Identification of mitofusin 1 and complement component 1q subcomponent-binding protein as mitochondrial targets of autoantibodies in systemic lupus erythematosus

Yann LC Becker[1,2,4], Jean-Philippe Gagné[2,8], Anne-Sophie Julien[3], Tania Lévesque[1,2,4], Isabelle Allaeys[1,2,4], Nadine Gougeard[5,6], Vicente Rubio[5,6], François-Michel Boisvert[7], Dominique Jean[7], Eric Wagner[4,8]; Guy G. Poirier[2,9] , Paul R. Fortin[1,10], Éric Boilard[1,2, 4].

[1] Centre de Recherche ARThrite - Arthrite, Recherche et Traitements, Université Laval, Québec, Qc, Canada.
[2] Axe Maladies infectieuses et immunitaires, Centre de Recherche du Centre Hospitalier Universitaire de Québec - Université Laval, Québec, Qc, Canada
[3] Département de mathématiques et statistique, Université Laval, Québec, Qc, Canada.
[4] Département de microbiologie et immunologie, Université Laval, Québec, Qc, Canada
[5] Structural Enzymopathology Unit, Instituto de Biomedicina de Valencia of the CSIC (IBV-CSIC), Valencia, Spain
[6] Group 739, Centro de Investigación Biomédica en Red para Enfermedades Raras (CIBERER-ISCIII), Madrid, Spain
[7] Department of Anatomy and Cell Biology, Université de Sherbrooke, Sherbrooke, Quebec, Canada
[8] Laboratoire d'Immunologie et Histocompatibilité, CHU de Québec-Université Laval, Département de Médecine de Laboratoire, Québec, Qc, Canada.
[9] Département de biologie moléculaire, de biochimie médicale et de pathologie, Faculté de Médecine, Université Laval, Québec, Qc, Canada
[10] Division de Rhumatologie, Département de Médecine, CHU de Québec – Université Laval, Québec, Qc, Canada.

Correspondence should be sent to

Eric Boilard, PhD : eric.boilard@crchudequebec.ulaval.ca

Centre de Recherche du CHU de Québec – Université Laval,

2705 Boulevard Laurier, Room T1-49

Quebec City, Quebec, G1V 4G2, Canada.

Telephone: (418) 525-4444 Ext : 46175

Authors' Twitter handles: Yann LC Becker: @YannBECKER4**, Eric Boilard:** @boilard_eric

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Conflict of Interest: YB, PRF and EB have filed a provisional patent related to the work presented herein.

ABSTRACT

Objective: Mitochondria are organelles that possess several bacterial features such as a double-stranded genome with hypomethylated CpG islets, formylated proteins, and cardiolipin-containing membrane. In systemic lupus erythematosus (SLE), mitochondria and their inner components are released into the extracellular space, potentially eliciting a pro-inflammatory response by the immune system. While cardiolipin and mitochondrial DNA and RNA are confirmed targets of autoantibodies, other antigenic mitochondrial proteins in SLE remain to be identified. Herein, we aim to characterize the protein repertoire recognized by anti-mitochondrial antibodies (AMA) in SLE patients.

Methods: Using shotgun proteomic profiling, we identified 1345 proteins, 431 of which were associated with the mitochondrial proteome. Immunoreactivities to several of these candidates were assessed by direct ELISA in serum sample from a local cohort (healthy: n=30, SLE: n=87) and associated with demographic and disease characteristics.

Results: We determined that IgGs to the C1q-binding protein (C1qBP) are significantly elevated in SLE patients included in our cohort (p=0.049) and are associated with positivity for lupus anticoagulant (p=0.049). IgG against the mitochondrial protein mitofusin 1 (Mfn1) displayed promising performances in the prediction of SLE diagnoses (aOR: 2.99, 95%CI: 1.39–6.43, p=0.0044) in our cohort. Moreover, anti-Mfn1 were associated with positivity to anti-phospholipids (p=0.011) and anti-dsDNA (p=0.0005).

Conclusion: This study presents the mitochondrial repertoire targeted in SLE, indicating that autoantibodies can recognize secreted and/or surface proteins of mitochondrial origin. Profiling of the AMA repertoire in large prospective cohorts may improve our knowledge on mitochondrial biomarkers and their usefulness for patient stratification.

INTRODUCTION

The mitochondrion, a peculiar organelle in charge of numerous cellular pathways, is derived from the endosymbiosis between an α-proteobacterium and a primitive eukaryotic cell (1,2). Despite their intracellular nature, whole mitochondria and/or mitochondrial components may be released into the extracellular milieu in conditions of necrosis, tissue damage (3–6), or cellular activation (7–10). The release of whole mitochondria and/or mitochondrial components [i.e. molecular patterns (mtDAMPs)] skews innate immunity toward a pro-inflammatory response (11–13). Mitochondrial antigens may also be targeted by the adaptive immune system as indicated by the presence of a humoral response, comprised of various types of anti-mitochondrial autoantibodies (AMA) (14–17), in various inflammatory and autoimmune conditions. However, both the pathophysiological pathway leading to the production of AMA and several of the antigens targeted by several AMA remain to be characterized (14,16).

Systemic lupus erythematosus (SLE) is a complex autoimmune disease in which the immune system generates autoantibodies recognizing self-epitopes. Antibodies directed against DNA and nuclear components are hallmarks of SLE (18). Autoantibodies against the mitochondrial phospholipid cardiolipin (aCL) are associated with both thrombotic and obstetric events in SLE and the antiphospholipid syndrome (APS) (19). Simultaneous presence of aCL and antibodies to the 60-kDa heat-shock protein (HSP60) were associated with arterial thrombosis (20). Studies have also revealed that the lupus autoantibody repertoire comprises immunoglobulins against mtDNA and mtRNA (15–17)

Despite the description of antibodies targeting mitochondrial antigens, the mitochondrial epitopes expressed on the outer membrane remains to be identified (14,15). Herein, we aim to characterize the antigenic protein repertoire recognized by AMA in SLE patients.

MATERIAL AND METHODS

The CHU de Québec – Université Laval Systemic Autoimmune Rheumatic Disease Biobank and DataBase repository (SARD-BDB).

Serum samples from healthy donors and lupus patients were gathered, in accordance with the Declaration of Helsinki, as previously reported (16). Additional information provided in **Supplementary methods**.

Mitochondrial samples:

Mitochondria were isolated, following previously published procedures (15). and subsequently lyzed. Additional information provided in **Supplementary methods**.

Sample preparation for mass spectrometry identification of mitochondrial antigens targeted by AMA in SLE:

Immunoprecipitations: All incubations and washings used gentle rotary mixing, and were performed at ambient temperature (about 21ºC) – unless indicated. In all experiments, 3mg of Dynabeads®-ProteinG were used. Before use, beads were washed three times with 1ml of 1X PBS (Wisent, Montréal, Qc, Canada). For retention of the beads in the tubes, a DynaMag™-2 (Thermo Fisher Scientific, Waltham, MA, USA) magnetic strip was used.

Total mitochondrial antigens: Dynabeads®-Protein G were incubated for 2hrs with 1mL pooled sera (Additional information provided in **Supplementary methods)** diluted to an IgG concentration of 24µg/ml in protease inhibitors-containing lysis buffer (see above). Dynabeads®-bound total IgG were then washed three times in 1.5mL PBS and once in the same volume of lysis buffer. Samples were incubated overnight at 4 ºC with 1.5ml of mitochondrial lysate brought to a protein concentration of 3mg/mL. Washing steps in 1.5mL total volume were then performed as as follows: thrice in lysis buffer, containing a protease inhibitor cocktail, and twice in PBS. Beads were then resuspended in 100µL of 75mM ammonium bicarbonate at pH8.0 and stored at -80°C until used.

Enrichment in mitochondrial outer membrane (MOM) antigens by panning: Intact mitochondria (0.5mg as quantitated by BCA assay) were incubated overnight at 4ºC with 1mL of diluted pooled sera (10%, in PBS with a protease inhibitor cocktail) from pooled samples of healthy individuals or lupus patients. Unbound serum components were removed by three 7,000g centrifugal washing steps, each performed for 10min at 4°C, with 1.5ml PBS. AwMA, bound to their outer membrane mitochondrial antigens were released by incubation in 1mL lysis buffer containing a protease inhibitor cocktail, overnight at 4°C to ensure the capture of IgGs by Dynabeads®-Protein G. Three washing steps were performed in PBS containing a protease inhibitor cocktail, followed by two final washes with PBS devoid of protease inhibitors. Samples were resuspended in 100µL ammonium bicarbonate buffer, pH8.0 and stored at -80°C.

Negative controls: The same procedure as for total mitochondrial antigens was performed, using an irrelevant monoclonal IgG (Clone IV.3, i.e. targeting FcγRIIa) instead of serum-containing IgG in order to mitigate non-specific capture of proteins caused by either polyreactive or natural antibodies that may target mitochondrial antigens.

Identification of mitochondrial antigens recognized by AMA:

On-bead proteolysis: isolated samples were resuspended in 200µL of 75mM ammonium bicarbonate pH8.0 and supplemented with 2µg of a trypsin/Lys-C mix (Promega, Madison, WI, USA). Proteins in the samples were digested overnight at 37°C on a rotating mixer. The digested products were acidified with trifluoroacetic acid and the peptides generated from the proteolytic digestion were isolated and washed on C18 tips (Thermo Fisher Scientific) according to the manufacturer's instructions. The purified peptides were then dried by vacuum centrifugation and stored at −80 °C before analysis by liquid chromatography with tandem mass spectrometry (LC-MS/MS. Additional information provided in **Supplementary methods**).

Detection of autoantibodies targeting selected mitochondrial antigens

The assessment of autoantibody levels against several mitochondrial antigens was performed either by direct ELISA, using diluted sera (1:100) from healthy individuals or patients with either primary biliary cirrhosis (PBC), SLE or APS – as previously described (15–17). To assess reactivity patterns in routine clinical testing, indirect immunofluorescence (IIF) assays were performed using HEp-2 cells (Bio-Rad laboratories, Hercules, CA, USA). Patient serum samples were tested at 1:80 and 1:160 dilutions using a PhD lx workstation (Bio-Rad laboratories). Polyclonal antibodies against C1qBP and Mfn1 were also tested for their reactivity patterns on HEp-2 cells. Reactivity patterns were assessed by a trained member of the personnel and validated by the laboratory director, using a BX53 immunofluorescence microscope (Olympus Corporation, Shinjuku, Japan). Pictures presented herein were subsequently acquired, using a (MODELE) confocal microscope. Additional information is provided in **Supplementary methods**.

Statistical analyses:

Sociodemographic, clinical and laboratory values are presented as either median ± inter-quartile range (IQR), n (%), or as mean ± SD. Groups were compared using the Kruskal-Wallis test with multiple comparisons to healthy donors. Spearman correlations were calculated to see associations between AMA and antibodies assessed in routine clinical serology tests. Youden's index was determined to set a cut-off value for positivity to anti-C1qBP and anti-Mfn1. Logistic regressions were performed to predict diagnosis, separately for C1qBP ad Mfn1. Additional information on these tests provided in **Supplementary methods**. Statistical analyses were performed with Prism 9 software (GraphPad Software Inc., La Jolla, CA, USA) and SAS version 9.4 (SAS Institute Inc., Cary, NC, USA), while figures were assembled with Photoshop CC 2019 version 20.0.4 (Adobe Systems Inc.).

RESULTS

We adopted two complementary approaches to identify proteins targeted by AMA in SLE: 1) we used mitochondrial lysates to examine the complete spectrum of mitochondrial proteins targeted by AMA and identified by immunoprecipitation, and 2) whole (i.e. intact) mitochondria were used to capture AMA recognizing components from the mitochondrial outer membrane (MOM). An irrelevant antibody, targeting a protein absent in mitochondria, was also utilized as a control. The latter strategy permitted to appreciate both the non-specific binding and potential endogenous proteins interacting with IgG (e.g. the complement pathway) (**Figure 1**).

A total of 1345 proteins were identified by the combined approaches, 252 of which were withdrawn as usual contaminants (**Supplementary Table 4**). When grouped for protein interactions, we observed an enrichment of three networks in SLE samples: the C1q complement component, the serin protease inhibitor (serpin) superfamily, and members of the pyruvate dehydrogenase complex. Analysis through gene ontology highlighted the mitochondrial metabolism as the functions / processes with the highest significance (**Figure 2c**).

The complement component 1q subcomponent-binding protein (C1qBP) is a mitochondrial protein that is stored within the mitochondrion and can be then addressed to the surface of the plasma membrane and/or shed into the extracellular space (21). Although C1qBP is not strictly a mitochondrial protein, its enrichment in SLE samples and its relevance to mitochondria and complement stimulated further analyses (Figure 2). When assessed by direct ELISA, IgG against C1qBP was significantly ($p=0.049$) elevated in patients with SLE (**Figure 3a**) in comparison with healthy individuals. In contrast, the levels of anti-C1qBP were not significantly increased in APS or PBC (**Figure 3a**), two diseases in which AMA are reported (22,23).

While antibodies in PBC target proteins from the mitochondria inner membrane (MIM), the inter-membrane space (IMS) or the matrix (MM) (14,24–26), previous findings determined that

antibodies may also recognize components on the surface of the outer membrane in SLE (15,17,27). Thus, we assessed the localizations of the proteins to identify members of the mitochondrial proteome. 431 mitochondrial proteins were assigned to the mitochondrion, 168 of which lacked references pertaining to their mitochondrial sublocalization. Ninety-three proteins were expressed within the MM, 6 in the IMS, 130 in the MIM and 35 in the MOM. Of note, 13 proteins were associated with more than one mitochondrial compartment (**Supplementary Table 4**).

A protein from the MOM, associated to the the pyruvate dehydrogenase complex but distinct from the antigenic targets of AMA-M2 and presenting an elevated score in our panning approach was selected – mitofusin-1 (Mfn1). IgGs against Mfn-1 were significantly increased in SLE in comparison with healthy individuals ($p=0.0044$). In contrast, they were not significantly increased in PBC and APS (**Figure 3b**). For comparisons, we tested the antigenicity of other mitochondrial proteins with known MIM or MM locations, but with lower prediction scores in our panning approach. The MM urea cycle enzymes ornithine carbamoyltransferase, carbamoyl-phosphate synthase and N-acetylglutamate synthase and the metabolic enzymes aspartate aminotransferase and aldehyde dehydrogenase; and the MIM beta and alpha subunits of, respectively, ATP synthase and electron transfer flavoprotein, two proteins implicated in oxidative phosphorylation and electron transfer, were tested. The levels of autoantibodies against these other candidates were not significantly increased in SLE patients in comparison to healthy individuals (**Supplementary Figure 1**).

Whether the autoantibodies to either of these two components, C1qBP and Mfn 1, are associated with a definable cytoplasmic immunofluorescent staining pattern on routine Hep-2 substrates, as seen with antibodies to pyruvate dehydrogenase complex in PBC sera (22,28), was determined next. Indirect immunofluorescence labeling of Hep2 cells with a commercial antibody against C1qBP produced an intense speckled staining of the nuclear region and a lower signal in the cytosol. Conversely, commercial anti-Mfn 1 displayed a reticular staining of the cytoplasm, typical of anti-mitochondrial antibodies (**Figure 4A**). $AwMA^{+}$ SLE sera displayed a wide variety of

patterns, but none was qualified as positive for mitochondrial staining. In contrast, PBC sera utilized using the same approach revealed an obvious cytosolic pattern, with no nuclear staining when observed using a regular fluorescence microscope. However, when the same slides were examined using a confocal microscope, the autoantibodies from 7 out of the 9 SLE patients tested displayed various intensities of cytoplasmic staining, reminiscent of those observed in PBC or observed using commercial antibodies against C1qBP and Mfn 1 (**Figure 4**, **Supplementary Table 5**).

Although it is acknowledged that the number of patients examined is insufficient to draw definite conclusions on the clinical implications of these findings, biostatistical analyses were performed to determine potential associations between anti-C1qBP or anti-Mfn1 with disease characteristics in the SLE patients included in our cohort. While neither anti-C1qBP nor anti-Mfn1 displayed significant association to the various clinical manifestations assessed using univariate and multivariate logistic regressions (i.e. thrombosis, carotid plaque, SDI≥1, SLEDAI-2K≥4, arthritis, nephropathies or dermatological disorders, *data not shown*), we assessed the ability of these two AMA to efficiently discriminate SLE samples from healthy controls using Youden's index. Calculated cut-off values were 0.064 for anti-C1qBP and 0.116 for anti-Mfn1. Antibodies to Mfn1 displayed suboptimal sensitivity, but good specificities, while anti-C1qBP had high sensitivity, but lower specificity (**Supplementary Table 6**). However, both autoantibodies showed high positive predictive values.

Moreover, SLE patients positive for the lupus anticoagulant (i.e. LA) displayed increased anti-C1qBP IgGs (**Table 1**). Anti-Mfn1 IgGs were increased in patients with positivity to anti-phospholipids (i.e. any, or a combination of the various anti-phospholipids assessed), as well as anti-double-stranded DNA autoantibodies (i.e. anti-dsDNA). When considering individual IgGs, anti-Mfn1 were increased in patients positive for anti-cardiolipin and neared significance in patients with anti-β_2 glycoprotein I (i.e. anti-β_2GPI). These results were further confirmed by the correlations between $OD_{405\,nm}$ measured for anti-Mfn1 and continuous variables available for anti-cardiolipin, anti-β_2GPI and anti-dsDNA (**Table 2**). When matched with levels of other AMA, levels of anti-C1qBP were associated with both AwMA-IgG and AmtDNA-IgG. Anti-Mfn1

271 correlated with all the AMA assessed in our cohort (**Table 2**). Of note, levels of anti-C1qBP also
272 correlated with those of anti-Mfn1 (r_s=0.49; p>0.0001).

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DISCUSSION

Patients with SLE display antibodies from various subclasses (e.g. IgG, IgM, IgA) against a wide array of self-antigens (29). The epitopes targeted by these autoantibodies comprise, but are not limited to (30), phospholipids [e.g. aPL, aCL, LA] (31), anti-β_2 GPI (32), nucleic acids (e.g. anti-dsDNA, AmtDNA, AmtRNA) (15,16), transcription factors and ribonucleoproteins [i.e. anti-nuclear antibodies (ANA)] (33). Furthermore, distinct autoantibodies targeting various types of mitochondrial biomolecules such as phospholipids (i.e. aCL targeting cardiolipin) (34), nucleic acids (i.e. mtDNA, mtRNA) (15,16) and antigens whose precise nature remains to be characterized (i.e. AMA-M5) were reported in SLE (14,35).

While various proteins involved in the mitochondrial processing of pyruvate (e.g. PDC-E2), sulfite oxidase and glycogen phosphorylase are mitochondrial proteins known to be targeted by AMA (i.e. respectively by AMA-M2, -M4 and -M9) in PBC (14), limited knowledge is available concerning the extent of the mitochondrial proteome targeted by AMA in SLE. Antibodies to cardiolipin, a phospholipid uniquely synthetized in mitochondria in humans are known to be associated with vascular and obstetrical events in SLE and APS (19,36,37). To date, the only mitochondrial protein with autoantibodies associated with disease manifestations in SLE is HSP60 (38). Herein, we used several approaches to enrich mitochondrial antigens. Thus, we identified 1093 different proteins with 431 (39.43%) of which were associated with the mitochondrial proteome (39). These mitochondrial proteins, targeted by circulating AMA, reveal the extent of the mitochondrial antigenicity in SLE. Of note, among all the previously known mitochondrial proteins targeted by AMA, each of the currently known protein antigen targeted by AMA – with the exception of glycogen phosphorylase – were detected by our mass spectrometry analyses.

Samples were treated with the benzonase nuclease in order to prevent the co-isolation of nucleic acid interacting proteins, such as mtRNA with bound ribonucleoproteins (mtRNP). Despite these precautions, our methods indicated the presence of non-mitochondrial proteins (e.g. complement proteins, ficolin-3, serpins). While we restricted the focus of our study on the proteins assigned to the mitochondrial proteome, such entities should be considered with caution as, in addition to their own potential antigenicities, they can be co-isolated in association with other biomolecules

(e.g. interactors, ligands). Anti-RNP autoantibodies such as anti-small nuclear ribonucleoproteins (snRNP), Ro/SSA and La/SSB are detected in mixed connective tissue disease as well as in SLE, Sjögren syndrome, scleroderma and myositis (40). Of note is that ANA of the anti-Th/To family were reported to cross-react with mitochondrial RNA processing in systemic sclerosis (41). These elements suggest that, while we substracted mtRNP given their recognition as common contaminants in proteomic analyses, further studies are needed to appreciate their immunogenicity and the overlap between AMA and ANA in various systemic autoimmune rheumatic diseases. Such studies could allow improvements to patient classification in cases of difficult diagnoses or overlapping syndromes. While we tested a handful of mitochondrial proteins, systematic characterization of patients' immunoreactivities to large subsets of mitochondrial antigens would be enhanced by the use of high-throughput screening methods such as nucleic acid programmable protein array.

Two proteins with significant immunogenicities stood out from the various candidates assessed due to their increase in SLE samples when compared to healthy individuals. First, C1qBP, a protein stored within the mitochondrion and dispatched to the MOM and/or the cell membrane, or secreted into the circulation (42,43), where it may be targeted by circulating AMA. Second, Mfn1, a protein embedded in the MOM that could be recognized by AMA upon the release of whole mitochondria into the extracellular space (44). Of note, neither autoantibodies to C1qBP or Mfn-1 were increased in PBC, another autoimmune condition characterized by the production of various AMA by patients (22). They were also not increased in APS, a disease that may be associated to SLE with pathogenic antibodies against cardiolipin (45). ~~We~~ Complement molecules in circulation, thus in the sera tested, may target mitochondria directly (46); we thus speculate that C1qBP potentially constitutes a circulating autoantigen enabling the formation of protein-protein scaffolds with C1q and/or IgGs allowing pro-inflammatory signaling (e.g. respectively through the classical complement pathway and signaling by Fcɣ receptors) (47). The strong correlation between anti-Mfn1 and AwMA suggests that mitofusin 1 might represent one of the main mitochondrial antigens of the MOM. Moreover, our previous work on AMA in SLE and the correlations of AMA with circulating mtDNA or anti-cardiolipin (**Tables 1 and 2**) showcase the mitochondrion as the source of various immunogenic biomolecules (10,15–17). When considering the preliminary

performances of the two identified AMA, both displayed high positive predictive values for the likelihood of an SLE diagnosis in samples from this cohort. Anti-C1qBP displayed suboptimal specificity, but high sensitivity, whereas anti-Mfn1 presented high specificity and suboptimal sensitivity (**Supplementary table 6**).

Routine detection of AMA is performed either by indirect immunofluorescence or ELISA (48). We observed that commercial antibodies against Mfn1 produce a classical mitochondrial staining, whereas anti-C1qBP shows staining of both nuclear and cytoplasmic regions of Hep2 cells. These observations are concordant with the fact that Mfn1 is known to be uniquely expressed at the surface of the mitochondrion, while C1qBP may also be found in other organelles such as the nucleus or the Golgi apparatus (49). Clinical observation of SLE sera positive for AwMA, using a fluorescence microscope as routinely performed in clinical laboratories, indicated that none of the 9 samples assessed displayed cytoplasmic staining. However, upon further scrutiny using a confocal microscope, a proportion of these patients displayed significant cytoplasmic fluorescence resembling that observed in PBC, along with nuclear staining. The use of confocal microscopy, rather than wide-field fluorescence imaging, may thus be more optimal to discriminate different subcellular stainings in conditions where the nucleus shows dominant staining. Every patient included in our cohort was positive for ANA, thus we could not assess indirect immunofluorescence patterns observed in $AwMA^{+}$ / ANA^{-} specimens. SLE being characterized by a wide repertoire of autoantibodies, confocal microscopy may thus be of use in order to visualize indirect immunofluorescence patterns across each cellular sublocalizations (29,30,50). The lack of specific indirect immunofluorescence pattern in our preliminary study suggests that direct ELISA may be more informative for the detection AMA, as this technique would provide quantitative information on the levels of autoantibodies specific to this target.

Our study has limitations. Due to the nature of the patient recruitment, the blood samples used for this study were collected at the time of patient inclusion into the cohort, not at time of first diagnosis. Thus, the levels of autoantibodies that we measured do not necessarily reflect the antibodies present at the time of diagnosis. Moreover, phlebotomies were not performed at time of occurrence of the clinical events. AMA levels were thus assessed for associations with histories of

any past and/or active clinical events. Furthermore, the sample size, the ethnic distribution of the patients and the relatively low clinical activity scores of the patients at the time of the phlebotomy may have influenced the various data assessed. Our preliminary findings presented herein should therefore be confirmed in large inception cohorts with a broader spectrum of autoantibody repertoires. Such studies would allow to appreciate fluctuations of AMA levels around the time of active disease manifestations in SLE and to assess the performances of AMA as biomarkers in SLE. Considering the dynamic range of antibody levels measured in patients with PBC and APS, the replication of the present study in larger cohorts of patients and the evaluation of other rheumatic conditions (e.g. myositis, scleroderma) would also provide information about the distribution of AMA in autoimmune diseases.

In conclusion, the autoantibodies repertoire in SLE targets multiple representatives of the mitochondrial proteome, notably C1qBP and Mfn1. Further studies may reveal whether the detection of AMA in SLE or other autoimmune conditions may improve diagnosis, prognosis and/or patient stratification in SLE.

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Figures:

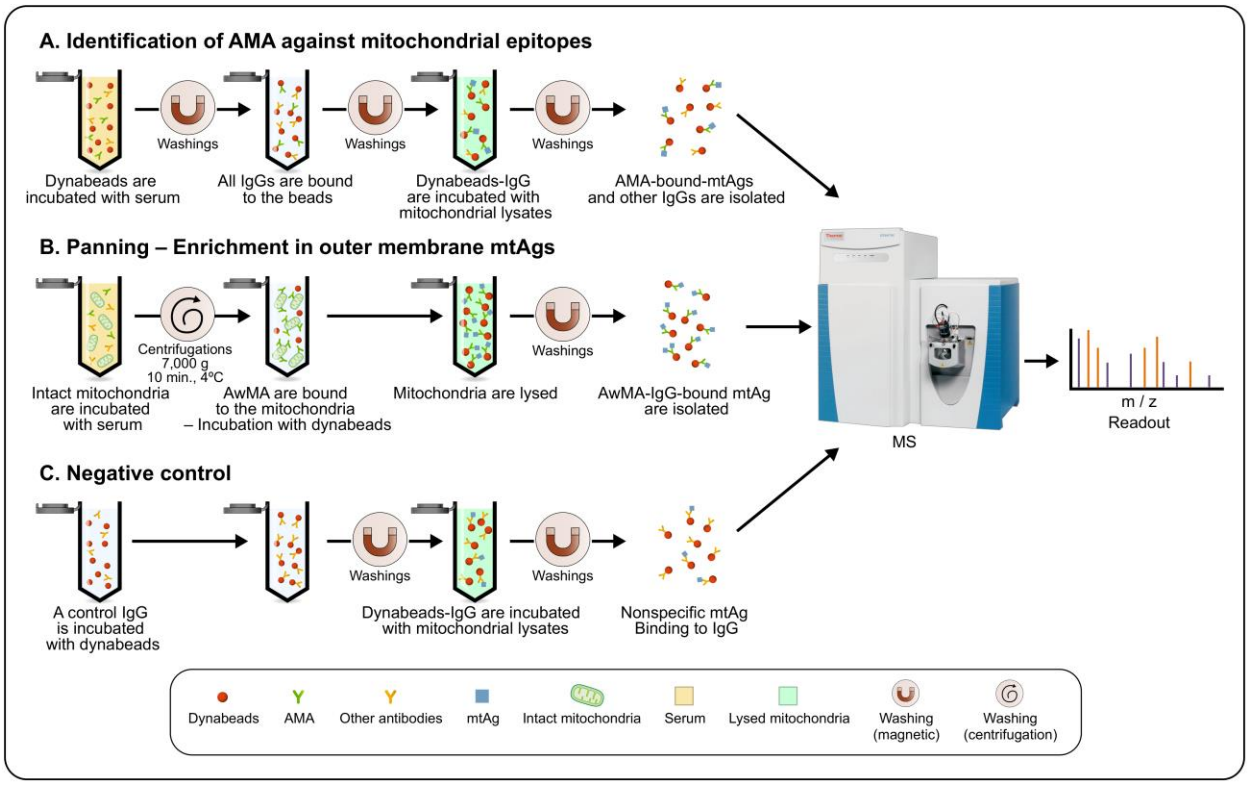

Figure 1: Workflow used for the detection of mitochondrial antigens targeted by anti-mitochondrial antibodies in SLE.

(a) Antibodies of the IgG subclass are isolated, using Dynabeads®-Protein G, from pooled sera from either 10 healthy donors or 10 SLE patients with high levels of anti-whole mitochondrial IgG (AwMA-IgG). Dynabeads®-bound IgG were subsequently incubated with mitochondrial lysates, allowing the affinity purification of mitochondrial antigens (mtAgs) from all sub-localizations. (b) Freshly isolated intact mitochondria were incubated with pooled sera. Mitochondria incubated with AwMA were then lysed and AwMA-IgG isolated with Dynabeads™. (c) An irrelevant monoclonal IgG targeting FcγRIIa – a protein absent from mitochondria, is bound to Dynabeads™ and incubated with mitochondrial lysates in order to identify non-specific binding of mtAgs. For each approach, samples were acquired in triplicate and mtAgs were identified by mass-spectrometry (MS).

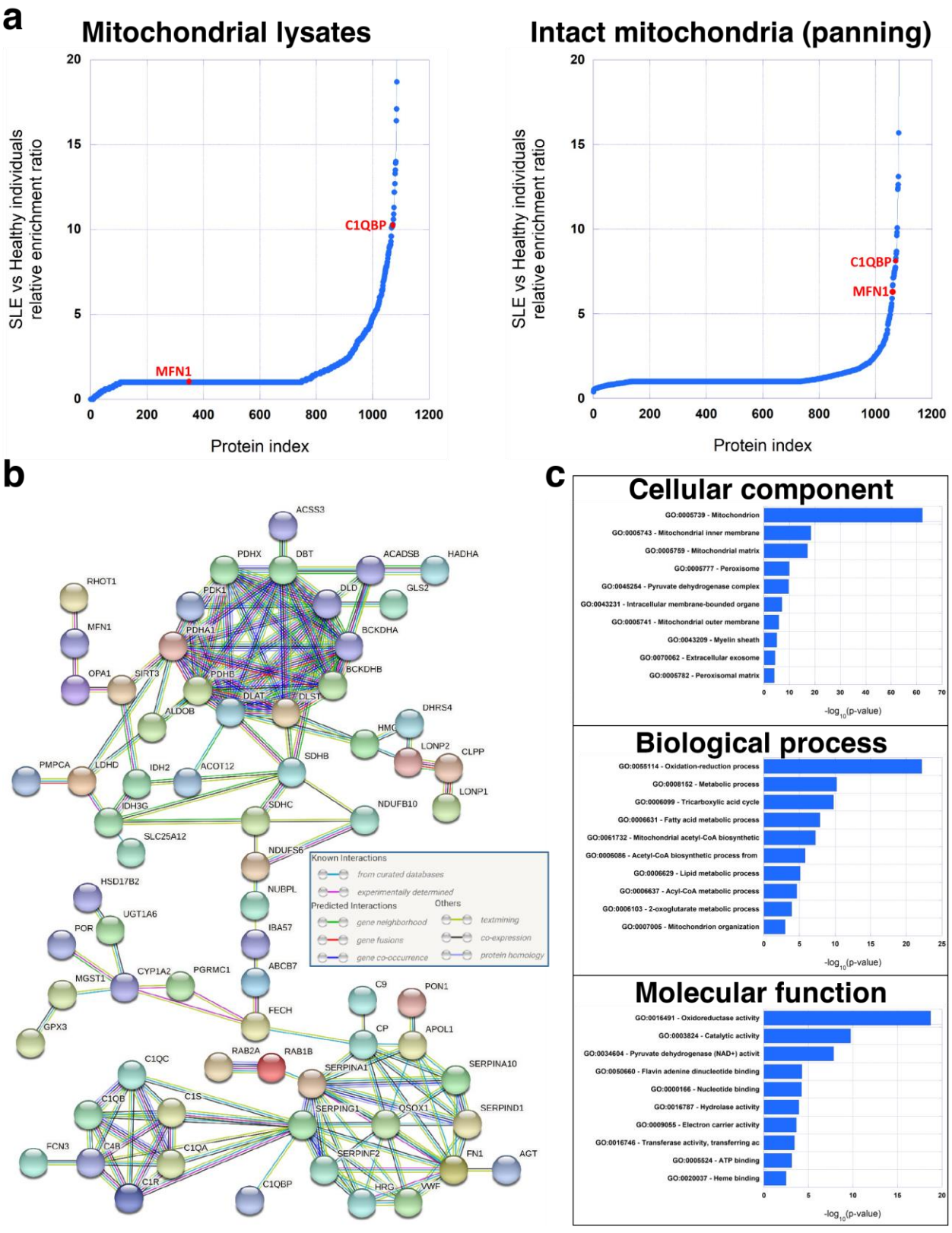
a
Mitochondrial lysates
Intact mitochondria (panning)
SLE vs Healthy individuals relative enrichment ratio
Protein index
C1QBP
MFN1
b
c
Cellular component
Biological process
Molecular function
Known Interactions
from curated databases
experimentally determined
Predicted Interactions
gene neighborhood
gene fusions
gene co-occurrence
Others
textmining
co-expression
protein homology

Figure 2: Mitochondrial hits identified and their mitochondrial sub-localization.

(a) Proteins are plotted in the order of increasing ratio. A ratio > 1 suggests enrichment in SLE patients relative to healthy individuals. Refer to **Supplementary Table 4 f**or a complete protein listing and calculated ratios. (b) High-confidence protein interaction network of proteins enriched in SLE patients (ratio>2). (c) Subcellular locations, processes and functions of the proteins targeted by AMA in SLE.

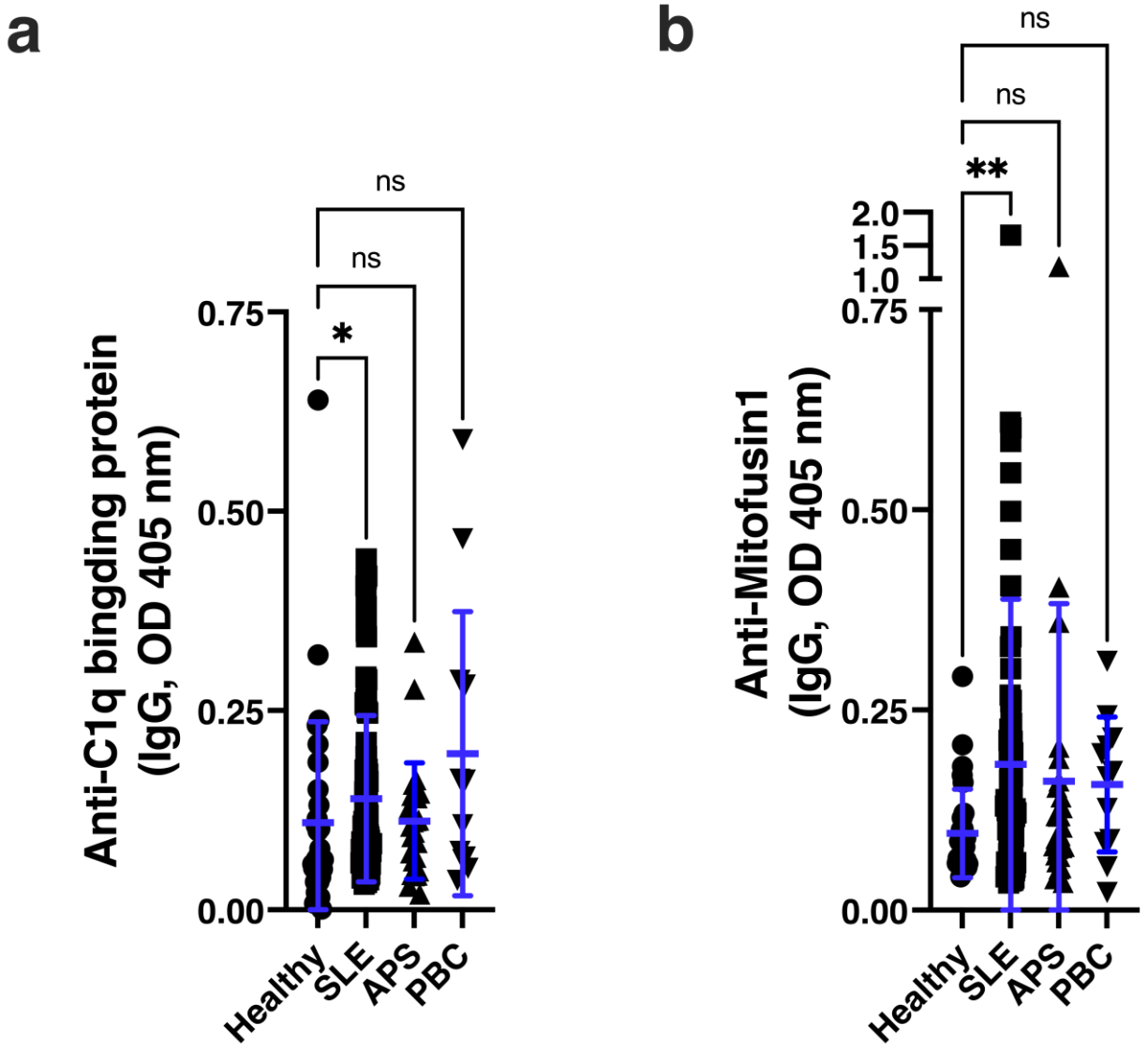

Figure 3: C1qBP and Mfn1 are two surface mitochondrial antigens with increased immunoreactivity in SLE.

Immunoreactivity against mitochondrial proteins was assessed by direct ELISA. (a) The receptor for the complement component C1q (C1qBP) is a protein stored within the mitochondrion and subsequently dispatched to the cell surface and/or released into the extracellular space. SLE patients display increased levels of IgGs targeting C1qBP, compared with healthy individuals (p=0.049). (b) Mitofusin 1 (Mfn1) is a protein expressed at the surface of the mitochondrion and is responsible for the fusion of mitochondrial outer membranes; anti-Mfn-1-IgG are significantly increased in patients with SLE, compared with healthy donors (p=0.0044). Of note neither autoantibodies were increased in APS and PBC. Healthy: n=30,

SLE: n=87, APS: n=27, PBC: n=12. Data are mean optical densities read at 405 nm ($OD_{405\ nm}$) ± standard deviation. Wilcoxon-Mann-Whitney test. Ns: $p \geq 0.05$; *: $p \leq 0.05$; **: $p < 0.01$.

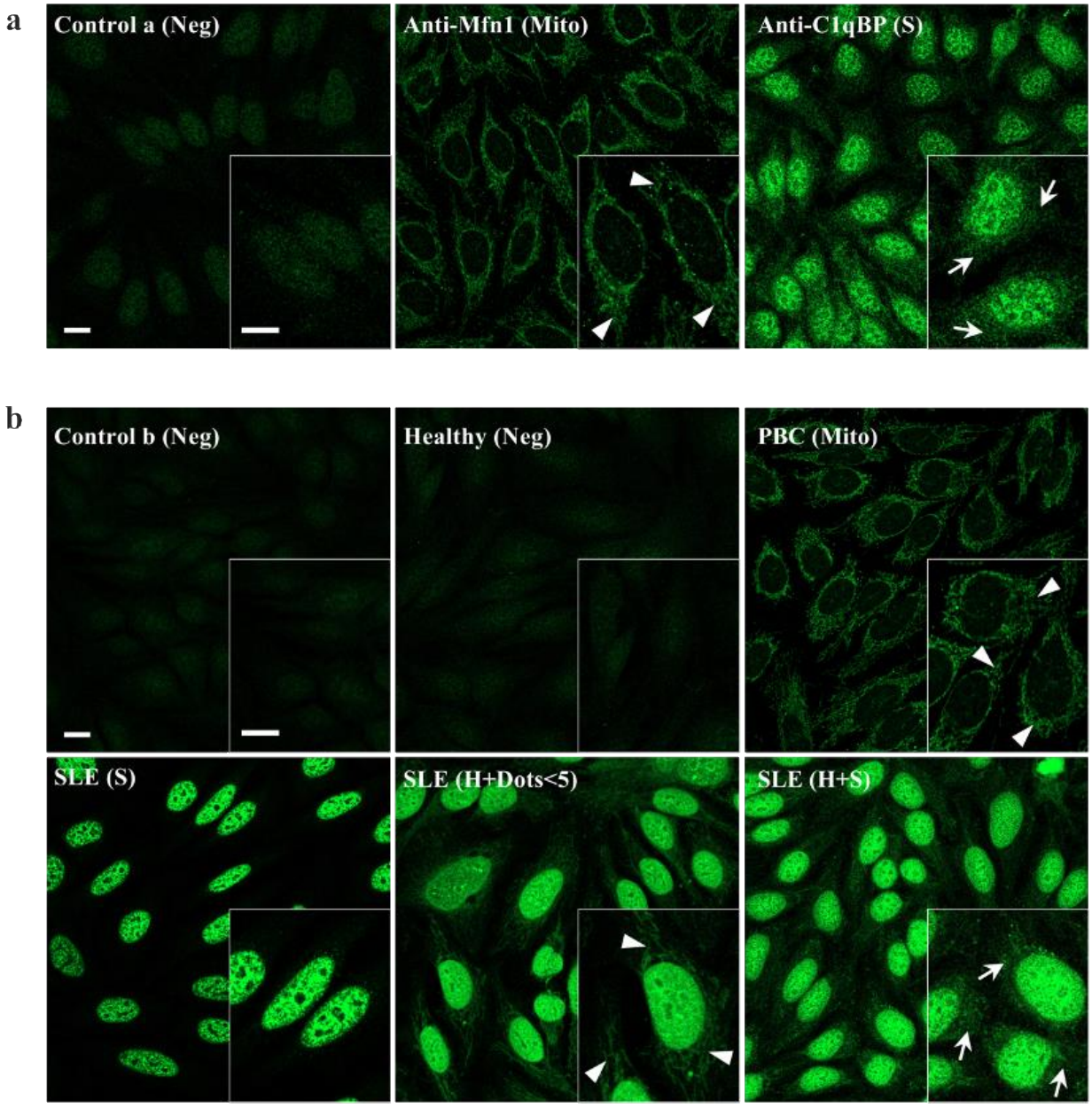

Figure 4: Indirect immunofluorescence (IIF) staining of Hep2 cells.

(a) HEp2 cells were stained with an isotype-matched irrelevant antibody (Control a), or commercial antibodies (5 µg/mL each) specific to either mitofusin 1 (Anti-Mfn1) or C1qBP (Anti-C1qBP). While anti-mfn1 displayed a reticular staining of the cytoplasm (arrowheads), typical of anti-mitochondrial antibodies (Mito), anti-C1qBP provided a speckled staining of the nucleus (S) and the cytoplasm (arrows). (b, *top row*) HEp2 cells, stained with a FITC-labelled anti-human IgG secondary antibody (Control b. (human serum-based negative control: Liquicheck negative

control, Bio-Rad Laboratories, Hercules, CA), or diluted sera (1:80) from healthy donors - negative for AwMA, provided no signal (Neg). Sera from PBC patients showed the typical mitochondrial-associated cytoplasmic reticular staining pattern provided by AMA. (b, *bottom row*) Routine clinical staining of Hep2 cells with $AwMA^+$ SLE sera allowed for the observation of various nuclear fluorescence patterns [i.e. speckled, homogenous (H), dots] but no sample was qualified as positive for AMA. However, confocal microscopy revealed that some samples may display cytoplasmic patterns resembling those seen in PBC. Scale bar account for 10 µm.

Tables:

Table 1: Qualitative associations between anti-C1qBP, anti-Mitofusin 1 and autoantibodies routinely assessed in SLE.

		Anti-C1qBP	Anti-Mitofusin 1
Anti-phospholipids	Negatives (n = 51)	0.09 ± 0.11	0.12 ± 0.11
	Positives (n = 23)	0.12 ± 0.21	0.18 ± 0.15
	p-value	0.097	**0.011**
Anti-cardiolipin	Negatives (n = 60)	0.09 ± 0.11	0.12 ± 0.10
	Positives (n = 14)	0.17 ± 0.27	0.25 ± 0.24
	p-value	0.053	**0.0004**
Anti-β_2 Glycoprotein I	Negatives (n = 64)	0.09 ± 0.11	0.12 ± 0.13
	Positives (n = 10)	0.11 ± 0.24	0.22 ± 0.25
	p-value	0.656	0.065
Lupus anticoagulant	Negatives (n = 67)	0.09 ± 0.10	0.12 ± 0.13
	Positives (n = 12)	0.13 ± 0.24	0.18 ± 0.12
	p-value	**0.049**	0.068
Anti-double-stranded DNA	Negatives (n = 62)	0.09 ± 0.10	0.12 ± 0.08
	Positives (n = 20)	0.10 ± 0.18	0.22 ± 0.23
	p-value	0.602	**0.0005**

Positivity to anti-phospholipids is defined here as the positivity to any, or a combination of the various anti-phospholipids assessed. Data are median ± IQR. Associations presented, herein, for anti-cardiolipin, anti-β2-GPI and anti-dsDNA were tested for IgGs.

559 **Table 2: Correlations between anti-C1qBP, anti-Mitofusin 1 and various continuous variables in**
560 **SLE patients.**

			Anti-C1qBP	Anti-Mitofusin 1
Clinical serology	Anti-cardiolipin antibodies (n = 80)		**r_s = 0.25**	**r_s = 0.45**
			p = 0.02	**p < 0.0001**
	Anti-β_2 Glycoprotein I (n = 80)		r_s = 0.12	**r_s = 0.26**
			p = 0.28	**p = 0.02**
	Anti-double-stranded DNA (n = 22)		r_s = 0.11	**r_s = 0.44**
			p = 0.63	**p = 0.04**
Anti-mitochondrial antibodies	Anti-whole mitochondria (AwMA)	IgG	**r_s = 0.32**	**r_s = 0.65**
			p = 0.003	**p < 0.0001**
		IgM	r_s = 0.08	**r_s = 0.31**
			p = 0.46	**p = 0.003**
	Anti-mitochondrial DNA (AmtDNA)	IgG	**r_s = 0.23**	**r_s = 0.52**
			p = 0.03	**p < 0.0001**
		IgM	r_s = 0.07	**r_s = 0.24**
			p = 0.50	**p = 0.03**
	Anti-mitochondrial RNA (AmtRNA)	IgG	r_s = 0.03	**r_s = 0.27**
			p = 0.75	**p = 0.01**
		IgM	r_s = 0.03	**r_s = 0.27**
			p = 0.82	**p = 0.01**

561

562 **Correlations presented, herein, for anti-cardiolipins or anti-β_2-GPI were tested for IgGs.**

Identification of mitofusin 1 and complement component 1q subcomponent-binding protein as mitochondrial targets in systemic lupus erythematosus

Yann LC Becker, M. Sc.[1,2,4]; Jean-Philippe Gagné, Ph. D.[2,8]; Anne-Sophie Julien, M. Sc.[3]; Tania Lévesque, DCS[1,2,4]; Isabelle Allaeys, Ph. D.[1,2,4]; Nadine Gougeard, BTS.[5,6]; Vicente Rubio, M.D., Ph. D.[5,6]; François-Michel Boisvert, Ph. D.[7]; Dominique Jean, Ph. D.[7]; Eric Wagner, Ph. D.[4,8]; Guy G. Poirier, Ph. D.[2,9]; Paul R. Fortin, M.D., MPH , FRCPC [1,10], Éric Boilard, Ph. D [1,2, 4].

[1] Centre de Recherche ARThrite - Arthrite, Recherche et Traitements, Université Laval, Québec, Qc, Canada.
[2] Axe Maladies infectieuses et immunitaires, Centre de Recherche du Centre Hospitalier Universitaire de Québec - Université Laval, Québec, Qc, Canada
[3] Département de mathématiques et statistique, Université Laval, Québec, Qc, Canada.
[4] Département de microbiologie et immunologie, Université Laval, Québec, Qc, Canada
[5] Structural Enzymopathology Unit, Instituto de Biomedicina de Valencia of the CSIC (IBV-CSIC), Valencia, Spain
[6] Group 739, Centro de Investigación Biomédica en Red para Enfermedades Raras (CIBERER-ISCIII), Madrid, Spain
[7] Department of Anatomy and Cell Biology, Université de Sherbrooke, Sherbrooke, Quebec, Canada
[8] Laboratoire d'Immunologie et Histocompatibilité, CHU de Québec-Université Laval, Département de Médecine de Laboratoire, Québec, Qc, Canada.
[9] Département de biologie moléculaire, de biochimie médicale et de pathologie, Faculté de Médecine, Université Laval, Québec, Qc, Canada
[10] Division de Rhumatologie, Département de Médecine, CHU de Québec – Université Laval, Québec, Qc, Canada.

Correspondence should be sent to

Eric Boilard, PhD : eric.boilard@crchudequebec.ulaval.ca

Centre de Recherche du CHU de Québec – Université Laval,

2705 Boulevard Laurier, Room T1-49

Quebec City, Quebec, G1V 4G2, Canada.

Telephone: (418) 525-4444 Ext : 46175

Authors' Twitter handles: Yann LC Becker: @YannBECKER4**, Eric Boilard:** @boilard_eric

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Supplementary information:

Supplementary methods

Human serum samples – healthy donors, and patients with SLE or APS from the CHU de Québec – Université Laval Systemic Autoimmune Rheumatic Disease Biobank and DataBase repository (SARD-BDB).

Human serum samples from healthy donors and patients with autoimmune conditions: This study was approved by the research ethics board of the CHU de Québec–Université Laval (CHUL. #B13-06-1243 and #B14-08-2108). Healthy volunteers (i.e. with no signs or symptoms of acute infection and not on medications) were recruited at the CHUL. Serum samples were obtained from peripheral blood punctures performed at the time of inclusion. In accordance with the Declaration of Helsinki, written consent was provided by each subject, and their clinical information and biological specimen were associated with an anonymized reference number. A convenience sample was used and no sample size calculation was done. SLE patients met ACR classification criteria and each of the 11 categories was documented (1,2). APS patients met the 2006 revised Sapporo Criteria (3), and PBC patients the 2018 PBC classification criteria (4).

Clinical data collection: Information on sociodemographic variables (e.g. age, sex, ethnicity. **Supplementary Table 1**) were collected at the first visit of the patients at the SARD-BDB. Smoking history was characterized as any the consumption of tobacco, past or present. Body metrics and blood pressure were measured at the time of the visit, and co-morbidities were documented as present of absent. Information about SLE indexes was collected during the clinical visit corresponding to the blood sample

drawn. Medications presented in **Supplementary Table 1** were defined as treatments, ongoing at the time of the visit – apart from corticosteroids, that was defined as the use of prednisone in the past year.

Each of the 11 categories of the ACR classification criteria was documented (1,2). Disease activity was assessed, using the SLE Disease Activity Index–2000 (SLEDAI-2K) (5,6). SLE damages were evaluated using the Systemic Lupus International Collaborating Clinics (SLICC)/ACR damage index (SDI) (**Supplementary Table 2**) (7,8). Positivity for the various clinical outcomes assessed (e.g. lupus nephritis, arthritis, dermatological manifestations, thrombovascular events) was defined as past or present reports of one or more of these events, as defined by the SLICC Classification criteria for SLE (9).

Data from SLE patients' serology: Blood samples drawn at the time of the visit in the SARD-BDB were used to assess the various autoantibodies measured. Serological data was obtained as part of the routine care and included measurements of anti-dsDNA, anticardiolipin and anti-β_2GPI antibodies by ELISA (i.e. laboratory cut-off of 40 UPL or above the 99th percentile of controls). Detection of LA activity was performed, following international guidelines for this assay (10). Detection of AMA (i.e. AwMA, AmtDNA, AmtRNA. IgG and IgM) was performed by our research laboratory, as previously published (11) (**Supplementary Table 3**).

Sample preparation for the identification of mitochondrial antigens targeted by AMA in SLE using mass spectrometry:

Preparation of mitochondrial lysates: Freshly isolated mitochondria were used for the panning of antibodies targeting the mitochondrial outer membrane (i.e. anti-whole mitochondria antibodies, AwMA). Dry-pelleted mitochondria were stored at -80°C until needed. Frozen mitochondria were resuspended in hypotonic lysis buffer (10mM HEPES, 2mM KCl, 0.1%

CHAPS, pH7.2) with protease inhibitors (cOmplete protease inhibitor cocktail; Roche, Basel, Switzerland) and underwent three cycles, alternating between thawing in a water bath (37°C) and freezing in an ethanol–dry ice bath, followed by a 15min sonication in an ice bath. Unbroken mitochondria were pelleted at 7,000g for 10min at 4°C and discarded. Supernatant protein (i.e. mitochondrial lysates) content was determined by the bicinchoninic acid method (BCA protein assay kit. Thermo Fisher Scientific, Waltham, MA, USA). Nucleic acids were digested by addition of benzonase nuclease (Sigma-Aldrich, St-Louis, MO, USA. 100 U/mL, 30min, 37°C). Lysates were stored at -80°C until use.

Serum selection and pooling: Optical densities at 405 nm ($OD_{405\ nm}$) for 1:150 dilutions of serum samples from the SARD-BDB were previously assessed with our direct AwMA-ELISA (11) and a cut-off value for positivity to AwMA-IgG was calculated for $OD_{405\ nm}$ values$\geq$0.30. To account for interpersonal variabilities in autoantibody production, equal volumes of sera from either ten healthy donors ($OD_{405\ nm}$ values ranging from 0.08 to 0.17), or from ten SLE patients positive for AwMA ($OD_{405\ nm}$, 0.68 to 3.00) were pooled and their IgG concentrations were determined by Human IgG total uncoated ELISA kit (Thermo Fisher Scientific). Experiments were performed in triplicate.

Identification of mitochondrial antigens recognized by AMA:

LC-MS/MS analysis: Trypsin/Lys-C-digested peptides were separated on a Dionex Ultimate 3000 nanoHPLC system coupled to a Q Exactive™ OrbiTrap mass spectrometer (Thermo Fisher). 10µl of sample (a total of 1.5µg) resuspended in 1% (vol/vol) formic acid were loaded with a constant

flow of 4 µl/min onto an Acclaim PepMap100 C18 column (0.3mm id × 5mm; Dionex Corporation, Sunnyvale, CA, USA). After trap enrichment, peptides were eluted onto an EasySpray PepMap C18 nano column (75µm × 50cm; Dionex Corporation) with a linear gradient of 8–40% solvent B (80% acetonitrile with 0.1% formic acid) over 240min with a constant flow of 200nl/min. The HPLC system was coupled to the mass spectrometer via an EasySpray source. The spray voltage was set to 2.0kV and the temperature of the column set to 40°C. Full scan MS survey spectra (m/z 350–1600) in profile mode were acquired in the Orbitrap with a resolution of 70,000 after accumulation of 1,000,000 ions. The ten most intense peptide ions from the preview scan in the Orbitrap were fragmented by collision-induced dissociation (normalized collision energy 25% and resolution of 17,500) after the accumulation of 50,000 ions. Maximal filling times were 250ms for the full scans and 60ms for the MS/MS scans. Precursor ion charge state screening was enabled and all unassigned charge states as well as single, 7 and 8 charged species were rejected. The dynamic exclusion list was restricted to a maximum of 500 entries with a maximum retention period of 40 seconds and a relative mass window of 10ppm. The lock mass option was enabled for survey scans to improve mass accuracy. Data were acquired using the XCalibur software (Thermo Fisher Scientific).

Mass spectrometry data analysis: Mass spectra data (.RAW files) were loaded into MaxQuant version 1.6.17.0 and searched against a protein database generated by merging the *Homo sapiens* and *Mus musculus* reference proteomes (Uniprot, versions 01-29-2021: 77 027 human and 55 470 mouse proteins) complemented with a list of common contaminants maintained by MaxQuant and concatenated with the reversed version of all sequences (decoy mode). The minimum peptide length was set to 7 amino acids and trypsin was specified as the protease allowing up to two missed

cleavages. The mass tolerance was set to 7ppm for the precursor ions and 20ppm for the fragment ions. The following parameters were used: fixed carbamidomethylation of cysteine (+57.0214 Da), oxidation of methionine (+15.9949 Da) as a variable modification and a peptide-spectrum and protein match false-discovery rate of 0.01.

Intensity-based label-free quantification (LFQ) values were used to estimate the relative abundance of proteins in each replicate groups, which correspond to the sum of all peak intensities over all tandem mass spectra assigned to a particular protein. Missing LFQ data imputation was estimated by using a noise value corresponding to the lowest 1% percentile of the LFQ distribution. This noise value was imputated for each sample when the intensity value is missing (i.e. undetected proteins) and selected as the minimum LFQ intensity for low abundance protein identification for which LFQ values fall below the 1% percentile background.

Filtering and data analysis of proteomic data: Matches to reverse proteins, proteins with zero intensity values in all datasets, proteins with negative MaxQuant scores and common contaminants were removed from the final protein repertoire. Identified proteins were cross-referenced using their Uniprot ID for their cellular localization and, when the information was available, for their mitochondrial sub-localization. Pathways involving the mitochondrial proteins identified were analyzed, using the Reactome pathway knowledge base https://reactome.org/ and the Database for Annotation, Visualization and Integrated Discovery (DAVID).

Detection of autoantibodies targeting selected mitochondrial antigens

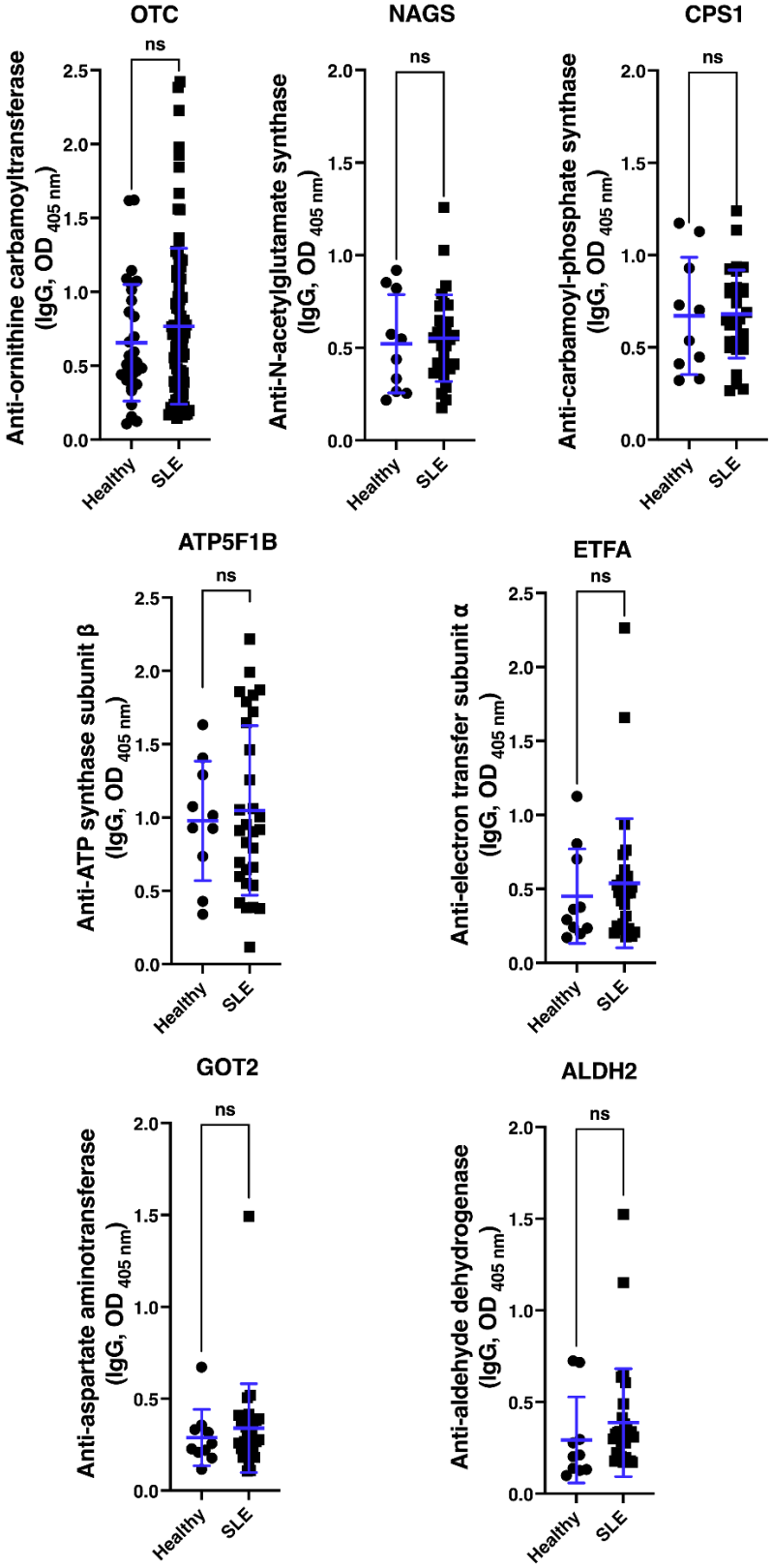
Enzyme-Linked Immunoassays (ELISAs): Detection of IgG, using various sources of mtAgs (i.e. whole/intact mitochondria, mtDNA, mtRNA) were performed as previously described (11–13). Immunoreactivity against other mitochondrial proteins were assessed. These proteins included the complement component 1 Q subcomponent-binding protein (C1qBP. Novus Biologicals, Centennial, CO, USA), mitofusin 1 (Mfn 1. Origene Technologies, Rockville, MD, USA) (Healthy: n=30, SLE: n=87, APS: n=27, PBC: n=12). Other mitochondrial proteins available, with MIM or MM locations identified by our proteomic approaches were assessed (Healthy: n=10; SLE n=30). These miscalleneous proteins were three representatives of the urea pathways [i.e. ornithine carbamoyltransferase (OTC), carbamoyl-phosphate synthase (CPS1) and N-acetylglutamate synthase (NAGS)] and two proteins implicated in electron transfer and oxidative phosphorylation [i.e. the beta subunit of the MIM complex ATP synthase (ATP5F1B. Cusabio, Wuhan, China) and electron transfer flavoprotein subunit alpha (ETFA. Origene Technologies)] as well as two proteins involved in metabolic processes [i.e. aspartate aminotransferase (GOT2. BioVision Inc., Milpitas, California, USA) and aldehyde dehydrogenase (ALDH2. RayBiotech Life, Peachtree Corners, GA, USA)]. OTC, CPS 1 and NAGS were prepared as published (14,15). Immunoreactivities against recombinant mitochondrial proteins were assessed by coating plates overnight at 4°C with 225ng protein in 25µL PBS 1X (i.e. 9ng/µL).

Statistical analyses:

The logistic regression models to predict diagnosis were adjusted for sex and age, and are expressed as their adjusted odds ratio (aOR), 95% confidence interval (95% CI) and p-value. Univariable and multivariable logistic and linear regressions were performed to predict clinical outcomes (thrombosis, presence of carotid plaque, presence of damage according to SLICC

Damage Index, presence of disease activity [SLEDAI-2k > 4], presence of nephropathies, presence of dermatological disorder and presence of arthritis, as well as continuous variables carotid intima-media thickness and Lupus Severity Index Score), separately for C1qBP and Mfn1. These models were adjusted for disease duration, age, BMI, sex, antimalarial drugs, and prednisone use.

Supplementary figure:



Supplementary Figure 1: Immunoreactivity of several mitochondrial proteins in SLE.

Autoantibodies against mitochondrial proteins implicated in the urea cycle (i.e. OTC, NAGS, CPS1), OxPhos (i.e. ATP5F1B, ETFA) and mitochondrial metabolism (i.e. GOT2, ALDH2) were assessed in serum samples from the SARD-BDB (Anti-OTC-IgG: Healthy n=30, SLE: n=87. Other autoantibodies: Healthy n=10, SLE: n=30). No differences were observed between the two groups for any of the antigens assessed. Data are mean optical densities read at 405 nm ($OD_{405\ nm}$) ± standard deviation. Wilcoxon-Mann Whitney test. Ns: $p > 0.05$.

Abbreviations: ALDH2: aldehyde dehydrogenase. ATP5F1B: ATP synthase – β subunit. CPS1: carbamoyl-phosphate synthase. ETFA: electron transfer flavoprotein subunit α. GOT2: Aspartate aminotransferase. NAGS: N-acetylglutamate synthase. OTC: ornithine carbamoyltransferase.

Supplementary tables

Supplementary Table 1: Sociodemographic and clinical characteristics of the SLE patients included in the SARD-BDB.

Variable		Sample size	Value [n (%) or median ± IQR]
Sex (%)	Female	87	72 (82.8)
	Male		15 (17.2)
Age, in years		86	49.58 ± 20.65
Ethnicity (%)	Caucasian	86	84 (97.7)
	Black		1 (1.2)
	Other		1 (1.2)
Disease duration, in years		87	5.00 ± 19
Body metrics	Waist, in cm	61	87 ± 17
	Hip, in cm	59	98 ± 10
	Waist / Hip ratio	59	0.86 ± 0.11
Blood pressure (mmHg)	Systolic	69	124 ± 15
	Diastolic	69	73 ± 12
Comorbidities (%)	Menopause	65	38 (58.5)
	Tobacco, *past or present*	83	35 (42.2)
	Obesity (*i.e. BMI ≥ 30*)	86	13 (15.1)
	Hypertension	87	11 (12.6)
	Diabetes	86	2 (2.3)
	Dyslipidaemia	87	7 (8.0)
Medications (%)	Corticosteroids	86	17 (19.8)
	Hydroxychloroquine	87	65 (74.7)
	Chloroquine	87	6 (6.9)
	Azathioprine	87	15 (17.2)
	Methotrexate	87	14 (16.1)
	Leflunomide	87	1 (1.1)
	Mycophenolate mofetil	87	10 (11.5)
	Mycophenolic acid	87	1 (1.1)
	Cyclophosphamide	87	2 (2.3)
	Anti-platelet / anticoagulants	86	13 (15.1)
	Hormones replacement (estrogen/progesterone)	87	2 (2.3)
	Contraception	87	5 (5.7)
	Diabetes medication	86	2 (2.3)
	Lipid lowering drug	86	14 (16.3)

Supplementary table 2: SLE disease characteristics of the patients included in the SARD-BDB.

	Variable	Sample size	Value [n(%) or median ± IQR]
Clinical Scores	ACR	86	5.00 ± 2.00
	LSI	86	5.62 ± 2.92
	SDI	86	0.00 ± 1.00
	SLEDAI - 2K	86	2.00 ± 6.00
American College of Rheumatology Classification criteria	Malar rash	86	20 (23.3)
	Discoid rash	86	13 (15.1)
	Photosensitivity	86	37 (43.0)
	Oral ulcers	86	27 (31.4)
	Arthritis	86	70 (81.4)
	Serositis	86	23 (26.7)
	Pleuritis	86	17 (19.8)
	Pericarditis	86	13 (15.1)
	Renal disorders	86	24 (27.9)
	Proteinuria	86	24 (27.9)
	Cellular casts	86	9 (10.5)
	Neurological disorders	86	4 (4.7)
	Seizure	86	4 (4.7)
	Psychosis	86	1 (1.2)
	Haematological disorders	86	69 (80.2)
	Haemolytic anemia	86	5 (5.8)
	Leucopenia	86	33 (38.4)
	Lymphopenia	86	51 (58.6)
	Thrombocytopenia	86	24 (59.3)
	Anti-nuclear antibodies	86	86 (100)
	Immunological disorders	86	63 (73.3)
	Anti-double-stranded DNA	86	49 (57.0)
	Anti-Smith	86	12 (14.0)
	Anti-phospholipids	86	42 (48.8)
	Anti-cardiolipin	86	29 (33.7)
	Lupus anticoagulant	86	23 (26.7)
	Venereal Disease Research Laboratory	86	2 (2.3)
Miscellaneous clinical information	Platelets	87	211 ± 82
	Red blood cells	87	5.60 ± 2.70
	Carotid-intima media thickness	34	0.61 ± 0.12
	Creatinine clearance	26	98.50 ± 22.00
	Thromboses	87	10 (11.5)
	Carotid plaque	64	24 (37.5)
	Dermatological manifestations	86	71 (82.6)

Supplementary table 3: Continuous variables acquired in blood samples acquired from SLE patients drawn at the time of their inclusion in the SARD-BDB.

	Variable	Sample size	Value (median ± IQR)
Clinical serology	Anti-cardiolipin - IgG	80	2.70 ± 6.30
	- IgM	80	6.95 ± 9.50
	Anti-β_2 Glycoprotein I - IgG	80	1.30 ± 0.80
	- IgM	80	2.15 ± 2.10
	Anti-double-stranded DNA	22	6.00 ± 21
Anti-mitochondrial antibodies	Anti-whole mitochondria - IgG	87	0.25 ± 0.19
	- IgM	87	0.41 ± 0.43
	Anti-mitochondrial DNA - IgG	87	0.35 ± 0.25
	- IgM	87	0.37 ± 0.49
	Anti-mitochondrial RNA - IgG	87	0.28 ± 0.47
	- IgM	87	0.37 ± 0.44
	Anti-C1qBP - IgG	87	0.13 ± 0.13
	Anti-Mitofusine 1 - IgG	87	0.09 ± 0.11

Supplementary table 4: Mass spectrometry identification of proteins associated with anti-mitochondrial autoantibodies in SLE.

See attached appendix

Supplementary table 5: Confocal microscopy observation in indirect immunofluorescence allows the detection of cytoplasmic patterns that are undetected using an epifluorescence microscope.

	Type of microscope	
	Epifluorescence	Confocal
Homogenous	7 (77.78 %)	7 (77.78 %)
Speckled	1 (11.11 %)	1 (11.11 %)
Nucleolar	1 (11.11 %)	1 (11.11 %)
Cytoplasmic/mitochondrial	0 (0 %)	7 (77.78 %)
Negative	1 (11.11 %)	1 (11.11 %)

Supplementary table 6: Performance of cut-off values for anti-C1qBP and anti-Mitofusin 1.

	Cut-off	Sensitivity	Specificity	PPV	NPV	AUC	p-value
Anti-C1qBP	0.064 (0.038 - 0.419)	0.79 (0.693 - 0.873)	0.53 (0.343 - 0.717)	0.83 (0.733 - 0.905)	0.47 (0.298 - 0.649)	0.65 (0.52 - 0.78)	**0.021**
Anti-Mitofusin 1	0.116 (0.088 - 0.125)	0.61 (0.499 - 0.712)	0.80 (0.614 - 0.923)	0.90 (0.792 - 0.962)	0.41 (0.2860 - 0.551)	0.69 (0.59 - 0.79)	**< 0.001**

Data are proportions (95% exact confidence interval), except for the cut-off with 95% bootstrap confidence interval. PPV=positive predictive value. NPV=negative predictive value. AUC=Area under the cuve. P-value for the test H_0: AUC=0.50, H_1 : AUC≠0.50.

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Uniprot Accession code	Uniprot Entry name	Description	Gene name	Total MS/MS count	Score	Total Intensity	Mol. weight [kDa]	Sequence length	Sequence coverage [%]	Peptides Lysates - Healthy	Peptides Lysates - SLE	Peptides Lysates - Control	Peptides Panning - Healthy	Peptides Panning - SLE	LFQ intensity Lysates - Healthy	LFQ intensity Lysates - SLE	Lysates Ratio SLE : HEALTHY	LFQ intensity Panning - Control	LFQ intensity Panning - Healthy	LFQ intensity Panning - SLE	Panning Ratio SLE : HEALTHY	MS/MS count Lysates - Healthy	MS/MS count Lysates - SLE	MS/MS count Lysates - Control	MS/MS count Panning - Healthy	MS/MS count Panning - SLE	Cellular compartment	Submitochondrial location
O75636	FCN3_HUMAN	Ficolin-3	FCN3	227	238,09	2,1E+11	32.903	299	44.5	0	8	0	0	10	1,1E+07	8,9E+08	82,9	1,5E+07	1,5E+07	7,1E+10	4830,9	0	41	0	0	186	Secreted	N/A
P35486	ODPA_MOUSE	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Pdha1	240	304,7	4,1E+10	43.231	390	63.8	8	17	1	2	22	1,2E+08	9,1E+08	7,6	1,5E+07	1,8E+07	2,9E+09	160,6	9	62	2	2	165	Mitochondrion	Matrix
Q6P3A8	ODBB_MOUSE	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	Bckdhb	180	323,31	7,5E+10	42.88	390	60.3	11	16	0	1	5	5,6E+08	4,6E+09	8,3	1,5E+07	1,5E+07	9,5E+08	64,4	20	136	0	2	22	Mitochondrion	Matrix
Q9D051	ODPB_MOUSE	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	Pdhb	273	285,63	5,0E+10	38.937	359	58.2	4	14	3	5	16	9,6E+07	7,5E+08	7,8	1,5E+08	7,5E+07	4,5E+09	59,5	7	72	6	7	181	Mitochondrion	Matrix
U3KQK0	U3KQK0_HUMAN	Histone H2B	H2BC15	25	10,606	2,6E+09	18.804	166	19.9	3	1	1	1	3	3,3E+08	1,1E+07	0,0	1,5E+07	1,5E+07	7,2E+08	48,7	5	3	1	2	14	Nucleus	N/A
Q8BMF4	ODP2_MOUSE	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	Dlat	292	285,41	7,5E+10	67.941	642	38.5	6	18	1	7	18	1,1E+08	1,1E+09	10,6	1,5E+07	9,4E+07	4,4E+09	47,3	7	100	2	12	171	Mitochondrion	Matrix
Q8BKZ9	ODPX_MOUSE	Pyruvate dehydrogenase protein X component, mitochondrial	Pdhx	53	48,91	7,1E+09	53.998	501	26.7	2	5	0	2	8	5,0E+07	8,2E+07	1,7	1,5E+07	3,0E+07	1,1E+09	35,0	2	18	0	4	29	Mitochondrion	Matrix
P02745	C1QA_HUMAN	Complement C1q subcomponent subunit A	C1QA	34	45,183	4,7E+09	26.016	245	18.4	5	5	0	0	3	1,2E+09	4,7E+08	0,4	1,5E+07	1,5E+07	4,9E+08	32,9	16	12	0	0	6	Secreted	N/A
Q99878	H2A1J_HUMAN	Histone H2A type 1-J	H2AC14	54	39,224	5,3E+09	13.936	128	36.7	7	3	1	1	4	1,4E+09	3,3E+08	0,2	1,5E+07	1,5E+07	4,8E+08	32,4	22	12	1	2	17	Nucleus	N/A
A0A0A0MSV6	A0A0A0MSV6_HUMAN	Complement C1q subcomponent subunit B (Fragment)	C1QB	103	34,176	8,6E+09	24.03	228	31.6	7	6	0	1	7	6,3E+08	2,1E+08	0,3	1,5E+07	1,5E+07	4,6E+08	31,4	35	24	0	1	43	Not specified	N/A
Q792Z1	Q792Z1_MOUSE	Trypsin 10	Try10	64	13,804	1,2E+10	26.221	246	8.1	2	2	1	1	1	2,3E+09	9,5E+08	0,4	1,5E+07	1,5E+07	4,5E+08	30,7	18	14	5	13	14	Not specified	N/A
P52503	NDUS6_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	Ndufs6	24	66,899	1,8E+09	13.02	116	64.7	4	5	1	0	2	1,7E+08	1,1E+08	0,7	1,5E+07	1,5E+07	4,1E+08	27,6	4	14	1	0	5	Mitochondrion	Inner membrane
P85094	ISC2A_MOUSE	Isochorismatase domain-containing protein 2A	Isoc2a	81	112,8	1,8E+10	22.417	206	58.7	7	9	0	0	4	7,7E+08	9,2E+08	1,2	1,5E+07	1,5E+07	3,9E+08	26,3	12	60	0	0	9	Cytoplasm, nucleus	N/A
A0A2R8Y4F5	A0A2R8Y4F5_HUMAN	Enoyl-CoA hydratase	HADHA	22	12,301	5,5E+09	79.466	728	9.6	5	6	5	4	6	3,5E+08	1,4E+09	3,9	1,5E+07	1,5E+07	3,4E+08	23,3	5	8	3	0	6	Not specified	N/A
I3L145	I3L145_HUMAN	Sex hormone-binding globulin	SHBG	32	32,359	1,5E+09	37.487	344	53.2	0	0	0	2	12	1,1E+07	1,1E+07	1,0	1,5E+07	2,9E+07	4,6E+08	15,7	0	0	0	2	30	Not specified	N/A
P04275	VWF_HUMAN	von Willebrand factor	VWF	98	90,987	3,0E+09	309.26	2813	11.8	0	9	0	5	24	1,1E+07	2,1E+07	2,0	1,5E+07	2,4E+07	3,2E+08	13,1	0	12	0	10	76	Secreted	N/A
P62806	H4_MOUSE	Histone H4	H4c1	117	29,43	8,6E+09	11.367	103	60.2	3	5	1	2	9	2,4E+08	3,1E+08	1,3	1,5E+07	6,1E+07	7,7E+08	12,6	16	25	2	4	70	Nucleus	N/A
D6REH1	D6REH1_MOUSE	Peroxisomal membrane protein 2	Pxmp2	26	33,392	8,7E+08	9.4381	87	64.4	1	3	0	1	7	1,1E+07	3,9E+07	3,7	1,5E+07	1,5E+07	1,8E+08	12,4	1	5	0	1	19	Not specified	N/A
Q3U3J1	Q3U3J1_MOUSE	2-oxoisovalerate dehydrogenase subunit alpha	Bckdha	396	279,84	6,2E+10	50.773	446	69.1	9	22	4	9	25	5,7E+07	2,6E+09	45,2	5,1E+07	1,3E+08	1,6E+09	12,4	13	165	11	30	177	Not specified	N/A
A0A087X232	A0A087X232_HUMAN	Complement C1s subcomponent	C1S	33	53,097	1,8E+09	75.905	682	21.6	5	8	0	1	7	1,2E+08	1,4E+08	1,2	1,5E+07	1,5E+07	1,5E+08	10,1	8	12	0	2	11	Not specified	N/A
Q8R104	SIR3_MOUSE	NAD-dependent protein deacetylase sirtuin-3	Sirt3	28	36,928	1,2E+09	36.614	334	16.2	4	4	0	1	3	1,2E+08	1,1E+08	0,9	1,5E+07	1,5E+07	1,4E+08	9,6	5	15	0	2	6	Cytoplasm, mitochondrion	Matrix
Q8BFP9	PDK1_MOUSE	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	Pdk1	59	47,127	3,1E+09	48.994	434	33.2	2	8	0	0	8	4,6E+07	2,4E+08	5,3	1,5E+07	1,5E+07	1,3E+08	8,7	4	35	0	0	20	Mitochondrion	Matrix
Q3UUI3	THEM4_MOUSE	Acyl-coenzyme A thioesterase THEM4	Them4	38	24,161	2,4E+09	26.031	230	25.2	4	3	0	1	4	9,1E+08	2,6E+08	0,3	1,5E+07	1,5E+07	1,3E+08	8,5	15	13	0	3	7	Cell membrane, cytoplasm, mitochondrion	Inner membrane, IMS
P52430	PON1_MOUSE	Serum paraoxonase/arylesterase 1	Pon1	19	33,453	1,2E+09	39.565	355	35.8	1	7	1	3	5	1,1E+07	7,9E+07	7,4	1,5E+07	1,5E+07	1,2E+08	8,3	1	10	1	2	5	Secreted	N/A
D3YYK0	D3YYK0_MOUSE	Protein ABHD11	Abhd11	34	60,477	3,5E+09	24.881	227	39.6	3	5	0	0	6	2,6E+08	2,8E+08	1,1	1,5E+07	1,5E+07	1,2E+08	8,1	3	19	0	0	12	Not specified	N/A
P35564	CALX_MOUSE	Calnexin	Canx	31	19,439	6,2E+08	67.277	591	14.7	0	4	0	2	6	1,1E+07	3,6E+07	3,4	1,5E+07	1,5E+07	1,1E+08	7,7	0	7	0	3	21	Endoplasmic reticulum	N/A
H7BX01	H7BX01_MOUSE	Dynamin-like 120 kDa protein, form S1	Opa1	100	101,67	2,6E+09	113.23	978	29.2	0	7	0	5	26	1,1E+07	3,4E+07	3,2	1,5E+07	3,6E+07	2,7E+08	7,7	0	11	0	9	80	Mitochondrion	Inner membrane
Q8R5L1	Q8R5L1_MOUSE	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1qbp	82	192,16	4,7E+10	31.025	279	32.3	4	7	3	0	2	3,5E+08	3,6E+09	10,2	2,6E+09	1,5E+07	1,1E+08	7,6	10	59	10	0	3	Cell membrane, mitochondrion	Not specified
Q91VA0	ACSM1_MOUSE	Acyl-coenzyme A synthetase ACSM1, mitochondrial	Acsm1	163	323,31	4,9E+10	64.76	573	64.2	12	24	5	2	5	9,4E+08	5,2E+09	5,5	1,1E+09	1,5E+07	1,1E+08	7,5	25	121	5	2	10	Mitochondrion	Matrix
A0A3B3ISR2	A0A3B3ISR2_HUMAN	Complement subcomponent C1r	C1R	35	71,57	1,4E+09	80.173	705	26.4	10	9	0	0	3	1,1E+08	1,7E+08	1,6	1,5E+07	1,5E+07	1,1E+08	7,4	16	12	0	0	7	Not specified	N/A
P02747	C1QC_HUMAN	Complement C1q subcomponent subunit C	C1QC	108	42,043	1,6E+10	25.773	245	25.3	5	4	0	3	4	1,8E+09	8,3E+08	0,5	1,5E+07	2,0E+08	1,4E+09	7,3	36	22	0	13	37	Secreted	N/A
Q9DBL7	COASY_MOUSE	Bifunctional coenzyme A synthase	Coasy	40	76,16	2,4E+09	62.022	563	29.8	5	9	0	1	7	9,8E+07	1,5E+08	1,5	1,5E+07	1,5E+07	1,1E+08	7,2	7	21	0	2	10	Cytoplasm, mitochondrion	Matrix
E9Q197	E9Q197_MOUSE	Glyoxalase domain-containing protein 4	Glod4	18	29,347	1,1E+09	31.207	279	21.5	0	3	0	1	3	1,1E+07	1,7E+08	16,4	1,5E+07	1,5E+07	1,1E+08	7,1	0	6	0	1	11	Not specified	N/A
Q9DCS9	NDUBA_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Ndufb10	34	9,274	1,3E+09	21.024	176	21	1	3	2	1	3	1,1E+07	1,1E+08	10,2	1,4E+08	1,5E+07	1,1E+08	7,1	1	10	3	3	17	Mitochondrion	Inner membrane
P53395	ODB2_MOUSE	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogen	Dbt	599	323,31	1,7E+11	53.246	482	69.5	16	29	7	13	28	7,4E+08	7,7E+09	10,3	1,8E+08	4,5E+08	3,0E+09	6,7	38	253	12	42	254	Mitochondrion	Matrix
P97450	ATP5J_MOUSE	ATP synthase-coupling factor 6, mitochondrial	Atp5pf	38	257,84	1,7E+09	12.496	108	44.4	1	4	3	1	2	1,1E+07	1,1E+07	1,0	2,7E+09	1,5E+07	9,8E+07	6,7	0	7	15	3	13	Mitochondrion	Inner membrane
Q8R3F5	FABD_MOUSE	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	Mcat	25	28,837	1,0E+09	41.928	381	19.2	2	5	0	1	3	6,0E+07	8,7E+07	1,5	1,5E+07	1,5E+07	9,3E+07	6,3	2	14	0	2	7	Mitochondrion	Not specified
Q811U4	MFN1_MOUSE	Mitofusin-1	Mfn1	25	31,243	6,9E+08	83.725	741	13.4	0	0	0	2	9	1,1E+07	1,1E+07	1,0	1,5E+07	2,4E+07	1,4E+08	5,9	0	0	0	3	22	Mitochondrion	Outer membrane
Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B	RAB1B	14	17,621	6,0E+08	22.171	201	27.9	1	3	0	1	3	1,1E+07	8,3E+07	7,8	1,5E+07	1,5E+07	8,3E+07	5,6	0	4	0	2	8	Cytoplasm, endoplasmic reticulum, Golgi apparatus	N/A
Q8R084	Q8R084_MOUSE	UDP-glucuronosyltransferase	Ugt2b1	22	21,644	6,5E+08	60.157	529	14.7	1	3	1	2	7	1,1E+07	9,2E+07	8,6	1,5E+07	1,5E+07	8,0E+07	5,4	0	6	0	3	13	Other	N/A
P54071	IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial	Idh2	424	323,31	1,8E+11	50.906	452	54	28	25	13	2	7	1,4E+10	1,2E+10	0,9	3,7E+09	1,5E+07	7,9E+07	5,4	139	231	39	2	13	Mitochondrion	Not specified
J3QP56	J3QP56_MOUSE	Acyl-protein thioesterase 1	Lypla1	24	66,833	3,2E+09	23.726	224	54	3	7	0	0	2	1,7E+08	3,1E+08	1,8	1,5E+07	1,5E+07	7,8E+07	5,3	3	19	0	0	2	Not specified	N/A
Q9DC61	MPPA_MOUSE	Mitochondrial-processing peptidase subunit alpha	Pmpca	52	101,53	4,6E+09	58.278	524	36.5	3	13	1	1	6	5,8E+07	8,1E+08	13,9	1,5E+07	1,5E+07	7,6E+07	5,2	3	37	1	1	10	Mitochondrion	Inner membrane, matrix
Q99JB2	STML2_MOUSE	Stomatin-like protein 2, mitochondrial	Stoml2	58	76,838	2,6E+09	38.384	353	35.7	0	1	0	3	12	1,1E+07	1,1E+07	1,0	1,5E+07	8,2E+07	4,0E+08	4,9	0	1	0	7	50	Cell membrane, cytoplasm, mitochondrion	Inner membrane, IMS
Q9Z0S1	BPNT1_MOUSE	3(2),5-bisphosphate nucleotidase 1	Bpnt1	19	13,873	3,7E+08	33.196	308	27.6	0	6	0	0	4	1,1E+07	2,2E+07	2,0	1,5E+07	1,5E+07	7,3E+07	4,9	0	10	0	0	9	Not specified	N/A
Q68FD5	CLH1_MOUSE	Clathrin heavy chain 1	Cltc	22	34,855	5,1E+08	191.55	1675	7.8	0	6	0	1	5	1,1E+07	3,9E+07	3,6	1,5E+07	1,5E+07	7,2E+07	4,9	0	7	0	3	12	Cytoplasm	N/A
Q01768	NDKB_MOUSE	Nucleoside diphosphate kinase B	Nme2	17	13,832	5,1E+08	17.363	152	49.3	0	5	0	1	4	1,1E+07	8,5E+07	7,9	1,5E+07	1,5E+07	7,1E+07	4,8	0	8	0	1	8	Cytoplasm, nucleus	N/A
Q8BMS4	COQ3_MOUSE	Ubiquinone biosynthesis O-methyltransferase, mitochondrial	Coq3	35	42,664	3,9E+09	40.956	370	20	3	5	0	1	2	1,5E+08	4,5E+08	3,1	1,5E+07	1,5E+07	6,9E+07	4,7	4	22	0	3	6	Mitochondrion	Inner membrane
O00391	QSOX1_HUMAN	Sulfhydryl oxidase 1	QSOX1	32	23,412	4,8E+08	82.577	747	16.5	0	0	0	2	9	1,1E+07	1,1E+07	1,0	1,5E+07	3,3E+07	1,5E+08	4,6	0	0	0	5	27	Secreted, Golgi apparatus	N/A
J3QNY6	J3QNY6_MOUSE	Bile salt export pump	Abcb11	12	13,933	2,9E+08	146.74	1321	3.9	0	4	0	0	3	1,1E+07	4,6E+07	4,3	1,5E+07	1,5E+07	6,7E+07	4,5	0	6	0	0	6	Endosome	N/A
P08697	A2AP_HUMAN	Alpha-2-antiplasmin	SERPINF2	36	69,131	2,3E+09	54.565	491	27.7	0	0	0	3	11	1,1E+07	1,1E+07	1,0	1,5E+07	1,3E+08	6,0E+08	4,5	0	0	0	3	33	Secreted	N/A
Q8K370	ACD10_MOUSE	Acyl-CoA dehydrogenase family member 10	Acad10	179	256,72	1,3E+10	118.98	1069	36.9	21	28	0	4	19	4,3E+08	4,2E+08	1,0	1,5E+07	4,1E+07	1,8E+08	4,4	31	105	0	7	36	Not specified	N/A
P61019	RAB2A_HUMAN	Ras-related protein Rab-2A	RAB2A	15	18,213	3,9E+08	23.545	212	25.9	0	3	0	1	5	1,1E+07	5,0E+07	4,7	1,5E+07	1,5E+07	6,4E+07	4,4	0	6	0	2	7	Endoplasmic reticulum, Golgi apparatus	N/A
Q922Q1	MARC2_MOUSE	Mitochondrial amidoxime reducing component 2	Mtarc2	109	87,342	8,0E+09	38.194	338	50.9	6	10	1	4	12	2,0E+08	1,8E+08	0,9	1,5E+07	2,3E+08	9,3E+08	4,0	8	24	3	15	59	Mitochondrion, peroxisome	Outer membrane
O08749	DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial	Dld	192	287,57	4,8E+10	54.272	509	42.8	9	17	6	3	8	1,5E+09	5,2E+09	3,6	8,4E+08	2,1E+08	8,2E+08	3,9	18	119	14	7	34	Cytoplasm, nucleus, mitochondrion	Matrix
P01009	A1AT_HUMAN	Alpha-1-antitrypsin	SERPINA1	260	319,47	6,0E+10	46.736	418	61	4	1	0	16	24	2,9E+07	1,1E+07	0,4	1,5E+07	2,0E+09	7,6E+09	3,8	6	2	0	58	194	Secreted, endoplasmic reticulum	N/A
Q8BGC4	PTGR3_MOUSE	Prostaglandin reductase-3	Zadh2	97	103,07	1,0E+10	40.528	377	44.8	8	13	1	3	10	7,1E+08	4,7E+08	0,7	1,5E+07	5,9E+07	2,3E+08	3,8	15	46	1	6	29	Peroxisome	N/A
E9PFZ2	E9PFZ2_HUMAN	Ceruloplasmin	CP	30	28,45	8,2E+08	108.82	946	18.1	1	0	0	2	13	1,1E+07	1,1E+07	1,0	1,5E+07	4,6E+07	1,7E+08	3,8	1	0	0	2	27	Not specified	N/A
Q91VA6	PDIP2_MOUSE	Polymerase delta-interacting protein 2	Poldip2	68	41,933	2,9E+09	41.87	368	46.5	5	11	0	0	8	8,5E+07	1,9E+08	2,3	1,5E+07	1,5E+07	5,5E+07	3,7	6	49	0	0	13	Nucleus, mitochondrion	Matrix
B7Z6Z4	B7Z6Z4_HUMAN	Myosin light polypeptide 6	MYL6	19	7,8066	4,5E+08	26.707	238	14.3	2	3	0	1	2	3,8E+07	5,7E+07	1,5	1,5E+07	1,5E+07	5,3E+07	3,6	2	4	0	5	8	Not specified	N/A
Q9DCM0	ETHE1_MOUSE	Persulfide dioxygenase ETHE1, mitochondrial	Ethe1	58	102	7,7E+09	27.738	254	64.6	4	9	2	0	2	2,7E+08	7,7E+08	2,9	1,5E+08	1,5E+07	5,2E+07	3,5	5	37	8	0	8	Cytoplasm, nucleus, mitochondrion	Matrix
Q9CWD8	NUBPL_MOUSE	Iron-sulfur protein NUBPL	Nubpl	15	11,062	2,4E+08	34.139	319	8.5	0	2	1	1	2	1,1E+07	3,6E+07	3,3	1,5E+07	1,5E+07	5,2E+07	3,5	0	7	1	1	6	Mitochondrion	Not specified
Q5RKZ7	MOCS1_MOUSE	Molybdenum cofactor biosynthesis protein 1	Mocs1	42	57,295	1,9E+09	69.858	636	23.1	3	11	0	0	3	4,9E+07	1,8E+08	3,7	1,5E+07	1,5E+07	5,1E+07	3,5	5	33	0	0	4	Not specified	N/A
Q9JKR6	HYOU1_MOUSE	Hypoxia up-regulated protein 1	Hyou1	76	97,051	3,1E+09	111.18	999	31.1	10	17	0	1	10	1,1E+08	7,5E+07	0,7	1,5E+07	1,5E+07	5,1E+07	3,4	13	44	0	1	18	Endoplasmic reticulum	N/A
Q8R1S0	COQ6_MOUSE	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial	Coq6	37	52,65	3,2E+09	51.392	476	21.6	3	9	0	1	4	7,2E+07	2,5E+08	3,5	1,5E+07	1,5E+07	5,0E+07	3,4	3	25	0	2	7	Mitochondrion, Golgi apparatus	Inner membrane
A0A494BAI5	A0A494BAI5_MOUSE	Ferrochelatase	Fech	136	159,69	6,0E+09	46.96	417	56.8	17	13	2	4	12	8,9E+08	1,5E+08	0,2	1,6E+08	1,0E+08	3,5E+08	3,4	54	40	2	6	34	Mitochondrion	Inner membrane
K9J7B2	K9J7B2_MOUSE	UDP-glucuronosyltransferase	Ugt1a6b	94	63,019	1,6E+10	60.49	531	24.3	4	7	3	7	11	1,3E+08	2,9E+08	2,2	6,5E+08	6,9E+08	2,3E+09	3,3	3	16	5	12	58	Other	N/A
Q9D172	GAL3A_MOUSE	Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondria	Gatd3a	68	105,94	1,5E+10	28.09	266	50.4	7	9	0	0	3	1,4E+09	1,8E+09	1,2	1,5E+07	1,5E+07	4,9E+07	3,3	12	52	0	0	4	Mitochondrion	Not specified
Q99L04	DHRS1_MOUSE	Dehydrogenase/reductase SDR family member 1	Dhrs1	29	249,25	9,2E+08	34.005	313	20.1	0	0	1	2	7	1,1E+07	1,1E+07	1,0	1,5E+07	7,6E+07	2,4E+08	3,2	0	0	1	4	24	Not specified	N/A
Q9UK55	ZPI_HUMAN	Protein Z-dependent protease inhibitor	SERPINA10	35	51,14	1,5E+09	50.706	444	39.9	0	0	0	4	16	1,1E+07	1,1E+07	1,0	1,5E+07	7,9E+07	2,5E+08	3,2	0	0	0	8	27	Secreted	N/A
E9QKK8	E9QKK8_MOUSE	Phospholipid-transporting ATPase	Atp11c	24	21,062	4,9E+08	127.81	1116	13.2	0	0	0	2	10	1,1E+07	1,1E+07	1,0	1,5E+07	5,0E+07	1,6E+08	3,1	0	0	0	3	21	Other	N/A
Q9DCY0	KEG1_MOUSE	Glycine N-acyltransferase-like protein Keg1	Keg1	117	124,42	1,8E+10	33.723	295	45.4	7	10	2	5	9	7,9E+08	9,4E+08	1,2	6,3E+07	1,4E+08	4,4E+08	3,1	23	54	4	8	28	Cytoplasm	N/A
A0A1W2P733	A0A1W2P733_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	9	10,999	2,5E+08	82.041	755	8.7	0	3	0	0	4	1,1E+07	5,0E+07	4,7	1,5E+07	1,5E+07	4,6E+07	3,1	0	3	0	0	6	Not specified	N/A
Q8CC88	VWA8_MOUSE	von Willebrand factor A domain-containing protein 8	Vwa8	365	304,31	1,9E+10	213.42	1905	42.8	19	46	2	18	56	1,3E+08	2,0E+08	1,6	3,7E+07	1,9E+08	5,9E+08	3,1	27	140	2	43	153	Mitochondrion	Not specified
Q60766	IRGM1_MOUSE	Immunity-related GTPase family M protein 1	Irgm1	45	37,128	1,4E+09	46.551	409	17.6	0	2	0	3	8	1,1E+07	3,7E+07	3,4	1,5E+07	8,4E+07	2,6E+08	3,0	0	4	0	7	34	Cell membrane, cytoplasm, Golgi apparatus, endolysosomal compartment	N/A
O88696	CLPP_MOUSE	ATP-dependent Clp protease proteolytic subunit, mitochondrial	Clpp	16	27,591	5,1E+08	29.8	272	22.1	0	4	0	2	3	1,1E+07	7,2E+07	6,7	1,5E+07	1,5E+07	4,5E+07	3,0	0	8	0	2	6	Mitochondrion	Matrix
P70404	IDHG1_MOUSE	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	Idh3g	15	44,588	1,6E+09	42.785	393	25.4	0	5	0	1	2	1,1E+07	4,3E+08	39,9	1,5E+07	1,5E+07	4,5E+07	3,0	0	11	0	2	2	Mitochondrion	Not specified
Q9DBK0	ACO12_MOUSE	Acetyl-coenzyme A thioesterase	Acot12	42	49,845	1,6E+09	61.761	556	25.4	2	9	0	1	7	2,8E+07	1,1E+08	3,9	1,5E+07	1,5E+07	4,5E+07	3,0	2	24	0	1	15	Cytoplasm	N/A
Q8K0D5	EFGM_MOUSE	Elongation factor G, mitochondrial	Gfm1	77	88,858	5,2E+09	83.549	751	24.4	12	14	0	1	6	2,0E+08	2,5E+08	1,2	1,5E+07	1,5E+07	4,5E+07	3,0	17	49	0	1	10	Mitochondrion	Not specified
Q91WS0	CISD1_MOUSE	CDGSH iron-sulfur domain-containing protein 1	Cisd1	92	90,195	8,0E+09	12.097	108	43.5	4	2	2	3	5	5,1E+07	8,2E+07	1,6	1,2E+08	3,9E+08	1,1E+09	2,9	9	7	7	11	58	Mitochondrion	Outer membrane
B1AXW5	B1AXW5_MOUSE	Peroxiredoxin-1 (Fragment)	Prdx1	31	14,841	6,0E+08	18.87	169	38.5	1	4	0	1	5	1,1E+07	4,6E+07	4,3	1,5E+07	1,5E+07	4,3E+07	2,9	1	9	0	3	18	Not specified	N/A
E9Q7N5	E9Q7N5_MOUSE	Ribosome-releasing factor 2, mitochondrial	Gfm2	24	77,285	1,1E+09	82.025	741	11.9	2	6	0	0	2	4,1E+07	1,7E+08	4,1	1,5E+07	1,5E+07	4,2E+07	2,9	2	19	0	0	3	Mitochondrion	Not specified
Q14DH7	ACSS3_MOUSE	Acyl-CoA synthetase short-chain family member 3, mitochondrial	Acss3	56	118,88	4,9E+09	74.517	682	35.2	9	15	1	0	2	1,3E+08	2,8E+08	2,1	1,5E+07	1,5E+07	4,2E+07	2,8	9	39	1	0	7	Mitochondrion	Matrix
Q571F8	GLSL_MOUSE	Glutaminase liver isoform, mitochondrial	Gls2	188	179,23	3,2E+10	66.365	602	48	14	21	3	5	15	4,2E+08	1,7E+09	4,0	8,5E+07	1,4E+08	3,9E+08	2,8	19	116	3	12	38	Mitochondrion	Not specified
Q61102	ABCB7_MOUSE	ATP-binding cassette sub-family B member 7, mitochondrial	Abcb7	35	24,791	4,8E+08	82.58	752	18.4	0	5	2	2	9	1,1E+07	2,6E+07	2,4	4,4E+07	4,5E+07	1,3E+08	2,8	0	6	3	5	21	Mitochondrion	Inner membrane
Q91YM4	FAKD4_MOUSE	FAST kinase domain-containing protein 4	Tbrg4	31	34,779	1,1E+09	71.513	630	18.3	1	8	0	0	3	1,1E+07	1,3E+08	12,2	1,5E+07	1,5E+07	4,0E+07	2,7	1	24	0	0	6	Mitochondrion	Matrix
Q6XVG2	CP254_MOUSE	Cytochrome P450 2C54	Cyp2c54	38	20,844	9,4E+08	55.857	490	33.1	1	5	4	11	18	1,1E+07	2,1E+07	1,9	1,5E+07	8,5E+07	2,3E+08	2,7	1	5	1	9	22	Endoplasmic reticulum, microsomes	N/A
Q8BH59	CMC1_MOUSE	Calcium-binding mitochondrial carrier protein Aralar1	Slc25a12	46	37,102	9,3E+08	74.569	677	24.8	4	4	2	8	13	1,1E+07	2,0E+07	1,9	1,5E+07	6,0E+07	1,6E+08	2,7	1	4	0	11	30	Mitochondrion	Inner membrane
A0A140TA29	A0A140TA29_HUMAN	C4a anaphylatoxin	C4B	122	68,347	1,9E+10	187.66	1698	51.4	27	45	0	37	62	3,6E+08	2,1E+08	0,6	1,5E+07	1,4E+09	3,7E+09	2,7	11	9	0	33	69	Secreted	N/A
P38060	HMGCL_MOUSE	Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	139	130,94	3,0E+10	34.238	325	53.8	10	12	3	3	8	1,3E+09	2,0E+09	1,5	1,5E+08	1,5E+08	4,1E+08	2,7	18	79	6	10	26	Mitochondrion, peroxisome	Matrix
Q9D2G2	ODO2_MOUSE	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydro	Dlst	164	91,919	2,0E+10	48.994	454	35.5	5	9	7	7	15	2,1E+08	6,7E+08	3,2	3,7E+08	2,1E+08	5,7E+08	2,7	8	55	13	17	71	Nucleus, mitochondrion	Matrix
P51658	DHB2_MOUSE	Estradiol 17-beta-dehydrogenase 2	Hsd17b2	49	33,243	7,2E+08	41.835	381	33.1	0	0	0	2	12	1,1E+07	1,1E+07	1,0	1,5E+07	6,8E+07	1,8E+08	2,6	0	0	0	9	40	Other	N/A
Q60936	COQ8A_MOUSE	Atypical kinase COQ8A, mitochondrial	Coq8a	179	257,66	1,6E+10	71.742	645	43.4	8	16	4	8	15	5,3E+08	8,2E+08	1,6	1,8E+08	5,6E+08	1,5E+09	2,6	11	68	12	27	61	Mitochondrion	Not specified
Q3TLP5	ECHD2_MOUSE	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Echdc2	56	128,16	1,1E+10	31.852	296	41.2	6	8	1	1	2	5,9E+08	8,4E+08	1,4	1,5E+07	1,5E+07	3,8E+07	2,6	9	37	1	1	8	Mitochondrion	Not specified
P01011	AACT_HUMAN	Alpha-1-antichymotrypsin	SERPINA3	44	28,236	1,2E+09	47.65	423	21.3	0	0	0	4	10	1,1E+07	1,1E+07	1,0	1,5E+07	6,9E+07	1,8E+08	2,5	0	0	0	10	34	Secreted	N/A
A2AKK5	ACNT1_MOUSE	Acyl-coenzyme A amino acid N-acyltransferase 1	Acnat1	30	30,472	1,2E+09	46.07	416	26.4	3	4	0	0	3	3,3E+08	5,8E+07	0,2	1,5E+07	1,5E+07	3,7E+07	2,5	7	16	0	0	7	Peroxisome	N/A
Q9CW42	MARC1_MOUSE	Mitochondrial amidoxime-reducing component 1	Mtarc1	73	76,801	5,5E+09	37.978	340	56.8	2	9	0	4	12	1,1E+07	9,6E+07	9,0	1,5E+07	2,3E+08	5,9E+08	2,5	2	29	0	8	34	Mitochondrion	Outer membrane
P02751	FINC_HUMAN	Fibronectin	FN1	173	157,91	8,2E+09	272.32	2477	24.3	3	16	0	9	34	1,3E+07	1,2E+08	9,3	1,5E+07	1,7E+08	4,3E+08	2,5	4	27	0	28	114	Secreted	N/A
Q9CQA3	SDHB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	Sdhb	84	42,245	5,3E+09	31.814	282	36.5	6	9	2	2	9	1,3E+08	4,4E+08	3,5	1,3E+08	5,7E+07	1,4E+08	2,5	17	34	2	5	26	Mitochondrion	Inner membrane
Q9DBL1	ACDSB_MOUSE	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Acadsb	59	127,72	7,0E+09	47.874	432	35	7	14	0	2	5	2,8E+08	4,5E+08	1,6	1,5E+07	9,2E+07	2,2E+08	2,5	8	35	0	4	12	Mitochondrion	Matrix
P04196	HRG_HUMAN	Histidine-rich glycoprotein	HRG	33	24,051	1,1E+09	59.578	525	16.4	4	2	0	3	7	9,9E+07	3,3E+07	0,3	1,5E+07	7,0E+07	1,7E+08	2,4	6	3	0	6	18	Secreted	N/A
Q8CG76	ARK72_MOUSE	Aflatoxin B1 aldehyde reductase member 2	Akr7a2	61	98,009	5,1E+09	40.612	367	35.7	5	9	1	3	6	2,5E+08	4,6E+08	1,8	1,5E+07	8,9E+07	2,1E+08	2,4	8	33	2	6	12	Cytoplasm, Golgi apparatus	N/A
P61620	S61A1_MOUSE	Protein transport protein Sec61 subunit alpha isoform 1	Sec61a1	17	7,659	2,9E+08	52.264	476	4.6	0	2	0	2	3	1,1E+07	1,8E+07	1,7	1,5E+07	4,6E+07	1,1E+08	2,4	0	3	0	4	10	Endoplasmic reticulum	N/A
O88441	MTX2_MOUSE	Metaxin-2	Mtx2	24	17,852	6,6E+08	29.758	263	28.1	0	0	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	7,3E+07	1,7E+08	2,4	0	0	0	4	20	Mitochondrion	Outer membrane
Q91VS7	MGST1_MOUSE	Microsomal glutathione S-transferase 1	Mgst1	174	35,471	1,5E+10	17.551	155	40	2	4	1	2	3	7,9E+08	3,9E+08	0,5	1,5E+07	6,5E+08	1,5E+09	2,4	9	17	6	24	118	Mitochondrion, microsomes	Outer membrane
A0A7I2V2D2	A0A7I2V2D2_HUMAN	Plasma protease C1 inhibitor	SERPING1	27	25,435	9,8E+08	53.213	482	15.1	1	2	0	4	6	1,1E+07	4,7E+07	4,4	1,5E+07	7,3E+07	1,7E+08	2,3	1	3	0	6	17	Not specified	N/A
Q925I1	ATAD3_MOUSE	ATPase family AAA domain-containing protein 3	Atad3	156	106,19	9,6E+09	66.741	591	38.1	2	4	1	14	26	2,6E+07	3,2E+07	1,2	1,5E+07	5,6E+08	1,3E+09	2,3	2	8	1	29	116	Mitochondrion	Inner membrane, matrix
P25688	URIC_MOUSE	Uricase	Uox	563	321,01	1,2E+11	35.039	303	63	25	21	15	13	20	9,2E+09	3,3E+09	0,4	2,7E+09	1,9E+09	4,4E+09	2,3	189	137	42	50	145	Mitochondrion, peroxisome	Not specified
Q8CGK3	LONM_MOUSE	Lon protease homolog, mitochondrial	Lonp1	252	323,31	2,5E+10	105.84	949	50.8	13	35	3	9	24	3,8E+08	9,0E+08	2,4	3,9E+07	1,4E+08	3,1E+08	2,3	18	137	4	24	69	Mitochondrion	Matrix
P99029	PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial	Prdx5	61	57,62	5,8E+09	21.897	210	57.1	4	11	1	3	5	2,2E+08	4,7E+08	2,1	1,5E+07	3,6E+07	8,2E+07	2,3	8	34	3	4	12	Cytoplasm, mitochondrion, peroxisome	Not specified
P02748	CO9_HUMAN	Complement component C9	C9	213	104,41	3,0E+10	63.173	559	28.6	0	1	0	16	19	1,1E+07	1,1E+07	1,0	1,5E+07	2,0E+09	4,6E+09	2,3	0	1	0	58	154	Secreted, cell membrane	N/A
Q9CYV5	TM135_MOUSE	Transmembrane protein 135	Tmem135	21	19,159	4,5E+08	52.363	458	15.5	0	0	0	2	8	1,1E+07	1,1E+07	1,0	1,5E+07	4,0E+07	9,1E+07	2,3	0	0	0	3	18	Mitochondrion, peroxisome	Not specified
Q9CPY7	AMPL_MOUSE	Cytosol aminopeptidase	Lap3	160	219,06	1,3E+10	56.141	519	53.6	11	22	2	5	13	2,5E+08	5,7E+08	2,3	8,2E+07	8,9E+07	2,0E+08	2,2	17	95	2	15	31	Cytoplasm	N/A
O55022	PGRC1_MOUSE	Membrane-associated progesterone receptor component 1	Pgrmc1	54	23,575	1,8E+09	21.694	195	45.6	1	3	1	4	8	1,1E+07	5,3E+07	5,0	1,5E+07	1,7E+08	3,8E+08	2,2	1	5	1	12	35	Mitochondrion, endoplasmic reticulum, microsomes	Outer membrane
Q91Y97	ALDOB_MOUSE	Fructose-bisphosphate aldolase B	Aldob	32	30,651	1,1E+09	39.507	364	31.3	2	7	0	1	3	1,1E+07	9,7E+07	9,1	1,5E+07	1,5E+07	3,2E+07	2,2	2	21	0	1	8	Cytoplasm	N/A
O88451	RDH7_MOUSE	Retinol dehydrogenase 7	Rdh7	98	47,88	7,8E+09	35.66	316	37.7	3	11	3	7	10	1,1E+08	2,5E+08	2,2	1,3E+08	6,2E+08	1,4E+09	2,2	4	25	10	16	43	Endoplasmic reticulum, microsomes	N/A
P00186	CP1A2_MOUSE	Cytochrome P450 1A2	Cyp1a2	103	66,891	4,4E+09	58.183	513	39.2	2	4	2	9	19	5,5E+07	5,4E+07	1,0	6,2E+07	3,2E+08	6,9E+08	2,2	2	11	2	27	61	Endoplasmic reticulum, microsomes	N/A
Q9CZB0	C560_MOUSE	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	Sdhc	11	4,9183	2,2E+08	18.382	169	14.2	0	1	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	3,5E+07	7,4E+07	2,1	0	2	0	3	6	Mitochondrion	Inner membrane
Q9WUZ9	ENTP5_MOUSE	Ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	23	38,288	1,3E+09	47.101	427	18.7	4	5	0	1	2	8,0E+07	1,3E+08	1,6	1,5E+07	1,5E+07	3,1E+07	2,1	3	15	0	2	3	Secreted, endoplasmic reticulum	N/A
P55096	ABCD3_MOUSE	ATP-binding cassette sub-family D member 3	Abcd3	238	182,79	3,1E+10	75.474	659	43.2	2	10	2	19	25	2,2E+07	2,2E+08	10,1	5,4E+07	1,2E+09	2,4E+09	2,1	3	30	4	53	148	Peroxisome	N/A
Q8JZR0	ACSL5_MOUSE	Long-chain-fatty-acid--CoA ligase 5	Acsl5	82	38,596	2,4E+09	76.205	683	28.7	1	7	4	9	14	1,1E+07	1,1E+07	1,0	1,5E+07	1,6E+08	3,4E+08	2,1	0	8	3	22	49	Cell membrane, mitochondrion, endoplasmic reticulum	Outer membrane
Q91VT4	CBR4_MOUSE	Carbonyl reductase family member 4	Cbr4	124	75,741	7,7E+09	25.414	236	55.9	11	7	2	3	6	1,3E+09	1,8E+08	0,1	6,6E+07	7,9E+07	1,7E+08	2,1	55	30	3	12	24	Mitochondrion	Matrix
A0A0R4IZY2	A0A0R4IZY2_MOUSE	Cytochrome P450 2D26	Cyp2d26	87	55,383	2,5E+09	56.949	500	42	0	8	2	7	17	1,1E+07	5,5E+07	5,2	2,7E+07	1,1E+08	2,2E+08	2,1	0	15	2	15	55	Not specified	N/A
P37040	NCPR_MOUSE	NADPH--cytochrome P450 reductase	Por	47	35,534	8,6E+08	77.043	678	28.5	0	4	0	4	17	1,1E+07	2,6E+07	2,4	1,5E+07	6,6E+07	1,4E+08	2,1	0	5	0	6	36	Cytoplasm, endoplasmic reticulum	N/A
P01019	ANGT_HUMAN	Angiotensinogen	AGT	50	44,526	4,5E+09	53.154	485	28.2	0	0	0	5	11	1,1E+07	1,1E+07	1,0	1,5E+07	3,4E+08	7,0E+08	2,1	0	0	0	13	37	Secreted	N/A
Q8CAK1	CAF17_MOUSE	Putative transferase CAF17 homolog, mitochondrial	Iba57	15	12,76	1,7E+08	38.399	358	7	1	2	0	1	2	1,1E+07	1,8E+07	1,7	1,5E+07	1,5E+07	3,1E+07	2,1	1	5	0	2	7	Mitochondrion	Not specified
Q7TNG8	LDHD_MOUSE	Probable D-lactate dehydrogenase, mitochondrial	Ldhd	100	168,04	1,1E+10	51.847	484	58.1	8	16	1	2	7	5,5E+08	6,5E+08	1,2	1,5E+07	5,0E+07	1,0E+08	2,1	14	68	3	4	11	Mitochondrion	Not specified
Q99LB2	DHRS4_MOUSE	Dehydrogenase/reductase SDR family member 4	Dhrs4	128	280,61	1,8E+10	29.884	279	58.8	9	13	3	2	4	1,3E+09	1,8E+09	1,4	4,2E+08	3,3E+07	6,9E+07	2,1	36	56	13	4	19	Peroxisome	N/A
P06702	S10A9_HUMAN	Protein S100-A9	S100A9	25	8,0888	4,4E+08	13.242	114	30.7	1	2	2	1	3	1,1E+07	1,1E+07	1,0	1,4E+08	1,5E+07	3,0E+07	2,1	1	4	5	1	14	Secreted, cell membrane, cytoplasm	N/A
Q8BG51	MIRO1_MOUSE	Mitochondrial Rho GTPase 1	Rhot1	42	24,034	9,6E+08	72.241	631	19.2	0	0	0	4	9	1,1E+07	1,1E+07	1,0	1,5E+07	5,6E+07	1,1E+08	2,0	0	0	0	10	32	Mitochondrion	Outer membrane
Q8R4H7	NAGS_MOUSE	N-acetylglutamate synthase, mitochondrial	Nags	59	36,364	1,8E+09	57.488	527	23.7	4	11	0	2	6	4,2E+07	8,5E+07	2,0	1,5E+07	2,3E+07	4,5E+07	2,0	4	30	0	6	19	Mitochondrion	Matrix
P05546	HEP2_HUMAN	Heparin cofactor 2	SERPIND1	200	238,75	2,4E+10	57.07	499	43.7	2	0	0	14	21	1,1E+07	1,1E+07	1,0	1,5E+07	1,7E+09	3,4E+09	2,0	1	0	0	63	136	Not specified	N/A
Q9DBN5	LONP2_MOUSE	Lon protease homolog 2, peroxisomal	Lonp2	74	62,267	1,6E+09	94.525	852	22.5	1	7	0	6	18	1,1E+07	4,8E+07	4,5	1,5E+07	6,6E+07	1,3E+08	2,0	1	12	0	10	51	Peroxisome	N/A
A0A087X1J7	A0A087X1J7_HUMAN	Glutathione peroxidase	GPX3	17	9,5107	7,4E+08	25.402	225	22.2	0	0	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+08	2,9E+08	2,0	0	0	0	4	13	Not specified	N/A
Q3TDQ1	STT3B_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	Stt3b	23	26,695	6,7E+08	93.245	823	10.6	0	0	0	2	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,0E+08	2,0E+08	2,0	0	0	0	6	17	Endoplasmic reticulum	N/A
O14791	APOL1_HUMAN	Apolipoprotein L1	APOL1	74	56,154	9,4E+09	43.974	398	38.7	5	4	0	6	13	4,5E+08	1,4E+08	0,3	1,5E+07	7,7E+08	1,5E+09	2,0	5	4	0	18	47	Secreted	N/A
Q6PB66	LPPRC_MOUSE	Leucine-rich PPR motif-containing protein, mitochondrial	Lrpprc	268	323,31	2,9E+10	156.61	1392	52.8	22	56	0	7	21	2,4E+08	8,8E+08	3,6	1,5E+07	3,8E+07	7,4E+07	2,0	27	195	0	7	39	Nucleus, mitochondrion	Not specified
P16460	ASSY_MOUSE	Argininosuccinate synthase	Ass1	75	85,575	2,9E+09	46.584	412	37.6	3	9	0	7	12	4,6E+07	9,5E+07	2,1	1,5E+07	1,1E+08	2,1E+08	1,9	3	24	0	9	39	Cytoplasm	N/A
Q9WU79	PROD_MOUSE	Proline dehydrogenase 1, mitochondrial	Prodh	127	323,31	8,4E+09	68.035	599	42.2	1	11	3	8	15	1,1E+07	4,7E+08	43,6	1,3E+08	4,4E+08	8,6E+08	1,9	2	32	2	15	76	Mitochondrion	Matrix
Q99M87	DNJA3_MOUSE	DnaJ homolog subfamily A member 3, mitochondrial	Dnaja3	32	48,822	1,7E+09	52.443	480	24.4	3	8	1	0	3	3,6E+07	1,8E+08	4,9	1,5E+07	1,5E+07	2,8E+07	1,9	4	21	1	0	6	Cell membrane, cytoplasm, mitochondrion	Matrix
O09174	AMACR_MOUSE	Alpha-methylacyl-CoA racemase	Amacr	93	94,594	9,0E+09	41.704	381	54.3	9	13	1	2	7	2,7E+08	4,8E+08	1,8	1,5E+07	2,8E+07	5,4E+07	1,9	14	55	1	4	19	Mitochondrion, peroxisome	Not specified
Q9WVL0	MAAI_MOUSE	Maleylacetoacetate isomerase	Gstz1	58	50,768	3,5E+09	24.275	216	49.1	4	7	0	2	4	1,6E+08	2,3E+08	1,4	1,5E+07	3,9E+07	7,3E+07	1,9	9	30	0	5	14	Cytoplasm	N/A
Q9CXJ4	MITOS_MOUSE	Mitochondrial potassium channel ATP-binding subunit	Abcb8	33	18,432	6,8E+08	77.999	717	13.8	0	0	0	4	7	1,1E+07	1,1E+07	1,0	1,5E+07	5,6E+07	1,1E+08	1,9	0	0	0	8	25	Mitochondrion	Inner membrane
Q9CXI0	COQ5_MOUSE	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	Coq5	42	39,556	1,3E+09	37.335	327	39.1	3	9	0	1	6	2,5E+07	6,8E+07	2,7	1,5E+07	1,5E+07	2,8E+07	1,9	2	26	0	1	13	Mitochondrion	Inner membrane
J3QN06	J3QN06_MOUSE	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Naxd	33	65,893	2,0E+09	29.133	272	51.5	6	9	0	0	2	1,2E+08	2,1E+08	1,7	1,5E+07	1,5E+07	2,8E+07	1,9	6	21	0	0	6	Mitochondrion	Not specified
P00738	HPT_HUMAN	Haptoglobin	HP	101	109,67	5,1E+09	45.205	406	25.1	3	2	0	9	15	2,1E+07	1,7E+07	0,8	1,5E+07	2,8E+08	5,3E+08	1,9	7	5	0	26	63	Secreted	N/A
Q8K2B3	SDHA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Sdha	226	245,45	2,0E+10	72.585	664	53.5	14	26	11	7	15	4,2E+08	1,1E+09	2,5	7,0E+08	2,0E+08	3,7E+08	1,9	41	104	16	15	50	Mitochondrion	Inner membrane
Q61578	ADRO_MOUSE	NADPH:adrenodoxin oxidoreductase, mitochondrial	Fdxr	51	127,19	1,6E+09	54.201	494	37.9	2	10	0	3	7	2,3E+07	1,3E+08	5,7	1,5E+07	4,1E+07	7,5E+07	1,9	3	27	0	7	14	Mitochondrion	Inner membrane
O54734	OST48_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	Ddost	85	62,618	4,2E+09	49.027	441	32.7	0	6	2	6	12	1,1E+07	7,7E+07	7,2	6,9E+07	2,9E+08	5,3E+08	1,8	0	16	6	14	49	Endoplasmic reticulum	N/A
P02649	APOE_HUMAN	Apolipoprotein E	APOE	175	169,05	1,7E+10	36.154	317	57.7	5	5	0	14	17	4,7E+07	5,0E+07	1,1	1,5E+07	8,8E+08	1,6E+09	1,8	7	6	0	58	104	Secreted	N/A
Q91X34	BAAT_MOUSE	Bile acid-CoA:amino acid N-acyltransferase	Baat	95	80,954	9,3E+09	46.481	420	41.7	5	11	0	4	7	2,2E+08	7,6E+08	3,5	1,5E+07	1,5E+08	2,8E+08	1,8	7	53	0	7	28	Cytoplasm, peroxisome	N/A
P50285	FMO1_MOUSE	Dimethylaniline monooxygenase [N-oxide-forming] 1	Fmo1	31	20,703	1,1E+09	59.914	532	19.4	1	5	0	2	7	1,1E+07	1,1E+08	10,3	1,5E+07	1,3E+08	2,3E+08	1,8	1	7	0	6	17	Endoplasmic reticulum, microsomes	N/A
B1AU25	B1AU25_MOUSE	Apoptosis-inducing factor 1, mitochondrial	Aifm1	110	76,88	6,3E+09	66.113	608	32.1	3	11	3	9	15	4,6E+07	2,8E+08	6,1	7,9E+07	3,8E+08	6,7E+08	1,8	4	31	3	23	49	Mitochondrion	Not specified
P23142	FBLN1_HUMAN	Fibulin-1	FBLN1	18	23,846	1,1E+09	77.213	703	11.2	0	0	0	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	2,0E+08	3,5E+08	1,8	0	0	0	6	12	Secreted	N/A
Q8JZN7	MIRO2_MOUSE	Mitochondrial Rho GTPase 2	Rhot2	38	10,594	4,1E+08	69.07	620	10.3	0	0	0	3	5	1,1E+07	1,1E+07	1,0	1,5E+07	4,0E+07	7,1E+07	1,8	0	0	0	11	27	Mitochondrion	Outer membrane
Q791V5	MTCH2_MOUSE	Mitochondrial carrier homolog 2	Mtch2	139	91,389	1,0E+10	33.499	303	39.6	1	6	1	7	8	1,1E+07	1,4E+08	13,5	1,5E+07	1,2E+09	2,1E+09	1,8	2	14	1	47	75	Mitochondrion	Inner membrane
Q9Z2I9	SUCB1_MOUSE	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	Sucla2	197	304,16	5,4E+10	50.113	463	54.4	15	21	3	7	12	3,7E+09	3,2E+09	0,8	2,5E+08	5,1E+08	9,0E+08	1,8	23	110	5	20	39	Mitochondrion	Not specified
Q99P30	NUDT7_MOUSE	Peroxisomal coenzyme A diphosphatase NUDT7	Nudt7	75	57,645	6,3E+09	26.856	236	40.3	5	7	2	2	4	3,0E+08	3,4E+08	1,1	1,1E+08	9,9E+07	1,7E+08	1,8	9	36	7	10	13	Peroxisome	N/A
P04114	APOB_HUMAN	Apolipoprotein B-100	APOB	2734	323,31	3,8E+11	515.6	4563	56.3	65	61	0	200	249	2,1E+08	1,3E+08	0,6	1,5E+07	4,5E+09	7,8E+09	1,7	89	75	0	925	1645	Secreted, cytoplasm	N/A
G3UX26	G3UX26_MOUSE	Outer mitochondrial membrane protein porin 2	Vdac2	65	39,655	7,0E+09	30.446	283	33.6	0	4	1	7	8	1,1E+07	3,1E+07	2,9	1,5E+07	4,9E+08	8,6E+08	1,7	0	7	1	20	37	Mitochondrion	Outer membrane
P97742	CPT1A_MOUSE	Carnitine O-palmitoyltransferase 1, liver isoform	Cpt1a	116	81,847	9,1E+09	88.25	773	29.6	1	6	1	10	20	1,1E+07	5,7E+07	5,3	1,5E+07	5,5E+08	9,6E+08	1,7	0	9	2	24	81	Mitochondrion	Outer membrane
Q8BGH2	SAM50_MOUSE	Sorting and assembly machinery component 50 homolog	Samm50	90	52,63	4,2E+09	51.863	469	33.3	0	0	0	5	14	1,1E+07	1,1E+07	1,0	1,5E+07	1,9E+08	3,2E+08	1,7	0	0	0	15	75	Cytoplasm, mitochondrion	Outer membrane
E9Q5K4	CP2CN_MOUSE	Cytochrome P450 2C44	Cyp2c23	43	19,091	7,1E+08	56.421	494	25.3	0	0	0	3	9	1,1E+07	1,1E+07	1,0	1,5E+07	8,6E+07	1,5E+08	1,7	0	0	0	12	31	Endoplasmic reticulum, microsomes	N/A
O35490	BHMT1_MOUSE	Betaine--homocysteine S-methyltransferase 1	Bhmt	68	37,262	2,7E+09	45.02	407	39.6	2	6	0	5	10	1,1E+07	6,0E+07	5,6	1,5E+07	2,3E+08	4,0E+08	1,7	5	13	0	11	39	Cytoplasm	N/A
Q61586	GPAT1_MOUSE	Glycerol-3-phosphate acyltransferase 1, mitochondrial	Gpam	88	49,806	2,3E+09	93.703	827	20.2	0	1	0	7	14	1,1E+07	1,1E+07	1,0	1,5E+07	9,6E+07	1,6E+08	1,7	0	1	0	19	68	Mitochondrion	Outer membrane
A0A0R4J0I6	A0A0R4J0I6_MOUSE	Acyl-CoA dehydrogenase family member 11	Acad11	225	151,73	1,9E+10	87.347	779	44.3	9	24	4	10	23	1,6E+08	8,1E+08	5,2	5,5E+07	2,6E+08	4,4E+08	1,7	19	88	8	33	77	Not specified	N/A
O35459	ECH1_MOUSE	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Ech1	45	188,67	5,0E+09	36.118	327	40.7	3	9	0	0	2	8,2E+07	7,9E+08	9,6	1,5E+07	1,5E+07	2,5E+07	1,7	5	33	0	0	7	Mitochondrion, peroxisome	Not specified
Q99KK9	SYHM_MOUSE	Histidine--tRNA ligase, mitochondrial	Hars2	14	227,1	3,4E+08	56.985	505	14.5	0	7	0	0	2	1,1E+07	5,5E+07	5,2	1,5E+07	1,5E+07	2,5E+07	1,7	0	12	0	0	2	Mitochondrion	Not specified
Q64521	GPDM_MOUSE	Glycerol-3-phosphate dehydrogenase, mitochondrial	Gpd2	201	164,19	6,7E+09	80.953	727	45.5	0	9	1	15	29	1,1E+07	7,5E+07	7,0	1,5E+07	3,5E+08	5,9E+08	1,7	0	16	0	46	139	Mitochondrion	Inner membrane
Q8VCW8	ACSF2_MOUSE	Medium-chain acyl-CoA ligase ACSF2, mitochondrial	Acsf2	310	323,31	6,6E+10	67.95	615	58.7	16	26	3	16	22	1,9E+09	2,7E+09	1,4	1,5E+08	4,7E+08	7,8E+08	1,7	33	174	8	38	57	Mitochondrion	Not specified
P00747	PLMN_HUMAN	Plasminogen	PLG	53	17,615	1,8E+09	90.568	810	8.9	0	1	0	5	6	1,1E+07	1,1E+07	1,0	1,5E+07	3,8E+08	6,4E+08	1,7	0	1	0	13	39	Secreted	N/A
Q63880	EST3A_MOUSE	Carboxylesterase 3A	Ces3a	37	28,45	2,2E+09	63.317	571	23.1	5	9	0	2	3	1,2E+08	1,3E+08	1,1	1,5E+07	7,3E+07	1,2E+08	1,7	7	19	0	2	9	Endoplasmic reticulum	N/A
Q9CQN1	TRAP1_MOUSE	Heat shock protein 75 kDa, mitochondrial	Trap1	232	323,31	2,9E+10	80.208	706	52.5	12	25	3	15	21	8,6E+08	9,1E+08	1,1	2,4E+07	4,2E+08	6,9E+08	1,7	21	98	5	32	76	Mitochondrion	Inner membrane, matrix
Q8VDD5	MYH9_MOUSE	Myosin-9	Myh9	165	159,32	4,6E+09	226.37	1960	24.7	10	22	0	12	31	7,9E+07	1,8E+08	2,3	1,5E+07	1,3E+08	2,2E+08	1,7	13	37	0	25	90	Cytoplasm	N/A
Q91WN4	KMO_MOUSE	Kynurenine 3-monooxygenase	Kmo	130	90,608	1,1E+10	54.531	479	40.1	2	5	4	9	18	1,1E+07	9,1E+07	8,5	1,4E+08	8,5E+08	1,4E+09	1,7	2	13	9	25	81	Mitochondrion	Outer membrane
Q99LC3	NDUAA_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Ndufa10	69	78,022	3,6E+09	40.603	355	49	3	9	0	4	12	4,9E+07	1,9E+08	3,9	1,5E+07	1,7E+08	2,8E+08	1,7	3	29	0	8	29	Mitochondrion	Matrix
P11352	GPX1_MOUSE	Glutathione peroxidase 1	Gpx1	145	157,14	1,9E+10	22.329	201	79.6	9	15	3	6	10	5,5E+08	1,2E+09	2,1	1,3E+08	9,5E+07	1,6E+08	1,7	12	78	8	13	34	Cytoplasm	N/A
Q14520	HABP2_HUMAN	Hyaluronan-binding protein 2	HABP2	10	45,364	4,0E+08	62.671	560	6.1	0	0	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	8,0E+07	1,3E+08	1,7	0	0	0	3	7	Secreted	N/A
Q91VA7	Q91VA7_MOUSE	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	Idh3b	64	58,082	4,5E+09	42.194	384	45.1	6	12	0	4	10	1,1E+08	3,2E+08	2,9	1,5E+07	6,8E+07	1,1E+08	1,6	6	31	0	6	21	Mitochondrion	Not specified
P67778	PHB_MOUSE	Prohibitin	Phb	295	200,62	4,5E+10	29.82	272	82.4	9	13	11	13	19	2,2E+08	4,7E+08	2,1	4,9E+08	1,6E+09	2,6E+09	1,6	27	43	29	65	131	Cell membrane, cytoplasm, nucleus, mitochondrion	Inner membrane
Q3UNZ8	QORL2_MOUSE	Quinone oxidoreductase-like protein 2	Cryzl2	16	75,712	4,6E+08	37.808	350	20.3	2	4	0	0	2	6,2E+07	4,4E+07	0,7	1,5E+07	1,5E+07	2,4E+07	1,6	2	12	0	0	2	Not specified	N/A
Q9DBG1	CP27A_MOUSE	Sterol 26-hydroxylase, mitochondrial	Cyp27a1	133	85,157	8,4E+09	60.719	533	46.9	3	16	4	8	17	7,0E+07	5,7E+08	8,1	1,6E+08	2,8E+08	4,5E+08	1,6	3	61	4	17	48	Mitochondrion	Inner membrane
Q9QXD1	ACOX2_MOUSE	Peroxisomal acyl-coenzyme A oxidase 2	Acox2	205	323,31	1,5E+10	76.862	681	52.3	9	27	3	9	24	2,9E+08	5,9E+08	2,0	7,0E+07	2,8E+08	4,5E+08	1,6	13	86	5	26	75	Peroxisome	N/A
Q91WD5	NDUS2_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	Ndufs2	100	55,484	2,1E+09	52.625	463	34.6	1	12	1	7	11	1,1E+07	6,4E+07	6,0	1,5E+07	1,0E+08	1,6E+08	1,6	1	27	1	17	54	Mitochondrion	Inner membrane
Q9R112	SQOR_MOUSE	Sulfide:quinone oxidoreductase, mitochondrial	Sqor	134	105,68	6,8E+09	50.282	450	54.7	6	16	3	8	14	1,5E+08	3,0E+08	2,1	1,0E+08	1,8E+08	2,8E+08	1,6	12	53	5	18	46	Mitochondrion	Not specified
Q8CAQ8	MIC60_MOUSE	MICOS complex subunit Mic60	Immt	439	323,31	4,5E+10	83.899	757	53.4	0	3	3	35	42	1,1E+07	1,1E+07	1,0	1,5E+07	1,1E+09	1,8E+09	1,6	0	5	4	137	293	Mitochondrion	Inner membrane
Q9CR62	M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier protein	Slc25a11	72	52,783	2,3E+09	34.155	314	43.6	1	8	2	7	13	1,1E+07	5,8E+07	5,4	3,8E+07	1,6E+08	2,5E+08	1,6	1	14	3	19	35	Mitochondrion	Inner membrane
Q8BIJ6	SYIM_MOUSE	Isoleucine--tRNA ligase, mitochondrial	Iars2	59	182,56	3,4E+09	112.8	1012	23.4	4	17	0	0	3	6,5E+07	2,5E+08	3,9	1,5E+07	1,5E+07	2,3E+07	1,6	5	46	0	0	8	Mitochondrion	Matrix
P16332	MUTA_MOUSE	Methylmalonyl-CoA mutase, mitochondrial	Mmut	135	323,31	2,0E+10	82.843	748	50.7	11	27	4	2	6	1,9E+08	1,0E+09	5,2	8,3E+07	2,9E+07	4,6E+07	1,6	17	93	7	4	14	Cytoplasm, mitochondrion	Matrix
O35488	S27A2_MOUSE	Very long-chain acyl-CoA synthetase	Slc27a2	154	93,869	1,0E+10	70.422	620	45.2	2	10	3	13	23	1,1E+07	7,8E+07	7,3	4,8E+07	9,1E+08	1,4E+09	1,6	2	25	7	36	84	Cell membrane, endoplasmic reticulum, microsomes, peroxisome	N/A
Q9DBW0	CP4V2_MOUSE	Cytochrome P450 4V2	Cyp4v2	16	14,526	2,0E+08	60.938	525	12	0	0	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	2,3E+07	3,7E+07	1,6	0	0	0	4	12	Endoplasmic reticulum	N/A
Q99623	PHB2_HUMAN	Prohibitin-2	PHB2	358	323,31	5,7E+10	33.296	299	63.5	10	12	13	17	18	5,9E+08	5,6E+08	1,0	1,3E+09	3,3E+09	5,2E+09	1,6	31	49	40	83	155	Cell membrane, cytoplasm, nucleus, mitochondrion	Inner membrane
Q9D023	MPC2_MOUSE	Mitochondrial pyruvate carrier 2	Mpc2	44	12,327	2,3E+09	14.286	127	46.5	0	5	1	3	4	1,1E+07	1,0E+08	9,6	1,5E+07	4,9E+08	7,6E+08	1,6	0	8	2	11	23	Mitochondrion	Inner membrane
Q9WUR9	KAD4_MOUSE	Adenylate kinase 4, mitochondrial	Ak4	76	41,118	3,5E+09	25.061	223	48.9	4	7	2	3	5	9,4E+07	2,7E+08	2,9	3,2E+07	5,7E+07	8,9E+07	1,6	6	39	5	5	21	Mitochondrion	Matrix
A0A6Q8PGE6	A0A6Q8PGE6_HUMAN	Ras-related protein Rab-7a	RAB7A	50	32,533	1,3E+09	20.963	183	48.1	0	4	0	3	6	1,1E+07	1,2E+08	11,3	1,5E+07	8,6E+07	1,3E+08	1,6	0	12	0	12	26	Not specified	N/A
D3Z041	D3Z041_MOUSE	Long-chain-fatty-acid--CoA ligase 1	Acsl1	359	197,91	3,0E+10	78.034	699	57.1	6	24	11	21	32	6,1E+07	2,9E+08	4,8	4,1E+08	1,4E+09	2,2E+09	1,6	15	76	18	55	195	Not specified	N/A
B1ATI0	B1ATI0_MOUSE	Aldehyde dehydrogenase	Aldh3a2	216	82,698	1,9E+10	59.276	532	30.3	9	11	5	14	16	1,9E+08	1,2E+08	0,6	1,7E+08	1,0E+09	1,6E+09	1,6	21	27	6	55	107	Not specified	N/A
A2ACG7	A2ACG7_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	Rpn2	96	108,23	7,7E+09	67.501	615	31.9	0	8	4	8	14	1,1E+07	1,4E+08	13,3	1,2E+08	4,7E+08	7,3E+08	1,5	0	19	4	15	58	Endoplasmic reticulum	N/A
Q99L13	3HIDH_MOUSE	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Hibadh	94	311,76	1,1E+10	35.44	335	37.9	8	11	3	4	6	2,2E+08	7,1E+08	3,2	5,2E+07	4,5E+07	7,0E+07	1,5	11	59	4	5	15	Mitochondrion	Not specified
Q9DCM2	GSTK1_MOUSE	Glutathione S-transferase kappa 1	Gstk1	126	142,44	1,1E+10	25.704	226	61.5	10	12	2	6	9	4,8E+08	4,0E+08	0,8	5,7E+07	2,7E+08	4,2E+08	1,5	20	55	5	12	34	Mitochondrion	Not specified
A0A0R4J0P1	A0A0R4J0P1_MOUSE	Isobutyryl-CoA dehydrogenase, mitochondrial	Acad8	76	95,984	7,5E+09	45.091	413	40.9	3	13	2	4	9	8,5E+07	3,4E+08	4,0	8,2E+07	1,9E+08	2,9E+08	1,5	3	34	3	8	28	Mitochondrion	Not specified
P55058	PLTP_HUMAN	Phospholipid transfer protein	PLTP	24	12,604	5,8E+08	54.739	493	7.7	0	0	0	3	3	1,1E+07	1,1E+07	1,0	1,5E+07	9,4E+07	1,4E+08	1,5	0	0	0	6	18	Secreted, nucleus	N/A
Q8BW75	AOFB_MOUSE	Amine oxidase [flavin-containing] B	Maob	144	113,84	8,0E+09	58.557	520	39.6	5	11	1	6	15	8,5E+07	1,6E+08	1,9	1,5E+07	4,7E+08	7,2E+08	1,5	8	28	4	23	81	Cytoplasm, mitochondrion	Outer membrane
Q8BGT5	ALAT2_MOUSE	Alanine aminotransferase 2	Gpt2	132	213,36	1,0E+10	57.943	522	49.6	11	19	1	7	10	4,3E+08	4,3E+08	1,0	1,5E+07	1,2E+08	1,8E+08	1,5	12	79	1	17	23	Not specified	N/A
Q7TMF3	NDUAC_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Ndufa12	38	17,495	4,9E+08	17.086	145	44.8	3	2	1	3	5	1,1E+07	4,3E+07	4,0	1,5E+07	5,7E+07	8,6E+07	1,5	4	4	3	7	20	Mitochondrion	Inner membrane
E9QLB2	E9QLB2_MOUSE	Lysophospholipase-like protein 1	Lyplal1	25	24,409	1,2E+09	26.34	239	46	2	7	0	0	2	4,2E+07	1,5E+08	3,6	1,5E+07	1,5E+07	2,2E+07	1,5	2	20	0	0	3	Not specified	N/A
P04004	VTNC_HUMAN	Vitronectin	VTN	155	65,451	1,5E+10	54.305	478	27.2	3	3	0	9	11	3,7E+07	3,0E+07	0,8	1,5E+07	1,0E+09	1,5E+09	1,5	8	7	0	50	90	Secreted	N/A
P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein	HSPA8	66	44,256	1,7E+09	70.897	646	25.7	2	6	2	7	14	1,1E+07	4,1E+07	3,8	1,5E+07	1,1E+08	1,7E+08	1,5	2	14	1	15	34	Cell membrane, cytoplasm, nucleus	N/A
P61922	GABT_MOUSE	4-aminobutyrate aminotransferase, mitochondrial	Abat	182	227,31	2,7E+10	56.451	500	60.6	18	25	0	2	5	1,0E+09	1,2E+09	1,2	1,5E+07	2,9E+07	4,3E+07	1,5	33	134	0	3	12	Mitochondrion	Matrix
O35386	PAHX_MOUSE	Phytanoyl-CoA dioxygenase, peroxisomal	Phyh	47	25,789	2,1E+09	38.607	338	29	3	9	0	2	3	9,0E+07	1,1E+08	1,2	1,5E+07	8,6E+07	1,3E+08	1,5	4	24	0	5	14	Peroxisome	N/A
Q9D826	SOX_MOUSE	Peroxisomal sarcosine oxidase	Pipox	133	109,84	3,2E+10	43.846	390	53.3	11	17	3	4	8	1,1E+09	2,5E+09	2,4	2,6E+08	1,2E+08	1,8E+08	1,5	23	82	3	6	19	Peroxisome	N/A
Q8JZQ2	AFG32_MOUSE	AFG3-like protein 2	Afg3l2	46	23,912	1,0E+09	89.518	802	17.2	0	1	0	4	13	1,1E+07	1,1E+07	1,0	1,5E+07	9,6E+07	1,4E+08	1,5	0	2	0	9	35	Mitochondrion	Inner membrane
Q9WUM5	SUCA_MOUSE	Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	Suclg1	378	323,31	2,0E+11	36.154	346	34.7	11	9	3	2	4	2,4E+10	3,7E+09	0,2	1,7E+08	6,6E+07	9,8E+07	1,5	224	113	16	7	18	Mitochondrion	Not specified
Q60932	VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1	Vdac1	179	103,7	2,5E+10	32.351	296	62.8	4	9	3	14	17	2,5E+07	6,7E+07	2,6	5,7E+07	1,2E+09	1,7E+09	1,5	6	23	5	47	98	Cell membrane, mitochondrion	Outer membrane
P01031	CO5_HUMAN	Complement C5	C5	99	69,297	3,1E+09	188.3	1676	19.1	0	0	0	10	27	1,1E+07	1,1E+07	1,0	1,5E+07	2,4E+08	3,5E+08	1,5	0	0	0	30	69	Secreted	N/A
Q78IK4	MIC27_MOUSE	MICOS complex subunit Mic27	Apool	48	28,712	2,2E+09	29.26	265	37.4	0	0	0	5	8	1,1E+07	1,1E+07	1,0	1,5E+07	2,0E+08	2,9E+08	1,5	0	0	0	11	37	Mitochondrion	Inner membrane
Q9DCT2	NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	Ndufs3	124	55,608	5,1E+09	30.149	263	35.4	3	8	4	7	11	5,5E+07	2,5E+08	4,6	1,3E+08	2,4E+08	3,6E+08	1,5	4	28	5	25	62	Mitochondrion	Inner membrane
Q9CQ69	QCR8_MOUSE	Cytochrome b-c1 complex subunit 8	Uqcrq	57	22,501	1,6E+09	9.7681	82	37.8	3	2	2	2	4	2,4E+08	7,8E+07	0,3	1,5E+08	1,7E+08	2,4E+08	1,5	12	7	5	8	25	Mitochondrion	Inner membrane
P12790	CP2B9_MOUSE	Cytochrome P450 2B9	Cyp2b9	31	15,903	4,4E+08	55.74	491	14.7	0	3	1	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	5,5E+07	8,0E+07	1,5	0	3	1	9	18	Endoplasmic reticulum, microsomes	N/A
Q91YQ5	RPN1_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Rpn1	162	148,96	9,5E+09	68.527	608	56.9	2	11	3	12	27	1,6E+07	1,1E+08	7,0	1,1E+08	6,1E+08	8,8E+08	1,5	3	20	5	31	103	Endoplasmic reticulum	N/A
Q3TJI8	Q3TJI8_MOUSE	Corticosteroid 11-beta-dehydrogenase isozyme 1	Hsd11b1	61	43,523	1,9E+09	28.689	262	32.8	2	4	0	6	10	3,6E+07	9,8E+07	2,7	1,5E+07	7,7E+07	1,1E+08	1,4	3	15	0	18	25	Not specified	N/A
Q8R1A8	Q8R1A8_MOUSE	Ornithine carbamoyltransferase, mitochondrial	Otc	258	284,18	6,2E+10	39.365	351	75.5	15	21	10	5	8	2,2E+09	2,6E+09	1,2	1,7E+09	1,7E+08	2,4E+08	1,4	54	146	28	8	22	Mitochondrion	Not specified
Q9CQX2	CYB5B_MOUSE	Cytochrome b5 type B	Cyb5b	31	41,466	2,0E+09	16.318	146	51.4	1	1	0	3	5	1,1E+07	1,1E+07	1,0	1,5E+07	4,2E+08	6,0E+08	1,4	0	4	0	4	23	Mitochondrion	Outer membrane
P01027	CO3_MOUSE	Complement C3	C3	32	32,159	9,1E+08	186.48	1663	13	4	16	0	7	13	1,1E+07	7,3E+07	6,9	1,5E+07	1,5E+07	2,1E+07	1,4	0	23	0	0	9	Secreted	N/A
Q9WTP6	KAD2_MOUSE	Adenylate kinase 2, mitochondrial	Ak2	22	39,205	4,8E+08	26.468	239	44.8	0	8	1	0	3	1,1E+07	6,4E+07	6,0	1,5E+07	1,5E+07	2,1E+07	1,4	0	15	1	0	6	Mitochondrion	IMS
Q8BGB8	COQ4_MOUSE	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial	Coq4	19	14,267	8,1E+08	30.084	266	16.2	0	4	0	0	2	1,1E+07	8,6E+07	8,0	1,5E+07	1,5E+07	2,1E+07	1,4	0	15	0	0	4	Mitochondrion	Inner membrane
Q5U458	DJC11_MOUSE	DnaJ homolog subfamily C member 11	Dnajc11	67	52,893	2,8E+09	63.232	559	30.8	0	0	0	7	18	1,1E+07	1,1E+07	1,0	1,5E+07	2,8E+08	4,1E+08	1,4	0	0	0	16	51	Mitochondrion	Outer membrane
Q9CQZ5	NDUA6_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	Ndufa6	41	21,636	1,6E+09	15.283	131	45.8	2	2	3	4	5	2,9E+08	6,5E+07	0,2	3,4E+08	1,7E+08	2,4E+08	1,4	3	3	9	7	19	Mitochondrion	Inner membrane
Q9CPP6	NDUA5_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Ndufa5	25	49,121	6,5E+08	13.36	116	50	0	3	3	2	5	1,1E+07	2,1E+07	2,0	1,2E+08	8,0E+07	1,1E+08	1,4	0	8	3	3	11	Mitochondrion	Inner membrane
P24270	CATA_MOUSE	Catalase	Cat	508	323,31	1,1E+11	59.795	527	71.3	24	32	17	12	18	1,2E+09	2,6E+09	2,2	2,3E+09	5,2E+08	7,4E+08	1,4	113	220	54	42	79	Peroxisome	N/A
Q05421	CP2E1_MOUSE	Cytochrome P450 2E1	Cyp2e1	129	143,03	5,0E+09	56.804	493	30.6	1	6	4	13	17	1,1E+07	6,4E+07	6,0	8,3E+07	6,0E+08	8,4E+08	1,4	2	16	7	38	66	Mitochondrion, endoplasmic reticulum, microsomes	Inner membrane
O88908	SOAT2_MOUSE	Sterol O-acyltransferase 2	Soat2	28	15,296	7,0E+08	60.597	525	10.5	0	0	0	3	5	1,1E+07	1,1E+07	1,0	1,5E+07	7,6E+07	1,1E+08	1,4	0	0	0	6	22	Endoplasmic reticulum	N/A
P10126	EF1A1_MOUSE	Elongation factor 1-alpha 1	Eef1a1	66	51,45	2,2E+09	50.113	462	30.5	2	6	2	4	7	4,9E+07	1,1E+08	2,2	2,6E+07	1,4E+08	2,0E+08	1,4	3	19	4	16	24	Cell membrane, cytoplasm, nucleus	N/A
P06727	APOA4_HUMAN	Apolipoprotein A-IV	APOA4	111	74,633	3,1E+09	45.371	396	58.8	0	0	0	15	23	1,1E+07	1,1E+07	1,0	1,5E+07	2,3E+08	3,2E+08	1,4	0	0	0	31	80	Secreted	N/A
Q9EQ20	MMSA_MOUSE	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Aldh6a1	451	323,31	2,3E+11	57.915	535	70.7	22	27	5	18	23	8,1E+09	9,1E+09	1,1	4,0E+08	2,8E+09	3,9E+09	1,4	65	213	9	51	113	Mitochondrion	Not specified
Q9D9P1	Q9D9P1_MOUSE	MICOS complex subunit Mic19	Chchd3	91	161,08	6,1E+09	20.375	175	37.1	0	0	0	9	11	1,1E+07	1,1E+07	1,0	1,5E+07	6,0E+08	8,4E+08	1,4	0	0	0	30	61	Not specified	N/A
E9PWK1	E9PWK1_MOUSE	Epoxide hydrolase	Ephx1	43	16,081	6,0E+08	50.969	441	20.2	0	1	0	5	7	1,1E+07	1,1E+07	1,0	1,5E+07	7,6E+07	1,1E+08	1,4	0	1	0	11	31	Endoplasmic reticulum, microsomes	N/A
Q99J39	DCMC_MOUSE	Malonyl-CoA decarboxylase, mitochondrial	Mlycd	89	119,41	6,9E+09	54.735	492	55.3	4	18	2	3	5	1,1E+08	6,9E+08	6,1	7,5E+07	1,2E+08	1,6E+08	1,4	6	53	4	10	16	Cytoplasm, mitochondrion, peroxisome	Matrix
Q61285	ABCD2_MOUSE	ATP-binding cassette sub-family D member 2	Abcd2	66	33,326	1,3E+09	83.482	741	16.7	0	0	0	5	11	1,1E+07	1,1E+07	1,0	1,5E+07	2,2E+08	3,0E+08	1,4	0	0	0	20	46	Peroxisome	N/A
Q3UEP4	Q3UEP4_MOUSE	UDP-glucuronosyltransferase	Ugt2b36	30	22,236	4,2E+08	61.041	530	22.1	1	5	2	4	9	1,1E+07	2,4E+07	2,3	1,5E+07	3,1E+07	4,3E+07	1,4	0	4	1	4	21	Other	N/A
A8DUK4	A8DUK4_MOUSE	Beta-globin	Hbb-bs	40	39,9	2,2E+09	15.748	147	66	3	8	0	2	2	2,7E+08	2,2E+08	0,8	1,5E+07	4,3E+07	5,9E+07	1,4	5	22	0	5	8	Not specified	N/A
P00734	THRB_HUMAN	Prothrombin	F2	83	42,401	3,2E+09	70.036	622	20.3	2	3	0	7	13	1,8E+08	4,8E+07	0,3	1,5E+07	2,9E+08	4,0E+08	1,4	3	2	0	27	51	Secreted	N/A
Q9WTP7	KAD3_MOUSE	GTP:AMP phosphotransferase AK3, mitochondrial	Ak3	212	168,58	3,4E+10	25.426	227	77.1	11	17	3	10	12	1,7E+09	1,2E+09	0,7	5,5E+07	7,6E+08	1,0E+09	1,4	24	97	3	29	59	Mitochondrion	Matrix
P01023	A2MG_HUMAN	Alpha-2-macroglobulin	A2M	245	152,99	1,1E+10	163.29	1474	31.8	6	3	0	24	35	1,1E+07	1,1E+07	1,0	1,5E+07	3,8E+08	5,2E+08	1,4	11	2	0	78	154	Secreted	N/A
P06396	GELS_HUMAN	Gelsolin	GSN	225	323,31	2,6E+10	85.696	782	50	5	0	0	20	33	2,4E+07	1,1E+07	0,4	1,5E+07	1,5E+09	2,1E+09	1,4	9	0	0	68	148	Secreted, cytoplasm	N/A
P50171	DHB8_MOUSE	Estradiol 17-beta-dehydrogenase 8	Hsd17b8	127	109,36	9,6E+09	26.588	259	55.2	6	10	3	5	6	4,9E+08	4,5E+08	0,9	9,5E+07	1,9E+08	2,5E+08	1,4	20	63	7	18	19	Mitochondrion	Matrix
A0A0R4J1H2	A0A0R4J1H2_MOUSE	Glycerate kinase	Glyctk	77	106,16	5,8E+09	55.334	523	29.8	7	10	0	6	6	4,3E+08	4,4E+08	1,0	1,5E+07	1,4E+08	1,9E+08	1,3	9	39	0	12	17	Not specified	N/A
P10909	CLUS_HUMAN	Clusterin	CLU	223	199,63	3,3E+10	52.494	449	38.8	7	3	0	18	21	1,0E+08	4,1E+07	0,4	1,5E+07	3,0E+09	4,0E+09	1,3	12	5	0	78	128	Secreted, cytoplasm, nucleus, mitochondrion, endoplasmic reticulum, microsomes	Not specified
P46978	STT3A_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	Stt3a	43	34,326	1,6E+09	80.597	705	14.5	0	1	0	4	13	1,1E+07	1,1E+07	1,0	1,5E+07	2,0E+08	2,6E+08	1,3	0	2	0	9	32	Endoplasmic reticulum	N/A
P31327	CPSM_HUMAN	Carbamoyl-phosphate synthase [ammonia], mitochondrial	CPS1	141	260,7	2,7E+11	164.94	1500	45.9	55	65	46	46	49	2,0E+10	3,1E+10	1,6	1,2E+09	2,4E+09	3,2E+09	1,3	27	69	11	12	22	Nucleus, mitochondrion	Not specified
E9Q8R5	E9Q8R5_MOUSE	TraB domain-containing protein	Trabd	20	14,206	4,1E+08	36.071	320	25.3	0	0	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	8,1E+07	1,1E+08	1,3	0	0	0	3	17	Not specified	N/A
A0A0R4IZZ5	A0A0R4IZZ5_MOUSE	C-type lectin domain family 4 member F	Clec4f	7	7,4117	7,7E+07	61.254	548	6.9	0	0	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,7E+07	2,2E+07	1,3	0	0	0	2	5	Not specified	N/A
Q9CQ75	NDUA2_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	Ndufa2	36	12,078	1,2E+09	10.916	99	34.3	2	1	3	2	2	3,3E+08	1,1E+07	0,0	4,9E+08	1,5E+08	2,0E+08	1,3	6	4	8	8	10	Mitochondrion	Inner membrane
Q9DBF1	AL7A1_MOUSE	Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	166	108,81	1,1E+10	58.861	539	46	8	14	0	10	15	1,7E+08	2,6E+08	1,5	1,5E+07	3,6E+08	4,7E+08	1,3	10	53	0	29	74	Cytoplasm, nucleus, mitochondrion	Not specified
Q6P8N8	Q6P8N8_MOUSE	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	Clpx	115	75,868	3,5E+09	67.335	620	36.5	7	15	1	6	16	6,1E+07	1,1E+08	1,8	1,5E+07	1,0E+08	1,4E+08	1,3	12	45	1	14	43	Mitochondrion	Not specified
Q922Q8	LRC59_MOUSE	Leucine-rich repeat-containing protein 59	Lrrc59	58	35,052	3,3E+09	34.877	307	29.6	5	3	2	3	4	6,3E+08	2,0E+08	0,3	1,5E+07	1,2E+08	1,6E+08	1,3	19	16	2	6	15	Nucleus, endoplasmic reticulum, microsomes	N/A
Q9CQQ7	AT5F1_MOUSE	ATP synthase F(0) complex subunit B1, mitochondrial	Atp5pb	117	43,499	5,9E+09	28.948	256	44.9	2	4	6	9	12	5,4E+07	4,4E+07	0,8	3,5E+08	7,0E+08	9,1E+08	1,3	3	12	18	32	52	Mitochondrion	Inner membrane
Q63886	UD11_MOUSE	UDP-glucuronosyltransferase 1A1	Ugt1a1	96	110,91	5,1E+09	60.047	535	24.7	5	10	5	7	9	3,3E+07	2,1E+08	6,4	7,4E+07	3,4E+08	4,4E+08	1,3	5	27	4	25	35	Endoplasmic reticulum	N/A
Q8BWF0	SSDH_MOUSE	Succinate-semialdehyde dehydrogenase, mitochondrial	Aldh5a1	93	77,119	9,9E+09	55.968	523	42.6	9	18	1	3	3	2,9E+08	5,0E+08	1,7	1,5E+07	6,0E+07	7,7E+07	1,3	16	65	1	3	8	Mitochondrion	Not specified
Q9DD20	MET7B_MOUSE	Methyltransferase-like protein 7B	Mettl7b	36	15,465	1,2E+09	28.049	244	29.9	0	2	0	4	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,6E+08	2,1E+08	1,3	0	7	0	7	22	Not specified	N/A
Q6PF96	Q6PF96_MOUSE	Electron transfer flavoprotein-ubiquinone oxidoreductase	Etfdh	128	91,115	6,0E+09	61.16	556	51.6	5	20	4	4	10	4,6E+07	3,0E+08	6,4	1,1E+08	1,3E+08	1,7E+08	1,3	6	73	5	12	32	Not specified	N/A
Q9CZS1	AL1B1_MOUSE	Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	197	314,74	3,1E+10	57.552	519	57.2	14	23	5	11	15	6,8E+08	1,1E+09	1,7	1,9E+08	1,7E+08	2,2E+08	1,3	18	113	10	18	38	Mitochondrion	Matrix
Q8VCH0	THIKB_MOUSE	3-ketoacyl-CoA thiolase B, peroxisomal	Acaa1b	341	323,31	1,7E+11	43.995	424	67.2	16	20	7	9	11	4,0E+09	5,5E+09	1,4	6,5E+08	2,0E+09	2,6E+09	1,3	60	174	19	30	58	Peroxisome	N/A
Q13790	APOF_HUMAN	Apolipoprotein F	APOF	19	8,0451	5,1E+08	35.399	326	8.3	0	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,0E+08	1,3E+08	1,3	0	0	0	9	10	Secreted	N/A
Q2TPA8	HSDL2_MOUSE	Hydroxysteroid dehydrogenase-like protein 2	Hsdl2	105	297,73	1,1E+10	54.208	490	59.2	11	19	1	4	8	5,5E+08	5,4E+08	1,0	1,5E+07	8,5E+07	1,1E+08	1,3	18	64	2	5	16	Peroxisome	N/A
Q9JHF5	Q9JHF5_MOUSE	V-type proton ATPase subunit a	Tcirg1	16	8,4596	2,2E+08	93.459	834	8.9	0	0	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	3,8E+07	4,8E+07	1,3	0	0	0	4	12	Other	N/A
Q9WVD5	ORNT1_MOUSE	Mitochondrial ornithine transporter 1	Slc25a15	69	58,887	2,8E+09	32.823	301	35.5	1	4	2	6	10	1,1E+07	9,6E+07	9,0	4,7E+07	2,3E+08	2,9E+08	1,3	1	8	2	15	43	Mitochondrion	Inner membrane
P35858	ALS_HUMAN	Insulin-like growth factor-binding protein complex acid labile subunit	IGFALS	16	16,261	1,8E+08	66.034	605	15.5	0	0	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	3,4E+07	4,3E+07	1,3	0	0	0	3	13	Secreted	N/A

Q64458	CP2CT_MOUSE	Cytochrome P450 2C29	Cyp2c29	133	151,63	8,0E+09	55.715	490	43.5	7	9	4	8	16	7,6E+07	1,3E+08	1,7	5,5E+07	4,6E+08	5,8E+08	1,3	16	27	6	25	59	Endoplasmic reticulim, microsomes	N/A
Q8BMS1	ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial	Hadha	732	323,31	1,3E+11	82.669	763	65.4	24	31	21	24	31	1,4E+09	3,2E+09	2,2	2,2E+09	3,9E+09	4,9E+09	1,3	84	272	53	108	215	Mitochondrion	Inner membrane
Q8VCZ9	HYPDH_MOUSE	Hydroxyproline dehydrogenase	Prodh2	39	44,256	1,5E+09	50.723	456	22.8	3	7	1	2	4	5,5E+07	1,3E+08	2,4	1,5E+07	3,1E+07	3,9E+07	1,3	3	19	2	4	11	Not specified	N/A
Q91X75	Q91X75_MOUSE	Cyp2a4 protein	Cyp2a5	51	39,084	1,4E+09	56.712	494	27.9	1	3	0	9	14	1,1E+07	4,5E+07	4,2	1,5E+07	1,8E+08	2,2E+08	1,2	1	5	0	14	31	Not specified	N/A
Q8VCR2	DHB13_MOUSE	17-beta-hydroxysteroid dehydrogenase 13	Hsd17b13	40	21,581	1,2E+09	33.458	304	29.3	0	3	1	3	9	1,1E+07	2,9E+07	2,7	1,5E+07	1,7E+08	2,1E+08	1,2	0	6	1	10	23	Endoplasmic reticulim	N/A
P0C0L4	CO4A_HUMAN	Complement C4-A	C4A	623	323,31	1,0E+11	192.78	1744	50.2	26	45	0	36	60	7,7E+08	2,8E+09	3,6	1,5E+07	6,5E+09	8,1E+09	1,2	54	83	0	146	340	Secreted	N/A
P97807	FUMH_MOUSE	Fumarate hydratase, mitochondrial	Fh	148	160,65	3,2E+10	54.356	507	56.2	10	18	5	1	5	1,1E+09	1,8E+09	1,7	1,3E+08	1,5E+07	1,8E+07	1,2	22	104	11	3	8	Cytoplasm, nucleus, mitochondrion	Not specified
Q9EP89	LACTB_MOUSE	Serine beta-lactamase-like protein LACTB, mitochondrial	Lactb	102	54,861	2,1E+09	60.705	551	30.3	3	7	0	5	13	8,0E+07	4,6E+07	0,6	1,5E+07	8,8E+07	1,1E+08	1,2	4	21	0	22	55	Mitochondrion	Not specified
Q9D6R2	IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Idh3a	104	104,17	1,1E+10	39.638	366	33.6	8	11	2	6	7	5,1E+08	5,5E+08	1,1	9,2E+07	2,1E+08	2,6E+08	1,2	11	49	8	11	25	Mitochondrion	Not specified
Q9Y277	VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3	VDAC3	45	38,373	5,9E+09	30.658	283	32.2	0	1	0	3	6	1,1E+07	1,1E+07	1,0	1,5E+07	7,7E+08	9,5E+08	1,2	0	4	0	11	30	Mitochondrion	Outer membrane
P24456	CP2DA_MOUSE	Cytochrome P450 2D10	Cyp2d10	69	36,971	2,5E+09	57.233	504	27.2	1	10	1	7	12	1,1E+07	1,1E+08	10,2	1,5E+07	1,8E+08	2,2E+08	1,2	1	22	1	12	33	Endoplasmic reticulim, microsomes	N/A
Q8R1I1	QCR9_MOUSE	Cytochrome b-c1 complex subunit 9	Uqcr10	28	49,136	2,4E+09	7.4454	64	50	2	2	2	2	3	3,2E+08	1,9E+08	0,6	1,5E+07	2,7E+08	3,3E+08	1,2	6	7	3	1	11	Mitochondrion	Inner membrane
Q60759	GCDH_MOUSE	Glutaryl-CoA dehydrogenase, mitochondrial	Gcdh	206	323,31	5,6E+10	48.605	438	58.4	11	15	5	9	11	1,1E+09	4,5E+09	4,1	8,2E+08	8,5E+08	1,0E+09	1,2	31	100	10	23	42	Mitochondrion	Matrix
P08113	ENPL_MOUSE	Endoplasmin	Hsp90b1	224	177,36	1,2E+10	92.475	802	44.1	14	19	5	12	29	4,9E+08	3,6E+08	0,7	6,4E+07	5,6E+08	6,8E+08	1,2	47	56	4	33	84	Endoplasmic/Sarcoplasmic reticula	N/A
Q5XG73	ACBD5_MOUSE	Acyl-CoA-binding domain-containing protein 5	Acbd5	42	16,497	1,0E+09	56.613	508	9.1	0	0	1	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,3E+08	1,6E+08	1,2	0	0	1	11	30	Peroxisome	N/A
Q9D1D4	TMEDA_MOUSE	Transmembrane emp24 domain-containing protein 10	Tmed10	14	10,432	2,3E+08	24.911	219	24.2	0	0	0	2	4	1,1E+07	1,1E+07	1,0	1,5E+07	4,4E+07	5,3E+07	1,2	0	0	0	2	12	Cell membrane, cytoplasm, endoplasmic reticulum, Golgi aparatus	N/A
P05202	AATM_MOUSE	Aspartate aminotransferase, mitochondrial	Got2	366	323,31	1,0E+11	47.411	430	71.9	29	28	7	4	6	8,6E+09	5,4E+09	0,6	3,8E+08	5,7E+07	6,9E+07	1,2	149	183	20	6	8	Cell membrane, mitochondrion	Matrix
Q8BWQ1	UD2A3_MOUSE	UDP-glucuronosyltransferase 2A3	Ugt2a3	45	89,528	1,8E+09	61.119	534	21.3	2	7	0	3	7	6,9E+07	1,4E+08	2,0	1,5E+07	1,0E+08	1,2E+08	1,2	3	13	0	6	23	Other	N/A
Q9QXX4	CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2	Slc25a13	481	235,71	3,8E+10	74.466	676	57	17	25	11	21	29	2,3E+08	3,5E+08	1,5	3,6E+08	1,0E+09	1,2E+09	1,2	48	114	30	99	190	Mitochondrion	Inner membrane
A0A0R3P9C8	A0A0R3P9C8_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	Ndufa9	114	80,474	2,5E+09	42.121	373	54.4	7	11	5	9	14	7,8E+07	6,7E+07	0,9	1,4E+08	1,6E+08	1,9E+08	1,2	13	29	11	21	40	Mitochondrion	Not specified
Q9Z0R9	FADS2_MOUSE	Acyl-CoA 6-desaturase	Fads2	18	15,032	4,8E+08	52.387	444	18	0	0	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	7,7E+07	9,2E+07	1,2	0	0	0	4	14	Endoplasmic reticulim	N/A
Q8C6B0	Q8C6B0_MOUSE	Methyltransferase-like 7A1	Mettl7a1	17	10,944	5,1E+08	28.096	244	16.4	0	2	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,0E+08	1,2E+08	1,2	0	2	0	4	11	Not specified	N/A
Q8JZN5	ACAD9_MOUSE	Complex I assembly factor ACAD9, mitochondrial	Acad9	128	93,757	7,4E+09	68.721	625	45.8	6	21	0	6	13	9,3E+07	3,9E+08	4,2	1,5E+07	1,2E+08	1,4E+08	1,2	8	62	0	13	45	Mitochondrion	Inner membrane
G3UWE1	G3UWE1_MOUSE	Very-long-chain enoyl-CoA reductase	Tecr	37	12,161	5,6E+08	34.244	293	19.5	0	0	0	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	5,5E+07	6,5E+07	1,2	0	0	0	8	29	Other	N/A
P54869	HMCS2_MOUSE	Hydroxymethylglutaryl-CoA synthase, mitochondrial	Hmgcs2	784	323,31	3,2E+11	56.822	508	66.5	19	25	16	20	24	7,8E+09	8,3E+09	1,1	3,6E+09	6,6E+09	7,7E+09	1,2	69	306	57	115	237	Mitochondrion	Not specified
P58710	GGLO_MOUSE	L-gulonolactone oxidase	Gulo	24	38,127	7,2E+08	50.478	440	18.6	1	3	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	7,0E+07	8,2E+07	1,2	1	6	0	7	10	Endoplasmic reticulim, microsomes	N/A
E9PXC3	E9PXC3_MOUSE	Cytochrome P450, family 2, subfamily c, polypeptide 69	Cyp2c69	115	61,231	4,8E+09	56.135	491	31	4	9	3	8	13	4,0E+07	5,8E+07	1,5	5,4E+07	4,0E+08	4,7E+08	1,2	6	27	4	28	50	Not specified	N/A
D3YZ54	D3YZ54_MOUSE	2-hydroxyacyl-CoA lyase 1	Hacl1	161	323,31	1,0E+10	60.995	554	49.6	9	19	5	4	8	1,9E+08	5,9E+08	3,0	1,7E+08	9,0E+07	1,0E+08	1,2	15	95	11	8	32	Not specified	N/A
P60709	ACTB_HUMAN	Actin, cytoplasmic 1	ACTB	189	137,28	2,1E+10	41.736	375	63.7	7	13	3	10	15	5,2E+08	1,2E+09	2,3	1,0E+08	7,8E+08	9,0E+08	1,2	8	76	3	42	60	Cytoplasm, nucleus	N/A
A0A494BAD7	A0A494BAD7_MOUSE	Acyl-CoA (8-3)-desaturase	Fads1	19	6,5611	2,4E+08	12.7	112	35.7	0	0	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	5,1E+07	5,8E+07	1,2	0	0	0	5	14	Not specified	N/A
Q9CQ54	NDUC2_MOUSE	NADH dehydrogenase [ubiquinone] 1 subunit C2	Ndufc2	41	11,367	1,1E+09	14.164	120	28.3	1	1	1	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,7E+08	2,0E+08	1,2	6	2	4	9	20	Mitochondrion	Inner membrane
Q9DCW5	Q9DCW5_MOUSE	Cytochrome c oxidase subunit	Cox6a1	48	23,662	2,6E+09	12.483	112	42	2	2	0	3	3	4,1E+08	2,2E+08	0,5	1,5E+07	5,9E+08	6,9E+08	1,2	4	9	0	8	27	Mitochondrion	Inner membrane
P02743	SAMP_HUMAN	Serum amyloid P-component	APCS	15	8,5622	3,2E+08	25.387	223	19.3	0	0	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	8,1E+07	9,4E+07	1,2	0	0	0	3	12	Secreted	N/A
Q62186	SSRD_MOUSE	Translocon-associated protein subunit delta	Ssr4	40	18,074	9,3E+08	18.936	172	32.6	0	2	1	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,3E+08	1,5E+08	1,2	0	2	2	8	28	Endoplasmic reticulim	N/A
Q9CXT8	MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta	Pmpcb	31	53,375	1,9E+09	54.614	489	26.2	2	9	0	1	3	6,1E+07	1,6E+08	2,7	1,5E+07	1,5E+07	1,7E+07	1,1	3	22	0	1	5	Mitochondrion	Matrix
P29622	KAIN_HUMAN	Kallistatin	SERPINA4	100	305,98	4,8E+09	48.541	427	49.9	0	0	0	14	17	1,1E+07	1,1E+07	1,0	1,5E+07	3,8E+08	4,3E+08	1,1	0	0	0	36	64	Secreted	N/A
Q8BFR5	EFTU_MOUSE	Elongation factor Tu, mitochondrial	Tufm	289	298,63	3,2E+10	49.508	452	53.1	13	19	7	17	19	7,6E+08	1,2E+09	1,5	3,6E+08	8,5E+08	9,8E+08	1,1	25	115	17	50	82	Mitochondrion	Not specified
Q99JY0	ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial	Hadhb	434	253,82	3,8E+10	51.386	475	55.6	22	20	13	17	24	7,4E+08	8,0E+08	1,1	1,1E+09	9,8E+08	1,1E+09	1,1	73	135	41	54	131	Mitochondrion, endoplasmic reticulum	Outer membrane, inner membrane
Q06033	ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3	ITIH3	86	84,121	4,7E+09	99.848	890	24.9	0	0	0	13	17	1,1E+07	1,1E+07	1,0	1,5E+07	3,5E+08	4,0E+08	1,1	0	0	0	24	62	Secreted	N/A
Q99PG0	AAAD_MOUSE	Arylacetamide deacetylase	Aadac	61	54,066	2,7E+09	45.25	398	41.5	2	8	1	4	10	1,1E+08	3,1E+08	2,8	1,5E+07	1,2E+08	1,4E+08	1,1	2	22	3	7	27	Endoplasmic reticulim, microsomes	N/A
P56593	CP2AC_MOUSE	Cytochrome P450 2A12	Cyp2a12	104	62,262	3,3E+09	56.179	492	46.7	0	3	0	12	23	1,1E+07	1,1E+07	1,0	1,5E+07	2,7E+08	3,0E+08	1,1	0	4	0	31	69	Microsomes	N/A
O55125	NIPS1_MOUSE	Protein NipSnap homolog 1	Nipsnap1	88	218,68	1,5E+10	33.363	284	51.8	6	10	4	2	3	3,4E+08	1,7E+09	5,0	6,5E+08	1,4E+08	1,6E+08	1,1	12	49	9	5	13	Not specified	N/A
P02765	FETUA_HUMAN	Alpha-2-HS-glycoprotein	AHSG	37	45,746	1,8E+09	39.34	367	13.9	3	2	0	3	3	1,4E+08	1,8E+08	1,3	1,5E+07	3,3E+08	3,6E+08	1,1	5	2	0	6	24	Secreted	N/A
Q99J99	THTM_MOUSE	3-mercaptopyruvate sulfurtransferase	Mpst	94	163	9,9E+09	33.097	297	58.6	6	11	2	2	3	2,9E+08	1,1E+09	3,8	1,5E+08	5,5E+07	6,1E+07	1,1	10	67	4	2	11	Cytoplasm, mitochondrion	Not specified
P20742	PZP_HUMAN	Pregnancy zone protein	PZP	31	15,571	3,0E+08	163.86	1482	8.7	0	0	0	8	12	1,1E+07	1,1E+07	1,0	1,5E+07	5,3E+07	5,8E+07	1,1	0	0	0	6	25	Secreted	N/A
Q96PD5	PGRP2_HUMAN	N-acetylmuramoyl-L-alanine amidase	PGLYRP2	62	56,392	5,7E+09	62.216	576	25	0	0	0	5	9	1,1E+07	1,1E+07	1,0	1,5E+07	9,6E+08	1,1E+09	1,1	0	0	0	15	47	Secreted	N/A
Q9DCS3	MECR_MOUSE	Enoyl-[acyl-carrier-protein] reductase, mitochondrial	Mecr	55	100,54	3,3E+09	40.342	373	44.5	3	10	0	2	6	7,4E+07	3,3E+08	4,5	1,5E+07	9,4E+07	1,0E+08	1,1	7	28	0	4	16	Mitochondrion	Not specified
A0A494BAW8	A0A494BAW8_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial (Fragment)	Ndufs8	24	8,9606	4,9E+08	7.6908	67	46.3	0	3	1	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	5,4E+07	5,9E+07	1,1	0	5	1	7	11	Mitochondrion	Not specified
Q9D0S9	HINT2_MOUSE	Histidine triad nucleotide-binding protein 2, mitochondrial	Hint2	73	221,67	1,9E+10	17.32	163	39.9	4	4	2	3	3	1,5E+09	2,1E+09	1,4	7,7E+08	5,5E+08	6,1E+08	1,1	16	38	4	4	11	Mitochondrion	Not specified
Q9D6M3	GHC1_MOUSE	Mitochondrial glutamate carrier 1	Slc25a22	65	36,883	1,7E+09	34.67	323	31.9	0	4	1	6	7	1,1E+07	5,1E+07	4,8	1,5E+07	1,8E+08	1,9E+08	1,1	0	10	2	20	33	Mitochondrion	Inner membrane
Q9D0M3	CY1_MOUSE	Cytochrome c1, heme protein, mitochondrial	Cyc1	86	54,587	4,8E+09	35.327	325	35.4	7	5	3	2	4	3,2E+08	4,3E+08	1,4	3,2E+08	2,2E+08	2,4E+08	1,1	23	20	13	11	19	Mitochondrion	Inner membrane
P04003	C4BPA_HUMAN	C4b-binding protein alpha chain	C4BPA	64	323,31	8,9E+09	67.033	597	30	9	12	0	4	4	4,6E+08	1,0E+09	2,2	1,5E+07	2,0E+08	2,2E+08	1,1	12	24	0	12	16	Secreted	N/A
Q925N2	SFXN2_MOUSE	Sideroflexin-2	Sfxn2	25	14,266	3,9E+08	36.141	322	15.2	0	1	0	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	6,6E+07	7,3E+07	1,1	0	1	0	6	18	Mitochondrion	Not specified
Q8K169	Q8K169_MOUSE	UDP-glucuronosyltransferase	Ugt2b5	123	44,578	6,3E+09	60.873	530	27	4	10	5	7	8	9,8E+07	2,0E+08	2,0	3,7E+08	4,1E+08	4,5E+08	1,1	8	31	15	18	51	Other	N/A
Q9ERS2	NDUAD_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Ndufa13	56	12,956	2,5E+09	16.859	144	29.2	3	4	3	4	5	2,8E+08	1,4E+08	0,5	2,9E+08	3,1E+08	3,3E+08	1,1	7	10	5	8	26	Nucleus, mitochondrion	Inner membrane
Q61425	HCDH_MOUSE	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Hadh	143	211,11	3,9E+10	34.463	314	78.3	10	13	1	3	7	1,7E+09	2,9E+09	1,7	1,5E+07	2,1E+08	2,3E+08	1,1	35	77	2	9	20	Mitochondrion	Matrix
P05154	IPSP_HUMAN	Plasma serine protease inhibitor	SERPINA5	13	9,8084	1,5E+08	45.674	406	11.1	0	0	0	2	4	1,1E+07	1,1E+07	1,0	1,5E+07	2,4E+07	2,6E+07	1,1	0	0	0	2	11	Secreted	N/A
Q61176	ARGI1_MOUSE	Arginase-1	Arg1	48	27,673	1,2E+09	34.807	323	26.3	3	5	0	3	6	1,2E+08	6,0E+07	0,5	1,5E+07	1,1E+08	1,1E+08	1,1	7	8	0	11	22	Cytoplasm	N/A
Q9CQR4	ACO13_MOUSE	Acyl-coenzyme A thioesterase 13	Acot13	75	86,249	9,2E+09	15.183	140	50.7	3	4	3	2	4	1,1E+09	7,2E+08	0,6	2,9E+08	1,6E+08	1,7E+08	1,1	14	33	12	5	11	Cytoplasm, nucleus, mitochondrion	Not specified
F2Z456	F2Z456_MOUSE	NADH-cytochrome b5 reductase	Cyb5r3	100	103,8	6,1E+09	34.929	313	46	6	9	3	8	11	1,5E+08	2,2E+08	1,5	1,4E+08	3,8E+08	4,1E+08	1,1	14	25	5	15	41	Not specified	N/A
Q91YP0	L2HDH_MOUSE	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2hgdh	47	78,854	2,1E+09	50.898	464	35.8	4	12	1	2	5	8,3E+07	1,3E+08	1,6	1,5E+07	8,0E+07	8,7E+07	1,1	5	27	1	3	11	Mitochondrion	Not specified
Q9D0F3	LMAN1_MOUSE	Protein ERGIC-53	Lman1	20	11,386	3,6E+08	57.788	517	6.8	0	0	0	2	4	1,1E+07	1,1E+07	1,0	1,5E+07	6,5E+07	7,0E+07	1,1	0	0	0	4	16	Endoplasmic reticulim, Golgi aparatus	N/A
P00739	HPTR_HUMAN	Haptoglobin-related protein	HPR	32	20,324	1,9E+09	39.029	348	32.2	2	3	0	11	13	1,1E+07	4,4E+07	4,1	1,5E+07	3,2E+08	3,4E+08	1,1	1	2	0	10	19	Secreted	N/A
P56654	CP237_MOUSE	Cytochrome P450 2C37	Cyp2c37	44	32,951	2,2E+09	55.606	490	32.9	1	5	4	13	15	1,1E+07	1,5E+08	14,0	1,5E+07	1,9E+08	2,1E+08	1,1	0	9	1	13	21	Endoplasmic reticulim, microsomes	N/A
Q8QZR3	EST2A_MOUSE	Pyrethroid hydrolase Ces2a	Ces2a	52	30,619	1,6E+09	61.94	558	15.4	0	4	0	6	7	1,1E+07	9,1E+07	8,5	1,5E+07	1,1E+08	1,1E+08	1,1	0	14	0	15	23	Microsomes	N/A
Q91VD9	NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Ndufs1	180	132,04	8,3E+09	79.776	727	44.3	7	16	15	12	22	1,1E+08	1,7E+08	1,6	3,2E+08	2,9E+08	3,1E+08	1,1	12	44	25	26	73	Mitochondrion	Inner membrane
P51881	ADT2_MOUSE	ADP/ATP translocase 2	Slc25a5	252	74,971	3,7E+10	32.931	298	48	8	11	8	8	12	1,0E+09	8,1E+08	0,8	1,9E+09	4,4E+09	4,6E+09	1,1	30	56	34	44	88	Mitochondrion	Inner membrane
Q15392	DHC24_HUMAN	Delta(24)-sterol reductase	DHCR24	13	4,4721	1,1E+08	60.101	516	2.3	0	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	2,9E+07	3,1E+07	1,1	0	0	0	3	10	Endoplasmic reticulim, Golgi aparatus	N/A
Q9CPQ8	ATP5L_MOUSE	ATP synthase subunit g, mitochondrial	Atp5mg	113	26,968	5,8E+09	11.424	103	54.4	4	3	3	5	7	4,3E+08	6,9E+07	0,2	3,7E+08	5,4E+08	5,7E+08	1,1	37	5	10	17	44	Mitochondrion	Inner membrane
Q9QZD8	DIC_MOUSE	Mitochondrial dicarboxylate carrier	Slc25a10	88	54,553	3,7E+09	31.715	287	39.7	1	7	2	9	11	1,1E+07	5,7E+07	5,3	5,9E+07	3,6E+08	3,8E+08	1,1	1	14	3	28	42	Mitochondrion	Inner membrane
P04899	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	20	9,58	3,0E+08	40.45	355	19.2	0	1	0	3	5	1,1E+07	1,1E+07	1,0	1,5E+07	6,7E+07	7,1E+07	1,1	0	2	0	8	10	Cell membrane, cytoplasm	N/A
Q8BJ64	CHDH_MOUSE	Choline dehydrogenase, mitochondrial	Chdh	90	88,749	3,1E+09	66.414	596	32.9	3	12	5	4	9	9,2E+07	1,8E+08	2,0	2,6E+08	9,5E+07	1,0E+08	1,1	8	39	10	6	27	Mitochondrion	Inner membrane
P51660	DHB4_MOUSE	Peroxisomal multifunctional enzyme type 2	Hsd17b4	475	323,31	4,5E+10	79.481	735	51.6	28	25	15	19	23	1,2E+09	8,7E+08	0,7	1,2E+09	1,7E+09	1,8E+09	1,1	110	117	42	85	121	Peroxisome	N/A
A0A087WSY5	A0A087WSY5_HUMAN	Carboxypeptidase B2	CPB2	24	12,754	2,7E+08	44.022	386	16.1	0	0	0	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	4,6E+07	4,9E+07	1,1	0	0	0	8	16	Not specified	N/A
Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	262	185,33	2,7E+10	103.36	930	41.6	2	4	0	26	36	1,3E+07	2,7E+07	2,2	1,5E+07	2,3E+09	2,4E+09	1,1	4	5	0	77	176	Secreted	N/A
Q91X77	CY250_MOUSE	Cytochrome P450 2C50	Cyp2c50	100	63,334	5,0E+09	55.764	490	32	2	5	5	13	17	1,7E+07	5,8E+07	3,4	5,5E+07	4,7E+08	4,9E+08	1,0	4	13	5	34	44	Endoplasmic reticulim, microsomes	N/A
Q4LDG0	S27A5_MOUSE	Bile acyl-CoA synthetase	Slc27a5	54	42,971	3,7E+09	76.202	689	25.3	0	4	1	8	11	1,1E+07	1,1E+07	1,0	1,5E+07	6,5E+08	6,8E+08	1,0	0	6	1	13	34	Cell membrane, endoplasmic reticulum, microsomes	N/A
Q8JZU2	TXTP_MOUSE	Tricarboxylate transport protein, mitochondrial	Slc25a1	67	67,001	4,0E+09	33.931	311	22.5	1	4	1	5	7	1,1E+07	2,5E+08	23,0	1,5E+07	5,2E+08	5,4E+08	1,0	1	9	5	10	42	Mitochondrion	Inner membrane
P50544	ACADV_MOUSE	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadvl	457	323,31	5,9E+10	70.875	656	62	20	32	19	24	29	8,9E+08	1,7E+09	1,9	6,4E+08	1,2E+09	1,3E+09	1,0	33	177	42	89	116	Mitochondrion	Inner membrane
O70503	DHB12_MOUSE	Very-long-chain 3-oxoacyl-CoA reductase	Hsd17b12	17	12,355	6,0E+08	34.741	312	23.1	0	0	0	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,4E+08	1,4E+08	1,0	0	0	0	4	13	Endoplasmic reticulim	N/A
Q9DCX2	ATP5H_MOUSE	ATP synthase subunit d, mitochondrial	Atp5pd	137	59,49	9,1E+09	18.749	161	83.2	5	10	7	4	13	1,8E+08	3,1E+08	1,7	1,2E+09	5,5E+08	5,7E+08	1,0	23	45	10	12	47	Mitochondrion	Inner membrane
Q9DBM2	ECHP_MOUSE	Peroxisomal bifunctional enzyme	Ehhadh	1254	323,31	4,5E+11	78.301	718	87.2	69	39	16	27	39	3,8E+10	3,3E+09	0,1	9,8E+08	1,8E+09	1,9E+09	1,0	659	260	52	102	181	Peroxisome	N/A
P34914	HYES_MOUSE	Bifunctional epoxide hydrolase 2	Ephx2	304	323,31	3,9E+10	62.515	554	75.5	11	29	4	14	19	3,1E+08	1,3E+09	4,2	1,1E+08	6,1E+08	6,3E+08	1,0	19	148	9	46	82	Cytoplasm, peroxisome	N/A
O35728	CP4AE_MOUSE	Cytochrome P450 4A14	Cyp4a14	48	53,941	1,9E+09	58.719	507	30.8	1	1	1	9	10	1,1E+07	1,1E+07	1,0	1,5E+07	2,8E+08	2,9E+08	1,0	0	1	1	18	28	Endoplasmic reticulim, microsomes	N/A
P63000	RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1	RAC1	7	7,7611	1,8E+08	21.45	192	20.8	0	1	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	6,2E+07	6,3E+07	1,0	0	1	0	2	4	Cell membrane, cytoplasm, endosome	N/A
Q9JM62	REEP6_MOUSE	Receptor expression-enhancing protein 6	Reep6	29	199,24	6,5E+08	22.204	201	11.4	0	2	0	2	2	1,1E+07	6,0E+07	5,6	1,5E+07	1,2E+08	1,3E+08	1,0	0	9	0	10	10	Cytoplasm, endoplasmic reticulum	N/A
A0A3B3ISJ1	A0A3B3ISJ1_HUMAN	Vitamin K-dependent protein S	PROS1	91	50,917	4,0E+09	73.757	662	21.3	2	8	0	9	10	1,1E+07	9,5E+07	8,9	1,5E+07	2,7E+08	2,7E+08	1,0	3	10	0	31	47	Secreted	N/A
Q8BH95	ECHM_MOUSE	Enoyl-CoA hydratase, mitochondrial	Echs1	319	305,79	4,8E+10	31.474	290	45.2	12	15	7	12	13	1,6E+09	1,1E+09	0,7	4,7E+08	8,0E+08	8,1E+08	1,0	46	109	21	49	94	Mitochondrion	Matrix
Q91YT0	NDUV1_MOUSE	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Ndufv1	121	130,98	5,1E+09	50.834	464	52.2	9	16	10	5	10	1,3E+08	1,9E+08	1,5	7,1E+08	2,7E+08	2,8E+08	1,0	13	44	14	15	35	Mitochondrion	Inner membrane
P52825	CPT2_MOUSE	Carnitine O-palmitoyltransferase 2, mitochondrial	Cpt2	138	164,27	8,2E+09	73.98	658	37.5	8	18	6	8	11	2,7E+08	3,4E+08	1,2	2,3E+08	3,2E+08	3,2E+08	1,0	18	57	10	19	34	Mitochondrion	Inner membrane
O35857	TIM44_MOUSE	Mitochondrial import inner membrane translocase subunit TIM44	Timm44	142	206,36	5,6E+09	51.091	452	43.4	6	13	1	10	17	1,2E+08	1,9E+08	1,6	1,5E+07	2,2E+08	2,3E+08	1,0	8	54	1	20	59	Mitochondrion	Inner membrane
Q8CHQ9	NT8F2_MOUSE	N-acetyltransferase family 8 member 2	Nat8f2	22	8,6903	6,6E+08	26.424	238	15.1	0	0	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,6E+08	1,6E+08	1,0	0	0	0	11	11	Other	N/A
Q9WU19	HAOX1_MOUSE	Hydroxyacid oxidase 1	Hao1	96	70,932	4,7E+09	41.001	370	47.8	7	13	1	4	9	1,3E+08	1,9E+08	1,4	1,5E+07	8,3E+07	8,4E+07	1,0	12	39	1	19	25	Peroxisome	N/A
Q8R164	BPHL_MOUSE	Valacyclovir hydrolase	Bphl	188	283,63	6,7E+10	32.851	291	67	13	20	7	1	4	1,2E+09	2,6E+09	2,2	2,1E+08	1,5E+07	1,5E+07	1,0	37	134	8	3	6	Cytoplasm	N/A
Q9CZ13	QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial	Uqcrc1	220	323,31	1,8E+10	52.851	480	48.8	14	17	12	9	12	1,2E+09	8,4E+08	0,7	2,6E+09	8,4E+08	8,5E+08	1,0	45	75	25	27	48	Mitochondrion	Inner membrane
P27773	PDIA3_MOUSE	Protein disulfide-isomerase A3	Pdia3	126	104,57	9,8E+09	56.678	505	53.1	9	26	6	1	5	7,5E+07	5,8E+08	7,7	1,9E+08	1,5E+07	1,5E+07	1,0	11	95	12	1	7	Endoplasmic reticulim	N/A
P29758	OAT_MOUSE	Ornithine aminotransferase, mitochondrial	Oat	64	124,99	7,2E+09	48.354	439	55.8	5	15	4	0	2	7,0E+07	6,4E+08	9,1	2,9E+07	1,5E+07	1,5E+07	1,0	7	48	6	0	3	Mitochondrion	Matrix
Q8K1R3	PNPT1_MOUSE	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	Pnpt1	23	46,219	1,1E+09	85.682	783	16	2	10	0	0	0	1,2E+07	1,1E+08	9,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	21	0	0	0	Cytoplasm, mitochondrion	IMS, matrix
Q9DCU9	HOGA1_MOUSE	4-hydroxy-2-oxoglutarate aldolase, mitochondrial	Hoga1	33	38,346	2,4E+09	34.644	321	42.4	2	9	0	0	1	2,9E+07	2,3E+08	7,8	1,5E+07	1,5E+07	1,5E+07	1,0	2	30	0	0	1	Mitochondrion	Not specified
A0A1L1SV25	A0A1L1SV25_MOUSE	Alpha-actinin-4	Actn4	18	28,827	7,0E+08	107.11	932	11.4	1	7	0	0	3	1,1E+07	6,9E+07	6,5	1,5E+07	1,5E+07	1,5E+07	1,0	1	14	0	0	3	Not specified	N/A
G5E8T9	G5E8T9_MOUSE	Hydroxyacylglutathione hydrolase, mitochondrial	Hagh	19	23,482	1,7E+09	34.103	309	26.2	2	6	0	0	0	4,0E+07	2,5E+08	6,4	1,5E+07	1,5E+07	1,5E+07	1,0	2	17	0	0	0	Mitochondrion	Not specified
Q99MN9	PCCB_MOUSE	Propionyl-CoA carboxylase beta chain, mitochondrial	Pccb	95	146,6	1,0E+10	58.408	541	53.4	8	19	2	0	0	1,5E+08	8,8E+08	6,0	5,0E+07	1,5E+07	1,5E+07	1,0	12	81	2	0	0	Mitochondrion	Matrix
Q9CZN7	GLYM_MOUSE	Serine hydroxymethyltransferase, mitochondrial	Shmt2	183	268,71	3,9E+10	55.758	504	72	14	25	7	0	0	2,6E+08	1,5E+09	5,8	8,2E+07	1,5E+07	1,5E+07	1,0	30	145	8	0	0	Cytoplasm, nucleus, mitochondrion	Inner membrane, matrix
Q71RI9	KAT3_MOUSE	Kynurenine--oxoglutarate transaminase 3	Kyat3	44	53,47	3,9E+09	51.126	455	29.9	3	11	1	0	0	5,4E+07	2,9E+08	5,5	1,5E+07	1,5E+07	1,5E+07	1,0	4	37	3	0	0	Not specified	N/A
Q9JK42	PDK2_MOUSE	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial	Pdk2	29	38,882	1,4E+09	46.04	407	41.5	2	11	0	0	3	3,0E+07	1,6E+08	5,3	1,5E+07	1,5E+07	1,5E+07	1,0	2	23	0	0	4	Mitochondrion	Matrix
Q9DC50	OCTC_MOUSE	Peroxisomal carnitine O-octanoyltransferase	Crot	52	82,081	3,4E+09	70.264	612	38.9	4	16	1	0	0	4,4E+07	2,3E+08	5,1	1,5E+07	1,5E+07	1,5E+07	1,0	6	45	1	0	0	Peroxisome	N/A
Q8R0Y6	AL1L1_MOUSE	Cytosolic 10-formyltetrahydrofolate dehydrogenase	Aldh1l1	31	36,936	8,3E+08	98.708	902	18.6	0	12	0	0	3	1,1E+07	5,4E+07	5,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	25	0	0	6	Cytoplasm	N/A
Q91W43	GCSP_MOUSE	Glycine dehydrogenase (decarboxylating), mitochondrial	Gldc	112	165,22	8,4E+09	113.27	1025	35.8	8	25	0	0	0	5,5E+07	2,7E+08	5,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	102	0	0	0	Mitochondrion	Not specified
Q3UEG6	AGT2_MOUSE	Alanine--glyoxylate aminotransferase 2, mitochondrial	Agxt2	83	117,73	6,0E+09	57.114	513	48.3	6	18	3	0	1	8,5E+07	4,2E+08	4,9	3,7E+07	1,5E+07	1,5E+07	1,0	7	69	6	0	1	Mitochondrion	Not specified
Q8K411	PREP_MOUSE	Presequence protease, mitochondrial	Pitrm1	36	47,014	1,0E+09	117.37	1036	19.4	3	13	0	0	0	1,6E+07	7,6E+07	4,8	1,5E+07	1,5E+07	1,5E+07	1,0	3	33	0	0	0	Mitochondrion	Matrix
A2ATU0	DHTK1_MOUSE	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	Dhtkd1	31	86,573	2,7E+09	102.79	921	21.5	3	11	0	0	0	6,1E+07	2,7E+08	4,4	1,5E+07	1,5E+07	1,5E+07	1,0	4	27	0	0	0	Mitochondrion	Not specified
Q3ULD5	MCCB_MOUSE	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	Mccc2	141	157,71	9,5E+09	61.378	563	51	7	24	5	0	4	1,0E+08	4,5E+08	4,3	3,5E+07	1,5E+07	1,5E+07	1,0	7	120	7	0	7	Mitochondrion	Matrix
Q91WM2	HDHD5_MOUSE	Haloacid dehalogenase-like hydrolase domain-containing 5	Hdhd5	29	56,097	3,0E+09	46.306	419	30.1	3	9	1	0	0	1,1E+08	4,6E+08	4,3	1,5E+07	1,5E+07	1,5E+07	1,0	5	23	1	0	0	Not specified	N/A
A0A0R4J0S3	A0A0R4J0S3_MOUSE	Reticulon-4-interacting protein 1, mitochondrial	Rtn4ip1	17	35,311	6,1E+08	43.399	396	30.8	2	8	0	1	0	1,2E+07	5,0E+07	4,1	1,5E+07	1,5E+07	1,5E+07	1,0	3	13	0	1	0	Mitochondrion	Not specified
Q9D6Y7	MSRA_MOUSE	Mitochondrial peptide methionine sulfoxide reductase	Msra	22	21,467	1,2E+09	25.988	233	36.9	2	6	0	0	0	4,1E+07	1,7E+08	4,1	1,5E+07	1,5E+07	1,5E+07	1,0	2	20	0	0	0	Cytoplasm, nucleus, mitochondrion	Not specified
Q91ZA3	PCCA_MOUSE	Propionyl-CoA carboxylase alpha chain, mitochondrial	Pcca	110	166,81	6,2E+09	79.921	724	52.9	7	31	3	0	1	7,6E+07	3,0E+08	3,9	3,6E+07	1,5E+07	1,5E+07	1,0	9	95	5	0	1	Mitochondrion	Matrix
P97478	COQ7_MOUSE	5-demethoxyubiquinone hydroxylase, mitochondrial	Coq7	31	61,392	1,9E+09	24.041	217	26.3	2	5	0	1	1	4,9E+07	1,8E+08	3,8	1,5E+07	1,5E+07	1,5E+07	1,0	3	25	0	1	2	Mitochondrion	Inner membrane
Q8BGA8	ACSM5_MOUSE	Acyl-coenzyme A synthetase ACSM5, mitochondrial	Acsm5	127	198,7	1,8E+10	64.328	578	67.5	13	26	2	0	0	3,7E+08	1,4E+09	3,7	6,5E+07	1,5E+07	1,5E+07	1,0	22	101	4	0	0	Mitochondrion	Matrix
Q14C51	PTCD3_MOUSE	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	Ptcd3	68	90,889	4,4E+09	77.795	685	31.4	5	15	0	0	4	6,4E+07	2,3E+08	3,5	1,5E+07	1,5E+07	1,5E+07	1,0	6	56	0	0	6	Mitochondrion	Not specified
Q80YD1	SUV3_MOUSE	ATP-dependent RNA helicase SUPV3L1, mitochondrial	Supv3l1	39	66,542	1,9E+09	87.004	779	26.4	3	13	0	0	2	3,8E+07	1,1E+08	2,8	1,5E+07	1,5E+07	1,5E+07	1,0	3	33	0	0	3	Nucleus, mitochondrion	Matrix
Q3UNX5	ACSM3_MOUSE	Acyl-coenzyme A synthetase ACSM3, mitochondrial	Acsm3	55	79,995	5,5E+09	65.622	580	30.9	7	14	0	1	2	1,1E+08	3,0E+08	2,7	1,5E+07	1,5E+07	1,5E+07	1,0	8	42	0	1	4	Mitochondrion	Matrix
A0A087WRE7	A0A087WRE7_MOUSE	Alcohol dehydrogenase iron-containing protein 1 (Fragment)	Adhfe1	41	72,85	8,2E+09	49.039	457	46.4	4	13	1	0	0	3,0E+08	7,7E+08	2,6	1,5E+07	1,5E+07	1,5E+07	1,0	6	34	1	0	0	Mitochondrion	Not specified
A0A1Y7VN70	A0A1Y7VN70_MOUSE	Glutaredoxin-related protein 5, mitochondrial	Glrx5	12	17,091	1,4E+09	12.168	118	28	2	2	0	0	1	9,4E+07	2,3E+08	2,5	1,5E+07	1,5E+07	1,5E+07	1,0	2	8	0	0	2	Mitochondrion	Not specified
P09671	SODM_MOUSE	Superoxide dismutase [Mn], mitochondrial	Sod2	44	90,36	5,5E+09	24.603	222	47.7	4	7	2	1	2	3,0E+08	7,4E+08	2,5	3,1E+08	1,5E+07	1,5E+07	1,0	7	22	3	7	5	Mitochondrion	Matrix
O88986	KBL_MOUSE	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	Gcat	104	246,34	1,5E+10	44.93	416	51	6	15	0	0	0	3,7E+08	9,2E+08	2,5	1,5E+07	1,5E+07	1,5E+07	1,0	12	92	0	0	0	Nucleus, mitochondrion	Not specified
Q9WVM8	AADAT_MOUSE	Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial	Aadat	21	10,575	9,3E+08	47.597	425	12.9	2	4	0	1	1	6,1E+07	1,5E+08	2,5	1,5E+07	1,5E+07	1,5E+07	1,0	2	12	0	1	6	Mitochondrion	Not specified
O88844	IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic	Idh1	52	63,437	2,8E+09	46.674	414	42	5	15	1	0	3	5,7E+07	1,3E+08	2,4	1,5E+07	1,5E+07	1,5E+07	1,0	5	42	3	0	2	Cytoplasm	N/A
Q8K0Z7	TACO1_MOUSE	Translational activator of cytochrome c oxidase 1	Taco1	36	49,44	3,0E+09	32.314	294	50.3	5	8	0	0	2	1,0E+08	2,4E+08	2,4	1,5E+07	1,5E+07	1,5E+07	1,0	7	24	0	0	5	Mitochondrion	Not specified
Q8R2K3	Q8R2K3_MOUSE	Single-stranded DNA-binding protein, mitochondrial	Ssbp1	15	13,929	7,7E+08	17.156	148	25.7	3	4	0	0	0	3,7E+07	8,7E+07	2,3	1,5E+07	1,5E+07	1,5E+07	1,0	5	10	0	0	0	Mitochondrion	Not specified
Q91VM9	IPYR2_MOUSE	Inorganic pyrophosphatase 2, mitochondrial	Ppa2	45	89,428	3,1E+09	38.114	330	49.7	5	13	0	0	0	1,2E+08	2,6E+08	2,2	1,5E+07	1,5E+07	1,5E+07	1,0	3	42	0	0	0	Mitochondrion	Not specified
Q9QXF8	GNMT_MOUSE	Glycine N-methyltransferase	Gnmt	22	48,34	1,1E+09	32.675	293	28.3	3	6	0	0	0	3,9E+07	8,6E+07	2,2	1,5E+07	1,5E+07	1,5E+07	1,0	3	19	0	0	0	Cytoplasm	N/A
Q9CZU6	CISY_MOUSE	Citrate synthase, mitochondrial	Cs	116	163,91	4,9E+10	51.736	464	37.5	10	14	2	0	0	1,4E+09	3,0E+09	2,1	1,5E+07	1,5E+07	1,5E+07	1,0	32	81	3	0	0	Mitochondrion	Matrix
Q8R0F8	FAHD1_MOUSE	Acylpyruvase FAHD1, mitochondrial	Fahd1	38	50,157	5,0E+09	25.172	227	34.4	3	5	2	0	1	4,0E+08	8,2E+08	2,1	2,3E+08	1,5E+07	1,5E+07	1,0	4	28	3	0	3	Cytoplasm, mitochondrion	Not specified
Q922B1	MACD1_MOUSE	ADP-ribose glycohydrolase MACROD1	Macrod1	31	83,856	4,5E+09	35.294	323	34.7	5	6	0	0	1	3,3E+08	6,6E+08	2,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	25	0	0	1	Nucleus	N/A
Q8C5H8	NAKD2_MOUSE	NAD kinase 2, mitochondrial	Nadk2	97	106,03	9,8E+09	50.858	452	43.8	11	14	1	2	2	2,8E+08	5,5E+08	2,0	1,5E+07	1,5E+07	1,5E+07	1,0	16	72	1	3	5	Mitochondrion	Not specified
P00329	ADH1_MOUSE	Alcohol dehydrogenase 1	Adh1	32	65,795	2,7E+09	39.771	375	34.1	5	8	0	0	1	1,3E+08	2,5E+08	1,9	1,5E+07	1,5E+07	1,5E+07	1,0	6	24	0	0	2	Cytoplasm	N/A
A0A087WP24	A0A087WP24_MOUSE	Protein ABHD14B (Fragment)	Abhd14b	18	7,8632	8,0E+08	14.948	142	21.1	2	3	0	1	1	6,7E+07	1,2E+08	1,8	1,5E+07	1,5E+07	1,5E+07	1,0	2	11	0	1	4	Not specified	N/A
P30837	AL1B1_HUMAN	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	15	22,577	4,7E+09	57.206	517	30.2	12	14	3	7	8	5,0E+08	8,8E+08	1,7	1,5E+07	1,5E+07	1,5E+07	1,0	3	12	0	0	0	Mitochondrion	Matrix
A0A0R4J023	A0A0R4J023_MOUSE	Methylglutaconyl-CoA hydratase, mitochondrial	Auh	33	25,994	2,6E+09	33.338	314	24.5	6	6	0	0	0	1,5E+08	2,3E+08	1,5	1,5E+07	1,5E+07	1,5E+07	1,0	10	23	0	0	0	Mitochondrion	Not specified
J3QMQ8	J3QMQ8_MOUSE	Thioredoxin-disulfide reductase	Txnrd2	40	56,367	3,5E+09	56.375	522	26.2	5	9	0	0	0	4,1E+08	6,1E+08	1,5	1,5E+07	1,5E+07	1,5E+07	1,0	14	26	0	0	0	Not specified	N/A
Q8CFA2	GCST_MOUSE	Aminomethyltransferase, mitochondrial	Amt	45	64,72	2,3E+09	44.008	403	28.5	4	9	1	1	1	2,3E+08	3,2E+08	1,4	1,5E+07	1,5E+07	1,5E+07	1,0	15	23	1	2	4	Mitochondrion	Not specified
Q9D9V3	ECHD1_MOUSE	Ethylmalonyl-CoA decarboxylase	Echdc1	14	16,577	7,2E+08	35.467	322	12.1	2	2	0	0	1	8,3E+07	1,1E+08	1,4	1,5E+07	1,5E+07	1,5E+07	1,0	3	7	0	0	4	Cytoplasm	N/A
P02776	PLF4_HUMAN	Platelet factor 4	PF4	19	15,5	1,1E+09	10.845	101	34.7	3	3	0	1	1	1,4E+08	1,8E+08	1,3	1,5E+07	1,5E+07	1,5E+07	1,0	6	9	0	1	3	Secreted	N/A
O35423	SPYA_MOUSE	Serine--pyruvate aminotransferase, mitochondrial	Agxt	140	223,07	4,6E+10	45.912	414	40.3	12	14	4	1	1	2,2E+09	2,7E+09	1,2	2,3E+08	1,5E+07	1,5E+07	1,0	26	104	6	1	3	Mitochondrion, peroxisome	Matrix
P47199	QOR_MOUSE	Quinone oxidoreductase	Cryz	22	68,649	1,2E+09	35.268	331	30.5	2	6	0	0	0	1,2E+08	1,5E+08	1,2	1,5E+07	1,5E+07	1,5E+07	1,0	2	20	0	0	0	Cytoplasm	N/A
A0A0R4J094	A0A0R4J094_MOUSE	Fumarylacetoacetate hydrolase domain-containing 2A	Fahd2a	35	85,842	3,8E+09	34.676	313	44.7	5	9	0	0	0	2,3E+08	2,8E+08	1,2	1,5E+07	1,5E+07	1,5E+07	1,0	6	29	0	0	0	Not specified	N/A
Q91Z53	GRHPR_MOUSE	Glyoxylate reductase/hydroxypyruvate reductase	Grhpr	34	64,087	3,2E+09	35.328	328	35.1	4	10	0	0	0	1,8E+08	2,0E+08	1,1	1,5E+07	1,5E+07	1,5E+07	1,0	5	29	0	0	0	Not specified	N/A
P24369	PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B	Ppib	54	50,605	3,9E+09	23.713	216	56	10	10	2	0	1	2,7E+08	3,0E+08	1,1	1,5E+07	1,5E+07	1,5E+07	1,0	25	26	2	0	1	Endoplasmic reticulim	N/A
Q8R4N0	CLYBL_MOUSE	Citramalyl-CoA lyase, mitochondrial	Clybl	58	53,632	4,6E+09	37.548	338	45.3	9	13	0	1	0	2,1E+08	2,3E+08	1,1	1,5E+07	1,5E+07	1,5E+07	1,0	13	44	0	1	0	Mitochondrion	Not specified
Q99LP6	GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial	Grpel1	14	32,931	1,0E+09	24.307	217	45.2	4	7	0	0	0	1,3E+08	1,3E+08	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	10	0	0	0	Mitochondrion	Matrix
Q9CXJ1	SYEM_MOUSE	Probable glutamate--tRNA ligase, mitochondrial	Ears2	22	47,266	8,8E+08	58.326	523	18.2	5	8	0	0	1	7,5E+07	7,6E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	16	0	0	1	Mitochondrion	Matrix
Q9CPN7	Q9CPN7_MOUSE	RIKEN cDNA 1810009J06 gene	1810009J06Rik	4	3,4869	8,4E+08	26.503	247	8.1	0	1	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	2	0	0	Not specified	N/A
Q9CPN9	Q9CPN9_MOUSE	RIKEN cDNA 2210010C04 gene	2210010C04Rik	21	5,6156	1,6E+09	26.422	247	4.9	1	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	9	3	3	3	Not specified	N/A
E9PVG8	E9PVG8_MOUSE	RIKEN cDNA 9530053A07 gene	9530053A07Rik	1	3,8642	6,2E+08	280.23	2581	0.9	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Not specified	N/A
P04217	A1BG_HUMAN	Alpha-1B-glycoprotein	A1BG	8	4,8474	5,3E+07	54.253	495	6.1	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	6	Secreted	N/A
Q14CH7	SYAM_MOUSE	Alanine--tRNA ligase, mitochondrial	Aars2	4	9,0374	8,3E+07	106.78	980	4.6	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	Mitochondrion	Not specified
Q9JI39	ABCBA_MOUSE	ATP-binding cassette sub-family B member 10, mitochondrial	Abcb10	7	9,6618	8,3E+07	77.187	715	8.8	0	0	0	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	6	Mitochondrion	Inner membrane
Q9DC29	ABCB6_MOUSE	ATP-binding cassette sub-family B member 6, mitochondrial	Abcb6	2	6,9356	1,6E+08	93.769	842	4	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Cell membrane, mitochondrion, endoplasmic reticulum, Golgi aparatus, endosome	Outer membrane
Q8VI47	MRP2_MOUSE	ATP-binding cassette sub-family C member 2	Abcc2	5	4,5036	4,3E+07	173.67	1543	1.9	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Cell membrane	N/A
A0A0R4J015	A0A0R4J015_MOUSE	Canalicular multispecific organic anion transporter 2	Abcc3	2	3,5722	1,7E+07	169.15	1522	2.4	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Not specified	N/A
Q91ZH7	ABHD3_MOUSE	Phospholipase ABHD3	Abhd3	9	5,5576	5,0E+07	46.232	411	6.1	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	8	Other	N/A
P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	5	3,4653	3,4E+08	70.389	655	10.1	5	7	4	5	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	2	Mitochondrion	Inner membrane
A0A5F9ZHJ0	A0A5F9ZHJ0_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	2	7,7742	1,5E+08	35.496	337	11.6	3	6	4	4	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	2	Mitochondrion	Not specified
Q8BGG9	ACNT2_MOUSE	Acyl-coenzyme A amino acid N-acyltransferase 2	Acnat2	4	3,9072	5,4E+07	46.595	420	15.5	1	2	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	2	Peroxisome	N/A
P58137	ACOT8_MOUSE	Acyl-coenzyme A thioesterase 8	Acot8	37	60,308	1,8E+09	35.827	320	30	1	7	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	35	0	0	0	Peroxisome	N/A
Q9R0X4	ACOT9_MOUSE	Acyl-coenzyme A thioesterase 9, mitochondrial	Acot9	9	12,687	5,5E+08	50.56	439	14.4	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	8	0	0	0	Mitochondrion	Not specified
A2A848	A2A848_MOUSE	Peroxisomal acyl-coenzyme A oxidase 1 (Fragment)	Acox1	9	33,224	2,6E+09	70.03	625	65.6	22	32	11	17	21	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	6	0	0	1	Peroxisome	N/A
D3Z2N6	D3Z2N6_MOUSE	Peroxisomal acyl-coenzyme A oxidase 3 (Fragment)	Acox3	2	2,9748	6,9E+07	9.4506	83	16.9	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Not specified	N/A
Q3URE1	ACSF3_MOUSE	Malonate--CoA ligase ACSF3, mitochondrial	Acsf3	35	49,247	2,1E+09	65.076	583	32.2	0	11	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	31	0	2	2	Mitochondrion	Not specified
Q6NUN0	ACSM5_HUMAN	Acyl-coenzyme A synthetase ACSM5, mitochondrial	ACSM5	4	3,1041	3,5E+08	64.759	579	19.9	6	9	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	0	0	Mitochondrion	Matrix
Q8BFZ3	ACTBL_MOUSE	Beta-actin-like protein 2	Actbl2	8	3,2414	1,9E+09	42.004	376	22.6	0	2	0	3	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	7	Cytoplasm	N/A
Q9D0L4	ADCK1_MOUSE	AarF domain-containing protein kinase 1	Adck1	4	6,0434	7,8E+07	59.735	525	7.2	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Secreted	N/A
E0CXW2	E0CXW2_MOUSE	Uncharacterized aarF domain-containing protein kinase 5	Adck5	18	19,752	2,2E+08	64.421	567	16.6	0	0	0	1	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	16	Not specified	N/A
Q3MIX3	ADCK5_HUMAN	Uncharacterized aarF domain-containing protein kinase 5	ADCK5	5	2,9816	3,4E+07	65.827	580	3.3	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Other	N/A
A0A286YCD7	A0A286YCD7_MOUSE	Adenosine kinase (Fragment)	Adk	2	6,5805	2,7E+07	22.914	205	10.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	Not specified	N/A
Q920A7	AFG31_MOUSE	AFG3-like protein 1	Afg3l1	10	8,205	2,7E+08	87.046	789	9.1	0	0	0	0	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	10	Mitochondrion	Inner membrane
Q9ESW4	AGK_MOUSE	Acylglycerol kinase, mitochondrial	Agk	4	6,3314	6,1E+07	46.975	421	13.3	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Mitochondrion	Inner membrane, IMS
Q9BSE5	SPEB_HUMAN	Agmatinase, mitochondrial	AGMAT	2	4,6902	2,6E+07	37.66	352	13.4	2	2	1	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	1	Mitochondrion	Not specified
Q9D1E8	PLCE_MOUSE	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	Agpat5	9	5,3204	1,0E+08	42.202	365	7.1	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	9	Nucleus, mitochondrion, endoplasmic reticulum	Not specified
P50247	SAHH_MOUSE	Adenosylhomocysteinase	Ahcy	3	4,9542	2,5E+07	47.688	432	6.2	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Cytoplasm	N/A
P70694	DHB5_MOUSE	Estradiol 17 beta-dehydrogenase 5	Akr1c6	2	4,3202	7,0E+07	37.047	323	9.3	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	Not specified	N/A
A0A0R4J0X2	A0A0R4J0X2_MOUSE	5-aminolevulinate synthase	Alas1	5	9,3072	1,3E+08	70.96	641	6.9	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	0	Mitochondrion	Matrix
P07724	ALBU_MOUSE	Albumin	Alb	17	17,36	3,9E+08	68.692	608	13.3	2	5	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	14	0	0	2	Secreted	N/A
P00352	AL1A1_HUMAN	Retinal dehydrogenase 1	ALDH1A1	3	4,8471	4,1E+09	54.861	501	5.6	4	4	1	4	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	Cytoplasm	N/A
P24549	AL1A1_MOUSE	Retinal dehydrogenase 1	Aldh1a1	4	3,394	5,3E+07	54.467	501	9.4	3	3	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cytoplasm	N/A
P05091	ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial	ALDH2	3	6,2308	2,6E+08	56.381	517	49.1	12	19	8	15	15	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Mitochondrion	Matrix
P16157	ANK1_HUMAN	Ankyrin-1	ANK1	17	15,179	1,5E+08	206.26	1881	5.2	0	0	0	0	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	17	Cytoplasm, sarcoplasmic reticulum	N/A
Q6P1H6	ANKL2_MOUSE	Ankyrin repeat and LEM domain-containing protein 2	Ankle2	1	3,3154	1,6E+09	106.2	964	2.6	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	Endoplasmic reticulim	N/A
A0A0C4DG84	A0A0C4DG84_HUMAN	Anthrax toxin receptor 2	ANTXR2	1	3,2984	1,6E+07	26.111	245	5.7	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	Other	N/A
H0YMW4	H0YMW4_HUMAN	Annexin	ANXA2	3	4,686	3,5E+07	41.899	367	12	0	1	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted	N/A
Q9D7N9	APMAP_MOUSE	Adipocyte plasma membrane-associated protein	Apmap	5	5,3513	8,8E+07	46.434	415	12.3	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Other	N/A
Q00623	APOA1_MOUSE	Apolipoprotein A-I	Apoa1	3	3,4722	1,3E+08	30.615	264	10.6	1	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	Secreted	N/A
E9Q1Y3	E9Q1Y3_MOUSE	Apolipoprotein B-100 (Fragment)	Apob	14	9,8758	3,3E+08	503.9	4456	3.7	1	4	0	11	13	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	7	5	Not specified	N/A
P55056	APOC4_HUMAN	Apolipoprotein C-IV	APOC4	5	3,5093	7,4E+07	14.553	127	18.1	0	1	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Secreted	N/A
P08226	APOE_MOUSE	Apolipoprotein E	Apoe	13	22,76	4,3E+08	35.866	311	20.3	2	5	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	9	0	0	3	Secreted	N/A
Q9DCZ4	MIC26_MOUSE	MICOS complex subunit Mic26	Apoo	12	9,6636	7,8E+08	22.604	198	24.7	1	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	2	9	Secreted, mitochondrion, endoplasmic reticulum, Golgi aparatus	Inner membrane
Q02013	AQP1_MOUSE	Aquaporin-1	Aqp1	9	4,7903	2,2E+08	28.793	269	10.8	0	0	0	2	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	6	3	Cell membrane	N/A
C9J1Z8	C9J1Z8_HUMAN	ADP-ribosylation factor 5 (Fragment)	ARF5	2	3,8425	4,1E+07	17.107	150	6.7	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	Not specified	N/A
A0A0U1RPP2	A0A0U1RPP2_MOUSE	Rho guanine nucleotide exchange factor 1 (Fragment)	Arhgef1	2	3,2458	4,5E+07	21.57	192	14.6	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	Not specified	N/A
A0A0N4SVB8	A0A0N4SVB8_MOUSE	ADP-ribosylation factor-like protein 8B	Arl8b	4	5,9981	1,3E+08	15.985	138	23.2	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	1	Cytoplasm, endolysosomal compartment	N/A
Q9NVT9	ARMC1_HUMAN	Armadillo repeat-containing protein 1	ARMC1	2	4,2916	6,7E+08	31.28	282	14.5	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	Cytoplasm, mitochondrion	Outer membrane
H7C0A3	H7C0A3_HUMAN	ARPC4-TTLL3 readthrough (Fragment)	ARPC4-TTLL3	4	3,0649	4,5E+07	19.288	167	11.4	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	3	Other	N/A
Q9WV54	ASAH1_MOUSE	Acid ceramidase	Asah1	3	2,975	2,1E+07	44.669	394	4.8	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted, lysosome	N/A
J3QPT6	J3QPT6_MOUSE	Asialoglycoprotein receptor 1 (Fragment)	Asgr1	5	8,317	1,6E+08	15.262	132	10.6	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Not specified	N/A
Q8CBM2	Q8CBM2_MOUSE	Aspartyl/asparaginyl beta-hydroxylase	Asph	15	15,797	2,9E+08	75.127	658	17.9	0	0	0	1	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	14	Other	N/A
A0A494B9Y0	A0A494B9Y0_MOUSE	Outer mitochondrial transmembrane helix translocase	Atad1	20	11,657	2,3E+08	36.244	322	22	0	0	0	1	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	19	Mitochondrion	Not specified
Q9EPE9	AT131_MOUSE	Endoplasmic reticulum transmembrane helix translocase	Atp13a1	6	9,4508	5,3E+07	132.39	1200	4.4	0	0	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	Endoplasmic reticulim	N/A
A0A0A6YX05	A0A0A6YX05_MOUSE	Sodium/potassium-transporting ATPase subunit beta (Fragment)	Atp1b1	10	21,877	1,7E+08	15.253	132	18.9	0	1	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	1	7	Cell membrane	N/A
F8W0P7	F8W0P7_HUMAN	ATP synthase subunit beta, mitochondrial (Fragment)	ATP5F1B	4	3,1154	4,6E+08	28.392	270	53.7	9	10	8	8	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	0	0	Mitochondrion	Not specified
A0A1Y7VLP0	A0A1Y7VLP0_MOUSE	ATP synthase subunit ATP5MPL, mitochondrial (Fragment)	Atp5mpl	32	3,3452	6,0E+08	6.5608	57	14	1	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	5	4	8	9	Mitochondrion	Not specified
A0A0R4J1C5	A0A0R4J1C5_MOUSE	ATP synthase mitochondrial F1 complex assembly factor 2	Atpaf2	5	8,1243	1,3E+08	34.287	298	11.1	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	4	0	0	0	Mitochondrion	Not specified
A0A1B0GS13	A0A1B0GS13_MOUSE	Apoptosis regulator BAX (Fragment)	Bax	2	3,4237	6,6E+07	12.513	114	22.8	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	Not specified	N/A
D3Z7R0	D3Z7R0_MOUSE	Protein-serine/threonine kinase (Fragment)	Bckdk	10	32,753	8,9E+08	24.351	214	38.3	0	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	0	0	0	Mitochondrion	Matrix
Q9CZP5	BCS1_MOUSE	Mitochondrial chaperone BCS1	Bcs1l	5	6,0154	4,2E+07	47.406	418	10	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Mitochondrion	Inner membrane
P21810	PGS1_HUMAN	Biglycan	BGN	3	3,0612	3,8E+07	41.654	368	3	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted	N/A
Q9D8S9	BOLA1_MOUSE	BolA-like protein 1	Bola1	2	28,582	1,2E+08	14.379	137	16.1	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Mitochondrion	Not specified
P43251	BTD_HUMAN	Biotinidase	BTD	12	8,7125	1,5E+08	61.132	543	4.2	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	4	8	Secreted	N/A
P98086	C1QA_MOUSE	Complement C1q subcomponent subunit A	C1qa	6	5,5273	1,0E+08	25.974	245	15.5	2	2	2	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	3	0	0	Secreted	N/A
P14106	C1QB_MOUSE	Complement C1q subcomponent subunit B	C1qb	14	18,906	3,1E+08	26.717	253	27.3	5	1	2	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	12	0	2	0	0	Secreted	N/A
Q02105	C1QC_MOUSE	Complement C1q subcomponent subunit C	C1qc	15	8,205	1,6E+08	25.991	246	15	3	0	2	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	11	0	4	0	0	Secreted	N/A
Q9NZP8	C1RL_HUMAN	Complement C1r subcomponent-like protein	C1RL	6	7,2578	7,3E+07	53.498	487	9.4	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	Secreted	N/A
P01029	CO4B_MOUSE	Complement C4-B	C4b	6	11,748	1,4E+08	192.91	1738	6.2	4	6	0	7	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	5	Secreted	N/A
P20851	C4BPB_HUMAN	C4b-binding protein beta chain	C4BPB	3	7,6209	2,4E+08	28.357	252	10.3	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Secreted	N/A
P13671	CO6_HUMAN	Complement component C6	C6	13	9,915	1,2E+08	104.79	934	5.9	0	1	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	11	Secreted	N/A
P10643	CO7_HUMAN	Complement component C7	C7	3	2,9662	3,9E+07	93.517	843	3.4	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted	N/A
P07360	CO8G_HUMAN	Complement component C8 gamma chain	C8G	1	3,1167	3,3E+07	22.277	202	8.4	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Secreted	N/A
P23589	CAH5A_MOUSE	Carbonic anhydrase 5A, mitochondrial	Ca5a	10	16,541	2,3E+08	34.072	299	19.7	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	0	0	0	Mitochondrion	Not specified
Q9NZT1	CALL5_HUMAN	Calmodulin-like protein 5	CALML5	3	4,5254	8,7E+07	15.892	146	15.8	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	Not specified	N/A
P14211	CALR_MOUSE	Calreticulin	Calr	6	7,6878	2,1E+08	47.994	416	13.7	0	4	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	1	0	0	Secreted, cytoplasm, nucleus, endoplasmic/Sarcoplasmic reticula	N/A
Q9H257	CARD9_HUMAN	Caspase recruitment domain-containing protein 9	CARD9	3	4,1342	4,7E+07	62.24	536	2.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	Cytoplasm	N/A
A2AIV8	CARD9_MOUSE	Caspase recruitment domain-containing protein 9	Card9	3	2,9897	9,1E+07	62.461	536	2.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	1	0	0	0	Cytoplasm	N/A
Q8BYM8	SYCM_MOUSE	Probable cysteine--tRNA ligase, mitochondrial	Cars2	1	3,9078	4,4E+07	61.271	551	2.5	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Mitochondrion	Matrix
Q9D024	CCD47_MOUSE	PAT complex subunit CCDC47	Ccdc47	9	8,8245	1,6E+08	55.843	483	7.2	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	6	Endoplasmic reticulim	N/A
Q3URS9	MITOK_MOUSE	Mitochondrial potassium channel	Ccdc51	22	17,547	4,9E+08	45.132	406	21.2	0	0	0	0	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	22	Mitochondrion	Inner membrane
D6RFL4	D6RFL4_HUMAN	Monocyte differentiation antigen CD14 (Fragment)	CD14	12	22,801	3,4E+08	23.313	213	22.5	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	12	Secreted, cell membrane, Golgi apparatus	N/A
O43866	CD5L_HUMAN	CD5 antigen-like	CD5L	10	19,128	6,9E+08	38.087	347	31.7	2	5	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	6	0	0	2	Secreted, cytoplasm	N/A
D3Z4M2	D3Z4M2_MOUSE	Ceramide synthase 2 (Fragment)	Cers2	8	3,6486	1,0E+08	15.505	130	23.1	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	7	Nucleus	N/A
Q8VCC2	EST1_MOUSE	Liver carboxylesterase 1	Ces1	16	28,692	4,8E+08	62.679	565	23.4	0	9	1	4	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	0	2	4	Cytoplasm, endoplasmic reticulum	N/A
H3BL34	H3BL34_MOUSE	Carboxylic ester hydrolase	Ces1e	6	6,1364	9,2E+07	61.51	561	10.9	0	4	1	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	4	Not specified	N/A
Q8BK48	EST2E_MOUSE	Pyrethroid hydrolase Ces2e	Ces2e	21	20,959	3,3E+08	62.317	559	16.1	0	4	0	3	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	7	0	3	11	Microsomes	N/A
Q8VCU1	EST3B_MOUSE	Carboxylesterase 3B	Ces3b	6	5,6929	1,8E+08	63.352	571	13.7	4	6	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	Endoplasmic reticulim	N/A
P11597	CETP_HUMAN	Cholesteryl ester transfer protein	CETP	11	12,637	2,8E+08	54.756	493	14.4	0	0	0	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	10	Secreted	N/A
H3BK95	H3BK95_MOUSE	Complement factor B (Fragment)	Cfb	4	11,059	4,6E+07	33.506	296	14.9	2	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	0	0	0	0	Secreted	N/A
P08603	CFAH_HUMAN	Complement factor H	CFH	19	15,984	4,1E+08	139.09	1231	6.8	1	1	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	3	14	Secreted	N/A
P18760	COF1_MOUSE	Cofilin-1	Cfl1	3	6,4892	8,2E+07	18.559	166	28.9	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	Cytoplasm, nucleus	N/A
Q05BF0	Q05BF0_MOUSE	Chchd1 protein	Chchd1	11	17,573	1,2E+09	8.3125	70	40	3	0	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	0	1	0	0	Not specified	N/A
A0A0R4J058	A0A0R4J058_MOUSE	Chitinase domain-containing protein 1	Chid1	15	32,422	4,3E+08	35.54	310	30.3	8	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	15	0	0	0	0	Not specified	N/A
B0R091	B0R091_MOUSE	Calcineurin B homologous protein 1	Chp1	3	3,584	2,9E+07	21.997	191	12	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Not specified	N/A
Z4YKM2	Z4YKM2_MOUSE	CDGSH iron-sulfur domain-containing protein 3, mitochondrial	Cisd3	5	4,3318	1,6E+08	13.155	115	20.9	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	0	1	Mitochondrion	Not specified
Q60649	CLPB_MOUSE	Caseinolytic peptidase B protein homolog	Clpb	2	3,7778	1,8E+07	76.003	677	3.8	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Mitochondrion	IMS
A0A1W2P729	A0A1W2P729_MOUSE	Protein canopy homolog 2 (Fragment)	Cnpy2	3	2,9388	6,4E+07	15.316	136	8.8	0	1	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	1	0	0	Not specified	N/A
Q12860	CNTN1_HUMAN	Contactin-1	CNTN1	13	7,6592	1,2E+08	113.32	1018	5.1	0	0	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	13	Cell membrane	N/A
Q9D2R6	COA3_MOUSE	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	Coa3	5	3,3107	7,3E+07	11.987	108	18.5	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Mitochondrion	Inner membrane
Q04857	CO6A1_MOUSE	Collagen alpha-1(VI) chain	Col6a1	6	5,9845	5,3E+07	108.49	1025	3.1	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	Secreted	N/A
P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain	COL6A3	8	8,5481	7,3E+07	343.67	3177	2.1	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	Secreted	N/A
D3YWD1	D3YWD1_MOUSE	Collagen, type VI, alpha 3 (Fragment)	Col6a3	3	4,9589	4,0E+07	185.73	1703	1.6	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Not specified	N/A
O88587	COMT_MOUSE	Catechol O-methyltransferase	Comt	18	15,998	3,7E+08	29.486	265	22.6	0	3	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	4	9	Cell membrane, cytoplasm	N/A
Q566J8	COQ8B_MOUSE	Atypical kinase COQ8B, mitochondrial	Coq8b	2	7,4445	8,5E+07	59.231	533	6.2	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Cell membrane, cytoplasm, mitochondrion	Not specified
P48771	CX7A2_MOUSE	Cytochrome c oxidase subunit 7A2, mitochondrial	Cox7a2	22	70,142	6,6E+08	9.2908	83	27.7	1	2	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	6	5	8	Mitochondrion	Inner membrane
P36551	HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	11	24,109	2,8E+08	50.151	454	12.3	1	5	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	9	0	0	1	Mitochondrion	IMS
H7BX88	H7BX88_MOUSE	Carnitine O-acetyltransferase	Crat	7	7,3163	2,3E+08	68.644	605	8.9	4	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	2	0	0	0	Not specified	N/A
G3XAM7	G3XAM7_HUMAN	Catenin (Cadherin-associated protein), alpha 1, 102kDa, isoform CRA_a	CTNNA1	6	6,4356	1,3E+08	92.721	841	7	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	Cell membrane, cytoplasm	N/A
D3YUH4	D3YUH4_MOUSE	Catenin beta-1 (Fragment)	Ctnnb1	3	4,7738	4,9E+07	19.287	174	17.2	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Not specified	N/A
D3Z2H7	D3Z2H7_MOUSE	Catenin delta-1	Ctnnd1	11	6,7353	1,5E+08	67.935	609	4.4	0	1	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	9	Not specified	N/A
P10605	CATB_MOUSE	Cathepsin B	Ctsb	6	14,888	2,3E+08	37.279	339	18.3	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	0	Secreted, cell membrane, lysosome	N/A
Q61093	CY24B_MOUSE	Cytochrome b-245 heavy chain	Cybb	5	3,1193	7,6E+07	65.304	570	3.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Cell membrane, endoplasmic reticulum	N/A
P27786	CP17A_MOUSE	Steroid 17-alpha-hydroxylase/17,20 lyase	Cyp17a1	7	8,6455	1,0E+08	57.637	507	16.8	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	Endoplasmic reticulim, microsomes	N/A
P15392	CP2A4_MOUSE	Cytochrome P450 2A4	Cyp2a4	12	7,2461	1,4E+08	56.781	494	28.7	1	2	0	7	14	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	10	Endoplasmic reticulim, microsomes	N/A
Q569X9	Q569X9_MOUSE	Cytochrome P450, family 2, subfamily c, polypeptide 67	Cyp2c67	6	3,7228	6,5E+07	56.144	491	25.7	2	6	2	7	12	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	4	Not specified	N/A
K7N6C2	K7N6C2_MOUSE	Cytochrome P450, family 2, subfamily c, polypeptide 68	Cyp2c68	5	6,376	1,3E+08	56.057	491	29.1	2	7	1	6	11	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Not specified	N/A
O54749	CP2J5_MOUSE	Cytochrome P450 2J5	Cyp2j5	10	8,9075	1,2E+08	57.783	501	9.8	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	9	Endoplasmic reticulim, microsomes	N/A

O09158	CP3AP_MOUSE	**Cytochrome P450 3A25**	Cyp3a25	7	6,8617	5,8E+07	58.121	503	7.6	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	Endoplasmic reticulim, microsomes	N/A
A2A977	A2A977_MOUSE	**Cytochrome P450 4A10**	Cyp4a10	8	10,604	7,2E+07	57.188	499	18.2	0	0	0	0	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	*Not specified*	N/A
Q99N18	Q99N18_MOUSE	**Cytochrome P450 CYP4F15**	Cyp4f15	4	7,2649	5,0E+07	61.266	534	7.1	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	*Not specified*	N/A
Q8K0C4	CP51A_MOUSE	**Lanosterol 14-alpha demethylase**	Cyp51a1	3	4,216	3,6E+07	56.775	503	7.4	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Endoplasmic reticulim, microsomes	N/A
A0A0R4J0N7	A0A0R4J0N7_MOUSE	**7-alpha-hydroxycholest-4-en-3-one 12-alpha-hydroxylase**	Cyp8b1	12	8,0497	8,1E+07	57.705	500	10	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	12	Endoplasmic reticulim	N/A
A0A087WR78	A0A087WR78_MOUSE	**D-2-hydroxyglutarate dehydrogenase, mitochondrial (Fragment)**	D2hgdh	1	8,947	5,6E+07	24.287	219	7.3	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Mitochondrion	*Not specified*
F5H895	F5H895_HUMAN	**Defender against cell death 1**	DAD1	8	2,9455	8,7E+07	7.2883	65	18.5	0	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	2	5	Endoplasmic reticulim	N/A
D3Z563	D3Z563_MOUSE	**Acyl-CoA-binding protein**	Dbi	2	2,9909	1,0E+08	7.2373	63	28.6	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
Q9CWT6	DDX28_MOUSE	**Probable ATP-dependent RNA helicase DDX28**	Ddx28	3	12,817	1,3E+08	59.514	540	5.6	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	Nucleus, mitochondrion	Matrix
W4VSN6	W4VSN6_MOUSE	**Alpha-defensin 22**	Defa22	1	3,9594	3,8E+07	10.535	93	15.1	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	Secreted	N/A
Q9QX60	DGUOK_MOUSE	**Deoxyguanosine kinase, mitochondrial**	Dguok	3	5,5326	1,2E+08	32.281	277	10.8	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	2	Cytoplasm, mitochondrion	*Not specified*
O88455	DHCR7_MOUSE	**7-dehydrocholesterol reductase**	Dhcr7	7	3,1326	2,5E+08	53.918	471	4	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	4	Endoplasmic reticulim	N/A
Q9CXR1	DHRS7_MOUSE	**Dehydrogenase/reductase SDR family member 7**	Dhrs7	5	3,8755	4,1E+07	38.167	338	8.9	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	*Not specified*	N/A
Z4YKT6	Z4YKT6_MOUSE	**Dehydrogenase/reductase SDR family member 7B**	Dhrs7b	10	11,179	7,8E+07	33.225	308	12	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	10	*Not specified*	N/A
P11532	DMD_HUMAN	**Dystrophin**	DMD	3	6,0858	7,2E+07	426.74	3685	1.1	0	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	1	Cell membrane, cytoplasm	N/A
P63037	DNJA1_MOUSE	**DnaJ homolog subfamily A member 1**	Dnaja1	4	4,3164	4,4E+07	44.868	397	6.3	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Cytoplasm, nucleus, mitochondrion, microsomes	*Not specified*
Q99KV1	DJB11_MOUSE	**DnaJ homolog subfamily B member 11**	Dnajb11	4	6,9936	3,5E+07	40.555	358	12.8	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	Endoplasmic reticulim	N/A
Q08554	DSC1_HUMAN	**Desmocollin-1**	DSC1	4	4,2398	6,4E+07	99.986	894	3.2	0	0	1	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	1	1	2	Cell membrane	N/A
Q02413	DSG1_HUMAN	**Desmoglein-1**	DSG1	17	12,354	4,3E+08	113.75	1049	6.6	1	2	2	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	4	3	2	5	Cell membrane	N/A
P15924	DESP_HUMAN	**Desmoplakin**	DSP	15	17,191	1,7E+08	331.77	2871	2.6	0	2	1	1	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	2	1	9	Cell membrane, cytoplasm	N/A
P97930	KTHY_MOUSE	**Thymidylate kinase**	Dtymk	6	8,2221	2,4E+08	23.914	212	21.7	1	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	*Not specified*	N/A
P97425	ECP2_MOUSE	**Eosinophil cationic protein 2**	Ear2	3	6,8199	2,5E+07	17.62	156	14.1	3	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	Cytoplasm	N/A
Q9NTX5	ECHD1_HUMAN	**Ethylmalonyl-CoA decarboxylase**	ECHDC1	6	8,1392	4,3E+08	33.698	307	7.5	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	4	0	0	0	Cytoplasm	N/A
Q16610	ECM1_HUMAN	**Extracellular matrix protein 1**	ECM1	5	4,1077	4,3E+07	60.673	540	3.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Secreted	N/A
Q9JMG1	EDF1_MOUSE	**Endothelial differentiation-related factor 1**	Edf1	8	20,286	1,8E+08	16.369	148	29.7	3	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	0	0	0	0	Cytoplasm, nucleus	N/A
Q9WVK4	EHD1_MOUSE	**EH domain-containing protein 1**	Ehd1	4	5,3475	4,4E+07	60.602	534	7.5	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cell membrane, cytoplasm, endosome	N/A
Q9NZN3	EHD3_HUMAN	**EH domain-containing protein 3**	EHD3	8	5,3692	5,2E+07	60.886	535	6.5	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	5	Cell membrane, cytoplasm, endosome	N/A
Q9JLJ4	ELOV2_MOUSE	**Elongation of very long chain fatty acids protein 2**	Elovl2	6	3,4237	2,4E+08	34.207	292	5.8	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	Endoplasmic reticulim	N/A
Z4YJW0	Z4YJW0_MOUSE	**ER membrane protein complex subunit 1**	Emc1	21	19,568	3,3E+08	111.56	997	10.8	0	0	0	1	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	20	Endoplasmic reticulim	N/A
Q9CRD2	EMC2_MOUSE	**ER membrane protein complex subunit 2**	Emc2	7	12,607	1,1E+08	34.934	297	21.5	0	0	0	0	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	Cytoplasm, endoplasmic reticulum	N/A
Q9P0I2	EMC3_HUMAN	**ER membrane protein complex subunit 3**	EMC3	5	7,097	1,2E+08	29.952	261	16.9	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Endoplasmic reticulim	N/A
Q9EP72	EMC7_MOUSE	**ER membrane protein complex subunit 7**	Emc7	13	7,2085	2,1E+08	26.31	241	16.6	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	4	9	Endoplasmic reticulim	N/A
M0R1B0	M0R1B0_HUMAN	**ER membrane protein complex subunit 8 (Fragment)**	EMC8	6	4,2894	8,5E+07	11.728	100	25	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	*Not specified*	N/A
O08600	NUCG_MOUSE	**Endonuclease G, mitochondrial**	Endog	4	6,2689	1,5E+07	32.19	294	7.8	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	2	Mitochondrion	*Not specified*
P17182	ENOA_MOUSE	**Alpha-enolase**	Eno1	3	4,9452	1,3E+08	47.14	434	6.9	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Cell membrane, cytoplasm	N/A
Q91X78	ERLN1_MOUSE	**Erlin-1**	Erlin1	2	3,7728	1,5E+07	39.182	348	14.1	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Endoplasmic reticulim	N/A
E5RHW4	E5RHW4_HUMAN	**Erlin-2 (Fragment)**	ERLIN2	14	10,828	4,9E+08	37.725	338	13.9	0	0	0	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	13	*Other*	N/A
Q9D1Q6	ERP44_MOUSE	**Endoplasmic reticulum resident protein 44**	Erp44	2	4,4371	3,4E+08	46.852	406	4.4	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Endoplasmic reticulim	N/A
Q6IPR1	ETFR1_HUMAN	**Electron transfer flavoprotein regulatory factor 1**	ETFRF1	6	6,0149	3,2E+08	10.864	90	17.8	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	0	Mitochondrion	*Not specified*
P00748	FA12_HUMAN	**Coagulation factor XII**	F12	10	5,7217	1,4E+08	67.791	615	4.4	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	9	Secreted	N/A
O08914	FAAH1_MOUSE	**Fatty-acid amide hydrolase 1**	Faah	17	22,871	1,1E+09	63.221	579	23.3	0	2	0	0	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	14	Endoplasmic reticulim, Golgi aparatus	N/A
Q96CS3	FAF2_HUMAN	**FAS-associated factor 2**	FAF2	4	5,2742	3,3E+07	52.623	445	6.7	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cytoplasm, endoplasmic reticulum	N/A
Q9D6U8	F162A_MOUSE	**Protein FAM162A**	Fam162a	3	4,181	3,5E+07	17.725	155	20.6	1	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	2	Mitochondrion	*Not specified*
Q99M01	SYFM_MOUSE	**Phenylalanine--tRNA ligase, mitochondrial**	Fars2	15	57,44	9,6E+08	52.336	451	16	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	13	0	0	0	Mitochondrion	Matrix
P19096	FAS_MOUSE	**Fatty acid synthase**	Fasn	11	17,759	1,4E+08	272.43	2504	5.3	0	2	0	0	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	9	Cytoplasm	N/A
Q922E6	FAKD2_MOUSE	**FAST kinase domain-containing protein 2, mitochondrial**	Fastkd2	2	4,6547	1,8E+08	78.947	689	5.2	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Mitochondrion	Matrix
B1AHL2	B1AHL2_HUMAN	**Fibulin-1**	FBLN1	7	3,9298	7,2E+07	78.329	721	8.9	0	0	0	2	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	6	Secreted	N/A
A0A0B4J1G1	A0A0B4J1G1_MOUSE	**Fc receptor, IgG, low affinity IIb**	Fcgr2b	12	9,6129	4,4E+08	32.976	293	19.1	4	0	0	1	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	0	0	2	0	*Not specified*	N/A
A0A0B4J1G0	FCGR4_MOUSE	**Low affinity immunoglobulin gamma Fc region receptor IV**	Fcgr4	5	4,6834	1,2E+08	28.398	249	8.8	1	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	0	3	Cell membrane	N/A
Q15485	FCN2_HUMAN	**Ficolin-2**	FCN2	11	19,435	3,8E+08	34.001	313	18.2	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	11	Secreted	N/A
Q920E5	FPPS_MOUSE	**Farnesyl pyrophosphate synthase**	Fdps	7	12,661	2,2E+08	40.581	353	15.3	1	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	6	0	0	0	Cytoplasm	N/A
P46656	ADX_MOUSE	**Adrenodoxin, mitochondrial**	Fdx1	9	8,4814	2,9E+08	20.123	188	20.7	1	2	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	4	4	0	0	Mitochondrion	Matrix
Q9UGM5	FETUB_HUMAN	**Fetuin-B**	FETUB	8	3,4558	3,9E+08	42.054	382	4.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	7	Secreted	N/A
P02671	FIBA_HUMAN	**Fibrinogen alpha chain**	FGA	22	18,164	1,7E+08	94.972	866	7.9	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	22	Secreted	N/A
Q8VCM7	FIBG_MOUSE	**Fibrinogen gamma chain**	Fgg	11	10,45	3,0E+08	49.391	436	9.4	1	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	9	0	0	1	Secreted	N/A
C9JEU5	C9JEU5_HUMAN	**Fibrinogen gamma chain**	FGG	8	5,5605	5,1E+07	50.322	445	10.8	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	Secreted	N/A
P45878	FKBP2_MOUSE	**Peptidyl-prolyl cis-trans isomerase FKBP2**	Fkbp2	5	3,0625	2,3E+08	15.344	140	8.6	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	3	0	0	0	Endoplasmic reticulim	N/A
Q8R123	FAD1_MOUSE	**FAD synthase**	Flad1	3	12,205	1,4E+08	54.766	492	11.8	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Cytoplasm	N/A
Q5D862	FILA2_HUMAN	**Filaggrin-2**	FLG2	9	7,1654	1,1E+08	248.07	2391	0.5	0	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	1	1	5	Cytoplasm	N/A
O08917	FLOT1_MOUSE	**Flotillin-1**	Flot1	25	20,778	3,5E+08	47.513	428	22.2	0	0	0	1	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	23	Cell membrane, endosome	N/A
Q5SS83	Q5SS83_MOUSE	**Flotillin**	Flot2	15	18,678	1,5E+08	47.116	428	24.8	0	0	0	0	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	15	Endosome	N/A
Q9CR13	FMC1_MOUSE	**Protein FMC1 homolog**	Fmc1	8	13,528	3,7E+08	12.694	113	13.3	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	3	Mitochondrion	*Not specified*
Q8VHG0	FMO4_MOUSE	**Dimethylaniline monooxygenase [N-oxide-forming] 4**	Fmo4	17	9,7753	2,7E+08	63.791	560	9.8	0	1	0	2	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	14	Endoplasmic reticulim, microsomes	N/A
F6TLV3	F6TLV3_MOUSE	**Fibronectin type-III domain-containing protein 3A (Fragment)**	Fndc3a	3	4,9337	5,2E+07	127.14	1154	2.3	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	*Not specified*	N/A
Q5CZC0	FSIP2_HUMAN	**Fibrous sheath-interacting protein 2**	FSIP2	2	3,1444	1,5E+08	780.6	6907	0.3	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	*Not specified*	N/A
A0A1B0GR60	A0A1B0GR60_MOUSE	**Ferritin**	Ftl1	2	3,6019	1,6E+07	17.999	160	10	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	*Not specified*	N/A
Q9CR59	G45IP_MOUSE	**Growth arrest and DNA damage-inducible proteins-interacting protein 1**	Gadd45gip1	7	4,6748	2,7E+08	25.82	222	12.2	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	7	0	0	0	Nucleus, mitochondrion	*Not specified*
Q8BHN3	GANAB_MOUSE	**Neutral alpha-glucosidase AB**	Ganab	15	31,794	6,3E+08	106.91	944	12.3	0	8	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	14	0	0	1	Endoplasmic reticulim, Golgi aparatus	N/A
E7EUT5	E7EUT5_HUMAN	**Glyceraldehyde-3-phosphate dehydrogenase**	GAPDH	2	3,5383	1,9E+07	27.87	260	20.4	1	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	1	*Not specified*	N/A
Q3TLZ6	Q3TLZ6_MOUSE	**Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial**	Gatb	2	3,1006	8,9E+07	52.541	472	3	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	Mitochondrion	*Not specified*
P21614	VTDB_MOUSE	**Vitamin D-binding protein**	Gc	5	10,976	1,6E+08	53.6	476	14.3	0	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	1	Secreted	N/A
P02774	VTDB_HUMAN	**Vitamin D-binding protein**	GC	3	3,4202	4,4E+07	52.917	474	6.1	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted	N/A
P28230	CXB1_MOUSE	**Gap junction beta-1 protein**	Gjb1	5	8,9165	8,1E+07	32.003	283	4.9	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Cell membrane	N/A
J3KMU5	J3KMU5_MOUSE	**Glycolipid transfer protein domain-containing protein 2**	Gltpd2	2	5,1387	3,3E+07	22.03	207	15	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	*Not specified*	N/A
P15105	GLNA_MOUSE	**Glutamine synthetase**	Glul	14	12,178	2,6E+08	42.119	373	12.3	0	2	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	1	9	Cell membrane, cytoplasm, mitochondrion, microsomes	*Not specified*
A0A1B0GT66	A0A1B0GT66_MOUSE	**Predicted gene, 49369 (Fragment)**	Gm49369	13	6,0089	3,5E+08	29.299	273	15	1	3	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	6	0	2	4	*Not specified*	N/A
D3YVW2	D3YVW2_MOUSE	**Golgi integral membrane protein 4**	Golim4	8	11,514	9,5E+07	79.904	683	8.5	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	7	*Not specified*	N/A
P40197	GPV_HUMAN	**Platelet glycoprotein V**	GP5	14	13,529	2,8E+08	60.958	560	16.1	0	0	0	1	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	11	*Other*	N/A
S4R1E5	S4R1E5_MOUSE	**Glutathione peroxidase**	Gpx4	12	3,0425	1,5E+08	17.937	157	8.9	0	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	4	6	*Not specified*	N/A
E9Q179	E9Q179_MOUSE	**G-rich sequence factor 1**	Grsf1	2	4,7948	6,8E+07	41.61	362	7.7	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
P47791	GSHR_MOUSE	**Glutathione reductase, mitochondrial**	Gsr	6	13,69	2,5E+08	53.662	500	15.4	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	0	Cytoplasm, mitochondrion	*Not specified*
A2AE89	A2AE89_MOUSE	**Glutathione transferase**	Gstm1	12	26,518	4,9E+08	28.556	244	25.8	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	11	0	0	0	*Not specified*	N/A
A0A494BAM8	A0A494BAM8_MOUSE	**Glutathione transferase (Fragment)**	Gstp2	2	10,417	1,1E+08	14.67	132	27.3	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
F6SMJ7	F6SMJ7_MOUSE	**GTP-binding protein 8 (Fragment)**	Gtpbp8	2	3,2704	5,8E+06	16.198	147	8.2	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	*Not specified*	N/A
P10922	H10_MOUSE	**Histone H1.0**	H1-0	6	6,8217	9,0E+07	20.861	194	11.3	2	0	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	0	1	0	0	Nucleus	N/A
P15864	H12_MOUSE	**Histone H1.2**	H1-2	3	4,6107	3,2E+07	21.266	212	12.7	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	Nucleus	N/A
C0HKE4	H2A1E_MOUSE	**Histone H2A type 1-E**	H2ac8	3	8,8826	4,7E+07	14.135	130	36.2	6	3	1	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	Nucleus	N/A
P01902	HA1D_MOUSE	**H-2 class I histocompatibility antigen, K-D alpha chain**	H2-K1	4	8,1341	3,2E+08	41.489	368	6.8	0	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	3	*Other*	N/A
K7EMV3	K7EMV3_HUMAN	**Histone H3**	H3-3B	28	30,72	7,4E+08	10.334	92	19.6	1	1	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	6	0	1	17	*Not specified*	N/A
A2A7A7	A2A7A7_MOUSE	**GDH/6PGL endoplasmic bifunctional protein**	H6pd	2	10,293	4,8E+07	89.909	797	3.3	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	*Not specified*	N/A
Q8K2C9	HACD3_MOUSE	**Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3**	Hacd3	10	6,0085	1,7E+08	43.131	362	14.9	0	0	1	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	1	1	8	Endoplasmic reticulim	N/A
Q9NYQ2	HAOX2_MOUSE	**Hydroxyacid oxidase 2**	Hao2	13	29,244	6,1E+08	38.699	353	24.6	2	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	11	0	0	0	Peroxisome	N/A
A0A0G2JDP0	A0A0G2JDP0_MOUSE	**HCLS1-associated protein X-1**	Hax1	3	4,2303	2,5E+07	31.315	277	7.6	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	*Not specified*	N/A
P69905	HBA_HUMAN	**Hemoglobin subunit alpha**	HBA1	15	8,3717	1,3E+09	15.257	142	43	3	1	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	7	6	*Not specified*	N/A
P68871	HBB_HUMAN	**Hemoglobin subunit beta**	HBB	13	8,0564	2,5E+08	15.998	147	46.9	1	3	0	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	4	8	*Not specified*	N/A
K7EMY7	K7EMY7_HUMAN	**Haloacid dehalogenase-like hydrolase domain-containing protein 2 (Fragment)**	HDHD2	1	3,8772	2,3E+07	16.413	146	8.9	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	*Not specified*	N/A
Q5T7C4	Q5T7C4_HUMAN	**High mobility group protein B1**	HMGB1	4	4,7026	4,6E+07	18.311	158	18.4	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	0	0	0	0	Nucleus	N/A
A0A338P6H8	A0A338P6H8_MOUSE	**Histidine-rich glycoprotein**	Hrg	1	2,9491	2,7E+07	22.257	199	8	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	*Not specified*	N/A
Q9EQ06	DHB11_MOUSE	**Estradiol 17-beta-dehydrogenase 11**	Hsd17b11	12	11,302	1,9E+08	32.88	298	15.1	1	1	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	3	6	Endoplasmic reticulim	N/A
A8Y5N4	A8Y5N4_MOUSE	**17-beta-hydroxysteroid dehydrogenase 13**	Hsd17b13	7	3,9214	1,4E+08	29.424	264	33.7	0	3	2	3	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	1	3	3	*Not specified*	N/A
Q7Z5P4	DHB13_HUMAN	**17-beta-hydroxysteroid dehydrogenase 13**	HSD17B13	6	3,7539	4,6E+07	33.655	300	12.3	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	Endoplasmic reticulim	N/A
O88736	DHB7_MOUSE	**3-keto-steroid reductase/17-beta-hydroxysteroid dehydrogenase 7**	Hsd17b7	7	3,5327	6,7E+07	37.316	334	8.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	4	Endoplasmic reticulim	N/A
P26150	3BHS3_MOUSE	**3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 3**	Hsd3b3	16	17,17	3,8E+08	42.031	373	27.3	0	0	0	1	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	14	Mitochondrion, endoplasmic reticulum	*Not specified*
Q8BTX9	HSDL1_MOUSE	**Inactive hydroxysteroid dehydrogenase-like protein 1**	Hsdl1	6	6,514	8,8E+07	36.867	330	14.8	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	Mitochondrion	*Not specified*
P11499	HS90B_MOUSE	**Heat shock protein HSP 90-beta**	Hsp90ab1	30	20,115	6,6E+09	83.28	724	16.7	3	4	1	3	7	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	16	0	0	11	Secreted, cell membrane, cytoplasm, nucleus	N/A
P48741	HSP77_HUMAN	**Putative heat shock 70 kDa protein 7**	HSPA7	8	3,2645	3,4E+08	40.244	367	6.5	1	2	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	2	*Not specified*	N/A
Q9Z2G9	HTAI2_MOUSE	**Oxidoreductase HTATIP2**	Htatip2	11	7,3527	1,3E+08	26.87	242	14.9	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	8	Cytoplasm, nucleus	N/A
P14735	IDE_HUMAN	**Insulin-degrading enzyme**	IDE	5	7,2021	3,0E+08	117.97	1019	5.5	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	0	Secreted, cell membrane, cytoplasm	N/A
A0A0C4DH35	HV335_HUMAN	**Probable non-functional immunoglobulin heavy variable 3-35**	IGHV3-35	6	8,4365	2,4E+08	12.81	117	9.4	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	3	0	0	0	Secreted, cell membrane	N/A
Q9DCE9	Q9DCE9_MOUSE	**Interferon gamma-induced GTPase**	Igtp	11	9,4714	2,5E+08	48.493	423	13.2	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	10	*Not specified*	N/A
Q9QZ85	IIGP1_MOUSE	**Interferon-inducible GTPase 1**	Iigp1	7	6,554	9,5E+07	47.571	413	8.7	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	Cytoplasm, nucleus, endoplasmic reticulum, Golgi apparatus	N/A
Q3UQ44	IQGA2_MOUSE	**Ras GTPase-activating-like protein IQGAP2**	Iqgap2	21	18,855	2,2E+08	180.53	1575	5.8	0	2	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	18	*Not specified*	N/A
J3QSS7	J3QSS7_HUMAN	**Iron-sulfur cluster assembly 2 homolog, mitochondrial**	ISCA2	3	4,0259	1,4E+08	11.442	108	11.1	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Mitochondrion	*Not specified*
D3Z0K9	D3Z0K9_MOUSE	**Iron-sulfur cluster assembly enzyme ISCU, mitochondrial (Fragment)**	Iscu	6	13,109	1,0E+08	14.692	136	25	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	Mitochondrion	*Not specified*
D6RGE2	D6RGE2_HUMAN	**Isochorismatase domain-containing protein 1 (Fragment)**	ISOC1	1	4,6581	9,1E+07	20.239	188	13.8	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	*Not specified*	N/A
Q9DCC7	ISC2B_MOUSE	**Isochorismatase domain-containing protein 2B**	Isoc2b	6	8,8422	2,3E+08	23.151	210	8.6	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	Cytoplasm, nucleus	N/A
Q61703	ITIH2_MOUSE	**Inter-alpha-trypsin inhibitor heavy chain H2**	Itih2	25	54,336	1,9E+09	105.93	946	23.7	13	1	0	8	10	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	25	0	0	0	0	Secreted	N/A
Q9DCX8	IYD1_MOUSE	**Iodotyrosine deiodinase 1**	Iyd	6	4,7104	9,9E+07	32.814	285	7.7	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	Cell membrane, cytoplasm	N/A
Q02257	PLAK_MOUSE	**Junction plakoglobin**	Jup	17	14,366	1,9E+08	81.8	745	10.2	1	0	1	1	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	2	1	12	Cytoplasm	N/A
K7EM02	K7EM02_HUMAN	**Katanin p60 ATPase-containing subunit A-like 2 (Fragment)**	KATNAL2	4	3,012	2,5E+08	13.999	128	9.4	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	*Not specified*	N/A
H0YAC1	H0YAC1_HUMAN	**Plasma kallikrein (Fragment)**	KLKB1	4	4,2967	3,4E+07	76.773	686	3.6	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	3	*Not specified*	N/A
Q99KR3	LACB2_MOUSE	**Endoribonuclease LACTB2**	Lactb2	19	16,699	7,1E+08	32.754	288	23.3	1	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	18	0	0	0	Mitochondrion	Matrix
Q8VDC0	SYLM_MOUSE	**Probable leucine--tRNA ligase, mitochondrial**	Lars2	3	4,5413	3,1E+07	101.48	902	3.2	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Mitochondrion	Matrix
P18428	LBP_HUMAN	**Lipopolysaccharide-binding protein**	LBP	34	31,11	1,7E+09	53.383	481	25.2	0	1	0	1	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	2	31	Secreted, cytoplasm	N/A
J3QSE5	J3QSE5_HUMAN	**Phosphatidylcholine-sterol acyltransferase (Fragment)**	LCAT	10	9,9922	3,5E+08	29.386	255	10.2	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	7	*Not specified*	N/A
P13796	PLSL_HUMAN	**Plastin-2**	LCP1	8	24,298	1,2E+08	70.288	627	11.6	0	0	0	0	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	Cytoplasm	N/A
A0A1B0GSX0	A0A1B0GSX0_MOUSE	**L-lactate dehydrogenase**	Ldha	14	13,181	3,6E+08	39.758	361	20.5	0	7	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	14	0	0	0	*Not specified*	N/A
Q86WU2	LDHD_HUMAN	**Probable D-lactate dehydrogenase, mitochondrial**	LDHD	7	19,791	3,6E+08	54.87	507	2.8	1	1	1	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	1	0	3	Mitochondrion	*Not specified*
A0A0R4J0R8	A0A0R4J0R8_MOUSE	**Leukocyte cell-derived chemotaxin-2**	Lect2	11	21,477	2,6E+08	16.391	151	29.8	3	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	11	0	0	0	0	*Not specified*	N/A
A0A0M3HEP3	A0A0M3HEP3_MOUSE	**Lipoyl synthase, mitochondrial**	Lias	13	34,45	1,1E+09	32.173	289	31.5	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	13	0	0	0	Mitochondrion	*Not specified*
Q9DBH5	LMAN2_MOUSE	**Vesicular integral-membrane protein VIP36**	Lman2	2	3,3736	1,9E+07	40.429	358	5.9	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Golgi aparatus	N/A
P08519	APOA_HUMAN	**Apolipoprotein(a)**	LPA	25	27,042	1,1E+09	501.31	4548	17.4	0	1	0	1	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	3	21	*Not specified*	N/A
Q91YX5	LGAT1_MOUSE	**Acyl-CoA:lysophosphatidylglycerol acyltransferase 1**	Lpgat1	10	3,1298	7,2E+07	43.088	370	8.1	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	8	Endoplasmic reticulim	N/A
P51884	LUM_HUMAN	**Lumican**	LUM	10	7,0969	7,6E+07	38.429	338	12.4	0	0	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	7	Secreted	N/A
P61626	LYSC_HUMAN	**Lysozyme C**	LYZ	1	8,3941	6,0E+07	16.537	148	27	2	1	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	Secreted	N/A
P17897	LYZ1_MOUSE	**Lysozyme C-1**	Lyz1	12	10,962	3,2E+08	16.794	148	39.9	4	1	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	2	2	0	0	Secreted	N/A
P08905	LYZ2_MOUSE	**Lysozyme C-2**	Lyz2	9	8,9904	2,5E+08	16.689	148	35.8	4	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	0	0	0	0	Secreted	N/A
Q9CQY5	MAGT1_MOUSE	**Magnesium transporter protein 1**	Magt1	11	7,1081	1,1E+08	37.969	335	12.8	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	10	Cell membrane, endoplasmic reticulum	N/A
Q64133	AOFA_MOUSE	**Amine oxidase [flavin-containing] A**	Maoa	5	4,2045	7,1E+07	59.601	526	7	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Cytoplasm, mitochondrion	Outer membrane
A0A0G2JFT4	A0A0G2JFT4_MOUSE	**Microtubule-associated protein (Fragment)**	Map4	4	4,7417	3,8E+07	27.872	276	9.4	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	0	0	0	0	Cytoplasm	N/A
A0A0R4J1H0	A0A0R4J1H0_MOUSE	**E3 ubiquitin-protein ligase MARCHF5**	Marchf5	7	7,1254	1,1E+08	27.363	244	11.1	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	*Not specified*	N/A
P48740	MASP1_HUMAN	**Mannan-binding lectin serine protease 1**	MASP1	22	26,617	3,2E+09	79.246	699	11	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	22	Secreted	N/A
O00187	MASP2_HUMAN	**Mannan-binding lectin serine protease 2**	MASP2	31	25,228	1,9E+09	75.702	686	13.4	0	0	0	0	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	31	Secreted	N/A
E9PWX8	E9PWX8_MOUSE	**Non-specific serine/threonine protein kinase**	Mast4	2	3,1302	9,8E+07	264.58	2426	1.1	0	1	0	1	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	0	*Not specified*	N/A
P41317	MBL2_MOUSE	**Mannose-binding protein C**	Mbl2	11	40,099	8,2E+08	25.957	244	21.7	1	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	10	0	0	0	Secreted	N/A
Q9D1I5	MCEE_MOUSE	**Methylmalonyl-CoA epimerase, mitochondrial**	Mcee	7	20,868	6,9E+08	19.017	178	18	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	7	0	0	0	Mitochondrion	*Not specified*
P14152	MDHC_MOUSE	**Malate dehydrogenase, cytoplasmic**	Mdh1	10	9,1315	1,7E+08	36.511	334	22.2	0	1	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	9	Cytoplasm	N/A
J3QMC5	J3QMC5_MOUSE	**Midasin**	Mdn1	3	2,9671	8,9E+08	629.58	5582	0.5	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Nucleus	N/A
E9Q5B2	E9Q5B2_MOUSE	**Methyltransferase-like 26**	Mettl26	7	9,6044	1,3E+08	12.037	107	16.8	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	5	0	0	0	*Not specified*	N/A
Q80U63	MFN2_MOUSE	**Mitofusin-2**	Mfn2	32	21,707	4,6E+08	86.187	757	14.3	0	0	0	1	11	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	31	Mitochondrion	Outer membrane
O35678	MGLL_MOUSE	**Monoglyceride lipase**	Mgll	5	10,877	7,6E+07	33.387	303	11.6	0	1	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	4	Cytoplasm	N/A
Q9CPU4	MGST3_MOUSE	**Microsomal glutathione S-transferase 3**	Mgst3	7	10,117	1,6E+08	16.958	153	18.3	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	7	Endoplasmic reticulim, microsomes	N/A
H3BJS5	H3BJS5_MOUSE	**Melanoma inhibitory activity protein 2 (Fragment)**	Mia2	6	7,4614	8,6E+07	30.773	269	17.8	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	*Not specified*	N/A
Q8BI84	TGO1_MOUSE	**Transport and Golgi organization protein 1 homolog**	Mia3	18	17,841	3,3E+08	213.67	1930	5	0	0	0	1	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	17	Endoplasmic reticulim	N/A
Q8R404	MIC13_MOUSE	**MICOS complex subunit MIC13**	Micos13	11	6,2833	2,6E+08	13.373	119	27.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	9	Mitochondrion	Inner membrane
E9PQV6	E9PQV6_HUMAN	**Calcium uptake protein 1, mitochondrial (Fragment)**	MICU1	3	4,4383	6,4E+07	28.15	246	13.8	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Mitochondrion	*Not specified*
A0A286YDC5	A0A286YDC5_MOUSE	**Mitochondrial intermediate peptidase**	Mipep	8	9,635	3,7E+08	64.322	568	8.5	0	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	2	Mitochondrion	*Not specified*
Q6ZQI3	MLEC_MOUSE	**Malectin**	Mlec	3	4,7478	6,7E+07	32.342	291	11.7	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Endoplasmic reticulim	N/A
Q8C7H1	MMAA_MOUSE	**Methylmalonic aciduria type A homolog, mitochondrial**	Mmaa	18	26,564	3,5E+08	45.932	415	21.7	0	5	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	12	0	0	6	Cytoplasm, mitochondrion	*Not specified*
Q80UM7	MOGS_MOUSE	**Mannosyl-oligosaccharide glucosidase**	Mogs	16	15,021	1,7E+08	91.83	834	8.5	1	2	1	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	1	0	12	Endoplasmic reticulim	N/A
D3YWY6	D3YWY6_MOUSE	**Mitochondrial pyruvate carrier**	Mpc1	29	3,9521	5,2E+08	9.7384	85	18.8	1	1	2	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	6	5	6	11	Mitochondrion	Inner membrane
A0A0J9YVC7	A0A0J9YVC7_MOUSE	**Protein Mpv17 (Fragment)**	Mpv17	3	3,2202	2,5E+07	11.814	105	10.5	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	2	*Other*	N/A
P03930	ATP8_MOUSE	**ATP synthase protein 8**	Mtatp8	27	125,42	2,6E+09	7.7662	67	14.9	0	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	10	6	7	Mitochondrion	*Not specified*
A0A3Q4EG99	A0A3Q4EG99_MOUSE	**Mitochondrial carrier homolog 1**	Mtch1	11	9,9426	2,2E+08	29.073	260	16.2	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	9	Mitochondrion	*Not specified*
A2AFW6	A2AFW6_MOUSE	**Mitochondrial carrier homolog 2**	Mtch2	3	2,9457	4,1E+07	32.345	294	37.8	1	6	1	6	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Mitochondrion	*Not specified*
B5MC22	B5MC22_HUMAN	**Mitochondrial 18 kDa protein**	MTFP1	19	9,0112	3,6E+08	15.556	143	17.5	0	1	1	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	3	3	11	Mitochondrion	*Not specified*
D3YZ89	D3YZ89_MOUSE	**Mitochondrial fission regulator 1 (Fragment)**	Mtfr1	1	3,0367	1,3E+07	18.59	168	7.1	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	Mitochondrion	*Not specified*
Q9D110	MTHFS_MOUSE	**5-formyltetrahydrofolate cyclo-ligase**	Mthfs	12	11,62	2,4E+08	23.201	203	29.1	0	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	0	0	2	Cytoplasm	N/A
Q91YJ5	IF2M_MOUSE	**Translation initiation factor IF-2, mitochondrial**	Mtif2	5	4,3078	1,2E+08	81.288	727	3	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	0	Mitochondrion	*Not specified*
P03888	NU1M_MOUSE	**NADH-ubiquinone oxidoreductase chain 1**	Mtnd1	3	3,2464	5,9E+07	36.059	318	2.5	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	1	Mitochondrion	Inner membrane
P03921	NU5M_MOUSE	**NADH-ubiquinone oxidoreductase chain 5**	Mtnd5	5	7,4756	5,0E+08	68.474	607	6.6	0	1	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	4	Mitochondrion	Inner membrane
A0A3Q4L2Q3	A0A3Q4L2Q3_MOUSE	**Poly(A) RNA polymerase, mitochondrial (Fragment)**	Mtpap	1	3,5016	3,6E+07	37.467	338	7.1	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Mitochondrion	*Not specified*
Q9CQF4	MRES1_MOUSE	**Mitochondrial transcription rescue factor 1**	Mtres1	2	4,6967	5,4E+07	27.847	240	5.4	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Mitochondrion	Matrix
O08601	MTP_MOUSE	**Microsomal triglyceride transfer protein large subunit**	Mttp	40	78,97	2,4E+09	99.098	894	22.6	0	16	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	40	0	0	0	Endoplasmic reticulim, Golgi aparatus	N/A
Q8R5C0	Q8R5C0_MOUSE	**Metaxin**	Mtx1	13	10,357	4,3E+08	35.646	317	18.3	0	0	0	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	12	Mitochondrion	Outer membrane
E9Q3X0	E9Q3X0_MOUSE	**Major vault protein**	Mvp	47	37,255	7,0E+08	96.856	870	24.1	0	2	0	0	15	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	46	Cytoplasm	N/A
Q7Z406	MYH14_HUMAN	**Myosin-14**	MYH14	8	3,0172	1,0E+08	227.87	1995	2.4	0	3	0	3	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	6	*Not specified*	N/A
P19105	ML12A_HUMAN	**Myosin regulatory light chain 12A**	MYL12A	1	2,952	1,3E+08	19.794	171	6.4	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	*Not specified*	N/A
E9Q405	E9Q405_MOUSE	**Unconventional myosin-XVIIIa**	Myo18a	4	19,183	1,2E+08	193.64	1700	2.9	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	*Not specified*	N/A
E9QNH6	E9QNH6_MOUSE	**Unconventional myosin-Ib**	Myo1b	8	8,2268	1,1E+08	125.03	1078	5	0	0	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	*Not specified*	N/A
Q9WTI7	MYO1C_MOUSE	**Unconventional myosin-Ic**	Myo1c	4	5,6829	7,1E+07	121.94	1063	4	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cell membrane, cytoplasm, nucleus	N/A
Q8BGV0	SYNM_MOUSE	**Probable asparagine--tRNA ligase, mitochondrial**	Nars2	6	6,1006	9,3E+07	53.961	477	6.3	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	0	Mitochondrion	Matrix
D3YU17	D3YU17_MOUSE	**Nicalin**	Ncln	6	7,1193	4,8E+07	62.779	562	8.9	0	0	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	*Not specified*	N/A
Q9QYG0	NDRG2_MOUSE	**Protein NDRG2**	Ndrg2	4	6,0078	4,2E+07	40.789	371	3.8	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	3	Cytoplasm	N/A
K7EQ77	K7EQ77_HUMAN	**Complex I-B14.7**	NDUFA11	2	4,1699	1,1E+08	12.671	120	19.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	Mitochondrion	Inner membrane
Q9Z1P6	NDUA7_MOUSE	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7**	Ndufa7	15	10,298	4,2E+08	12.575	113	52.2	4	1	1	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	2	1	1	4	Mitochondrion	Inner membrane
F6ZFT1	F6ZFT1_MOUSE	**Acyl carrier protein (Fragment)**	Ndufab1	11	9,8453	4,8E+08	14.309	127	18.1	0	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	1	2	2	*Not specified*	N/A
Q9D1H6	NDUF4_MOUSE	**NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4**	Ndufaf4	5	10,025	1,0E+08	20.082	173	8.1	0	1	1	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	1	0	1	Mitochondrion	*Not specified*
A0A3B2WD93	A0A3B2WD93_MOUSE	**Protein arginine methyltransferase NDUFAF7 (Fragment)**	Ndufaf7	7	26,633	2,3E+08	32.058	288	17.4	1	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	1	Mitochondrion	*Not specified*
O09111	NDUBB_MOUSE	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial**	Ndufb11	5	3,1019	1,5E+08	17.444	151	19.2	0	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	3	Mitochondrion	Inner membrane
D3Z568	D3Z568_MOUSE	**Complex I-SGDH**	Ndufb5	23	12	8,3E+08	14.038	119	31.9	1	1	1	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	4	1	1	15	Mitochondrion	Inner membrane
Q9CR61	NDUB7_MOUSE	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7**	Ndufb7	3	8,9908	8,4E+07	16.331	137	11.7	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Mitochondrion	Inner membrane, IMS
Q9D6J5	NDUB8_MOUSE	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial**	Ndufb8	20	8,3839	3,3E+08	21.876	186	25.8	0	2	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	4	10	Mitochondrion	Inner membrane
Q9CQJ8	NDUB9_MOUSE	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9**	Ndufb9	6	13,098	3,3E+08	21.984	179	32.4	0	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	1	Mitochondrion	Inner membrane
Q8BK30	NDUV3_MOUSE	**NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial**	Ndufv3	1	4,0732	2,0E+08	11.813	104	26	0	0	1	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	Mitochondrion	Inner membrane
Q8VDK1	NIT1_MOUSE	**Deaminated glutathione amidase**	Nit1	10	30,085	3,5E+08	35.705	323	28.5	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	0	0	0	Cytoplasm, mitochondrion	*Not specified*
Q86X76	NIT1_HUMAN	**Deaminated glutathione amidase**	NIT1	1	3,6863	8,7E+07	35.896	327	9.5	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Cytoplasm, mitochondrion	*Not specified*
Q9JHW2	NIT2_MOUSE	**Omega-amidase NIT2**	Nit2	14	32,985	7,5E+08	30.501	276	44.9	1	8	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	13	0	0	0	Cytoplasm	N/A
Q3TL44	NLRX1_MOUSE	**NLR family member X1**	Nlrx1	11	11,74	2,7E+08	107.83	975	7.1	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	11	Mitochondrion	Outer membrane
Q3V3C7	Q3V3C7_MOUSE	**Nicotinamide-nucleotide adenylyltransferase**	Nmnat3	2	3,7294	1,4E+08	20.256	179	10.6	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
Q6GQT9	NOMO1_MOUSE	**Nodal modulator 1**	Nomo1	5	5,9072	4,2E+07	133.42	1214	3.5	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Endoplasmic reticulim	N/A
Q9DCN1	NUD12_MOUSE	**NAD-capped RNA hydrolase NUDT12**	Nudt12	18	32,702	7,3E+08	51.51	462	20.8	0	5	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	13	0	1	4	Cytoplasm, peroxisome	N/A
P11930	NUD19_MOUSE	**Nucleoside diphosphate-linked moiety X motif 19**	Nudt19	18	53,568	9,7E+08	40.32	357	27.5	1	8	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	14	0	0	3	Peroxisome	N/A
Q9CR24	NUDT8_MOUSE	**Nucleoside diphosphate-linked moiety X motif 8**	Nudt8	13	21,532	6,1E+08	23.252	210	32.9	1	5	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	11	0	0	1	*Not specified*	N/A
F8VWK9	F8VWK9_HUMAN	**2-5-oligoadenylate synthase 3**	OAS3	2	3,3246	9,7E+08	19.485	177	8.5	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
Q9CRD0	OCAD1_MOUSE	**OCIA domain-containing protein 1**	Ociad1	12	8,0134	1,8E+08	27.61	247	13	0	0	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	9	Endosome	N/A
Q5TBF5	Q5TBF5_HUMAN	**Mimecan (Fragment)**	OGN	1	10,592	2,4E+07	30.456	268	6	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	*Not specified*	N/A
Q505D7	OPA3_MOUSE	**Optic atrophy 3 protein homolog**	Opa3	15	8,624	3,6E+08	20.11	179	33.5	0	1	0	1	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	13	Mitochondrion	*Not specified*
Q9CR10	OXLD1_MOUSE	**Oxidoreductase-like domain-containing protein 1**	Oxld1	2	6,094	7,9E+07	22.178	201	7.5	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
Q8VE38	OXND1_MOUSE	**Oxidoreductase NAD-binding domain-containing protein 1**	Oxnad1	6	14,845	2,8E+08	34.727	311	16.1	2	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	*Not specified*	N/A
Q9D404	OXSM_MOUSE	**3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial**	Oxsm	31	101,77	2,5E+09	48.627	459	48.6	2	11	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	28	1	0	0	Mitochondrion	*Not specified*
Q8VDG7	PAFA2_MOUSE	**Platelet-activating factor acetylhydrolase 2, cytoplasmic**	Pafah2	13	10,457	3,5E+08	43.561	390	15.6	0	2	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	10	Cytoplasm, endoplasmic reticulum	N/A
P16331	PH4H_MOUSE	**Phenylalanine-4-hydroxylase**	Pah	2	11,73	5,6E+07	51.899	453	7.5	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
D6RF62	D6RF62_HUMAN	**AIR carboxylase**	PAICS	2	7,482	3,1E+07	37.111	333	4.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	*Not specified*	N/A
Q9CQV1	TIM16_MOUSE	**Mitochondrial import inner membrane translocase subunit TIM16**	Pam16	7	17,274	4,2E+08	13.784	125	44.8	2	1	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	1	0	0	4	Mitochondrion	Inner membrane
Q6TCG2	PAQR9_MOUSE	**Membrane progesterone receptor epsilon**	Paqr9	11	5,0197	1,4E+08	42.741	375	5.6	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	9	Cell membrane	N/A
A0A0R4J1R7	A0A0R4J1R7_MOUSE	**4a-hydroxytetrahydrobiopterin dehydratase**	Pcbd2	6	11,284	1,4E+08	11.74	103	43.7	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	6	0	0	0	*Not specified*	N/A
P05165	PCCA_HUMAN	**Propionyl-CoA carboxylase alpha chain, mitochondrial**	PCCA	14	14,802	7,3E+08	80.058	728	22.3	5	15	2	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	11	1	0	0	Mitochondrion	Matrix
A0A2I3BQL9	A0A2I3BQL9_MOUSE	**Phosphoenolpyruvate carboxykinase (GTP) (Fragment)**	Pck2	8	20,445	6,0E+08	65.936	599	9.7	1	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	8	0	0	0	*Not specified*	N/A
P08003	PDIA4_MOUSE	**Protein disulfide-isomerase A4**	Pdia4	11	27,856	3,0E+08	71.982	638	13.5	0	6	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	10	1	0	0	Endoplasmic reticulim	N/A
A0A0R4J1V0	A0A0R4J1V0_MOUSE	**Na(+)/H(+) exchange regulatory cofactor NHE-RF3**	Pdzk1	8	14,315	9,9E+07	56.497	519	9.1	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	5	*Not specified*	N/A
Q5BL07	PEX1_MOUSE	**Peroxisome biogenesis factor 1**	Pex1	16	16,657	1,9E+08	141.43	1284	6.6	0	0	0	0	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	16	Cytoplasm, peroxisome	N/A
Q9Z211	PX11A_MOUSE	**Peroxisomal membrane protein 11A**	Pex11a	5	4,1199	5,9E+07	28.153	246	13.4	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Peroxisome	N/A
E9PXK7	E9PXK7_MOUSE	**Peroxisomal membrane protein 11B**	Pex11b	6	9,0396	7,1E+07	27.003	245	10.2	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	*Not specified*	N/A
Q6P6M5	PX11C_MOUSE	**Peroxisomal membrane protein 11C**	Pex11g	5	8,7012	1,0E+08	27.151	241	5	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Peroxisome	N/A
Q8VC48	PEX12_MOUSE	**Peroxisome assembly protein 12**	Pex12	3	5,0895	2,4E+07	40.633	359	10.6	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Peroxisome	N/A
Q9R0A0	PEX14_MOUSE	**Peroxisomal membrane protein PEX14**	Pex14	4	4,2683	8,0E+07	41.207	376	5.6	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cytoplasm, peroxisome	N/A
Q91XC9	PEX16_MOUSE	**Peroxisomal membrane protein PEX16**	Pex16	5	4,7107	3,3E+07	38.677	336	6.5	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	5	Peroxisome	N/A
Q8BGI5	PEX26_MOUSE	**Peroxisome assembly protein 26**	Pex26	14	7,9231	1,9E+08	34.016	305	9.8	2	2	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	2	0	1	9	Peroxisome	N/A
E9QA46	E9QA46_MOUSE	**Peroxisomal assembly protein PEX3**	Pex3	8	4,8918	8,9E+07	40.639	359	2.8	0	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	4	4	Peroxisome	N/A
Q99LC9	PEX6_MOUSE	**Peroxisome assembly factor 2**	Pex6	22	22,146	2,2E+08	104.55	981	13.5	0	0	0	2	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	20	Cytoplasm, peroxisome	N/A
Q9Z126	PLF4_MOUSE	**Platelet factor 4**	Pf4	7	4,6165	4,2E+08	11.243	105	20	2	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	0	0	0	0	Secreted	N/A
O70570	PIGR_MOUSE	**Polymeric immunoglobulin receptor**	Pigr	3	5,9747	1,1E+08	84.998	771	4	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted, cell membrane	N/A
Q9CWW6	PIN4_MOUSE	**Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4**	Pin4	6	7,8973	4,8E+07	13.815	131	10.7	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	0	0	0	0	Cytoplasm, nucleus	N/A
F7C386	F7C386_MOUSE	**Phosphatidylserine decarboxylase proenzyme, mitochondrial (Fragment)**	Pisd	4	6,8229	4,8E+07	40.675	359	7.2	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	3	Mitochondrion	*Not specified*
E9Q509	E9Q509_MOUSE	**Pyruvate kinase**	Pklr	6	8,0738	1,1E+08	58.82	543	5.5	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	4	*Not specified*	N/A
B4DNK4	B4DNK4_HUMAN	**Pyruvate kinase**	PKM	1	3,0476	5,6E+07	49.897	457	5.9	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	*Not specified*	N/A
Q15149	PLEC_HUMAN	**Plectin**	PLEC	3	3,4079	1,5E+07	531.78	4684	0.4	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	Cytoplasm	N/A
P20918	PLMN_MOUSE	**Plasminogen**	Plg	3	3,4528	2,4E+07	90.807	812	3.9	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Secreted	N/A
E9PXB0	E9PXB0_MOUSE	**Calcium-independent phospholipase A2-gamma**	Pnpla8	6	3,8534	5,6E+07	62.351	558	4.7	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	*Not specified*	N/A
Q9QZM2	DPOG2_MOUSE	**DNA polymerase subunit gamma-2, mitochondrial**	Polg2	2	3,2855	1,2E+07	51.466	459	5.2	0	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	1	Mitochondrion	*Not specified*
Q62087	PON3_MOUSE	**Serum paraoxonase/lactonase 3**	Pon3	5	2,9749	1,1E+08	39.351	354	7.3	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Secreted	N/A
Q8BXN7	PPM1K_MOUSE	**Protein phosphatase 1K, mitochondrial**	Ppm1k	2	10,795	2,9E+08	40.918	372	3.8	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Mitochondrion	Matrix
A0A0A6YX50	A0A0A6YX50_MOUSE	**Protoporphyrinogen oxidase (Fragment)**	Ppox	5	4,287	5,3E+07	41.247	389	5.9	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	4	Mitochondrion	Inner membrane
O08807	PRDX4_MOUSE	**Peroxiredoxin-4**	Prdx4	12	12,182	3,2E+08	31.052	274	23	0	5	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	8	0	2	2	Secreted, cytoplasm, endoplasmic reticulum	N/A
D3Z3S1	D3Z3S1_MOUSE	**Prolactin regulatory element-binding protein**	Preb	12	14,661	1,1E+08	37.965	350	22	0	0	0	1	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	11	*Not specified*	N/A
Q9JK53	PRELP_MOUSE	**Prolargin**	Prelp	2	4,4409	1,8E+07	43.292	378	3.4	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Secreted	N/A
Q92954	PRG4_HUMAN	**Proteoglycan 4**	PRG4	13	6,6001	2,1E+08	151.06	1404	2.6	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	3	10	Secreted	N/A
O08795	GLU2B_MOUSE	**Glucosidase 2 subunit beta**	Prkcsh	4	4,7443	1,4E+08	58.792	521	4	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	Endoplasmic reticulim	N/A
E7EQL6	E7EQL6_HUMAN	**Proline dehydrogenase**	PRODH	11	4,8679	5,7E+08	56.255	492	13.6	1	2	1	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	5	2	2	*Not specified*	N/A
Q9Z1R9	Q9Z1R9_MOUSE	**Protease, serine 1 (trypsin 1)**	Prss1	8	3,6642	1,6E+11	26.134	246	8.1	1	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	3	2	1	*Not specified*	N/A
H0Y8D1	H0Y8D1_HUMAN	**Trypsin-1 (Fragment)**	PRSS1	24	16,515	3,9E+09	15.421	142	14.1	1	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	6	3	3	5	*Not specified*	N/A
P35030	TRY3_HUMAN	**Trypsin-3**	PRSS3	25	141,55	8,7E+09	32.528	304	4.3	1	1	1	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	4	3	6	7	Secreted	N/A
D3Z0A8	D3Z0A8_MOUSE	**Peroxiredoxin-like 2 activated in M-CSF stimulated monocytes (Fragment)**	Prxl2a	12	7,8391	1,1E+08	11.265	103	25.2	0	1	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	2	8	Cytoplasm	N/A
Q8BWM0	PGES2_MOUSE	**Prostaglandin E synthase 2**	Ptges2	8	9,269	1,7E+08	43.323	384	11.5	0	1	0	0	4	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	6	Cytoplasm, nucleus, Golgi aparatus	N/A
Q66GT5	PTPM1_MOUSE	**Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1**	Ptpmt1	3	6,1152	2,3E+07	21.942	193	13	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	3	Mitochondrion	Inner membrane
Q8R2Y8	PTH2_MOUSE	**Peptidyl-tRNA hydrolase 2, mitochondrial**	Ptrh2	8	7,2984	1,2E+08	19.526	181	18.2	0	1	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	7	Mitochondrion	*Not specified*
A2ADA5	PUSL1_MOUSE	**tRNA pseudouridine synthase-like 1**	Pusl1	4	3,8561	2,2E+08	31.992	291	4.5	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	0	0	*Not specified*	N/A
B4DWH1	B4DWH1_HUMAN	**Peroxisomal membrane protein 4**	PXMP4	4	3,3082	5,1E+07	15.69	144	6.9	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	*Not specified*	N/A
A2AKD6	A2AKD6_MOUSE	**Peroxisomal membrane protein 4**	Pxmp4	1	2,9385	1,3E+07	10.365	92	16.3	0	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	1	*Not specified*	N/A
A0A0G2JGY0	A0A0G2JGY0_MOUSE	**Dihydropteridine reductase**	Qdpr	4	3,783	5,2E+07	14.821	139	17.3	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	*Not specified*	N/A
P61027	RAB10_MOUSE	**Ras-related protein Rab-10**	Rab10	15	11,075	3,0E+08	22.541	200	16	0	2	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	5	7	Cytoplasm, endoplasmic reticulum, Golgi aparatus, endosome	N/A
Q50HX3	Q50HX3_MOUSE	**RAB14 protein variant**	Rab14	16	16,944	3,0E+08	21.888	197	44.2	0	0	0	0	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	16	*Not specified*	N/A
Q9NP72	RAB18_HUMAN	**Ras-related protein Rab-18**	RAB18	13	9,9126	2,3E+08	22.977	206	28.2	0	0	0	0	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	13	Cell membrane	N/A
P35282	RAB21_MOUSE	**Ras-related protein Rab-21**	Rab21	4	4,1629	4,7E+07	24.106	222	12.2	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	Cytoplasm, endoplasmic reticulum, Golgi aparatus, endosome	N/A
Q9CZE3	RAB32_MOUSE	**Ras-related protein Rab-32**	Rab32	5	3,6048	5,9E+07	25.068	223	9.9	0	0	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	2	3	Cytoplasm, mitochondrion	Outer membrane
P35278	RAB5C_MOUSE	**Ras-related protein Rab-5C**	Rab5c	20	12,998	2,9E+08	23.412	216	31	0	1	0	1	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	1	17	Cell membrane, cytoplasm, endosome	N/A
Q9NRW1	RAB6B_HUMAN	**Ras-related protein Rab-6B**	RAB6B	8	5,3126	6,2E+08	23.461	208	10.6	1	1	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	0	4	Cytoplasm, endoplasmic reticulum, Golgi aparatus	N/A
P61006	RAB8A_HUMAN	**Ras-related protein Rab-8A**	RAB8A	2	3,0076	6,8E+07	23.668	207	12.1	0	1	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	2	Cell membrane, cytoplasm, Golgi aparatus, endosome	N/A
A2AFP5	A2AFP5_MOUSE	**RAB9, member RAS oncogene family (Fragment)**	Rab9	6	6,4303	6,6E+07	22.946	202	18.8	0	0	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	1	5	Cytoplasm	N/A
Q9QVY8	RAI2_MOUSE	**Retinoic acid-induced protein 2**	Rai2	3	4,8788	3,2E+07	57.123	529	1.3	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	*Not specified*	N/A

Q9QYR9	ACOT2_MOUSE	**Acyl-coenzyme A thioesterase 2, mitochondrial**	Acot2	47	92,569	1,7E+09	49.656	453	36.9	3	10	1	4	8	1,1E+07	1,2E+08	10,9	1,5E+07	6,9E+07	4,1E+07	0,6	1	24	0	5	17	Mitochondrion	Matrix
P20108	PRDX3_MOUSE	**Thioredoxin-dependent peroxide reductase, mitochondrial**	Prdx3	65	92,113	5,7E+09	28.127	257	51.8	5	8	0	4	3	1,7E+08	2,7E+08	1,5	1,5E+07	2,9E+08	1,7E+08	0,6	6	32	0	11	16	Cytoplasm, mitochondrion, endosome	*Not specified*
Q3UMR5	MCU_MOUSE	**Calcium uniporter protein, mitochondrial**	Mcu	23	12,72	2,5E+08	39.681	350	14.6	0	0	0	4	5	1,1E+07	1,1E+07	1,0	1,5E+07	7,9E+07	4,7E+07	0,6	0	0	0	11	12	Mitochondrion	Inner membrane
Q91WU0	EST1F_MOUSE	**Carboxylesterase 1F**	Ces1f	41	43,338	1,3E+09	61.612	561	29.6	1	11	3	3	5	1,1E+07	1,4E+08	12,7	1,5E+07	7,2E+07	4,2E+07	0,6	1	23	3	2	12	Cytoplasm, microsomes	N/A
H9KUZ3	H9KUZ3_MOUSE	**Sialoadhesin**	Siglec1	8	4,7504	4,5E+07	173.36	1605	1.9	0	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	2,6E+07	1,5E+07	0,6	0	0	0	2	6	*Not specified*	N/A
Q9CQZ6	NDUB3_MOUSE	**NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3**	Ndufb3	25	8,9723	3,1E+08	11.692	104	18.3	1	1	1	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	7,7E+07	4,4E+07	0,6	3	2	3	6	11	Mitochondrion	Inner membrane
K7ER74	K7ER74_HUMAN	**Apolipoprotein C-II**	APOC4-APOC2	27	14,223	1,3E+09	20.049	178	36	0	1	0	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	4,7E+08	2,6E+08	0,6	0	2	0	10	15	Secreted	N/A
J3QP71	J3QP71_MOUSE	**Basigin (Fragment)**	Bsg	16	4,888	4,5E+08	21.602	197	11.7	0	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	2,5E+08	1,4E+08	0,6	0	0	0	7	9	Cell membrane	N/A
Q8QZS1	HIBCH_MOUSE	**3-hydroxyisobutyryl-CoA hydrolase, mitochondrial**	Hibch	92	110,72	1,0E+10	43.037	385	56.1	4	16	1	2	4	3,7E+08	6,8E+08	1,8	1,5E+07	3,9E+08	2,0E+08	0,5	7	68	1	6	10	Mitochondrion	*Not specified*
Q9QYR7	ACOT3_MOUSE	**Acyl-coenzyme A thioesterase 3**	Acot3	72	105,1	5,7E+09	47.489	432	42.6	10	13	3	5	10	1,9E+08	3,5E+08	1,8	1,5E+07	1,7E+08	8,6E+07	0,5	8	42	0	4	18	Peroxisome	N/A
Q96Q89	KI20B_HUMAN	**Kinesin-like protein KIF20B**	KIF20B	43	28,669	7,4E+10	210.63	1820	0.5	1	1	1	1	1	3,2E+10	1,1E+07	0,0	3,9E+10	3,8E+10	1,5E+10	0,4	10	1	8	13	11	Cytoplasm, nucleus	N/A

Common contaminants (ribosomal proteins, IgGs, keratins)

Uniprot Accession code	Uniprot Entry name	Description	Gene name	Total MS/MS count	Score	Total Intensity	Mol. weight [kDa]	Sequence length	Sequence coverage [%]	Peptides Lysates - Healthy	Peptides Lysates - SLE	Peptides Lysates - Control	Peptides Panning - Healthy	Peptides Panning - SLE	LFQ intensity Lysates - Healthy	LFQ intensity Lysates - SLE	Lysates Ratio SLE : HEALTHY	LFQ intensity Panning - Control	LFQ intensity Panning - Healthy	LFQ intensity Panning - SLE	Panning Ratio SLE : HEALTHY	MS/MS count Lysates - Healthy	MS/MS count Lysates - SLE	MS/MS count Lysates - Control	MS/MS count Panning - Healthy	MS/MS count Panning - SLE	Cellular compartment	Submitochondrial location
E9QJS0	E9QJS0_MOUSE	**28S ribosomal protein S10, mitochondrial**	Mrps10	12	18,948	8,3E+08	18.698	160	45	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	12	0	0	0	Secreted, mitochondrion	*Not specified*
Q3U8Y1	Q3U8Y1_MOUSE	**28S ribosomal protein S11, mitochondrial**	Mrps11	22	18,33	4,5E+08	20.251	191	14.1	2	3	0	1	2	4,2E+07	4,3E+07	1,0	1,5E+07	1,5E+07	1,8E+07	1,2	6	11	0	1	4	Mitochondrion	*Not specified*
E9PUY1	E9PUY1_MOUSE	**28S ribosomal protein S12, mitochondrial (Fragment)**	Mrps12	9	40,904	5,8E+08	13.874	125	28.8	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	1	0	0	0	Mitochondrion	*Not specified*
D3Z2K2	D3Z2K2_MOUSE	**28S ribosomal protein S14, mitochondrial**	Mrps14	9	15,025	3,6E+08	14.279	122	23	1	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	7	0	0	2	Mitochondrion	*Not specified*
Q9DC71	RT15_MOUSE	**28S ribosomal protein S15, mitochondrial**	Mrps15	11	11,114	5,4E+08	29.463	258	19.8	1	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	10	0	0	0	Mitochondrion	*Not specified*
A6ND22	A6ND22_HUMAN	**28S ribosomal protein S16, mitochondrial**	MRPS16	5	5,5725	3,6E+08	11.15	99	39.4	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	0	Mitochondrion	*Not specified*
Q9CQE3	RT17_MOUSE	**28S ribosomal protein S17, mitochondrial**	Mrps17	16	25,396	1,5E+09	13.382	120	51.7	1	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	13	0	0	1	Mitochondrion	*Not specified*
Q99N85	RT18A_MOUSE	**28S ribosomal protein S18a, mitochondrial**	Mrps18a	5	9,2755	1,0E+08	22.321	196	21.9	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	0	Mitochondrion	*Not specified*
Q99N84	RT18B_MOUSE	**28S ribosomal protein S18b, mitochondrial**	Mrps18b	9	13,786	2,0E+08	28.702	254	13.8	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	9	0	0	0	Mitochondrion	*Not specified*
Q924T2	RT02_MOUSE	**28S ribosomal protein S2, mitochondrial**	Mrps2	12	22,267	1,1E+09	32.313	291	17.5	2	3	0	0	0	5,3E+07	1,3E+08	2,4	1,5E+07	1,5E+07	1,5E+07	1,0	2	10	0	0	0	Mitochondrion	*Not specified*
D3YVZ9	D3YVZ9_MOUSE	**28S ribosomal protein S21, mitochondrial (Fragment)**	Mrps21	17	39,494	1,6E+09	5.1089	44	61.4	1	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	10	0	0	3	Mitochondrion	*Not specified*
Q9CXW2	RT22_MOUSE	**28S ribosomal protein S22, mitochondrial**	Mrps22	21	19,751	2,0E+09	41.192	359	27.6	3	7	0	1	2	2,4E+07	2,6E+08	11,0	1,5E+07	1,5E+07	2,2E+07	1,5	3	15	0	1	2	Mitochondrion	*Not specified*
Q8VE22	RT23_MOUSE	**28S ribosomal protein S23, mitochondrial**	Mrps23	41	33,426	2,8E+09	20.348	177	49.2	4	6	0	2	3	1,1E+08	2,2E+08	2,1	1,5E+07	2,4E+07	2,3E+07	1,0	4	25	0	3	9	Mitochondrion	*Not specified*
Q9CQV5	RT24_MOUSE	**28S ribosomal protein S24, mitochondrial**	Mrps24	17	22,137	9,6E+08	18.901	167	23.4	1	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	14	0	0	2	Mitochondrion	*Not specified*
Q80ZS3	RT26_MOUSE	**28S ribosomal protein S26, mitochondrial**	Mrps26	16	21,431	7,5E+08	23.443	200	20.5	1	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	14	0	0	1	Mitochondrion	*Not specified*
Q8BK72	RT27_MOUSE	**28S ribosomal protein S27, mitochondrial**	Mrps27	31	34,524	2,0E+09	47.778	415	25.8	2	9	1	0	1	6,2E+07	1,9E+08	3,1	1,5E+07	1,5E+07	1,5E+07	1,0	2	26	1	0	2	Cytoplasm, mitochondrion	*Not specified*
Q9CY16	RT28_MOUSE	**28S ribosomal protein S28, mitochondrial**	Mrps28	9	13,076	3,4E+08	20.52	186	31.7	1	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	7	0	0	1	Mitochondrion	*Not specified*
Q9ER88	RT29_MOUSE	**28S ribosomal protein S29, mitochondrial**	Dap3	48	67,802	4,3E+09	44.699	391	39.1	3	11	0	0	3	6,2E+07	4,0E+08	6,4	1,5E+07	1,5E+07	2,1E+07	1,4	4	40	0	0	4	Mitochondrion	*Not specified*
Q9D0G0	RT30_MOUSE	**28S ribosomal protein S30, mitochondrial**	Mrps30	53	82,482	2,4E+09	49.939	442	43.4	5	12	1	0	0	6,9E+07	1,5E+08	2,2	1,5E+07	1,5E+07	1,5E+07	1,0	4	48	1	0	0	Mitochondrion	*Not specified*
Q61733	RT31_MOUSE	**28S ribosomal protein S31, mitochondrial**	Mrps31	26	31,276	1,2E+09	43.88	384	30.5	0	8	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	26	0	0	0	Mitochondrion	*Not specified*
Q9D2R8	RT33_MOUSE	**28S ribosomal protein S33, mitochondrial**	Mrps33	12	9,1075	8,4E+08	12.459	106	28.3	3	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	6	0	0	0	Mitochondrion	*Not specified*
Q9JIK9	RT34_MOUSE	**28S ribosomal protein S34, mitochondrial**	Mrps34	29	61,984	1,7E+09	25.826	218	54.1	2	10	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	23	0	0	4	Mitochondrion	*Not specified*
A0A0R4J0L6	A0A0R4J0L6_MOUSE	**28S ribosomal protein S35, mitochondrial**	Mrps35	27	70,449	8,7E+08	35.917	320	42.5	0	9	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	25	0	0	2	Mitochondrion	*Not specified*
Q9CQX8	RT36_MOUSE	**28S ribosomal protein S36, mitochondrial**	Mrps36	10	16,401	2,7E+08	11.101	102	69.6	1	3	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	9	0	0	0	Mitochondrion	*Not specified*
Q99N87	RT05_MOUSE	**28S ribosomal protein S5, mitochondrial**	Mrps5	27	22,977	1,2E+09	48.206	432	19.7	1	7	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	23	0	0	3	Mitochondrion	*Not specified*
P58064	RT06_MOUSE	**28S ribosomal protein S6, mitochondrial**	Mrps6	9	7,8927	5,1E+08	14.308	125	25.6	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	7	0	0	0	Mitochondrion	*Not specified*
Q80X85	RT07_MOUSE	**28S ribosomal protein S7, mitochondrial**	Mrps7	56	185,84	1,7E+09	28.062	242	45.9	5	9	0	0	3	9,9E+07	2,3E+08	2,3	1,5E+07	1,5E+07	5,1E+07	3,4	19	30	0	0	7	Mitochondrion	*Not specified*
Q9D7N3	RT09_MOUSE	**28S ribosomal protein S9, mitochondrial**	Mrps9	37	57,392	2,0E+09	44.929	390	34.4	1	10	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	31	0	0	5	Mitochondrion	*Not specified*
Q99N96	RM01_MOUSE	**39S ribosomal protein L1, mitochondrial**	Mrpl1	20	28,244	6,5E+08	37.596	336	28	2	7	0	0	0	2,9E+07	5,5E+07	1,9	1,5E+07	1,5E+07	1,5E+07	1,0	2	18	0	0	0	Mitochondrion	*Not specified*
Q3TBW2	RM10_MOUSE	**39S ribosomal protein L10, mitochondrial**	Mrpl10	20	60,526	1,7E+09	29.395	262	39.3	2	6	0	0	0	4,4E+07	1,7E+08	3,8	1,5E+07	1,5E+07	1,5E+07	1,0	2	18	0	0	0	Mitochondrion	*Not specified*
Q9CQF0	RM11_MOUSE	**39S ribosomal protein L11, mitochondrial**	Mrpl11	41	131,96	2,5E+09	20.68	192	51	6	6	0	0	0	3,5E+08	1,6E+08	0,5	1,5E+07	1,5E+07	1,5E+07	1,0	24	17	0	0	0	Mitochondrion	*Not specified*
Q9DB15	RM12_MOUSE	**39S ribosomal protein L12, mitochondrial**	Mrpl12	20	33,335	2,6E+09	21.708	201	24.9	1	5	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	18	1	0	0	Mitochondrion	*Not specified*
Q9D1P0	RM13_MOUSE	**39S ribosomal protein L13, mitochondrial**	Mrpl13	37	27,045	1,8E+09	20.677	178	54.5	4	7	2	0	0	7,0E+07	1,5E+08	2,1	6,8E+07	1,5E+07	1,5E+07	1,0	5	29	3	0	0	Mitochondrion	*Not specified*
Q9D1I6	RM14_MOUSE	**39S ribosomal protein L14, mitochondrial**	Mrpl14	16	38,41	9,1E+08	15.874	145	44.8	5	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	16	0	0	0	0	Mitochondrion	*Not specified*
Q9CPR5	RM15_MOUSE	**39S ribosomal protein L15, mitochondrial**	Mrpl15	35	59,762	1,3E+09	33.541	295	44.7	0	11	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	35	0	0	0	Mitochondrion	*Not specified*
Q9D8P4	RM17_MOUSE	**39S ribosomal protein L17, mitochondrial**	Mrpl17	6	6,3796	7,3E+08	20.249	176	15.3	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	Mitochondrion	*Not specified*
Q9CQL5	RM18_MOUSE	**39S ribosomal protein L18, mitochondrial**	Mrpl18	6	6,9305	1,9E+08	20.677	180	11.7	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	5	0	0	0	Mitochondrion	*Not specified*
Q9D338	RM19_MOUSE	**39S ribosomal protein L19, mitochondrial**	Mrpl19	16	21,227	1,2E+09	33.578	292	19.2	1	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	15	0	0	0	Mitochondrion	*Not specified*
B1B1D8	B1B1D8_MOUSE	**39S ribosomal protein L2, mitochondrial**	Mrpl2	13	8,5278	1,7E+08	33.099	304	17.8	3	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	8	0	0	0	Mitochondrion	*Not specified*
Q9CQL4	RM20_MOUSE	**39S ribosomal protein L20, mitochondrial**	Mrpl20	12	12,399	4,6E+08	17.595	149	28.2	0	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	12	0	0	0	Mitochondrion	*Not specified*
Q9D1N9	RM21_MOUSE	**39S ribosomal protein L21, mitochondrial**	Mrpl21	28	31,532	1,6E+09	23.366	209	23.9	0	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	28	0	0	0	Mitochondrion	*Not specified*
Q8BU88	RM22_MOUSE	**39S ribosomal protein L22, mitochondrial**	Mrpl22	9	12,218	2,6E+08	23.805	206	21.4	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	9	0	0	0	Mitochondrion	*Not specified*
O35972	RM23_MOUSE	**39S ribosomal protein L23, mitochondrial**	Mrpl23	27	39,097	1,8E+09	17.121	146	61	3	7	0	0	0	3,4E+07	1,0E+08	3,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	24	0	0	0	Mitochondrion	*Not specified*
Q9CQ06	RM24_MOUSE	**39S ribosomal protein L24, mitochondrial**	Mrpl24	8	13,323	6,0E+08	24.944	216	14.8	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	7	0	0	0	Mitochondrion	*Not specified*
Q99N92	RM27_MOUSE	**39S ribosomal protein L27, mitochondrial**	Mrpl27	13	21,039	1,4E+09	15.944	148	33.8	4	1	1	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	2	1	0	2	Mitochondrion	*Not specified*
Q9D1B9	RM28_MOUSE	**39S ribosomal protein L28, mitochondrial**	Mrpl28	19	9,7683	6,2E+08	30.169	257	13.6	1	4	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	16	0	0	2	Mitochondrion	*Not specified*
D3Z456	D3Z456_MOUSE	**39S ribosomal protein L3, mitochondrial**	Mrpl3	13	17,329	5,3E+08	33.994	304	21.4	0	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	13	0	0	0	Mitochondrion	*Not specified*
Q9D7N6	RM30_MOUSE	**39S ribosomal protein L30, mitochondrial**	Mrpl30	2	3,5549	9,3E+07	18.342	160	25.6	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	Mitochondrion	*Not specified*
Q9DCI9	RM32_MOUSE	**39S ribosomal protein L32, mitochondrial**	Mrpl32	19	21,459	4,0E+08	21.733	187	32.6	6	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	16	3	0	0	0	Mitochondrion	*Not specified*
Q9CQP0	RM33_MOUSE	**39S ribosomal protein L33, mitochondrial**	Mrpl33	24	22,611	1,1E+09	7.4158	65	53.8	5	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	24	0	0	0	0	Mitochondrion	*Not specified*
Q99N91	RM34_MOUSE	**39S ribosomal protein L34, mitochondrial**	Mrpl34	22	28,306	3,3E+09	10.531	92	26.1	5	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	21	1	0	0	0	Mitochondrion	*Not specified*
Q921S7	RM37_MOUSE	**39S ribosomal protein L37, mitochondrial**	Mrpl37	31	37,54	9,7E+08	48.34	423	34.3	0	10	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	31	0	0	0	Mitochondrion	*Not specified*
Q8K2M0	RM38_MOUSE	**39S ribosomal protein L38, mitochondrial**	Mrpl38	10	17,03	9,8E+08	45.029	380	21.8	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	9	0	0	0	Mitochondrion	*Not specified*
Q9JKF7	RM39_MOUSE	**39S ribosomal protein L39, mitochondrial**	Mrpl39	16	17,86	7,2E+08	38.549	336	17	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	15	0	0	0	Mitochondrion	*Not specified*
Q9DCU6	RM04_MOUSE	**39S ribosomal protein L4, mitochondrial**	Mrpl4	19	88,719	2,6E+09	33.073	294	22.8	1	5	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	18	0	0	0	Mitochondrion	*Not specified*
D3Z7C0	D3Z7C0_MOUSE	**39S ribosomal protein L40, mitochondrial**	Mrpl40	20	22,744	9,6E+08	19.378	162	43.2	1	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	18	0	0	0	Mitochondrion	*Not specified*
Q9CQN7	RM41_MOUSE	**39S ribosomal protein L41, mitochondrial**	Mrpl41	20	16,832	6,4E+08	15.261	135	50.4	1	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	18	0	0	0	Mitochondrion	*Not specified*
Q5RL20	Q5RL20_MOUSE	**39S ribosomal protein L43, mitochondrial**	Mrpl43	23	21,895	6,4E+08	17.877	159	37.7	1	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	22	0	0	0	Mitochondrion	*Not specified*
Q9CY73	RM44_MOUSE	**39S ribosomal protein L44, mitochondrial**	Mrpl44	21	37,354	9,4E+08	37.527	333	27.3	0	6	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	21	0	0	0	Mitochondrion	*Not specified*
Q9D0Q7	RM45_MOUSE	**39S ribosomal protein L45, mitochondrial**	Mrpl45	21	50,622	1,4E+09	35.41	306	21.9	4	4	0	0	0	1,9E+08	1,8E+08	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	13	0	0	0	Mitochondrion	*Not specified*
Q9EQI8	RM46_MOUSE	**39S ribosomal protein L46, mitochondrial**	Mrpl46	23	37,104	1,1E+09	32.131	283	30.7	2	7	0	0	0	5,3E+07	1,2E+08	2,3	1,5E+07	1,5E+07	1,5E+07	1,0	2	21	0	0	0	Mitochondrion	*Not specified*
Q8K2Y7	RM47_MOUSE	**39S ribosomal protein L47, mitochondrial**	Mrpl47	11	36,612	6,9E+08	29.725	252	15.5	0	4	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	11	0	0	0	Mitochondrion	*Not specified*
A0A140LHT6	A0A140LHT6_MOUSE	**39S ribosomal protein L48, mitochondrial**	Mrpl48	8	5,6256	4,3E+08	12.954	113	20.4	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	8	0	0	0	Mitochondrion	*Not specified*
Q9CQ40	RM49_MOUSE	**39S ribosomal protein L49, mitochondrial**	Mrpl49	16	25,551	1,4E+09	19.133	166	36.1	2	5	0	0	0	5,3E+07	1,6E+08	3,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	13	0	0	0	Mitochondrion	*Not specified*
Q8VDT9	RM50_MOUSE	**39S ribosomal protein L50, mitochondrial**	Mrpl50	17	29,393	1,3E+09	18.213	159	58.5	1	7	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	17	0	0	0	Mitochondrion	*Not specified*
Q9D1H8	RM53_MOUSE	**39S ribosomal protein L53, mitochondrial**	Mrpl53	15	31,696	1,1E+09	12.737	118	49.2	2	4	0	0	1	1,2E+08	1,3E+08	1,1	1,5E+07	1,5E+07	1,5E+07	1,0	2	11	0	0	2	Mitochondrion	*Not specified*
Q9CPW3	RM54_MOUSE	**39S ribosomal protein L54, mitochondrial**	Mrpl54	2	3,3935	2,9E+07	15.422	135	7.4	0	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Mitochondrion	*Not specified*
Q9CZ83	RM55_MOUSE	**39S ribosomal protein L55, mitochondrial**	Mrpl55	4	2,9933	6,8E+07	15.121	127	11.8	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	0	Mitochondrion	*Not specified*
Q99N94	RM09_MOUSE	**39S ribosomal protein L9, mitochondrial**	Mrpl9	23	26,415	9,2E+08	30.244	265	24.2	2	5	0	0	0	2,1E+07	7,3E+07	3,4	1,5E+07	1,5E+07	1,5E+07	1,0	4	19	0	0	0	Mitochondrion	*Not specified*
P63325	RS10_MOUSE	**40S ribosomal protein S10**	Rps10	10	8,0532	3,3E+08	18.916	165	14.5	3	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	0	0	0	3	Cytoplasm, nucleus	N/A
Q921R2	Q921R2_MOUSE	**40S ribosomal protein S13**	Rps13	77	65,611	3,2E+09	16.142	140	45	11	3	2	1	7	1,8E+09	5,7E+07	0,0	2,1E+08	1,5E+07	7,0E+07	4,7	41	9	7	1	19	*Not specified*	N/A
A0A2R8Y811	A0A2R8Y811_HUMAN	**40S ribosomal protein S14 (Fragment)**	RPS14	25	18,348	3,3E+08	16.159	150	39.3	4	1	0	1	6	4,5E+07	1,1E+07	0,2	1,5E+07	1,5E+07	8,3E+07	5,6	8	1	0	3	13	*Not specified*	N/A
I3L3P7	I3L3P7_HUMAN	**40S ribosomal protein S15a**	RPS15A	16	7,6389	1,9E+08	11.477	100	32	0	2	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	3,8E+07	4,5E+07	1,2	0	4	0	3	9	*Not specified*	N/A
M0R210	M0R210_HUMAN	**40S ribosomal protein S16**	RPS16	67	22,459	1,2E+09	14.419	129	53.5	0	1	0	5	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,2E+08	2,1E+08	1,7	0	3	0	22	42	*Not specified*	N/A
F6YVP7	F6YVP7_MOUSE	**40S ribosomal protein S18**	Rps18-ps6	47	20,484	1,0E+09	17.671	152	38.8	2	1	0	5	7	3,3E+07	1,1E+07	0,3	1,5E+07	6,7E+07	1,4E+08	2,1	4	1	0	16	26	*Not specified*	N/A
Q9CZX8	RS19_MOUSE	**40S ribosomal protein S19**	Rps19	27	38,111	1,3E+09	16.085	145	44.8	8	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	24	0	0	1	2	*Not specified*	N/A
P25444	RS2_MOUSE	**40S ribosomal protein S2**	Rps2	10	13,365	3,5E+08	31.231	293	16	0	2	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	1	6	*Not specified*	N/A
P60867	RS20_MOUSE	**40S ribosomal protein S20**	Rps20	13	11,168	1,9E+08	13.373	119	22.7	3	1	0	1	2	9,6E+07	1,1E+07	0,1	1,5E+07	1,5E+07	3,0E+07	2,0	7	1	0	1	4	Cytoplasm	N/A
P62266	RS23_HUMAN	**40S ribosomal protein S23**	RPS23	16	7,3821	4,4E+08	15.807	143	16.1	2	0	0	2	3	1,8E+08	1,1E+07	0,1	1,5E+07	1,2E+08	1,5E+08	1,3	4	0	0	7	5	Cytoplasm, endoplasmic reticulum	N/A
A0A2R8Y8A0	A0A2R8Y8A0_HUMAN	**40S ribosomal protein S24 (Fragment)**	RPS24	4	6,1027	7,4E+07	10.248	90	30	0	0	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	4	*Not specified*	N/A
A0A1L1SQA8	A0A1L1SQA8_MOUSE	**40S ribosomal protein S25**	Rps25	24	7,9964	5,3E+08	10.309	93	32.3	2	0	0	3	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,2E+08	1,2E+08	1,0	3	0	0	6	15	*Not specified*	N/A
P62854	RS26_HUMAN	**40S ribosomal protein S26**	RPS26	11	6,1433	2,7E+08	13.015	115	20.9	0	1	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	3	7	Cytoplasm, endoplasmic reticulum	N/A
G3UYV7	G3UYV7_MOUSE	**40S ribosomal protein S28 (Fragment)**	Rps28	3	4,1294	1,7E+08	6.3442	56	21.4	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	*Not specified*	N/A
P62273	RS29_HUMAN	**40S ribosomal protein S29**	RPS29	10	3,7597	8,4E+07	6.6767	56	19.6	1	0	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	0	0	1	2	Cytoplasm, endoplasmic reticulum	N/A
F2Z2S8	F2Z2S8_HUMAN	**40S ribosomal protein S3**	RPS3	29	13,971	5,8E+08	13.069	117	43.6	0	1	0	3	6	1,1E+07	1,1E+07	1,0	1,5E+07	8,1E+07	8,9E+07	1,1	0	1	0	8	20	Mitochondrion	Inner membrane
P62862	RS30_MOUSE	**40S ribosomal protein S30**	Fau	24	9,8937	2,3E+09	6.6478	59	20.3	3	0	2	0	1	1,8E+09	1,1E+07	0,0	6,0E+08	1,5E+07	1,5E+07	1,0	13	0	7	0	4	*Not specified*	N/A
D6RB09	D6RB09_HUMAN	**40S ribosomal protein S3a (Fragment)**	RPS3A	8	7,5567	1,1E+08	22.459	193	20.7	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	8	Cytoplasm	N/A
P62702	RS4X_MOUSE	**40S ribosomal protein S4, X isoform**	Rps4x	44	31,906	1,4E+09	29.597	263	39.9	0	2	1	3	10	1,1E+07	1,1E+07	1,0	1,5E+07	1,1E+08	2,4E+08	2,1	0	3	1	11	29	Cytoplasm	N/A
P62754	RS6_MOUSE	**40S ribosomal protein S6**	Rps6	41	20,618	8,5E+08	28.68	249	20.5	4	1	0	4	6	6,3E+07	1,1E+07	0,2	1,5E+07	7,2E+07	1,1E+08	1,5	11	2	0	8	20	*Not specified*	N/A
P62082	RS7_MOUSE	**40S ribosomal protein S7**	Rps7	5	17,448	2,1E+08	22.127	194	25.8	3	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	1	0	0	1	Cytoplasm	N/A
Q5JR95	Q5JR95_HUMAN	**40S ribosomal protein S8**	RPS8	50	30,95	1,2E+09	21.879	188	42.6	1	4	0	3	8	1,1E+07	4,0E+07	3,7	1,5E+07	9,3E+07	1,1E+08	1,1	1	10	0	13	26	*Not specified*	N/A
Q6ZWN5	RS9_MOUSE	**40S ribosomal protein S9**	Rps9	26	14,391	6,9E+08	22.591	194	28.9	0	2	0	2	7	1,1E+07	2,4E+07	2,2	1,5E+07	5,0E+07	9,3E+07	1,9	0	4	0	5	17	Cytoplasm	N/A
F8WD59	F8WD59_HUMAN	**40S ribosomal protein SA (Fragment)**	RPSA	13	7,9852	2,4E+08	12.647	116	34.5	1	3	0	1	2	1,1E+07	2,9E+07	2,7	1,5E+07	1,5E+07	3,2E+07	2,2	1	5	0	1	6	*Not specified*	N/A
P14869	RLA0_MOUSE	**60S acidic ribosomal protein P0**	Rplp0	30	38,03	1,8E+09	34.216	317	34.4	2	6	0	1	4	5,9E+07	1,4E+08	2,3	1,5E+07	1,5E+07	7,6E+07	5,2	2	16	0	1	11	Cytoplasm, nucleus	N/A
P99027	RLA2_MOUSE	**60S acidic ribosomal protein P2**	Rplp2	7	13,367	5,1E+08	11.651	115	24.3	0	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	5	0	0	2	*Not specified*	N/A
F8W7C6	F8W7C6_HUMAN	**60S ribosomal protein L10**	RPL10	35	15,944	9,0E+08	18.565	163	23.3	3	0	0	3	5	3,7E+07	1,1E+07	0,3	1,5E+07	9,9E+07	2,2E+08	2,2	5	0	0	7	23	*Not specified*	N/A
Q5VVC8	Q5VVC8_HUMAN	**60S ribosomal protein L11**	RPL11	24	7,199	6,3E+08	19.024	167	13.8	0	2	1	2	2	1,1E+07	6,3E+07	5,9	1,5E+07	1,5E+08	1,8E+08	1,2	0	6	1	9	8	*Not specified*	N/A
P35979	RL12_MOUSE	**60S ribosomal protein L12**	Rpl12	81	80,651	8,7E+09	17.804	165	58.8	8	6	2	2	2	1,2E+09	2,8E+08	0,2	7,8E+07	1,5E+07	1,5E+07	1,0	40	31	4	2	4	*Not specified*	N/A
P47963	RL13_MOUSE	**60S ribosomal protein L13**	Rpl13	47	257,49	1,1E+09	24.305	211	36	4	3	1	5	6	5,0E+07	8,8E+07	1,8	1,5E+07	1,1E+08	1,3E+08	1,2	13	8	2	9	15	*Not specified*	N/A
A0A1B0GSQ6	A0A1B0GSQ6_MOUSE	**60S ribosomal protein L13a (Fragment)**	Rpl13a	19	6,1098	3,0E+08	19.031	167	18	0	1	0	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,1E+08	9,6E+07	0,8	0	2	0	5	12	*Not specified*	N/A
Q9CR57	RL14_MOUSE	**60S ribosomal protein L14**	Rpl14	36	16,137	1,6E+09	23.564	217	17.1	1	3	1	2	3	1,1E+07	9,8E+07	9,2	1,5E+07	1,4E+08	1,8E+08	1,3	5	7	2	9	13	*Not specified*	N/A
A0A087WXM6	A0A087WXM6_HUMAN	**60S ribosomal protein L17 (Fragment)**	RPL17	12	7,2058	4,1E+08	19.586	169	23.7	0	1	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	1	7	*Not specified*	N/A
A0A1B0GQU8	A0A1B0GQU8_MOUSE	**60S ribosomal protein L18**	Rpl18	57	27,854	2,2E+09	18.101	159	35.8	3	5	1	5	5	9,8E+07	1,2E+08	1,3	1,5E+07	1,9E+08	2,4E+08	1,3	8	17	1	11	20	Endoplasmic reticulum	N/A
M0R3D6	M0R3D6_HUMAN	**60S ribosomal protein L18a (Fragment)**	RPL18A	17	8,2347	4,9E+08	16.714	141	21.3	1	3	0	2	2	1,1E+07	3,7E+07	3,5	1,5E+07	3,9E+07	5,7E+07	1,5	1	7	0	3	6	*Not specified*	N/A
Q9CQM8	Q9CQM8_MOUSE	**60S ribosomal protein L21**	Rpl21	13	5,3279	1,5E+08	18.579	160	16.2	1	1	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	1	0	0	10	*Not specified*	N/A
P67984	RL22_MOUSE	**60S ribosomal protein L22**	Rpl22	30	11,118	7,8E+08	14.759	128	39.1	2	3	1	1	2	6,7E+07	7,0E+07	1,0	1,5E+07	1,5E+07	6,1E+07	4,1	4	11	3	3	9	*Not specified*	N/A
C9JD32	C9JD32_HUMAN	**60S ribosomal protein L23 (Fragment)**	RPL23	5	6,1695	3,7E+08	9.6694	91	38.5	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	1	0	0	1	*Not specified*	N/A
P62751	RL23A_MOUSE	**60S ribosomal protein L23a**	Rpl23a	31	17,026	9,9E+08	17.695	156	42.3	6	1	2	0	3	3,3E+08	1,1E+07	0,0	1,3E+08	1,5E+07	9,8E+07	6,6	12	5	4	0	10	*Not specified*	N/A
C9JXB8	C9JXB8_HUMAN	**60S ribosomal protein L24**	RPL24	34	17,733	1,6E+09	14.369	121	24.8	2	0	1	2	2	6,2E+08	1,1E+07	0,0	1,5E+07	2,1E+08	1,8E+08	0,9	9	0	3	9	13	*Not specified*	N/A
B1ARA3	B1ARA3_MOUSE	**60S ribosomal protein L26 (Fragment)**	Rpl26	7	6,5981	1,3E+08	12.217	103	24.3	4	0	0	0	2	7,3E+07	1,1E+07	0,1	1,5E+07	1,5E+07	2,5E+07	1,7	6	0	0	0	1	*Not specified*	N/A
P61358	RL27_MOUSE	**60S ribosomal protein L27**	Rpl27	13	5,2971	2,0E+08	15.798	136	20.6	0	2	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	3	7	Cytoplasm, endoplasmic reticulum	N/A
P14115	RL27A_MOUSE	**60S ribosomal protein L27a**	Rpl27a	20	4,8875	9,2E+08	16.605	148	14.2	1	2	0	2	2	1,1E+07	7,6E+07	7,2	1,5E+07	1,5E+07	2,7E+08	18,0	2	6	0	2	10	*Not specified*	N/A
P41105	RL28_MOUSE	**60S ribosomal protein L28**	Rpl28	10	10,781	2,1E+08	15.733	137	26.3	4	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	0	0	0	0	*Not specified*	N/A
A0A1L1SS27	A0A1L1SS27_MOUSE	**60S ribosomal protein L29 (Fragment)**	Rpl29	4	4,159	4,8E+07	15.719	140	15.7	2	0	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	1	0	0	*Not specified*	N/A
P27659	RL3_MOUSE	**60S ribosomal protein L3**	Rpl3	7	13,527	2,8E+08	46.109	403	8.2	0	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	4	Cytoplasm, nucleus	N/A
A0A2I3BQF4	A0A2I3BQF4_MOUSE	**60S ribosomal protein L30**	Rpl30	22	26,411	3,9E+08	10.457	94	62.8	4	2	0	0	1	1,6E+08	5,1E+07	0,3	1,5E+07	1,5E+07	1,5E+07	1,0	12	9	0	0	1	*Not specified*	N/A
P62900	RL31_MOUSE	**60S ribosomal protein L31**	Rpl31	21	12,89	1,2E+09	14.463	125	26.4	3	1	2	1	2	5,9E+08	1,1E+07	0,0	1,2E+08	1,5E+07	1,9E+07	1,3	9	3	4	1	4	*Not specified*	N/A
F2Z388	F2Z388_HUMAN	**60S ribosomal protein L35**	RPL35	27	33,651	1,1E+09	10.645	96	34.4	5	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	19	3	0	0	5	*Not specified*	N/A
P18077	RL35A_HUMAN	**60S ribosomal protein L35a**	RPL35A	5	6,8294	2,5E+08	12.538	110	22.7	0	1	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	4	*Not specified*	N/A
Q6ZWZ4	Q6ZWZ4_MOUSE	**60S ribosomal protein L36**	Rpl36	6	4,8518	7,5E+07	12.254	105	21	0	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	4	0	0	2	*Not specified*	N/A
C9J4Z3	C9J4Z3_HUMAN	**60S ribosomal protein L37a**	RPL37A	2	4,6313	1,6E+07	7.624	68	44.1	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	0	0	*Not specified*	N/A
J3KT73	J3KT73_HUMAN	**60S ribosomal protein L38**	RPL38	12	11,4	4,1E+08	7.5649	64	37.5	1	0	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	7,6E+07	7,7E+07	1,0	5	0	0	3	4	*Not specified*	N/A
Q9D8E6	RL4_MOUSE	**60S ribosomal protein L4**	Rpl4	56	29,996	2,0E+09	47.153	419	34.8	2	7	0	2	9	5,8E+07	8,3E+07	1,4	1,5E+07	8,5E+07	2,7E+08	3,1	3	16	0	5	32	*Not specified*	N/A
P47911	RL6_MOUSE	**60S ribosomal protein L6**	Rpl6	62	34,577	2,3E+09	33.509	296	24.7	0	3	1	7	7	1,1E+07	9,1E+07	8,5	1,5E+07	1,8E+08	2,4E+08	1,3	0	8	1	20	33	Cytoplasm, endoplasmic reticulum	N/A
P14148	RL7_MOUSE	**60S ribosomal protein L7**	Rpl7	42	86,583	1,6E+09	31.419	270	33	1	3	1	4	10	1,1E+07	6,7E+07	6,3	1,5E+07	1,7E+08	2,2E+08	1,3	1	4	1	9	27	*Not specified*	N/A
P62424	RL7A_HUMAN	**60S ribosomal protein L7a**	RPL7A	56	45,909	2,3E+09	29.995	266	37.2	2	6	0	4	8	1,1E+07	1,1E+08	10,2	1,5E+07	1,2E+08	1,2E+08	1,0	9	16	0	9	22	*Not specified*	N/A
E9PKZ0	E9PKZ0_HUMAN	**60S ribosomal protein L8 (Fragment)**	RPL8	60	20,893	9,7E+08	22.389	205	23.4	2	2	1	3	5	6,0E+07	3,1E+07	0,5	1,5E+07	1,3E+08	2,5E+08	2,0	12	11	2	12	23	*Not specified*	N/A
P51410	RL9_MOUSE	**60S ribosomal protein L9**	Rpl9	16	9,9177	5,1E+08	21.881	192	40.1	1	0	0	2	5	1,1E+07	1,1E+07	1,0	1,5E+07	1,2E+08	1,2E+08	1,0	2	0	0	2	12	*Not specified*	N/A
P01868	IGHG1_MOUSE	**Ig gamma-1 chain C region secreted form**	Ighg1	9	10,743	6,1E+08	35.704	324	14.5	4	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	0	0	0	0	Secreted	N/A
P01867	IGG2B_MOUSE	**Ig gamma-2B chain C region**	Igh-3	1	4,3819	1,3E+08	44.259	404	22.8	3	0	6	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	1	0	0	Secreted, cell membrane	N/A
P18528	HVM57_MOUSE	**Ig heavy chain V region 6.96**		35	26,516	1,4E+09	11.007	98	30.6	2	3	0	0	1	3,8E+08	1,3E+08	0,3	1,5E+07	1,5E+07	1,5E+07	1,0	11	15	0	0	9	*Not specified*	N/A
P01790	HVM21_MOUSE	**Ig heavy chain V region M511**		34	25,032	5,2E+09	13.652	122	22.1	2	2	0	1	1	1,0E+09	5,8E+08	0,6	1,5E+07	1,5E+07	1,5E+07	1,0	14	16	0	1	3	*Not specified*	N/A
P01629	KV2A4_MOUSE	**Ig kappa chain V-II region 2S1.3**		7	8,2357	1,7E+09	12.221	112	11.6	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	3	0	0	1	*Not specified*	N/A
P01628	KV2A3_MOUSE	**Ig kappa chain V-II region MOPC 511**		6	6,1708	3,3E+08	12.496	113	14.2	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	4	0	0	0	*Not specified*	N/A
P01657	KV3A5_MOUSE	**Ig kappa chain V-III region PC 2413**		14	5,9363	2,6E+09	11.949	111	8.1	1	0	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	7	0	0	2	*Not specified*	N/A
P01635	KV5A3_MOUSE	**Ig kappa chain V-V region K2 (Fragment)**		7	6,1695	6,0E+07	12.581	115	20	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	0	0	0	0	*Not specified*	N/A
P04945	KV6AB_MOUSE	**Ig kappa chain V-VI region NQ2-6.1**		3	5,2464	3,7E+07	11.713	108	29.6	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	*Not specified*	N/A
A0A087WUZ2	A0A087WUZ2_HUMAN	**IgGFc-binding protein**	FCGBP	1	2,9732	3,5E+07	174.12	1642	2.3	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	*Not specified*	N/A
A0A0J9YY99	A0A0J9YY99_HUMAN	**Ig-like domain-containing protein (Fragment)**		61	147,85	9,9E+09	12.965	117	32.5	4	3	0	1	2	2,2E+09	1,3E+09	0,6	1,5E+07	1,5E+07	1,0E+08	7,0	29	26	0	0	6	*Not specified*	N/A
A0A0G2JRQ6	A0A0G2JRQ6_HUMAN	**Ig-like domain-containing protein (Fragment)**		3	3,5392	9,5E+07	12.748	117	13.7	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	*Not specified*	N/A
P01876	IGHA1_HUMAN	**Immunoglobulin heavy constant alpha 1**	IGHA1	193	323,31	5,0E+10	37.654	353	55.5	12	12	0	5	8	9,8E+08	2,2E+09	2,2	1,5E+07	3,8E+08	2,1E+09	5,5	49	79	0	12	53	Secreted, cell membrane	N/A
A0A0A0MS08	A0A0A0MS08_HUMAN	**Immunoglobulin heavy constant gamma 1 (Fragment)**	IGHG1	649	323,31	1,5E+12	43.911	399	58.6	22	19	1	5	9	6,5E+10	4,2E+10	0,6	1,5E+07	7,0E+08	1,4E+09	2,1	291	321	1	10	26	*Not specified*	N/A
P01859	IGHG2_HUMAN	**Immunoglobulin heavy constant gamma 2**	IGHG2	262	323,31	2,3E+11	35.9	326	54	19	15	0	3	6	3,8E+10	1,5E+10	0,4	1,5E+07	8,0E+08	2,9E+08	0,4	152	101	0	3	6	Secreted, cell membrane	N/A
A0A075B5P3	A0A075B5P3_MOUSE	**Immunoglobulin heavy constant gamma 2B (Fragment)**	Ighg2b	42	39,042	4,1E+09	36.568	336	33	5	1	5	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	14	1	27	0	0	*Not specified*	N/A
F6TQW2	F6TQW2_MOUSE	**Immunoglobulin heavy constant gamma 2C (Fragment)**	Ighg2c	10	11,311	4,4E+08	44.095	404	23	5	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	0	0	0	0	*Not specified*	N/A
A0A4W9A917	A0A4W9A917_HUMAN	**Immunoglobulin heavy constant gamma 3 (Fragment)**	IGHG3	1210	323,31	1,6E+12	41.215	377	71.9	22	21	0	4	7	1,1E+11	5,0E+10	0,4	1,5E+07	3,1E+08	7,8E+08	2,5	538	602	0	27	43	*Not specified*	N/A
A0A075B5P5	A0A075B5P5_MOUSE	**Immunoglobulin heavy constant gamma 3 (Fragment)**	Ighg3	10	10,779	3,0E+08	36.198	330	17.3	4	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	1	0	0	0	*Not specified*	N/A
P01861	IGHG4_HUMAN	**Immunoglobulin heavy constant gamma 4**	IGHG4	52	56,179	1,6E+10	35.94	327	54.7	14	12	0	2	4	3,6E+09	1,1E+09	0,3	1,5E+07	1,5E+07	1,5E+07	1,0	29	23	0	0	0	Secreted, cell membrane	N/A
P01871	IGHM_HUMAN	**Immunoglobulin heavy constant mu**	IGHM	388	319,56	4,8E+10	49.439	453	47.5	14	15	0	10	16	4,8E+08	1,3E+09	2,8	1,5E+07	5,6E+08	2,1E+09	3,7	70	108	0	62	148	Secreted, cell membrane	N/A
A0A075B7D0	A0A075B7D0_HUMAN	**Immunoglobulin heavy variable 1/OR15-1 (non-functional) (Fragment)**	IGHV1OR15-1	12	2,9839	1,4E+09	13.012	117	10.3	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	6	0	0	0	*Not specified*	N/A
A0A0C4DH31	HV118_HUMAN	**Immunoglobulin heavy variable 1-18**	IGHV1-18	12	8,6851	2,3E+08	12.82	117	26.5	3	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	8	0	0	0	Secreted, cell membrane	N/A
P23083	HV102_HUMAN	**Immunoglobulin heavy variable 1-2**	IGHV1-2	20	15,805	7,3E+08	13.085	117	22.2	3	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	13	7	0	0	0	Secreted, cell membrane	N/A
A0A0C4DH33	HV124_HUMAN	**Immunoglobulin heavy variable 1-24**	IGHV1-24	2	9,2364	3,5E+07	12.824	117	12.8	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Secreted, cell membrane	N/A
A0A0C4DH29	HV103_HUMAN	**Immunoglobulin heavy variable 1-3**	IGHV1-3	7	8,8951	3,0E+08	13.008	117	22.2	2	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	5	0	0	0	Secreted, cell membrane	N/A
P01743	HV146_HUMAN	**Immunoglobulin heavy variable 1-46**	IGHV1-46	10	13,039	2,7E+08	12.933	117	22.2	2	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	3	0	0	0	Secreted, cell membrane	N/A
P01742	HV169_HUMAN	**Immunoglobulin heavy variable 1-69**	IGHV1-69	23	30,227	1,2E+09	12.659	117	54.7	3	4	0	0	1	1,6E+08	1,0E+08	0,7	1,5E+07	1,5E+07	1,5E+07	1,0	10	12	0	0	1	Secreted, cell membrane	N/A
A0A0B4J1V2	HV226_HUMAN	**Immunoglobulin heavy variable 2-26**	IGHV2-26	18	14,611	1,9E+09	13.182	119	17.6	1	2	0	0	0	2,1E+08	2,7E+08	1,3	1,5E+07	1,5E+07	1,5E+07	1,0	10	8	0	0	0	Secreted, cell membrane	N/A
A0A075B7D8	A0A075B7D8_HUMAN	**Immunoglobulin heavy variable 3/OR15-7 (pseudogene) (Fragment)**	IGHV3OR15-7	15	5,392	7,9E+08	13.08	119	20.2	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	8	0	0	0	*Not specified*	N/A
A0A075B7B8	A0A075B7B8_HUMAN	**Immunoglobulin heavy variable 3/OR16-12 (non-functional) (Fragment)**	IGHV3OR16-12	6	3,4695	9,6E+08	12.874	117	18.8	2	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	3	0	0	0	*Not specified*	N/A
P01766	HV313_HUMAN	**Immunoglobulin heavy variable 3-13**	IGHV3-13	4	3,2377	1,6E+07	12.506	116	19	2	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	0	0	0	0	Secreted, cell membrane	N/A
A0A0B4J1V0	HV315_HUMAN	**Immunoglobulin heavy variable 3-15**	IGHV3-15	13	13,15	1,6E+08	12.926	119	30.3	5	2	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	4	0	0	3	Secreted, cell membrane	N/A
P0DP04	HV43D_HUMAN	**Immunoglobulin heavy variable 3-43D**	IGHV3-43D	13	9,6948	3,9E+08	13.017	118	34.7	3	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	6	0	0	0	Secreted, cell membrane	N/A
A0A0A0MS15	HV349_HUMAN	**Immunoglobulin heavy variable 3-49**	IGHV3-49	22	25,389	2,4E+09	13.056	119	44.5	4	3	0	0	2	4,3E+08	4,1E+08	1,0	1,5E+07	1,5E+07	7,3E+07	4,9	8	8	0	0	6	Secreted, cell membrane	N/A
P01780	HV307_HUMAN	**Immunoglobulin heavy variable 3-7**	IGHV3-7	88	82,212	1,5E+10	12.943	117	39.3	4	3	0	1	3	2,1E+09	6,9E+08	0,3	1,5E+07	1,5E+07	6,2E+07	4,2	41	35	0	2	10	Secreted, cell membrane	N/A
A0A4W8ZXM2	A0A4W8ZXM2_HUMAN	**Immunoglobulin heavy variable 3-72**	IGHV3-72	198	170,14	7,5E+10	11.167	101	74.3	7	4	0	2	2	2,2E+10	5,4E+09	0,2	1,5E+07	5,6E+08	1,3E+09	2,4	94	65	0	14	25	*Not specified*	N/A
A0A0B4J1V6	HV373_HUMAN	**Immunoglobulin heavy variable 3-73**	IGHV3-73	7	8,8274	2,0E+08	12.858	119	31.9	4	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	6	0	0	0	Secreted, cell membrane	N/A
P06331	HV434_HUMAN	**Immunoglobulin heavy variable 4-34**	IGHV4-34	43	35,366	2,8E+09	13.815	123	43.9	5	3	0	0	2	3,8E+08	2,8E+08	0,7	1,5E+07	1,5E+07	1,5E+08	9,8	14	20	0	0	9	Secreted, cell membrane	N/A
A0A075B6R2	HV404_HUMAN	**Immunoglobulin heavy variable 4-4**	IGHV4-4	4	6,795	2,6E+08	12.848	117	31.6	1	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	1	Secreted, cell membrane	N/A
A0A075B5Q9	A0A075B5Q9_MOUSE	**Immunoglobulin heavy variable 5-15**	Ighv5-15	5	3,9267	1,1E+08	12.943	116	23.3	1	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	3	0	0	0	*Not specified*	N/A
A0A0C4DH38	HV551_HUMAN	**Immunoglobulin heavy variable 5-51**	IGHV5-51	29	27,144	3,4E+09	12.674	117	47	4	3	0	0	1	4,8E+08	6,2E+08	1,3	1,5E+07	1,5E+07	1,5E+07	1,0	10	17	0	0	2	Secreted, cell membrane	N/A
A0A075B5Q2	A0A075B5Q2_MOUSE	**Immunoglobulin heavy variable 5-9 (Fragment)**	Ighv5-9	24	8,1262	1,3E+09	12.795	117	18.8	2	2	0	0	1	3,5E+08	1,6E+08	0,4	1,5E+07	1,5E+07	1,5E+07	1,0	13	10	0	0	1	*Not specified*	N/A
A0A0B4J1U7	HV601_HUMAN	**Immunoglobulin heavy variable 6-1**	IGHV6-1	24	3,4591	3,2E+09	13.481	121	13.2	2	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	8	0	3	4	Secreted, cell membrane	N/A
A0A075B5S9	A0A075B5S9_MOUSE	**Immunoglobulin heavy variable 9-4**	Ighv9-4	3	3,0654	2,0E+08	10.934	98	12.2	0	0	1	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	3	0	0	*Not specified*	N/A
A0A075B5V6	A0A075B5V6_MOUSE	**Immunoglobulin heavy variable V1-42**	Ighv1-42	10	12,406	1,6E+08	10.776	98	33.7	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	8	2	0	0	0	*Not specified*	N/A
D6RD17	D6RD17_HUMAN	**Immunoglobulin J chain (Fragment)**	JCHAIN	43	23,029	3,0E+09	18.02	157	28.7	3	4	0	1	2	1,4E+08	2,7E+08	1,9	1,5E+07	1,5E+07	3,1E+08	21,1	10	21	0	4	8	*Not specified*	N/A
A0A140T8N1	A0A140T8N1_MOUSE	**Immunoglobulin kappa chain variable 1-88 (Fragment)**	Igkv1-88	22	148,39	1,1E+10	13.167	120	29.2	4	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	9	0	1	2	*Not specified*	N/A
A0A0B4J1J1	A0A0B4J1J1_MOUSE	**Immunoglobulin kappa chain variable 5-45 (Fragment)**	Igkv5-45	2	5,243	3,0E+08	12.718	115	27	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	1	0	0	0	*Not specified*	N/A
A0A075B5N4	A0A075B5N4_MOUSE	**Immunoglobulin kappa chain variable 8-27**	Igkv8-27	5	3,3061	1,2E+08	10.976	100	24	3	3	0	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	1	0	0	0	*Not specified*	N/A
P01834	IGKC_HUMAN	**Immunoglobulin kappa constant**	IGKC	691	323,31	4,0E+11	11.765	107	84.1	9	7	0	5	5	3,4E+10	1,4E+10	0,4	1,5E+07	9,4E+08	1,7E+09	1,8	325	279	0	16	71	Secreted, cell membrane	N/A
A0A5H1ZRK8	A0A5H1ZRK8_MOUSE	**Immunoglobulin kappa constant (Fragment)**	Igkc	8	44,227	1,5E+09	11.778	107	30.8	0	0	3	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	8	0	0	*Not specified*	N/A
P0DP09	KV113_HUMAN	**Immunoglobulin kappa variable 1-13**	IGKV1-13	12	12,469	5,1E+08	12.569	117	13.7	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	4	0	0	4	Secreted, cell membrane	N/A
A0A0B4J1H8	A0A0B4J1H8_MOUSE	**Immunoglobulin kappa variable 1-133 (Fragment)**	Igkv1-133	5	3,8699	1,4E+08	13.237	120	10.8	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	1	0	0	0	*Not specified*	N/A
P04430	KV116_HUMAN	**Immunoglobulin kappa variable 1-16**	IGKV1-16	12	12,662	3,1E+08	12.618	117	29.1	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	3	0	0	0	Secreted, cell membrane	N/A
P01599	KV117_HUMAN	**Immunoglobulin kappa variable 1-17**	IGKV1-17	47	62,201	2,1E+09	12.778	117	26.5	5	3	0	0	1	3,3E+08	1,2E+08	0,4	1,5E+07	1,5E+07	1,5E+07	1,0	22	20	0	0	5	Secreted, cell membrane	N/A
A0A2Q2TTZ9	A0A2Q2TTZ9_HUMAN	**Immunoglobulin kappa variable 1-33**	IGKV1D-33	52	28,615	7,7E+09	11.842	108	31.5	2	2	0	0	2	1,1E+09	5,6E+08	0,5	1,5E+07	1,5E+07	2,9E+08	19,4	24	17	0	0	11	*Not specified*	N/A
P01602	KV105_HUMAN	**Immunoglobulin kappa variable 1-5**	IGKV1-5	29	32,578	3,5E+09	12.781	117	27.4	4	3	0	0	0	5,2E+08	3,0E+08	0,6	1,5E+07	1,5E+07	1,5E+07	1,0	19	10	0	0	0	Secreted, cell membrane	N/A
A0A0C4DH72	KV106_HUMAN	**Immunoglobulin kappa variable 1-6**	IGKV1-6	36	11,098	2,1E+09	12.697	117	26.5	4	2	0	0	1	2,4E+08	1,2E+08	0,5	1,5E+07	1,5E+07	1,5E+07	1,0	13	15	0	0	8	Secreted, cell membrane	N/A
A0A0C4DH67	KV108_HUMAN	**Immunoglobulin kappa variable 1-8**	IGKV1-8	26	18,971	1,6E+09	12.537	115	29.6	2	2	0	0	1	2,3E+08	1,2E+08	0,5	1,5E+07	1,5E+07	1,5E+07	1,0	9	14	0	0	3	Secreted, cell membrane	N/A
P01611	KVD12_HUMAN	**Immunoglobulin kappa variable 1D-12**	IGKV1D-12	2	3,197	2,3E+08	12.62	117	29.1	1	2	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	Secreted, cell membrane	N/A
A0A0C4DH68	KV224_HUMAN	**Immunoglobulin kappa variable 2-24**	IGKV2-24	30	28,63	3,0E+09	13.079	120	38.3	5	4	0	0	1	6,2E+08	1,3E+08	0,2	1,5E+07	1,5E+07	1,5E+07	1,0	19	10	0	0	1	Secreted, cell membrane	N/A
P06310	KV230_HUMAN	**Immunoglobulin kappa variable 2-30**	IGKV2-30	10	10,201	5,3E+08	13.185	120	41.7	4	1	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	10	0	0	0	0	Secreted, cell membrane	N/A
A0A5H1ZRS2	A0A5H1ZRS2_HUMAN	**Immunoglobulin kappa variable 2D-28**	IGKV2D-28	11	33,33	2,5E+09	11.043	102	43.1	3	2	0	2	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	2	0	2	3	*Not specified*	N/A
A0A5H1ZRS9	A0A5H1ZRS9_HUMAN	**Immunoglobulin kappa variable 2D-29**	IGKV2D-29	5	5,6602	7,1E+07	11.192	102	43.1	4	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	0	0	0	0	*Not specified*	N/A
P04433	KV311_HUMAN	**Immunoglobulin kappa variable 3-11**	IGKV3-11	40	42,613	1,2E+10	12.575	115	26.1	2	3	0	1	2	2,5E+09	1,6E+09	0,7	1,5E+07	1,5E+07	3,6E+08	24,3	12	18	0	3	7	Secreted, cell membrane	N/A
P01624	KV315_HUMAN	**Immunoglobulin kappa variable 3-15**	IGKV3-15	26	20,171	2,5E+09	12.496	115	26.1	3	3	0	1	3	4,1E+08	3,0E+08	0,7	1,5E+07	1,5E+07	1,1E+08	7,4	10	10	0	0	6	Secreted, cell membrane	N/A
P01619	KV320_HUMAN	**Immunoglobulin kappa variable 3-20**	IGKV3-20	68	307,87	3,0E+10	12.557	116	46.6	5	5	0	2	4	3,9E+09	2,2E+09	0,6	1,5E+07	1,8E+08	2,8E+08	1,6	26	29	0	2	11	Secreted, cell membrane	N/A
P06312	KV401_HUMAN	**Immunoglobulin kappa variable 4-1**	IGKV4-1	42	20,781	5,2E+09	13.38	121	29.8	4	4	0	1	3	1,4E+09	5,6E+08	0,4	1,5E+07	1,5E+07	1,3E+08	8,9	18	20	0	1	3	Secreted, cell membrane	N/A
A0A075B677	A0A075B677_MOUSE	**Immunoglobulin kappa variable 4-53**	Igkv4-53	1	2,9665	1,9E+07	10.366	97	18.6	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	*Not specified*	N/A
A0A075B5M7	A0A075B5M7_MOUSE	**Immunoglobulin kappa variable 5-39**	Igkv5-39	8	6,1138	8,3E+07	10.345	95	47.4	3	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	1	0	0	0	*Not specified*	N/A
A0A0C4DH24	KV621_HUMAN	**Immunoglobulin kappa variable 6-21**	IGKV6-21	7	2,9808	7,3E+07	12.43	114	10.5	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	7	0	0	0	0	Secreted, cell membrane	N/A
A0A0A0MT36	KVD21_HUMAN	**Immunoglobulin kappa variable 6D-21**	IGKV6D-21	5	5,0125	1,5E+08	12.34	114	10.5	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	2	0	0	0	Secreted, cell membrane	N/A
A0A140T8M4	A0A140T8M4_MOUSE	**Immunoglobulin kappa variable 8-19**	Igkv8-19	8	3,6641	8,3E+07	11.116	101	23.8	2	2	0	1	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	3	0	0	0	*Not specified*	N/A
A0A075B5N3	A0A075B5N3_MOUSE	**Immunoglobulin kappa variable 8-28**	Igkv8-28	21	4,9589	1,0E+10	10.903	101	23.8	3	3	0	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	9	9	0	2	1	*Not specified*	N/A
P0DOY3	IGLC3_HUMAN	**Immunoglobulin lambda constant 3**	IGLC3	138	56,536	4,2E+10	11.265	106	88.7	6	5	1	2	3	5,1E+09	2,1E+09	0,4	1,5E+07	1,5E+07	3,2E+08	22,0	61	42	0	2	33	Secreted, cell membrane	N/A
A0A0B4J1U3	LV136_HUMAN	**Immunoglobulin lambda variable 1-36**	IGLV1-36	7	7,42	2,9E+08	12.478	117	17.9	2	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	1	0	0	0	Secreted, cell membrane	N/A
P01703	LV140_HUMAN	**Immunoglobulin lambda variable 1-40**	IGLV1-40	21	12,879	7,4E+08	12.301	118	17.8	2	1	0	0	2	1,0E+08	1,1E+07	0,1	1,5E+07	1,5E+07	3,2E+07	2,2	9	7	0	0	5	Secreted, cell membrane	N/A
P01700	LV147_HUMAN	**Immunoglobulin lambda variable 1-47**	IGLV1-47	52	25,805	5,9E+09	12.283	117	29.1	3	3	0	1	2	1,2E+09	7,2E+08	0,6	1,5E+07	1,5E+07	1,2E+08	8,3	21	17	0	4	10	Secreted, cell membrane	N/A
P01701	LV151_HUMAN	**Immunoglobulin lambda variable 1-51**	IGLV1-51	17	18,615	7,1E+08	12.249	117	17.9	1	2	0	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	7	0	0	5	Secreted, cell membrane	N/A
P01704	LV214_HUMAN	**Immunoglobulin lambda variable 2-14**	IGLV2-14	15	9,4648	4,0E+08	12.597	120	13.3	1	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	6	6	0	0	3	Secreted, cell membrane	N/A
A0A075B6J9	LV218_HUMAN	**Immunoglobulin lambda variable 2-18**	IGLV2-18	5	3,8508	2,8E+08	12.412	118	11	1	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	3	0	0	0	Secreted, cell membrane	N/A
A0A075B6K4	LV310_HUMAN	**Immunoglobulin lambda variable 3-10**	IGLV3-10	10	8,7079	3,3E+08	12.441	115	34.8	3	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	4	6	0	0	0	Secreted, cell membrane	N/A
P01714	LV319_HUMAN	**Immunoglobulin lambda variable 3-19**	IGLV3-19	7	6,4192	1,6E+08	12.042	112	27.7	1	3	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	6	0	0	0	Secreted, cell membrane	N/A
P80748	LV321_HUMAN	**Immunoglobulin lambda variable 3-21**	IGLV3-21	54	89,406	7,5E+09	12.446	117	39.3	4	4	0	0	2	1,6E+09	7,7E+08	0,5	1,5E+07	1,5E+07	1,8E+08	12,0	20	28	0	0	6	Secreted, cell membrane	N/A
P01717	LV325_HUMAN	**Immunoglobulin lambda variable 3-25**	IGLV3-25	11	15,131	3,2E+08	12.011	112	36.6	2	3	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	5	0	0	1	Secreted, cell membrane	N/A
P01721	LV657_HUMAN	**Immunoglobulin lambda variable 6-57**	IGLV6-57	14	22,977	6,8E+08	12.566	117	35.9	2	2	0	0	0	7,8E+07	1,0E+08	1,3	1,5E+07	1,5E+07	1,5E+07	1,0	5	9	0	0	0	Secreted, cell membrane	N/A
A0A075B6I0	LV861_HUMAN	**Immunoglobulin lambda variable 8-61**	IGLV8-61	5	11,803	4,3E+08	12.814	122	20.5	2	1	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	1	0	0	2	Secreted, cell membrane	N/A
A0A0B4J1Y8	LV949_HUMAN	**Immunoglobulin lambda variable 9-49**	IGLV9-49	9	10,876	4,6E+08	13.024	123	30.1	4	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	4	0	0	0	Secreted, cell membrane	N/A
B9A064	IGLL5_HUMAN	**Immunoglobulin lambda-like polypeptide 5**	IGLL5	234	323,31	1,6E+11	23.063	214	39.7	6	6	1	2	3	3,1E+10	1,3E+10	0,4	1,5E+07	6,6E+08	1,4E+09	2,2	105	94	1	9	25	Secreted	N/A
O76009	KT33A_HUMAN	**Keratin, type I cuticular Ha3-I**	KRT33A	2	10,273	7,8E+07	45.94	404	31.4	9	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	0	0	*Not specified*	N/A
A2A513	A2A513_MOUSE	**Keratin, type I cytoskeletal 10**	Krt10	2	5,0471	7,2E+07	57.04	561	20	7	10	7	6	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	2	0	0	0	*Not specified*	N/A
P13645	K1C10_HUMAN	**Keratin, type I cytoskeletal 10**	KRT10	582	323,31	1,2E+11	58.826	584	56.3	29	31	24	21	30	2,9E+09	3,1E+09	1,1	8,6E+09	4,4E+09	4,0E+09	0,9	104	164	85	83	146	Secreted	N/A
K7ERE3	K7ERE3_HUMAN	**Keratin, type I cytoskeletal 13**	KRT13	3	7,0387	1,3E+08	45.26	415	17.8	5	9	3	4	6	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	*Not specified*	N/A
Q61781	K1C14_MOUSE	**Keratin, type I cytoskeletal 14**	Krt14	6	3,3074	1,2E+08	52.866	484	25.8	9	9	6	6	15	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	1	4	Cytoplasm, nucleus	N/A
P02533	K1C14_HUMAN	**Keratin, type I cytoskeletal 14**	KRT14	178	152,42	8,9E+09	51.561	472	52.1	17	18	12	11	25	3,0E+08	3,2E+08	1,1	7,7E+08	5,2E+08	4,5E+08	0,9	32	37	19	19	71	Cytoplasm, nucleus	N/A
P08779	K1C16_HUMAN	**Keratin, type I cytoskeletal 16**	KRT16	64	82,545	2,4E+09	51.267	473	49.9	14	14	8	9	23	3,1E+08	4,0E+07	0,1	5,6E+07	1,3E+08	4,0E+08	3,2	12	7	3	10	32	*Not specified*	N/A
Q04695	K1C17_HUMAN	**Keratin, type I cytoskeletal 17**	KRT17	7	8,419	1,8E+08	48.105	432	28.2	7	10	7	8	15	1,1E+07	2,6E+07	2,4	1,5E+07	1,5E+07	1,6E+07	1,1	1	3	0	0	3	Cytoplasm	N/A
P05784	K1C18_MOUSE	**Keratin, type I cytoskeletal 18**	Krt18	13	12,586	2,3E+08	47.538	423	21.7	0	1	2	2	8	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	13	Cytoplasm, nucleus	N/A
Q7Z3Y8	K1C27_HUMAN	**Keratin, type I cytoskeletal 27**	KRT27	16	25,912	1,0E+09	49.822	459	25.1	5	9	1	1	2	6,7E+07	1,3E+08	1,9	1,5E+07	1,5E+07	1,5E+07	1,0	4	12	0	0	0	Cytoplasm	N/A
Q9NSB2	KRT84_HUMAN	**Keratin, type II cuticular Hb4**	KRT84	13	60,378	1,1E+09	64.842	600	26.7	1	12	2	1	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	13	0	0	0	*Not specified*	N/A
P78386	KRT85_HUMAN	**Keratin, type II cuticular Hb5**	KRT85	3	6,5196	7,2E+07	55.802	507	10.1	5	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	*Not specified*	N/A
O43790	KRT86_HUMAN	**Keratin, type II cuticular Hb6**	KRT86	15	42,285	5,3E+08	53.5	486	22.8	9	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	15	0	0	0	0	*Not specified*	N/A
P04264	K2C1_HUMAN	**Keratin, type II cytoskeletal 1**	KRT1	839	323,31	2,0E+11	66.038	644	58.2	32	32	35	31	36	1,5E+10	1,1E+10	0,8	3,0E+10	1,7E+10	1,1E+10	0,7	152	191	151	123	222	Cell membrane	N/A
Q7Z794	K2C1B_HUMAN	**Keratin, type II cytoskeletal 1b**	KRT77	3	6,1968	4,0E+07	61.901	578	7.6	2	5	3	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	0	*Not specified*	N/A
P35908	K22E_HUMAN	**Keratin, type II cytoskeletal 2 epidermal**	KRT2	508	323,31	9,1E+10	65.432	639	66	30	26	34	21	36	4,4E+09	4,2E+09	1,0	1,0E+10	4,8E+09	4,7E+09	1,0	70	117	92	66	163	*Not specified*	N/A
P19013	K2C4_HUMAN	**Keratin, type II cytoskeletal 4**	KRT4	4	8,3383	1,1E+08	56.143	520	14	2	6	2	1	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	3	0	0	1	*Not specified*	N/A
P13647	K2C5_HUMAN	**Keratin, type II cytoskeletal 5**	KRT5	147	70,475	4,7E+09	62.378	590	37.5	19	19	18	12	19	1,4E+08	2,1E+08	1,5	2,9E+08	1,9E+08	1,6E+08	0,9	26	28	21	30	42	*Not specified*	N/A
P02538	K2C6A_HUMAN	**Keratin, type II cytoskeletal 6A**	KRT6A	134	97,648	6,7E+09	60.044	564	39	20	18	12	11	19	5,3E+08	2,8E+08	0,5	4,2E+08	3,0E+08	4,5E+08	1,5	35	33	10	14	42	*Not specified*	N/A
Q3SY84	K2C71_HUMAN	**Keratin, type II cytoskeletal 71**	KRT71	29	24,207	2,1E+09	57.291	523	17.6	5	9	3	2	3	1,9E+08	1,8E+08	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	5	13	1	3	7	Cytoplasm	N/A
Q6IME9	K2C72_MOUSE	**Keratin, type II cytoskeletal 72**	Krt72	5	3,736	2,4E+08	56.75	520	9.4	3	5	3	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	3	0	0	0	*Not specified*	N/A
Q86Y46	K2C73_HUMAN	**Keratin, type II cytoskeletal 73**	KRT73	3	8,7571	1,1E+08	58.923	540	15	5	8	3	2	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	2	0	0	0	*Not specified*	N/A
Q8N1N4	K2C78_HUMAN	**Keratin, type II cytoskeletal 78**	KRT78	5	4,1694	7,8E+07	56.865	520	6.3	0	2	1	0	2	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	1	0	4	*Not specified*	N/A
P11679	K2C8_MOUSE	**Keratin, type II cytoskeletal 8**	Krt8	27	19,126	5,2E+08	54.565	490	22	2	3	3	3	9	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	3	0	1	22	Cytoplasm, nucleus	N/A
A0A087WT19	A0A087WT19_HUMAN	**Keratin-associated protein 10-9**	KRTAP10-9	3	6,8659	2,8E+08	19.72	192	10.4	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	3	0	0	0	0	*Not specified*	N/A
A8MUX0	KR161_HUMAN	**Keratin-associated protein 16-1**	KRTAP16-1	2	3,5281	1,6E+08	53.912	517	2.7	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	0	0	*Not specified*	N/A
Q9BYT5	KRA22_HUMAN	**Keratin-associated protein 2-2**	KRTAP2-2	2	11,051	1,3E+08	12.957	123	18.7	2	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	0	0	0	0	*Not specified*	N/A
Q9BYR2	KRA45_HUMAN	**Keratin-associated protein 4-5**	KRTAP4-5	1	20,882	1,6E+08	19.363	181	10.5	1	0	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	1	0	0	0	0	*Not specified*	N/A
Q5T749	KPRP_HUMAN	**Keratinocyte proline-rich protein**	KPRP	1	3,732	9,5E+07	64.135	579	4.1	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	1	0	0	0	Cytoplasm	N/A
A0A3B2WDD2	A0A3B2WDD2_MOUSE	**Ribosomal protein**	Rpl10a	24	22,521	1,1E+09	21.636	190	26.3	1	5	0	0	1	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	2	21	0	0	1	*Not specified*	N/A
Q9CQF8	RT63_MOUSE	**Ribosomal protein 63, mitochondrial**	Mrpl57	8	4,4414	4,1E+08	11.952	102	12.7	0	1	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	8	0	0	0	Mitochondrion	*Not specified*
A0A2R8YEM3	A0A2R8YEM3_HUMAN	**Ribosomal protein L15 (Fragment)**	RPL15	31	19,415	9,9E+08	19.968	169	29	1	2	0	1	4	1,1E+07	4,1E+07	3,8	1,5E+07	1,5E+07	1,4E+08	9,8	1	9	0	6	15	*Not specified*	N/A
J3QR09	J3QR09_HUMAN	**Ribosomal protein L19**	RPL19	6	4,5785	7,0E+07	23.134	193	18.1	0	0	0	0	3	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	0	0	0	0	6	*Not specified*	N/A
Q9D6S7	RRFM_MOUSE	**Ribosome-recycling factor, mitochondrial**	Mrrf	20	33,662	7,4E+08	29.05	262	29.4	4	2	0	0	0	1,1E+07	1,1E+07	1,0	1,5E+07	1,5E+07	1,5E+07	1,0	12	8	0	0	0	Mitochondrion	*Not specified*