed in and purified from *Escherichia coli* for use in an activity assay to determine if the cysteine labeled in the mass spectrometry experiment is essential for the protein function. With additional knowledge of cysteines that help progress disease states, new small molecule inhibitors can be developed to target these cysteines and impede the function that is beneficial for the disease.

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LIST OF ABBREVIATIONS

Standard 3-letter and 1-letter codes are used for the 20 natural amino acids.

ABPP	activity-based protein profiling
ACN	acetonitrile
BL21	*E. coli* expression molecular biology strain with T7 polymerase for pET system
C18	C18-reversed phase silica gel
dH_2O	deionized water
DMEM	Dulbecco’s modified eagle medium
DMEM/F12	Dulbecco's modified eagle medium: nutrient mixture F-12
DMSO	dimethylsulfoxide
DTT	dithiothreitol
EGF	epidermal growth factor
EGFR	epidermal growth factor receptor
FBS	fetal bovine serum
GAPDH	glyceraldehyde 3-phosphate dehydrogenase
GDP	guanosine diphosphate
GTP	guanosine triphosphate
HPLC	high performance liquid chromatography
HRP	horseradish peroxidase
IA	iodoacetamide

IA-alkyne	iodoacetamide alkyne probe (N-(hex-5-yn-1-yl)-2-iodoacetamide)
iNOS	inducible nitric oxide synthase
IPTG	isopropyl β-D-1-thiogalactopyranoside
Irg1 (Acod1)	immune-responsive gene 1 (aconitate decarboxylase 1)
IsoTOP-ABPP	isotopic tandem orthogonal proteolysis - activity-based protein profiling
KRAS	GTPase important for cell signaling pathways
LB media	Luria broth media
LC	liquid chromatography
LPS	lipopolysaccharides
MeOH	methanol
MS	mass spectrometry
Ni-NTA	nickel-charged affinity resin used to purify recombinant proteins containing a polyhistidine (6xHis) sequence
OD_{600}	optical density of cultures measured by absorbance at 600 nm
PBS	phosphate buffered saline (137 mM NaCl, 2.7 mM KCl, pH 7.4)
PSA	Amphotericin B, Penicillin, Streptomycin solution
ReDiMe	reductive dimethylation
ROS	reactive oxygen species
SCX	strong cation exchange resin

SDS	sodium dodecyl sulfate
SDS-PAGE	sodium dodecyl sulfate polyacrylamide gel electrophoresis
TBS	tris-buffer saline
TBS-T	tris-buffer saline with 1% Tween-20
TBTA	tris(benzyltriazolylmethyl)amine
TCA	trichloroacetic acid
TCA cycle	tricarboxylic acid cycle (citric acid cycle)
TCEP	tris(2-carboxyethyl)phosphine hydrochloride
TEAB	tetraethylammonium bromide
TFA	trifluoroacetic acid
Tris	tris(hydroxymethyl)aminomethane

1.0 CHAPTER 1: CYSTEINE PROFILING IN CANCER AND THE IMMUNE RESPONSE

1.1 INTRODUCTION

Cysteine is one of the 20 natural amino acids that are the building blocks for proteins. Cysteines, which contain a reactive thiol, often play major roles in protein function and stability. This unique amino acid has nucleophilic properties, can form disulfides with other thiols and can be reversibly oxidized to an extent. Due to their reactivity, cysteines are also susceptible to a wide variety of post-translational modifications, which can further attune the protein's function. Cysteines are often highly conserved residues, suggesting that they were harnessed in early evolution to support protein structure and activity. They are also widespread throughout proteomes, with most proteins containing at least one cysteine residue.[1] Though often conserved residues, eukaryotic proteomes only have about a 1.9% cysteine composition, indicating that this amino acid is only incorporated when it is truly essential.[2] The critical roles and distinctive properties of cysteine make it appealing to study from a proteomics perspective.

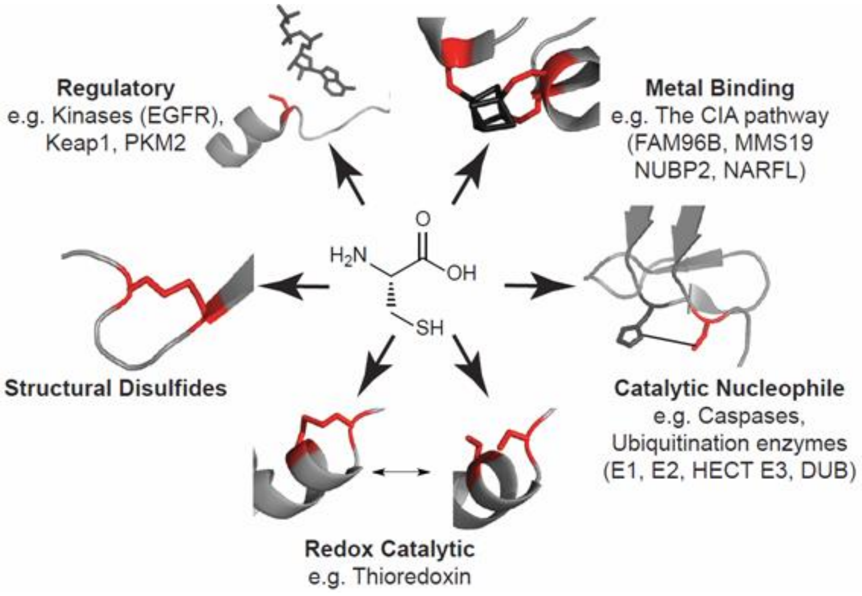

Figure 1-1. Functional roles performed by cysteine residues.[3]

Reactive cysteines have several known cellular functions, as illustrated in Figure 1-1. A common functional role of cysteine is as a catalytic nucleophile. Cysteine is the only amino acid with a thiol, which makes its nucleophilic reactivity very unique. An example of a catalytic cysteine is in arginine deaminase, which uses active site Cys406 to catalyze the hydrolysis of L-arginine to citrulline. It is proposed that the cysteine binding to the electrophilic carbon on arginine mediates the displacement of an ammonia, which is a crucial step for the formation of citrulline.[4]

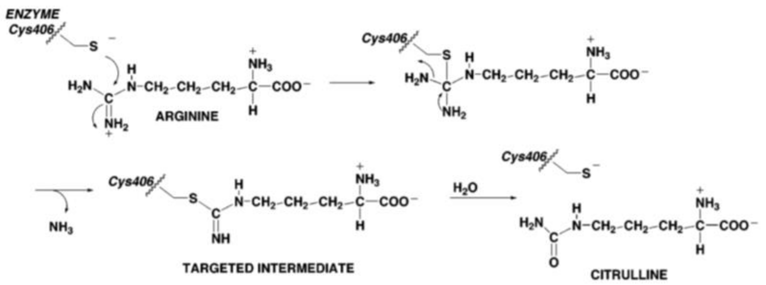

Figure 1-2. Cysteine acting as a catalytic nucleophile in the hydrolysis of arginine.[4]

Cysteines can also catalyze redox reactions, such as radical transfer in the RNRase family. Fe-dependent RNRases in *E.coli* generate radicals on a cysteine residue by transferring an electron to the catalytic tyrosine. The thiyl radical is reduced by an electron from the ribonucleotide substrate, which allows the synthesis of the deoxyribonucleotides to proceed.[5,6] Not all cysteines have catalytic functions on their own; some cysteines require modifications in order to become catalytic, such as metal coordination.[7]

Cysteines participate in metal coordination to promote protein stability, function or regulation. Cysteine can coordinate stably with several transition elements including zinc, iron and copper.[1] The most common coordination involves cysteine and iron in varying ratios ([Fe_2S_2], [Fe_3S_4] and [Fe_4S_4]). These iron-sulfur complexes are found in more than 120 classes of proteins. The clusters bring a new function of regulating one-electron redox processes to the proteins involved.[8] Radical SAM enzymes are an interesting subset of iron-sulfur proteins. In this enzyme family, a motif containing three cysteines coordinate three of the four irons in the cluster. The fourth iron is coordinated by an S-adenosyl-L-methionine (SAM) molecule, which is then cleaved by the enzyme into a methionine and a 5′-deoxyadenosyl radical, a powerful oxidant.[9]

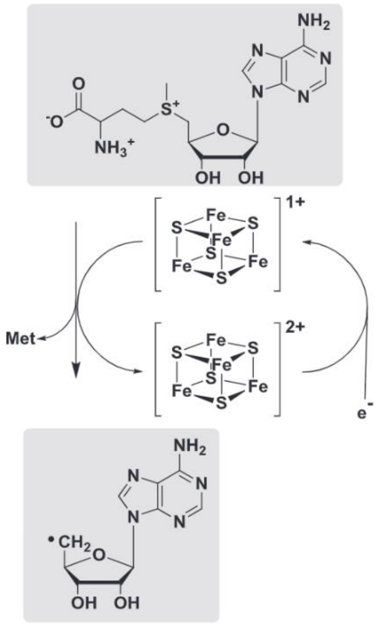

Figure 1-3. Cysteine-coordinated iron-sulfur complex participating in radical reaction with a SAM molecule.[9]

The electron needed for this radical reaction is provided by the essential $[Fe_4S_4]^{1+}$ cluster. Another electron from an outside source is then needed to reduce the newly formed $[Fe_4S_4]^{2+}$ cluster.[9] Without the coordination of metal complexes by cysteines, many proteins would not be able to perform their intended functions.

Protein folding mostly occurs in the endoplasmic reticulum, which is a highly reducing environment. For proteins that require disulfide bonds for proper folding, this ensures that the cysteines are available (not oxidized by other cellular components) to form a disulfide pair. The most common enzymes that control the formation and reduction of disulfide bonds are the members of the protein disulfide isomerase family (PDI).[10] These oxidoreductases are able to form disulfide bonds by transferring them from their own cysteine residues.[11]

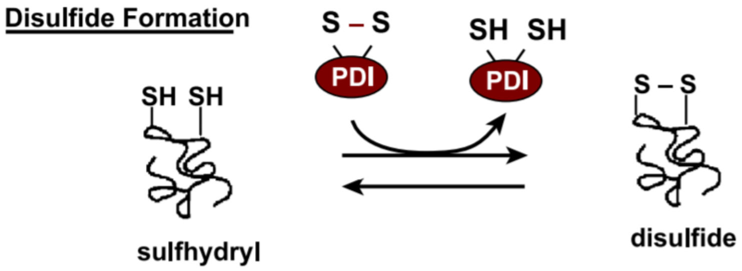

Figure 1-4. Protein disulfide isomerase transfers its disulfide bond to proteins in the endoplasmic reticulum.[11]

Disulfide bonds are essential to proper protein folding, as they often stabilize the folded state of the protein over the unfolded state as well as align the residues in the correct formation.[12] Structural disulfides can be essential for the structure-activity relationship of a protein; if a protein is not folded correctly it may have disrupted functionality. Redox active disulfides, however, directly regulate protein activity in response to cellular conditions. Exposure to reactive oxygen species (ROS) can oxidize protein thiols which can then interact with nearby intra- or inter-molecular thiols to form a disulfide bond. These non-native disulfide bonds can limit protein activity under oxidative stress conditions.[13] Several reports have discussed an intermolecular disulfide bond in GAPDH between the active site cysteine and an adjacent cysteine that forms upon exposure to various oxidizing agents. This disulfide reversibly inactivates the GAPDH by preventing binding of the active site to the substrate. The inactivation of GAPDH, in turn, regulates the glycolysis pathway in response to the presence of oxidative stress.[14] Many proteins rely on successfully formed disulfide bonds in order to fold properly and thus be able to perform their function. Disulfides bonds are also essential for cells to regulate their responses to oxidative stress.

Cysteine post-translational modifications, illustrated in Figure 1-5, are a way to add or remove functionalities from cysteine-containing proteins. As mentioned above, cysteines are susceptible to oxidation by reactive oxygen species due to their nucleophilicity. Oxidation of cysteines by ROS is a way for the cells to respond to oxidative stress. The function of this oxidation is often protective; proteins can deplete the reactive ROS molecules, which prevents oxidative damage of other cellular components. The oxidation reactions can also participate in redox signaling cascades, which can initiate more downstream stress responses.[15] S-palmitoylation is a cysteine modification where the thiol is acylated with palmitic acid (C16:0). This acylation can occur with longer chain or unsaturated fatty acids as well, but palmitic acid is the most common acylation modification. The central function of this modification is to serve as a membrane targeting mechanism; fully formed and folded proteins that are destined for the membrane will receive this modification and the protein will be trafficked to the lipid bilayer. A less well-studied function of S-palmitoylation is its role in cell differentiation. There are several examples of synaptic genes encoding for S-palmitoylated proteins in cells that are destined to become neurons. These proteins are often essential for neuronal development and function, including neurotransmitter receptors and transporters. The variation in S-palmitoylation composition across cell types assists in differentiation during development.[16] Post translational modifications can add new functionalities to proteins in response to outside stressors and they can assist with the canonical protein activity.

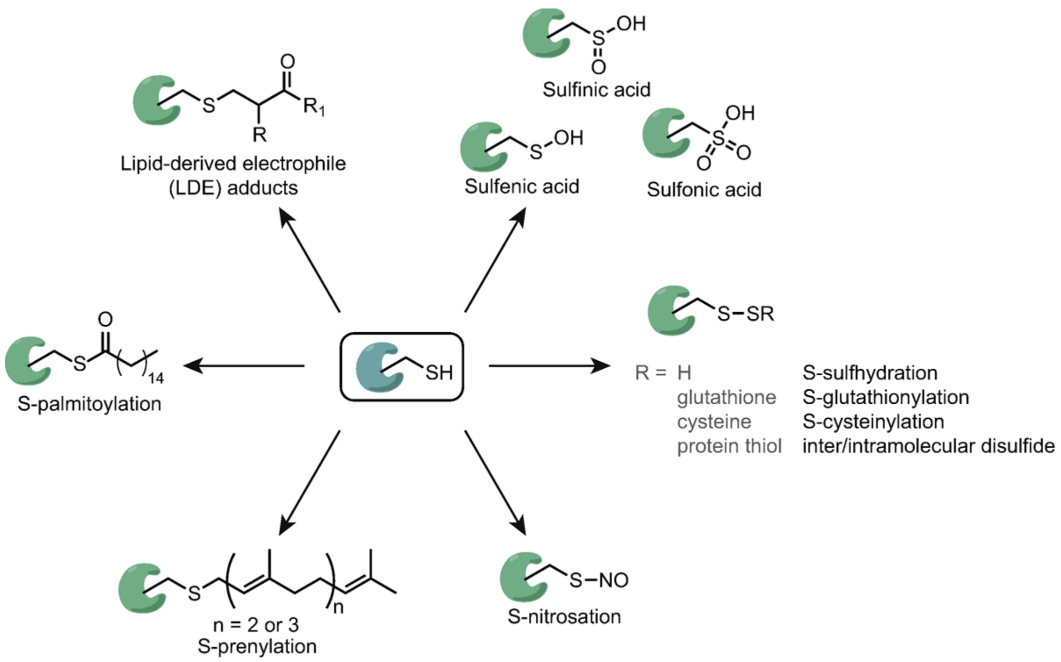

Figure 1-5. Variety of post-translational modifications of cysteines that can further alter the structure or function of a protein.[17]

The significance and flexibility of cysteine residues also make them noteworthy in several diseases. Parkin (PARK2), which is an E3 ubiquitin ligase, can be inactivated by sulfonlyation or S-nitrosylation of cysteine residues. These modifications prevent PARK2 from performing its vital function of degrading misfolded proteins, which leads to accumulation of these proteins, neuronal cell death and, eventually, the development of Parkinson's disease.[18,19] Interestingly, some diseases, particularly cancer, are influenced by mutations where a protein gains a non-canonical cysteine. The frequency of these mutations in cancer cases indicate that the acquired cysteines play a role in tumorigenesis. Fibroblast growth factor receptor 3 (FGFR3) is among the proteins that most commonly express a "gain of cysteine" mutation in cancer.[20] A tumor sequencing study found that S249C was the most frequent missense mutation. This mutation leads to the formation of a new intermolecular disulfide bond in the receptor, which increases homodimerization and downstream signaling to encourage cancer cell proliferation.[21] The frequency with which cysteines influence diseases, whether through noncanonical modification or change in protein activity due to an acquired cysteine, have led them to be considered more as novel targets for therapeutics.

The nucleophilicity of cysteine residues makes them excellent targets for electrophilic small molecule therapeutics, in particular. Proteins with "gain of cysteine" mutations already have several examples of small molecules that target the acquired cysteines. The small molecules can be tailored to specifically target the acquired cysteine so that they don't target other thiols on the protein or the wildtype protein. An example is the oncoprotein KRAS mutation G12C, which causes the protein to favor GTP over GDP. This mutation is seen commonly in Ras-driven lung adenocarcinomas.[20] A covalent inhibitor of this acquired cysteine was able to be developed. The inhibitor irreversibly bound to the G12C mutation and inhibited the activity of the mutant protein while having no effect on the wildtype protein.[22] EGFR inhibitors offer some examples of small molecules that target canonical, but non-catalytic, cysteines. Inhibition of EGFR is therapeutically relevant because it can lead to apoptosis of tumor cells that are overproducing the protein kinase. Some small molecule drugs, such as afatinib, target this protein kinase, whose dysregulation due to mutations is indicative of aggressive tumors and poor prognosis in cancer patients, at sites other than cysteine. These drugs have shown clinical success for non-small cell lung cancer treatment. However, their reversible interactions can lead to decreased efficacy once the drug falls off the target and resistance due to new point mutations. Novel small molecule *N*-(3-(3-phenylureido)quinoxalin-6-yl) acrylamide derivatives were designed to irreversibly bind Cys797 of EGFR and they have had promising inhibitory effects so far on several tumor cell types.[23] Cysteine-targeting therapeutics are attractive, because they can be engineered to target cysteine specifically and covalently bind to the nucleophilic amino acid.

In conclusion, cysteines have a wide variety of important functions related to protein activity and structure, despite being one of the least incorporated amino acids. They are also susceptible to post translational modifications, which can alter or eliminate protein function. There exists substantial evidence that cysteine mutation, incorporation or modification can lead to the progression of several diseases. This has resulted in a larger focus on identifying and studying cysteines that contribute to the disease state as well as a burst of cysteine-targeting therapeutics.

It stands to reason that if a cysteine can be identified as playing a significant role in advancing a disease, then it would also potentially be a suitable target for new small molecule inhibitors, which could have therapeutic effects. To explore this concept, two disease models were probed for disease-relevant cysteines that would be appropriate candidates for inhibitor development.

The first step for this process is to identify therapeutically relevant cysteines to target. The two disease models that were chosen to undergo comparative proteomics were breast cancer, through the human MCF10 progression series, and immunoactivation, through the Raw 246.7 mouse macrophage cells. The MCF10 progression series was derived from benign breast tissue to first create an immortalized, non-tumorigenic breast tissue cell line; the MCF10A cells.[24] From MCF10A cells, the pre-malignant MCF10AT cell line was established. These cells were created through the transfection of the oncogene

HRAS into MCF10A cells. The MCF10A cells produce lesions and exhibit characteristics of the beginning stages of proliferative breast disease in mice.[25] The fully malignant MCF10CA1a cell line, which is capable of metastasis, was produced through continuous passage and transplantation of the MCF10AT cells until they produced full carcinomas. Given that all three cell lines are derived from the same genetic source, a more direct comparison between diseased and healthy cells can occur without having to account for initial genetic variation.[26] Analysis of the genetic or proteomic profile changes across the progression of the cancer can lead to a better understanding of breast cancer development and the genes and proteins that participate.

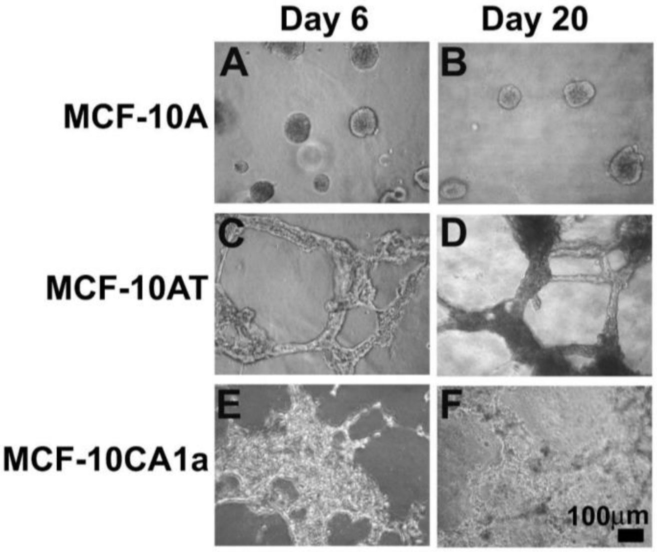

Figure 1-6. Cell culture comparison of the MCF10 progression cell line. MCF10A, the non-tumorigenic breast tissue cells, show the most typical morphology. The fully malignant MCF10CA1a cells show the morphological characteristics associated with tumor cells.[27]

Another cell line that allows for the direct comparison of diseased and healthy cells is the Raw 246.7 mouse macrophage cell line. This cell line originated from the Abelson leukemia virus transformed cell line derived from BALB/c mice. These cells are capable of phagocytosis and pinocytosis. The macrophages can be activated by the addition of lipopolysaccharides (LPS) to simulate an infection. This activation causes the macrophages to accumulate lipids, increase phagocytosis and gain the ability to kill target cells by antibody dependent cytotoxicity. The activated cells also produce large quantities of inducible nitric oxide synthase (iNOS), which can be used as a biomarker for successful activation.[28,29,30] The activated Raw cells can be directly compared to their inactive counterparts from the same source. This again allows for a comparison without concern for initial genetic variability and can lead to insights about changes in the genetic and proteomic profile once the immune system is stimulated.

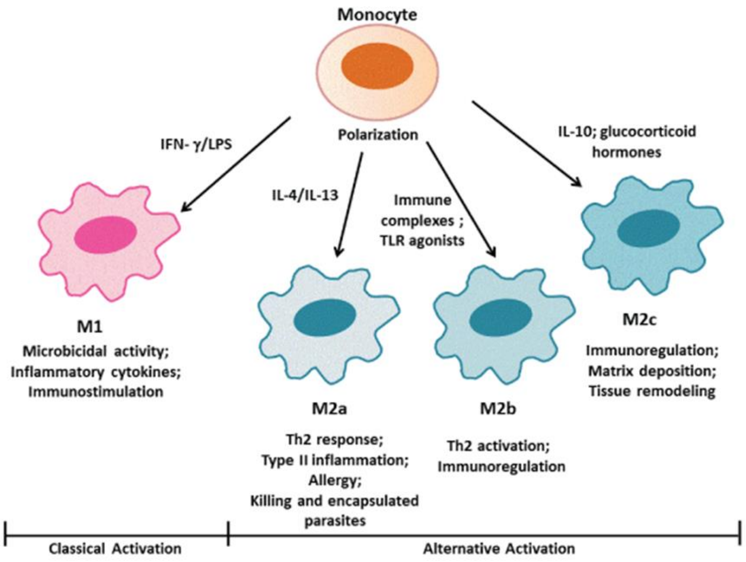

Figure 1-7. Methods for stimulating monocytes to trigger the inflammatory and immune response. Activation by LPS generates M1 macrophages, which have cellular defense activity, produce cytokines and prompt the immune system.[31]

Comparison of cysteine availability between healthy and diseased proteomes can be used to determine which cysteines play roles in diseases. Identification of these changes can lead to a better understanding of the disease proteomes. It can also reveal if cysteine modifications, disulfide bonds or the proteins themselves are necessary for the diseased cells to thrive. Methods for detecting, identifying and comparing labeled cysteine residues in two samples using isotope labeling and mass spectrometry have been developed; isotopic Tandem Orthogonal Proteolysis-Activity-Based Protein Profiling (isoTOP ABPP). Available cysteines are covalently labeled with isotopically tagged iodoacetamide alkyne (diseased sample typically labeled with the light isotope tag). The alkyne handle is then used for "click chemistry" to attach a biotin handle for use in sequestration of labeled proteins. The isolated proteins are cleaved into peptides by trypsin and the samples are analyzed by LC/LC-MS/MS to annotate the labeled cysteines.[32,33,34] This analysis allows for a direct comparison of the cysteine labeling in two different samples.

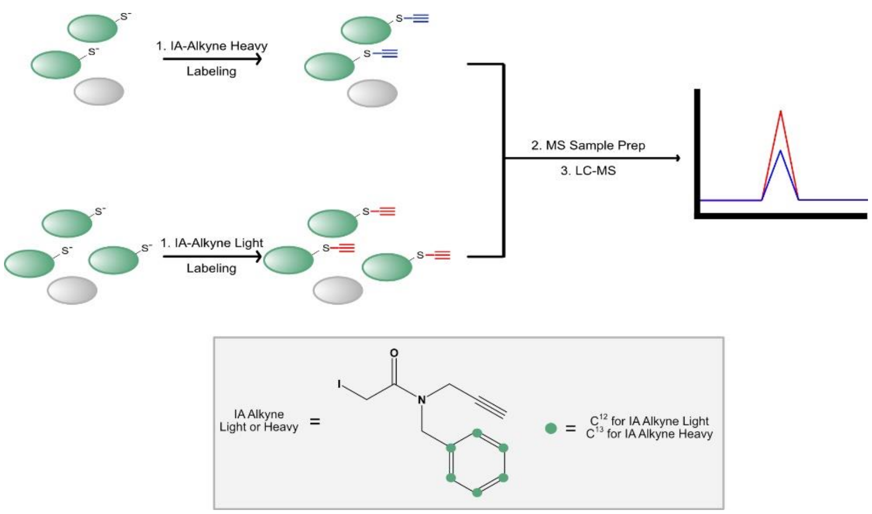

Figure 1-8. Simplified protocol for isotopically labeling two samples with IA-alkyne light and heavy. Differences in labeling due to cysteine availability changes between the two samples are detected by the mass spectrometer.

Some small molecule inhibitor research has been conducted already on these two model systems. Signal transducer and activator of transcription 3 (STAT3) is a transcription factor that is activated in many cancers. An anti-inflammatory natural product, curcumin, derived from turmeric, has been shown to inhibit STAT3 in the MCF10 cell line. It was elucidated that the natural product targets Cys259 on STAT3. This interaction inhibits STAT3 signaling, which results in restriction of tumor cell growth and apoptosis.[35] Artemisolide, an NF-κB inhibitor isolated from the *Artemisia* asiatica plant, inhibits immune activation by LPS in Raw 246.7 cells. The target of this natural product was revealed to be Cys179 of IκB kinase β (IKKβ). This drug molecule has potential therapeutic benefits for NF-κB-dependent inflammatory disorders.[36] Although cysteine-targeting therapeutics exist for these two disease systems, there is no evidence of rational drug design based on reactive cysteine proteomic data to determine the best cysteine targets for new inhibitors. The overall objective of this study is to initiate rational drug design by first identifying novel cysteine residues that play an influential role in breast cancer and the immune response by isoTOP ABPP and determine if they are suitable candidates for small molecule inhibitor development.

1.2 RESULTS AND DISCUSSION

1.2.1 Identification of upregulated and reactive cysteine residues

A protocol was designed for measuring cysteine availability differences between the diseased and healthy proteomes using the isoTOP ABPP protocol, seen in Figure 1-9. An increase of availability of a cysteine in diseased proteome could indicate a loss of a modification, breaking of a disulfide bond or an increase of the cysteine-containing protein expression due to the disease. On the other hand, decreased cysteine availability could suggest a gain of a modification, formation of a disulfide bond or a decrease in expression due to the disease.

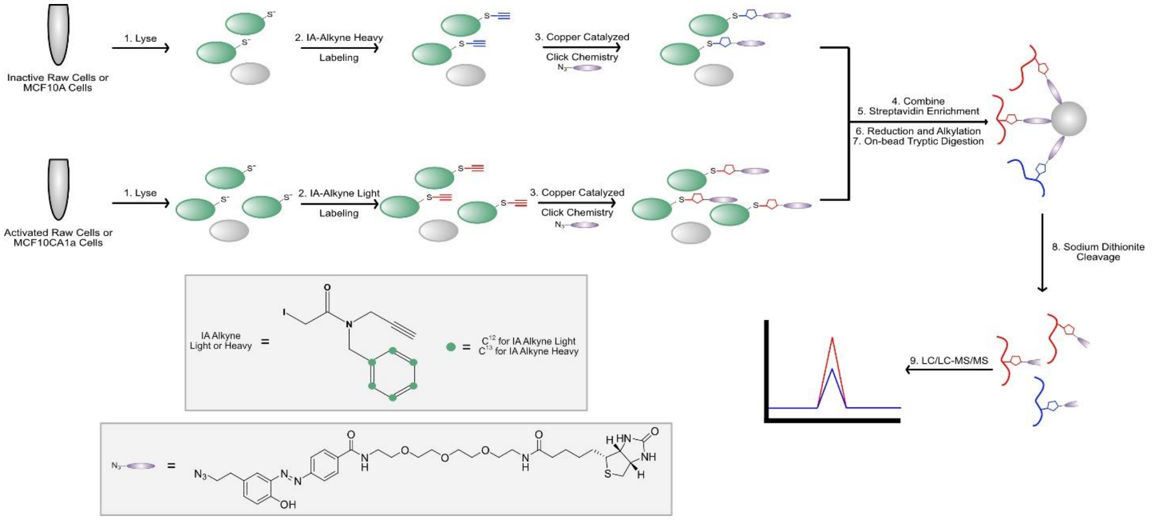

Figure 1-9. The simplified isoTOP ABPP platform. A detailed description of the method can be found in the experimental procedures.

Lysates from fully malignant MCF10CA1a cells were compared to lysates from non-tumorigenic MCF10A cells to observe the effect that tumorigenesis has on the cysteine proteome. This data is seen in Figure 1-10 and Table 1-1. Figure 1-10 shows the general trend of cysteine availability changes within the proteome; points above and below the black dotted lines are considered significant based on our restrictions. The log ratios show the fold change of cysteine labeling of the MCF10CA1a proteome versus the MCF10A proteome. It is clear that tumorigenesis causes changes within the cysteine proteome of MCF10 cells.

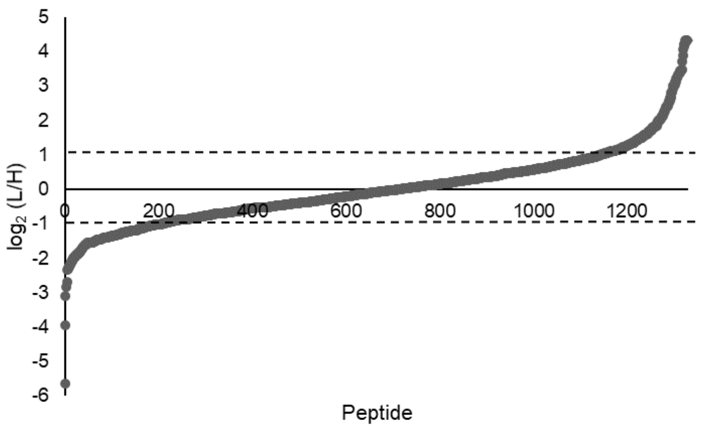

Figure 1-10. Log fold change of cysteine labeling in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy). Changes of labeling can be due to changes in cysteine reactivity or levels of protein expression. Measured using isoTOP ABPP labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant.

Table 1-1 gives more detailed data for the peptides with the top 5 most increased and most decreased changes in cysteine labeling due to tumorigenesis. The decreased peptides have log ratios less than -1 because the cysteines were labeled more in the healthy MCF10A proteome sample (labeled with heavy IA-alkyne), indicating a gain of modification or decrease of protein expression upon tumorigenesis. The increased peptides have log ratios greater than 1 because the cysteines were labeled more in the diseased MCF10CA1a proteome sample (labeled with light IA-alkyne), indicating a loss of modification or increase of protein expression upon tumorigenesis.

Table 1-1. Top hits with increased and decreased cysteine labeling in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**$\log_2$(L/H)**
Decreased	Serum deprivation-response protein	SDPR	-5.64385
	Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	-3.94341
	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	-3.12029
	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	-2.83650
	Protein unc-93 homolog B1	UNC93B1	-2.68965
Increased	Bifunctional 3-phosphoadenosine 5-phosphosulfate	PAPSS1	4.32192
	E3 ubiquitin-protein ligase UBR5	UBR5	4.32192
	GMP synthase	GMPS	4.32192
	Cornifin-A	SPRR1A	4.32192
	Uridine phosphorylase 1	UPP1	4.32192

Lysates from activated Raw cells were compared to lysates from inactive Raw cells to observe the effect that immune activation has on the cysteine proteome. The cells were activated using LPS. This data is seen in Figure 1-11 and Table 1-2. Figure 1-11 shows the general trend of cysteine availability changes within the proteome; points above and below the black dotted lines are considered significant based on our restrictions. The log ratios show the fold change of cysteine labeling of the activated Raw proteome versus the inactive Raw proteome. This data shows that immune activation has an effect on the cysteine proteome of Raw cells. Cysteine residues that are known to participate in disulfide bonds, metal binding and post-translational modifications are also highlighted in Figure 1-11. A few disulfide bonds appear to be broken when the Raw cells become activated, shown by an increase of cysteine availability after activation. Other disulfide bonds emerge due to LPS activation, shown by a decrease of cysteine availability. Overall, there is no clear trend of forming or breaking disulfide bonds after Raw cell activation. Most of the metal binding sites are only changed insignificantly except one, Metallothionein-2, which shows increased availability, indicating a loss of the metal cofactor. Availability of cysteines known to have post translational modifications also generally remains unchanged except one, Cytoskeleton-associated protein 4, which shows decreased availability, indicating a gain of the S-palmitoylation modification when the cells are activated. A more in-depth review of the specific proteins involved in these differences observed could elucidate what benefit these changes serve for the diseased cells.

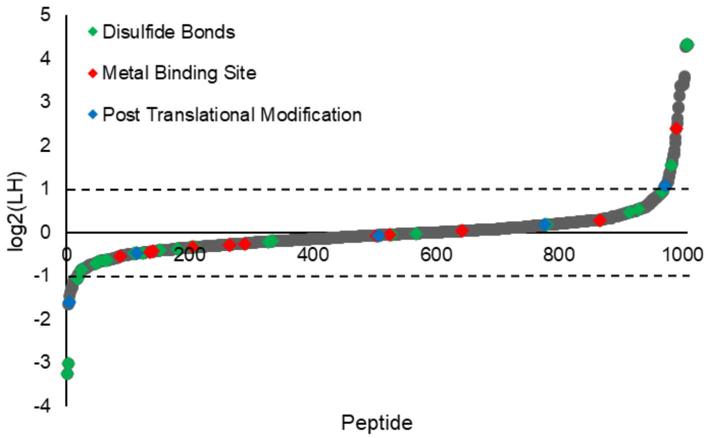

Figure 1-11. Log fold change of cysteine labeling in the activated Raw proteome (labeled with IA-alkyne light) versus the inactive Raw proteome (labeled with IA-alkyne heavy). Changes of labeling can be due to changes in cysteine reactivity or levels of protein expression. Measured using isoTOP ABPP labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant. Cysteines with known functions are highlighted.

Table 1-2 gives more detailed data for the peptides with the top 5 most increased and most decreased changes in cysteine labeling due to immune activation. The decreased peptides have log ratios less than -1 because the cysteines were labeled more in the inactive Raw proteome sample (labeled with heavy IA-alkyne), indicating a gain of modification or decrease of protein expression upon LPS activation. The increased peptides have log ratios greater than 1 because the cysteines were labeled more in the activated Raw proteome sample (labeled with light IA-alkyne), indicating a loss of modification or increase of protein expression upon LPS activation.

Table 1-2. Top hits with increased and decreased cysteine labeling in the activated Raw cell proteome (labeled with IA-alkyne light) versus the inactive Raw proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**log$_2$(L/H)**
Decreased	Gamma-interferon-inducible lysosomal thiol reductase	Ifi30	-3.25153
	Gamma-interferon-inducible lysosomal thiol reductase	Ifi30	-3.01936
	Probable arginine--tRNA ligase, mitochondrial	Rars2	-1.64385
	Cytoskeleton-associated protein 4	Ckap4	-1.59946
	Catechol O-methyltransferase domain-containing protein	Comtd1	-1.47393
Increased	Interleukin-1 alpha	Il1a	4.27575
	Immune-responsive gene 1 protein	Irg1	4.32192
	C-C motif chemokine 5	Ccl5	4.32192
	Prostaglandin G/H synthase 2	Ptgs2	4.32192
	C-X-C motif chemokine 10	Cxcl10	4.32192

Based on the data presented, it is clear that both tumorigenesis and immune activated have effects of the cysteine proteome. However, it is impossible, using this data, to determine if the variations in cysteine availability observed are due to a change of protein expression (leading to different amounts of the cysteine available to label) or to changes in modifications or disulfide bonds (leading to newly exposed or hindered cysteines).

It was decided that reductive dimethylation would be used to measure overall changes in protein expression; the general protocol is illustrated in Figure 1-12.[37]

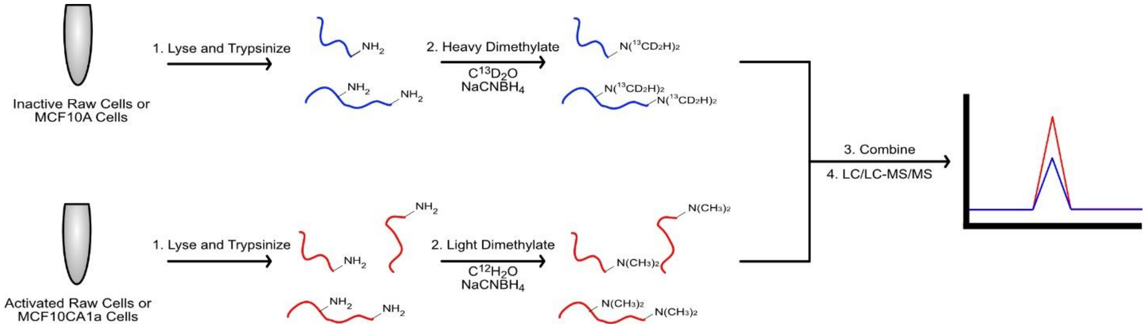

Figure 1-12. The simplified ReDiMe platform. A detailed description of the method can be found in the experimental procedures.

The dimethylation labeling occurs on the amino groups of the N-terminus and any lysine residues of the peptides within the sample. Every peptide will at least have an N-terminus, so this method labels every peptide regardless of differences in cysteine availability. The data collected from this protocol can thus be used to determine the changes in protein expression cause by the diseased state. An increase of dimethylation labeling indicates an increase of protein expression, while a decrease of dimethylation labeling indicates a decrease of protein expression in the diseased proteome. Lysates from the malignant MCF10CA1a cells were compared to lysates from the healthy MCF1A cells using ReDiMe labeling. This data is included in Figure 1-13 and Table 1-3. Figure 1-13 shows the trend of protein expression changes caused by tumorigenesis of the MCF10 cells; the peptides showing the most increased and decreased protein expression are highlighted.

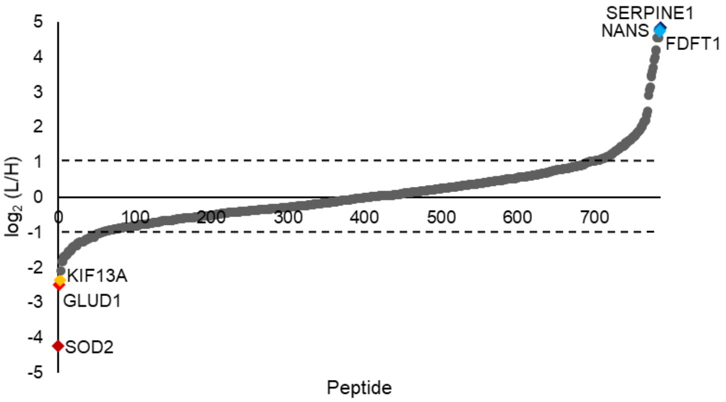

Figure 1-13. Log fold change of protein expression in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy). Measured using ReDiMe labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant. The top 3 peptides with decreased protein expression and the top 3 peptides with increased protein expression in the MCF10CA1a proteome are highlighted.

Table 1-3 gives more detailed data for the peptides that show the largest changes in protein expression caused by tumorigenesis. The decreased peptides have log ratios less than -1 because they were labeled more in the MCF10A proteome sample (labeled with heavy IA-alkyne), indicating decrease of protein expression upon tumorigenesis. The increased peptides have log ratios greater than 1 because the peptides were labeled more in the MCF10CA1a proteome sample (labeled with light IA-alkyne), indicating an increase of protein expression upon tumorigenesis.

Table 1-3. Top hits with increased and decreased protein expression in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**log$_2$(L/H)**
Decreased	Superoxide dismutase	SOD2	-4.25956
	Glutamate dehydrogenase 1, mitochondrial	GLUD1	-2.49296
	Kinesin-like protein KIF13A	KIF13A	-2.35973
	Brain acid soluble protein 1	BASP1	-2.09408
	Polymerase I and transcript release factor	PTRF	-1.83227
Increased	Laminin subunit gamma-2	LAMC2	4.54408
	Perilipin-3	PLIN3	4.55144
	Squalene synthase	FDFT1	4.73627
	Sialic acid synthase	NANS	4.79756
	Plasminogen activator inhibitor 1	SERPINE1	4.83211

Lysates from the activated Raw cells were compared to lysates from the inactive Raw cells using ReDiMe labeling. The cells were activated using LPS. This data is illustrated in Figure 1-14 and Table 1-4. Figure 1-14 shows the trend of protein expression changes caused by activation of the Raw cells; two proteins of interest are highlighted. These proteins were chosen to highlight due to the severity of the increase of their expression caused by LPS activation and their relevant functions. IRG1 (immune responsive gene 1) has been reported to be highly expressed in mammalian macrophages during inflammation, but it is unknown if the cysteine identified in the isoTOP ABPP experiment is essential for protein function. IRG1 produces itaconate from cis-aconitate, which interrupts the citric acid cycle. Itaconate was previously shown to be antimicrobial by inhibiting isocitrate lyase, which is essential for bacterial growth.[38] This suggests that an increase of IRG1 expression is essential for the immune response. SQSTM1 (sequestosome 1), which is a stress-related protein, is mostly linked to the function of autophagy and degradation of ubiquitinated proteins. It has been found that accumulation of SQSTM1 can activate NF-κB signaling, which regulates the inflammatory process.[39] This shows that SQSTM1 is also essential for the success of the immune response, but it is again unknown if the cysteine residue identified plays a critical role in this function.

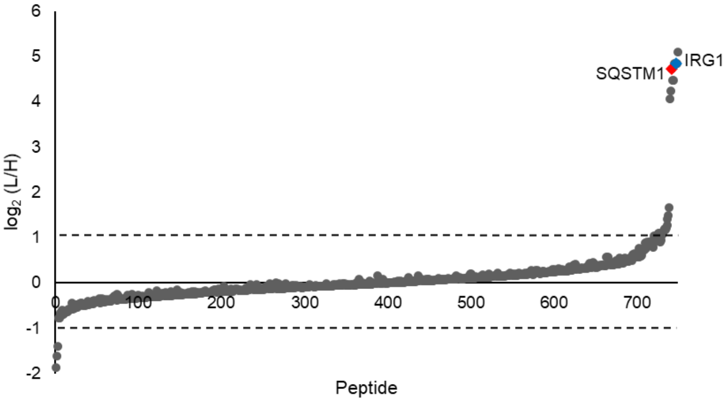

Figure 1-14. Log fold change of protein expression in the activated Raw cell proteome (labeled with IA-alkyne light) versus the inactive Raw cell proteome (labeled with IA-alkyne heavy). Measured using ReDiMe labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant. Two peptides of interest are highlighted, SQSTM1 and IRG1; both show increased expression after activation of the Raw cells by LPS.

Table 1-4 gives more detailed data for the peptides that show the largest changes in protein expression caused by LPS activation. The decreased peptides have log ratios less than -1 because they were labeled more in the inactive Raw proteome sample (labeled with heavy IA-alkyne), indicating decrease of protein expression upon LPS activation. The increased peptides have log ratios greater than 1 because the peptides were labeled more in the activated Raw proteome sample (labeled with light IA-alkyne), indicating an increase of protein expression upon LPS activation.

Table 1-4. Top hits with increased and decreased protein expression in the activated Raw cell proteome (labeled with IA-alkyne light) versus the inactive Raw cell proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**log$_2$(L/H)**
Decreased	MLV-related proviral Env polyprotein	Env1	-1.86020
	Lysozyme C-2	Lyz2	-1.60851
	Keratin, type II cytoskeletal 73	Krt73	-1.40068
	Endoplasmic reticulum resident protein 29	Erp29	-0.77173
	Malectin	Mlec	-0.78129
Increased	Interleukin-1 receptor antagonist protein	Il1rn	4.84449
	Nitric oxide synthase, inducible	Nos2	4.84449
	Immune-responsive gene 1 protein	Irg1	4.84449
	Prostaglandin G/H synthase 2	Ptgs2	4.84449
	Transcription factor jun-B	Junb	5.09451

Apart from being used to measure protein expression changes, the ReDiMe data can also be used to correct the original cysteine labeling data. For all peptides that are found in both datasets, the cysteine labeling ratio can be corrected with the corresponding ReDiMe ratio to account for changes in protein expression. The resulting dataset will show changes in cysteine labeling due only to changes in cysteine reactivity, such as loss or gain of a post translational modification or the cleavage or formation of a disulfide bond. This correction was performed for both the MCF10 cell and the Raw cell datasets; this data is seen in Figure 1-15, Table 1-5, Figure 1-16 and Table 1-6. Figure 1-15 shows the trend of calculated cysteine reactivity changes caused by tumorigenesis of the MCF10 cells; the peptides showing the most increased and decreased protein expression are highlighted.

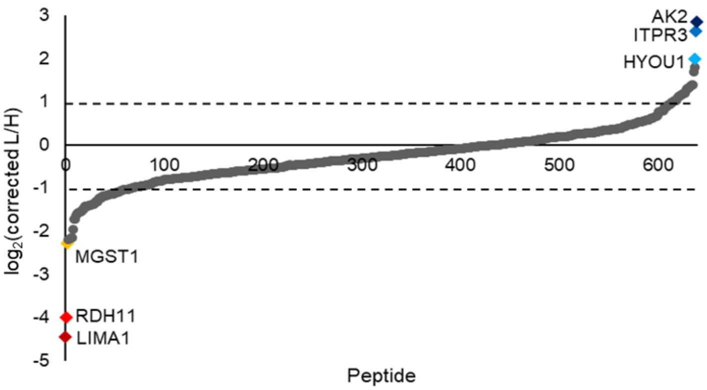

Figure 1-15. Log fold change of cysteine reactivity in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy). Calculated by correcting cysteine labeling data with the protein abundance data from the ReDiMe labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant. The top 3 peptides with decreased cysteine reactivity and the top 3 peptides with increased cysteine reactivity in the MCF10CA1a proteome are highlighted.

Table 1-5 gives more detailed data for the cysteine residues that show the largest changes in calculated cysteine reactivity caused by tumorigenesis. The decreased cysteine residues have log ratios less than -1 because they were labeled more in the MCF10A proteome sample (labeled with heavy IA-alkyne), indicating gain of modification or formation of a disulfide bond upon tumorigenesis. The increased cysteine residues have log ratios greater than 1 because the cysteines were labeled more in the MCF10CA1a proteome sample (labeled with light IA-alkyne), indicating loss of modification or breakage of a disulfide bond upon tumorigenesis.

Table 1-5. Top hits with increased and decreased cysteine reactivity in the MCF10CA1a proteome (labeled with IA-alkyne light) versus the MCF10A proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**$\log_2$(L/H)**
Decreased	LIM domain and actin-binding protein 1	LIMA1	-4.45110
	Retinol dehydrogenase 11	RDH11	-3.99724
	Microsomal glutathione S-transferase 1	MGST1	-2.27983
	Perilipin-3	PLIN3	-2.19530
	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	-2.17450
Increased	Filamin-B	FLNB	1.68440
	Insulin-like growth factor 2 mRNA-binding protein	IGF2BP3	1.79880
	Hypoxia up-regulated protein 1	HYOU1	1.98590
	Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	2.62319
	Adenylate kinase 2, mitochondrial	AK2	2.84004

Figure 1-16 shows the trend of calculated cysteine reactivity changes caused by activation of the Raw cells; IRG1 and SQSTM1 are again highlighted. IRG1 shows little to no significant change in cysteine reactivity following LPS activation. This indicates that the increase of protein expression was truly the only cause of increased cysteine labeling. Interestingly, the cysteine on SQSTM1 shows a decrease of cysteine reactivity despite the increased accumulation of the protein.

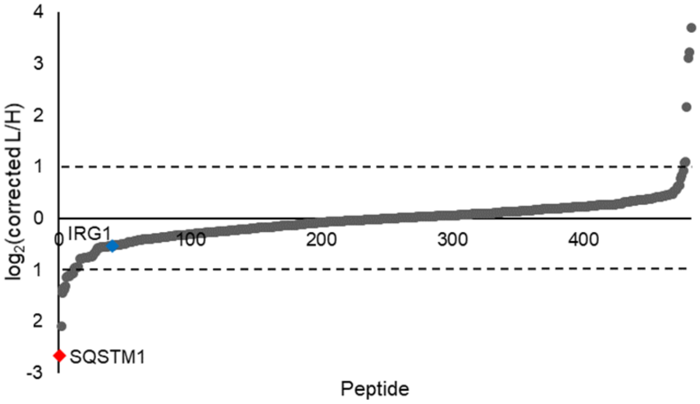

Figure 1-16. Log fold change of cysteine reactivity in the activated Raw cell proteome (labeled with IA-alkyne light) versus the inactive Raw cell proteome (labeled with IA-alkyne heavy). Calculated by correcting cysteine labeling data with the protein abundance data from the ReDiMe labeling. A fold change of greater than 2 [$-1 < \log_2(L/H) > 1$] is considered significant. Both highlighted targets of interest, SQSTM1 and IRG1, have decreased and unchanged cysteine reactivity following activation of the Raw cells by LPS respectively.

Table 1-6 gives more detailed data for the cysteines that show the largest changes in calculated cysteine reactivity changes caused by LPS activation. The decreased cysteine residues have log ratios less than -1 because they were labeled more in the inactive Raw proteome sample (labeled with heavy IA-alkyne), indicating a gain of modification or formation of a disulfide bond following activation. The increased cysteine residues have log ratios greater than 1 because the cysteines were labeled more in the activated Raw proteome sample (labeled with light IA-alkyne), indicating loss of modification or breakage of a disulfide bond upon LPS activation.

Table 1-6. Top hits with increased and decreased cysteine reactivity in the activated Raw cell proteome (labeled with IA-alkyne light) versus the inactive Raw cell proteome (labeled with IA-alkyne heavy).

	Peptide	**Symbol**	**$\log_2$(L/H)**
Decreased	Sequestosome-1	Sqstm1	-2.66903
	Sequestosome-1	Sqstm1	-2.09508
	Eukaryotic translation initiation factor 4 gamma 1	Eif4g1	-1.44581
	Clathrin light chain A	Clta	-1.37377
	Peroxiredoxin-5, mitochondrial	Prdx5	-1.30041
Increased	Peptidyl-prolyl cis-trans isomerase A	Ppia	1.10986
	Poly(rC)-binding protein 2	Pcbp2	2.15179
	Peroxisomal multifunctional enzyme type 2	Hsd17b4	3.10074
	Lon protease homolog, mitochondrial	Lonp1	3.22406
	Cytochrome b-c1 complex subunit 2, mitochondrial	Uqcrc2	3.69442

The included data show that there are significant changes in protein expression and cysteine reactivity upon tumorigenesis and immune activation. Many possible small molecule inhibitor targets have been identified. The next step in the process is to study these targets further to determine if they are suitable for inhibitor development.

1.2.2 IRG1 as a potential small molecule inhibitor target

In order to determine if a cysteine-targeting, small molecule inhibitor will be therapeutic, it first must be discerned if the cysteine identified in the data is essential for the activity of the protein that benefits the disease. To begin this process, immune responsive gene 1 (IRG1) was chosen from the Raw dataset to focus on. This protein was chosen due to its expression changes as well as its importance for immune activation, as described above. This cysteine initially showed an increase of availability following activation of the Raw cells by LPS. Through ReDiMe labeling, it was elucidated that this increase of cysteine availability was due to an increase of IRG1 expression caused by the activation. To first validate the mass spectrometry data, a Western blot was performed to compare the expression of IRG1 in activated and inactive Raw cells (Figure 1-17). A Western blot was also conducted to confirm the expression changes of SQSTM1 as well, but this protein has not been followed up any further so far. The Western blots confirm that both IRG1 and SQSTM1 show increased expression upon activation of the Raw cells by LPS.

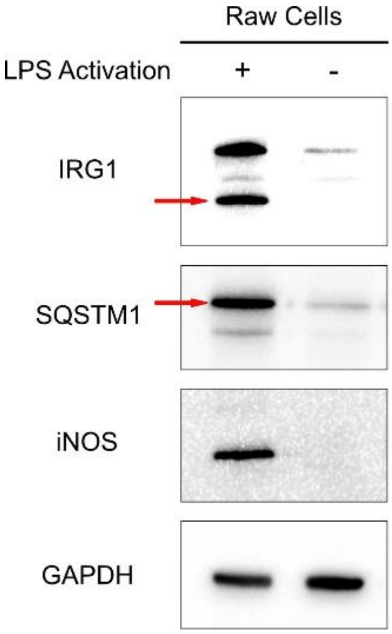

Figure 1-17. Western blot confirming an increase of IRG1 and SQSTM1 expression after activation of Raw cells by LPS for 12 hours. iNOS used as control to confirm successful activation by LPS. GAPDH used as gel loading control.

Next, IRG1 needed to be overexpressed in *E. coli* and purified for future use in an activity assay. A plasmid containing IRG1 (Acod1) was successfully transformed into BL21 cells, which was confirmed via sequencing. The overexpression was able to be induced by IPTG, as shown in Figure 1-18. The conditions for overexpression should be optimized to allow for the maximum yield of recombinant protein possible.

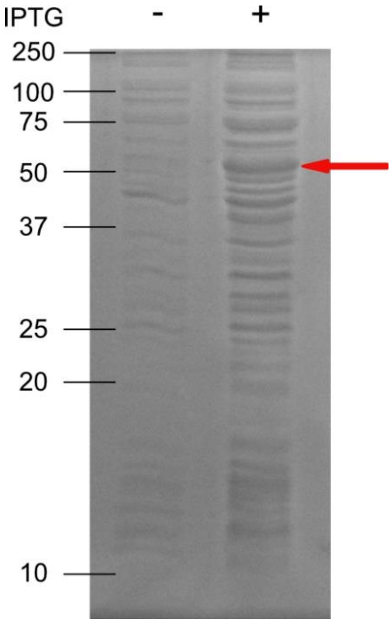

Figure 1-18. Overexpression of recombinant murine Acod1. The overexpression band (indicated by the red arrow) is seen at just above 50 kDa, at the expected weight of 52 kDa.

The recombinant IRG1 was purified using a Ni-NTA column (Figure 1-19). The image shows successful elution of a His-tagged protein that is mostly pure by the second round of elution. The protein appears on the gel at the expected mass for IRG1.

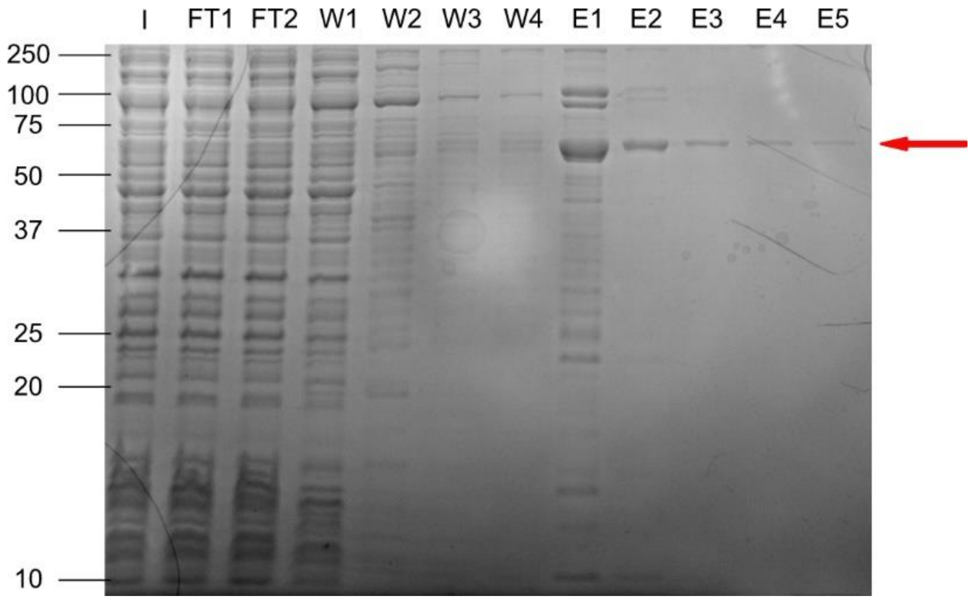

Figure 1-19. Purification of recombinant murine Acod1. The purified protein band (indicated by the red arrow) is seen at just above 50 kDa in the elutions, at the expected weight of 52 kDa. I is the input lane (what was loaded on the column), FT lanes are the flow through collections after adding the lysate to the column, W lanes are the flow through collections during the wash steps and E lanes are the flow through collections during the elution steps.

The identity of the purified protein was confirmed through a Western blot. The blot shows distinct IRG1 bands in the elution lanes. The anti-His tag antibody also confirms that the purified protein is indeed the His-tagged recombinant IRG1 (Figure 1-20).

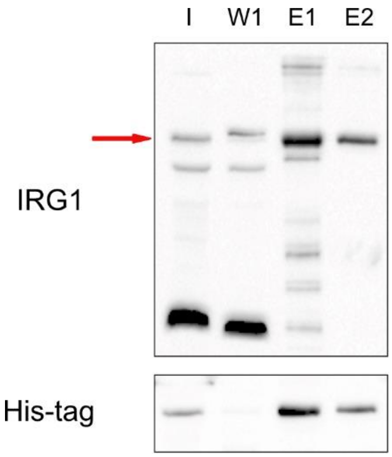

Figure 1-20. Western blot confirming identity of the purified protein. Anti-His antibody used to confirm that the purified protein was His-tagged. Anti-IRG1 antibody used to confirm that the purified protein is the desired Acod1 protein (indicated by the red arrow). I is the input lane (what was loaded on the column), W is the flow through collections during the wash steps and E lanes are the flow through collections during the elution steps.

These images show that IRG1 was able to be successfully recombinantly expressed in *E. coli* and purified for use in a future activity assay. The goal of this activity assay will be to determine if the cysteine identified in the mass spectrometry data is essential for the protein function. To accomplish this, a mutant version of the protein that has a serine residue in place of the cysteine will also need to be expressed and purified. The activity of these two proteins can then be compared using an assay. If the cysteine is necessary for the protein's function, then the mutant IRG1 should not be able to produce itaconate if given the precursor, cis-aconitate. If it is discovered that the cysteine residue is necessary, then IRG1 should be a suitable focus for development of a cysteine-targeting, small molecule inhibitor.

1.3 CONCLUSIONS

The data presented in this thesis shows that the cysteine proteome is affected by tumorigenesis and immune activation. Some cysteine-containing proteins experience changes in overall expression level due to the introduction of the disease state. Other proteins have cysteine residues that change in reactivity following tumorigenesis or macrophage activation, most likely due to changes in modifications or disulfide bonds. The identification of these proteins that are affected by the disease state can lead to discovery of suitable targets for small molecule inhibitors. IRG1, a protein that has increased expression in Raw cells following LPS activation, is one of these possible targets. The protein was successfully recombinantly expressed and purified from *E. coli*, although an optimization of the overexpression should lead to a higher yield of purified protein. Further studies on this protein should include an activity assay of the wildtype protein compared to a C → S mutant in order to determine if the cysteine residue identified in this study is essential for function. An essential cysteine residue in IRG1 could make an appropriate focus of a rational drug design study. More future work on this project should include follow-up studies of other proteins and cysteine residues that were identified as possibly essential for the disease states investigated.

1.4 EXPERIMENTAL PROCEDURES

General procedures and materials

All materials were purchased from Sigma Aldrich or Fisher Scientific unless otherwise noted. Insulin was purchased from Santa Cruz Biotechnologies. Fetal bovine serum was purchased from Atlanta Biologics. The DC Protein Assay kit, SDS, acrylamide, coomassie stain and Poly-Prep® Chromatography Columns were purchased from Bio-Rad. The DTT was purchased from Invitrogen. The diazo biotin-azide was purchased from Click Chemistry Tools. The iodoacetamide was purchased from Acros Organics. The sequencing grade trypsin was purchased from Promega. The C18 and SCX resin were purchased from Phemonenex. The α-GAPDH rabbit antibody, α-iNOS rabbit antibody, α-SQSTM1 rabbit antibody, α-6x His-tag rabbit antibody and α-rabbit HRP-linked secondary antibody were purchased from Cell Signaling. The α-IRG1 rabbit antibody was purchased from Antibodies-Online.

MCF10A and MCF10CA1a cell culture and harvesting

MCF10A and MCF10CA1a cells were grown at 37 °C under 5% CO_2 in DMEM/F12 media supplemented with 5% Horse serum, 1% PSA, 20 ng/mL EGF (resuspended in sterile dH_2O), 0.5 mg/mL Hydrocortisone (resuspended in 200 proof ethanol), 100ng/mL Cholera Toxin (resuspended in sterile dH_2O) and 10 μg/mL Insulin (resuspended in sterile dH_2O containing 1% glacial acetic acid). MCF10A and MCF10CA1a cells grown to 100% confluency. The cells were washed with PBS, harvested by scraping and the pellets were washed again with PBS. The pellets were resuspended in 500 μL PBS and lysed by sonication (10 pulses 3 times at 75% amplitude) to give whole-cell lysates. These lysates were isolated by centrifugation (5 mins, 1000 rcf) to pellet un-lysed cells and cell debris. The supernatant was collected and the pellet was discarded. The protein concentrations were determined using the Bio-Rad DC™ Protein Assay kit. Lysates were diluted to 2 mg/mL and stored at -80 °C until further analysis.

Raw 264.7 cell culture, activation and harvesting

Raw 264.7 cells were grown at 37 °C under 5% CO_2 in DMEM supplemented with 10% FBS and 1% PSA. For LPS activated cells, cells were treated with 100 ng/mL LPS 12 hours prior to harvesting. Raw cells grown to 100% confluency. The cells were washed with PBS, harvested by scraping and the pellets were washed again with PBS. The pellets were resuspended in 500 μL PBS and lysed by sonication (10 pulses 3 times at 75% amplitude) to give whole-cell lysates. These lysates were isolated by centrifugation (5 mins, 1000 rcf) to pellet un-lysed cells and cell debris. The supernatant was collected and the pellet was discarded. The protein concentrations were determined using the Bio-Rad DC™ Protein Assay kit. Lysates were diluted to 2 mg/mL and stored at -80 °C until further analysis.

IsoTOP-ABPP Procedures

IA-alkyne heavy and light labeling

MCF10A/MCF10CA1a or Raw inactive/Raw activated lysates were aliquoted to undergo IA alkyne heavy or light labeling (2 mg/mL, 500 μL). MCF10A and Raw inactive lysates were labeled with IA-alkyne heavy (100 μM from 10 mM DMSO stock). MCF10CA1a and activated Raw lysates were labeled with IA-alkyne light (100 μM from 10 mM DMSO stock). The lysates were labeled at room temperature for 1 hour.

Click chemistry and streptavidin enrichment

Diazo biotin-azide (100 μM from 5 mM DMSO stock), TCEP (1 mM from fresh 50 mM stock in water), TBTA ligand (100 μM from 1.7 mM stock in 1:4 DMSO: *t*-butanol) and copper (II) sulfate (1 mM from 50 mM stock in water) were added to the labeled lysates. The samples were allowed to react at room temperature for 1 hour with periodic vortexing. The samples were centrifuged (4 mins, 6500xg, 4 °C) to pellet the precipitated protein. The pellets were resuspended in cold MeOH (500 μL) by sonication (55% amplitude) and the samples were combined pairwise (MCF10A with MCF10CA1a and Raw inactive with Raw activated). The samples were centrifuged (4 mins, 6500xg, 4 °C) and the supernatants were removed. The methanol wash was repeated. The pellets were then resuspended in 1.2% SDS in PBS (1 mL) by sonication (55% amplitude) and heating (5 mins, 80-90 °C). The solubilized samples were diluted with PBS (5 mL) and incubated with washed streptavidin beads (100 μL) for 16 hours at 4 °C then at room temperature for 2.5 hours. The beads were washed with 0.2% SDS in PBS (5 mL), PBS (3x 5 mL) and water (3x 5 mL). The beads were pelleted in between washes by centrifugation (3 mins, 1400xg).

On-bead trypsin digestion

The washed beads were resuspended in 6 M urea in PBS (500 μL). The streptavidin bound proteins were reduced by incubation with DTT (10 mM from 200 mM stock in water, 20 mins, 65 °C). The samples were then alkylated with iodoacetamide (20 mM from 400 mM stock in water, 30 mins, 37 °C with rotating). The alkylation reaction was quenched with PBS (950 μL) and the beads were pelleted by centrifugation (2 mins, 1400xg). The beads were resuspended in a pre-mixed solution of 2 M urea in PBS (200 μL), 100 mM calcium chloride (2 μL) and trypsin solution (4 μL of 20 μg lyophilized powder resuspended in 40 μL trypsin buffer, overnight, 37 °C with shaking).

Cleavage of peptides from streptavidin beads

The beads were washed with PBS (3x 500 μL) and water (3x 500 μL). The beads were incubated with 50 mM sodium hydrosulfite (50 μL, 1 hour with rotating). The beads were spun down and the cleaved peptides were collected. The cleavage was repeated 2 more times with 75 μL of 50 mM sodium hydrosulfite. The beads were washed with water (2x 75 μL) and the washes were added to the collected cleaved peptides. Formic acid (17.5 μL) was added to the samples and they were stored at -20 °C until analyzed by mass spectrometry.

Liquid chromatography/mass spectrometry

LC/MS analysis was performed on a ThermoFisher LTQ Orbitrap Discovery™ mass spectrometer coupled to an Agilent 1100 series HPLC. Samples were pressure loaded onto a 250 µm fused silica desalting column packed with 4 cm of Aqua C18. The peptides were eluted onto a biphasic column (100 µm fused silica with a 5 µm tip, packed with 10 cm of C18 and 4 cm of SCX) using a gradient of 5-100% Buffer B (80% acetonitrile, 20% water, 0.1% formic acid) in Buffer A (95% water, 5% acetonitrile, 0.1% formic acid). The peptides were eluted from the SCX onto the C18 and into the mass spectrometer using a series of salt steps (Step 1: no salt; Step 2: 25% ammonium acetate; Step 3: 50% ammonium acetate; Step 4: 80% ammonium acetate; Step 5: 100% ammonium acetate).[32] The flow rate through the column was 0.25 µL/min and the spray voltage was set to 2.75 kV. One full MS scan (400-1800 mW) was followed by 8 data dependent scans of the n^{th} most intense scans with dynamic inclusion enabled.

MS Data Analysis

The generated tandem MS data were searched using the SEQUEST algorithm[40] against the human IPI database (for the MCF10a/MCF10CA1a samples) or the mouse IPI database (for the Raw samples). A static modification of +57 on Cys was specified to account for iodoacetamide alkylation and differential modifications of +312.1481 (for IA-alkyne heavy) and +306.1981 (for IA-alkyne light) were added to account for probe labeling of available cysteines. The SEQUEST output files were filtered using DTASelect 2.0.[41] Restrictions were set so peptides in the given dataset were required to be fully tryptic and contain the desired probe modification (based on the differential modification); the peptide false-discovery rate was set below 5%. Calculation of light/heavy ratios was performed using CIMAGE quantification.[32] The full datasets can be found in the Appendix as Table A-1.

ReDiMe Procedures

TCA precipitation, reduction, alkylation and trypsin digestion

MCF10A/MCF10CA1a or Raw inactive/Raw activated lysates were aliquoted to undergo ReDiMe labeling (1 mg/mL, 100 μL). The protein was precipitated with 100% TCA (5 μL, 1 hour or overnight, -80 °C). The samples were thawed and the precipitated protein was pelleted by centrifugation (10 mins, 15K rpm). The protein pellets were washed with ice-cold acetone (500 μL), resuspended by sonication. The protein was again pelleted by centrifugation (10 mins, 5K rpm). The acetone was removed and the pellets were air-dried. The protein pellets were resuspended in 8 M urea in PBS (30 μL) by sonication. 100 mM TEAB in water (70 μL) was added to the samples and the proteins were reduced by incubation with DTT (3 mM from 1 M stock in water, 15 mins, 75 °C). The samples were then alkylated at room temperature with iodoacetamide (2.5 mM from 500 mM stock in water, 30 mins). The reaction was quenched with PBS (120 µL). 100 mM calcium chloride in water was added to the samples (2.5 µL) and the proteins were digested with trypsin (4 µL of 20 µg lyophilized powder resuspended in 40 µL PBS, overnight, 37 °C with shaking).

Reductive dimethylation

20% formaldehyde (4 µL) was added to the MCF10A and Raw inactive samples. 20% heavy formaldehyde (4 µL) was added to the MCF10CA1a and activated Raw samples. 0.6 M sodium cyanoborohydride (20 µL) was added to all samples. The proteins were labeled with a 2 hour incubation in the fume hood. The samples were placed on ice and the reactions were quenched with 20% ammonium hydroxide (4 µL). Formic acid (8 µL) was added to the samples. The samples were combined pairwise (MCF10A with MCF10CA1a and Raw inactive with Raw activated). The samples were desalted using a Sep-Pack column. The columns were washed with 5 mL Buffer B (90% ACN, 10 mM ammonium bicarbonate) and 5 mL Buffer A (5% ACN, 10 mM ammonium bicarbonate). The sample was loaded on the column. The column was washed again with 5 mL Buffer B. The peptides were eluted with Buffer B (2x 750 µL). The solvent was removed by SpeedVac.

Offline HPLC-fractionation

The peptides were resuspended in Buffer A (400 µL) by sonication. The sample was fractionated by high pH reverse-phase high-pressure liquid chromatography using a two-buffer gradient system at a flow rate of 500 µL/min on an Agilent 1100 series HPLC coupled to a Gilson FC 203B fraction collector. The sample was loaded in 0% Buffer B for 2 minutes, then the peptides were separated using a linear gradient from 20% to 35% Buffer B over 60 minutes. 96 fractions were collected in a deep-well 96-well plate. The 96 fractions were combined into 12 samples (one from each column of the 96-well plate) and the solvent was removed by lyophilization. The fractions were each resuspended in Buffer A (8 μL) by sonication. The fractions were combined again to have a final total of 6 samples (1 and 7, 2 and 8, 3 and 9, 4 and 10, 5 and 11, and 6 and 12 were combined). These samples were transferred to LC vials.

Mass spectrometry with autosampler

MS analysis was performed on a ThermoFisher LTQ Orbitrap XL^{TM} coupled to a ThermoFisher Easy-nLC 1000^{TM} autosampler. The 6 offline fractionated samples were place in the autosampler tray. The peptides (6 μL of the sample) were separated over a 100 μm fused silica column packed with 10 cm C18. A gradient of 6% to 25% MS Buffer B (80% ACN/H_2O, 0.1% formic acid) in MS Buffer A (95% H_2O, 5% ACN, 0.1% formic acid) over 165 minutes at a flow rate of 300 nL/min was used to elute the peptides. The gradient ended with a 10 minute wash with 100% MS Buffer B and a re-equilibration of the column with 100% MS Buffer A (9 μL) before the start of the gradient for the subsequent sample. This was repeated for each of the 6 samples.

MS Data Analysis

The generated tandem MS data were searched using the SEQUEST algorithm[40] against the human IPI database (for the MCF10a/MCF10CA1a samples) or the mouse IPI database (for the Raw samples). A static modification of +34.06315 (for heavy dimethylation) and +28.01313 (for light dimethylation) on Lys and the N-terminus was added to account for dimethylation of these residues. The SEQUEST output files were filtered using DTASelect 2.0.[41] Restrictions were set so peptides in the given dataset were required to be fully tryptic and contain the desired probe modification (based on the differential modification); the peptide false-discovery rate was set below 5%. Calculation of light/heavy ratios was performed using CIMAGE quantification.[32] The full datasets can be found in the Appendix as Table A-2.

Western blot analysis

Lysates were mixed 1:1 with 2x loading buffer. The lysate/loading buffer mixtures (15 μL) were separated by SDS-PAGE (70 minutes, 175 V) on a 12.5% polyacrylamide gel. The gels were then transferred by electroblotting into nitrocellulose membranes (100 minutes, 75 V). The blots were washed with TBS-T (3x 10 mL). The membranes were blocked with 5% non-fat dry milk in TBS-T at room temperature (1-2 hours). The blots were washed with TBS-T (3x 10 mL) then treated with the primary antibodies (anti-GAPDH, anti-IRG1, anti-SQSTM1, anti-iNOS or anti-6x His-tag, 1:1,000 in TBS-T, overnight, 4 °C). The blots were washed with TBS-T (3x 10 mL) then treated with the α-rabbit HRP-linked secondary antibody (1:10,000 in TBS-T, 2 hours) at room temperature. The blots were washed with TBS (3x 10 mL), treated with HRP super signal chemiluminescence reagents (5 mins) and imaged using a Bio-Rad ChemiDoc^{TM} MP Imaging System.

Transformation of plasmid containing murine Irg1 (Acod1) gene

A pET-24b (+) vector containing the murine Acod1 gene, a kanamycin resistant gene, a T7 promoter and a C-terminus His-tag were ordered from GenScript. The vector (5 µL) was incubated with BL21 competent cells (50 µL) on ice (30 mins). The cells were heat shocked (45 sec, 42 °C) then incubated on ice again (2 mins). The transformed cells were incubated (1 hour, 37 °C with shaking) with antibiotic-free liquid LB media (950 µL). The cells (600 µL) were then plated on pre-warmed LB-agar plates containing kanamycin (50 µg/mL) and the plates were incubated overnight (37 °C) to allow the transformed cells to form colonies. Portions of the colonies were added to liquid LB media (5 mL) containing kanamycin (50 µg/mL). The liquid cultures were allowed to grow up overnight (37 °C with shaking). A portion of the liquid culture (820 µL) was aliquoted to make glycerol stocks (180 µL of 80% glycerol) of the transformed cells. The remainder of the liquid cultures underwent an Epoch mini-prep protocol to extract the DNA. The DNA was sent for sequencing by GeneWiz to confirm that the genome contained the Acod1 gene.

Overexpression and purification of Acod1

A scraping of the frozen glycerol stock of the competent cells transformed with the plasmid containing the Acod1 gene was added to liquid LB media (5 mL) containing kanamycin (50 µg/mL). The starter culture was allowed to grow overnight (37 °C with shaking). A portion of the starter culture (2.5 mL) was added to a larger flask containing liquid LB media (500 mL) with kanamycin (50 µg/mL). The cells were allowed to incubate (37 °C with shaking) until the cellular density reached an OD_{600} of 0.6-0.8. IPTG (500 µL, 142 mg/mL) was added to the large culture to induce the lac operon and initiate the overexpression of the target protein. The overexpression took place overnight (25 °C with shaking). Aliquots (1 mL) each of pre-induction and post-induction of overexpression were lysed (10 pulses 3x, 75% amplitude) and separated by SDS-PAGE (70 mins, 150 V) on a 12.5% acrylamide gel to visualize the overexpression of the Acod1 protein by coomassie staining. The large culture was centrifuged (10 mins, 5,000 rpm) and the supernatant was discarded. The cell pellet was resuspended in PBS (4 mL) and lysed by sonication (40 pulses 4x, 90% amplitude). The cell debris was pelleted by centrifugation (10 mins, 15,000 rpm) and the supernatant was saved for purification. The target protein was purified by the HisPur^{TM} Ni-NTA resin protocol with native conditions and using Poly-Prep® Chromatography Columns as the gravity flow columns. The input was flowed through the resin twice to optimize binding of the His-tagged protein target. Four washes and five elutions were done to purify the Acod1 protein. Aliquots were taken at each step and were separated by SDS-PAGE (70 mins, 150 V) on a 12.5% acrylamide gel to visualize the purification of the Acod1 protein by coomassie staining.

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APPENDIX

Table A-1. Mass spectrometry results from isotopic labeling of MCF10A and MCF10CA1a lysates. Three replicates were run. If a peptide was found in at least two samples, the average ratio is presented in the table as light/heavy. The average ratios for cysteine labeling and ReDiMe labeling are included.

ipi	description	symbol	sequence	cysteine	abundance
O95810	SDPR Serum deprivation-response protein	SDPR	R.MDRQC*AQVK.R	0.02	-
Q96CM8	ACSF2 Acyl-CoA synthetase family member 2, mitochondrial	ACSF2	R.MVSTPIGGLSYVQGC*TK.K	0.065	-
P49419	ALDH7A1 Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	R.RSTC*TINYSK.D	0.115	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.MC*LFAGFQR.K	0.14	0.632000822
Q9H1C4	UNC93B1 Protein unc-93 homolog B1	UNC93B1	R.RPC*PYEQAQGGDGPEEQ.-	0.155	-
P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.ALNALC*DGLIDELNQALK.T	0.2	0.338874153
P02533	KRT14 Keratin, type I cytoskeletal 14	KRT14	R.ISSVLAGGSC*R.A	0.203333333	0.542756477
P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.IC*PVETLVEEAIQCAEK.I	0.205	0.338874153
Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.ILSC*GEVIHVK.I	0.21	0.548250855
Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.AVTNHSVYC*STK.G	0.213333333	-
P30084	ECHS1 Enoyl-CoA hydratase, mitochondrial	ECHS1	K.AFAAGADIKEMQNLSFQDC*YSSK.F	0.22	0.338874153
P29590	PML Protein PML	PML	R.LQDLSSC*ITQGK.D	0.223333333	-
P31930	UQCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	R.NALVSHLDGTTPVC*EDIGR.S	0.23	0.475645938
Q7Z4W1	DCXR L-xylulose reductase	DCXR	R.GVPGAIVNVSSQC*SQR.A	0.233333333	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.GNFTLPEVAEC*FDEITYVELQK.E	0.236666667	0.632000822
P31930	UQCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	R.LC*TSATESEVAR.G	0.24	0.475645938
P31930	UQCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	K.YIYDQC*PAVAGYGPIEQLPDYNR.I	0.243333333	0.475645938
Q7Z434	MAVS Mitochondrial antiviral-signaling protein	MAVS	K.QGAESDQAEPIIC*SSGAEAPANSLPSK.V	0.245	-
Q14151	SAFB2 Scaffold attachment factor B2	SAFB2	K.FDFDAC*NEVPPAPK.E	0.25	0.533411033
P13647	KRT5 Keratin, type II cytoskeletal 5	KRT5	K.KQC*ANLQNAIADAEQR.G	0.253333333	0.321940894

O95182	NDUFA7 NADH dehydrogenase	NDUFA7	K.LSNNYYC*TR.D	0.26	-
P13647	KRT5 Keratin, type II cytoskeletal 5	KRT5	R.VSLAGAC*GVGGYGSR.S	0.26	0.321940894
P78347	GTF2I General transcription factor II-I	GTF2I	R.SILSPGGSC*GPIK.V	0.265	-
Q16666	IFI16 Gamma-interferon-inducible protein 16	IFI16	K.INQLC*SQTK.G	0.266666667	-
Q07065	CKAP4 Cytoskeleton-associated protein 4	CKAP4	K.SSSSSSASAAAAAAAASSSASC*SR.R	0.27	0.790717073
P31040	SDHA Succinate dehydrogenase	SDHA	K.TLNEADC*ATVPPAIR.S	0.27	0.611915798
Q04695	KRT17 Keratin, type I cytoskeletal 17	KRT17	R.LGSAGGLGSTLGGSSYSSC*YSFGSGGGYGSSFGGVDGLLAGGEK.A	0.273333333	0.561971617
P49419	ALDH7A1 Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	K.GSDC*GIVNVNIPTSGAEIGGAFGGEK.H	0.273333333	-
Q5T440	IBA57 Putative transferase CAF17, mitochondrial	IBA57	R.VWAVLPSSPEAC*GAASLQER.A	0.275	-
P31930	UQCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	K.AVELLGDIVQNC*SLEDSQIEK.E	0.276666667	0.475645938
Q9Y2Q5	LAMTOR2 Ragulator complex protein LAMTOR2	LAMTOR2	R.VANLLLC*MYAK.E	0.28	-
O14880	MGST3 Microsomal glutathione S-transferase 3	MGST3	K.VEYPIMYSTDPENGHIFNC*IQR.A	0.283333333	-
P07858	CTSB Cathepsin B	CTSB	K.IC*EPGYSPTYK.Q	0.283333333	0.810742706
Q9HA77	CARS2 Probable cysteine--tRNA ligase, mitochondrial	CARS2	R.QPLLEAC*DTLR.R	0.29	-
Q7RTV0	PHF5A PHD finger-like domain-containing protein 5A	PHF5A	R.IC*DEC*NYGSYQGR.C	0.295	-
P55265	ADAR Double-stranded RNA-specific adenosine deaminase	ADAR	K.LGNSC*EFR.L	0.296666667	0.799095285
P40939	HADHA Trifunctional enzyme subunit alpha, mitochondrial	HADHA	K.TGIEQGSDAGYLC*ESQK.F	0.3	0.515490895
Q14103	HNRNPD Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	K.FGEVVDC*TLKLDPITGR.S	0.31	0.687448312
Q9BYG3	MKI67IP MKI67 FHA domain-interacting nucleolar phosphoprot	MKI67IP	K.TVDSQGPTPVC*TPTFLER.R	0.315	-
Q96FJ2	DYNLL2 Dynein light chain 2, cytoplasmic	DYNLL2	K.NADMSEDMQQDAVDC*ATQAMEK.Y	0.315	-
Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.DKSTNC*FGDNDPIDVCEIGSK.I	0.32	0.548250855
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.TCNC*ETEDYGEK.F	0.325	0.632000822
Q04695	KRT17 Keratin, type I cytoskeletal 17	KRT17	R.LSGGLGAGSC*R.L	0.326666667	0.561971617
O95299	NDUFA10 NADH dehydrogenase	NDUFA10	R.SRVITVDGNIC*TGK.G	0.326666667	0.552758353
Q9NSE4	IARS2 Isoleucine--tRNA ligase, mitochondrial	IARS2	K.KPGLEEAVESAC*AMR.D	0.326666667	0.491745037
Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochon	ISCU	K.LHC*SMLAEDAIK.A	0.33	-
P09622	DLD Dihydrolipoyl dehydrogenase, mitochondrial	DLD	K.NETLGGTC*LNVGCIPSK.A	0.336666667	0.564583947
Q49A26	GLYR1 Putative oxidoreductase GLYR1	GLYR1	R.TAEKC*DLFIQEGAR.L	0.34	-

P26440	IVD Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	R.GSNTC*ELIFEDCKIPAANILGHENK.G	0.34	0.45464191
P15924	DSP Desmoplakin	DSP	R.ELDEC*FAQANDQMEILDSLIR.E	0.34	0.281381454
P21953	BCKDHB 2-oxoisovalerate dehydrogenase subunit beta, mitoc	BCKDHB	R.SGDLFNC*GSLTIR.S	0.34	-
Q6P1X6	C8orf82 UPF0598 protein C8orf82	C8orf82	R.YEAAFPFLSPC*GR.E	0.34	-
P23434	GCSH Glycine cleavage system H protein, mitochondrial	GCSH	K.SC*YEDGWLIK.M	0.34	-
P22695	UQCRC2 Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	R.ENMAYTVEC*LR.G	0.343333333	0.416975234
Q16666	IFI16 Gamma-interferon-inducible protein 16	IFI16	K.IIAIANYVC*R.N	0.345	-
P22830	FECH Ferrochelatase, mitochondrial	FECH	R.AIAFTQYPQYSC*STTGSSLNAIYR.Y	0.345	-
Q12955	ANK3 Ankyrin-3	ANK3	K.IRDTSQEPC*GR.L	0.345	-
P07858	CTSB Cathepsin B	CTSB	R.GQDHC*GIESEVVAGIPR.T	0.345	0.810742706
Q16698	DECR1 2,4-dienoyl-CoA reductase, mitochondrial	DECR1	K.GMTTLLSSLGAQC*VIASR.K	0.345	0.55322366
P21912	SDHB Succinate dehydrogenase	SDHB	K.C*GPMVLDALIK.I	0.345	0.514097652
Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	R.GQPC*SQNYR.L	0.346666667	0.548250855
Q8IVF2	AHNAK2 Protein AHNAK2	AHNAK2	K.EKEDTDVADGC*R.E	0.35	0.912419509
P22570	FDXR NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	R.ALEIPGEELPGVC*SAR.A	0.35	0.819347319
P15924	DSP Desmoplakin	DSP	R.GVITDQNSDGYC*QTGTMSR.H	0.35	0.281381454
B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVDGADTTPEELAALFAPYGTVMSC*AVMK.Q	0.355	-
P04899	GNAI2 Guanine nucleotide-binding protein G(i) subunit al	GNAI2	K.IIHEDGYSEEEC*R.Q	0.355	0.68573891
O95299	NDUFA10 NADH dehydrogenase	NDUFA10	K.C*EVLQYSAR.E	0.355	0.552758353
Q13825	AUH Methylglutaconyl-CoA hydratase, mitochondrial	AUH	R.SEVPGIFC*AGADLK.E	0.36	-
Q9UKU7	ACAD8 Isobutyryl-CoA dehydrogenase, mitochondrial	ACAD8	R.KDAVALC*SMAK.L	0.36	-
Q14151	SAFB2 Scaffold attachment factor B2	SAFB2	K.ILDILGETC*K.S	0.36	0.533411033
Q9H9J2	MRPL44 39S ribosomal protein L44, mitochondrial	MRPL44	K.TAFVNSC*YIK.S	0.363333333	-
O75390	CS Citrate synthase, mitochondrial	CS	R.GFSIPEC*QK.L	0.363333333	0.649222553
P42167	TMPO Lamina-associated polypeptide 2, isoforms beta/gam	TMPO	K.EMFPYEASTPTGISASC*R.R	0.363333333	0.559613822
Q9HCC0	MCCC2 Methylcrotonoyl-CoA carboxylase beta chain, mitoch	MCCC2	K.MVAAVAC*AQVPK.I	0.365	-
Q02338	BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondria	BDH1	K.METYC*SSGSTDTSPVIDAVTHALTATTPYTR.Y	0.365	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	R.APQC*LGK.F	0.366666667	0.632000822

P15924	DSP Desmoplakin	DSP	R.DANSENC*NK.N	0.366666667	0.281381454
Q99590	SCAF11 Protein SCAF11	SCAF11	K.VYQPVSC*PLSDLSENVESVVNEEK.I	0.37	-
O95478	NSA2 Ribosome biogenesis protein NSA2 homolog	NSA2	K.ATFC*LPILGVK.K	0.37	-
P22626	HNRNPA2B1 Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	K.LTDC*VVMR.D	0.373333333	0.550731006
P61586	RHOA Transforming protein RhoA	RHOA	R.IGAFGYMEC*SAK.T	0.373333333	1.448484848
Q8IXK0	PHC2 Polyhomeotic-like protein 2	PHC2	R.C*SDNSSYEEPLSPISASSSTSR.R	0.375	-
O75380	NDUFS6 NADH dehydrogenase	NDUFS6	R.VIAC*DGGGGALGHPK.V	0.375	-
P03928	MT-ATP8 ATP synthase protein 8	MT-ATP8	K.IC*SLHSLPPQS.-	0.375	-
P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.GAVVGIDLGTTNSC*VAVMEGK.Q	0.375	0.857285499
H7C455	Uncharacterized protein	Uncharacterized	K.NLSTFAVDGKDC*K.V	0.375	0.456413829
I3L0E3	MRPS17 28S ribosomal protein S17, mitochondrial	MRPS17	K.VIDPVTGKPC*AGTTYLESPLSSETTQLSK.N	0.376666667	-
P84090	ERH Enhancer of rudimentary homolog	ERH	R.TYADYESVNEC*MEGVCK.M	0.38	0.664801865
P61224	RAP1B Ras-related protein Rap-1b	RAP1B	R.VKDTDDVPMILVGNKC*DLEDER.V	0.38	0.821408604
Q9H2U2	PPA2 Inorganic pyrophosphatase 2, mitochondrial	PPA2	K.C*NGGAINCTNVQISDSPFR.C	0.38	0.548250855
Q86VU5	COMTD1 Catechol O-methyltransferase domain-containing pro	COMTD1	R.LLTLEQPQGDSMMTC*EQAQLLANLAR.L	0.38	-
Q86VU5	COMTD1 Catechol O-methyltransferase domain-containing pro	COMTD1	K.VLQPPKGDVAAEC*VR.N	0.38	-
Q9P0J1	PDP1	PDP1	R.SAATC*LQTR.G	0.385	-
Q9NRP4	ACN9 Protein ACN9 homolog, mitochondrial	ACN9	K.AC*FGTFLPEEK.L	0.385	-
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	R.AAEC*NIVVTQPR.R	0.385	0.631166662
P60953	CDC42 Cell division control protein 42 homolog	CDC42	K.YVEC*SALTQK.G	0.39	-
Q8WUY1	THEM6 UPF0670 protein THEM6	THEM6	R.AHTVLAASC*AR.H	0.39	-
P28838	LAP3 Cytosol aminopeptidase	LAP3	R.SAGAC*TAAAFLK.E	0.39	1.280825496
P51553	IDH3G Isocitrate dehydrogenase	IDH3G	R.HAC*VPVDFEEVHVSSNADEEDIR.N	0.39	0.611421911
P56381	ATP5E ATP synthase subunit epsilon, mitochondrial	ATP5E	R.YSQIC*AK.A	0.39	-
P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.VDGMDILC*VR.E	0.393333333	0.751340103
P43304	GPD2 Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2	K.LYDLVAGSNC*LK.S	0.393333333	-
O75390	CS Citrate synthase, mitochondrial	CS	K.LPC*VAAK.I	0.393333333	0.649222553
Q9NP73	ALG13 UDP-N-acetylglucosamine transferase subunit ALG13	ALG13	K.ADLVISHAGAGSC*LETLEK.G	0.395	-
O75431	MTX2 Metaxin-2	MTX2	K.TLDQVLEDVDQC*CQALSQR.L	0.395	-

Q9H1K1	ISCU Iron-sulfur cluster assembly enzyme ISCU, mitochon	ISCU	K.NVGTGLVGAPAC*GDVMK.L	0.395	-
Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	R.ISELSGC*TPDPR.I	0.396666667	-
B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	K.IFVGNVSAAC*TSQELR.S	0.396666667	-
P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	K.AC*GDSTLTQITAGLDPVGR.I	0.396666667	0.582816672
Q06136	KDSR 3-ketodihydrosphingosine reductase	KDSR	R.LISETTSVC*KPEQVAK.Q	0.4	-
Q5U5X0	LYRM7 LYR motif-containing protein 7	LYRM7	R.KDLLVENVPYC*DAPTQK.Q	0.403333333	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.AVVVC*PK.D	0.403333333	0.632000822
P43304	GPD2 Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2	R.NYLSC*DVEVR.R	0.405	-
P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSC*GPAQC*QETIR.T	0.405	1.035508042
Q3ZCQ8	TIMM50 Mitochondrial import inner membrane translocase su	TIMM50	R.VVVVDC*KK.E	0.405	0.761959114
Q16718	NDUFA5 NADH dehydrogenase	NDUFA5	K.TTGLVGLAVC*NTPHER.L	0.405	0.605977547
P12236	SLC25A6 ADP/ATP translocase 3	SLC25A6	K.GIVDC*IVR.I	0.405	0.589060365
Q86SX6	GLRX5 Glutaredoxin-related protein 5, mitochondrial	GLRX5	K.GTPEQPQC*GFSNAVVQILR.L	0.41	-
H3BQZ7	Uncharacterized protein	Uncharacterized	K.SRDLLVQQASQC*LSK.L	0.41	0.688392323
P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	K.IIC*QGFTGK.Q	0.41	0.451691986
P15924	DSP Desmoplakin	DSP	R.QMGQPC*DAYQK.R	0.41	0.281381454
P23919	DTYMK Thymidylate kinase	DTYMK	K.LVEALC*AAGHR.A	0.415	-
Q02338	BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondria	BDH1	K.FGVEAFSDC*LR.Y	0.415	-
Q96D53	ADCK4 Uncharacterized aarF domain-containing protein kin	ADCK4	R.IVQTLC*TVR.G	0.415	-
P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	R.TFVSGAC*DASIK.L	0.416666667	0.582816672
P82912	MRPS11 28S ribosomal protein S11, mitochondrial	MRPS11	K.ASHNNTQIQVVSASNEPLAFASC*GTEGFR.N	0.42	-
P00966	ASS1 Argininosuccinate synthase	ASS1	R.FELSC*YSLAPQIK.V	0.42	-
Q9Y4W6	AFG3L2 AFG3-like protein 2	AFG3L2	K.LASLTPGFSGADVANVC*NEAALIAAR.H	0.42	0.767424912
P12235	SLC25A4 ADP/ATP translocase 1	SLC25A4	R.EFHGLGDC*IIK.I	0.42	0.662535166
P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	R.LGYILTC*PSNLGTGLR.A	0.42	0.383051559
P50213	IDH3A Isocitrate dehydrogenase	IDH3A	R.IEAAC*FATIK.D	0.423333333	0.561584903
Reverse_Q9P2Y5	UVRAG UV radiation resistance-associated gene protein	UVRAG	K.LGDLC*VK.W	0.425	-

P19367	HK1 Hexokinase-1	HK1	K.TVC*GVVSR.R	0.425	0.585075333
Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	K.IDATQVEVNPFGETPEGQVVC*FDAK.I	0.426666667	0.576446159
P08559	PDHA1 Pyruvate dehydrogenase E1 component subunit alpha,	PDHA1	R.FAAAYC*R.S	0.426666667	0.751340103
Q9NUP9	LIN7C Protein lin-7 homolog C	LIN7C	R.VLQSEFC*NAVR.E	0.43	-
O75746	SLC25A12 Calcium-binding mitochondrial carrier protein Aral	SLC25A12	K.NSFDC*FK.K	0.43	-
P14649	MYL6B Myosin light chain 6B	MYL6B	K.ILYSQC*GDVMR.A	0.43	-
P19367	HK1 Hexokinase-1	HK1	R.AILQQLGLNSTC*DDSILVK.T	0.43	0.585075333
P07858	CTSB Cathepsin B	CTSB	R.EQWPQC*PTIK.E	0.433333333	0.810742706
Q16891	IMMT Mitochondrial inner membrane protein	IMMT	K.ANC*SDNEFTQALTAAIPPESLTR.G	0.433333333	0.749093946
P62879	GNB2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB2	R.ELPGHTGYLSC*CR.F	0.433333333	0.582816672
P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	R.QAVLGAGLPISTPC*TTINK.V	0.433333333	0.491243112
Q16134	ETFDH Electron transfer flavoprotein-ubiquinone oxidored	ETFDH	R.FC*PAGVYEFVPVEQGDGFR.L	0.435	-
Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	R.GLMAIDC*PHTGIVDYR.Q	0.435	-
P52948	NUP98 Nuclear pore complex protein Nup98-Nup96	NUP98	K.ADTSQEIC*SPR.L	0.436666667	-
P08754	GNAI3 Guanine nucleotide-binding protein G(k) subunit al	GNAI3	R.DGGVQAC*FSR.S	0.44	0.80986791
P09543	CNP 2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	K.DKPELQFPFLQDEDTVATLLEC*K.T	0.44	-
Q13425	SNTB2 Beta-2-syntrophin	SNTB2	R.LVHSGSGC*R.S	0.44	-
O15228	GNPAT Dihydroxyacetone phosphate acyltransferase	GNPAT	K.NALAAC*VR.L	0.44	-
P55795	HNRNPH2 Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	R.GLPWSC*SADEVMR.F	0.44	0.851502648
Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	R.LDFVC*SFLQK.N	0.44	0.568591307
O00159	MYO1C Unconventional myosin-Ic	MYO1C	R.LLQFYAETC*PAPER.G	0.44	0.526340326
F5H5P2	Uncharacterized protein	Uncharacterized	R.DYPLELFMAQC*YGNISDLGK.G	0.445	-
Q9BSD7	NTPCR Cancer-related nucleoside-triphosphatase	NTPCR	R.NADC*SSGPGQR.V	0.445	-
Q9Y2X3	NOP58 Nucleolar protein 58	NOP58	K.TYDPSGDSTLPTC*SK.K	0.446666667	0.60872295
Q96ER9	CCDC51 Coiled-coil domain-containing protein 51	CCDC51	K.TC*SQMAGVVQLVK.S	0.446666667	-
Q9UKJ3	GPATCH8 G patch domain-containing protein 8	GPATCH8	K.VSETQMC*ESNSSK.E	0.45	-
Q14137	BOP1 Ribosome biogenesis protein BOP1	BOP1	K.KTTEEQVQASTPC*PR.T	0.45	-
P12235	SLC25A4 ADP/ATP translocase 1	SLC25A4	R.YFAGNLASGGAAGATSLC*FVYPLDFAR.T	0.45	0.662535166
Q9BVP2	GNL3 Guanine nucleotide-binding protein-like 3	GNL3	K.KLYC*QELK.K	0.45	0.877819754

P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	R.FEC*GEGEEAAETE.-	0.453333333	0.747319347
Q9Y2Q5	LAMTOR2 Ragulator complex protein LAMTOR2	LAMTOR2	K.FILMDC*MEGR.V	0.455	-
Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	R.AAGPLLTDEC*R.T	0.456666667	-
P62873	GNB1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB1	K.AC*ADATLSQITNNIDPVGR.I	0.456666667	0.582816672
P08670	VIM Vimentin	VIM	R.QVQSLTC*EVDALK.G	0.456666667	0.5374952
Q8TBP6	SLC25A40 Solute carrier family 25 member 40	SLC25A40	K.LGENETC*IPIVAGIVAR.F	0.46	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.GKVC*FEMK.V	0.46	0.632000822
O95299	NDUFA10 NADH dehydrogenase	NDUFA10	R.KQC*VDHYNEVK.S	0.46	0.552758353
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LAAQSC*ALSLVR.Q	0.463333333	0.631166662
Q9BU76	MMTAG2 Multiple myeloma tumor-associated protein 2	MMTAG2	R.APC*AGPSR.E	0.465	-
P11498	PC Pyruvate carboxylase, mitochondrial	PC	R.ADFAQAC*QDAGVR.F	0.465	0.455462673
Q15392	DHCR24 Delta(24)-sterol reductase	DHCR24	R.GLEAIC*AK.F	0.47	-
P01111	NRAS GTPase NRas	NRAS	R.VKDSDDVPMVLVGNKC*DLPTR.T	0.47	2.095579134
O15525	MAFG Transcription factor MafG	MAFG	R.GYAASC*R.V	0.473333333	-
P31040	SDHA Succinate dehydrogenase	SDHA	R.VGSVLQEGC*GK.I	0.473333333	0.611915798
Q8NFF5	FLAD1 FAD synthase	FLAD1	K.LTLDSEEEGPLEEC*LAYLTAR.L	0.475	-
P35658	NUP214 Nuclear pore complex protein Nup214	NUP214	R.TSC*KDDEAVVQAPR.H	0.475	0.601631702
B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	R.VIEC*DVVK.D	0.476666667	-
Q9NX24	NHP2 H/ACA ribonucleoprotein complex subunit 2	NHP2	K.ADPDGPEAQAEAC*SGER.T	0.476666667	0.704512856
Q8N163	KIAA1967 DBIRD complex subunit KIAA1967	KIAA1967	R.VHLTPYTVDSPIC*DFLELQR.R	0.48	-
Q9Y446	PKP3 Plakophilin-3	PKP3	K.SVENAVC*VLR.N	0.48	0.661092802
P62873	GNB1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	GNB1	R.ELAGHTGYLSC*CR.F	0.48	0.582816672
Q96I99	SUCLG2 Succinyl-CoA ligase	SUCLG2	R.SC*NGPVLVGSPQGGVDIEEVAASNPELIFK.E	0.48	0.576446159
P48047	ATP5O ATP synthase subunit O, mitochondrial	ATP5O	R.GEVPC*TVTSASPLEEATLSELK.T	0.48	0.456858595
O75521	ECI2 Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	K.LHAVNAEEC*NVLQGR.W	0.483333333	-
Q00325	SLC25A3 Phosphate carrier protein, mitochondrial	SLC25A3	K.GWAPTFLGYSMQGLC*K.F	0.485	0.704777215
Q7Z2W4	ZC3HAV1 Zinc finger CCCH-type antiviral protein 1	ZC3HAV1	R.SC*TPSPDQISHR.A	0.486666667	-
Q9Y6N5	SQRDL Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	K.KYDGYTSC*PLVTGYNR.V	0.486666667	1.602774875
P51553	IDH3G Isocitrate dehydrogenase	IDH3G	K.LGDGLFLQC*CR.E	0.486666667	0.611421911
O75521	ECI2 Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	R.WLSDEC*TNAVVNFLSR.K	0.49	-

Q96DV4	MRPL38 39S ribosomal protein L38, mitochondrial	MRPL38	K.QDQPIDFSEDARPSPC*YQLAQR.T	0.49	-
Q9NVS2	MRPS18A 28S ribosomal protein S18a, mitochondrial	MRPS18A	R.DNVC*YSR.T	0.49	-
Q06587	RING1 E3 ubiquitin-protein ligase RING1	RING1	K.GEYC*QTR.Y	0.49	-
Q9BYD6	MRPL1 39S ribosomal protein L1, mitochondrial	MRPL1	K.IATLDMSSDQIAANLQAVINEVC*R.H	0.49	0.993240093
Q15149	PLEC Plectin	PLEC	R.LLEAQAC*TGGIIDPSTGER.F	0.49	0.941752628
P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.MEEFKDQLPADEC*NK.L	0.49	0.857285499
Q14684	RRP1B Ribosomal RNA processing protein 1 homolog B	RRP1B	R.VFC*VEEEDSESSLQK.R	0.49	-
Q02252	ALDH6A1 Methylmalonate-semialdehyde dehydrogenase	ALDH6A1	K.ERVC*NLIDSGTK.E	0.493333333	-
Q9Y4W6	AFG3L2 AFG3-like protein 2	AFG3L2	K.FKDVAGC*EEAK.L	0.493333333	0.767424912
O75947	ATP5H ATP synthase subunit d, mitochondrial	ATP5H	K.SC*AEWVSLSK.A	0.493333333	0.523716386
P82921	MRPS21 28S ribosomal protein S21, mitochondrial	MRPS21	K.NRADPWQGC*.-	0.495	-
Q6P161	MRPL54 39S ribosomal protein L54, mitochondrial	MRPL54	K.GAVTSEALKDPDVC*TDPVQLTTYAMGVNIYK.E	0.495	-
O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.LC*DSYEIRPGK.H	0.495	0.891887933
Q9H9P8	L2HGDH L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	K.AC*FLGATVK.Y	0.496666667	-
B0LM41	RBM14/RBM4 fusion Transcriptional coactivator CoAZ	RBM14/RBM4	R.TAPGMGDQSGC*YR.C	0.496666667	-
O00330	PDHX Pyruvate dehydrogenase protein X component, mitoch	PDHX	K.STVPHAYATADC*DLGAVLK.V	0.5	-
P49189	ALDH9A1 4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	K.TVC*VEMGDVESAF.-	0.5	1.452758353
Q9H0L4	CSTF2T Cleavage stimulation factor subunit 2 tau variant	CSTF2T	K.LC*VQNSHQEAR.N	0.505	-
P62910	RPL32 60S ribosomal protein L32	RPL32	K.SYC*AEIAHNVSSK.N	0.505	-
P21912	SDHB Succinate dehydrogenase	SDHB	R.C*HTIMNCTR.T	0.505	0.514097652
Q14197	ICT1 Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	R.NLADC*LQK.I	0.506666667	1.034654235
P55769	NHP2L1 NHP2-like protein 1	NHP2L1	R.ACGVSRPVIAC*SVTIK.E	0.506666667	0.842852039
Q9UHB6	LIMA1 LIM domain and actin-binding protein 1	LIMA1	K.KMENC*LGESR.H	0.51	11.15537336
Q96DI7	SNRNP40 U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	R.C*SSLQAPIMLLSGHEGEVYCCK.F	0.51	0.857751699
Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	R.VDVAVNC*AGIAVASK.T	0.51	0.708885495
P21796	VDAC1 Voltage-dependent anion-selective channel protein	VDAC1	R.EHINLGC*DMDFDIAGPSIR.G	0.51	0.586841001
O43837	IDH3B Isocitrate dehydrogenase	IDH3B	K.LGDGLFLQC*C*EEVAELYPK.I	0.51	0.553613054
Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.KLGNNC*VFAPADVTSEK.D	0.513333333	0.708885495

P05141	SLC25A5 ADP/ATP translocase 2	SLC25A5	K.GTDIMYTGTLDC*WR.K	0.513333333	0.600767177
H3BQZ7	Uncharacterized protein	Uncharacterized	K.ANFSLPEKC*DYMDEVTYGELEKEEAQPIVTK.Y	0.515	0.688392323
Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	K.ILAC*DDLDEAAR.M	0.516666667	0.602403344
P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.LGGTIDDC*ELVEGLVLTQK.V	0.52	1.106498674
P36578	RPL4 60S ribosomal protein L4	RPL4	R.YAIC*SALAASALPALVMSK.G	0.52	0.776301476
Q9BWJ5	SF3B5 Splicing factor 3B subunit 5	SF3B5	K.MLQPC*GPPADKPEEN.-	0.523333333	-
P55769	NHP2L1 NHP2-like protein 1	NHP2L1	K.KLLDLVQQSC*NYK.Q	0.523333333	0.842852039
Q9NVH1	DNAJC11 DnaJ homolog subfamily C member 11	DNAJC11	K.VIDVTVPLQC*LVK.D	0.525	-
Q8IZL8	PELP1 Proline-, glutamic acid- and leucine-rich protein	PELP1	R.KGDSNANSDVC*AAALR.G	0.525	-
P05141	SLC25A5 ADP/ATP translocase 2	SLC25A5	R.GLGDC*LVK.I	0.526666667	0.600767177
P07602	PSAP Proactivator polypeptide	PSAP	R.LGPGMADIC*K.N	0.526666667	0.800459949
P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.DGLTDVYNKIHMGSC*AENTAK.K	0.526666667	0.491243112
Q8IY81	FTSJ3 pre-rRNA processing protein FTSJ3	FTSJ3	K.QQLPQTPPSC*LK.T	0.53	1.322660736
P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.TIYAGNALC*TVK.C	0.53	0.913986907
O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.SLLPGC*QSVISR.L	0.533333333	1.214913949
P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	K.TGYSFVNC*K.K	0.533333333	0.747319347
O15533	TAPBP Tapasin	TAPBP	K.WASGLTPAQNC*PR.A	0.535	-
Q9Y4C8	RBM19 Probable RNA-binding protein 19	RBM19	R.ITVEFC*K.S	0.535	-
Q9NX63	CHCHD3 Coiled-coil-helix-coiled-coil-helix domain-contain	CHCHD3	R.ERIC*SEEER.A	0.535	0.690267842
Q9UMS4	PRPF19 Pre-mRNA-processing factor 19	PRPF19	R.QELSHALYQHDAAC*R.V	0.535	0.688157436
P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.AC*QIFVR.N	0.536666667	0.459448597
P04843	RPN1 Dolichyl-diphosphooligosaccharide--protein glycosy	RPN1	K.TEGSDLC*DR.V	0.536666667	0.804201163
P56962	STX17 Syntaxin-17	STX17	K.LTSSC*PDLPSQTDKK.C	0.54	-
Q9BUJ2	HNRNPUL1 Heterogeneous nuclear ribonucleoprotein U-like pro	HNRNPUL1	R.WDVLIQQATQC*LNR.L	0.54	-
Q9BRJ2	MRPL45 39S ribosomal protein L45, mitochondrial	MRPL45	R.SIHLAC*TAGIFDAYVPPEGDAR.I	0.54	-
O75533	SF3B1 Splicing factor 3B subunit 1	SF3B1	R.VAIGPC*R.M	0.54	0.84270557
P55809	OXCT1 Succinyl-CoA:3-ketoacid coenzyme A transferase 1,	OXCT1	K.STGC*DFAVSPK.L	0.54	0.612400754
P50151	GNG10 Guanine nucleotide-binding protein G(I)/G(S)/G(O)	GNG10	K.VSQAAAELQQYCMQNAC*K.D	0.543333333	-
P60763	RAC3 Ras-related C3 botulinum toxin substrate 3	RAC3	R.AVLC*PPPVK.K	0.543333333	-
P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	R.VPTANVSVVDLTC*R.L	0.543333333	0.7724129

P62318	SNRPD3 Small nuclear ribonucleoprotein Sm D3	SNRPD3	K.VLHEAEGHIVTC*ETNTGEVYR.G	0.545	1.153576436
P33316	DUT Deoxyuridine 5-triphosphate nucleotidohydrolase,	DUT	R.IAQLIC*ER.I	0.545	-
Q15286	RAB35 Ras-related protein Rab-35	RAB35	R.WLHEINQNC*DDVCR.I	0.546666667	-
Q9H936	SLC25A22 Mitochondrial glutamate carrier 1	SLC25A22	R.VYTSMSDC*LIK.T	0.546666667	-
O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.LTLSC*EEFVK.I	0.546666667	1.214913949
P12235	SLC25A4 ADP/ATP translocase 1	SLC25A4	K.GADIMYTGTVDC*WR.K	0.546666667	0.662535166
P02533	KRT14 Keratin, type I cytoskeletal 14	KRT14	R.C*EMEQQNQEYK.I	0.55	0.542756477
P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.VC*ASGMK.A	0.55	0.491243112
P82675	MRPS5 28S ribosomal protein S5, mitochondrial	MRPS5	R.GWSGNSWGGISLGPPDPGPC*GETYEDFDTR.I	0.55	-
Q53H12	AGK Acylglycerol kinase, mitochondrial	AGK	K.ATVFLNPAAC*K.G	0.55	-
P50336	PPOX Protoporphyrinogen oxidase	PPOX	R.GQPVC*GLSLQAEGR.W	0.55	-
Q8N0V3	RBFA Putative ribosome-binding factor A, mitochondrial	RBFA	K.VSLTPDFSAC*R.A	0.55	-
P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.GLPWSC*SADEVQR.F	0.55	0.836485992
B4DLN1	SLC25A10 cDNA FLJ60124, highly similar to Mitochondrial dic	SLC25A10	R.TDGILALYSGLSASLC*R.Q	0.55	0.692764962
O00159	MYO1C Unconventional myosin-Ic	MYO1C	R.NLKETMC*SSK.N	0.55	0.526340326
P50336	PPOX Protoporphyrinogen oxidase	PPOX	R.LGPEVASLAMDSLC*R.G	0.553333333	-
P11388	TOP2A DNA topoisomerase 2-alpha	TOP2A	K.LC*NIFSTK.F	0.555	-
H3BQZ7	Uncharacterized protein	Uncharacterized	R.NFILDQC*NVYNSGQR.R	0.555	0.688392323
Q8IWX8	CHERP Calcium homeostasis endoplasmic reticulum protein	CHERP	K.LALEQQQLIC*K.Q	0.555	-
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.MREVC*DEVK.A	0.556666667	1.061903741
P11182	DBT Lipoamide acyltransferase component of branched-ch	DBT	K.AASLGLLQFPILNASVDENC*QNITYK.A	0.556666667	1.03779171
A1L0T0	ILVBL Acetolactate synthase-like protein	ILVBL	K.VLHDAQQQC*R.D	0.56	-
Q9UJA2	CRLS1 Cardiolipin synthase	CRLS1	K.YFNPC*YATAR.L	0.56	-
Q6P4A7	SFXN4 Sideroflexin-4	SFXN4	R.QLLC*TNEDVSSPASADQR.I	0.56	-
P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E	0.56	0.632853736
P10620	MGST1 Microsomal glutathione S-transferase 1	MGST1	K.VFANPEDC*VAFGK.G	0.563333333	2.735664336
Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.SC*SGVEFSTSGHAYTDTGK.A	0.563333333	0.487586743
Q9UDR5	AASS Alpha-aminoadipic semialdehyde synthase, mitochond	AASS	K.YNINPVSMDIC*K.Q	0.565	-
Q96EL3	MRPL53 39S ribosomal protein L53, mitochondrial	MRPL53	R.STNLNC*SVIADVR.H	0.565	-

Q9H6K4	OPA3 Optic atrophy 3 protein	OPA3	R.AQLC*NPGR.S	0.565	-
P24752	ACAT1 Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	K.QGEYGLASIC*NGGGGASAMLIQK.L	0.566666667	0.491243112
Q02978	SLC25A11 Mitochondrial 2-oxoglutarate/malate carrier protei	SLC25A11	R.GC*IPTMAR.A	0.57	-
P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.TFDLYANVRPC*VSIEGYK.T	0.57	0.561584903
P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.DKFNEC*GHVLYADIK.M	0.57	0.459448597
P12532	CKMT1B Creatine kinase U-type, mitochondrial	CKMT1B	R.GLSLPPAC*TR.A	0.57	0.383051559
P63279	UBE2I SUMO-conjugating enzyme UBC9	UBE2I	K.QILLGIQELLNEPNIQDPAQAEAYTIYC*QNR.V	0.57	-
O95716	RAB3D Ras-related protein Rab-3D	RAB3D	R.LVDVIC*EK.M	0.57	-
P49821	NDUFV1 NADH dehydrogenase	NDUFV1	K.HESCGQC*TPCR.E	0.57	0.545019157
Q96DI7	SNRNP40 U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	R.RGPQLVC*TGSDDGTVK.L	0.575	0.857751699
Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	R.C*DVIAQGIVMAVK.D	0.575	0.602403344
P02533	KRT14 Keratin, type I cytoskeletal 14	KRT14	K.GSC*GIGGGIGGGSSR.I	0.576666667	0.542756477
P49748	ACADVL Very long-chain specific acyl-CoA dehydrogenase, m	ACADVL	K.ELGAFGLQVPSELGGVGLC*NTQYAR.L	0.58	0.995332637
P43897	TSFM Elongation factor Ts, mitochondrial	TSFM	K.ALETC*GGDLK.Q	0.58	0.747319347
P14868	DARS Aspartate--tRNA ligase, cytoplasmic	DARS	R.LEYC*EALAMLR.E	0.58	-
P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	K.NLDKEYLPIGGLAEFC*K.A	0.58	0.907056417
P25705	ATP5A1 ATP synthase subunit alpha, mitochondrial	ATP5A1	K.YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR.D	0.58	0.473538211
O75367	H2AFY Core histone macro-H2A.1	H2AFY	K.NC*LALADDK.K	0.583333333	0.920713769
Q9H9J2	MRPL44 39S ribosomal protein L44, mitochondrial	MRPL44	R.QSGGTTALPLYFVGLYC*DK.K	0.585	-
P63167	DYNLL1 Dynein light chain 1, cytoplasmic	DYNLL1	K.NADMSEEMQQDSVEC*ATQALEK.Y	0.586666667	-
Q07955	SRSF1 Serine/arginine-rich splicing factor 1	SRSF1	R.EAGDVC*YADVYR.D	0.586666667	0.990386625
P53597	SUCLG1 Succinyl-CoA ligase	SUCLG1	R.LIGPNC*PGVINPGECK.I	0.586666667	0.451691986
Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.VC*NYGLTFTQK.W	0.586666667	0.487586743
P49959	MRE11A Double-strand break repair protein MRE11A	MRE11A	K.VTQAIQSFC*LEK.I	0.59	-
P04899	GNAI2 Guanine nucleotide-binding protein G(i) subunit al	GNAI2	K.NNLKDC*GLF.-	0.59	0.68573891
Q9Y446	PKP3 Plakophilin-3	PKP3	R.SAVDLSC*SR.R	0.59	0.661092802
P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.GDEC*ELLGHSK.N	0.59	0.632853736
O43837	IDH3B Isocitrate dehydrogenase	IDH3B	K.LGDGLFLQC*CEEVAELYPK.I	0.59	0.553613054
O95202	LETM1 LETM1 and EF-hand domain-containing protein 1, mit	LETM1	K.LFEDELTLDNLTRPQLVALC*K.L	0.59	0.926329609

P38405	GNAL Guanine nucleotide-binding protein G(olf) subunit	GNAL	R.VFNDC*R.D	0.593333333	-
O75431	MTX2 Metaxin-2	MTX2	K.NYSNLLAFC*R.R	0.596666667	-
P22695	UQCRC2 Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	R.NALANPLYC*PDYR.I	0.596666667	0.416975234
P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.AEGSDVANAVLDGADC*IMLSGETAK.G	0.6	1.042960105
P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G	0.6	1.041240879
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.FNNYVDC*MKK.F	0.6	0.995679161
P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.AAVEEGIVLGGGC*ALLR.C	0.6	0.714611187
Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	K.C*LNNLAASQLK.L	0.6	-
Q96SK2	TMEM209 Transmembrane protein 209	TMEM209	R.SQAPC*ANKDEADLSSK.Q	0.606666667	-
Q96EL3	MRPL53 39S ribosomal protein L53, mitochondrial	MRPL53	R.VQFC*PFEK.N	0.606666667	-
P49748	ACADVL Very long-chain specific acyl-CoA dehydrogenase, m	ACADVL	R.LFVALQGC*MDK.G	0.606666667	0.995332637
P23284	PPIB Peptidyl-prolyl cis-trans isomerase B	PPIB	R.DKPLKDVIIADC*GK.I	0.606666667	0.982430851
P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	K.VTDDLVC*LVYK.T	0.61	-
P03897	MT-ND3 NADH-ubiquinone oxidoreductase chain 3	MT-ND3	K.STPYEC*GFDPMSPAR.V	0.61	-
P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.HSMNPFC*EIAVEEAVR.L	0.61	1.035508042
Q96GQ7	DDX27 Probable ATP-dependent RNA helicase DDX27	DDX27	K.AC*IPVGLLGK.D	0.61	1.0000777
P53007	SLC25A1 Tricarboxylate transport protein, mitochondrial	SLC25A1	R.GIGDC*VR.Q	0.61	0.904011825
O15382	BCAT2 Branched-chain-amino-acid aminotransferase, mitoch	BCAT2	R.EVFGSGTAC*QVCPVHR.I	0.61	0.877830024
Q01081	U2AF1 Splicing factor U2AF 35 kDa subunit	U2AF1	K.DKVNC*SFYFK.I	0.61	1.090154418
P60709	ACTB Actin, cytoplasmic 1	ACTB	K.EKLC*YVALDFEQEMATAASSSSLEK.S	0.613333333	1.610252838
Q15233	NONO Non-POU domain-containing octamer-binding protein	NONO	R.C*SEGSFLLTTFPR.P	0.615	0.775898686
P46776	RPL27A 60S ribosomal protein L27a	RPL27A	K.RNQSFC*PTVNLDK.L	0.616666667	-
P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	K.KNINC*SIEESFQR.F	0.616666667	-
O15213	WDR46 WD repeat-containing protein 46	WDR46	K.VPAELIC*LDPR.A	0.616666667	-
P02795	MT2A Metallothionein-2	MT2A	K.KSC*CSCCPVGCAK.C	0.62	-
P35270	SPR Sepiapterin reductase	SPR	K.GKLVDC*K.V	0.62	-
Q96T23	RSF1 Remodeling and spacing factor 1	RSF1	R.VTDLVDYVC*NSEQL.-	0.62	-
Q4G0J3	LARP7 La-related protein 7	LARP7	R.SRPTSEGSDIESTEPQKQC*SK.K	0.62	-
O00264	PGRMC1 Membrane-associated progesterone receptor componen	PGRMC1	R.GLATFC*LDK.E	0.62	1.38697318

Q9BZE1	MRPL37 39S ribosomal protein L37, mitochondrial	MRPL37	R.NHIENQDEC*VLNVISHAR.L	0.62	1.327428127
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.AALEALGSC*LNNK.Y	0.62	1.061903741
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	K.NTC*TSVYTK.D	0.62	0.995679161
Q9Y277	VDAC3 Voltage-dependent anion-selective channel protein	VDAC3	K.YMLDC*R.T	0.62	0.487586743
Q5HYI8	RABL3 Rab-like protein 3	RABL3	R.TAFLAEDFNPEEINLDC*TNPR.Y	0.62	-
Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	K.LNQVC*FDDDGTSSPQDR.L	0.623333333	-
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.SQETEC*TYFSTPLLLGK.K	0.623333333	0.706639338
P49792	RANBP2 E3 SUMO-protein ligase RanBP2	RANBP2	R.VWLWTAC*DFADGER.K	0.625	-
Q7Z3D6	C14orf159 UPF0317 protein C14orf159, mitochondrial	C14orf159	K.APPGC*LTPER.I	0.625	-
P52597	HNRNPF Heterogeneous nuclear ribonucleoprotein F	HNRNPF	R.DLSYC*LSGMYDHR.Y	0.625	1.183898222
Q9UJZ1	STOML2 Stomatin-like protein 2	STOML2	R.ERESLNASIVDAINQAADC*WGIR.C	0.625	0.870134591
P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.GSDFDC*ELR.L	0.626666667	1.041240879
Q9HC36	RNMTL1 RNA methyltransferase-like protein 1	RNMTL1	R.SAAGAGC*SK.V	0.626666667	-
Q14197	ICT1 Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1	R.LTISYC*R.S	0.626666667	1.034654235
Q9NUQ2	AGPAT5 1-acyl-sn-glycerol-3-phosphate acyltransferase eps	AGPAT5	K.ATHVAFDC*MK.N	0.63	-
Q8N335	GPD1L Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	K.NIVAVGAGFC*DGLR.C	0.63	-
P39023	RPL3 60S ribosomal protein L3	RPL3	K.GC*VVGTK.K	0.63	1.564851879
P13804	ETFA Electron transfer flavoprotein subunit alpha, mito	ETFA	R.LGGEVSC*LVAGTK.C	0.63	0.913986907
P04406	GAPDH Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	K.IISNASC*TTNCLAPLAK.V	0.63	0.7724129
H3BQZ7	Uncharacterized protein	Uncharacterized	R.LQEALDAEMLEDEAGGGGAGPGGAC*K.A	0.63	0.688392323
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.EGVVEC*SFVK.S	0.633333333	0.706639338
Q5JTH9	RRP12 RRP12-like protein	RRP12	K.AAQHGVC*SVLK.G	0.635	-
Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGAC*GLR.Y	0.635	0.802797203
Q14980	NUMA1 Nuclear mitotic apparatus protein 1	NUMA1	K.HPSSPEC*LVSAQK.V	0.635	0.568591307
P15924	DSP Desmoplakin	DSP	K.AC*GSEIMQK.K	0.64	0.281381454
P35270	SPR Sepiapterin reductase	SPR	R.TVVNISSLC*ALQPFK.G	0.64	-
Q9Y512	SAMM50 Sorting and assembly machinery component 50 homolo	SAMM50	R.IC*DGVQFGAGIR.F	0.64	-
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.C*VANNQVETLEK.L	0.643333333	0.800215238

Q8N983	MRPL43 39S ribosomal protein L43, mitochondrial	MRPL43	R.PCC*VPR.V	0.643333333	-
P17676	CEBPB CCAAT/enhancer-binding protein beta	CEBPB	K.AEPGFEPADC*KR.K	0.643333333	-
Q8TAE8	GADD45GIP1 Growth arrest and DNA damage-inducible proteins-in	GADD45 GIP1	R.EQHIAEC*MAK.M	0.645	-
Q9Y4W6	AFG3L2 AFG3-like protein 2	AFG3L2	R.MC*MTLGGR.V	0.645	0.767424912
P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.SRGC*AVVEFK.M	0.645	0.459448597
O00567	NOP56 Nucleolar protein 56	NOP56	R.IDC*FSEVPTSVFGEK.L	0.646666667	0.761383954
Q15149	PLEC Plectin	PLEC	R.VPLDVAC*AR.G	0.646666667	0.941752628
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	K.IAC*LDFSLQK.T	0.65	1.079708223
Q96ER9	CCDC51 Coiled-coil domain-containing protein 51	CCDC51	R.QVHSC*LEGLR.E	0.65	-
Q00839	HNRNPU Heterogeneous nuclear ribonucleoprotein U	HNRNPU	K.DC*EVVMMIGLPGAGK.T	0.65	0.632000822
Q13162	PRDX4 Peroxiredoxin-4	PRDX4	R.TREEEC*HFYAGGQVYPGEASR.V	0.655	1.134099617
P35221	CTNNA1 Catenin alpha-1	CTNNA1	R.LESIISGAALMADSSC*TR.D	0.655	0.916168761
P07858	CTSB Cathepsin B	CTSB	R.DQGSC*GSCWAFGAVEAISDR.I	0.66	0.810742706
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	R.QALVEFEDVLGAC*NAVNYAADNQIYIAGHPAFVNYSTSQK.I	0.66	0.753256705
Q9Y2R9	MRPS7 28S ribosomal protein S7, mitochondrial	MRPS7	K.NC*EPMIGLVPILK.G	0.66	1.173076477
P09497	CLTB Clathrin light chain B	CLTB	K.VAQLC*DFNPK.S	0.663333333	-
O76021	RSL1D1 Ribosomal L1 domain-containing protein 1	RSL1D1	R.EINDC*IGGTVLNISK.S	0.663333333	1.027661228
Q9H0U6	MRPL18 39S ribosomal protein L18, mitochondrial	MRPL18	R.NVVAC*ESIGR.V	0.665	-
P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	K.STC*IYGGAPK.G	0.665	1.757924068
Q9H0A0	NAT10 N-acetyltransferase 10	NAT10	R.IVSGC*PLPEACELYYVNR.D	0.665	0.893763452
P62753	RPS6 40S ribosomal protein S6	RPS6	K.LNISFPATGC*QK.L	0.666666667	-
O75533	SF3B1 Splicing factor 3B subunit 1	SF3B1	K.VQENC*IDLVGR.I	0.666666667	0.84270557
Q9BPW8	NIPSNAP1 Protein NipSnap homolog 1	NIPSNAP 1	R.FSGGYPALMDC*MNK.L	0.666666667	0.652379677
Q8N335	GPD1L Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L	K.FC*ETTIGSK.V	0.67	-
Q7L0Y3	TRMT10C Mitochondrial ribonuclease P protein 1	TRMT10C	R.LNLATEC*LPLDK.Y	0.673333333	1.201010101
P35221	CTNNA1 Catenin alpha-1	CTNNA1	R.IVAEC*NAVR.Q	0.673333333	0.916168761
Q9NRW3	APOBEC3C Probable DNA dC- dU-editing enzyme APOBEC-3C	APOBEC 3C	R.NQVDSETHC*HAER.C	0.675	-
Q8NI37	PPTC7 Protein phosphatase PTC7 homolog	PPTC7	R.AGGGGGGDYGLVTAGC*GFGK.D	0.675	-
Q9H0A0	NAT10 N-acetyltransferase 10	NAT10	K.ESLQDTQPVGVLVDC*C*K.T	0.675	0.893763452
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.IHDVLC*K.L	0.675	0.800215238

Q99714	HSD17B10 3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	K.VC*NFLASQVPFPSR.L	0.675	0.708885495
P21796	VDAC1 Voltage-dependent anion-selective channel protein	VDAC1	K.YQIDPDAC*FSAK.V	0.676666667	0.586841001
P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	K.LLEAGNFIC*QALNR.K	0.68	-
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.YYGGAEVVDEIELLC*QR.R	0.68	1.061903741
P61978	HNRNPK Heterogeneous nuclear ribonucleoprotein K	HNRNPK	K.LFQEC*CPHSTDR.V	0.68	1.041240879
P84103	SRSF3 Serine/arginine-rich splicing factor 3	SRSF3	R.DSC*PLDCK.V	0.68	1.037541641
B4DLN1	SLC25A10 cDNA FLJ60124, highly similar to Mitochondrial dic	SLC25A10	R.GALVTVGQLSC*YDQAK.Q	0.68	0.692764962
Q9HD33	MRPL47 39S ribosomal protein L47, mitochondrial	MRPL47	K.SGAAWTC*QQLR.N	0.683333333	-
Q5J8M3	EMC4 ER membrane protein complex subunit 4	EMC4	R.C*WDIALGPLK.Q	0.683333333	-
Q9Y2X3	NOP58 Nucleolar protein 58	NOP58	K.EEPLSEEEPC*TSTAIASPEKK.K	0.685	0.60872295
Q9BSH4	TACO1 Translational activator of cytochrome c oxidase 1	TACO1	K.EGGPNPEHNSNLANILEVC*R.S	0.686666667	-
P24390	KDELR1 ER lumen protein retaining receptor 1	KDELR1	K.SRSC*AGISGK.S	0.69	-
Q8NDX6	ZNF740 Zinc finger protein 740	ZNF740	R.MCQGC*QSK.T	0.69	-
Q7L2E3	DHX30 Putative ATP-dependent RNA helicase DHX30	DHX30	R.QAAAAAC*QLFK.G	0.69	-
Q15050	RRS1 Ribosome biogenesis regulatory protein homolog	RRS1	R.C*AGPTPEAELQALAR.D	0.69	0.983372183
Q8IVF2	AHNAK2 Protein AHNAK2	AHNAK2	R.LDLTGPHFESSILSPC*EDVTLTK.Y	0.69	0.912419509
P61224	RAP1B Ras-related protein Rap-1b	RAP1B	R.QWNNC*AFLESSAK.S	0.69	0.821408604
P52272	HNRNPM Heterogeneous nuclear ribonucleoprotein M	HNRNPM	K.GC*GVVKFESPEVAER.A	0.69	0.459448597
P60604	UBE2G2 Ubiquitin-conjugating enzyme E2 G2	UBE2G2	R.VC*ISILHAPGDDPMGYESSAER.W	0.69	-
O76021	RSL1D1 Ribosomal L1 domain-containing protein 1	RSL1D1	R.SDSEDIC*LFTK.D	0.69	1.027661228
O75439	PMPCB Mitochondrial-processing peptidase subunit beta	PMPCB	R.VTC*LESGLR.V	0.69	0.939328743
P53007	SLC25A1 Tricarboxylate transport protein, mitochondrial	SLC25A1	R.NTWDC*GLQILK.K	0.69	0.904011825
Q00325	SLC25A3 Phosphate carrier protein, mitochondrial	SLC25A3	K.FAC*FER.T	0.69	0.704777215
P49411	TUFM Elongation factor Tu, mitochondrial	TUFM	K.GEETPVIVGSALC*ALEGR.D	0.69	0.632853736
Q9Y2S7	POLDIP2 Polymerase delta-interacting protein 2	POLDIP2	R.DC*PHISQR.S	0.693333333	-
Q14318	FKBP8 Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	R.SC*SLVLEHQPDNIK.A	0.693333333	-
Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVGVEVPDVELEC*PDAK.L	0.693333333	0.970800847

P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.WNTDNTLGTEIAIEDQIC*QGLK.L	0.693333333	0.943164626
Q15149	PLEC Plectin	PLEC	R.GC*LDEETSR.A	0.693333333	0.941752628
Q96QR8	PURB Transcriptional activator protein Pur-beta	PURB	R.GGGGGPC*GFQPASR.G	0.696666667	-
Q8NBN7	RDH13 Retinol dehydrogenase 13	RDH13	K.DYVTGGAC*PSK.A	0.696666667	-
O75348	ATP6V1G1 V-type proton ATPase subunit G 1	ATP6V1G1	R.GSC*STEVEKETQEK.M	0.696666667	-
P07237	P4HB Protein disulfide-isomerase	P4HB	R.ITEFC*HR.F	0.696666667	1.035758112
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	K.VFNDTC*R.S	0.696666667	0.800215238
P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.IYGFYDEC*K.R	0.7	-
O95861	BPNT1 3(2),5-bisphosphate nucleotidase 1	BPNT1	K.TC*ATDLQTK.A	0.7	-
P04075	ALDOA Fructose-bisphosphate aldolase A	ALDOA	R.ALANSLAC*QGK.Y	0.7	2.123474801
Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.GPFVEAEVPDVDLEC*PDAK.L	0.7	0.970800847
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.AILQENGC*LSDSDMFSQAGLR.S	0.7	0.800215238
P35659	DEK Protein DEK	DEK	K.GQKLC*EIER.I	0.7	0.583586528
P62241	RPS8 40S ribosomal protein S8	RPS8	K.LLAC*IASR.P	0.7	1.120108244
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	K.NTC*PGDR.S	0.7	1.061903741
Q9NYK5	MRPL39 39S ribosomal protein L39, mitochondrial	MRPL39	K.DC*DPGEVNK.A	0.703333333	1.036900392
Q13242	SRSF9 Serine/arginine-rich splicing factor 9	SRSF9	R.NGYDYGQC*R.L	0.703333333	1.150322857
O60832	DKC1 H/ACA ribonucleoprotein complex subunit 4	DKC1	K.DSAVNAIC*YGAK.I	0.706666667	-
P36873	PPP1CC Serine/threonine-protein phosphatase PP1-gamma cat	PPP1CC	R.GNHEC*ASINR.I	0.706666667	-
Q9Y3E5	PTRH2 Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	R.VC*FGMLPK.S	0.71	-
P62273	RPS29 40S ribosomal protein S29	RPS29	K.YGLNMC*R.Q	0.71	-
O75691	UTP20 Small subunit processome component 20 homolog	UTP20	K.IPTPADVC*K.V	0.71	-
O94906	PRPF6 Pre-mRNA-processing factor 6	PRPF6	R.AGSVATC*QAVMR.A	0.71	-
O94832	MYO1D Unconventional myosin-Id	MYO1D	K.SNC*VLEAFGNAK.T	0.71	-
P82932	MRPS6 28S ribosomal protein S6, mitochondrial	MRPS6	K.EC*EGIVPVPLAEK.L	0.713333333	0.748068662
Q8NFF5	FLAD1 FAD synthase	FLAD1	R.LHYGTDPC*TGQPFR.F	0.715	-
Q8IVH4	MMAA Methylmalonic aciduria type A protein, mitochondri	MMAA	R.AC*LAEAITLVESTHSR.K	0.715	-
O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.QMFEPVSC*TFTYLLGDR.E	0.715	1.214913949
Q9Y673	ALG5 Dolichyl-phosphate beta-glucosyltransferase	ALG5	K.GLNDLQPWPNQMAIAC*GSR.A	0.716666667	-

P49458	SRP9 Signal recognition particle 9 kDa protein	SRP9	R.HSDGNLC*VK.V	0.72	-
Q6YP21	CCBL2 Kynurenine--oxoglutarate transaminase 3	CCBL2	K.LSAIPVSAFC*NSETK.S	0.72	-
Q9P032	NDUFAF4 NADH dehydrogenase	NDUFAF4	K.AAETC*QEPK.E	0.72	-
O43795	MYO1B Unconventional myosin-Ib	MYO1B	K.NGSVPTC*K.R	0.72	0.665578866
Q9Y6C9	MTCH2 Mitochondrial carrier homolog 2	MTCH2	K.YCGLC*DSIITIYR.E	0.723333333	-
P31943	HNRNPH1 Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	R.DLNYC*FSGMSDHR.Y	0.723333333	0.836485992
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.SSVNC*PFSSQDMK.Y	0.723333333	0.631166662
Q9Y324	FCF1 rRNA-processing protein FCF1 homolog	FCF1	K.GTYADDC*LVQR.V	0.725	-
P23246	SFPQ Splicing factor, proline- and glutamine-rich	SFPQ	R.C*SEGVFLLTTTPR.P	0.725	0.852238566
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SQMESMLISGYALNC*VVGSQGMPK.R	0.725	1.079708223
P49207	RPL34 60S ribosomal protein L34	RPL34	R.AYGGSMC*AK.C	0.726666667	1.496089989
Q15149	PLEC Plectin	PLEC	K.VLSSSGSEAAVPSVC*FLVPPPNQEAQEAVTR.L	0.726666667	0.941752628
Q9P2R7	SUCLA2 Succinyl-CoA ligase	SUCLA2	R.IC*NQVLVCER.K	0.726666667	0.602403344
Q9HAV7	GRPEL1 GrpE protein homolog 1, mitochondrial	GRPEL1	K.LYGIQAFC*K.D	0.73	1.327729104
Q9Y3B4	SF3B14 Pre-mRNA branch site protein p14	SF3B14	K.NACDHLSGFNVC*NR.Y	0.73	0.858090186
O00567	NOP56 Nucleolar protein 56	NOP56	R.LVAFC*PFASSQVALENANAVSEGVVHEDLR.L	0.73	0.761383954
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	R.VFNVFC*LYGNVEK.V	0.73	0.753256705
P49748	ACADVL Very long-chain specific acyl-CoA dehydrogenase, m	ACADVL	R.TSAVPSPC*GK.Y	0.733333333	0.995332637
H3BQZ7	Uncharacterized protein	Uncharacterized	K.EGC*TEVSLLR.V	0.733333333	0.688392323
Q7L8L6	FASTKD5 FAST kinase domain-containing protein 5	FASTKD5	R.NQYC*YGSR.D	0.735	-
Q9NVV4	MTPAP Poly(A) RNA polymerase, mitochondrial	MTPAP	R.FSHQASGFQC*DLTTNNR.I	0.735	-
Q9Y2Z2	MTO1 Protein MTO1 homolog, mitochondrial	MTO1	K.TDQYLC*DADR.L	0.735	-
P49756	RBM25 RNA-binding protein 25	RBM25	K.AKENDENC*GPTTTVFVGNISEK.A	0.735	0.949824505
P25445	FAS Tumor necrosis factor receptor superfamily member	FAS	K.ANLC*TLAEK.I	0.736666667	-
Q9Y3B7	MRPL11 39S ribosomal protein L11, mitochondrial	MRPL11	R.GVSINQFC*K.E	0.736666667	-
P22087	FBL rRNA 2-O-methyltransferase fibrillarin	FBL	K.ANC*IDSTASAEAVFASEVK.K	0.74	0.664358885
Q9UKS6	PACSIN3 Protein kinase C and casein kinase substrate in ne	PACSIN3	R.IGLYPANYVEC*VGA.-	0.74	-
Q6P2I3	FAHD2B Fumarylacetoacetate hydrolase domain-containing pr	FAHD2B	K.TFDTFC*PLGPALVTK.D	0.743333333	-
Q9BSC4	NOL10 Nucleolar protein 10	NOL10	K.IYSLSC*GK.S	0.743333333	-
Q9UHD8	SEPT9 Septin-9	43717	R.SQEATEAAPSC*VGDMADTPR.D	0.743333333	-

P42765	ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	K.EAEVVLC*GGTESMSQAPYC*VR.N	0.743333333	0.967278443
Q5JVF3	PCID2 PCI domain-containing protein 2	PCID2	K.QNPFPPLSTVC*.-	0.745	-
Q7RTV0	PHF5A PHD finger-like domain-containing protein 5A	PHF5A	R.IC*DECNYGSYQGR.C	0.746666667	-
Q9NW81	ATP5SL ATP synthase subunit s-like protein	ATP5SL	R.LYPLADSLQELSLAGC*PR.I	0.746666667	-
Q6NUK1	SLC25A24 Calcium-binding mitochondrial carrier protein SCaM	SLC25A24	K.TGQYSGIYDC*AK.K	0.746666667	1.028735632
Q96N66	MBOAT7 Lysophospholipid acyltransferase 7	MBOAT7	R.AGGGPTLQC*PPPSSPEK.A	0.75	-
P38646	HSPA9 Stress-70 protein, mitochondrial	HSPA9	K.AKC*ELSSSVQTDINLPYLTMDSSGPK.H	0.75	0.857285499
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.SC*GSLLPELK.L	0.75	0.800215238
P36776	LONP1 Lon protease homolog, mitochondrial	LONP1	R.ALC*GLDESK.A	0.75	0.798535309
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.TIIPLISQC*TPK.V	0.75	0.706639338
P50213	IDH3A Isocitrate dehydrogenase	IDH3A	K.C*SDFTEEICR.R	0.75	0.561584903
P61006	RAB8A Ras-related protein Rab-8A	RAB8A	K.C*DVNDKR.Q	0.753333333	-
P48735	IDH2 Isocitrate dehydrogenase	IDH2	K.DLAGC*IHGLSNVK.L	0.755	-
O43684	BUB3 Mitotic checkpoint protein BUB3	BUB3	R.TPC*NAGTFSQPEK.V	0.755	1.709681698
P55265	ADAR Double-stranded RNA-specific adenosine deaminase	ADAR	K.NFYLC*PV.-	0.755	0.799095285
P49207	RPL34 60S ribosomal protein L34	RPL34	K.SAC*GVCPGR.L	0.756666667	1.496089989
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.WC*EYGLTFTEK.W	0.756666667	0.943164626
Q5JTH9	RRP12 RRP12-like protein	RRP12	R.VTVC*QALR.T	0.76	-
O43159	RRP8 Ribosomal RNA-processing protein 8	RRP8	K.AQLSGLQLQPC*LYK.R	0.76	-
Q6PI48	DARS2 Aspartate--tRNA ligase, mitochondrial	DARS2	K.TAELLNAC*K.K	0.76	-
P04181	OAT Ornithine aminotransferase, mitochondrial	OAT	K.VLPMNTGVEAGETAC*K.L	0.76	1.016908251
O14966	RAB7L1 Ras-related protein Rab-7L1	RAB7L1	K.C*DLSPWAVSR.D	0.763333333	-
Q9H936	SLC25A22 Mitochondrial glutamate carrier 1	SLC25A22	R.GVNEDTYSGILDC*AR.K	0.763333333	-
Q86U28	ISCA2 Iron-sulfur cluster assembly 2 homolog, mitochondr	ISCA2	R.LTDSC*VQR.L	0.763333333	-
Q7L0Y3	TRMT10C Mitochondrial ribonuclease P protein 1	TRMT10C	K.TLMEC*VSNTAK.K	0.763333333	1.201010101
P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*C*TLR.I	0.765	0.674151774
O95249	GOSR1 Golgi SNAP receptor complex member 1	GOSR1	K.LC*TSYSHSSTR.D	0.765	-
O60488	ACSL4 Long-chain-fatty-acid--CoA ligase 4	ACSL4	R.VGAPLIC*CEIK.L	0.765	1.787687664
Q07955	SRSF1 Serine/arginine-rich splicing factor 1	SRSF1	R.GPAGNNDC*R.I	0.766666667	0.990386625
O00217	NDUFS8 NADH dehydrogenase	NDUFS8	K.LCEAIC*PAQAITIEAEPR.A	0.766666667	0.672173548

Q9BW27	NUP85 Nuclear pore complex protein Nup85	NUP85	K.EADASPASAGIC*R.I	0.77	-
P02545	LMNA Prelamin-A/C	LMNA	K.AQNTWGC*GNSLR.T	0.77	1.127681769
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.VC*EDLDTSVNLAWTSGTNC*TR.F	0.77	0.943164626
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.LQISHEAAAC*ITGLR.A	0.77	0.631166662
P55084	HADHB Trifunctional enzyme subunit beta, mitochondrial	HADHB	K.EGGQYGLVAAC*AAGGQGHAMIVEAYPK.-	0.77	0.501654922
Q9Y2X3	NOP58 Nucleolar protein 58	NOP58	K.IISDNLTYC*K.C	0.773333333	0.60872295
P19447	ERCC3 TFIIH basal transcription factor complex helicase	ERCC3	R.SGVIVLPC*GAGK.S	0.773333333	-
P30050	RPL12 60S ribosomal protein L12	RPL12	R.C*TGGEVGATSALAPK.I	0.773333333	1.375625396
Q9BQ69	MACROD1 O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	K.LEVDAIVNAANSSLLGGGGVDGC*IHR.A	0.775	-
Q14690	PDCD11 Protein RRP5 homolog	PDCD11	K.VGQYLNC*IVEK.V	0.775	1.177203065
Q08211	DHX9 ATP-dependent RNA helicase A	DHX9	K.NFLYAWC*GK.R	0.775	0.631166662
O14950	MYL12B Myosin regulatory light chain 12B	MYL12B	R.NAFAC*FDEEATGTIQEDYLR.E	0.776666667	0.832946619
Q13838	DDX39B Spliceosome RNA helicase DDX39B	DDX39B	K.HFILDEC*DK.M	0.78	-
Q9NVV5	AIG1 Androgen-induced gene 1 protein	AIG1	-.MALVPC*QVLR.M	0.78	-
P54886	ALDH18A1 Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	R.GDEC*GLALGR.L	0.783333333	0.743305736
P36954	POLR2I DNA-directed RNA polymerase II subunit RPB9	POLR2I	R.NCDYQQEADNSC*IYVNK.I	0.783333333	-
O95678	KRT75 Keratin, type II cytoskeletal 75	KRT75	K.LLEGEEC*R.L	0.783333333	0.967100715
J3KR12	Uncharacterized protein	Uncharacterized	R.SLLINAVEASC*IR.T	0.785	-
Q13242	SRSF9 Serine/arginine-rich splicing factor 9	SRSF9	R.EAGDVC*YADVQK.D	0.785	1.150322857
Q99798	ACO2 Aconitate hydratase, mitochondrial	ACO2	R.DLGGIVLANACGPC*IGQWDR.K	0.785	0.748687583
P35659	DEK Protein DEK	DEK	K.SIC*EVLDLER.S	0.785	0.583586528
P27635	RPL10 60S ribosomal protein L10	RPL10	K.MLSC*AGADR.L	0.786666667	-
P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.ERPTPSLNNNC*TTSEDSLVLYNR.V	0.786666667	-
Q9Y6C9	MTCH2 Mitochondrial carrier homolog 2	MTCH2	K.TYC*CDLK.M	0.79	-
Q13084	MRPL28 39S ribosomal protein L28, mitochondrial	MRPL28	K.TPKEDLC*SK.F	0.79	-
P08754	GNAI3 Guanine nucleotide-binding protein G(k) subunit al	GNAI3	K.NNLKEC*GLY.-	0.79	0.80986791
P62826	RAN GTP-binding nuclear protein Ran	RAN	R.VC*ENIPIVLCGNK.V	0.79	0.797493056
Q13813	SPTAN1 Spectrin alpha chain, non-erythrocytic 1	SPTAN1	R.C*NSLEEIK.A	0.793333333	-
O15091	KIAA0391 Mitochondrial ribonuclease P protein 3	KIAA0391	R.DHKAC*LPDAK.T	0.793333333	-
O76021	RSL1D1 Ribosomal L1 domain-containing protein 1	RSL1D1	K.SGSC*SAIR.I	0.793333333	1.027661228

P42765	ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	K.ISREEC*DKYALQSQQR.W	0.793333333	0.967278443
P37198	NUP62 Nuclear pore glycoprotein p62	NUP62	R.KVEEVTKVC*EGR.R	0.795	0.80577392
P38117	ETFB Electron transfer flavoprotein subunit beta	ETFB	K.EVIAVSC*GPAQCQETIR.T	0.796666667	1.035508042
P14923	JUP Junction plakoglobin	JUP	K.GIMEEDEAC*GR.Q	0.8	0.503413445
Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	K.SSGQSAQLLSHEPGDPPC*LR.R	0.8	-
Q02218	OGDH 2-oxoglutarate dehydrogenase, mitochondrial	OGDH	K.AEQFYC*GDTEGK.K	0.8	0.896915218
Q92785	DPF2 Zinc finger protein ubi-d4	DPF2	K.KGPDGLALPNNYCDFC*LGDSK.I	0.805	-
Q9HBH5	RDH14 Retinol dehydrogenase 14	RDH14	R.QAAEC*GPEPGVSGVGELIVR.E	0.805	-
Q5PRF9	SAMD4B Protein Smaug homolog 2	SAMD4B	K.C*LTHEAFTETQK.K	0.805	-
P04843	RPN1 Dolichyl-diphosphooligosaccharide--protein glycosy	RPN1	K.VAC*ITEQVLTLVNK.R	0.805	0.804201163
P62820	RAB1A Ras-related protein Rab-1A	RAB1A	K.LLVGNKC*DLTTK.K	0.81	1.803326814
Q07020	RPL18 60S ribosomal protein L18	RPL18	K.GC*GTVLLSGPR.K	0.81	1.161750127
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.DC*LINAAK.T	0.813333333	1.079708223
Q92621	NUP205 Nuclear pore complex protein Nup205	NUP205	R.C*QDVSAGSLQELALLTGIISK.A	0.815	-
Q9BZG1	RAB34 Ras-related protein Rab-34	RAB34	R.DRVLAELPQC*LR.K	0.82	-
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	R.PMC*IPPSYADLGK.A	0.82	0.943164626
P23497	SP100 Nuclear autoantigen Sp-100	SP100	K.RKDTTSDKDDSLGSQQTNEQC*AQK.A	0.82	-
P63208	SKP1 S-phase kinase-associated protein 1	SKP1	K.ENQWC*EEK.-	0.823333333	-
Q7L0Y3	TRMT10C Mitochondrial ribonuclease P protein 1	TRMT10C	K.SSVQEEC*VSTISSSKDEDPLAATR.E	0.823333333	1.201010101
Q9Y2Q3	GSTK1 Glutathione S-transferase kappa 1	GSTK1	K.ETTEAAC*R.Y	0.823333333	0.863613143
Q13795	ARFRP1 ADP-ribosylation factor-related protein 1	ARFRP1	K.TAFSDC*TSK.I	0.825	-
O75694	NUP155 Nuclear pore complex protein Nup155	NUP155	R.YVENPSQVLNC*ER.R	0.825	-
P41252	IARS Isoleucine--tRNA ligase, cytoplasmic	IARS	K.MGITEYNNQC*R.A	0.825	-
P34897	SHMT2 Serine hydroxymethyltransferase, mitochondrial	SHMT2	R.GLELIASENFC*SR.A	0.825	1.061903741
P50454	SERPINH1 Serpin H1	SERPINH1	K.QHYNC*EHSK.I	0.825	0.87977208
P55265	ADAR Double-stranded RNA-specific adenosine deaminase	ADAR	K.KLTEC*QLK.N	0.826666667	0.799095285
P62829	RPL23 60S ribosomal protein L23	RPL23	R.ISLGLPVGAVINC*ADNTGAK.N	0.826666667	1.254643696
Q15005	SPCS2 Signal peptidase complex subunit 2	SPCS2	R.SGGSGGC*SGAGGASNCGTGSGR.S	0.83	1.449880771
O00567	NOP56 Nucleolar protein 56	NOP56	K.GLTDLSAC*K.A	0.83	0.761383954
O00483	NDUFA4 NADH dehydrogenase	NDUFA4	R.LALFNPDVC*WDR.N	0.83	0.314955925
O95140	MFN2 Mitofusin-2	MFN2	R.RFEEC*ISQSAVK.T	0.833333333	-
Q9BV79	MECR Trans-2-enoyl-CoA reductase, mitochondrial	MECR	R.LALNC*VGGK.S	0.836666667	-

P42765	ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	K.EAEVVLC*GGTESMSQAPYCVR.N	0.836666667	0.967278443
Q02218	OGDH 2-oxoglutarate dehydrogenase, mitochondrial	OGDH	R.FGLEGC*EVLIPALK.T	0.836666667	0.896915218
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LNVC*VSK.Q	0.836666667	0.753256705
O60216	RAD21 Double-strand-break repair protein rad21 homolog	RAD21	K.TGAESISLLELC*R.N	0.84	-
Q9H6R4	NOL6 Nucleolar protein 6	NOL6	R.QAVDSPAASFC*R.G	0.84	-
Q9Y265	RUVBL1 RuvB-like 1	RUVBL1	K.EVYEGEVTELTPC*ETENPMGGYGK.T	0.84	1.046386946
P55735	SEC13 Protein SEC13 homolog	SEC13	R.FASGGC*DNLIK.L	0.843333333	-
Q9BZE4	GTPBP4 Nucleolar GTP-binding protein 1	GTPBP4	R.TLLLC*GYPNVGK.S	0.845	-
P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.QITSYGETC*PGLEQYAIKK.F	0.845	-
Q9Y265	RUVBL1 RuvB-like 1	RUVBL1	K.VPFC*PMVGSEVYSTEIK.K	0.845	1.046386946
Q13185	CBX3 Chromobox protein homolog 3	CBX3	R.LTWHSC*PEDEAQ.-	0.846666667	1.067653547
P35579	MYH9 Myosin-9	MYH9	R.EDQSILC*TGESGAGK.T	0.846666667	1.03316543
P42704	LRPPRC Leucine-rich PPR motif-containing protein, mitocho	LRPPRC	R.YC*QEPR.G	0.846666667	0.800215238
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.SC*SGVEFSTSGSSNTDTGK.V	0.85	0.943164626
Q96FV9	THOC1 THO complex subunit 1	THOC1	K.SQNTVFC*GR.I	0.85	-
P10515	DLAT Dihydrolipoyllysine-residue acetyltransferase comp	DLAT	K.ASALAC*LK.V	0.85	0.668595772
O76021	RSL1D1 Ribosomal L1 domain-containing protein 1	RSL1D1	K.AVDALLTHC*K.S	0.853333333	1.027661228
P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	R.C*IPALDSLTPANEDQK.I	0.853333333	0.714611187
Q53R41	FASTKD1 FAST kinase domain-containing protein 1	FASTKD1	R.IEAVLPQC*DLNNLSSFATSVLR.W	0.855	-
O15091	KIAA0391 Mitochondrial ribonuclease P protein 3	KIAA0391	K.TIESIQLSPEEYEC*LK.G	0.855	-
P25398	RPS12 40S ribosomal protein S12	RPS12	K.LVEALC*AEHQINLIK.V	0.855	-
P14625	HSP90B1 Endoplasmin	HSP90B1	R.LTESPC*ALVASQYGWSGNMER.I	0.856666667	1.206935848
P07355	ANXA2 Annexin A2	ANXA2	K.GLGTDEDSLIEIIC*SR.T	0.856666667	1.858546562
Q92785	DPF2 Zinc finger protein ubi-d4	DPF2	K.TGQPEELVSC*SDC*GR.S	0.86	-
O00567	NOP56 Nucleolar protein 56	NOP56	K.IGAAIQEELGYNC*QTGGVIAEILR.G	0.86	0.761383954
O96008	TOMM40 Mitochondrial import receptor subunit TOM40 homolo	TOMM40	R.TPGAATASASGAAEDGAC*GCLPNPGTFEECHR.K	0.86	0.678116264
P62910	RPL32 60S ribosomal protein L32	RPL32	K.ELEVLLMC*NK.S	0.86	-
Q8NBU5	ATAD1 ATPase family AAA domain-containing protein 1	ATAD1	R.DAALLC*VR.E	0.863333333	-
Q53GQ0	HSD17B12 Estradiol 17-beta-dehydrogenase 12	HSD17B12	K.MININILSVC*K.M	0.865	-
Q12788	TBL3 Transducin beta-like protein 3	TBL3	R.FLGPEDSHVVVASNSPC*LK.V	0.865	0.788655789

O00567	NOP56 Nucleolar protein 56	NOP56	K.IINDNATYC*R.L	0.866666667	0.761383954
P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LGVENC*YFPMFVSQSALEK.E	0.87	-
O43143	DHX15 Putative pre-mRNA-splicing factor ATP-dependent RN	DHX15	K.IAPQYYDMSNFPQC*EAK.R	0.87	1.10986791
Q9ULX6	AKAP8L A-kinase anchor protein 8-like	AKAP8L	R.GQC*MSGASR.L	0.87	-
P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	R.GDGPIC*LVLAPTR.E	0.87	1.757924068
P14174	MIF Macrophage migration inhibitory factor	MIF	K.LLC*GLLAER.L	0.875	-
Q96CQ1	SLC25A36 Solute carrier family 25 member 36	SLC25A36	R.MGAFEC*VR.K	0.875	-
Q10713	PMPCA Mitochondrial-processing peptidase subunit alpha	PMPCA	K.HGGIC*DCQTSR.D	0.875	1.048767963
O95571	ETHE1 Protein ETHE1, mitochondrial	ETHE1	R.TDFQQGC*AK.T	0.876666667	1.214913949
Q12769	NUP160 Nuclear pore complex protein Nup160	NUP160	R.NHDGEC*TAAPTNR.Q	0.88	-
O96011	PEX11B Peroxisomal membrane protein 11B	PEX11B	R.LLMEQESSAC*SR.R	0.88	-
Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.EGTDSSQGIPQLVSNISAC*QVIAEAVR.T	0.88	1.164058355
Q9UI30	TRMT112 tRNA methyltransferase 112 homolog	TRMT112	R.IC*PVEFNPNFVAR.M	0.885	-
Q14232	EIF2B1 Translation initiation factor eIF-2B subunit alpha	EIF2B1	K.IGTNQMAVC*AK.A	0.885	-
Q9H0A0	NAT10 N-acetyltransferase 10	NAT10	R.YC*YYNETHK.I	0.885	0.893763452
Q6PI48	DARS2 Aspartate--tRNA ligase, mitochondrial	DARS2	R.LIC*LVTGSPSIR.D	0.886666667	-
Q16611	BAK1 Bcl-2 homologous antagonist/killer	BAK1	R.QEC*GEPALPSASEEQVAQDTEEVFR.S	0.886666667	-
P07947	YES1 Tyrosine-protein kinase Yes	YES1	K.YRPENTPEPVSTSVSHYGAEPTTVSPC*PSSSAK.G	0.886666667	-
P46779	RPL28 60S ribosomal protein L28	RPL28	R.NC*SSFLIK.R	0.89	-
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.QPAIMPGQSYGLEDGSC*SYK.D	0.893333333	0.753256705
P07203	GPX1 Glutathione peroxidase 1	GPX1	K.LITWSPVC*R.N	0.896666667	1.302576606
P51151	RAB9A Ras-related protein Rab-9A	RAB9A	R.QVSTEEAQAWC*R.D	0.896666667	-
Q9Y3U8	RPL36 60S ribosomal protein L36	RPL36	R.EVC*GFAPYER.R	0.9	-
O60831	PRAF2 PRA1 family protein 2	PRAF2	R.LAAPDPC*DPQR.W	0.9	-
Q9NXE4	SMPD4 Sphingomyelin phosphodiesterase 4	SMPD4	K.ASIQEC*ILPDSPLYHNK.V	0.9	-
Q96GQ7	DDX27 Probable ATP-dependent RNA helicase DDX27	DDX27	K.DIC*ACAATGTGK.T	0.9	1.0000777
P35221	CTNNA1 Catenin alpha-1	CTNNA1	K.AAAGEFADDPC*SSVK.R	0.9	0.916168761
Q8IX01	SUGP2 SURP and G-patch domain-containing protein 2	SUGP2	R.GADQKPTSADC*AVR.A	0.903333333	-
Q92667	AKAP1 A-kinase anchor protein 1, mitochondrial	AKAP1	R.ADPAIKEPLPVEDVC*PK.V	0.903333333	-
A3KMH1	VWA8 von Willebrand factor A domain-containing protein	VWA8	R.LLSQPC*ASDR.F	0.905	-

Q8IVF2	AHNAK2 Protein AHNAK2	AHNAK2	K.VDPEC*SVEDSK.L	0.905	0.912419509
P07355	ANXA2 Annexin A2	ANXA2	K.ALLYLC*GGDD.-	0.906666667	1.858546562
P32969	RPL9P9 60S ribosomal protein L9	RPL9P9	R.TIC*SHVQNMIK.G	0.906666667	1.134606007
P61225	RAP2B Ras-related protein Rap-2b	RAP2B	K.ALAEEWSC*PFMETSAK.N	0.906666667	-
Q03135	CAV1 Caveolin-1	CAV1	R.VYSIYVHTVC*DPLFEAVGK.I	0.91	-
Q9H845	ACAD9 Acyl-CoA dehydrogenase family member 9, mitochondr	ACAD9	R.GSNTC*EVHFENTK.I	0.91	1.534918147
Q9BVP2	GNL3 Guanine nucleotide-binding protein-like 3	GNL3	R.C*PQVEEAIVQSGQK.K	0.91	0.877819754
P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.GC*FQAEIVPVTTTVHDDK.G	0.91	-
P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	K.KLVIVGDGAC*GK.T	0.91	1.448484848
P62316	SNRPD2 Small nuclear ribonucleoprotein Sm D2	SNRPD2	K.NNTQVLINC*R.N	0.91	1.020478883
P10809	HSPD1 60 kDa heat shock protein, mitochondrial	HSPD1	K.C*EFQDAYVLLSEK.K	0.91	0.714611187
P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.DVNLRPEQLGDIC*VGNVLQPGAGAIMAR.I	0.92	-
Q7L5N7	LPCAT2 Lysophosphatidylcholine acyltransferase 2	LPCAT2	R.TTSGGEWPQILVFPEGTC*TNR.S	0.92	-
P14923	JUP Junction plakoglobin	JUP	R.VREAMC*PGVSGEDSSLLLATQVEGQATNLQR.L	0.92	0.503413445
Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.LEGDLTGPSVDVEVPDVELEC*PDAK.L	0.923333333	0.970800847
O43681	ASNA1 ATPase ASNA1	ASNA1	K.NQISPFISQMC*NMLGLGDMNADQLASK.L	0.925	-
P61247	RPS3A 40S ribosomal protein S3a	RPS3A	K.NC*LTNFHGMDLTR.D	0.925	1.217598621
Q8N9T8	KRI1 Protein KRI1 homolog	KRI1	R.LLGPTVMLGGC*EFSR.Q	0.93	-
Q6P1K8	GTF2H2D General transcription factor IIH subunit 2-like pr	GTF2H2D	R.AKYC*ELPVECK.I	0.93	-
Q96I24	FUBP3 Far upstream element-binding protein 3	FUBP3	R.SSGC*FPNMAAK.V	0.93	1.487645688
O94905	ERLIN2 Erlin-2	ERLIN2	K.ADAEC*YTAMK.I	0.933333333	1.013948504
P42765	ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	R.LC*GSGFQSIVNGCQEICVK.E	0.933333333	0.967278443
Q05086	UBE3A Ubiquitin-protein ligase E3A	UBE3A	K.VYEILELC*R.E	0.935	-
O00148	DDX39A ATP-dependent RNA helicase DDX39A	DDX39A	K.HFVLDEC*DK.M	0.935	1.065984335
Q14683	SMC1A Structural maintenance of chromosomes protein 1A	SMC1A	R.NSSAQAFLGPENPEEPYLDGINYNC*VAPGKR.F	0.935	-
Q8NBU5	ATAD1 ATPase family AAA domain-containing protein 1	ATAD1	K.SKDAAFQNVLTHVC*LD.-	0.935	-
P56589	PEX3 Peroxisomal biogenesis factor 3	PEX3	R.TC*NMTVLSMLPTLR.E	0.935	-
Q00765	REEP5 Receptor expression-enhancing protein 5	REEP5	K.NC*MTDLLAK.L	0.936666667	1.421833722
Q15149	PLEC Plectin	PLEC	R.LQLEAC*ETR.T	0.936666667	0.941752628
Q8TDN6	BRIX1 Ribosome biogenesis protein BRX1 homolog	BRIX1	R.HATAEEVEEEERDRIPGPVC*K.G	0.94	-
P62330	ARF6 ADP-ribosylation factor 6	ARF6	R.NWYVQPSC*ATSGDGLYEGLTWLTSNYK.S	0.94	-

P78346	RPP30 Ribonuclease P protein subunit p30	RPP30	K.AAVSTNC*R.A	0.943333333	-
O95363	FARS2 Phenylalanine--tRNA ligase, mitochondrial	FARS2	K.QFC*VSNINQK.V	0.943333333	-
P36578	RPL4 60S ribosomal protein L4	RPL4	R.SGQGAFGNMC*R.G	0.943333333	0.776301476
Q92520	FAM3C Protein FAM3C	FAM3C	R.DNWVFC*GGK.G	0.945	-
P78316	NOP14 Nucleolar protein 14	NOP14	K.C*NHPSLAEGNK.A	0.95	-
Q9Y2R4	DDX52 Probable ATP-dependent RNA helicase DDX52	DDX52	R.SVANVIQQAGC*PVPEYIK.G	0.95	-
P62280	RPS11 40S ribosomal protein S11	RPS11	K.C*PFTGNVSIR.G	0.95	-
Q9NXE4	SMPD4 Sphingomyelin phosphodiesterase 4	SMPD4	K.ADSINKPFAQQC*QDLVK.V	0.953333333	-
P42677	RPS27 40S ribosomal protein S27	RPS27	R.LTEGC*SFR.R	0.953333333	-
P26368	U2AF2 Splicing factor U2AF 65 kDa subunit	U2AF2	K.SIEIPRPVDGVEVPGC*GK.I	0.955	1.26037296
Q9H845	ACAD9 Acyl-CoA dehydrogenase family member 9, mitochondr	ACAD9	R.AYIC*AHPLDR.T	0.955	1.534918147
Q96I24	FUBP3 Far upstream element-binding protein 3	FUBP3	K.IQIASESSGIPERPC*VLTGTPESIEQAK.R	0.955	1.487645688
P62913	RPL11 60S ribosomal protein L11	RPL11	K.LC*LNICVGESGDR.L	0.955	1.317300324
Q96AG4	LRRC59 Leucine-rich repeat-containing protein 59	LRRC59	K.VAGDC*LDEK.Q	0.96	1.851088248
P62241	RPS8 40S ribosomal protein S8	RPS8	R.LDVGNFSWGSEC*C*TR.K	0.963333333	1.120108244
P14618	PKM Pyruvate kinase isozymes M1/M2	PKM	R.NTGIIC*TIGPASR.S	0.963333333	1.042960105
Q9NYH9	UTP6 U3 small nucleolar RNA-associated protein 6 homolo	UTP6	K.EQESC*NMANIR.E	0.966666667	-
Q8N1F7	NUP93 Nuclear pore complex protein Nup93	NUP93	R.C*GDLLAASQVVNR.A	0.97	-
Q9BU23	LMF2 Lipase maturation factor 2	LMF2	K.DSGAASEQATAAPNPC*SSSSR.T	0.97	-
P62330	ARF6 ADP-ribosylation factor 6	ARF6	R.HYYTGTQGLIFVVDC*ADR.D	0.97	-
O00212	RHOD Rho-related GTP-binding protein RhoD	RHOD	K.VVLVGDGGC*GK.T	0.97	-
Q6P4A7	SFXN4 Sideroflexin-4	SFXN4	R.SYTC*KPLER.S	0.97	-
O00116	AGPS Alkyldihydroxyacetonephosphate synthase, peroxisom	AGPS	K.YGSVAFPNFEQGVAC*LR.E	0.97	-
P82933	MRPS9 28S ribosomal protein S9, mitochondrial	MRPS9	K.LLTSQC*GAAEEEFVQR.F	0.97	0.700526038
Q14137	BOP1 Ribosome biogenesis protein BOP1	BOP1	R.DLQPFPTC*QALVYR.G	0.973333333	-
Q9Y6I9	TEX264 Testis-expressed sequence 264 protein	TEX264	R.LFTESC*SISPK.L	0.973333333	-
Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.ADIDVSGPKVDVEC*PDVNIEGPEGK.W	0.973333333	0.970800847
P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.SC*QFVAVR.R	0.975	-
P51553	IDH3G Isocitrate dehydrogenase	IDH3G	R.TSLDLYANVIHC*K.S	0.975	0.611421911
Q99797	MIPEP Mitochondrial intermediate peptidase	MIPEP	R.ACSTPPGPQTVLIFDELSDSLC*R.V	0.976666667	-
Q96N66	MBOAT7 Lysophospholipid acyltransferase 7	MBOAT7	R.NIDC*YSTDFC*VR.V	0.98	-

P32780	GTF2H1 General transcription factor IIH subunit 1	GTF2H1	K.DLFAEC*AK.I	0.98	-
P56192	MARS Methionine--tRNA ligase, cytoplasmic	MARS	R.LFVSDGVPGC*LPVLAAAGR.A	0.98	-
P62241	RPS8 40S ribosomal protein S8	RPS8	K.NC*IVLIDSTPYR.Q	0.98	1.120108244
Q96TC7	FAM82A2 Regulator of microtubule dynamics protein 3	FAM82A2	R.C*HMEENQR.V	0.983333333	-
Q15149	PLEC Plectin	PLEC	K.AFC*GFEDPR.T	0.983333333	0.941752628
P02795	MT2A Metallothionein-2	MT2A	K.CAQGCIC*K.G	0.985	-
O94901	SUN1 SUN domain-containing protein 1	SUN1	R.C*SETYETK.T	0.985	-
P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.C*VVVGDGAVGK.T	0.99	-
Q6YN16	HSDL2 Hydroxysteroid dehydrogenase-like protein 2	HSDL2	R.LAGC*TVFITGASR.G	0.99	1.514803204
P84095	RHOG Rho-related GTP-binding protein RhoG	RHOG	R.YLEC*SALQQDGVK.E	0.99	-
Q99959	PKP2 Plakophilin-2	PKP2	K.SIGC*FGSR.S	0.99	-
Q9BQG0	MYBBP1A Myb-binding protein 1A	MYBBP1A	K.AGTDPSHMPTGPQAASC*LDLNLVTR.V	0.99	0.855089355
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.GANDFMC*DEMER.S	0.993333333	1.079708223
P62249	RPS16 40S ribosomal protein S16	RPS16	K.TATAVAHC*K.R	0.996666667	-
O43172	PRPF4 U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	K.DVNLASC*AADGSVK.L	0.996666667	-
P33240	CSTF2 Cleavage stimulation factor subunit 2	CSTF2	K.LC*VQNSPQEAR.N	0.996666667	-
Q99829	CPNE1 Copine-1	CPNE1	R.VRNC*SSPEFSK.T	1	-
P62280	RPS11 40S ribosomal protein S11	RPS11	R.DVQIGDIVTVGEC*RPLSK.T	1.003333333	-
O60504	SORBS3 Vinexin	SORBS3	R.LC*DDGPQLPTSPR.L	1.005	-
C9J2C7	NT5C1B-RDH14 Protein NT5C1B-RDH14	NT5C1B-RDH14	R.LDVLINNAGIFQC*PYMK.T	1.005	-
A0FGR8	ESYT2 Extended synaptotagmin-2	ESYT2	R.AC*DLPAWVHFPDTER.A	1.005	1.078912467
P32322	PYCR1 Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	R.C*MTNTPVVVR.E	1.006666667	-
Q9Y3T9	NOC2L Nucleolar complex protein 2 homolog	NOC2L	K.VQENSAYIC*SR.R	1.01	-
Q9NVH0	EXD2 Exonuclease 3-5 domain-containing protein 2	EXD2	R.SELEDFPVLGIDC*EWVNLEGK.A	1.01	-
P35250	RFC2 Replication factor C subunit 2	RFC2	K.TTSILC*LAR.A	1.01	-
Q9BS26	ERP44 Endoplasmic reticulum resident protein 44	ERP44	R.VDC*DQHSDIAQR.Y	1.01	2.499222999
Q5SWX8	ODR4 Protein odr-4 homolog	ODR4	R.STATVQIC*SGSVNLK.G	1.013333333	-
P46782	RPS5 40S ribosomal protein S5	RPS5	K.AQC*PIVER.L	1.013333333	1.141043503
P01112	HRAS GTPase HRas	HRAS	R.VKDSDDVPMVLVGNKC*DLAAR.T	1.015	2.222121301
O94874	UFL1 E3 UFM1-protein ligase 1	UFL1	K.FINDC*TELFR.E	1.015	-
O43772	SLC25A20 Mitochondrial carnitine/acylcarnitine carrier prot	SLC25A20	K.YTGTLDC*AK.K	1.015	-

Q06323	PSME1 Proteasome activator complex subunit 1	PSME1	K.VDVFREDLC*TK.T	1.02	-
Q9Y3A4	RRP7A Ribosomal RNA-processing protein 7 homolog A	RRP7A	R.LLSTC*GLVQSVELQEKPDLAESPK.E	1.02	-
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	K.ILATGANVILTTGGIDDMC*LK.Y	1.023333333	1.079708223
Q9BQG0	MYBBP1A Myb-binding protein 1A	MYBBP1A	K.GNTAEGC*VHETQEK.Q	1.023333333	0.855089355
Q8N5K1	CISD2 CDGSH iron-sulfur domain-containing protein 2	CISD2	K.VVNEINIEDLC*LTK.A	1.026666667	-
Q15149	PLEC Plectin	PLEC	R.LC*FEGLR.S	1.026666667	0.941752628
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GC*DVVVIPAGVPR.K	1.026666667	0.706639338
P34932	HSPA4 Heat shock 70 kDa protein 4	HSPA4	K.FLEMC*NDLLAR.V	1.03	-
Q14839	CHD4 Chromodomain-helicase-DNA-binding protein 4	CHD4	K.STAPETAIEC*TQAPAPASEDEK.V	1.03	-
P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.AHEILPNLVCC*SAK.N	1.03	-
P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	K.C*FIVGADNVGSK.Q	1.03	0.994331467
P56182	RRP1 Ribosomal RNA processing protein 1 homolog A	RRP1	K.FIDPFC*R.I	1.035	-
P37198	NUP62 Nuclear pore glycoprotein p62	NUP62	K.DIIEHLNTSGAPADTSDPLQQIC*K.I	1.035	0.80577392
Q8IWA0	WDR75 WD repeat-containing protein 75	WDR75	K.INMPHEDC*ITALCFCNAEK.S	1.04	-
P83731	RPL24 60S ribosomal protein L24	RPL24	K.C*ESAFLSK.R	1.04	1.287567988
P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	K.DETVSDC*SPHIANIGR.L	1.043333333	1.398534416
P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	R.QC*SSGLQAVASIAGGIR.N	1.045	-
Q14690	PDCD11 Protein RRP5 homolog	PDCD11	R.LSC*QNLGAVLDDVPVQGFFK.K	1.045	1.177203065
P35221	CTNNA1 Catenin alpha-1	CTNNA1	R.TIADHCPDSAC*K.Q	1.045	0.916168761
P60981	DSTN Destrin	DSTN	K.C*STPEEIKK.R	1.046666667	-
Q06330	RBPJ Recombining binding protein suppressor of hairless	RBPJ	R.IIQFQATPC*PK.E	1.046666667	-
Q9Y324	FCF1 rRNA-processing protein FCF1 homolog	FCF1	K.AKLDLVQSMMDC*LYAK.C	1.05	-
Q9NP64	ZCCHC17 Nucleolar protein of 40 kDa	ZCCHC17	R.THMSSC*R.V	1.05	-
Reverse_P09488	GSTM1 Glutathione S-transferase Mu 1	GSTM1	K.LNPFADLC*K.P	1.05	-
P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	K.NC*GC*LGASPNLEQLQEENLK.L	1.05	-
P07814	EPRS Bifunctional glutamate/proline--tRNA ligase	EPRS	K.LNQWC*NVVR.W	1.05	-
P00558	PGK1 Phosphoglycerate kinase 1	PGK1	R.GCITIIGGGDTATC*C*AK.W	1.05	2.060742706
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.VEQLFQVMNGILAQDSAC*SQR.A	1.05	0.995679161
P67936	TPM4 Tropomyosin alpha-4 chain	TPM4	K.EENVGLHQTLDQTLNELNC*I.-	1.05	0.673150604
O75694	NUP155 Nuclear pore complex protein Nup155	NUP155	K.ISNQVDLSNVC*AQYR.Q	1.053333333	-
P63010	AP2B1 AP-2 complex subunit beta	AP2B1	K.TAAVC*VAK.L	1.053333333	1.258272379

Q9BTA9	WAC WW domain-containing adapter protein with coiled-c	WAC	R.STC*SLTPALAAHFSENLIK.H	1.055	-
Q92989	CLP1 Polyribonucleotide 5-hydroxyl-kinase Clp1	CLP1	K.VGAPTIPDSC*LPLGMSQEDNQLK.L	1.055	-
P09382	LGALS1 Galectin-1	LGALS1	R.EAVFPFQPGSVAEVC*ITFDQANLTVK.L	1.055	2.964675937
Q9ULV4	CORO1C Coronin-1C	CORO1C	R.NGSLIC*TASK.D	1.055	2.340713055
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.SLHDALC*VVK.R	1.056666667	1.079708223
Q9P2E9	RRBP1 Ribosome-binding protein 1	RRBP1	R.SKC*EELSGLHGQLQEAR.A	1.065	1.595024516
P51398	DAP3 28S ribosomal protein S29, mitochondrial	DAP3	K.TFSEAC*LMVR.K	1.065	0.785547786
Q8IVF2	AHNAK2 Protein AHNAK2	AHNAK2	R.LC*EGTPQEGGLR.A	1.066666667	0.912419509
P60900	PSMA6 Proteasome subunit alpha type-6	PSMA6	R.GKDC*AVIVTQK.K	1.07	3.316180371
O43390	HNRNPR Heterogeneous nuclear ribonucleoprotein R	HNRNPR	K.SAFLC*GVMK.T	1.073333333	0.891887933
P51149	RAB7A Ras-related protein Rab-7a	RAB7A	K.RAQAWC*YSK.N	1.073333333	2.25383365
Q9P2I0	CPSF2 Cleavage and polyadenylation specificity factor su	CPSF2	R.IGLEGC*LCQDFYR.I	1.075	-
Q9HB40	SCPEP1 Retinoid-inducible serine carboxypeptidase	SCPEP1	K.TFFSC*HK.E	1.075	-
Q13637	RAB32 Ras-related protein Rab-32	RAB32	K.DSSQSPSQVDQFC*K.E	1.08	-
Q9Y6I9	TEX264 Testis-expressed sequence 264 protein	TEX264	R.KLC*AYPR.L	1.08	-
Q06136	KDSR 3-ketodihydrosphingosine reductase	KDSR	K.LGPVDMLVNC*AGMAVSGK.F	1.08	-
Q15370	TCEB2 Transcription elongation factor B polypeptide 2	TCEB2	R.ADDTFEALC*IEPFSSPPELPDVMKPQDSGSSANEQAVQ.-	1.08	-
P17987	TCP1 T-complex protein 1 subunit alpha	TCP1	R.IC*DDELILIK.N	1.08	1.079708223
P42166	TMPO Lamina-associated polypeptide 2, isoform alpha	TMPO	K.SGIQPLC*PER.S	1.083333333	0.532789433
Q9UJX3	ANAPC7 Anaphase-promoting complex subunit 7	ANAPC7	R.NALANQSDC*VLHR.I	1.085	-
Q96SK2	TMEM209 Transmembrane protein 209	TMEM209	R.MGC*PELQIGEASITSLK.Q	1.085	-
O15270	SPTLC2 Serine palmitoyltransferase 2	SPTLC2	R.ANGC*VANGEVR.N	1.085	-
P14923	JUP Junction plakoglobin	JUP	R.LVQNC*LWTLR.N	1.085	0.503413445
P62917	RPL8 60S ribosomal protein L8	RPL8	K.AQLNIGNVLPVGTMPEGTIVC*CLEEKPGDR.G	1.086666667	1.233430682
Q9NXE4	SMPD4 Sphingomyelin phosphodiesterase 4	SMPD4	K.SHVYSLEGQDC*K.Y	1.09	-
Q9HD45	TM9SF3 Transmembrane 9 superfamily member 3	TM9SF3	R.NLSGQPNFPC*R.V	1.09	-
O43818	RRP9 U3 small nucleolar RNA-interacting protein 2	RRP9	R.EC*CVTAGGR.D	1.09	-
P50991	CCT4 T-complex protein 1 subunit delta	CCT4	R.TLSGMESYC*VR.A	1.09	1.106498674
Q02218	OGDH 2-oxoglutarate dehydrogenase, mitochondrial	OGDH	R.VVNAPIFHVNSDDPEAVMYVC*K.V	1.09	0.896915218
P62857	RPS28 40S ribosomal protein S28	RPS28	R.TGSQGQC*TQVR.V	1.093333333	-
Q04941	PLP2 Proteolipid protein 2	PLP2	R.LSAPGC*WAACTNFSR.T	1.093333333	-

Q13769	THOC5 THO complex subunit 5 homolog	THOC5	K.YREC*LSNK.E	1.095	-
P04632	CAPNS1 Calpain small subunit 1	CAPNS1	R.YSDESGNMDFDNFISC*LVR.L	1.095	-
Q8N4Q0	ZADH2 Zinc-binding alcohol dehydrogenase domain-containi	ZADH2	R.DC*PVPLPGDGDLLVR.N	1.1	-
Q9BQG0	MYBBP1A Myb-binding protein 1A	MYBBP1A	R.SC*FEDPEWK.Q	1.1	0.855089355
Q14684	RRP1B Ribosomal RNA processing protein 1 homolog B	RRP1B	K.EVLC*PESQSPNGVR.F	1.103333333	-
Q8NC56	LEMD2 LEM domain-containing protein 2	LEMD2	R.KTDEFC*QAK.Q	1.105	-
P62306	SNRPF Small nuclear ribonucleoprotein F	SNRPF	R.C*NNVLYIR.G	1.11	-
P13639	EEF2 Elongation factor 2	EEF2	K.STLTDSLVC*K.A	1.11	1.141161393
E9PLN8	Uncharacterized protein	Uncharacterized	R.ALC*DVGTAISCSR.V	1.11	-
P53582	METAP1 Methionine aminopeptidase 1	METAP1	R.VCETDGC*SSEAK.L	1.11	-
O00194	RAB27B Ras-related protein Rab-27B	RAB27B	R.NWMSQLQANAYC*ENPDIVLIGNK.A	1.11	-
Q5JTH9	RRP12 RRP12-like protein	RRP12	K.SSGTFLSGLSDC*TNVTFSK.V	1.113333333	-
P0C7P0	CISD3 CDGSH iron-sulfur domain-containing protein 3, mit	CISD3	R.MVALC*TCK.A	1.115	-
Q96H72	SLC39A13 Zinc transporter ZIP13	SLC39A13	R.GTATAC*R.L	1.116666667	-
P60866	RPS20 40S ribosomal protein S20	RPS20	K.VC*ADLIR.G	1.12	0.980340094
P22061	PCMT1 Protein-L-isoaspartate(D-aspartate) O-methyltransf	PCMT1	K.ALDVGSGSGILTAC*FAR.M	1.123333333	-
P38606	ATP6V1A V-type proton ATPase catalytic subunit A	ATP6V1A	R.VLDALFPCVQGGTTAIPGAFGC*GK.T	1.125	-
P47756	CAPZB F-actin-capping protein subunit beta	CAPZB	K.GC*WDSIHVVEVQEK.S	1.125	1.398534416
Q8WVV9	HNRPLL Heterogeneous nuclear ribonucleoprotein L-like	HNRPLL	K.LC*FSTSSHL.-	1.126666667	-
Q02487	DSC2 Desmocollin-2	DSC2	R.GGHTEVDNC*R.Y	1.126666667	-
Q9NX20	MRPL16 39S ribosomal protein L16, mitochondrial	MRPL16	R.C*EFEEVQGFLDQVAHK.L	1.126666667	-
Q96EY8	MMAB Cob(I)yrinic acid a,c-diamide adenosyltransferase,	MMAB	K.IQCTLQDVGSALATPC*SSAR.E	1.13	-
Q7L014	DDX46 Probable ATP-dependent RNA helicase DDX46	DDX46	R.GAEIIVC*TPGR.M	1.13	-
Q92685	ALG3 Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosy	ALG3	R.SGSAAQAEGLC*K.Q	1.13	-
P50914	RPL14 60S ribosomal protein L14	RPL14	K.C*MQLTDFILK.F	1.13	1.212745492
P60903	S100A10 Protein S100-A10	S100A10	K.DLDQC*R.D	1.13	-
Q15005	SPCS2 Signal peptidase complex subunit 2	SPCS2	R.SGGSGGC*SGAGGASNC*GTGSGR.S	1.13	1.449880771
Q5JTH9	RRP12 RRP12-like protein	RRP12	K.GC*QAEADR.A	1.133333333	-
Q9BW61	DDA1 DET1- and DDB1-associated protein 1	DDA1	R.FHADSVC*K.A	1.135	-
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	K.INQVFHGSC*ITEGNELTK.T	1.135	0.995679161

Q32NC0	C18orf21 UPF0711 protein C18orf21	C18orf21	R.GLHDSC*PGQAR.Y	1.136666667	-
P19338	NCL Nucleolin	NCL	K.EALNSC*NKR.E	1.14	1.275929052
Q08257	CRYZ Quinone oxidoreductase	CRYZ	K.AGESVLVHGASGGVGLAAC*QIAR.A	1.14	1.137665782
Q52LJ0	FAM98B Protein FAM98B	FAM98B	K.AAEGGLSSPEFSELC*IWLGSQIK.S	1.14	-
Q15149	PLEC Plectin	PLEC	K.YLTC*PK.T	1.14	0.941752628
P01112	HRAS GTPase HRas	HRAS	R.TGEGFLC*VFAINNTK.S	1.143333333	2.222121301
Q9HCY8	S100A14 Protein S100-A14	S100A14	R.DLVTQQLPHLMPSNC*GLEEK.I	1.143333333	1.774753726
Q9Y4P3	TBL2 Transducin beta-like protein 2	TBL2	R.FLASC*GDR.A	1.145	-
P30044	PRDX5 Peroxiredoxin-5, mitochondrial	PRDX5	K.ALNVEPDGTGLTC*SLAPNIISQL.-	1.146666667	1.115373005
Q16643	DBN1 Drebrin	DBN1	K.APPPVFYNKPPEIDITC*WDADPVPEEEEGFEGGD.-	1.15	5.071865427
P62829	RPL23 60S ribosomal protein L23	RPL23	K.EC*ADLWPR.I	1.15	1.254643696
Q96AG3	SLC25A46 Solute carrier family 25 member 46	SLC25A46	R.DNTGILEC*VK.E	1.15	-
P26599	PTBP1 Polypyrimidine tract-binding protein 1	PTBP1	K.LSLDGQNIYNAC*CTLR.I	1.15	0.674151774
P00505	GOT2 Aspartate aminotransferase, mitochondrial	GOT2	R.VGAFTMVC*K.D	1.153333333	0.907056417
Q9UJX3	ANAPC7 Anaphase-promoting complex subunit 7	ANAPC7	K.VRPSTGNSASTPQSQC*LPSEIEVK.Y	1.156666667	-
Q9NPD3	EXOSC4 Exosome complex component RRP41	EXOSC4	K.SC*EMGLQLR.Q	1.16	-
Q9NX40	OCIAD1 OCIA domain-containing protein 1	OCIAD1	R.VFAEC*NDESFWFR.S	1.165	-
P61026	RAB10 Ras-related protein Rab-10	RAB10	K.C*DMDDKR.V	1.166666667	2.031608749
Q96CS3	FAF2 FAS-associated factor 2	FAF2	R.KLEC*LPPEPSPDDPESVK.I	1.166666667	1.721212121
Q9UNE7	STUB1 E3 ubiquitin-protein ligase CHIP	STUB1	R.KYPEAAAC*YGR.A	1.17	-
P54136	RARS Arginine--tRNA ligase, cytoplasmic	RARS	K.NC*GCLGASPNLEQLQEENLK.L	1.17	-
Q9HCY8	S100A14 Protein S100-A14	S100A14	K.IANLGSC*NDSK.L	1.17	1.774753726
Q14690	PDCD11 Protein RRP5 homolog	PDCD11	R.ALEC*LPSKEHVDVIAK.F	1.17	1.177203065
P60468	SEC61B Protein transport protein Sec61 subunit beta	SEC61B	K.NASC*GTR.S	1.17	-
P35579	MYH9 Myosin-9	MYH9	R.C*NGVLEGIR.I	1.173333333	1.03316543
Q15269	PWP2 Periodic tryptophan protein 2 homolog	PWP2	R.GNLNFTC*DGNSVISPVGNR.V	1.18	-
Q9NYH9	UTP6 U3 small nucleolar RNA-associated protein 6 homolo	UTP6	K.LLSEC*QYK.Q	1.18	-
O00541	PES1 Pescadillo homolog	PES1	R.C*YVQPQWVFDSVNAR.L	1.18	-
Q15365	PCBP1 Poly(rC)-binding protein 1	PCBP1	R.LVVPATQC*GSLIGK.G	1.183333333	1.057454295
P02538	KRT6A Keratin, type II cytoskeletal 6A	KRT6A	K.KQC*ANLQAAIADAEQR.G	1.183333333	1.046728112
Q9UDY2	TJP2 Tight junction protein ZO-2	TJP2	R.SHFEC*EK.E	1.185	-
P35914	HMGCL Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL	K.VAQATC*K.L	1.186666667	-

P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	K.YLEC*SALTQR.G	1.19	-
O15446	CD3EAP DNA-directed RNA polymerase I subunit RPA34	CD3EAP	R.VLSSC*PQAGEATLLAPSTEAGGGLTCASAPQGTLR.I	1.19	-
P15880	RPS2 40S ribosomal protein S2	RPS2	R.GC*TATLGNFAK.A	1.193333333	1.289446186
O95573	ACSL3 Long-chain-fatty-acid--CoA ligase 3	ACSL3	R.SVNSLDGLASVLYPGC*DTLDK.V	1.193333333	-
P60866	RPS20 40S ribosomal protein S20	RPS20	K.TPC*GEGSK.T	1.193333333	0.980340094
Q00610	CLTC Clathrin heavy chain 1	CLTC	R.AHIAQLC*EK.A	1.195	1.826780627
P14324	FDPS Farnesyl pyrophosphate synthase	FDPS	R.GQICWYQKPGVGLDAINDANLLEAC*IYR.L	1.2	-
O00566	MPHOSPH10 U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	K.ATGRPEC*FLTIQEGLASK.F	1.2	-
Q9NRX1	PNO1 RNA-binding protein PNO1	PNO1	R.TAIC*NLILGNPPSK.V	1.2	-
Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.EFEFSQLPLKVEFLEC*SAK.G	1.203333333	1.744055944
Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.GIEELFLDLC*K.R	1.205	-
P39023	RPL3 60S ribosomal protein L3	RPL3	K.TVFAEHISDEC*K.R	1.205	1.564851879
O00541	PES1 Pescadillo homolog	PES1	K.AGEGTYALDSESC*MEK.L	1.206666667	-
O95573	ACSL3 Long-chain-fatty-acid--CoA ligase 3	ACSL3	R.LLLC*GGAPLSATTQR.F	1.215	-
P00338	LDHA L-lactate dehydrogenase A chain	LDHA	R.VIGSGC*NLDSAR.F	1.216666667	-
Q15149	PLEC Plectin	PLEC	R.C*DNFTSSWR.D	1.216666667	0.941752628
Q8NFW8	CMAS N-acylneuraminate cytidylyltransferase	CMAS	R.VGLSGAPADAC*STAQK.A	1.22	-
P07602	PSAP Proactivator polypeptide	PSAP	R.GSAVWC*QNVK.T	1.22	0.800459949
P37802	TAGLN2 Transgelin-2	TAGLN2	K.DGTVLC*ELINALYPEGQAPVK.K	1.22	3.624708625
Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	K.FSIQTMC*PIEGEGNIAR.F	1.223333333	-
Q9NVN8	GNL3L Guanine nucleotide-binding protein-like 3-like pro	GNL3L	R.AC*SVGAVPGITK.F	1.225	-
Q9UJX2	CDC23 Cell division cycle protein 23 homolog	CDC23	K.LHEQLTESEQAAQC*YIK.Y	1.225	-
O75691	UTP20 Small subunit processome component 20 homolog	UTP20	K.TNC*CESSEQIKR.L	1.225	-
Q53S33	BOLA3 BolA-like protein 3	BOLA3	K.VTDISGGC*GAMYEIK.I	1.225	-
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	K.C*LMDQATDPNILGR.T	1.225	0.995679161
Q92575	UBXN4 UBX domain-containing protein 4	UBXN4	K.SETSVANGSQSESSVSTPSASFEPNNTC*ENSQSR.N	1.23	-
Q9NX70	MED29 Mediator of RNA polymerase II transcription subuni	MED29	K.DIHTALLDC*ANK.V	1.23	-
P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.DKMC*SMVK.K	1.23	1.217598621
P07203	GPX1 Glutathione peroxidase 1	GPX1	R.FQTIDIEPDIEALLSQGPSC*A.-	1.233333333	1.302576606
P05388	RPLP0 60S acidic ribosomal protein P0	RPLP0	R.AGAIAPC*EVTVPAQNTGLGPEK.T	1.236666667	0.994331467

Q09666	AHNAK Neuroblast differentiation-associated protein AHNA	AHNAK	K.SSGC*DVNLPGVNVK.L	1.24	0.970800847
Q16851	UGP2 UTP--glucose-1-phosphate uridylyltransferase	UGP2	K.LNGGLGTSMGC*K.G	1.243333333	-
P22307	SCP2 Non-specific lipid-transfer protein	SCP2	K.ALADAQIPYSAVDQACVGYVFGDSTC*GQR.A	1.246666667	1.292336272
P50914	RPL14 60S ribosomal protein L14	RPL14	R.ALVDGPC*TQVR.R	1.25	1.212745492
O94906	PRPF6 Pre-mRNA-processing factor 6	PRPF6	R.AAQDLC*EEALR.H	1.255	-
Q9H8H0	NOL11 Nucleolar protein 11	NOL11	K.ESTSC*PVVQKR.A	1.255	-
P61247	RPS3A 40S ribosomal protein S3a	RPS3A	K.AC*QSIYPLHDVFVR.K	1.255	1.217598621
Q14574	DSC3 Desmocollin-3	DSC3	K.GGNQTLESC*R.G	1.256666667	-
P14923	JUP Junction plakoglobin	JUP	R.AGDKDDITEPAVC*ALR.H	1.26	0.503413445
P09211	GSTP1 Glutathione S-transferase P	GSTP1	K.ASC*LYGQLPK.F	1.263333333	1.650504157
Q16630	CPSF6 Cleavage and polyadenylation specificity factor su	CPSF6	R.ELHGQNPVVTPC*NK.Q	1.263333333	1.098408488
Q9Y4W2	LAS1L Ribosomal biogenesis protein LAS1L	LAS1L	R.LFNC*SASLDWPR.M	1.265	-
J3KR12	Uncharacterized protein	Uncharacterized	K.MLLDSEQHPC*QLK.D	1.266666667	-
P09110	ACAA1 3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	K.ARDC*LIPMGITSENVAER.F	1.27	-
P21964	COMT Catechol O-methyltransferase	COMT	R.LITIEINPDC*AAITQR.M	1.273333333	-
Q01780	EXOSC10 Exosome component 10	EXOSC10	R.SFPGFQAFC*ETQGDR.L	1.273333333	-
P0CW22	RPS17L 40S ribosomal protein S17-like	RPS17L	K.RVC*EEIAIIPSK.K	1.273333333	-
Q86Y07	VRK2 Serine/threonine-protein kinase VRK2	VRK2	R.SAESC*ATWK.V	1.273333333	-
O60313	OPA1 Dynamin-like 120 kDa protein, mitochondrial	OPA1	K.EGC*TVSPETISLNVK.G	1.273333333	1.450428244
Q12849	GRSF1 G-rich sequence factor 1	GRSF1	R.YIELFLNSC*PK.G	1.275	-
Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	R.YNFFTGC*PK.A	1.276666667	1.164058355
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.ASLNGADIYSGC*C*TLK.I	1.276666667	0.753256705
Q5TGZ0	MINOS1 Mitochondrial inner membrane organizing system pro	MINOS1	R.C*LADAVVK.I	1.28	-
Q99575	POP1 Ribonucleases P/MRP protein subunit POP1	POP1	K.LGTLAPFCC*PWEQLTQDWESR.V	1.28	-
Q9ULV4	CORO1C Coronin-1C	CORO1C	K.SIKDTIC*NQDER.I	1.28	2.340713055
P23497	SP100 Nuclear autoantigen Sp-100	SP100	K.MFEDSQDSC*R.N	1.283333333	-
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.GYGLFAGPC*K.V	1.283333333	0.995679161
Q9C0I4	THSD7B Thrombospondin type-1 domain-containing protein 7B	THSD7B	K.PYNGGRPC*PK.L	1.285	-
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.YWLC*AATGPSIK.I	1.285	1.206366048
P25398	RPS12 40S ribosomal protein S12	RPS12	K.KLGEWVGLC*K.I	1.29	-

Q15149	PLEC Plectin	PLEC	K.LQMEAGLC*EEQLNQADALLQSDVR.L	1.29	0.941752628
Q99832	CCT7 T-complex protein 1 subunit eta	CCT7	K.C*AMTALSSK.L	1.295	1.164058355
Q96I51	WBSCR16 Williams-Beuren syndrome chromosomal region 16 pro	WBSCR16	R.VLQVSC*GR.A	1.3	-
P41091	EIF2S3 Eukaryotic translation initiation factor 2 subunit	EIF2S3	R.SC*GSSTPDEFPTDIPGTK.G	1.3	-
P62851	RPS25 40S ribosomal protein S25	RPS25	K.ATYDKLC*K.E	1.3	1.301856764
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.SQGC*SEQVLTVLK.T	1.3	0.995679161
A6NJ78	METTL15 Probable methyltransferase-like protein 15	METTL15	K.AGVQPGTFDGVLMDLGC*SSMQLDTPER.G	1.305	-
P61158	ACTR3 Actin-related protein 3	ACTR3	K.LGYAGNTEPQFIIPSC*IAIK.E	1.305	-
P02538	KRT6A Keratin, type II cytoskeletal 6A	KRT6A	R.ISIGGGSC*AISGGYGSR.A	1.306666667	1.046728112
P45880	VDAC2 Voltage-dependent anion-selective channel protein	VDAC2	K.VC*EDLDTSVNLAWTSGTNCTR.F	1.306666667	0.943164626
Q15149	PLEC Plectin	PLEC	R.HGEKVEEC*QR.F	1.306666667	0.941752628
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.LAAVVSAC*K.Q	1.31	0.995679161
Q99536	VAT1 Synaptic vesicle membrane protein VAT-1 homolog	VAT1	R.AC*GLNFADLMAR.Q	1.315	-
Q96CS3	FAF2 FAS-associated factor 2	FAF2	R.NTLC*APEVISLINTR.M	1.32	1.721212121
Q8IVF2	AHNAK2 Protein AHNAK2	AHNAK2	R.GC*GLGDVPVSQPCGEGIAPTPEDPLQPSCR.K	1.325	0.912419509
Q8TDN6	BRIX1 Ribosome biogenesis protein BRX1 homolog	BRIX1	K.MTGNC*LK.G	1.326666667	-
O60361	NME2P1 Putative nucleoside diphosphate kinase	NME2P1	R.GDFC*IQVGR.N	1.34	-
Q9Y4P3	TBL2 Transducin beta-like protein 2	TBL2	R.SGRPAC*QK.A	1.34	-
Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	K.KSSGEIVYC*GQVFEK.S	1.34	-
P09382	LGALS1 Galectin-1	LGALS1	K.DSNNLC*LHFNPR.F	1.34	2.964675937
P62241	RPS8 40S ribosomal protein S8	RPS8	R.LDVGNFSWGSEC*CTR.K	1.34	1.120108244
P62888	RPL30 60S ribosomal protein L30	RPL30	K.YYRVC*TLAIIDPGDSDIIR.S	1.34	-
P62701	RPS4X 40S ribosomal protein S4, X isoform	RPS4X	K.FDTGNLC*MVTGGANLGR.I	1.35	1.483793729
Q08AG7	MZT1 Mitotic-spindle organizing protein 1	MZT1	R.LC*EQGINPEALSSVIK.E	1.355	-
P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	R.IIPGFMC*QGGDFTR.H	1.356666667	1.60441908
Q969H6	POP5 Ribonuclease P/MRP protein subunit POP5	POP5	R.SC*LLEEEEESGEEAAEAME.-	1.365	-
Q9UL03	INTS6 Integrator complex subunit 6	INTS6	R.SYSVC*SPR.M	1.365	-
Q9NY93	DDX56 Probable ATP-dependent RNA helicase DDX56	DDX56	R.QAQSMIQQLATYC*AR.D	1.365	-
P62888	RPL30 60S ribosomal protein L30	RPL30	K.LVILANNC*PALR.K	1.366666667	-

Q9NZJ7	MTCH1 Mitochondrial carrier homolog 1	MTCH1	R.RVSSGSC*FALE.-	1.37	-
P30153	PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa reg	PPP2R1A	R.LNIISNLDC*VNEVIGIR.Q	1.37	-
Q9UGP8	SEC63 Translocation protein SEC63 homolog	SEC63	K.EQSIC*AAEEQPAEDGQGETNK.N	1.375	-
Q9UHD8	SEPT9 Septin-9	43717	K.LTVIDTPGFGDHINNENC*WQPIMK.F	1.375	-
P30519	HMOX2 Heme oxygenase 2	HMOX2	K.C*PFYAAEQDKGALEGSSCPFR.T	1.375	2.088586127
Q9UHX1	PUF60 Poly(U)-binding-splicing factor PUF60	PUF60	R.ALAIMC*R.V	1.375	1.656366048
P08758	ANXA5 Annexin A5	ANXA5	K.ALLLLC*GEDD.-	1.376666667	2.600530504
P10588	NR2F6 Nuclear receptor subfamily 2 group F member 6	NR2F6	R.FGAGGGAAGAVLGIDNVC*ELAAR.L	1.38	-
P60174	TPI1 Triosephosphate isomerase	TPI1	K.VPADTEVVC*APPTAYIDFAR.Q	1.38	3.671618037
P78527	PRKDC DNA-dependent protein kinase catalytic subunit	PRKDC	R.APPC*EYKDWLTK.M	1.38	0.995679161
P25398	RPS12 40S ribosomal protein S12	RPS12	R.QAHLC*VLASNCDEPMYVK.L	1.385	-
Q9P2X0	DPM3 Dolichol-phosphate mannosyltransferase subunit 3	DPM3	R.VATFHDC*EDAAR.E	1.385	-
P60174	TPI1 Triosephosphate isomerase	TPI1	R.IIYGGSVTGATC*K.E	1.385	3.671618037
P23396	RPS3 40S ribosomal protein S3	RPS3	R.AC*YGVLR.F	1.386666667	1.258836821
Q9ULV4	CORO1C Coronin-1C	CORO1C	R.VTWDSSFC*AVNPR.F	1.39	2.340713055
Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	R.YC*ENKFNDK.H	1.393333333	-
Q9ULV4	CORO1C Coronin-1C	CORO1C	K.C*DLISIPK.K	1.395	2.340713055
Q9Y305	ACOT9 Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	K.SLEIC*HPQER.N	1.396666667	1.166572891
P40926	MDH2 Malate dehydrogenase, mitochondrial	MDH2	K.GYLGPEQLPDC*LK.G	1.4	0.706639338
Q99873	PRMT1 Protein arginine N-methyltransferase 1	PRMT1	K.VIGIEC*SSISDYAVK.I	1.4	-
O60264	SMARCA5 SWI/SNF-related matrix-associated actin-dependent	SMARCA5	K.ATNVC*TR.F	1.403333333	-
O60318	MCM3AP 80 kDa MCM3-associated protein	MCM3AP	R.STEC*AQEGR.I	1.405	-
Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	K.IWNVIYEENC*FKPQTIK.R	1.405	2.194330574
Q12931	TRAP1 Heat shock protein 75 kDa, mitochondrial	TRAP1	K.FEDRSPAAEC*LSEK.E	1.405	0.563923943
O95232	LUC7L3 Luc7-like protein 3	LUC7L3	R.SDLGPC*EK.I	1.406666667	-
P25398	RPS12 40S ribosomal protein S12	RPS12	K.VVGC*SCVVVK.D	1.413333333	-
P21964	COMT Catechol O-methyltransferase	COMT	K.IVDAVIQEHQPSVLLELGAYC*GYSAVR.M	1.415	-
P78346	RPP30 Ribonuclease P protein subunit p30	RPP30	R.LTIIVSDPSHC*NVLR.A	1.415	-
P50416	CPT1A Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	R.TLETANC*MSSQTK.N	1.416666667	-
Q9NRW3	APOBEC3C Probable DNA dC- dU-editing enzyme APOBEC-3C	APOBEC3C	R.LYYFQYPC*YQEGLR.S	1.416666667	-

P62424	RPL7A 60S ribosomal protein L7a	RPL7A	K.TC*TTVAFTQVNSEDKGALAK.L	1.416666667	1.408236208
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.LC*FSTAQHAS.-	1.416666667	0.753256705
O43929	ORC4 Origin recognition complex subunit 4	ORC4	K.YPNC*PTDVR.Q	1.42	-
Q14573	ITPR3 Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	K.LVC*DLITSTK.N	1.42	1.551669659
O94925	GLS Glutaminase kidney isoform, mitochondrial	GLS	K.FSPDLWGVSVC*TVDGQR.H	1.423333333	2.027619252
O95757	HSPA4L Heat shock 70 kDa protein 4L	HSPA4L	R.GC*ALQCAILSPAFK.V	1.43	-
P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.INISEGNC*PER.I	1.433333333	-
O00154	ACOT7 Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	R.HC*NSQNGER.C	1.433333333	4.269860408
P28074	PSMB5 Proteasome subunit beta type-5	PSMB5	K.VIEINPYLLGTMAGGAADC*SFWER.L	1.435	-
P09382	LGALS1 Galectin-1	LGALS1	R.FNAHGDANTIVC*NSK.D	1.436666667	2.964675937
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.AEPPQC*TSLAWSADGQTLFAGYTDNLVR.V	1.44	1.206366048
Q92597	NDRG1 Protein NDRG1	NDRG1	K.MADC*GGLPQISQPAK.L	1.443333333	-
Q6N075	MFSD5 Major facilitator superfamily domain-containing pr	MFSD5	R.AC*SNPSFLR.F	1.445	-
P50991	CCT4 T-complex protein 1 subunit delta	CCT4	K.ITGC*ASPGK.T	1.446666667	1.106498674
Q8NI36	WDR36 WD repeat-containing protein 36	WDR36	R.SLSPDC*GGSIEVMQSFLK.M	1.45	-
Q13155	AIMP2 Aminoacyl tRNA synthase complex-interacting multif	AIMP2	R.SC*ENLAPFNTALK.L	1.453333333	-
P16615	ATP2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase	ATP2A2	K.TGTLTTNQMSVC*R.M	1.453333333	1.828168511
Q8TC12	RDH11 Retinol dehydrogenase 11	RDH11	K.MLSSGVC*TSTVQLPGK.V	1.455	23.23551161
P56537	EIF6 Eukaryotic translation initiation factor 6	EIF6	R.ASFENNCEIGC*FAK.L	1.455	1.745776956
P50990	CCT8 T-complex protein 1 subunit theta	CCT8	K.IAVYSC*PFDGMITETK.G	1.46	-
Q9Y394	DHRS7 Dehydrogenase/reductase SDR family member 7	DHRS7	R.TELATYPGIIVSNIC*PGPVQSNIVENSLAGEVTK.T	1.46	2.574787664
O43264	ZW10 Centromere/kinetochore protein zw10 homolog	ZW10	R.LAPILC*DGTATFVDLVPGFR.R	1.465	-
Q9Y3A3	MOB4 MOB-like protein phocein	MOB4	R.HTLDGAAC*LLNSNK.Y	1.47	-
Q13123	IK Protein Red	IK	R.SKADC*PTMEAQTTLTTNDIVISK.L	1.475	-
Q99986	VRK1 Serine/threonine-protein kinase VRK1	VRK1	K.VGLPIGQGGFGC*IYLADMNSSESVGSDAPCVVK.V	1.475	-
P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YLAEVAC*GDDR.K	1.475	2.33273406
O95573	ACSL3 Long-chain-fatty-acid--CoA ligase 3	ACSL3	R.NTPLC*DSFVFR.K	1.476666667	-
O60313	OPA1 Dynamin-like 120 kDa protein, mitochondrial	OPA1	R.TQEQC*VHNETK.N	1.476666667	1.450428244
Q9NR30	DDX21 Nucleolar RNA helicase 2	DDX21	K.DSEDNPQTLLFSATC*PHWVFNVAK.K	1.48	1.764879565
Q13795	ARFRP1 ADP-ribosylation factor-related protein 1	ARFRP1	K.VVTSEALC*GVPVLVLANK.Q	1.483333333	-

P13646	KRT13 Keratin, type I cytoskeletal 13	KRT13	R.SEMEC*QNQEYK.M	1.483333333	1.036224312
O43169	CYB5B Cytochrome b5 type B	CYB5B	K.DPSKNDTC*K.S	1.485	1.606702748
P26641	EEF1G Elongation factor 1-gamma	EEF1G	K.AAAPAPEEEMDEC*EQALAAEPK.A	1.486666667	-
P23396	RPS3 40S ribosomal protein S3	RPS3	K.GC*EVVVSGK.L	1.486666667	1.258836821
Q969V5	MUL1 Mitochondrial ubiquitin ligase activator of NFKB 1	MUL1	R.TTHLWNDC*SK.I	1.49	-
O60716	CTNND1 Catenin delta-1	CTNND1	R.YQEAAPNVANNTGPHAASC*FGAK.K	1.49	0.811250435
Q13636	RAB31 Ras-related protein Rab-31	RAB31	K.VC*LLGDTGVGK.S	1.49	-
Q9UGP8	SEC63 Translocation protein SEC63 homolog	SEC63	R.APTLASLENC*MK.L	1.5	-
O60716	CTNND1 Catenin delta-1	CTNND1	K.SNAAAYLQHLC*YR.N	1.5	0.811250435
P16144	ITGB4 Integrin beta-4	ITGB4	R.ISGNLDAPEGGFDAILQTAVC*TR.D	1.505	0.884180443
Q12788	TBL3 Transducin beta-like protein 3	TBL3	R.RDPEAC*EK.L	1.506666667	0.788655789
P11172	UMPS Uridine 5-monophosphate synthase	UMPS	R.LHSVC*TLSK.M	1.51	-
P68104	EEF1A1 Elongation factor 1-alpha 1	EEF1A1	K.SGDAAIVDMVPGKPMC*VESFSDYPPLGR.F	1.52	2.069556752
P61106	RAB14 Ras-related protein Rab-14	RAB14	K.SC*LLHQFTEK.K	1.52	3.122154346
A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.ADHQPLTEASYVNLPTIALC*NTDSPLR.Y	1.525	-
P04062	GBA Glucosylceramidase	GBA	R.VPMASC*DFSIR.T	1.525	0.661442006
P19012	KRT15 Keratin, type I cytoskeletal 15	KRT15	R.C*EMEAQNQEYK.M	1.526666667	1.545868946
O95758	PTBP3 Polypyrimidine tract-binding protein 3	PTBP3	R.DRPPC*SPSR.V	1.53	-
P60981	DSTN Destrin	DSTN	K.LGGSLIVAFEGC*PV.-	1.53	-
Q8TCD1	C18orf32 UPF0729 protein C18orf32	C18orf32	K.GADMNGLPTKGPTEIC*DK.K	1.53	-
P46782	RPS5 40S ribosomal protein S5	RPS5	K.TIAEC*LADELINAAK.G	1.53	1.141043503
Q96GQ7	DDX27 Probable ATP-dependent RNA helicase DDX27	DDX27	R.QLAQFCNITTC*LAVGGLDVK.S	1.53	1.0000777
P14866	HNRNPL Heterogeneous nuclear ribonucleoprotein L	HNRNPL	K.ASLNGADIYSGC*CTLK.I	1.533333333	0.753256705
P36551	CPOX Coproporphyrinogen-III oxidase, mitochondrial	CPOX	R.C*SSFMAPPVTDLGELR.R	1.535	1.853846154
P16615	ATP2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase	ATP2A2	R.ANAC*NSVIK.Q	1.543333333	1.828168511
P23396	RPS3 40S ribosomal protein S3	RPS3	R.GLC*AIAQAESLR.Y	1.543333333	1.258836821
P61513	RPL37A 60S ribosomal protein L37a	RPL37A	K.YTC*SFCGK.T	1.545	-
Q9P2E9	RRBP1 Ribosome-binding protein 1	RRBP1	K.HMAAASAEC*QNYAK.E	1.545	1.595024516
Q9NXE4	SMPD4 Sphingomyelin phosphodiesterase 4	SMPD4	R.FAGQMAALC*SR.D	1.55	-
P63104	YWHAZ 14-3-3 protein zeta/delta	YWHAZ	R.YDDMAAC*MK.S	1.55	1.952838732
P37235	HPCAL1 Hippocalcin-like protein 1	HPCAL1	R.LLQC*DPSSASQF.-	1.55	1.099067599
Q9UL25	RAB21 Ras-related protein Rab-21	RAB21	K.VVLLGEGC*VGK.T	1.556666667	-
P36578	RPL4 60S ribosomal protein L4	RPL4	R.GPC*IIYNEDNGIIK.A	1.56	0.776301476

P02538	KRT6A Keratin, type II cytoskeletal 6A	KRT6A	R.GSGGLGGAC*GGAGFGSR.S	1.57	1.046728112
Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	K.NTPSFLIAC*NK.Q	1.573333333	1.744055944
A6NDY0	PABPN1L Embryonic polyadenylate-binding protein 2	PABPN1L	R.VTILC*DK.F	1.576666667	-
O95297	MPZL1 Myelin protein zero-like protein 1	MPZL1	R.DYTGC*STSESLSPVK.Q	1.58	-
O00161	SNAP23 Synaptosomal-associated protein 23	SNAP23	K.CCGLCVCPC*NR.T	1.583333333	-
Q8IY81	FTSJ3 pre-rRNA processing protein FTSJ3	FTSJ3	R.LAC*DFLAR.G	1.583333333	1.322660736
Q9H930	SP140L Nuclear body protein SP140-like protein	SP140L	R.KESDQAC*GK.M	1.585	-
Q05086	UBE3A Ubiquitin-protein ligase E3A	UBE3A	K.GAPNNSC*SEIK.M	1.6	-
P41250	GARS Glycine--tRNA ligase	GARS	R.SC*YDLSCHAR.A	1.6	-
Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	R.DTQTSITDSC*AVYR.V	1.603333333	1.744055944
P49368	CCT3 T-complex protein 1 subunit gamma	CCT3	K.IPGGIIEDSC*VLR.G	1.603333333	1.340450928
P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	K.QIC*VVMLESPPK.G	1.61	-
Q8IY81	FTSJ3 pre-rRNA processing protein FTSJ3	FTSJ3	R.ALLDLC*AAPGGWLQVAAK.F	1.61	1.322660736
O75683	SURF6 Surfeit locus protein 6	SURF6	K.AEEATEAQEVVEATPEGAC*TEPR.E	1.613333333	-
P30519	HMOX2 Heme oxygenase 2	HMOX2	K.GALEGSSC*PFR.T	1.616666667	2.088586127
Q96HW7	INTS4 Integrator complex subunit 4	INTS4	K.LHQTIYNQAC*K.L	1.63	-
Q8N9T8	KRI1 Protein KRI1 homolog	KRI1	R.LDYEDIIDDLPC*R.F	1.63	-
Q15149	PLEC Plectin	PLEC	K.FLEGTSC*IAGVFVDATK.E	1.635	0.941752628
Q8NFW8	CMAS N-acylneuraminate cytidylyltransferase	CMAS	K.VNNSC*QK.-	1.636666667	-
P09651	HNRNPA1 Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	K.YHTVNGHNC*EVR.K	1.64	0.632258929
O15144	ARPC2 Actin-related protein 2/3 complex subunit 2	ARPC2	R.NC*FASVFEK.Y	1.64	-
Q14974	KPNB1 Importin subunit beta-1	KPNB1	K.NSAKDC*YPAVQK.T	1.64	1.45744983
Q9UGP8	SEC63 Translocation protein SEC63 homolog	SEC63	K.KNEPPLTC*PYSLK.A	1.643333333	-
P63220	RPS21 40S ribosomal protein S21	RPS21	K.TYAIC*GAIR.R	1.643333333	-
P40429	RPL13A 60S ribosomal protein L13a	RPL13A	R.C*EGINISGNFYR.N	1.646666667	1.105973528
P46782	RPS5 40S ribosomal protein S5	RPS5	R.VNQAIWLLC*TGAR.E	1.65	1.141043503
P54819	AK2 Adenylate kinase 2, mitochondrial	AK2	K.NLETPLC*K.N	1.653333333	1.458016951
P60174	TPI1 Triosephosphate isomerase	TPI1	K.IAVAAQNC*YK.V	1.655	3.671618037
Q00610	CLTC Clathrin heavy chain 1	CLTC	R.IHEGC*EEPATHNALAK.I	1.656666667	1.826780627
O60716	CTNND1 Catenin delta-1	CTNND1	K.EVHLGAC*GALK.N	1.66	0.811250435
P61163	ACTR1A Alpha-centractin	ACTR1A	R.AC*YLSINPQKDETLETEK.A	1.665	-
P49790	NUP153 Nuclear pore complex protein Nup153	NUP153	K.CVACETPKPGTC*VK.R	1.67	-

Q5RKV6	EXOSC6 Exosome complex component MTR3	EXOSC6	R.APPGGC*EER.E	1.673333333	-
Q9Y696	CLIC4 Chloride intracellular channel protein 4	CLIC4	K.AGSDGESIGNC*PFSQR.L	1.675	-
Q8WWQ0	PHIP PH-interacting protein	PHIP	R.FLEDGPC*QQAAQVLIR.E	1.675	-
Q96KR1	ZFR Zinc finger RNA-binding protein	ZFR	R.NVNLVLLC*SEKPSK.T	1.675	-
E7EQZ4	SMN1 Survival motor neuron protein	SMN1	K.NGDIC*ETSGKPK.T	1.676666667	-
Q01780	EXOSC10 Exosome component 10	EXOSC10	R.VMQYHGC*R.S	1.68	-
P49591	SARS Serine--tRNA ligase, cytoplasmic	SARS	K.YAGLSTC*FR.Q	1.68	-
P61247	RPS3A 40S ribosomal protein S3a	RPS3A	R.LFC*VGFTK.K	1.683333333	1.217598621
Q02040	AKAP17A A-kinase anchor protein 17A	AKAP17A	K.SFLAC*LDGK.T	1.685	-
Q9NVU7	SDAD1 Protein SDA1 homolog	SDAD1	K.TVNVITTAC*FSK.V	1.69	-
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.LWNTLGVC*K.Y	1.7	1.206366048
E7EQ34	GOSR2 Golgi SNAP receptor complex member 2	GOSR2	K.QVHEIQSC*MGR.L	1.703333333	-
Q9UIS9	MBD1 Methyl-CpG-binding domain protein 1	MBD1	R.YLGPAC*DLTLFDFK.Q	1.725	-
Q9NQR4	NIT2 Omega-amidase NIT2	NIT2	R.VGLGIC*YDMR.F	1.726666667	-
P53634	CTSC Dipeptidyl peptidase 1	CTSC	R.YYSSEYHYVGGFYGGC*NEALMK.L	1.73	2.842736829
P48556	PSMD8 26S proteasome non-ATPase regulatory subunit 8	PSMD8	K.C*GEELGR.L	1.735	-
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	K.VWNLANC*K.L	1.736666667	1.206366048
E7ETI0	ARPC4-TTLL3 Protein ARPC4-TTLL3	ARPC4-TTLL3	R.ATLQAALC*LENFSSQVVER.H	1.743333333	2.070599005
Q9Y399	MRPS2 28S ribosomal protein S2, mitochondrial	MRPS2	R.DC*GEYAHTR.Y	1.743333333	0.785547786
P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.YMAC*CLLYR.G	1.745	-
Q6UXV4	APOOL Apolipoprotein O-like	APOOL	R.TATGC*YIGWCK.G	1.745	-
P36578	RPL4 60S ribosomal protein L4	RPL4	R.FC*IWTESAFR.K	1.745	0.776301476
P04632	CAPNS1 Calpain small subunit 1	CAPNS1	K.TDGFGIDTC*R.S	1.75	-
Q9NQT5	EXOSC3 Exosome complex component RRP40	EXOSC3	K.DMEPEMVCIDSC*GR.A	1.75	-
P53701	HCCS Cytochrome c-type heme lyase	HCCS	R.AYEYVEC*PIR.G	1.756666667	-
P31689	DNAJA1 DnaJ homolog subfamily A member 1	DNAJA1	K.GAVEC*CPNCR.G	1.756666667	-
O43159	RRP8 Ribosomal RNA-processing protein 8	RRP8	R.QRPASLVVADFGC*GDCR.L	1.756666667	-
P53634	CTSC Dipeptidyl peptidase 1	CTSC	R.NWAC*FTGK.K	1.763333333	2.842736829
P16615	ATP2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase	ATP2A2	R.NYLEPGKEC*VQPATK.S	1.763333333	1.828168511
P19012	KRT15 Keratin, type I cytoskeletal 15	KRT15	K.AGLENSLAETEC*R.Y	1.766666667	1.545868946
P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	K.AYHEQLSVAEITNAC*FEPANQMVK.C	1.773333333	-

Q15149	PLEC Plectin	PLEC	R.GAYRDC*LGR.L	1.773333333	0.941752628
Q13823	GNL2 Nucleolar GTP-binding protein 2	GNL2	K.VC*NVAPIAGETK.V	1.776666667	-
H3BN98	Uncharacterized protein	Uncharacterized	R.FHEIC*SNLVK.T	1.776666667	-
Reverse_Q9BYM8	RBCK1 RanBP-type and C3HC4-type zinc finger-containing p	RBCK1	-.HCNQC*SPHCPIGNVRCRCGGSTDGPGGPGWR.P	1.8	-
O94925	GLS Glutaminase kidney isoform, mitochondrial	GLS	R.LKEC*MDMLR.L	1.8	2.027619252
Q6UB35	MTHFD1L Monofunctional C1-tetrahydrofolate synthase, mitoc	MTHFD1L	R.GDAHEC*FVSPVAK.A	1.803333333	2.017623628
Q16643	DBN1 Drebrin	DBN1	K.EGTQASEGYFSQSQEEEFAQSEELC*AK.A	1.806666667	5.071865427
Q9Y5M8	SRPRB Signal recognition particle receptor subunit beta	SRPRB	R.AVLLVGLC*DSGK.T	1.81	1.744055944
Q9NRP0	OSTC Oligosaccharyltransferase complex subunit OSTC	OSTC	R.VPFLVLEC*PNLK.L	1.81	-
O00154	ACOT7 Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	R.ADLPPC*GAC*ITGR.I	1.81	4.269860408
P09382	LGALS1 Galectin-1	LGALS1	K.IKC*VAFD.-	1.826666667	2.964675937
Q8NF37	LPCAT1 Lysophosphatidylcholine acyltransferase 1	LPCAT1	R.LPADTC*LLEFAR.L	1.83	-
Q14442	PIGH Phosphatidylinositol N-acetylglucosaminyltransfera	PIGH	R.SFSDIC*GGR.L	1.833333333	-
O00425	IGF2BP3 Insulin-like growth factor 2 mRNA-binding protein	IGF2BP3	K.GNVETC*AK.A	1.833333333	0.526923077
Q7Z2K6	ERMP1 Endoplasmic reticulum metallopeptidase 1	ERMP1	R.AQEPLVDGC*SGGGR.T	1.836666667	1.676456876
Q8IWA4	MFN1 Mitofusin-1	MFN1	R.LC*QQVDITQK.Q	1.84	-
Q16576	RBBP7 Histone-binding protein RBBP7	RBBP7	R.VHIPNDDAQFDASHC*DSDKGEFGGFGSVTGK.I	1.84	1.067012298
P07737	PFN1 Profilin-1	PFN1	K.C*YEMASHLR.R	1.845	2.239078674
I3L2F9	Uncharacterized protein	Uncharacterized	K.TAVC*DIPPR.G	1.85	-
Q96AG4	LRRC59 Leucine-rich repeat-containing protein 59	LRRC59	K.ATILDLSC*NK.L	1.85	1.851088248
Q13148	TARDBP TAR DNA-binding protein 43	TARDBP	R.NPVSQC*MR.G	1.85	0.802797203
Q5VZF2	MBNL2 Muscleblind-like protein 2	MBNL2	K.SC*QVENGR.V	1.863333333	-
Q8N4Q0	ZADH2 Zinc-binding alcohol dehydrogenase domain-containi	ZADH2	K.SLGC*DRPINYK.T	1.865	-
P37802	TAGLN2 Transgelin-2	TAGLN2	K.NMAC*VQR.T	1.873333333	3.624708625
Q9BRJ6	C7orf50 Uncharacterized protein C7orf50	C7orf50	R.RSGAELALDYLC*R.W	1.875	-
Q8NE71	ABCF1 ATP-binding cassette sub-family F member 1	ABCF1	R.IC*IVGPNGVGK.S	1.875	-
Q00610	CLTC Clathrin heavy chain 1	CLTC	K.VIQC*FAETGQVQK.I	1.875	1.826780627
P49721	PSMB2 Proteasome subunit beta type-2	PSMB2	R.NLADC*LR.S	1.88	-
Q9NR30	DDX21 Nucleolar RNA helicase 2	DDX21	K.GKLGVC*FDVPTASVTEIQEK.W	1.88	1.764879565

Q7L5N1	COPS6 COP9 signalosome complex subunit 6	COPS6	K.TC*NTMNQFVNK.F	1.885	-
B0V043	VARS Valyl-tRNA synthetase	VARS	R.IC*LQPPPTSR.T	1.886666667	-
P57088	TMEM33 Transmembrane protein 33	TMEM33	R.LC*LQSIAFISR.L	1.9	-
P16152	CBR1 Carbonyl reductase	CBR1	K.SC*SPELQQK.F	1.905	-
Q8TB61	SLC35B2 Adenosine 3-phospho 5-phosphosulfate transporter	SLC35B2	K.AC*VFGNEPK.A	1.915	-
Q15397	KIAA0020 Pumilio domain-containing protein KIAA0020	KIAA0020	R.GAIILSSLLQSC*DLEVANK.V	1.915	-
Q8N8A6	DDX51 ATP-dependent RNA helicase DDX51	DDX51	R.VVAAAFQSEDPADPC*ALLQR.R	1.92	-
Q16186	ADRM1 Proteasomal ubiquitin receptor ADRM1	ADRM1	R.VPQC*PSGR.V	1.92	-
Q00610	CLTC Clathrin heavy chain 1	CLTC	R.LPVVIGGLLDVDC*SEDVIK.N	1.92	1.826780627
Q9NQZ5	STARD7 StAR-related lipid transfer protein 7, mitochondri	STARD7	R.KNEGSC*GPAR.I	1.93	-
P25789	PSMA4 Proteasome subunit alpha type-4	PSMA4	R.YLLQYQEPIPC*EQLVTALCDIK.Q	1.935	3.819893899
P48556	PSMD8 26S proteasome non-ATPase regulatory subunit 8	PSMD8	K.C*YYFDYK.E	1.945	-
Q8IY81	FTSJ3 pre-rRNA processing protein FTSJ3	FTSJ3	R.HESAEIFVVC*QGFLAPDKVDSK.F	1.95	1.322660736
Q8TAA5	GRPEL2 GrpE protein homolog 2, mitochondrial	GRPEL2	K.TTEC*ISEESEPEDQKLTLEK.V	1.955	-
P17844	DDX5 Probable ATP-dependent RNA helicase DDX5	DDX5	R.LIDFLEC*GK.T	1.97	1.757924068
Q15149	PLEC Plectin	PLEC	R.SEFERLEC*LQR.I	1.97	0.941752628
O15270	SPTLC2 Serine palmitoyltransferase 2	SPTLC2	R.NTGSC*QEAAAK.V	1.973333333	-
Q96MW5	COG8 Conserved oligomeric Golgi complex subunit 8	COG8	R.LEPAGPAC*PEGGR.A	1.98	-
P49757	NUMB Protein numb homolog	NUMB	R.AFSYIC*R.D	1.98	-
Q15366	PCBP2 Poly(rC)-binding protein 2	PCBP2	R.AITIAGIPQSIIEC*VK.Q	1.99	1.359498611
O60716	CTNND1 Catenin delta-1	CTNND1	K.TPAILEASAGAIQNLC*AGR.W	2	0.811250435
Q9UNM6	PSMD13 26S proteasome non-ATPase regulatory subunit 13	PSMD13	K.SSDEAVILC*K.T	2.023333333	-
Q96TA1	FAM129B Niban-like protein 1	FAM129B	K.GPTKEELC*K.S	2.03	-
A6NE09	RPSAP58 Protein RPSAP58	RPSAP58	R.YVDIAIPC*NNK.G	2.033333333	-
Q13501	SQSTM1 Sequestosome-1	SQSTM1	R.FSFC*C*SPEPEAEAEAAAGPGPCER.L	2.035	-
Q8N4Q0	ZADH2 Zinc-binding alcohol dehydrogenase domain-containi	ZADH2	K.CHVIGTC*SSDEK.S	2.035	-
P55036	PSMD4 26S proteasome non-ATPase regulatory subunit 4	PSMD4	R.SNPENNVGLITLANDC*EVLTTLTPDTGR.I	2.04	-
O94901	SUN1 SUN domain-containing protein 1	SUN1	K.TGC*ETVDAVQER.V	2.05	-
O95573	ACSL3 Long-chain-fatty-acid--CoA ligase 3	ACSL3	R.VGAPLVC*CEIK.L	2.06	-
I3L2F9	Uncharacterized protein	Uncharacterized	K.NMMAAC*DPR.H	2.07	-

P62937	PPIA Peptidyl-prolyl cis-trans isomerase A	PPIA	K.ITIADC*GQLE.-	2.073333333	1.60441908
P53701	HCCS Cytochrome c-type heme lyase	HCCS	K.GC*PVNTEPSGPTCEK.K	2.073333333	-
Q96HP0	DOCK6 Dedicator of cytokinesis protein 6	DOCK6	R.AGC*ALSAESSR.T	2.073333333	-
Q13823	GNL2 Nucleolar GTP-binding protein 2	GNL2	K.C*DLVPTWATK.R	2.075	-
P18031	PTPN1 Tyrosine-protein phosphatase non-receptor type 1	PTPN1	K.C*AQYWPQK.E	2.09	2.485236985
P63244	GNB2L1 Guanine nucleotide-binding protein subunit beta-2-	GNB2L1	R.FSPNSSNPIIVSC*GWDK.L	2.103333333	1.206366048
O60716	CTNND1 Catenin delta-1	CTNND1	K.NC*DGVPALVR.L	2.12	0.811250435
Q99436	PSMB7 Proteasome subunit beta type-7	PSMB7	R.ATEGMVVADKNC*SK.I	2.13	-
P07437	TUBB Tubulin beta chain	TUBB	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F	2.13	1.679464852
P09496	CLTA Clathrin light chain A	CLTA	R.LC*DFNPK.S	2.133333333	-
Q04917	YWHAH 14-3-3 protein eta	YWHAH	K.NC*NDFQYESK.V	2.133333333	2.254189999
Q15185	PTGES3 Prostaglandin E synthase 3	PTGES3	K.HLNEIDLFHC*IDPNDSK.H	2.145	-
Q96HE7	ERO1L ERO1-like protein alpha	ERO1L	K.HDDSSDNFC*EADDIQSPEAEYVDLLLNPER.Y	2.153333333	2.194330574
P61106	RAB14 Ras-related protein Rab-14	RAB14	K.FMADC*PHTIGVEFGTR.I	2.155	3.122154346
P28062	PSMB8 Proteasome subunit beta type-8	PSMB8	K.LLSNMMC*QYR.G	2.16	-
P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LNEC*VDHTPK.L	2.17	-
P68366	TUBA4A Tubulin alpha-4A chain	TUBA4A	R.SIQFVDWC*PTGFK.V	2.17	-
P49368	CCT3 T-complex protein 1 subunit gamma	CCT3	R.TLIQNC*GASTIR.L	2.17	1.340450928
O60841	EIF5B Eukaryotic translation initiation factor 5B	EIF5B	K.KGQEVC*VK.I	2.175	-
Q8WX93	PALLD Palladin	PALLD	K.VSSC*EQR.L	2.18	-
Q9P2T1	GMPR2 GMP reductase 2	GMPR2	K.VGIGPGSVC*TTR.K	2.18	-
Q9UBM7	DHCR7 7-dehydrocholesterol reductase	DHCR7	K.VIEC*SYTSADGQR.H	2.183333333	-
P54646	PRKAA2 5-AMP-activated protein kinase catalytic subunit	PRKAA2	R.TSC*GSPNYAAPEVISGR.L	2.185	-
P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.NVC*TEAGMFAIR.A	2.2	-
P23528	CFL1 Cofilin-1	CFL1	K.HELQANC*YEEVKDR.C	2.2	3.760742706
Q9BQ70	TCF25 Transcription factor 25	TCF25	R.SGC*ALTDAVAPGNK.G	2.205	-
P27348	YWHAQ 14-3-3 protein theta	YWHAQ	R.YDDMATC*MK.A	2.205	2.33273406
P49916	LIG3 DNA ligase 3	LIG3	K.AADETLC*QTK.V	2.21	-
Q52LJ0	FAM98B Protein FAM98B	FAM98B	R.INDALSC*EYECR.R	2.225	-
Q6NUQ4	TMEM214 Transmembrane protein 214	TMEM214	R.SSGFLPASQQAC*AK.L	2.236666667	-
Q9H6Y2	WDR55 WD repeat-containing protein 55	WDR55	R.TC*EERPAEDGSDEEDPDSMEAPTR.I	2.24	-
Q9Y5B9	SUPT16H FACT complex subunit SPT16	SUPT16H	R.INFYC*PGSALGR.N	2.256666667	-
Q56VL3	OCIAD2 OCIA domain-containing protein 2	OCIAD2	R.HC*LLTCEECK.I	2.266666667	-

O43865	AHCYL1 Putative adenosylhomocysteinase 2	AHCYL1	K.LC*VPAMNVNDSVTK.Q	2.29	-
O15355	PPM1G Protein phosphatase 1G	PPM1G	R.GTEAGQVGEPGIPTGEAGPSC*SSASDKLPR.V	2.29	-
P53634	CTSC Dipeptidyl peptidase 1	CTSC	R.NQASC*GSCYSFASMGMLEAR.I	2.306666667	2.842736829
B5ME19	EIF3CL Eukaryotic translation initiation factor 3 subunit	EIF3CL	K.TC*HSFIINEK.M	2.325	-
Q9Y4K1	AIM1 Absent in melanoma 1 protein	AIM1	K.SNLPNC*ANSDTDFMGLFK.S	2.325	-
P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.AVASQLDC*NFLK.V	2.33	-
Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R	2.35	3.21617144
P78345	RPP38 Ribonuclease P protein subunit p38	RPP38	R.SVPAC*QVPR.L	2.356666667	-
O00303	EIF3F Eukaryotic translation initiation factor 3 subunit	EIF3F	K.TC*FSPNR.V	2.36	-
P62191	PSMC1 26S protease regulatory subunit 4	PSMC1	K.AIC*TEAGLMALR.E	2.36	-
Q7Z2T5	TRMT1L TRMT1-like protein	TRMT1L	K.FLC*YLSQAGFR.V	2.375	-
Q14204	DYNC1H1 Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	K.VQYPQSQAC*K.M	2.39	-
Q27J81	INF2 Inverted formin-2	INF2	K.LGPQDSDPTEANLESADPELC*IR.L	2.406666667	-
Q13601	KRR1 KRR1 small subunit processome component homolog	KRR1	R.ILQDDVAC*DIIK.I	2.41	-
P43490	NAMPT Nicotinamide phosphoribosyltransferase	NAMPT	R.DLLNC*SFK.C	2.415	-
Q9GZR7	DDX24 ATP-dependent RNA helicase DDX24	DDX24	R.SLVFANSISC*IK.R	2.443333333	-
Q9H307	PNN Pinin	PNN	R.VESVEPSENEASKELEPEMEFEIEPDKEC*K.S	2.45	-
Q86VP6	CAND1 Cullin-associated NEDD8-dissociated protein 1	CAND1	K.NC*IGDFLK.T	2.46	-
P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	R.VFIMDSC*DELIPEYLNFIR.G	2.47	2.469233449
Q27J81	INF2 Inverted formin-2	INF2	K.AQLVLAAC*ESLLTSR.Q	2.48	-
P23743	DGKA Diacylglycerol kinase alpha	DGKA	K.TC*VPDLSDKR.L	2.495	-
P18031	PTPN1 Tyrosine-protein phosphatase non-receptor type 1	PTPN1	R.HEASDFPC*R.V	2.5	2.485236985
P55072	VCP Transitional endoplasmic reticulum ATPase	VCP	K.AIANEC*QANFISIK.G	2.51	3.391969206
P57721	PCBP3 Poly(rC)-binding protein 3	PCBP3	R.LVVPASQC*GSLIGK.G	2.516666667	-
O15269	SPTLC1 Serine palmitoyltransferase 1	SPTLC1	R.LLQEIVDQC*MNR.S	2.52	-
Q9H4I3	TRABD TraB domain-containing protein	TRABD	R.TASLVLSLPAAQYC*LQR.V	2.53	-
Q5T8P6	RBM26 RNA-binding protein 26	RBM26	K.ALC*IDQLDVFLQK.E	2.53	-
Q27J81	INF2 Inverted formin-2	INF2	K.C*SNEEVAAMIR.A	2.54	-
P34932	HSPA4 Heat shock 70 kDa protein 4	HSPA4	R.CTPAC*ISFGPK.N	2.56	-
Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	K.YNNC*WLAR.T	2.586666667	3.21617144

P51858	HDGF Hepatoma-derived growth factor	HDGF	K.C*GDLVFAK.M	2.625	2.976259947
P28062	PSMB8 Proteasome subunit beta type-8	PSMB8	K.VIEINPYLLGTMSGC*AADCQYWER.L	2.66	-
P78417	GSTO1 Glutathione S-transferase omega-1	GSTO1	K.LLPDDPYEKAC*QK.M	2.665	-
Q9ULC4	MCTS1 Malignant T-cell-amplified sequence 1	MCTS1	K.FDEKENVSNC*IQLK.T	2.685	-
P11940	PABPC1 Polyadenylate-binding protein 1	PABPC1	K.VVC*DENGSK.G	2.696666667	2.505312185
Q9UQ80	PA2G4 Proliferation-associated protein 2G4	PA2G4	R.MGVVEC*AK.H	2.706666667	-
Q27J81	INF2 Inverted formin-2	INF2	R.ELADYLC*EDAQQLSLEDTFSTMK.A	2.725	-
Q9HAS0	C17orf75 Protein Njmu-R1	C17orf75	K.NNMNC*EAR.G	2.735	-
P49321	NASP Nuclear autoantigenic sperm protein	NASP	K.SVSGTDVQEEC*R.E	2.75	-
Q9H553	ALG2 Alpha-1,3/1,6-mannosyltransferase ALG2	ALG2	R.GAAVC*AYVR.M	2.77	-
Q02487	DSC2 Desmocollin-2	DSC2	K.GGHQTSESC*R.G	2.82	-
Q6P1M0	SLC27A4 Long-chain fatty acid transport protein 4	SLC27A4	R.AGMAAVASPTGNC*DLER.F	2.82	-
Q9Y5Z9	UBIAD1 UbiA prenyltransferase domain-containing protein 1	UBIAD1	K.AGDRDPLGNDC*PEQDRLPQR.S	2.825	-
P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.LC*PNSTGAEIR.S	2.83	-
P22102	GART Trifunctional purine biosynthetic protein adenosin	GART	R.SAGVQC*FGPTAEAAQLESSKR.F	2.835	-
P35998	PSMC2 26S protease regulatory subunit 7	PSMC2	R.TDAC*FIR.V	2.845	-
P57772	EEFSEC Selenocysteine-specific elongation factor	EEFSEC	K.AGQATEGHC*PR.Q	2.845	-
P06400	RB1 Retinoblastoma-associated protein	RB1	K.AVGQGC*VEIGSQR.Y	2.91	-
Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	R.YVAAAFPSAC*GK.T	2.91	3.21617144
Q9NP72	RAB18 Ras-related protein Rab-18	RAB18	K.LDNWLNELETYC*TR.N	2.96	-
Q14573	ITPR3 Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	R.GDLPDPIGTGLDPDWSAIAATQC*R.L	2.975	1.551669659
P61158	ACTR3 Actin-related protein 3	ACTR3	R.LPACVVDC*GTGYTK.L	2.986666667	-
Q56VL3	OCIAD2 OCIA domain-containing protein 2	OCIAD2	K.QSLLFC*PK.S	3.003333333	-
Q6ZWT7	MBOAT2 Lysophospholipid acyltransferase 2	MBOAT2	K.FDEGENSLGQNSFSTTNNVC*NQNQEIASR.H	3.005	-
P30050	RPL12 60S ribosomal protein L12	RPL12	K.EILGTAQSVGC*NVDGR.H	3.02	1.375625396
Q52LJ0	FAM98B Protein FAM98B	FAM98B	K.TAC*AINK.V	3.043333333	-
Q8WVM8	SCFD1 Sec1 family domain-containing protein 1	SCFD1	K.ALTDAGC*NLNPLQYIK.Q	3.045	-
O00299	CLIC1 Chloride intracellular channel protein 1	CLIC1	K.IGNC*PFSQR.L	3.053333333	-
P08134	RHOC Rho-related GTP-binding protein RhoC	RHOC	R.ISAFGYLEC*SAK.T	3.193333333	1.448484848
P08238	HSP90AB1 Heat shock protein HSP 90-beta	HSP90AB1	K.AKFENLC*K.L	3.196666667	2.469233449
Q9NSY1	BMP2K BMP-2-inducible protein kinase	BMP2K	K.SEGGSGGGAAGGGAGGAGAGAGC*GSGGSSVGVR.V	3.21	-

P18085	ARF4 ADP-ribosylation factor 4	ARF4	K.NIC*FTVWDVGGQDR.I	3.22	-
Q9NU22	MDN1 Midasin	MDN1	R.FAASNPC*GNIQR.S	3.23	-
P43686	PSMC4 26S protease regulatory subunit 6B	PSMC4	K.ISGADINSIC*QESGMLAVR.E	3.246666667	-
P18669	PGAM1 Phosphoglycerate mutase 1	PGAM1	R.YADLTEDQLPSC*ESLKDTIAR.A	3.29	-
P31947	SFN 14-3-3 protein sigma	SFN	K.GAVEKGEELSC*EER.N	3.323333333	-
Q9NP72	RAB18 Ras-related protein Rab-18	RAB18	K.TC*DGVQC*AFEELVEK.I	3.335	-
Q9NPF5	DMAP1 DNA methyltransferase 1-associated protein 1	DMAP1	R.YYHIC*AK.L	3.435	-
P62333	PSMC6 26S protease regulatory subunit 10B	PSMC6	R.DHQPC*IIFMDEIDAIGGR.R	3.435	-
O15269	SPTLC1 Serine palmitoyltransferase 1	SPTLC1	K.YGVGTC*GPR.G	3.483333333	-
Q9NQC3	RTN4 Reticulon-4	RTN4	K.YSNSALGHVNC*TIK.E	3.503333333	2.747907903
Q16643	DBN1 Drebrin	DBN1	K.VMYGFC*SVK.D	3.53	5.071865427
P40222	TXLNA Alpha-taxilin	TXLNA	R.VTEAPC*YPGAPSTEASGQTGPQEPTSAR.A	3.53	-
O75369	FLNB Filamin-B	FLNB	K.SSFLVDC*SK.A	3.543333333	5.514802311
Q9UNH7	SNX6 Sorting nexin-6	SNX6	K.GNLQLLQNC*LAVLNGDT.-	3.55	-
Q96FX7	TRMT61A tRNA (adenine(58)-N(1))-methyltransferase catalyti	TRMT61A	R.FCSFSPC*IEQVQR.T	3.56	-
Q14247	CTTN Src substrate cortactin	CTTN	K.HC*SQVDSVR.G	3.596666667	-
A0JLT2	MED19 Mediator of RNA polymerase II transcription subuni	MED19	K.SGAGC*GPFYLMR.E	3.68	-
Q02543	RPL18A 60S ribosomal protein L18a	RPL18A	R.DLTTAGAVTQC*YR.D	3.795	-
O75475	PSIP1 PC4 and SFRS1-interacting protein	PSIP1	R.C*IEALDELASLQVTMQQAQK.H	3.805	-
P15153	RAC2 Ras-related C3 botulinum toxin substrate 2	RAC2	R.AVLC*PQPTR.Q	3.976666667	-
O00154	ACOT7 Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	R.ADLPPC*GACITGR.I	3.986666667	4.269860408
Q9Y4L1	HYOU1 Hypoxia up-regulated protein 1	HYOU1	R.VEFEELC*ADLFER.V	4.03	1.017395886
Q08J23	NSUN2 tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2	R.NNSGEEFDC*AFR.L	4.073333333	-
O75369	FLNB Filamin-B	FLNB	K.C*LATGPGIASTVK.T	4.075	5.514802311
P62979	RPS27A Ubiquitin-40S ribosomal protein S27a	RPS27A	K.C*CLTYCFNKPEDK.-	4.16	-
P29401	TKT Transketolase	TKT	K.QAFTDVATGSLGQGLGAAC*GMAYTGK.Y	4.175	8.395977458
Q86W92	PPFIBP1 Liprin-beta-1	PPFIBP1	R.INNFEPNC*LR.R	4.265	-
Q9UBE0	SAE1 SUMO-activating enzyme subunit 1	SAE1	R.YCFSEMAPVC*AVVGGILAQEIVK.A	4.365	-
O75369	FLNB Filamin-B	FLNB	R.SSTETC*YSAIPK.A	4.423333333	5.514802311
O75369	FLNB Filamin-B	FLNB	K.GAGTGGLGLTVEGPC*EAK.I	4.446666667	5.514802311
P61289	PSME3 Proteasome activator complex subunit 3	PSME3	R.LDEC*EEAFQGTK.V	4.645	-
P05455	SSB Lupus La protein	SSB	K.FSGDLDDQTC*R.E	4.7	3.078779841
Q9P258	RCC2 Protein RCC2	RCC2	K.AVQDLC*GWR.I	4.71	-
Q9HBH0	RHOF Rho-related GTP-binding protein RhoF	RHOF	K.IVIVGDGGC*GK.T	4.865	-

O75369	FLNB Filamin-B	FLNB	K.SGC*IVNNLAEFTVDPK.D	4.966666667	5.514802311
O60664	PLIN3 Perilipin-3	PLIN3	K.TVC*DAAEK.G	5.12	23.44877243
Q01813	PFKP 6-phosphofructokinase type C	PFKP	K.AAC*NLLQR.G	5.25	-
O75369	FLNB Filamin-B	FLNB	K.VAVTEGC*QPSR.V	5.253333333	5.514802311
Q9NXG2	THUMPD1 THUMP domain-containing protein 1	THUMPD1	R.RC*DAGGPR.Q	5.275	-
P01112	HRAS GTPase HRas	HRAS	K.LNPPDESGPGC*MSCK.C	5.335	2.222121301
Q92797	SYMPK Symplekin	SYMPK	R.KYC*EDESR.T	5.59	-
O75369	FLNB Filamin-B	FLNB	K.NRMDGTYAC*SYTPVK.A	5.71	5.514802311
P49915	GMPS GMP synthase	GMPS	K.TVGVQGDC*R.S	5.965	-
O75369	FLNB Filamin-B	FLNB	K.AEISC*IDNK.D	5.97	5.514802311
O75369	FLNB Filamin-B	FLNB	K.VDIQTEDLEDGTC*K.V	6.26	5.514802311
Q8TD30	GPT2 Alanine aminotransferase 2	GPT2	K.GYMGEC*GYR.G	6.365	-
P53396	ACLY ATP-citrate synthase	ACLY	K.FIC*TTSAIQNR.F	6.55	-
Q9NVH0	EXD2 Exonuclease 3-5 domain-containing protein 2	EXD2	R.NNLLC*NGLSLK.S	6.973333333	-
P04035	HMGCR 3-hydroxy-3-methylglutaryl-coenzyme A reductase	HMGCR	K.INLQDLQGAC*TK.K	7.1	-
O75369	FLNB Filamin-B	FLNB	R.APSVATVGSIC*DLNLK.I	7.205	5.514802311
P53602	MVD Diphosphomevalonate decarboxylase	MVD	R.DGDPLPSSLSC*K.V	7.566666667	-
Q04637	EIF4G1 Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	K.AISEPNFSVAYANMC*R.C	8.055	-
P49327	FASN Fatty acid synthase	FASN	K.AFDTAGNGYC*R.S	8.06	-
O75369	FLNB Filamin-B	FLNB	K.IEYNDQNDGSC*DVK.Y	8.086666667	5.514802311
Q16822	PCK2 Phosphoenolpyruvate carboxykinase	PCK2	K.VEC*VGDDIAWMR.F	8.21	3.21617144
P35321	SPRR1A Cornifin-A	SPRR1A	K.VPEPC*QPK.V	8.71	-
Q01813	PFKP 6-phosphofructokinase type C	PFKP	K.TNC*NVAVINVGAPAAGMNAAVR.S	8.746666667	-
P29034	S100A2 Protein S100-A2	S100A2	K.YSC*QEGDK.F	9.286666667	-
P31949	S100A11 Protein S100-A11	S100A11	K.ISSPTETERC*IESLIAVFQK.Y	9.493333333	8.853645205
Q14573	ITPR3 Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	R.LGFVDVQNC*ISR.-	9.56	1.551669659
Q13045	FLII Protein flightless-1 homolog	FLII	R.NQLTSLPSAIC*K.L	9.563333333	-
P04083	ANXA1 Annexin A1	ANXA1	K.MYGISLC*QAILDETK.G	9.85	10.84983344
Q8TD30	GPT2 Alanine aminotransferase 2	GPT2	R.ILQACGGNSLGSYSASQGVNC*IR.E	10.01	-
P36952	SERPINB5 Serpin B5	SERPINB5	K.AC*LENLGLK.H	10.31666667	15.09331779
P37268	FDFT1 Squalene synthase	FDFT1	K.C*LGHPEEFYNLVR.F	10.345	26.65390063
P54819	AK2 Adenylate kinase 2, mitochondrial	AK2	R.LAENFC*VCHLATGDMLR.A	10.44	1.458016951
O75369	FLNB Filamin-B	FLNB	K.SPFVVQVGEAC*NPNACR.A	10.91	5.514802311

Q9Y224	C14orf166 UPF0568 protein C14orf166	C14orf166	K.LTALDYHNPAGFNC*K.D	10.94	-
P04083	ANXA1 Annexin A1	ANXA1	K.ILVALC*GGN.-	11.00666667	10.84983344
P31153	MAT2A S-adenosylmethionine synthase isoform type-2	MAT2A	K.VAC*ETVAK.T	11.13	-
P37268	FDFT1 Squalene synthase	FDFT1	K.YQTVIADIC*R.R	13.09	26.65390063
O60664	PLIN3 Perilipin-3	PLIN3	R.DIAQQLQATC*TSLGSSIQGLPTNVK.D	14.655	23.44877243
Q13753	LAMC2 Laminin subunit gamma-2	LAMC2	K.NLENIRDNLPPGC*YNTQALEQQ.-	16.79333333	23.32949745
O75369	FLNB Filamin-B	FLNB	K.NGSC*GVSYIAQEPGNYEVSIK.F	17.725	5.514802311
P37268	FDFT1 Squalene synthase	FDFT1	R.TQNLPNC*QLISR.S	18.43	26.65390063
Q14534	SQLE Squalene monooxygenase	SQLE	K.AC*FLYFK.L	18.58	-
P29317	EPHA2 Ephrin type-A receptor 2	EPHA2	K.FTTEIHPSC*VTR.Q	19.02	16.06652734
Q16831	UPP1 Uridine phosphorylase 1	UPP1	K.AESHNDC*PVR.L	20	-
O60502	MGEA5 Bifunctional protein NCOAT	MGEA5	R.ANSSVVSVNC*K.G	20	-
O43252	PAPSS1 Bifunctional 3-phosphoadenosine 5-phosphosulfate	PAPSS1	R.GC*TVWLTGLSGAGK.T	20	-
O95071	UBR5 E3 ubiquitin-protein ligase UBR5	UBR5	K.LPNLEC*IQNANK.G	20	-
P49915	GMPS GMP synthase	GMPS	R.VICAEEPYIC*K.D	20	-
P35321	SPRR1A Cornifin-A	SPRR1A	K.VPEPC*PSTVTPAPAQQK.T	20	-
Q16831	UPP1 Uridine phosphorylase 1	UPP1	R.IGTSGGIGLEPGTVVITEQAVDTC*FK.A	20	-

Table A-2. Mass spectrometry results from isotopic labeling of inactive Raw and activated Raw lysates. Three replicates were run. If a peptide was found in at least two samples, the average ratio is presented in the table as light/heavy. The average ratios for cysteine labeling and ReDiMe labeling are included.

ipi	description	symbol	sequence	cysteine	abundance
Q9ESY9	Ifi30 Gamma-interferon-inducible lysosomal thiol reducta	Ifi30	R.VSLYYESLC*GAC*R.Y	0.105	-
Q9ESY9	Ifi30 Gamma-interferon-inducible lysosomal thiol reducta	Ifi30	R.VSLYYESLC*GACR.Y	0.123333333	-
Q3U186	Rars2 Probable arginine--tRNA ligase, mitochondrial	Rars2	K.AVLQQVTEDGC*K.Y	0.32	-
Q8BMK4	Ckap4 Cytoskeleton-associated protein 4	Ckap4	R.SSAATANASSASC*SR.R	0.33	-
Q8BIG7	Comtd1 Catechol O-methyltransferase domain-containing pro	Comtd1	R.LLTLEQPQGDSMMTC*EQAQLLANLAR.L	0.36	-
Q9EST5	Anp32b Acidic leucine-rich nuclear phosphoprotein 32 fami	Anp32b	K.SLDLFGC*EVTNR.S	0.385	0.813214286
Q9DCM0	Ethe1 Protein ETHE1, mitochondrial	Ethe1	R.TDFQQGC*AK.T	0.405	-

P46061	Rangap1 Ran GTPase-activating protein 1	Rangap1	K.AFSC*SSFNSNTFLTR.L	0.415	-
Q61207	Psap Sulfated glycoprotein 1	Psap	K.TC*SGGSAVLCR.D	0.42	0.71218254
P13864	Dnmt1 DNA (cytosine-5)-methyltransferase 1	Dnmt1	K.SQLC*DLETK.L	0.423333333	-
P13864	Dnmt1 DNA (cytosine-5)-methyltransferase 1	Dnmt1	R.DGLTEKEC*VR.E	0.46	-
O08585	Clta Clathrin light chain A	Clta	R.LC*DFNPK.S	0.463333333	1.200714286
Q8CH77	Nav1 Neuron navigator 1	Nav1	K.VAPGPSSGC*TPGQVPGSSALSSPR.R	0.47	-
B2RXS4	Plxnb2 Plexin-B2	Plxnb2	K.VLNC*DTISQVK.E	0.47	-
Q91WU5	As3mt Arsenite methyltransferase	As3mt	K.TSADLQTNAC*VTR.A	0.475	-
Q9QZQ8	H2afy Core histone macro-H2A.1	H2afy	K.NC*LALADDR.K	0.476666667	0.991071429
P10605	Ctsb Cathepsin B	Ctsb	R.DQGSC*GSC*WAFGAVEAISDR.T	0.48	0.813928571
Q9Z110	Aldh18a1 Delta-1-pyrroline-5-carboxylate synthase	Aldh18a1	R.GDEC*GLALGR.L	0.503333333	0.843968254
Q9JHS3	Lamtor2 Ragulator complex protein LAMTOR2	Lamtor2	R.VANLLLC*MYAK.E	0.505	-
D3YU93	Rpl7a-ps3 Uncharacterized protein	Rpl7a-ps3	K.TC*TTVAFTQVNSEDKGALAK.L	0.52	-
Q00PI9	Hnrnpul2 Heterogeneous nuclear ribonucleoprotein U-like pro	Hnrnpul2	R.LQEALDAEMLEDEAGVGGAGPGGAC*K.A	0.52	1.107142857
O88986	Gcat 2-amino-3-ketobutyrate coenzyme A ligase, mitochon	Gcat	R.C*ILDSELEGIR.G	0.53	-
Q8VBT6	Apobr Apolipoprotein B receptor	Apobr	R.TC*EQKEEEEEVVR.A	0.543333333	-
Q9DAU1	Cnpy3 Protein canopy homolog 3	Cnpy3	K.GKDTSC*LAER.W	0.555	-
Q9D8S9	Bola1 BolA-like protein 1	Bola1	R.ENPQLDISPPC*LGGSK.K	0.555	-
P08249	Mdh2 Malate dehydrogenase, mitochondrial	Mdh2	K.GC*DVVVIPAGVPR.K	0.555	0.923849206
Q6NZJ6	Eif4g1 Eukaryotic translation initiation factor 4 gamma 1	Eif4g1	K.AISEPNFSVAYANMC*R.C	0.56	1.525535714
P55194	Sh3bp1 SH3 domain-binding protein 1	Sh3bp1	K.ALEMTC*AIQNQLAR.I	0.56	-
D3YVE6	Uncharacterized protein	Uncharacterized	K.MGVPYC*IIK.E	0.56	0.822936508
P38060	Hmgcl Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	K.NANC*SIEESFQR.F	0.565	-
Q8CI11	Gnl3 Guanine nucleotide-binding protein-like 3	Gnl3	K.LLGDFQQSC*GK.D	0.573333333	-
P61979	Hnrnpk Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	K.IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK.G	0.573333333	1.121111111
Q8CHP8	Pgp Phosphoglycolate phosphatase	Pgp	K.SNQESDC*MFK.K	0.575	-
P05202	Got2 Aspartate aminotransferase, mitochondrial	Got2	R.VGAFTVVC*K.D	0.58	0.834047619
Q8CIE6	Copa Coatomer subunit alpha	Copa	K.IQVPNC*DEIFYAGTGNLLLR.D	0.59	1.015714286
Q9CPV4	Glod4 Glyoxalase domain-containing protein 4	Glod4	R.HEEFEEGC*K.A	0.595	-
Q91VI7	Rnh1 Ribonuclease inhibitor	Rnh1	R.ELDLSNNC*MGGPGVLQLLESLK.Q	0.595	0.706071429

P08113	Hsp90b1 Endoplasmin	Hsp90b1	R.LTESPC*ALVASQYGWSGNMER.I	0.596666667	0.663571429
P35601	Rfc1 Replication factor C subunit 1	Rfc1	K.NIIGQQGDQSC*ANK.L	0.6	-
Q8BXV2	Bri3bp BRI3-binding protein	Bri3bp	R.GSPGGLC*SPSVEEK.L	0.603333333	-
G3UZK1	Gm20503 Guanine nucleotide-binding protein subunit gamma	Gm20503	K.VSQAAAELQQYC*IQNAC*K.D	0.605	-
Q922Q1	Marc2 MOSC domain-containing protein 2, mitochondrial	43526	K.GVSVC*ETECTDMGLR.C	0.605	-
Q9WU62	Incenp Inner centromere protein	Incenp	K.TPSPPC*PANK.V	0.605	-
Q62465	Vat1 Synaptic vesicle membrane protein VAT-1 homolog	Vat1	R.AC*GLNFADLMGR.Q	0.605	1.028055556
Q9D0J4	Arl2 ADP-ribosylation factor-like protein 2	Arl2	K.QDLPGALSC*NAIQEALELDSIR.S	0.606666667	-
P17918	Pcna Proliferating cell nuclear antigen	Pcna	K.LMDLDVEQLGIPEQEYSC*VIK.M	0.61	0.799583333
P10605	Ctsb Cathepsin B	Ctsb	K.SC*EAGYSPSYK.E	0.613333333	0.813928571
Q99KC8	Vwa5a von Willebrand factor A domain-containing protein	Vwa5a	K.SAC*SAIQK.K	0.615	-
E9PVX6	Mki67 Protein Mki67	Mki67	K.LATAAEQTC*SGLPGLSSVDISNFGDSINK.S	0.625	-
Q8CE90	Map2k7 Dual specificity mitogen-activated protein kinase	Map2k7	R.SAGC*AAYMAPER.I	0.625	-
P10605	Ctsb Cathepsin B	Ctsb	R.GENHC*GIESEIVAGIPR.T	0.625	0.813928571
Q921F2	Tardbp TAR DNA-binding protein 43	Tardbp	K.VAQSLC*GEDLIIK.G	0.633333333	0.897142857
P10605	Ctsb Cathepsin B	Ctsb	R.EQWSNC*PTIGQIR.D	0.633333333	0.813928571
Q99K70	Rragc Ras-related GTP-binding protein C	Rragc	K.DFGYGVEEEEEEAAAGGGGGAGAGGGC*GPGGADSSKPR.I	0.635	-
Q64737	Gart Trifunctional purine biosynthetic protein adenosin	Gart	R.AFTNPEDAC*SFITSANFPALVVK.A	0.635	0.839285714
Q80VL1	Tdrkh Tudor and KH domain-containing protein	Tdrkh	R.VLLISGFPVQVC*K.A	0.636666667	-
Q8K2B3	Sdha Succinate dehydrogenase	Sdha	R.VGSVLQEGC*EK.I	0.64	0.727579365
Q9D287	Bcas2 Pre-mRNA-splicing factor SPF27	Bcas2	K.NDITAWQEC*VNNSMAQLEHQAVR.I	0.64	-
Q9DAW6	Prpf4 U4/U6 small nuclear ribonucleoprotein Prp4	Prpf4	K.DVNLASC*AADGSVK.L	0.64	-
Q9Z1P6	Ndufa7 NADH dehydrogenase	Ndufa7	K.LSNNYYC*TR.D	0.64	-
Q8R081	Hnrnpl Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	K.ASLNGADIYSGC*CTLK.I	0.64	0.904444444
P38060	Hmgcl Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	R.GYVSC*ALGC*PYEGK.V	0.643333333	-
P10605	Ctsb Cathepsin B	Ctsb	R.DQGSC*GSCWAFGAVEAISDR.T	0.643333333	0.813928571
O88796	Rpp30 Ribonuclease P protein subunit p30	Rpp30	R.PSEADDESLPVC*K.K	0.645	-
P31750	Akt1 RAC-alpha serine/threonine-protein kinase	Akt1	K.TFC*GTPEYLAPEVLEDNDYGR.A	0.645	-
Q9CZN7	Shmt2 Protein Shmt2	Shmt2	R.YYGGAEVVDEIELLC*QR.R	0.645	0.942698413
Q91VI7	Rnh1 Ribonuclease inhibitor	Rnh1	R.TNELGDGGVGLVLQGLQNPTC*K.I	0.645	0.706071429

J3QMM7	Carkd ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Carkd	R.IGIVGGC*QEYTGAPYFAGISALK.V	0.65	-
P08752	Gnai2 Guanine nucleotide-binding protein G(i) subunit al	Gnai2	K.IIHEDGYSEEEC*R.Q	0.65	0.720238095
Q99N11	Dusp22 Dual specificity protein phosphatase 22	Dusp22	R.SC*ANPNLGFQR.Q	0.65	-
G3UZK1	Gm20503 Guanine nucleotide-binding protein subunit gamma	Gm20503	K.VSQAAAELQQYCIQNAC*K.D	0.65	-
Q00PI9	Hnrnpul2 Heterogeneous nuclear ribonucleoprotein U-like pro	Hnrnpul2	K.SRDLLVQQASQC*LSK.L	0.65	1.107142857
P50136	Bckdha 2-oxoisovalerate dehydrogenase subunit alpha, mito	Bckdha	R.DYPLELFMSQC*YGNVNDPGK.G	0.653333333	-
P25206	Mcm3 DNA replication licensing factor MCM3	Mcm3	R.TVLIAC*NVK.Q	0.656666667	-
Q9DBD5	Pelp1 Proline-, glutamic acid- and leucine-rich protein	Pelp1	R.NANSDVC*AAALR.G	0.66	-
Q8CCF0	Prpf31 U4/U6 small nuclear ribonucleoprotein Prp31	Prpf31	K.MPAC*NIMLLGAQR.K	0.66	-
Q99M31	Hspa14 Heat shock 70 kDa protein 14	Hspa14	K.VVLC*GGSSR.I	0.66	-
Q9R0B7	Znf346 Zinc finger protein 346	Znf346	K.NQC*LFTSTQCK.V	0.66	-
Q91YS8	Camk1 Calcium/calmodulin-dependent protein kinase type 1	Camk1	K.MEDPGSVLSTAC*GTPGYVAPEVLAQKPYSK.A	0.663333333	-
Q1HFZ0	Nsun2 tRNA (cytosine(34)-C(5))-methyltransferase	Nsun2	R.NNSGEEFDC*AFR.L	0.666666667	1.147142857
Q9CR47	Nsa2 Ribosome biogenesis protein NSA2 homolog	Nsa2	K.ATFC*LPILGVK.K	0.67	-
Q9QY06	Myo9b Unconventional myosin-IXb	Myo9b	R.NADGSIQYLPIQLLAQPTAAC*R.L	0.675	-
Q7TPV4	Mybbp1a Myb-binding protein 1A	Mybbp1a	K.SPAESC*DVLGDIQTC*IK.K	0.675	1.121150794
Q99LC5	Etfa Electron transfer flavoprotein subunit alpha, mito	Etfa	R.LGGEVSC*LVAGTK.C	0.676666667	1.026785714
Q6NXI6	Rprd2 Regulation of nuclear pre-mRNA domain-containing p	Rprd2	R.VDVC*STETLK.C	0.685	-
Q9QXK7	Cpsf3 Cleavage and polyadenylation specificity factor su	Cpsf3	R.NFNYHILSPC*DLSNYTDLAMSTVK.Q	0.685	-
Q8WTY4	Ciapin1 Anamorsin	Ciapin1	K.APSC*GEGK.K	0.685	-
P58064	Mrps6 28S ribosomal protein S6, mitochondrial	Mrps6	K.EC*DGIVPVPLEEK.L	0.69	-
P08752	Gnai2 Guanine nucleotide-binding protein G(i) subunit al	Gnai2	R.QLFALSC*AAEEQGMLPEDLSGVIR.R	0.69	0.720238095
O35737	Hnrnph1 Heterogeneous nuclear ribonucleoprotein H	Hnrnph1	R.GLPWSC*SADEVQR.F	0.695	0.981507937
P61290	Psme3 Proteasome activator complex subunit 3	Psme3	R.LDEC*EEAFQGTK.V	0.696666667	-
Q8CGC7	Eprs Bifunctional glutamate/proline--tRNA ligase	Eprs	K.KLGVENC*YFPIFVSQAALEK.E	0.696666667	-
Q9QZD8	Slc25a10 Mitochondrial dicarboxylate carrier	Slc25a10	R.GALVTVGQLSC*YDQAK.Q	0.7	-

Q80ZQ9	Fam206a Protein FAM206A	Fam206a	R.ISYQISNNC*SR.L	0.7	-
Q8BGX2	Uncharacterized protein C19orf52 homolog	Uncharacterized	R.DYAEAC*GDAAAAAR.A	0.7	-
Q9QZK7	Dok3 Docking protein 3	Dok3	R.APDIC*GVVAAAIAR.Q	0.7	-
Q924H2	Med15 Mediator of RNA polymerase II transcription subuni	Med15	K.QQDLC*QPLLDAVLANIR.S	0.7	-
P61979	Hnrnpk Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	K.GSDFDC*ELR.L	0.7	1.121111111
Q3UFY7	Nt5c3l Cytosolic 5-nucleotidase III-like protein	Nt5c3l	K.NSSVC*ENSSYFQQLQNK.T	0.705	-
Q6PB66	Lrpprc Leucine-rich PPR motif-containing protein, mitocho	Lrpprc	R.VFESTC*SSGSPGSNQALLLLR.S	0.705	-
P30999	Ctnnd1 Catenin delta-1	Ctnnd1	K.TPAILEASAGAIQNLC*AGR.W	0.705	-
Q6NZJ6	Eif4g1 Eukaryotic translation initiation factor 4 gamma 1	Eif4g1	K.NHDEESLEC*LC*R.L	0.705	1.525535714
Q9Z2X1	Hnrnpf Heterogeneous nuclear ribonucleoprotein F	Hnrnpf	R.YGDSEFTVQSTTGHC*VHMR.G	0.705	0.991031746
Q64737	Gart Trifunctional purine biosynthetic protein adenosin	Gart	R.LLDGDEGPNTGGMGAYC*PAPQVSK.D	0.705	0.839285714
Q80X68	Csl Citrate synthase	Csl	R.GYSIPEC*QK.M	0.706666667	0.797619048
Q9CQA9	Ntpcr Cancer-related nucleoside-triphosphatase homolog	Ntpcr	R.NAGSSC*GPK.H	0.71	-
Q9EQI8	Mrpl46 39S ribosomal protein L46, mitochondrial	Mrpl46	R.FLLDSDGLSC*L.-	0.71	-
Q921G6	Lrch4 Leucine-rich repeat and calponin homology domain-c	Lrch4	R.AAGAGASAPSTQATC*NGPPK.S	0.71	-
Q91VA7	Idh3b Isocitrate dehydrogenase 3 (NAD) beta	Idh3b	K.LGDGLFLQC*C*EEVAELYPK.I	0.71	0.870535714
Q9R1J0	Nsdhl Sterol-4-alpha-carboxylate 3-dehydrogenase, decarb	Nsdhl	R.VQFFIGDLC*NQQDLYPALK.G	0.713333333	-
Q8VDD8	Wash1 WAS protein family homolog 1	Wash1	K.TQC*SLAGQLYAVPLIQPDLR.R	0.715	-
Q9WUU7	Ctsz Cathepsin Z	Ctsz	K.GGTGDSYNLAIESAC*TFGDPIV.-	0.715	0.941964286
Q9WUU7	Ctsz Cathepsin Z	Ctsz	K.HGIPDETC*NNYQAK.D	0.715	0.941964286
O09106	Hdac1 Histone deacetylase 1	Hdac1	K.VMEMFQPSAVVLQC*GSDSLSGDR.L	0.715	0.867559524
Q9DAV9	Tmem38b Trimeric intracellular cation channel type B	Tmem38b	R.GAGGAVVTAC*EQLLK.G	0.715	-
P63168	Dynll1 Dynein light chain 1, cytoplasmic	Dynll1	K.NADMSEEMQQDSVEC*ATQALEK.Y	0.716666667	-
Q91YR9	Ptgr1 Prostaglandin reductase 1	Ptgr1	R.TGPC*PQGPAPEVVIYQQLR.M	0.72	-
Q5SYH2	Tmem199 Transmembrane protein 199	Tmem199	R.NVTC*QDAQC*GGTLSDLGK.Q	0.72	-
P10126	Eef1a1 Elongation factor 1-alpha 1	Eef1a1	K.DGSASGTTLLEALDC*ILPPTRPTDK.P	0.72	1.213769841
O55143	Atp2a2 Sarcoplasmic/endoplasmic reticulum calcium ATPase	Atp2a2	R.NYLEQPGKEC*VQPATK.S	0.72	0.6875
P62702	Rps4x 40S ribosomal protein S4, X isoform	Rps4x	K.FDTGNLC*MVTGGANLGR.I	0.72	0.787301587
Q8C2Q3	Rbm14 RNA-binding protein 14	Rbm14	K.IFVGNVSAAC*TSQELR.S	0.723333333	1.12452381

P17751	Tpi1 Triosephosphate isomerase	Tpi1	K.C*LGELICTLNAANVPAGTEVVCAPPTAYIDFAR.Q	0.723333333	1.061984127
Q9WUU7	Ctsz Cathepsin Z	Ctsz	K.DQDC*DKFNQCGTCTEFK.E	0.723333333	0.941964286
Q9EP97	Senp3 Sentrin-specific protease 3	Senp3	K.SPLDPDSGLLSC*TLPNGFGGLSGPEGER.S	0.725	-
P49718	Mcm5 DNA replication licensing factor MCM5	Mcm5	K.AIAC*LLFGGSR.K	0.73	-
Q9Z2D8	Mbd3 Methyl-CpG-binding domain protein 3	Mbd3	R.DGEAPLDKAC*AEEEEEEEEEEEEPEPERV.-	0.73	-
P50431	Shmt1 Serine hydroxymethyltransferase, cytosolic	Shmt1	R.AVLEALGSC*LNNK.Y	0.73	-
P17225	Ptbp1 Polypyrimidine tract-binding protein 1	Ptbp1	K.LSLDGQNIYNAC*CTLR.I	0.73	0.976150794
O08997	Atox1 Copper transport protein ATOX1	Atox1	K.KVC*IDSEHSSDTLLATLNK.T	0.73	-
D3Z738	Gm10222 Uncharacterized protein	Gm10222	K.VSNTYGTDYVQNLNLLQC*.-	0.733333333	-
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	K.WC*EYGLTFTEK.W	0.733333333	0.781468254
O09110	Map2k3 Dual specificity mitogen-activated protein kinase	Map2k3	K.QVVEEPSPQLPADQFSPEFVDFTSQC*LR.K	0.735	-
Q60631	Grb2 Growth factor receptor-bound protein 2	Grb2	K.VLNEEC*DQNWYK.A	0.735	-
P83870	Phf5a PHD finger-like domain-containing protein 5A	Phf5a	R.IC*DEC*NYGSYQGR.C	0.735	-
Q8QZT1	Acat1 Acetyl-CoA acetyltransferase, mitochondrial	Acat1	K.DGLTDVYNKIHMGNC*AENTAK.K	0.735	0.947579365
Q9ESD6	Cmtm7 CKLF-like MARVEL transmembrane domain-containing p	Cmtm7	R.TTC*SSGGALGPGQPSEGLLDR.V	0.735	-
P84104	Srsf3 Serine/arginine-rich splicing factor 3	Srsf3	R.DSC*PLDCK.V	0.736666667	0.991607143
P50580	Pa2g4 Proliferation-associated protein 2G4	Pa2g4	R.MGVVEC*AK.H	0.736666667	0.961904762
Q8VCH0	Acaa1b 3-ketoacyl-CoA thiolase B, peroxisomal	Acaa1b	R.QC*SSGLQAVANIAGGIR.N	0.74	-
Q80Y14	Glrx5 Glutaredoxin-related protein 5, mitochondrial	Glrx5	K.GTPEQPQC*GFSNAVVQILR.L	0.74	-
Q64737	Gart Trifunctional purine biosynthetic protein adenosin	Gart	R.FGDPEC*QVILPLLK.S	0.74	0.839285714
P62880	Gnb2 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	Gnb2	R.TFVSGAC*DASIK.L	0.74	0.752678571
Q61595	Ktn1 Kinectin	Ktn1	K.AC*VAGTSDAEAVK.V	0.74	-
Q3TX08	Trmt1 tRNA (guanine(26)-N(2))-dimethyltransferase	Trmt1	K.FSAAC*GPPVTPECEHCGQR.H	0.74	-
P08249	Mdh2 Malate dehydrogenase, mitochondrial	Mdh2	K.EGVVEC*SFVQSK.E	0.74	0.923849206
Q61316	Hspa4 Heat shock 70 kDa protein 4	Hspa4	R.GC*ALQCAILSPAFK.V	0.74	0.88422619
Q921H8	Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1a	R.NGSYDIGMAC*GVESMSLSGMGNPGNISSR.L	0.74	0.799206349
Q99N85	Mrps18a 28S ribosomal protein S18a, mitochondrial	Mrps18a	K.DNVC*YSR.R	0.746666667	-
P97808	Fxyd5 FXYD domain-containing ion transport regulator 5	Fxyd5	R.QLSQFC*LNR.H	0.75	-

Q9D8Y7	Tnfaip8l2 Tumor necrosis factor alpha-induced protein 8-like	Tnfaip8l2	R.SGC*FGPGELALATR.F	0.75	-
Q9WUU7	Ctsz Cathepsin Z	Ctsz	K.DQDCDKFNQC*GTCTEFK.E	0.753333333	0.941964286
Q7TPV4	Mybbp1a Myb-binding protein 1A	Mybbp1a	K.LHGADTEDSEDQAANC*LDLDFVTR.V	0.753333333	1.121150794
Q8CI70	Lrrc20 Leucine-rich repeat-containing protein 20	Lrrc20	K.LVSFPIC*IYK.V	0.755	-
Q6P3A8	Bckdhb 2-oxoisovalerate dehydrogenase subunit beta, mitoc	Bckdhb	R.SGDLFNC*GSLTIR.A	0.755	-
P70404	Idh3g Isocitrate dehydrogenase	Idh3g	K.LGDGLFLQC*CR.E	0.755	-
Q9WTP6	Ak2 Adenylate kinase 2, mitochondrial	Ak2	K.LAENFC*VCHLATGDMLR.A	0.755	0.947777778
Q9EQP2	Ehd4 EH domain-containing protein 4	Ehd4	R.FMC*SQLPNQVLK.S	0.755	0.921964286
Q61316	Hspa4 Heat shock 70 kDa protein 4	Hspa4	R.WNSPAEEGLSDC*EVFPK.N	0.755	0.88422619
Q9CQA9	Ntpcr Cancer-related nucleoside-triphosphatase homolog	Ntpcr	R.VGSQPLPGKPEC*R.V	0.756666667	-
O35855	Bcat2 Branched-chain-amino-acid aminotransferase, mitoch	Bcat2	R.AWIGGVGDC*K.L	0.756666667	1.462797619
P62334	Psmc6 26S protease regulatory subunit 10B	Psmc6	R.NVC*TEAGMFAIR.A	0.756666667	0.94015873
Q8BNU0	Armc6 Armadillo repeat-containing protein 6	Armc6	R.AAHPDC*EDVAK.A	0.76	-
Q8CGC7	Eprs Bifunctional glutamate/proline--tRNA ligase	Eprs	K.MC*EIVFEDPK.T	0.76	-
Q9Z1G3	Atp6v1c1 V-type proton ATPase subunit C 1	Atp6v1c1	K.IDC*NLLEFK.-	0.76	-
Q60870	Reep5 Receptor expression-enhancing protein 5	Reep5	K.NC*MTDLLAK.L	0.76	-
Q9QXV3	Ing1 Inhibitor of growth protein 1	Ing1	R.VLHC*IQR.A	0.76	-
Q8QZT1	Acat1 Acetyl-CoA acetyltransferase, mitochondrial	Acat1	R.QATLGAGLPISTPC*TTVNK.V	0.76	0.947579365
Q6PIC6	Atp1a3 Sodium/potassium-transporting ATPase subunit alpha	Atp1a3	K.LIIVEGC*QR.Q	0.76	0.750634921
P60898	Polr2i DNA-directed RNA polymerase II subunit RPB9	Polr2i	R.NCDYQQEADNSC*IYVNK.I	0.76	-
P19253	Rpl13a 60S ribosomal protein L13a	Rpl13a	R.C*EGINISGNFYR.N	0.763333333	0.920079365
Q921H8	Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1a	K.ARDC*LTPMGMTSENVAER.F	0.763333333	0.799206349
Q9JKF1	Iqgap1 Ras GTPase-activating-like protein IQGAP1	Iqgap1	K.VNTSSALANISLALEQGC*AVTLLK.A	0.766666667	-
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.LTTPTYGDLNHLVSATMSGVTTC*LR.F	0.766666667	0.934563492
O35737	Hnrnph1 Heterogeneous nuclear ribonucleoprotein H	Hnrnph1	R.FFSDC*K.I	0.77	0.981507937
Q3UBZ5	Mif4gd MIF4G domain-containing protein	Mif4gd	R.VANVIVDHSLQDC*VFSK.E	0.77	-
O88952	Lin7c Protein lin-7 homolog C	Lin7c	R.VLQSEFC*NAVR.E	0.77	-
Q9D0E1	Hnrnpm Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	R.GC*AVVEFK.M	0.773333333	-

Q921F2	Tardbp TAR DNA-binding protein 43	Tardbp	R.YRNPVSQC*MR.G	0.773333333	0.897142857
Q8K1S2	Unc5d Netrin receptor UNC5D	Unc5d	K.C*NGEWVHQNEHVSEESLDESSGLK.V	0.773333333	-
Q8BYC6	Taok3 Serine/threonine-protein kinase TAO3	Taok3	R.LDEAQEAEC*QALR.L	0.773333333	-
Q9CZB0	Sdhc Succinate dehydrogenase cytochrome b560 subunit, m	Sdhc	K.SLC*LGPTLIYSAK.F	0.775	-
Q68FD5	Cltc Clathrin heavy chain 1	Cltc	R.C*NEPAVWSQLAK.A	0.775	0.891309524
Q3V3R1	Mthfd1l Monofunctional C1-tetrahydrofolate synthase, mitoc	Mthfd1l	R.GDAPEC*FVSPLAK.A	0.775	0.874166667
P29758	Oat Ornithine aminotransferase, mitochondrial	Oat	K.VLPMNTGVEAGETAC*K.L	0.776666667	1.140277778
Q61233	Lcp1 Plastin-2	Lcp1	K.EGIC*AIGGTSEQSSVGTQHSYSEEEK.Y	0.776666667	0.943095238
Q00PI9	Hnrnpul2 Heterogeneous nuclear ribonucleoprotein U-like pro	Hnrnpul2	R.NFILDQC*NVYNSGQR.R	0.78	1.107142857
Q8BFR5	Tufm Elongation factor Tu, mitochondrial	Tufm	K.NMITGTAPLDGC*ILVVAANDGPMPQTR.E	0.78	0.968888889
P57759	Erp29 Endoplasmic reticulum resident protein 29	Erp29	K.GQGVYLGMPGC*LPAYDALAGEFIK.A	0.78	0.585714286
P63168	Dynll1 Dynein light chain 1, cytoplasmic	Dynll1	K.YNPTWHC*IVGR.N	0.78	-
Q9DBJ1	Pgam1 Phosphoglycerate mutase 1	Pgam1	R.YADLTEDQLPSC*ESLK.D	0.78	1.147698413
P60335	Pcbp1 Poly(rC)-binding protein 1	Pcbp1	R.VMTIPYQPMPASSPVIC*AGGQDR.C	0.78	1.046111111
Q8R081	Hnrnpl Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	K.QPAIMPGQSYGLEDGSC*SYK.D	0.78	0.904444444
Q8BVQ5	Ppme1 Protein phosphatase methylesterase 1	Ppme1	K.QC*EGITSPEGSK.S	0.783333333	-
Q8VEK3	Hnrnpu Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	K.AVVVC*PK.D	0.783333333	1.013134921
Q8CGC7	Eprs Bifunctional glutamate/proline--tRNA ligase	Eprs	R.VAC*QGEVVR.K	0.785	-
Q8C1S0	Med19 Mediator of RNA polymerase II transcription subuni	Med19	R.LHTGPLPEQC*R.L	0.785	-
Q9D6R2	Idh3a Isocitrate dehydrogenase	Idh3a	K.IEAAC*FATIK.D	0.785	1.003650794
P38060	Hmgcl Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	K.LLEAGDFIC*QALNR.K	0.786666667	-
P61750	Arf4 ADP-ribosylation factor 4	Arf4	K.NIC*FTVWDVGGQDK.I	0.786666667	-
Q9CPR4	Rpl17 60S ribosomal protein L17	Rpl17	K.KQC*VPFR.R	0.786666667	0.912380952
Q791V5	Mtch2 Mitochondrial carrier homolog 2	Mtch2	K.TYC*YDLR.M	0.79	-
Q9R060	Nubp1 Cytosolic Fe-S cluster assembly factor NUBP1	Nubp1	R.LC*ASGAGAAPDPAVEEIR.E	0.79	-
Q9ER88	Dap3 28S ribosomal protein S29, mitochondrial	Dap3	R.FLSNC*NPEQLER.L	0.79	-
D3Z5N9	Gm5449 Protein Gm5848	Gm5449	K.NNTQVLINC*R.N	0.79	-
Q8BH04	Pck2 Phosphoenolpyruvate carboxykinase	Pck2	R.YVAAAFPSAC*GK.T	0.79	-

P49718	Mcm5 DNA replication licensing factor MCM5	Mcm5	R.KC*NMDQAGRPK.C	0.79	-
Q3UNA4	Nxt2 NTF2-related export protein 2	Nxt2	K.IASDC*FR.F	0.79	-
P51410	Rpl9 60S ribosomal protein L9	Rpl9	R.TIC*SHVQNMIK.G	0.79	0.95015873
P16675	Ctsa Lysosomal protective protein	Ctsa	K.SGLNIYNLYAPC*AGGVPGR.H	0.79	0.776904762
Q05816	Fabp5 Fatty acid-binding protein, epidermal	Fabp5	K.MIVEC*VMNNATCTR.V	0.79	0.72172619
P62259	Ywhae 14-3-3 protein epsilon	Ywhae	K.LIC*CDILDVLDK.H	0.793333333	0.976825397
Q8BIQ5	Cstf2 Cleavage stimulation factor subunit 2	Cstf2	K.LC*VQNSPQEAR.N	0.795	-
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	K.TNHIGHTGYLNTVTVSPDGSLC*ASGGK.D	0.795	0.894325397
Q9EQQ2	Yipf5 Protein YIPF5	Yipf5	K.QYAGC*DYSQQGR.F	0.795	-
Q9CQB5	Cisd2 CDGSH iron-sulfur domain-containing protein 2	Cisd2	K.VVNEINIEDLC*LTK.A	0.796666667	-
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	R.PMC*IPPPYADLGK.A	0.796666667	0.781468254
Q60932	Vdac1 Voltage-dependent anion-selective channel protein	Vdac1	K.YQVDPDAC*FSAK.V	0.796666667	0.774047619
P62827	Ran GTP-binding nuclear protein Ran	Ran	R.VC*ENIPIVLC*GNK.V	0.8	0.985238095
A2AGH6	Med12 Mediator of RNA polymerase II transcription subuni	Med12	K.TPQLNPC*QSDGNKPTVGIR.S	0.8	-
P62983	Rps27a Ubiquitin-40S ribosomal protein S27a	Rps27a	R.EC*PSDEC*GAGVFMGSHFDR.H	0.8	1.528174603
P58252	Eef2 Elongation factor 2	Eef2	R.YVEPIEDVPC*GNIVGLVGVDQFLVK.T	0.8	1.011428571
P45376	Akr1b1 Aldose reductase	Akr1b1	R.VC*ALMSCAK.H	0.8	0.795
Q9CPY3	Cdca5 Sororin	Cdca5	R.SFFGFEGPDDLPGVSPVVC*SK.L	0.803333333	-
P24547	Impdh2 Inosine-5-monophosphate dehydrogenase 2	Impdh2	R.VGMGSGSIC*ITQEVLACGRPQATAVYK.V	0.803333333	0.931190476
Q8BMS1	Hadha Trifunctional enzyme subunit alpha, mitochondrial	Hadha	R.KYESAYGTQFTPC*QLLLDHANNSSK.K	0.803333333	0.839285714
Q9CRC6	UPF0693 protein C10orf32 homolog	UPF0693	K.VNTC*GTDVIALTK.Q	0.805	-
P62196	Psmc5 26S protease regulatory subunit 8	Psmc5	K.FVVDVDKNIDINDVTPNC*R.V	0.805	-
Q9WUK4	Rfc2 Replication factor C subunit 2	Rfc2	R.FALAC*NASDK.I	0.805	-
Q8K2A7	Ints10 Integrator complex subunit 10	Ints10	K.VTEQC*FNTLER.S	0.806666667	-
B9EJ54	Nup205 MCG21756, isoform CRA_b	Nup205	K.KPISTTNLQDPGVLGC*PR.T	0.806666667	-
Q6PDY2	Ado 2-aminoethanethiol dioxygenase	Ado	K.EASGSAC*DLPR.E	0.806666667	-
Q60597	Ogdh 2-oxoglutarate dehydrogenase, mitochondrial	Ogdh	R.FGLEGC*EVLIPALK.T	0.806666667	0.727678571
P62918	Rpl8 60S ribosomal protein L8	Rpl8	K.AQLNIGNVLPVGTMPEGTIVC*CLEEKPGDR.G	0.81	0.98202381
P97351	Rps3a 40S ribosomal protein S3a	Rps3a	R.LFC*VGFTK.K	0.81	0.975
P68368	Tuba4a Tubulin alpha-4A chain	Tuba4a	K.TIGGGDDSFTTFFC*ETGAGK.H	0.81	0.90781746

Q61263	Soat1 Sterol O-acyltransferase 1	Soat1	K.SASLDNGGC*ALTTFSILEEMK.K	0.81	-
Q9CR59	Gadd45gip1 Growth arrest and DNA damage-inducible proteins-in	Gadd45gip1	R.IAEC*MAK.M	0.81	-
E9PVA8	Gcn1l1 Protein Gcn1l1	Gcn1l1	K.ILDVASLEALNEC*SR.R	0.81	-
Q8BUI3	LRWD1 Leucine-rich repeat and WD repeat-containing prote	LRWD1	K.DTASTC*SQVENLDR.E	0.81	-
Q9CR47	Nsa2 Ribosome biogenesis protein NSA2 homolog	Nsa2	K.VC*FVGDGFTR.K	0.81	-
Q0VGB7	Ppp4r2 Serine/threonine-protein phosphatase 4 regulatory	Ppp4r2	K.NVMVVSCVC*PSSEK.N	0.81	-
Q5SSL4	Abr Active breakpoint cluster region-related protein	Abr	K.C*SQSNNQFQK.I	0.81	-
P70404	Idh3g Isocitrate dehydrogenase	Idh3g	R.TSLDLYANVIHC*K.S	0.81	-
Q99JY0	Hadhb Trifunctional enzyme subunit beta, mitochondrial	Hadhb	K.DGGQYALVAAC*AAGGQGHAMIVEAYPK.-	0.813333333	-
P62814	Atp6v1b2 V-type proton ATPase subunit B, brain isoform	Atp6v1b2	K.KTSC*EFTGDILR.T	0.813333333	0.983214286
P46061	Rangap1 Ran GTPase-activating protein 1	Rangap1	K.LNNC*GMGIGGGK.I	0.815	-
O35643	Ap1b1 AP-1 complex subunit beta-1	Ap1b1	K.TAAVC*VAK.L	0.815	-
B2RSH2	Gnai1 Guanine nucleotide-binding protein G(i) subunit al	Gnai1	K.NNLKDC*GLF.-	0.815	-
O35972	Mrpl23 39S ribosomal protein L23, mitochondrial	Mrpl23	R.C*PGIPSWFGL.-	0.816666667	-
P05214	Tuba3b Tubulin alpha-3 chain	Tuba3b	K.AYHEQLSVAEITNAC*FEPANQMVK.C	0.816666667	-
Q3THE2	Myl12b Myosin regulatory light chain 12B	Myl12b	R.NAFAC*FDEEATGTIQEDYLR.E	0.82	1.211488095
P05202	Got2 Aspartate aminotransferase, mitochondrial	Got2	K.EYLPIGGLAEFC*K.A	0.82	0.834047619
Q3UIA2	Arhgap17 Rho GTPase-activating protein 17	Arhgap17	K.LQYLWTTC*QK.L	0.82	-
P47713	Pla2g4a Cytosolic phospholipase A2	Pla2g4a	R.C*SVSLSNVEAR.K	0.82	-
P62482	Kcnab2 Voltage-gated potassium channel subunit beta-2	Kcnab2	K.IGVGAMTWSPLAC*GIVSGK.Y	0.82	-
E9QP49	Ehbp1l1 EH domain-binding protein 1-like protein 1	Ehbp1l1	R.FQDTSQYVC*AELQALEQEQGQIDGR.A	0.82	-
P14152	Mdh1 Malate dehydrogenase, cytoplasmic	Mdh1	K.VIVVGNPANTNC*LTASK.S	0.82	0.915357143
Q6ZWV3	Rpl10 60S ribosomal protein L10	Rpl10	K.SC*GKDGFHIR.V	0.82	0.824722222
Q6P542	Abcf1 ATP-binding cassette sub-family F member 1	Abcf1	R.ALSIPPNIDVLLC*EQEVVADETPAVQAVLR.A	0.825	-
Q8CGC7	Eprs Bifunctional glutamate/proline--tRNA ligase	Eprs	K.ERPAPAVSSTC*ATAEDSSVLYSR.V	0.825	-
Q9WUK4	Rfc2 Replication factor C subunit 2	Rfc2	K.TTSILC*LAR.A	0.825	-
P27659	Rpl3 60S ribosomal protein L3	Rpl3	K.GC*VVGTK.K	0.825	0.932896825

Q99KI0	Aco2 Aconitate hydratase, mitochondrial	Aco2	R.DVGGIVLANACGPC*IGQWDR.K	0.825	0.937103175
O55234	Psmb5 Proteasome subunit beta type-5	Psmb5	K.KVIEINPYLLGTMAGGAADC*SFWER.L	0.826666667	-
Q9CQA3	Sdhb Succinate dehydrogenase	Sdhb	R.C*HTIMNCTQTCPK.G	0.826666667	0.737857143
Q8BUE4	Aifm2 Apoptosis-inducing factor 2	Aifm2	R.VPLADKELLPC*VR.Q	0.83	-
P17918	Pcna Proliferating cell nuclear antigen	Pcna	K.C*AGNEDIITLR.A	0.83	0.799583333
Q9ERK4	Cse1l Exportin-2	Cse1l	K.LSTAC*PGR.V	0.83	-
P47856	Gfpt1 Glucosamine--fructose-6-phosphate aminotransferase	Gfpt1	K.C*QNALQQVVAR.Q	0.83	-
Q62433	Ndrg1 Protein NDRG1	Ndrg1	K.MADC*GGLPQISQPAK.L	0.83	-
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	K.YTVQDESHSEWVSC*VR.F	0.83	0.894325397
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	K.WNTDNTLGTEIAIEDQIC*QGLK.L	0.83	0.781468254
O88844	Idh1 Isocitrate dehydrogenase	Idh1	K.SEGGFIWAC*K.N	0.833333333	0.808392857
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	K.SC*SGVEFSTSGSSNTDTGK.V	0.833333333	0.781468254
Q922H4	Gmppa Mannose-1-phosphate guanyltransferase alpha	Gmppa	K.LLPAITILGC*R.V	0.835	-
Q3UFM5	Nom1 Nucleolar MIF4G domain-containing protein 1	Nom1	R.TTSESEAC*ESR.S	0.835	-
Q61074	Ppm1g Protein phosphatase 1G	Ppm1g	R.YGQNC*QK.V	0.835	-
P62874	Gnb1 Guanine nucleotide-binding protein G(I)/G(S)/G(T)	Gnb1	R.VSC*LGVTDDGMAVATGSWDSFLK.I	0.835	0.752678571
P63038	Hspd1 60 kDa heat shock protein, mitochondrial	Hspd1	K.C*EFQDAYVLLSEK.K	0.836666667	1.066666667
P59999	Arpc4 Actin-related protein 2/3 complex subunit 4	Arpc4	R.ATLQAALC*LENFSSQVVER.H	0.836666667	1.05172619
Q91VA7	Idh3b Isocitrate dehydrogenase 3 (NAD) beta	Idh3b	K.LGDGLFLQC*CEEVAELYPK.I	0.836666667	0.870535714
Q00PI9	Hnrnpul2 Heterogeneous nuclear ribonucleoprotein U-like pro	Hnrnpul2	K.ANFSLPEKC*DYMDEVTYGELEKEEAQPIVTK.Y	0.836666667	1.107142857
Q9Z2I8	Suclg2 Succinyl-CoA ligase	Suclg2	K.IDATQVEVNPFGETPEGQVVC*FDAK.I	0.836666667	0.691964286
Q9WVJ2	Psmd13 26S proteasome non-ATPase regulatory subunit 13	Psmd13	K.SSDEAVILC*K.T	0.84	-
Q6P5B0	Rrp12 RRP12-like protein	Rrp12	R.VTVC*QALR.T	0.84	-
Q99LN9	Dohh Deoxyhypusine hydroxylase	Dohh	R.LEWLQQHPGEATC*AGPYLSVDPAPPAAEQDVGR.L	0.84	-
P25206	Mcm3 DNA replication licensing factor MCM3	Mcm3	K.GC*YTSGTFR.T	0.84	-
O54774	Ap3d1 AP-3 complex subunit delta-1	Ap3d1	K.LEDPDPGVQSAAVNVIC*ELAR.R	0.84	-
Q8WTY4	Ciapin1 Anamorsin	Ciapin1	K.NCTC*GLAEELER.E	0.84	-
P62717	Rpl18a 60S ribosomal protein L18a	Rpl18a	R.DLTTAGAVTQC*YR.D	0.843333333	-
P97351	Rps3a 40S ribosomal protein S3a	Rps3a	K.LITEDVQGKNC*LTNFHGMDLTR.D	0.843333333	0.975
E9Q070	Gm8730 Uncharacterized protein	Gm8730	R.AGAIAPC*EVTVPAQNTGLGPEK.T	0.843333333	0.860634921

H7BX26	Cep170 Centrosomal protein of 170 kDa	Cep170	K.SSPVNNHSSPSQTPALC*PPETR.A	0.845	-
Q62348	Tsn Translin	Tsn	R.GFNKETAAAC*GEK.-	0.845	-
Q9WTX5	Skp1 S-phase kinase-associated protein 1	Skp1	K.GLLDVTC*K.T	0.846666667	-
Q9DCL9	Paics Multifunctional protein ADE2	Paics	K.C*GETAFIAPQCEMIPIEWVCR.R	0.846666667	-
P62717	Rpl18a 60S ribosomal protein L18a	Rpl18a	K.KSSGEIVYC*GQVFEK.S	0.846666667	-
Q9Z1F9	Uba2 SUMO-activating enzyme subunit 2	Uba2	R.VLVVGAGGIGC*ELLK.N	0.85	-
Q99LG4	Ttc5 Tetratricopeptide repeat protein 5	Ttc5	R.VETPLLLVVNGKPQNSSSQASATVASRPQC*E.-	0.85	-
Q9JJT9	Phax Phosphorylated adapter RNA export protein	Phax	K.VLGGGSAAC*APVSHYR.T	0.85	-
Q8BFR5	Tufm Elongation factor Tu, mitochondrial	Tufm	K.GEETPVIVGSALC*ALEQR.D	0.85	0.968888889
P97930	Dtymk Thymidylate kinase	Dtymk	K.QVLLC*FQQLMEEK.N	0.85	-
Q3UJB9	Edc4 Enhancer of mRNA-decapping protein 4	Edc4	R.LC*AQLEGLQSTVTDHVER.A	0.85	-
Q9QUR7	Pin1 Peptidyl-prolyl cis-trans isomerase NIMA-interacti	Pin1	K.IKSGEEDFESLASQFSDC*SSAK.A	0.853333333	-
J3QPE8	Uncharacterized protein	Uncharacterized	K.SC*SGVEFSTSGHAYTDTGK.A	0.853333333	0.745535714
Q99JX7	Nxf1 Nuclear RNA export factor 1	Nxf1	R.SC*MAATLR.I	0.855	-
Q924C1	Xpo5 Exportin-5	Xpo5	K.TDSSQEAEAQANC*R.V	0.855	-
Q3TBW2	Mrpl10 39S ribosomal protein L10, mitochondrial	Mrpl10	K.EQNEGDC*ATSANEK.L	0.855	-
Q9D172	D10Jhu81e ES1 protein homolog, mitochondrial	D10Jhu81e	K.NLSTFAVDGKDC*K.V	0.855	-
E9Q1N8	Rps2-ps5 Uncharacterized protein	Rps2-ps5	K.KLLMMAGIDDC*YTSAR.G	0.855	-
Q8BM55	Tmem214 Transmembrane protein 214	Tmem214	R.SSGLLPVGQQVC*AR.L	0.855	-
P46460	Nsf Vesicle-fusing ATPase	Nsf	R.VFPPEIVEQMGC*K.H	0.855	-
Q68FD5	Cltc Clathrin heavy chain 1	Cltc	R.LPVVIGGLLDVDC*SEDVIK.N	0.855	0.891309524
Q8BMS1	Hadha Trifunctional enzyme subunit alpha, mitochondrial	Hadha	K.ALMGLYNGQVLC*K.K	0.856666667	0.839285714
Q9D0E1	Hnrnpm Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	K.MEEESGAPC*VPSGNGAPGPK.G	0.86	-
Q8BGE6	Atg4b Cysteine protease ATG4B	Atg4b	R.ANLPC*AGAAALPTDSER.H	0.86	-
P60605	Ube2g2 Ubiquitin-conjugating enzyme E2 G2	Ube2g2	R.VC*ISILHAPGDDPMGYESSAER.W	0.86	-
P20152	Vim Vimentin	Vim	R.QVQSLTC*EVDALK.G	0.86	1.045714286
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.TAVC*DIPPR.G	0.86	0.934563492
Q6ZWV3	Rpl10 60S ribosomal protein L10	Rpl10	K.AKVDEFPLC*GHMVSDEYEQLSSEALEAAR.I	0.86	0.824722222
P48962	Slc25a4 ADP/ATP translocase 1	Slc25a4	R.YFAGNLASGGAAGATSLC*FVYPLDFAR.T	0.86	0.764404762
E9Q070	Gm8730 Uncharacterized protein	Gm8730	K.C*FIVGADNVGSK.Q	0.863333333	0.860634921
A2AD25	Gm4987 Novel protein silmilar to ribosomal protein L32	Gm4987	K.ELEVLLMC*NK.S	0.863333333	-
Q8BH59	Slc25a12 Calcium-binding mitochondrial carrier protein Aral	Slc25a12	R.DGSIPLPAEILAGGC*AGGSQVIFTNPLEIVK.I	0.865	-

Q9DCJ5	Ndufa8 NADH dehydrogenase	Ndufa8	K.LVNGC*ALNFFR.Q	0.865	-
O35465	Fkbp8 Peptidyl-prolyl cis-trans isomerase FKBP8	Fkbp8	K.VDMTC*EEEEELLQLK.V	0.865	-
P42932	Cct8 T-complex protein 1 subunit theta	Cct8	K.AHEILPELVC*CSAK.N	0.865	0.980634921
P68254	Ywhaq 14-3-3 protein theta	Ywhaq	R.YLAEVAC*GDDR.K	0.866666667	1.065992063
Q3UJB9	Edc4 Enhancer of mRNA-decapping protein 4	Edc4	K.SC*QAMFQQINDSFR.L	0.866666667	-
Q8VEK3	Hnrnpu Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	K.DC*EVVMMIGLPGAGK.T	0.866666667	1.013134921
P62267	Rps23 40S ribosomal protein S23	Rps23	K.ITAFVPNDGC*LNFIEENDEVLVAGFGR.K	0.866666667	0.928928571
Q9Z266	Snapin SNARE-associated protein Snapin	Snapin	R.EQIDNLATELC*R.I	0.87	-
Q99LC8	Eif2b1 Translation initiation factor eIF-2B subunit alpha	Eif2b1	K.IGTNQMAVC*AK.A	0.87	-
Q8R3C0	Mcmbp Mini-chromosome maintenance complex-binding protei	Mcmbp	R.DASALLDPMEC*TDMAEEQR.V	0.87	-
P40124	Cap1 Adenylyl cyclase-associated protein 1	Cap1	R.LEAVSHTSDMHC*GYGDSPSK.G	0.87	1.196865079
P51410	Rpl9 60S ribosomal protein L9	Rpl9	R.MRTGVAC*SVSQAQK.D	0.87	0.95015873
P16110	Lgals3 Galectin-3	Lgals3	R.RVIVC*NTK.Q	0.87	0.81515873
P62717	Rpl18a 60S ribosomal protein L18a	Rpl18a	K.C*HTPPLYR.M	0.87	-
Q922Q4	Pycr2 Pyrroline-5-carboxylate reductase 2	Pycr2	R.C*MTNTPVVVR.E	0.87	1.211309524
Q9R0Q6	Arpc1a Actin-related protein 2/3 complex subunit 1A	Arpc1a	R.STVLSLDWHPNNVLLAAGSC*DFK.C	0.873333333	-
Q8VEK3	Hnrnpu Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	K.EKPYFPIPEDC*TFIQNVPLEDR.V	0.873333333	1.013134921
Q8VEK3	Hnrnpu Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	K.GNFTLPEVAEC*FDEITYVELQK.E	0.873333333	1.013134921
J3QPE8	Uncharacterized protein	Uncharacterized	K.VC*NYGLTFTQK.W	0.873333333	0.745535714
Q8BNV1	Trmt2a tRNA (uracil-5-)-methyltransferase homolog A	Trmt2a	K.GGTC*AVAAPFDTVHIPEATK.Q	0.875	-
P97377	Cdk2 Cyclin-dependent kinase 2	Cdk2	R.APEILLGC*K.Y	0.875	-
B2RY56	Rbm25 RNA-binding protein 25	Rbm25	K.LKENDENC*GPTTTVFVGNISEK.A	0.875	-
Q8BVA5	UPF0554 protein C2orf43 homolog	UPF0554	K.FATPFLC*QFR.Y	0.875	-
P60335	Pcbp1 Poly(rC)-binding protein 1	Pcbp1	R.AITIAGVPQSVTEC*VK.Q	0.876666667	1.046111111
E9Q616	Ahnak Protein Ahnak	Ahnak	K.ISMQDVDLSLGSC*K.L	0.88	1.119007937
Q61458	Ccnh Cyclin-H	Ccnh	R.TC*LSQLLDIMK.S	0.88	-
Q9CQ48	Nudcd2 NudC domain-containing protein 2	Nudcd2	R.DAANC*WTSLLESEYAADPWVQDQMQR.K	0.88	-
Q8BH43	Wasf2 Wiskott-Aldrich syndrome protein family member 2	Wasf2	R.QTLPSDTSELEC*R.T	0.88	-
Q3TXS7	Psmd1 26S proteasome non-ATPase regulatory subunit 1	Psmd1	K.SNC*KPSTFAYPAPLEVPK.E	0.88	-
P49138	Mapkapk2 MAP kinase-activated protein kinase 2	Mapkapk2	K.ETTSHNSLTTPC*YTPYYVAPEVLGPEK.Y	0.88	-
Q80X85	Mrps7 28S ribosomal protein S7, mitochondrial	Mrps7	K.NC*EPVIGLVPILK.G	0.88	-

P60335	Pcbp1 Poly(rC)-binding protein 1	Pcbp1	R.INISEGNC*PER.I	0.88	1.046111111
P62814	Atp6v1b2 V-type proton ATPase subunit B, brain isoform	Atp6v1b2	R.GPVVLAEDFLDIMGQPINPQC*R.I	0.88	0.983214286
Q99NB9	Sf3b1 Splicing factor 3B subunit 1	Sf3b1	K.VQENC*IDLVGR.I	0.88	0.956845238
Q3TW96	Uap1l1 UDP-N-acetylhexosamine pyrophosphorylase-like prot	Uap1l1	K.NFVAFEVC*R.E	0.88	0.943571429
Q61316	Hspa4 Heat shock 70 kDa protein 4	Hspa4	R.SVMDATQIAGLNC*LR.L	0.88	0.88422619
Q8VBZ3	Clptm1 Cleft lip and palate transmembrane protein 1 homol	Clptm1	K.ATSGAC*TASQPQEAPPKPAEDK.K	0.88	0.755059524
Q78PY7	Snd1 Staphylococcal nuclease domain-containing protein	Snd1	R.LSEC*EEQAK.A	0.88	0.984880952
P24270	Cat Catalase	Cat	R.LGPNYLQIPVNC*PYR.A	0.88	0.901785714
O54692	Zw10 Centromere/kinetochore protein zw10 homolog	Zw10	R.LAPILC*DGTTTFVDLVPGFR.R	0.883333333	-
Q922Q4	Pycr2 Pyrroline-5-carboxylate reductase 2	Pycr2	R.SLLINAVEASC*IR.T	0.883333333	1.211309524
Q61749	Eif2b4 Translation initiation factor eIF-2B subunit delta	Eif2b4	R.VQTDAFVSNELDDPDDLQC*K.R	0.885	-
Q9QUI0	Rhoa Transforming protein RhoA	Rhoa	R.IGAFGYMEC*SAK.T	0.885	1
Q8BH95	Echs1 Enoyl-CoA hydratase, mitochondrial	Echs1	R.TFQDC*YSSK.F	0.886666667	-
Q8CIG8	Prmt5 Protein arginine N-methyltransferase 5	Prmt5	R.DLNC*VPEIADTLGAVAK.Q	0.886666667	-
Q9Z2I9	Sucla2 Succinyl-CoA ligase	Sucla2	K.ILAC*DDLDEAAK.M	0.89	0.779761905
Q9ERK4	Cse1l Exportin-2	Cse1l	K.NLFEDQNTLTSIC*EK.V	0.89	-
Q9QZE5	Copg1 Coatomer subunit gamma-1	Copg1	K.HPSAVTAC*NLDLENLVTDSNR.S	0.89	-
Q9DBL1	Acadsb Short/branched chain specific acyl-CoA dehydrogena	Acadsb	R.ASSTC*QLTFENVKVPETNILGK.I	0.89	-
Q8BMJ2	Lars Leucine--tRNA ligase, cytoplasmic	Lars	K.NMETFC*EESR.K	0.89	1.201706349
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.NMMAAC*DPR.H	0.89	0.934563492
Q9D8E6	Rpl4 60S ribosomal protein L4	Rpl4	R.FC*IWTESAFR.K	0.89	0.926944444
Q9D8E6	Rpl4 60S ribosomal protein L4	Rpl4	R.GPC*IIYNEDNGIIK.A	0.89	0.926944444
Q6ZWU9	Rps27 40S ribosomal protein S27	Rps27	K.ARLTEGC*SFR.R	0.893333333	-
O54984	Asna1 ATPase Asna1	Asna1	K.NQISPFISQMC*NMLGLGDMNADQLASK.L	0.893333333	-
Q9DBA9	Gtf2h1 General transcription factor IIH subunit 1	Gtf2h1	K.DLFAEC*AK.I	0.895	-
Q9D898	Arpc5l Actin-related protein 2/3 complex subunit 5-like p	Arpc5l	K.FVDEHEEAAAAAGEPGPDPC*EVDGLLR.Q	0.895	-
Q9CQC6	Bzw1 Basic leucine zipper and W2 domain-containing prot	Bzw1	K.ERFDPTQFQDC*IIQGLTETGTDLEAVAK.F	0.895	-
Q9R1Q7	Plp2 Proteolipid protein 2	Plp2	R.LSAPGC*WLACTSFSR.T	0.895	-
P62307	Snrpf Small nuclear ribonucleoprotein F	Snrpf	R.C*NNVLYIR.G	0.895	-
D3YXK2	Safb Scaffold attachment factor B1	Safb	K.AIEDEGGNPDEIEVTSEC*NK.K	0.895	1.087797619

Q99JY9	Actr3 Actin-related protein 3	Actr3	K.LGYAGNTEPQFIIPSC*IAIK.E	0.895	0.977619048
Q9DBT5	Ampd2 AMP deaminase 2	Ampd2	K.C*GVPFTDLLDAAK.S	0.896666667	-
Q6NSR8	Npepl1 Probable aminopeptidase NPEPL1	Npepl1	R.ASEDPLLNLVSPLDC*EVDAQEGDNMGR.D	0.896666667	-
P40124	Cap1 Adenylyl cyclase-associated protein 1	Cap1	K.GKINSITVDNC*K.K	0.896666667	1.196865079
Q9R1T2	Sae1 SUMO-activating enzyme subunit 1	Sae1	K.GSGIVEC*LGPQ.-	0.896666667	0.989107143
Q8BY71	Hat1 Histone acetyltransferase type B catalytic subunit	Hat1	K.VDENFDC*VEADDVEGK.I	0.896666667	-
Q8BP67	Rpl24 60S ribosomal protein L24	Rpl24	K.VELC*SFSGYK.I	0.896666667	0.906865079
O70311	Nmt2 Glycylpeptide N-tetradecanoyltransferase 2	Nmt2	R.AMELLSAC*QGPAR.N	0.9	-
E9PW43	Gm10320 Protein Gm10320	Gm10320	K.NASC*GTR.S	0.9	-
P08249	Mdh2 Malate dehydrogenase, mitochondrial	Mdh2	K.ETEC*TYFSTPLLLGK.K	0.9	0.923849206
Q68FD5	Cltc Clathrin heavy chain 1	Cltc	K.VIQC*FAETGQVQK.I	0.9	0.891309524
P05214	Tuba3b Tubulin alpha-3 chain	Tuba3b	R.AVC*MLSNTTAIAEAWAR.L	0.9	-
Q922B2	Dars Aspartate--tRNA ligase, cytoplasmic	Dars	R.LEYC*EALAMLR.E	0.9	-
F8VQK7	Gm16519 Protein Gm16519	Gm16519	R.C*TGGEVGATSALAPK.I	0.9	-
Q9D0E1	Hnrnpm Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	K.AC*QIFVR.N	0.9	-
G5E8V9	Arfip1 Protein Arfip1	Arfip1	K.EGVTEAGAPQGSSAPPLPC*VLSPSR.V	0.9	-
O35286	Dhx15 Putative pre-mRNA-splicing factor ATP-dependent RN	Dhx15	K.RGVAC*TQPR.R	0.9	-
P68368	Tuba4a Tubulin alpha-4A chain	Tuba4a	K.RSIQFVDWC*PTGFK.V	0.9	0.90781746
Q9CYN2	Spcs2 Signal peptidase complex subunit 2	Spcs2	R.SGGGGGSSGAGGGPSC*GTSSSR.S	0.9	0.864583333
Q9D1Q4	Dpm3 Dolichol-phosphate mannosyltransferase subunit 3	Dpm3	R.VATFHDC*EDAAR.E	0.903333333	-
P61164	Actr1a Alpha-centractin	Actr1a	K.YC*FPNYVGRPK.H	0.903333333	-
Q07417	Acads Short-chain specific acyl-CoA dehydrogenase, mitoc	Acads	R.IGIASQALGIAQASLDC*AVK.Y	0.903333333	-
Q8BP67	Rpl24 60S ribosomal protein L24	Rpl24	K.C*ESAFLSK.R	0.903333333	0.906865079
P51881	Slc25a5 ADP/ATP translocase 2	Slc25a5	K.GLGDC*LVK.I	0.903333333	0.75547619
O35075	Dscr3 Down syndrome critical region protein 3 homolog	Dscr3	R.VETCGC*AEGYAR.D	0.905	-
Q9DBR0	Akap8 A-kinase anchor protein 8	Akap8	K.TNDGGLAAGSPAMHVASFAPEPC*TDNSDSLIAK.I	0.905	-
Q9WV80	Snx1 Sorting nexin-1	Snx1	K.LQEVEC*EEQR.L	0.905	-
Q9WUA2	Farsb Phenylalanine--tRNA ligase beta subunit	Farsb	K.TKEYTAC*ELMNIYK.T	0.905	-
D3YYI5	Gm7293 Glyceraldehyde-3-phosphate dehydrogenase	Gm7293	K.IVSNASC*TTNCLAPLAK.V	0.905	1.285634921
Q7TPV4	Mybbp1a Myb-binding protein 1A	Mybbp1a	R.YPVIC*K.N	0.905	1.121150794

P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	K.LWNTLGVC*K.Y	0.905	0.894325397
Q61510	Trim25 E3 ubiquitin/ISG15 ligase TRIM25	Trim25	K.NTVMC*AVVEQFLQAEQAR.T	0.906666667	-
P62245	Rps15a 40S ribosomal protein S15a	Rps15a	R.LNKC*GVISPR.F	0.906666667	0.89077381
Q61316	Hspa4 Heat shock 70 kDa protein 4	Hspa4	K.LMSANASDLPLSIEC*FMNDIDVSGTMNR.G	0.906666667	0.88422619
Q3UA06	Trip13 Pachytene checkpoint protein 2 homolog	Trip13	K.QALPC*VAESPAVHVEVLQR.S	0.91	-
Q99LE6	Abcf2 ATP-binding cassette sub-family F member 2	Abcf2	K.TLSFYFPPC*GK.I	0.91	-
Q8K1E0	Stx5 Syntaxin-5	Stx5	R.DRTQEFQSAC*K.S	0.91	-
Q9CPR4	Rpl17 60S ribosomal protein L17	Rpl17	R.INPYMSSPC*HIEMILTEK.E	0.91	0.912380952
Q07417	Acads Short-chain specific acyl-CoA dehydrogenase, mitoc	Acads	K.IGC*FALSEPGNGSDAGAASTTAR.E	0.91	-
E9Q616	Ahnak Protein Ahnak	Ahnak	K.GPSVDVEVPDVDLEC*PDAK.L	0.913333333	1.119007937
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.EAESC*DC*LQGFQLTHSLGGGTGSGMGTLLISK.I	0.913333333	0.934563492
P51881	Slc25a5 ADP/ATP translocase 2	Slc25a5	K.GTDIMYTGTLDC*WR.K	0.913333333	0.75547619
Q9WUA3	Pfkp 6-phosphofructokinase type C	Pfkp	K.WDC*VSSILQVGGTIIGSAR.C	0.915	0.971011905
J3QK52	Noc2l Nucleolar complex protein 2 homolog	Noc2l	R.AAVATTQGEQEAAETC*R.F	0.915	-
P37913	Lig1 DNA ligase 1	Lig1	K.GLFVAC*R.H	0.915	-
P32921	Wars Tryptophan--tRNA ligase, cytoplasmic	Wars	R.NC*DSDATK.A	0.915	1.16922619
O08807	Prdx4 Peroxiredoxin-4	Prdx4	R.ENEC*HFYAGGQVYPGEASR.V	0.915	0.829404762
Q9JIK5	Ddx21 Nucleolar RNA helicase 2	Ddx21	K.KDAQELSQNTC*IK.Q	0.92	1.307698413
Q60715	P4ha1 Prolyl 4-hydroxylase subunit alpha-1	P4ha1	R.HAAC*PVLVGNK.W	0.92	1.300595238
P40142	Tkt Transketolase	Tkt	R.MAAISESNINLC*GSHCGVSIGEDGPSQMALEDLAMFR.S	0.92	0.955833333
Q8BHD7	Ptbp3 Polypyrimidine tract-binding protein 3	Ptbp3	K.MALDGQNIYNACC*TLR.I	0.92	-
Q8BK67	Rcc2 Protein RCC2	Rcc2	K.GNLYSFGC*PEYGQLGHNSDGK.F	0.92	1.082202381
P35486	Pdha1 Pyruvate dehydrogenase E1 component subunit alpha,	Pdha1	K.NFYGGNGIVGAQVPLGAGIALAC*K.Y	0.923333333	-
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	R.YWLC*AATGPSIK.I	0.923333333	0.894325397
O09110	Map2k3 Dual specificity mitogen-activated protein kinase	Map2k3	K.TMDAGC*KPYMAPER.I	0.925	-
Q8BU30	Iars Isoleucine--tRNA ligase, cytoplasmic	Iars	K.VMPFSTAC*GTPLSNFESNQNYK.D	0.925	-
O70252	Hmox2 Heme oxygenase 2	Hmox2	K.GTLGGSNC*PFQTTVAVLR.K	0.925	-
E9Q035	Gm20425 Protein Gm20425	Gm20425	K.NSPSLLIAC*NK.Q	0.925	1.210714286
Q6PAM1	Txlna Alpha-taxilin	Txlna	K.AAQPGALC*DVSEELSR.Q	0.926666667	-

P62242	Rps8 40S ribosomal protein S8	Rps8	K.NC*IVLIDSTPYR.Q	0.926666667	0.784285714
Q9ESZ8	Gtf2i General transcription factor II-I	Gtf2i	K.YC*VEEEEK.A	0.93	-
Q9CZG3	Commd8 COMM domain-containing protein 8	Commd8	K.NFSEEETLQQLNQLNSC*HQEAVLK.C	0.93	-
P27659	Rpl3 60S ribosomal protein L3	Rpl3	K.TVFAEHISDEC*K.R	0.93	0.932896825
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	K.AEPPQC*TSLAWSADGQTLFAGYTDNLVR.V	0.93	0.894325397
P23198	Cbx3 Chromobox protein homolog 3	Cbx3	R.LTWHSC*PEDEAQ.-	0.93	0.892063492
Q9JHS3	Lamtor2 Ragulator complex protein LAMTOR2	Lamtor2	K.FILMDC*MEGR.V	0.933333333	-
P62889	Rpl30 60S ribosomal protein L30	Rpl30	K.LVILANNC*PALR.K	0.933333333	0.945912698
Q61753	Phgdh D-3-phosphoglycerate dehydrogenase	Phgdh	K.NAGTC*LSPAVIVGLLR.E	0.933333333	0.79797619
Q8R3D1	Tbc1d13 TBC1 domain family member 13	Tbc1d13	K.SLDDSQC*GITYK.M	0.935	-
Q9Z2Z6	Slc25a20 Mitochondrial carnitine/acylcarnitine carrier prot	Slc25a20	R.LQTQPPSLSGQPPMYSGTLDC*FR.K	0.935	-
Q8K4Z5	Sf3a1 Splicing factor 3A subunit 1	Sf3a1	R.EVLDQVC*YR.V	0.935	-
P58252	Eef2 Elongation factor 2	Eef2	K.EGALC*EENMR.G	0.935	1.011428571
Q8R081	Hnrnpl Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	K.MNVC*VSK.Q	0.935	0.904444444
E9Q616	Ahnak Protein Ahnak	Ahnak	K.LQGNIGMDAC*ASK.I	0.936666667	1.119007937
P62702	Rps4x 40S ribosomal protein S4, X isoform	Rps4x	R.EC*LPLIIFLR.N	0.936666667	0.787301587
Q9JIF0	Prmt1 Protein arginine N-methyltransferase 1	Prmt1	K.VIGIEC*SSISDYAVK.I	0.936666667	-
Q91VR8	Brk1 Protein BRICK1	Brk1	K.ISDFLNSFDMSC*R.S	0.936666667	-
Q9CR57	Rpl14 60S ribosomal protein L14	Rpl14	K.C*MQLTDFILK.F	0.936666667	0.872857143
P97461	Rps5 40S ribosomal protein S5	Rps5	R.VNQAIWLLC*TGAR.E	0.936666667	0.852698413
Q9QYA2	Tomm40 Mitochondrial import receptor subunit TOM40 homolo	Tomm40	R.TPGAAASGAAAASEDGSC*GCLPNPGTFEECHR.K	0.936666667	0.723214286
P39054	Dnm2 Dynamin-2	Dnm2	K.LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK.S	0.936666667	-
Q99LI9	Clp1 Polyribonucleotide 5-hydroxyl-kinase Clp1	Clp1	K.VGAPTIPDSC*LPLGMSQEDNQLK.L	0.94	-
Q8C079	Fam40a Protein FAM40A	Fam40a	R.THSNPDFLPVDNC*LQSVLGQR.V	0.94	-
Q9CQ28	Atpbd4 ATP-binding domain-containing protein 4	Atpbd4	R.VYTQC*EGDEVEDLYELLK.L	0.94	-
Q68FL4	Ahcyl2 Putative adenosylhomocysteinase 3	Ahcyl2	K.AGKLC*VPAMNVNDSVTK.Q	0.94	-
Q9DCS3	Mecr Trans-2-enoyl-CoA reductase, mitochondrial	Mecr	R.LALNC*VGGK.S	0.94	-
P53996	Cnbp Cellular nucleic acid-binding protein	Cnbp	R.EQC*CYNCGKPGHLAR.D	0.94	-
Q9D8E6	Rpl4 60S ribosomal protein L4	Rpl4	R.YAIC*SALAASALPALVMSK.G	0.94	0.926944444
P62242	Rps8 40S ribosomal protein S8	Rps8	K.LLAC*IASR.P	0.94	0.784285714
Q9R0Q7	Ptges3 Prostaglandin E synthase 3	Ptges3	K.HLNEIDLFHC*IDPNDSK.H	0.943333333	-
D3YXK2	Safb Scaffold attachment factor B1	Safb	K.ILDILGETC*K.S	0.943333333	1.087797619

P62889	Rpl30 60S ribosomal protein L30	Rpl30	K.YYRVC*TLAIIDPGDSDIIR.S	0.943333333	0.945912698
P40124	Cap1 Adenylyl cyclase-associated protein 1	Cap1	K.TDGC*HAYLSK.N	0.945	1.196865079
O88876	Dhrs3 Short-chain dehydrogenase/reductase 3	Dhrs3	R.FSGTYTC*MNTFK.G	0.945	-
Q9D023	Mpc2 Mitochondrial pyruvate carrier 2	Mpc2	K.WGLVC*AGLADMAR.P	0.945	-
Q3TX08	Trmt1 tRNA (guanine(26)-N(2))-dimethyltransferase	Trmt1	R.FC*EERPPADPVATVTEGAAK.I	0.945	-
P83882	Rpl36a 60S ribosomal protein L36a	Rpl36a	R.C*KHFELGGDK.K	0.945	-
Q78IK4	Apool Apolipoprotein O-like	Apool	K.IAYPLGLATLGATVC*YPAQSVIIAK.I	0.946666667	-
P35293	Rab18 Ras-related protein Rab-18	Rab18	K.LDNWLNELETYC*TR.N	0.946666667	-
Q9D1R9	Rpl34 60S ribosomal protein L34	Rpl34	K.SAC*GVC*PGR.L	0.946666667	0.978412698
Q76MZ3	Ppp2r1a Serine/threonine-protein phosphatase 2A 65 kDa reg	Ppp2r1a	K.DC*EAEVR.A	0.946666667	0.97125
Q03265	Atp5a1 ATP synthase subunit alpha, mitochondrial	Atp5a1	K.YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR.D	0.946666667	0.918214286
P35282	Rab21 Ras-related protein Rab-21	Rab21	K.VVLLGEGC*VGK.T	0.946666667	-
P26039	Tln1 Talin-1	Tln1	K.TMQFEPSTMVYDAC*R.M	0.95	1.237539683
Q8C7Q4	Rbm4 RNA-binding protein 4	Rbm4	K.LHVGNISPTC*TNQELR.A	0.95	-
P46471	Psmc2 26S protease regulatory subunit 7	Psmc2	R.SVC*TEAGMFAIR.A	0.95	1.305059524
Q61233	Lcp1 Plastin-2	Lcp1	K.AAC*LPLPGYR.V	0.95	0.943095238
O70325	Gpx4 Phospholipid hydroperoxide glutathione peroxidase,	Gpx4	R.YAEC*GLR.I	0.95	-
O08734	Bak1 Bcl-2 homologous antagonist/killer	Bak1	K.VGC*DESPSPSEQQVAQDTEEVFR.S	0.95	-
Q91YQ5	Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosy	Rpn1	K.VAC*ITEQVLTLVNK.R	0.95	0.924087302
P14131	Rps16 40S ribosomal protein S16	Rps16	K.KTATAVAHC*K.R	0.95	0.833769841
Q921E2	Rab31 Ras-related protein Rab-31	Rab31	K.C*DLSDIR.E	0.953333333	-
Q9DB20	Atp5o ATP synthase subunit O, mitochondrial	Atp5o	R.GEVPC*TVTTASPLDDAVLSELK.T	0.953333333	1.003769841
P60335	Pcbp1 Poly(rC)-binding protein 1	Pcbp1	R.LVVPATQC*GSLIGK.G	0.953333333	1.046111111
P42669	Pura Transcriptional activator protein Pur-alpha	Pura	R.AAC*EQLHQQQQQQEETTAATLLLQGEEEGEED.-	0.955	-
Q9DBC7	Prkar1a cAMP-dependent protein kinase type I-alpha regulat	Prkar1a	R.SLREC*ELYVQK.H	0.955	-
A2AD25	Gm4987 Novel protein silmilar to ribosomal protein L32	Gm4987	K.SYC*AEIAHNVSSK.N	0.955	-
P62274	Rps29 40S ribosomal protein S29	Rps29	K.YGLNMC*R.Q	0.955	-
Q9QZD8	Slc25a10 Mitochondrial dicarboxylate carrier	Slc25a10	R.TDGFLALYNGLSASLC*R.Q	0.955	-
P54071	Idh2 Isocitrate dehydrogenase	Idh2	K.SSGGFVWAC*K.N	0.955	0.79281746
O08553	Dpysl2 Dihydropyrimidinase-related protein 2	Dpysl2	R.GLYDGPVC*EVSVTPK.T	0.956666667	0.977619048

Q91V41	Rab14 Ras-related protein Rab-14	Rab14	K.FMADC*PHTIGVEFGTR.I	0.956666667	0.92202381
Q9WTX5	Skp1 S-phase kinase-associated protein 1	Skp1	K.ENQWC*EEK.-	0.96	-
Q8BUE4	Aifm2 Apoptosis-inducing factor 2	Aifm2	K.FNEVSC*QQAAIQAYED MVK.Q	0.96	-
P83882	Rpl36a 60S ribosomal protein L36a	Rpl36a	R.LEC*VEPNC*R.S	0.96	-
Q9JIK5	Ddx21 Nucleolar RNA helicase 2	Ddx21	K.LSVAC*FYGGTPYGGQIE R.M	0.96	1.307698413
P31230	Aimp1 Aminoacyl tRNA synthase complex-interacting multif	Aimp1	R.LSTPLQTNC*TASESVVQ SPSVATTASPATK.E	0.96	0.946190476
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	R.FSPNSSNPIIVSC*GWDK .L	0.96	0.894325397
P68040	Gnb2l1 Guanine nucleotide-binding protein subunit beta-2-	Gnb2l1	K.VWNLANC*K.L	0.96	0.894325397
Q11136	Pepd Xaa-Pro dipeptidase	Pepd	R.TVEEIEACMAGC*DK.A	0.96	-
F8VPN3	Gm5160 Peptidyl-prolyl cis-trans isomerase	Gm5160	R.IIPGFMC*QGGDFTR.H	0.963333333	-
Q3U1G5	Isg20l2 Interferon-stimulated 20 kDa exonuclease-like 2	Isg20l2	K.C*HMVNATPFK.T	0.963333333	-
P17182	Eno1 Alpha-enolase	Eno1	R.SGETEDTFIADLVVGLC* TGQIK.T	0.963333333	1.030793651
Q5SQX6	Cyfip2 Cytoplasmic FMR1-interacting protein 2	Cyfip2	K.C*NEQPNRVEIYEK.T	0.965	-
P60867	Rps20 40S ribosomal protein S20	Rps20	K.SLEKVC*ADLIR.G	0.965	0.99984127
P62827	Ran GTP-binding nuclear protein Ran	Ran	R.VC*ENIPIVLCGNK.V	0.965	0.985238095
Q9JHW4	Eefsec Selenocysteine-specific elongation factor	Eefsec	R.LDADIHTNTC*R.L	0.965	-
O88545	Cops6 COP9 signalosome complex subunit 6	Cops6	K.TC*NTMNQFVNK.F	0.965	-
Q9R060	Nubp1 Cytosolic Fe-S cluster assembly factor NUBP1	Nubp1	R.GASCQGC*PNQR.L	0.965	-
Q8BG73	Sh3bgrl2 SH3 domain-binding glutamic acid-rich-like protein	Sh3bgrl2	R.VFVASC*SGFVAIK.K	0.965	-
Q5EG47	Prkaa1 5-AMP-activated protein kinase catalytic subunit	Prkaa1	R.TSC*GSPNYAAPEVISGR .L	0.965	-
P06151	Ldha L-lactate dehydrogenase A chain	Ldha	K.DYC*VTANSK.L	0.966666667	0.832460317
Q63850	Nup62 Nuclear pore glycoprotein p62	Nup62	K.DIIEHLNMAGGPADTSDP LQQIC*K.I	0.966666667	-
Q9CSN1	Snw1 SNW domain-containing protein 1	Snw1	K.IPPC*ISNWK.N	0.966666667	1.30952381
P08249	Mdh2 Malate dehydrogenase, mitochondrial	Mdh2	K.GYLGPEQLPDC*LK.G	0.966666667	0.923849206
Q61990	Pcbp2 Poly(rC)-binding protein 2	Pcbp2	R.AITIAGIPQSIIEC*VK.Q	0.97	1.017896825
O88708	Orc4 Origin recognition complex subunit 4	Orc4	K.YSNC*PTDVR.Q	0.97	-
P53569	Cebpz CCAAT/enhancer-binding protein zeta	Cebpz	K.TVAEQRPESC*PVSK.A	0.97	-
P80318	Cct3 T-complex protein 1 subunit gamma	Cct3	R.TLIQNC*GASTIR.L	0.97	1.037222222
P52480	Pkm Pyruvate kinase isozymes M1/M2	Pkm	R.GIFPVLC*K.D	0.97	0.923690476
Q3ULJ0	Gpd1l Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	R.ITVVDDADTVELC*GALK. N	0.97	-

Q9CPP0	Npm3 Nucleoplasmin-3	Npm3	R.LSC*QPMLSVDDFQLQPPVTFR.L	0.97	-
Q9CZ30	Ola1 Obg-like ATPase 1	Ola1	K.STFFNVLTNSQASAENFPFC*TIDPNESR.V	0.973333333	-
P06151	Ldha L-lactate dehydrogenase A chain	Ldha	K.NRVIGSGC*NLDSAR.F	0.973333333	0.832460317
Q9EST3	Eif4enif1 Eukaryotic translation initiation factor 4E transp	Eif4enif1	R.SSC*STPLSQTSR.Y	0.975	-
P62754	Rps6 40S ribosomal protein S6	Rps6	K.LNISFPATGC*QK.L	0.975	1.035198413
Q9D1R9	Rpl34 60S ribosomal protein L34	Rpl34	R.AYGGSMC*AK.C	0.975	0.978412698
Q9CPY7	Lap3 Cytosol aminopeptidase	Lap3	R.QVIDC*QLADVNNLGK.Y	0.976666667	0.911626984
P14115	Rpl27a 60S ribosomal protein L27a	Rpl27a	K.RNQSFC*PTVNLDK.L	0.976666667	0.883769841
Q01853	Vcp Transitional endoplasmic reticulum ATPase	Vcp	R.QAAPC*VLFFDELDSIAK.A	0.976666667	1.075039683
P52480	Pkm Pyruvate kinase isozymes M1/M2	Pkm	R.NTGIIC*TIGPASR.S	0.976666667	0.923690476
P52482	Ube2e1 Ubiquitin-conjugating enzyme E2 E1	Ube2e1	K.ELADITLDPPPNC*SAGPK.G	0.98	-
Q9Z0H3	Smarcb1 SWI/SNF-related matrix-associated actin-dependent	Smarcb1	R.NTGDADQWC*PLLETLTDAEMEK.K	0.98	-
Q99KJ8	Dctn2 Dynactin subunit 2	Dctn2	R.C*DQDAQNPLSAGLQGAC*LMETVELLQAK.V	0.98	-
Q9ER00	Stx12 Syntaxin-12	Stx12	R.DFNSIIQTC*SGNIQR.I	0.98	-
Q9JHU4	Dync1h1 Cytoplasmic dynein 1 heavy chain 1	Dync1h1	R.IQFVGAC*NPPTDPGR.K	0.98	-
P70279	Surf6 Surfeit locus protein 6	Surf6	K.KIC*AQPGPER.Q	0.98	-
Q8C5R8	Prps1l1 Ribose-phosphate pyrophosphokinase	Prps1l1	K.FSNQETC*VEIGESVR.G	0.98	-
P23611	Irf8 Interferon regulatory factor 8	Irf8	R.VFCSGNAVVC*K.G	0.98	-
P70445	Eif4ebp2 Eukaryotic translation initiation factor 4E-bindin	Eif4ebp2	R.TVAISDAAQLPQDYC*TTPGGTLFSTTPGGTR.I	0.98	-
Q00PI9	Hnrnpul2 Heterogeneous nuclear ribonucleoprotein U-like pro	Hnrnpul2	K.VTQNLPMKEGC*TEVSLLR.V	0.98	1.107142857
P19096	Fasn Fatty acid synthase	Fasn	R.SFDDSGSGYC*R.S	0.98	1.037916667
Q9D8N0	Eef1g Elongation factor 1-gamma	Eef1g	K.AAAPAPEEEMDEC*EQALAAEPK.A	0.98	0.913571429
Q9CPY7	Lap3 Cytosol aminopeptidase	Lap3	R.SAGAC*TAAAFLR.E	0.98	0.911626984
P50516	Atp6v1a V-type proton ATPase catalytic subunit A	Atp6v1a	R.VLDALFPCVQGGTTAIPGAFGC*GK.T	0.98	0.824761905
P62281	Rps11 40S ribosomal protein S11	Rps11	K.C*PFTGNVSIR.G	0.983333333	0.856587302
P62702	Rps4x 40S ribosomal protein S4, X isoform	Rps4x	K.KIC*MQR.F	0.983333333	0.787301587
Q8VEH3	Arl8a ADP-ribosylation factor-like protein 8A	Arl8a	R.EICCYSISC*K.E	0.983333333	-
Q91VR2	Atp5c1 ATP synthase subunit gamma, mitochondrial	Atp5c1	R.GLC*GAIHSSVAK.Q	0.983333333	0.786547619
Q9CR00	Psmd9 26S proteasome non-ATPase regulatory subunit 9	Psmd9	K.GIGMNEPLVDC*EGYPR.A	0.985	-
P97351	Rps3a 40S ribosomal protein S3a	Rps3a	R.DKMC*SMVK.K	0.985	0.975
P51859	Hdgf Hepatoma-derived growth factor	Hdgf	K.SC*AAEPEVEPEAHEGDGDKK.G	0.985	0.901904762

Q9D0L8	Rnmt mRNA cap guanine-N7 methyltransferase	Rnmt	R.LPENTPPC*QQVDQPK.M	0.985	-
P10107	Anxa1 Annexin A1	Anxa1	K.KYGISLC*QAILDETKGDYEK.I	0.985	0.954603175
P35285	Rab22a Ras-related protein Rab-22A	Rab22a	K.VC*LLGDTGVGK.S	0.986666667	-
Q99K48	Nono Non-POU domain-containing octamer-binding protein	Nono	R.FAC*HSASLTVR.N	0.99	1.160039683
Q8CBE3	Wdr37 WD repeat-containing protein 37	Wdr37	R.INVC*VGQK.I	0.99	-
P23116	Eif3a Eukaryotic translation initiation factor 3 subunit	Eif3a	K.NIC*QQVNIK.S	0.99	1.120178571
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	R.SLHDALC*VVK.R	0.99	1.069007937
P58252	Eef2 Elongation factor 2	Eef2	K.STLTDSLVC*K.A	0.99	1.011428571
Q9CR57	Rpl14 60S ribosomal protein L14	Rpl14	R.ALVDGPC*TR.V	0.99	0.872857143
Q8K2Q9	Kiaa1598 Shootin-1	Kiaa1598	K.TLEAEFNNPC*PLTPEPGEGPR.K	0.99	-
Q9D0T1	Nhp2l1 NHP2-like protein 1	Nhp2l1	R.ACGVSRPVIAC*SVTIK.E	0.99	1.175595238
P32067	Ssb Lupus La protein homolog	Ssb	K.FSGDLDDQTC*R.E	0.99	0.828511905
P62242	Rps8 40S ribosomal protein S8	Rps8	R.LDVGNFSWGSEC*C*TR.K	0.99	0.784285714
Q8VEK3	Hnrnpu Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	K.MC*LFAGFQR.K	0.993333333	1.013134921
Q6P5F9	Xpo1 Exportin-1	Xpo1	K.LDINLLDNVVNC*LYHGEGAQQR.M	0.993333333	-
P63323	Rps12 40S ribosomal protein S12	Rps12	K.KLGEWVGLC*K.I	0.993333333	0.950753968
P62281	Rps11 40S ribosomal protein S11	Rps11	R.DVQIGDIVTVGEC*R.P	0.993333333	0.856587302
Q9D1A2	Cndp2 Cytosolic non-specific dipeptidase	Cndp2	K.DVGAETLLHSC*K.K	0.995	1.434920635
P14206	Rpsa 40S ribosomal protein SA	Rpsa	R.YVDIAIPC*NNK.G	0.995	0.918809524
P54071	Idh2 Isocitrate dehydrogenase	Idh2	K.DLAGC*IHGLSNVK.L	0.995	0.79281746
Q60605	Myl6 Myosin light polypeptide 6	Myl6	K.ILYSQC*GDVMR.A	0.996666667	1.11265873
Q9CQR2	Rps21 40S ribosomal protein S21	Rps21	K.TYGIC*GAIR.R	0.996666667	1.16702381
Q9R1T2	Sae1 SUMO-activating enzyme subunit 1	Sae1	R.YCFSEMAPVC*AVVGGILAQEIVK.A	0.996666667	0.989107143
Q9ESL4	Mltk Mitogen-activated protein kinase kinase kinase MLT	Mltk	K.FDDLQFFENC*GGGSFGSVYR.A	1	-
Q9CR51	Atp6v1g1 V-type proton ATPase subunit G 1	Atp6v1g1	K.AKEAAALGSHGSC*SSEVEK.E	1	-
D3YXL3	Gm5830 Uncharacterized protein	Gm5830	K.LPQPPEGQC*YSN.-	1	-
Q68FL6	Mars Methionine--tRNA ligase, cytoplasmic	Mars	K.DNVPFHGLVFPC*SVLGAEDNYTLVK.H	1	-
Q8VCG1	Dut Deoxyuridine triphosphatase, isoform CRA_b	Dut	R.IAQLIC*ER.I	1	-
P80315	Cct4 T-complex protein 1 subunit delta	Cct4	K.AQDIEAGDGTTSVVIIAGSLLDSC*TK.L	1	1.040198413
O70194	Eif3d Eukaryotic translation initiation factor 3 subunit	Eif3d	K.FMTPVIQDNPSGWGPC*AVPEQFR.D	1	1.037857143
P80313	Cct7 T-complex protein 1 subunit eta	Cct7	R.YNFFTGC*PK.A	1	0.953333333
Q9D8E6	Rpl4 60S ribosomal protein L4	Rpl4	R.SGQGAFGNMC*R.G	1	0.926944444

Q9CQ60	Pgls 6-phosphogluconolactonase	Pgls	R.TGALC*WFLDEAAAR.L	1	0.895297619
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	R.SQIESMLINGYALNC*VVGSQGMPK.R	1.003333333	1.069007937
P11499	Hsp90ab1 Heat shock protein HSP 90-beta	Hsp90ab1	R.GFEVVYMTEPIDEYC*VQQLK.E	1.003333333	0.913214286
Q9CXK8	Nip7 60S ribosome subunit biogenesis protein NIP7 homol	Nip7	K.LAANISGDKLVSLGTC*FGK.F	1.005	-
Q9DBR1	Xrn2 5-3 exoribonuclease 2	Xrn2	R.NSPGC*QVASNPR.Q	1.005	-
Q80XN0	Bdh1 D-beta-hydroxybutyrate dehydrogenase, mitochondria	Bdh1	K.METYC*NSGSTDTSSVINAVTHALTAATPYTR.Y	1.005	-
Q7TQI3	Otub1 Ubiquitin thioesterase OTUB1	Otub1	K.QEPLGSDSEGVNC*LAYDEAIMAQQDR.I	1.005	-
Q6ZWV3	Rpl10 60S ribosomal protein L10	Rpl10	K.MLSC*AGADR.L	1.005	0.824722222
P07356	Anxa2 Annexin A2	Anxa2	K.ALLYLC*GGDD.-	1.006666667	1.099404762
P62245	Rps15a 40S ribosomal protein S15a	Rps15a	R.QVLIRPC*SK.V	1.006666667	0.89077381
P62852	Rps25 40S ribosomal protein S25	Rps25	K.ATYDKLC*K.E	1.006666667	0.817222222
Q6P5F9	Xpo1 Exportin-1	Xpo1	K.TSSDPTC*VEK.E	1.01	-
Q9CPS7	Pno1 RNA-binding protein PNO1	Pno1	R.TAIC*NLILGNPPSK.V	1.01	-
Q3ULJ0	Gpd1l Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	K.NIVAVGAGFC*DGLR.C	1.01	-
Q6PAC3	Dcaf13 DDB1- and CUL4-associated factor 13	Dcaf13	K.FNPVETFLLGSC*ASDR.N	1.01	-
Q3ULJ0	Gpd1l Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	K.FC*ETTIGSK.V	1.01	-
Q9JHU4	Dync1h1 Cytoplasmic dynein 1 heavy chain 1	Dync1h1	K.VQYPQSQAC*K.M	1.01	-
Q5U4D9	Thoc6 THO complex subunit 6 homolog	Thoc6	K.AQVPGSSPGLLSLSLNQQPAAPEC*K.V	1.01	-
D3Z2H9	Tpm3-rs7 Uncharacterized protein	Tpm3-rs7	K.CTKEEHLC*TQR.M	1.01	1.3275
P40124	Cap1 Adenylyl cyclase-associated protein 1	Cap1	R.ALLATASQC*QQPAGNK.L	1.01	1.196865079
P38647	Hspa9 Stress-70 protein, mitochondrial	Hspa9	K.MEEFKDQLPADEC*NK.L	1.01	1.10531746
Q8BK67	Rcc2 Protein RCC2	Rcc2	K.AVQDLC*GWR.I	1.01	1.082202381
P17225	Ptbp1 Polypyrimidine tract-binding protein 1	Ptbp1	K.RGSDELFSTC*VSNGPFIMSSSASAANGNDSK.K	1.01	0.976150794
P62242	Rps8 40S ribosomal protein S8	Rps8	R.LDVGNFSWGSEC*CTR.K	1.01	0.784285714
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	K.VC*EDFDTSVNLAWTSGTNCTR.F	1.01	0.781468254
P40124	Cap1 Adenylyl cyclase-associated protein 1	Cap1	K.NSLDC*EIVSAK.S	1.013333333	1.196865079
P68510	Ywhah 14-3-3 protein eta	Ywhah	K.NC*NDFQYESK.V	1.013333333	1.116309524
Q920E5	Fdps Farnesyl pyrophosphate synthase	Fdps	K.SLIEQC*SAPLPPSIFMELANK.I	1.013333333	0.893095238
E9Q1N8	Rps2-ps5 Uncharacterized protein	Rps2-ps5	R.GC*TATLGNFAK.A	1.015	-
Q9D6K5	Synj2bp Synaptojanin-2-binding protein	Synj2bp	R.NAGC*AVSLR.V	1.015	-
P12382	Pfkl 6-phosphofructokinase, liver type	Pfkl	K.MGMEAVMALLEATPDTPAC*VVSLSGNQSVR.L	1.015	1.048809524

P80315	Cct4 T-complex protein 1 subunit delta	Cct4	K.TGC*NVLLIQK.S	1.015	1.040198413
O70503	Hsd17b12 Estradiol 17-beta-dehydrogenase 12	Hsd17b12	R.AFQVWC*VGNEALVGPR.L	1.016666667	-
P10107	Anxa1 Annexin A1	Anxa1	K.GDRC*QDLSVNQDLADTDAR.A	1.016666667	0.954603175
Q9CXW4	Rpl11 60S ribosomal protein L11	Rpl11	K.LC*LNICVGESGDR.L	1.016666667	0.874126984
Q9CR08	Pop4 Ribonuclease P protein subunit p29	Pop4	R.DLC*NGLKPDTQPQMIQAK.L	1.02	-
Q9WUA3	Pfkp 6-phosphofructokinase type C	Pfkp	R.NESC*SVNYTTDFIYQLYSEEGK.G	1.02	0.971011905
Q9WVA4	Tagln2 Transgelin-2	Tagln2	K.NMAC*VQR.T	1.02	0.922896825
P62908	Rps3 40S ribosomal protein S3	Rps3	R.AC*YGVLR.F	1.02	0.868134921
Q9DCW4	Etfb Electron transfer flavoprotein subunit beta	Etfb	K.EIIAVSCGPSQC*QETIR.T	1.023333333	1.051388889
P83870	Phf5a PHD finger-like domain-containing protein 5A	Phf5a	R.IC*DECNYGSYQGR.C	1.023333333	-
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	R.DC*LINAAK.T	1.023333333	1.069007937
P61164	Actr1a Alpha-centractin	Actr1a	R.AC*YLSINPQK.D	1.025	-
Q8K3X4	Irf2bpl Interferon regulatory factor 2-binding protein-lik	Irf2bpl	K.EGVPGADMLPQPYLDASC*PMLPTALVSLSR.A	1.025	-
Q8BTM8	Flna Filamin-A	Flna	K.VGTEC*GNQK.V	1.025	1.496984127
Q8BMS1	Hadha Trifunctional enzyme subunit alpha, mitochondrial	Hadha	R.SAVLISSKPGC*FVAGADINMLSSCTTPQEATR.I	1.025	0.839285714
P60710	Actb Actin, cytoplasmic 1	Actb	K.EKLC*YVALDFEQEMATAASSSSLEK.S	1.026666667	1.31265873
Q99JY9	Actr3 Actin-related protein 3	Actr3	R.YSYVC*PDLVK.E	1.026666667	0.977619048
Q7TMK9	Syncrip Heterogeneous nuclear ribonucleoprotein Q	Syncrip	K.SAFLC*GVMK.T	1.026666667	0.855357143
Q9D1M0	Sec13 Protein SEC13 homolog	Sec13	K.FASGGC*DNLIK.L	1.03	-
Q8R0X2	Cacul1 CDK2-associated and cullin domain-containing prote	Cacul1	K.SC*DAAAAVAK.T	1.03	-
P41105	Rpl28 60S ribosomal protein L28	Rpl28	R.NC*SSFLIK.R	1.03	-
Q9QWH1	Phc2 Polyhomeotic-like protein 2	Phc2	R.YNVGC*TK.R	1.03	-
Q99JB2	Stoml2 Stomatin-like protein 2	Stoml2	R.ESLNANIVDAINQAADC*WGIR.C	1.03	1.197916667
P80318	Cct3 T-complex protein 1 subunit gamma	Cct3	K.IPGGIIEDSC*VLR.G	1.03	1.037222222
Q9CZD3	Gars Glycine--tRNA ligase	Gars	R.SCYDLSC*HAR.A	1.03	1.035595238
Q9D6R2	Idh3a Isocitrate dehydrogenase	Idh3a	K.C*SDFTEEICR.R	1.03	1.003650794
P40142	Tkt Transketolase	Tkt	R.TVPFC*STFAAFFTR.A	1.03	0.955833333
P00493	Hprt1 Hypoxanthine-guanine phosphoribosyltransferase	Hprt1	K.SYC*NDQSTGDIK.V	1.03	0.895416667
P63038	Hspd1 60 kDa heat shock protein, mitochondrial	Hspd1	R.AAVEEGIVLGGGC*ALLR.C	1.033333333	1.066666667
Q8BH04	Pck2 Phosphoenolpyruvate carboxykinase	Pck2	R.QC*PIMDPAWEAPEGVPIDAIIFGGR.R	1.033333333	-
P80315	Cct4 T-complex protein 1 subunit delta	Cct4	K.IGLIQFC*LSAPK.T	1.033333333	1.040198413
P62908	Rps3 40S ribosomal protein S3	Rps3	K.GC*EVVVSGK.L	1.033333333	0.868134921

P62858	Rps28 40S ribosomal protein S28	Rps28	R.TGSQGQC*TQVR.V	1.035	0.981865079
Q80VJ3	Rcl Deoxyribonucleoside 5-monophosphate N-glycosidase	Rcl	R.YFEAYLPQGTASSSNPSAC*LNPTVLEK.I	1.036666667	-
Q76MZ3	Ppp2r1a Serine/threonine-protein phosphatase 2A 65 kDa reg	Ppp2r1a	R.LNIISNLDC*VNEVIGIR.Q	1.036666667	0.97125
P48036	Anxa5 Annexin A5	Anxa5	K.ALLLLC*GGEDD.-	1.04	0.949087302
P97496	Smarcc1 SWI/SNF complex subunit SMARCC1	Smarcc1	R.NLTGDVC*AVMR.V	1.04	-
Q91V92	Acly ATP-citrate synthase	Acly	K.YIC*TTSAIQNR.F	1.04	-
Q3TRM8	Hk3 Hexokinase-3	Hk3	R.TQLQQIQASLLC*SMEQALK.G	1.04	-
P56546	Ctbp2 C-terminal-binding protein 2	Ctbp2	K.DLATVAFC*DAQSTQEIHEK.V	1.04	-
Q9D0T1	Nhp2l1 NHP2-like protein 1	Nhp2l1	R.AC*GVSRPVIACSVTIK.E	1.04	1.175595238
P63323	Rps12 40S ribosomal protein S12	Rps12	K.VVGC*SC*VVVK.D	1.04	0.950753968
Q9CZN7	Shmt2 Protein Shmt2	Shmt2	R.GLELIASENFC*SR.A	1.04	0.942698413
P62334	Psmc6 26S protease regulatory subunit 10B	Psmc6	R.AVASQLDC*NFLK.V	1.04	0.94015873
P62908	Rps3 40S ribosomal protein S3	Rps3	R.GLC*AIAQAESLR.Y	1.04	0.868134921
Q3THS6	Mat2a S-adenosylmethionine synthase isoform type-2	Mat2a	K.VAC*ETVAK.T	1.043333333	2.274940476
Q9D0B0	Srsf9 Serine/arginine-rich splicing factor 9	Srsf9	R.NGYDYGQC*R.L	1.043333333	1.358630952
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	R.IC*DDELILIK.N	1.043333333	1.069007937
P11499	Hsp90ab1 Heat shock protein HSP 90-beta	Hsp90ab1	R.LVSSPC*CIVTSTYGWTANMER.I	1.043333333	0.913214286
Q6P1H6	Ankle2 Ankyrin repeat and LEM domain-containing protein 2	Ankle2	R.YLIGSGDNPTIVQEGC*R.Y	1.045	-
Q60854	Serpinb6 Serpin B6	Serpinb6	K.C*SGNGGGDVHQGFQSLLTEVNK.T	1.045	-
Q05144	Rac2 Ras-related C3 botulinum toxin substrate 2	Rac2	R.AVLC*PQPTR.Q	1.045	1.095515873
Q61990	Pcbp2 Poly(rC)-binding protein 2	Pcbp2	R.LVVPASQC*GSLIGK.G	1.045	1.017896825
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	R.GANDFMC*DEMER.S	1.046666667	1.069007937
O35737	Hnrnph1 Heterogeneous nuclear ribonucleoprotein H	Hnrnph1	R.DLNYC*FSGMSDHR.Y	1.046666667	0.981507937
Q6IRU2	Tpm4 Tropomyosin alpha-4 chain	Tpm4	K.EENVGLHQTLDQTLNELNC*I.-	1.05	-
P47856	Gfpt1 Glucosamine--fructose-6-phosphate aminotransferase	Gfpt1	R.GYDSAGVGLDGGNDKDWEANAC*K.I	1.05	-
P60766	Cdc42 Cell division control protein 42 homolog	Cdc42	K.YVEC*SALTQK.G	1.05	-
Q501J6	Ddx17 Probable ATP-dependent RNA helicase DDX17	Ddx17	R.GDGPIC*LVLAPTR.E	1.05	1.012063492
Q9Z1D1	Eif3g Eukaryotic translation initiation factor 3 subunit	Eif3g	K.EDLNC*QEEEDPMNK.L	1.053333333	-
O70503	Hsd17b12 Estradiol 17-beta-dehydrogenase 12	Hsd17b12	K.LININVLSVC*K.V	1.053333333	-
P62830	Rpl23 60S ribosomal protein L23	Rpl23	K.EC*ADLWPR.I	1.053333333	0.952896825
P62830	Rpl23 60S ribosomal protein L23	Rpl23	R.ISLGLPVGAVINC*ADNTGAK.N	1.053333333	0.952896825

Q9CZN7	Shmt2 Protein Shmt2	Shmt2	R.AALEALGSC*LNNK.Y	1.053333333	0.942698413
P62334	Psmc6 26S protease regulatory subunit 10B	Psmc6	R.DHQPC*IIFMDEIDAIGGR.R	1.053333333	0.94015873
P11499	Hsp90ab1 Heat shock protein HSP 90-beta	Hsp90ab1	R.VFIMDSC*DELIPEYLNFIR.G	1.053333333	0.913214286
Q9DCH4	Eif3f Eukaryotic translation initiation factor 3 subunit	Eif3f	K.TC*FSPNR.V	1.055	1.310119048
Q8BKS9	Kiaa0020 Pumilio domain-containing protein KIAA0020	Kiaa0020	K.ESGKEGC*FAK.T	1.055	1.237559524
P26638	Sars Serine--tRNA ligase, cytoplasmic	Sars	K.YAGLSTC*FR.Q	1.055	0.911190476
Q8VCI5	Pex19 Peroxisomal biogenesis factor 19	Pex19	R.VGSDASSQQEFTSC*LK.E	1.06	-
E9Q9A9	Oas2 2-5-oligoadenylate synthase 2	Oas2	K.VPVMQTPGSC*GGQIYPTVGGVTK.-	1.06	-
Q9QXB9	Drg2 Developmentally-regulated GTP-binding protein 2	Drg2	R.KPNSVVISC*GMK.L	1.06	-
Q91ZJ5	Ugp2 UTP--glucose-1-phosphate uridylyltransferase	Ugp2	K.LNGGLGTSMGC*K.G	1.06	-
O54988	Slk STE20-like serine/threonine-protein kinase	Slk	K.MTGESEC*LNPSAQSR.I	1.06	-
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.VSDTVVEPYNATLSVHQLVENTDETYC*IDNEALYDICFR.T	1.06	0.934563492
P68368	Tuba4a Tubulin alpha-4A chain	Tuba4a	K.YMAC*CLLYR.G	1.063333333	0.90781746
J3QPA0	Uncharacterized protein	Uncharacterized	R.ADPWLGC*.-	1.063333333	-
P35293	Rab18 Ras-related protein Rab-18	Rab18	K.TC*DGVQCAFEELVEK.I	1.065	-
P26638	Sars Serine--tRNA ligase, cytoplasmic	Sars	R.TIC*AILENYQAEK.G	1.065	0.911190476
P07901	Hsp90aa1 Heat shock protein HSP 90-alpha	Hsp90aa1	R.VFIMDNC*EELIPEYLNFIR.G	1.065	0.843888889
Q8BVY0	Rsl1d1 Protein Rsl1d1	Rsl1d1	K.QKVTEEC*EEAIPQLVPIGETPDKENVK.M	1.066666667	-
E9Q035	Gm20425 Protein Gm20425	Gm20425	K.EFEFSQLPLKVEFLEC*SAK.G	1.066666667	1.210714286
P19096	Fasn Fatty acid synthase	Fasn	K.EQGVTFPSGEVQEQLIC*SLYQPAGLAPESLEYIEAHGTGTK.V	1.07	1.037916667
Q8R010	Aimp2 Aminoacyl tRNA synthase complex-interacting multif	Aimp2	K.FSVQTMC*PIEGEGNIAR.F	1.07	-
P80313	Cct7 T-complex protein 1 subunit eta	Cct7	R.QLC*DNAGFDATNILNK.L	1.07	0.953333333
Q60930	Vdac2 Voltage-dependent anion-selective channel protein	Vdac2	K.VC*EDFDTSVNLAWTSGTNC*TR.F	1.07	0.781468254
P52480	Pkm Pyruvate kinase isozymes M1/M2	Pkm	R.AEGSDVANAVLDGADC*IMLSGETAK.G	1.073333333	0.923690476
P34884	Mif Macrophage migration inhibitory factor	Mif	K.LLC*GLLSDR.L	1.073333333	-
Q99K01	Pdxdc1 Pyridoxal-dependent decarboxylase domain-containin	Pdxdc1	R.GEDVDQLITC*IQSK.L	1.075	-
P62983	Rps27a Ubiquitin-40S ribosomal protein S27a	Rps27a	R.EC*PSDECGAGVFMGSHFDR.H	1.075	1.528174603
Q8BGD9	Eif4b Eukaryotic translation initiation factor 4B	Eif4b	K.DGNKVDVVGATQGQAGSC*SR.G	1.075	1.062559524
Q99LW6	Yaf2 YY1-associated factor 2	Yaf2	K.SAPASSAAGDQHSQGSC*SSDSTER.G	1.075	-
Q8CFE2	UPF0609 protein C4orf27 homolog	UPF0609	R.TAGAGPQC*EK.T	1.075	-

P18760	Cfl1 Cofilin-1	Cfl1	K.MLPDKDC*R.Y	1.075	1.170833333
Q9WVA3	Bub3 Mitotic checkpoint protein BUB3	Bub3	R.TPC*NAGTFSQPEK.V	1.075	1.087103175
O88990	Actn3 Alpha-actinin-3	Actn3	K.EGLLLWC*QR.K	1.08	-
Q9CRA8	Exosc5 Exosome complex component RRP46	Exosc5	R.SPVC*SLR.H	1.08	-
O35295	Purb Transcriptional activator protein Pur-beta	Purb	R.FFFDVGC*NK.Y	1.08	-
P11983	Tcp1 T-complex protein 1 subunit alpha	Tcp1	K.VLC*ELADLQDK.E	1.08	1.069007937
Q9D0I9	Rars Arginine--tRNA ligase, cytoplasmic	Rars	K.NC*GC*LEASPSLEQLR.E	1.08	1.066785714
Q9CZD3	Gars Glycine--tRNA ligase	Gars	K.NGEC*FR.A	1.08	1.035595238
Q9CTH6	Fcf1 rRNA-processing protein FCF1 homolog	Fcf1	K.AKLDLVQSMMDC*LYAK.C	1.083333333	-
D3YYI5	Gm7293 Glyceraldehyde-3-phosphate dehydrogenase	Gm7293	K.GILGYTEDQVVSC*DFNSNSHSSTFDAGAGIALNDNFVK.L	1.083333333	1.285634921
Q9Z2X1	Hnrnpf Heterogeneous nuclear ribonucleoprotein F	Hnrnpf	R.DLSYC*LSGMYDHR.Y	1.083333333	0.991031746
Q61233	Lcp1 Plastin-2	Lcp1	K.VDTDGNGYISC*NELNDLFK.A	1.083333333	0.943095238
P12382	Pfkl 6-phosphofructokinase, liver type	Pfkl	R.LPLMEC*VQVTK.D	1.085	1.048809524
P46471	Psmc2 26S protease regulatory subunit 7	Psmc2	R.TDAC*FIR.V	1.086666667	1.305059524
P07356	Anxa2 Annexin A2	Anxa2	K.GLGTDEDSLIEIIC*SR.T	1.086666667	1.099404762
D3Z3R1	Gm5745 60S ribosomal protein L36	Gm5745	R.DMIREVC*GFAPYER.R	1.09	1.03327381
O88712	Ctbp1 C-terminal-binding protein 1	Ctbp1	R.PLVALLDGRDC*TVEMPILK.D	1.09	-
Q8VI84	Noc3l Nucleolar complex protein 3 homolog	Noc3l	R.YC*NEAAPETPLDFAK.C	1.09	-
P97461	Rps5 40S ribosomal protein S5	Rps5	K.AQC*PIVER.L	1.09	0.852698413
P46471	Psmc2 26S protease regulatory subunit 7	Psmc2	K.IDPTVTMMQVEEKPDVTYSDVGGC*K.E	1.093333333	1.305059524
P68254	Ywhaq 14-3-3 protein theta	Ywhaq	R.YDDMATC*MK.A	1.093333333	1.065992063
Q91WK2	Eif3h Eukaryotic translation initiation factor 3 subunit	Eif3h	R.MDSLLIAGQINTYC*QNIK.E	1.095	-
O35465	Fkbp8 Peptidyl-prolyl cis-trans isomerase FKBP8	Fkbp8	K.C*LNNLAASQLK.L	1.095	-
P63037	Dnaja1 DnaJ homolog subfamily A member 1	Dnaja1	K.GAVEC*CPNCR.G	1.096666667	-
Q8C0C7	Farsa Phenylalanine--tRNA ligase alpha subunit	Farsa	K.VNLQMVYDSPVC*R.L	1.096666667	-
P40142	Tkt Transketolase	Tkt	K.QAFTDVATGSLGQGLGAAC*GMAYTGK.Y	1.096666667	0.955833333
Q8K124	Plekho2 Pleckstrin homology domain-containing family O mem	Plekho2	K.LLNQVLGSEPPPVC*AESLLSQAVEQLR.Q	1.1	-
P68037	Ube2l3 Ubiquitin-conjugating enzyme E2 L3	Ube2l3	K.GQVC*LPVISAENWKPATK.T	1.1	-
Q61029	Tmpo Lamina-associated polypeptide 2, isoforms beta/del	Tmpo	K.EMFPYEASTPTGISASC*R.R	1.103333333	1.59265873
Q6ZWQ9	Myl12a Protein Myl12a	Myl12a	R.NAFAC*FDEEAIGTIQEDYLR.E	1.103333333	1.211488095
Q61656	Ddx5 Probable ATP-dependent RNA helicase DDX5	Ddx5	R.LIDFLEC*GK.T	1.103333333	1.135992063
P19096	Fasn Fatty acid synthase	Fasn	K.LGMLSPDGTC*R.S	1.105	1.037916667
P05214	Tuba3b Tubulin alpha-3 chain	Tuba3b	R.TIQFVDWC*PTGFK.V	1.106666667	-

P80315	Cct4 T-complex protein 1 subunit delta	Cct4	K.KLGGTIDDC*ELVEGLVLTQK.V	1.106666667	1.040198413
P80314	Cct2 T-complex protein 1 subunit beta	Cct2	R.SLHDALC*VLAQTVK.D	1.11	1.094603175
O70145	Ncf2 Neutrophil cytosol factor 2	Ncf2	K.AFVEGC*AAK.N	1.11	-
P63323	Rps12 40S ribosomal protein S12	Rps12	K.VVGC*SCVVVK.D	1.113333333	0.950753968
Q9CXW4	Rpl11 60S ribosomal protein L11	Rpl11	K.LC*LNIC*VGESGDR.L	1.113333333	0.874126984
Q7TSC1	Prrc2a Protein PRRC2A	Prrc2a	R.GGPPC*KPPAPEDEDEAWR.Q	1.115	-
E9Q555	Rnf213 E3 ubiquitin-protein ligase RNF213	Rnf213	R.VLDC*LQGISYR.L	1.115	-
Q9JJG9	Noa1 Nitric oxide-associated protein 1	Noa1	K.STLFNTLLESDYC*TAK.G	1.115	-
Q80XC2	Trmt61a tRNA (adenine(58)-N(1))-methyltransferase catalyti	Trmt61a	R.FCSFSPC*IEQVQR.T	1.115	-
P42208	Sept2 Septin-2	43710	R.LTVVDTPGYGDAINC*RDC*FK.T	1.115	1.328968254
P63276	Rps17 40S ribosomal protein S17	Rps17	K.RVC*EEIAIIPSKK.L	1.116666667	1.372460317
P52480	Pkm Pyruvate kinase isozymes M1/M2	Pkm	K.C*CSGAIIVLTK.S	1.116666667	0.923690476
O08638	Myh11 Myosin-11	Myh11	R.EDQSILC*TGESGAGK.T	1.12	-
P05064	Aldoa Fructose-bisphosphate aldolase A	Aldoa	R.YASIC*QQNGIVPIVEPEILPDGDHDLKR.C	1.12	1.174047619
P68372	Tubb4b Tubulin beta-4B chain	Tubb4b	K.EAESC*DCLQGFQLTHSLGGGTGSGMGTLLISK.I	1.12	0.934563492
Q9WUM5	Suclg1 Succinyl-CoA ligase	Suclg1	K.IIC*QGFTGK.Q	1.125	-
Q8VBT6	Apobr Apolipoprotein B receptor	Apobr	R.AQGTQC*PGAESEDQAMLSR.E	1.125	-
P80315	Cct4 T-complex protein 1 subunit delta	Cct4	R.TLSGMESYC*VR.A	1.125	1.040198413
Q9Z1N2	Orc1 Origin recognition complex subunit 1	Orc1	R.LHVSAVPDSLPC*R.E	1.126666667	-
O70475	Ugdh UDP-glucose 6-dehydrogenase	Ugdh	K.ASVGFGGSC*FQK.D	1.13	-
P10639	Txn Thioredoxin	Txn	K.C*MPTFQFYK.K	1.13	0.77547619
Q9Z2L7	Crlf3 Cytokine receptor-like factor 3	Crlf3	R.NDAESSGVLYSSAPTYFC*GQTLTFR.V	1.13	-
P50543	S100a11 Protein S100-A11	S100a11	R.C*IESLIAVFQK.Y	1.133333333	-
Q9D8C4	Ifi35 Interferon-induced 35 kDa protein homolog	Ifi35	R.VNLEDC*R.L	1.135	-
E9PZF0	Gm20390 Nucleoside diphosphate kinase A	Gm20390	R.GDFC*IQVGR.N	1.135	1.047301587
P16381	D1Pas1 Putative ATP-dependent RNA helicase Pl10	D1Pas1	R.DLMAC*AQTGSGK.T	1.135	0.969047619
P99029	Prdx5 Peroxiredoxin-5, mitochondrial	Prdx5	K.GVLFGVPGAFTPGC*SK.T	1.136666667	2.799603175
D3YYI5	Gm7293 Glyceraldehyde-3-phosphate dehydrogenase	Gm7293	K.IVSNASC*TTNC*LAPLAK.V	1.136666667	1.285634921
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	K.IVNDNATYC*R.L	1.14	0.998511905
Q8BP47	Nars Asparagine--tRNA ligase, cytoplasmic	Nars	R.LMTDTINEPILLC*R.F	1.14	0.953333333
P62717	Rpl18a 60S ribosomal protein L18a	Rpl18a	K.VEEIAAGKC*R.R	1.14	-
Q3TJZ6	Fam98a Protein FAM98A	Fam98a	R.EKTAC*AINK.V	1.14	-
Q9D0I9	Rars Arginine--tRNA ligase, cytoplasmic	Rars	K.NC*GCLEASPSLEQLR.E	1.14	1.066785714

Q3V3R1	Mthfd1l Monofunctional C1-tetrahydrofolate synthase, mitoc	Mthfd1l	K.IDRYTQQGFGNLPIC*MAK.T	1.14	0.874166667
Q8K301	Ddx52 Probable ATP-dependent RNA helicase DDX52	Ddx52	R.SVANVIQQAGC*PVPEYIK.G	1.145	-
Q8R5A3	Apbb1ip Amyloid beta A4 precursor protein-binding family B	Apbb1ip	R.SSDTC*GSPALPSK.V	1.145	-
P62192	Psmc1 26S protease regulatory subunit 4	Psmc1	K.AIC*TEAGLMALR.E	1.145	1.140357143
O08749	Dld Dihydrolipoyl dehydrogenase, mitochondrial	Dld	K.NETLGGTC*LNVGCIPSK.A	1.145	1.055198413
Q8BR63	Fam177a1 Protein FAM177A1	Fam177a1	R.ESGC*AAAGETEAAAATAFR.D	1.15	-
P63101	Ywhaz 14-3-3 protein zeta/delta	Ywhaz	R.YDDMAAC*MK.S	1.15	1.011428571
P60843	Eif4a1 Eukaryotic initiation factor 4A-I	Eif4a1	K.VVMALGDYMGASC*HACIGGTNVR.A	1.153333333	1.053968254
Q9JKP5	Mbnl1 Muscleblind-like protein 1	Mbnl1	R.GTCSRPDTEC*K.F	1.155	-
Q6PAQ4	Rexo4 RNA exonuclease 4	Rexo4	R.VQQAEHC*SIQDAQAAMR.L	1.155	-
Q9D1R9	Rpl34 60S ribosomal protein L34	Rpl34	K.SAC*GVCPGR.L	1.155	0.978412698
Q78XF5	Ostc Oligosaccharyltransferase complex subunit OSTC	Ostc	R.VPFLVLEC*PNLK.L	1.156666667	-
P61759	Vbp1 Prefoldin subunit 3	Vbp1	K.DGC*GLETAAGNGR.R	1.156666667	-
P18760	Cfl1 Cofilin-1	Cfl1	K.HELQANC*YEEVK.D	1.156666667	1.170833333
Q8R010	Aimp2 Aminoacyl tRNA synthase complex-interacting multif	Aimp2	K.SC*ENLAPFSTALQLLK.-	1.16	-
P19096	Fasn Fatty acid synthase	Fasn	R.DPETLLGYSMVGC*QR.A	1.16	1.037916667
P06151	Ldha L-lactate dehydrogenase A chain	Ldha	K.GLYGINEDVFLSVPC*ILGQNGISDVVK.V	1.16	0.832460317
Q8R180	Ero1l ERO1-like protein alpha	Ero1l	K.SKENTFYNWLEGLC*VEK.R	1.16	-
Q9WUA3	Pfkp 6-phosphofructokinase type C	Pfkp	R.LKAAC*NLAR.L	1.16	0.971011905
Q8VCH0	Acaa1b 3-ketoacyl-CoA thiolase B, peroxisomal	Acaa1b	K.AGLTVNDIDIFEINEAFASQAVYC*VEK.L	1.163333333	-
P83882	Rpl36a 60S ribosomal protein L36a	Rpl36a	R.LEC*VEPNCR.S	1.163333333	-
Q9D0I9	Rars Arginine--tRNA ligase, cytoplasmic	Rars	R.LQEVFGC*AIR.A	1.163333333	1.066785714
Q8BKC5	Ipo5 Importin-5	Ipo5	R.VAAAESMPLLLEC*AR.V	1.165	-
O08800	Serpinb8 Serpin B8	Serpinb8	K.ISEVLSPGTVC*PLTK.L	1.165	-
P48678	Lmna Prelamin-A/C	Lmna	K.AQNTWGC*GSSLR.T	1.165	1.18047619
Q9JIK5	Ddx21 Nucleolar RNA helicase 2	Ddx21	K.DSEDNPQTLLFSATC*PHWVFNVAK.K	1.166666667	1.307698413
Q8VC74	Cox18 Mitochondrial inner membrane protein COX18	Cox18	R.DLSAAFC*AK.F	1.17	-
Q80U93	Nup214 Nuclear pore complex protein Nup214	Nup214	K.AC*LQVGTSEEMK.M	1.17	-
Q3THS6	Mat2a S-adenosylmethionine synthase isoform type-2	Mat2a	K.TC*NVLVALEQQSPDIAQGVHLDR.N	1.173333333	2.274940476
Q6ZQL4	Wdr43 WD repeat-containing protein 43	Wdr43	R.DISNC*WAPTVETAITK.V	1.173333333	-
P28063	Psmb8 Proteasome subunit beta type-8	Psmb8	K.VIEINPYLLGTMSGC*AADCQYWER.L	1.173333333	-

Q8BKC5	Ipo5 Importin-5	Ipo5	K.LC*GDTNLNNMQR.Q	1.175	-
Q9R1P0	Psma4 Proteasome subunit alpha type-4	Psma4	R.YLLQYQEPIPC*EQLVTALCDIK.Q	1.176666667	1.068531746
Q9WVJ2	Psmd13 26S proteasome non-ATPase regulatory subunit 13	Psmd13	R.LELWC*TDVK.S	1.176666667	-
Q01853	Vcp Transitional endoplasmic reticulum ATPase	Vcp	K.GVLFYGPPGC*GK.T	1.18	1.075039683
P80316	Cct5 T-complex protein 1 subunit epsilon	Cct5	K.ESNPALGIDC*LHK.G	1.18	0.982321429
P16381	D1Pas1 Putative ATP-dependent RNA helicase Pl10	D1Pas1	K.IGLDFC*K.Y	1.18	0.969047619
Q9R0P3	Esd S-formylglutathione hydrolase	Esd	K.CPALYWLSGLTC*TEQNFISK.S	1.183333333	1.20297619
Q99JY9	Actr3 Actin-related protein 3	Actr3	R.LPACVVDC*GTGYTK.L	1.183333333	0.977619048
Q61024	Asns Asparagine synthetase	Asns	K.AMTEDGFLAVC*SEAK.G	1.185	1.200714286
P80315	Cct4 T-complex protein 1 subunit delta	Cct4	K.ITGC*TSPGK.T	1.185	1.040198413
Q9D1A2	Cndp2 Cytosolic non-specific dipeptidase	Cndp2	K.NKPC*ITYGLR.G	1.19	1.434920635
P17751	Tpi1 Triosephosphate isomerase	Tpi1	K.IAVAAQNC*YK.V	1.19	1.061984127
Q9WUA3	Pfkp 6-phosphofructokinase type C	Pfkp	R.LGITNLC*VIGGDGSLTGANLFR.K	1.19	0.971011905
P58252	Eef2 Elongation factor 2	Eef2	R.VTDGALVVVDCVSGVC*VQTETVLR.Q	1.19	1.011428571
Q9D187	Fam96b Mitotic spindle-associated MMXD complex subunit MI	Fam96b	R.VAAALENTHLLEVVNQC*LSAR.S	1.193333333	-
Q5SUA5	Myo1g Unconventional myosin-Ig	Myo1g	K.STC*VLEAFGNAR.T	1.195	-
Q9JKF1	Iqgap1 Ras GTPase-activating-like protein IQGAP1	Iqgap1	K.QIPAITC*IQSQWR.G	1.195	-
Q99KN2	Ciao1 Probable cytosolic iron-sulfur protein assembly pr	Ciao1	R.LASC*SDDR.T	1.195	-
Q9CRB2	Nhp2 H/ACA ribonucleoprotein complex subunit 2	Nhp2	K.AAPEESEAQAEGC*SEER.T	1.2	-
Q9DCE5	Pak1ip1 p21-activated protein kinase-interacting protein 1	Pak1ip1	R.AANGMASLPPAAEPC*PDQPK.T	1.2	-
Q9QZB7	Actr10 Actin-related protein 10	Actr10	R.IPDWC*SLNNPPLEMMFDVGK.A	1.2	-
P80313	Cct7 T-complex protein 1 subunit eta	Cct7	K.EGTDSSQGIPQLVSNISAC*QVIAEAVR.T	1.2	0.953333333
Q8R180	Ero1l ERO1-like protein alpha	Ero1l	K.HDDSSDSFC*EIDDIQSPDAEYVDLLLNPER.Y	1.2	-
P55096	Abcd3 ATP-binding cassette sub-family D member 3	Abcd3	R.SGANVLIC*GPNGC*GK.S	1.2	-
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	K.IGAAIQEELGYNC*QTGGVIAEILR.G	1.203333333	0.998511905
Q8BMA6	Srp68 Signal recognition particle 68 kDa protein	Srp68	R.FESFC*LDPSLVTK.Q	1.205	-
P42208	Sept2 Septin-2	43710	R.LTVVDTPGYGDAINC*R.D	1.205	1.328968254
P09411	Pgk1 Phosphoglycerate kinase 1	Pgk1	K.TGQATVASGIPAGWMGLDC*GTESSKK.Y	1.205	1.171031746
P60764	Rac3 Ras-related C3 botulinum toxin substrate 3	Rac3	K.YLEC*SALTQR.G	1.206666667	-

O35226	Psmd4 26S proteasome non-ATPase regulatory subunit 4	Psmd4	R.SNPENNVGLITLANDC*EVLTTLTPDTGR.I	1.21	-
O89110	Casp8 Caspase-8	Casp8	K.IFFIQAC*QGSNFQK.G	1.21	-
Q8BZA9	Tigar Fructose-2,6-bisphosphatase TIGAR	Tigar	K.AAGEEC*PMFTPPGGETVEQVK.M	1.21	-
Q9Z315	Sart1 U4/U6.U5 tri-snRNP-associated protein 1	Sart1	K.SLPSAVYC*IEDK.M	1.21	-
Q61656	Ddx5 Probable ATP-dependent RNA helicase DDX5	Ddx5	R.ELAQQVQQVAAEYC*R.A	1.21	1.135992063
P31938	Map2k1 Dual specificity mitogen-activated protein kinase	Map2k1	K.LC*DFGVSGQLIDSMANSFVGTR.S	1.213333333	-
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	K.GLTDLSAC*K.A	1.213333333	0.998511905
Q9DCX1	Mad2l1bp MAD2L1-binding protein	Mad2l1bp	R.LAPFGVDQGLNTAAC*LR.R	1.215	-
P62983	Rps27a Ubiquitin-40S ribosomal protein S27a	Rps27a	K.C*CLTYCFNKPEDK.-	1.215	1.528174603
Q9WUA3	Pfkp 6-phosphofructokinase type C	Pfkp	R.LPLMEC*VQMTQDVQK.A	1.215	0.971011905
Q9D8X5	Cnot8 CCR4-NOT transcription complex subunit 8	Cnot8	K.QNEDVDC*AQEK.M	1.22	-
Q9D6M3	Slc25a22 Mitochondrial glutamate carrier 1	Slc25a22	R.MYASMSDC*LIK.T	1.22	-
P05064	Aldoa Fructose-bisphosphate aldolase A	Aldoa	R.ALANSLAC*QGK.Y	1.22	1.174047619
P18760	Cfl1 Cofilin-1	Cfl1	K.AVLFC*LSEDKK.N	1.22	1.170833333
P63323	Rps12 40S ribosomal protein S12	Rps12	R.QAHLC*VLASNCDEPMYVK.L	1.22	0.950753968
Q99KI0	Aco2 Aconitate hydratase, mitochondrial	Aco2	R.VGLIGSC*TNSSYEDMGR.S	1.22	0.937103175
Q9Z2U1	Psma5 Proteasome subunit alpha type-5	Psma5	K.GPQLFHMDPSGTFVQC*DAR.A	1.223333333	1.28765873
Q6DFW4	Nop58 Nucleolar protein 58	Nop58	K.TYDPSGDSTLPTC*SK.K	1.225	-
P09411	Pgk1 Phosphoglycerate kinase 1	Pgk1	K.DC*VGPEVENACANPAAGTVILLENLR.F	1.226666667	1.171031746
P09411	Pgk1 Phosphoglycerate kinase 1	Pgk1	R.GCITIIGGGDTATC*C*AK.W	1.236666667	1.171031746
O08992	Sdcbp Syntenin-1	Sdcbp	K.LYPELSQYMGLSLNEAEIC*ESMPMVSGAPAQGQLVAR.P	1.24	-
P32921	Wars Tryptophan--tRNA ligase, cytoplasmic	Wars	K.GIFGFTDSDC*IGK.I	1.24	1.16922619
P80313	Cct7 T-complex protein 1 subunit eta	Cct7	R.INALTAASEAAC*LIVSVDETIK.N	1.24	0.953333333
Q9EQH3	Vps35 Vacuolar protein sorting-associated protein 35	Vps35	R.TQC*ALAASK.L	1.25	-
Q8BFY6	Pef1 Peflin	Pef1	R.SAIPAMQLDC*FIK.V	1.25	-
P24547	Impdh2 Inosine-5-monophosphate dehydrogenase 2	Impdh2	R.HGFC*GIPITDTGR.M	1.253333333	0.931190476
O88574	Sap30 Histone deacetylase complex subunit SAP30	Sap30	K.AQLVEIVGC*HFK.S	1.255	-
Q9ESV0	Ddx24 ATP-dependent RNA helicase DDX24	Ddx24	R.NIESALSC*LSR.Q	1.256666667	-
P42932	Cct8 T-complex protein 1 subunit theta	Cct8	K.IAVYSC*PFDGMITETK.G	1.256666667	0.980634921
Q8BV66	Ifi44 Interferon-induced protein 44	Ifi44	K.C*LQNYFGGK.R	1.26	-

Q9QUJ7	Acsl4 Long-chain-fatty-acid--CoA ligase 4	Acsl4	K.TAEDYC*VDENGQR.W	1.26	-
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	R.IDC*FSEVPTSVFGEK.L	1.26	0.998511905
Q61233	Lcp1 Plastin-2	Lcp1	K.KLENC*NYAVDLGK.N	1.26	0.943095238
Q9D8N0	Eef1g Elongation factor 1-gamma	Eef1g	K.VPAFEGDDGFC*VFESNAIAYYVSNEELR.G	1.26	0.913571429
P14115	Rpl27a 60S ribosomal protein L27a	Rpl27a	K.IKGVGGAC*VLVA.-	1.275	0.883769841
Q6DFW4	Nop58 Nucleolar protein 58	Nop58	K.IISDNLTYC*K.C	1.276666667	-
Q9CQU5	Zwint ZW10 interactor	Zwint	R.NQSYLQLLC*SLQNK.L	1.285	-
O55135	Eif6 Eukaryotic translation initiation factor 6	Eif6	R.ASFENNCEVGC*FAK.L	1.285	1.27765873
Q04735	Cdk16 Cyclin-dependent kinase 16	Cdk16	R.LEHEEGAPC*TAIR.E	1.295	-
Q9CZT6	Uncharacterized protein C3orf26 homolog	Uncharacterized	K.TQQPTEC*FLTQTK.E	1.295	-
Q8CB96	Rassf4 Ras association domain-containing protein 4	Rassf4	K.SDASC*IIQR.R	1.295	-
P16858	Gapdh Glyceraldehyde-3-phosphate dehydrogenase	Gapdh	R.VPTPNVSVVDLTC*R.L	1.3	1.108055556
P26039	Tln1 Talin-1	Tln1	K.NC*GQMSEIEAK.V	1.3	1.237539683
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	R.LVAFC*PFSSSQVALENANAVSEGVVHEDLR.L	1.303333333	0.998511905
A2A432	Cul4b Cullin-4B	Cul4b	R.DSASPSTSSFC*LGVPVATSSHVPIQK.K	1.305	-
D3Z5M2	Gm10110 Protein Gm10110	Gm10110	K.VVC*DENGSK.G	1.31	1.149206349
P61079	Ube2d3 Ubiquitin-conjugating enzyme E2 D3	Ube2d3	K.VLLSICSLLC*DPNPDDPLVPEIAR.I	1.31	-
Q61093	Cybb Cytochrome b-245 heavy chain	Cybb	R.GSSACC*STR.I	1.315	0.965396825
Q9QYB1	Clic4 Chloride intracellular channel protein 4	Clic4	R.DEFTNTC*PSDKEVEIAYSDVAK.R	1.32	-
Q8BZJ7	Dcun1d2 DCN1-like protein 2	Dcun1d2	R.AATQC*EFSK.K	1.32	-
P97371	Psme1 Proteasome activator complex subunit 1	Psme1	K.VDVFREDLC*SK.T	1.33	1.011190476
A6H5X4	Phf11l PHD finger protein 11-like	Phf11l	R.LVDETASESDYEGIETLLFDC*GLFK.D	1.33	-
Q9JKL4	Ndufaf3 NADH dehydrogenase	Ndufaf3	R.GFTIC*GNR.V	1.335	-
Q80W47	Wipi2 WD repeat domain phosphoinositide-interacting prot	Wipi2	K.GQDANLEAYTDDLGAVGGAC*LEDEASALR.L	1.335	-
Q9D6Z1	Nop56 Nucleolar protein 56	Nop56	R.LAALALASSENSSTPEEC*EEVNEK.S	1.34	0.998511905
P62331	Arf6 ADP-ribosylation factor 6	Arf6	R.NWYVQPSC*ATSGDGLYEGLTWLTSNYK.S	1.346666667	-
P60710	Actb Actin, cytoplasmic 1	Actb	R.C*PEALFQPSFLGMESCGIHETTFNSIMK.C	1.35	1.31265873
O88796	Rpp30 Ribonuclease P protein subunit p30	Rpp30	R.LTIIVTDPAHC*NVLR.A	1.36	-
P54823	Ddx6 Probable ATP-dependent RNA helicase DDX6	Ddx6	K.GNEFEDYC*LK.R	1.366666667	-
P43883	Plin2 Perilipin-2	Plin2	R.NLTQQLQTTC*QTVLVNAQGLPQNIQDQAK.H	1.37	-
P47757	Capzb F-actin-capping protein subunit beta	Capzb	K.GC*WDSIHVVEVQEK.S	1.37	1.077777778
Q60953	Pml Protein PML	Pml	R.DYQEIAGQLSC*LEAVLQR.I	1.376666667	-
Q9D0T1	Nhp2l1 NHP2-like protein 1	Nhp2l1	K.KLLDLVQQSC*NYK.Q	1.38	1.175595238

O08528	Hk2 Hexokinase-2	Hk2	K.ASGC*EGEDVVTLLK.E	1.386666667	-
Q8VI93	Oas3 2-5-oligoadenylate synthase 3	Oas3	K.QAIDAILC*CLR.E	1.39	-
P16675	Ctsa Lysosomal protective protein	Ctsa	K.EC*SHITFLTIK.G	1.39	0.776904762
Q8VI36	Pxn Paxillin	Pxn	K.NSSASNTQDGVGSLC*SR.A	1.39	-
P97371	Psme1 Proteasome activator complex subunit 1	Psme1	K.KGDEDDKGPPC*GPVNCNEK.I	1.395	1.011190476
Q3THK7	Gmps GMP synthase	Gmps	R.VICAEEPYIC*K.D	1.4	-
Q9R0P3	Esd S-formylglutathione hydrolase	Esd	K.AYDATC*LVK.A	1.4	1.20297619
O08709	Prdx6 Peroxiredoxin-6	Prdx6	R.DFTPVC*TTELGR.A	1.405	1.057619048
Q9D3J9	Uncharacterized protein CXorf21 homolog	Uncharacterized	R.TVLQANSNPVFESPTLAAVGIC*R.D	1.415	-
Q8BGT7	Smndc1 Survival of motor neuron-related-splicing factor 3	Smndc1	K.VGVGTC*GIADKPMTQYQDTSK.Y	1.415	-
Q922U1	Prpf3 U4/U6 small nuclear ribonucleoprotein Prp3	Prpf3	R.VLGFSEPTVVTAALNC*VGK.G	1.415	-
P54775	Psmc4 26S protease regulatory subunit 6B	Psmc4	K.ISGADINSIC*QESGMLAVR.E	1.423333333	1.114583333
P61082	Ube2m NEDD8-conjugating enzyme Ubc12	Ube2m	K.TC*DISFSDPDDLLNFK.L	1.425	1.068928571
Q9D7S9	Chmp5 Charged multivesicular body protein 5	Chmp5	K.APPPSLTDC*IGTVDSR.A	1.43	-
Q99KK2	Cmas N-acylneuraminate cytidylyltransferase	Cmas	R.VGLSAVPADAC*SGAQK.A	1.44	-
Q8VDJ3	Hdlbp Vigilin	Hdlbp	K.AAC*LESAQEPAGAWSNK.I	1.44	1.195198413
P20108	Prdx3 Thioredoxin-dependent peroxide reductase, mitochon	Prdx3	K.AFQFVETHGEVC*PANWTPESPTIKPSPTASK.E	1.44	1.03125
O08528	Hk2 Hexokinase-2	Hk2	K.FLSQIESDC*LALLQVR.A	1.445	-
P97369	Ncf4 Neutrophil cytosol factor 4	Ncf4	K.NLLSLPVC*VLMDPDVR.I	1.46	-
E9Q555	Rnf213 E3 ubiquitin-protein ligase RNF213	Rnf213	K.SGESLPADC*PVR.S	1.47	-
Q8BP47	Nars Asparagine--tRNA ligase, cytoplasmic	Nars	R.DVC*LYPR.F	1.473333333	0.953333333
P97765	Wbp2 WW domain-binding protein 2	Wbp2	K.DC*EIKQPVFGANFIK.G	1.485	-
Q6ZQ58	Larp1 La-related protein 1	Larp1	R.TASISSSPSEGTPAVGSYGC*TPQSLPK.F	1.485	-
Q60710	Samhd1 SAM domain and HD domain-containing protein 1	Samhd1	K.TSSC*LQEVSK.V	1.486666667	1.39452381
Q9CZ13	Uqcrc1 Cytochrome b-c1 complex subunit 1, mitochondrial	Uqcrc1	K.YFYDQC*PAVAGYGPIEQLPDYNR.I	1.49	0.863095238
P35550	Fbl rRNA 2-O-methyltransferase fibrillarin	Fbl	K.ANC*IDSTASAEAVFASEVK.K	1.503333333	1.163412698
J3QPN4	Uncharacterized protein	Uncharacterized	R.ADQQYEC*VAEIGEGAYGK.V	1.505	-
P36371	Tap2 Antigen peptide transporter 2	Tap2	R.VLILDEATSALDAQC*EQALQNWR.S	1.505	-
O89053	Coro1a Coronin-1A	Coro1a	K.ADQC*YEDVR.V	1.52	1.156309524
P31266	Rbpj Recombining binding protein suppressor of hairless	Rbpj	K.NADLC*IASGTK.V	1.53	-
E9Q3L4	AI607873 Protein AI607873	AI607873	K.C*TTQLTQGAASGTGK.A	1.545	-
Q07076	Anxa7 Annexin A7	Anxa7	R.LGTDESC*FNMILATR.S	1.565	-

P70460	Vasp Vasodilator-stimulated phosphoprotein	Vasp	K.SSSSVTTSEAHPSTPC*SSDDSDLER.V	1.57	1.385357143
Q62159	Rhoc Rho-related GTP-binding protein RhoC	Rhoc	K.LVIVGDGAC*GK.T	1.575	1
Q80X41	Vrk1 Serine/threonine-protein kinase VRK1	Vrk1	K.LGLPIGQGGFGC*IYLADTNSSKPVGSDAPCVVK.V	1.59	-
Q99JX3	Gorasp2 Golgi reassembly-stacking protein 2	Gorasp2	R.VSDC*TPAVEKPVSDADASEPS.-	1.616666667	-
P15379	Cd44 CD44 antigen	Cd44	K.EPSETPDQC*MTADETR.N	1.643333333	1.416666667
Q9DBU3	Riok3 Serine/threonine-protein kinase RIO3	Riok3	K.AGIPC*PTVVLLK.K	1.665	-
Q9JIH2	Nup50 Nuclear pore complex protein Nup50	Nup50	K.C*NNSNQPPSSGPASSTACPGNAYHK.Q	1.665	-
Q8CAS9	Parp9 Poly	Parp9	K.FGCISTLSC*PTLAGSSSPAQR.V	1.695	-
Q8K1M6	Dnm1l Dynamin-1-like protein	Dnm1l	K.YIETSELC*GGAR.I	1.705	-
Q9WUM4	Coro1c Coronin-1C	Coro1c	K.SELSC*APK.K	1.71	0.892738095
Q8BVW3	Trim14 Tripartite motif-containing protein 14	Trim14	K.LIQDCLEC*LATK.K	1.725	-
O08528	Hk2 Hexokinase-2	Hk2	K.MLPTYVC*ATPDGTEK.G	1.73	-
O35892	Sp100 Nuclear autoantigen Sp-100	Sp100	K.MYEDLLDSC*R.S	1.746666667	-
P45377	Akr1b8 Aldose reductase-related protein 2	Akr1b8	R.AC*LLPETVNMEEYPYDAEY.-	1.756666667	-
Q04750	Top1 DNA topoisomerase 1	Top1	R.AVAILC*NHQR.A	1.79	-
P31266	Rbpj Recombining binding protein suppressor of hairless	Rbpj	R.IIQFQATPC*PK.E	1.805	-
P10126	Eef1a1 Elongation factor 1-alpha 1	Eef1a1	K.PMC*VESFSDYPPLGR.F	1.813333333	1.213769841
P02802	Mt1 Metallothionein-1	Mt1	K.SC*CSCCPVGCSK.C	1.835	-
Q6Q899	Ddx58 Probable ATP-dependent RNA helicase DDX58	Ddx58	K.GKNTIICAPTGC*GK.T	1.845	-
Q9QUH0	Glrx Glutaredoxin-1	Glrx	K.DC*IGGCSDLISMQQTGELMTR.L	1.866666667	-
Q9QUJ7	Acsl4 Long-chain-fatty-acid--CoA ligase 4	Acsl4	K.GYDAPLC*NLILFK.K	1.876666667	-
Q9QYB1	Clic4 Chloride intracellular channel protein 4	Clic4	K.AGSDGESIGNC*PFSQR.L	1.906666667	-
Q9R233	Tapbp Tapasin	Tapbp	R.SLSPEQNC*PR.A	1.915	1.828869048
P11928	Oas1a 2-5-oligoadenylate synthase 1A	Oas1a	K.SAVNVVC*DFLK.E	1.936666667	-
Q8BKC5	Ipo5 Importin-5	Ipo5	K.IC*DIAAELAR.N	1.955	-
Q91Z49	Fyttd1 UAP56-interacting factor	Fyttd1	R.TSTTNGGILTVSIDNPGAVQC*PVTQKPR.L	2.045	-
Q9CZL2	Uncharacterized protein C4orf32 homolog	Uncharacterized	R.GGAGSAGGEC*DEDGAAPAGR.V	2.105	-
P30681	Hmgb2 High mobility group protein B2	Hmgb2	K.MSSYAFFVQTC*R.E	2.115	1.516369048
P99029	Prdx5 Peroxiredoxin-5, mitochondrial	Prdx5	K.ALNVEPDGTGLTC*SLAPNILSQL.-	2.136666667	2.799603175
P22892	Ap1g1 AP-1 complex subunit gamma-1	Ap1g1	R.FTC*TVNR.I	2.15	-
E9Q3L4	AI607873 Protein AI607873	AI607873	R.LTNITC*EPGNK.L	2.22	-
Q9QUJ7	Acsl4 Long-chain-fatty-acid--CoA ligase 4	Acsl4	R.VGAPLIC*CEIK.L	2.24	-
Q91VE6	Mki67ip MKI67 FHA domain-interacting nucleolar phosphoprot	Mki67ip	K.SSVDSQGPTPVC*TPTFLER.R	2.35	1.107103175

P17742	Ppia Peptidyl-prolyl cis-trans isomerase A	Ppia	K.KITISDC*GQL.-	2.445	1.132857143
Q8CFI7	Polr2b DNA-directed RNA polymerase II subunit RPB2	Polr2b	R.DC*QIAHGAAQFLR.E	2.565	-
Q99LE6	Abcf2 ATP-binding cassette sub-family F member 2	Abcf2	R.LAHEDAEC*EK.L	2.665	-
P51670	Ccl9 C-C motif chemokine 9	Ccl9	R.GFQVC*ANPSDR.R	2.915	-
Q9WVK4	Ehd1 EH domain-containing protein 1	Ehd1	R.FMC*AQLPNPVLDSISIIDTPGILSGEK.Q	2.933333333	2.669642857
Q3UDK1	Trafd1 TRAF-type zinc finger domain-containing protein 1	Trafd1	R.TMNNVASC*NR.L	3.015	-
Q60766	Irgm1 Immunity-related GTPase family M protein 1	Irgm1	R.DDDNMGEC*LK.V	3.16	2.324404762
O35228	Ebi3 Interleukin-27 subunit beta	Ebi3	R.LGVATQQQSQPC*LQR.S	3.47	-
P28033	Cebpb CCAAT/enhancer-binding protein beta	Cebpb	K.AEPGFEPADC*KR.A	3.52	-
P52927	Hmga2 High mobility group protein HMGI-C	Hmga2	K.QQQEPTC*EPSPK.R	3.755	-
Q64337	Sqstm1 Sequestosome-1	Sqstm1	R.AGDGRPC*PTAESASAPPEDPNVNFLK.N	4.165	26.48958333
Q61990	Pcbp2 Poly(rC)-binding protein 2	Pcbp2	R.YSTGSDSASFPHTTPSMC*LNPDLEGPPLEAYTIQGQYAIPQPDLTK.L	4.523333333	1.017896825
P02798	Mt2 Metallothionein-2	Mt2	K.SC*CSCCPVGCAK.C	5.26	-
E9Q3L4	AI607873 Protein AI607873	AI607873	K.GLEC*INK.H	5.72	-
Q64337	Sqstm1 Sequestosome-1	Sqstm1	R.FSFC*FSPEPEAEAQAAAGPGPCER.L	6.2	26.48958333
Q8VI94	Oasl1 2-5-oligoadenylate synthase-like protein 1	Oasl1	R.ALGPSC*PSSEVYANLIK.A	7.275	-
Q8CGK3	Lonp1 Lon protease homolog, mitochondrial	Lonp1	R.TLC*GLDESK.A	7.35	0.786587302
P28033	Cebpb CCAAT/enhancer-binding protein beta	Cebpb	K.AAPAAC*FAGPPAAPAK.A	8.89	-
P28667	Marcksl1 MARCKS-related protein	Marcksl1	K.EGGGDSSASSPTEEEQEQGEMSAC*SDEGTAQEGK.A	10.205	16.72761905
A2AJI0	Map7d1 MAP7 domain-containing protein 1	Map7d1	R.SASASPLTPC*SAPR.S	10.4	-
Q3UHD6	Snx27 Sorting nexin-27	Snx27	R.NGGGGGGSGLHC*AGNGGGGGGGPR.V	10.44	-
P51660	Hsd17b4 Peroxisomal multifunctional enzyme type 2	Hsd17b4	K.NNIHC*NTIAPNAGSR.M	10.495	1.223392857
E9Q2I4	C130039O16Rik Protein C130039O16Rik	C130039O16Rik	K.RKRC*PFGDQEPAAK.E	10.54	-
Q9DB77	Uqcrc2 Cytochrome b-c1 complex subunit 2, mitochondrial	Uqcrc2	K.NALANPLYC*PDYR.M	10.555	0.81531746
Q9R0Q7	Ptges3 Prostaglandin E synthase 3	Ptges3	K.LTFSC*LGGSDNFK.H	10.99	-
Q8BVK9	Sp110 Sp110 nuclear body protein	Sp110	R.AVPLLGC*IQEGK.T	11.695	-
Q64337	Sqstm1 Sequestosome-1	Sqstm1	K.C*SVC*PDYDLCSVCEGK.G	12.11	26.48958333
P01582	Il1a Interleukin-1 alpha	Il1a	K.SFYDASYGSLHETC*TDQFVSLR.T	19.37	-
P30882	Ccl5 C-C motif chemokine 5	Ccl5	K.C*SNLAVVFVTR.R	20	-
P17515	Cxcl10 C-X-C motif chemokine 10	Cxcl10	K.LEIIPASLSC*PR.V	20	-
P54987	Irg1 Immune-responsive gene 1 protein	Irg1	K.LEDLEDC*SVLTR.L	20	28.73015873

Q05769	Ptgs2 Prostaglandin G/H synthase 2	Ptgs2	K.IINTASIQSLIC*NNVK.G	20	28.73015873