Deficiency of MMP17/MT4-MMP Proteolytic Activity Predisposes to Aortic Aneurysm in Mice

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ABSTRACT

Rationale: Aortic dissection or rupture resulting from aneurysm causes 1-2% of deaths in developed countries. These disorders are associated with mutations in genes that impact vascular smooth muscle cell (VSMC) differentiation and contractility or extracellular matrix (ECM) composition and assembly. However, up to 75% of patients with a family history of aortic aneurysms do not have an identified genetic syndrome.

Objective: To determine the role of the protease MMP17/MT4-MMP in the arterial wall and its possible relevance in human aortic pathology.

Methods and Results: Screening of patients with inherited thoracic aortic aneurysm and dissections (TAAD) identified a missense mutation (R373H) in the *MMP17* gene that prevented expression of the protease in human transfected cells. Using a loss-of-function genetic mouse model, we demonstrated that the lack of Mmp17 resulted in the presence of dysfunctional VSMCs and altered ECM in the vessel wall; and it led to increased susceptibility to angiotensin II-induced thoracic aortic aneurysm (TAA). We also showed that Mmp17-mediated Opn cleavage regulated VSMC maturation via JNK signaling during aorta wall development. Some features of the arterial phenotype were prevented by reexpression of catalytically active Mmp17 or the N-terminal osteopontin (Opn) fragment in Mmp17-null neonates.

Conclusions: Mmp17 proteolytic activity regulates VSMC phenotype in the arterial vessel wall, and its absence predisposes to thoracic aortic aneurysm in mice. The rescue of part of the vessel wall phenotype by a lentiviral strategy opens avenues for therapeutic intervention in these life-threatening disorders.

Keywords:

MMP17, aorta, cardiovascular diseases, aneurysms, osteopontin, matrix metalloproteinases.

Nonstandard Abbreviations and Acronyms:

AAA	abdominal aortic aneurysm
COMP	cartilage oligomeric matrix protein
ECM	extracellular matrix
ERK	extracellular signal-regulated kinases
FBN1	fibrillin-1
GO	gene ontology
GPI	glycosylphosphatidylinositol
HEK	human embryonic kidney
IRES	internal ribosome entry site
iTRAQ	isobaric tag for relative and absolute quantification
JNK	c-Jun N-terminal kinase
Ki67	protein encoded by MKI67 gene
LDS	Loeys-Dietz syndrome
LV	lentivirus
MFS	Marfan syndrome
MMP	matrix metalloproteinase
MT-MMP	membrane-type MMP
mTOR	mammalian target of rapamycin
OPN	osteopontin
PDGF	platelet-derived growth factor
pH3	phosphorylated histone H3
Q-RT-PCR	quantitative-reverse transcriptase PCR
RGD	arginine (R), glycine (G), aspartic acid (D)
SFFV	spleen focus-forming virus
SILAC	stable isotope labeling of amino acids in culture
SM-MHC	smooth muscle myosin heavy chain
TAAD	thoracic aortic aneurysms and dissections
TEM	transmission electron microscopy
TGF	transforming growth factor
TIMP	tissue Inhibitor of metalloproteinase
THBS	thrombospondin
VSMC	vascular smooth muscle cell
WES	whole exome sequencing

INTRODUCTION

Aortic aneurysm predisposes the aorta to dissection or rupture, and causes 1-2% of deaths in developed countries.¹ Thoracic aortic aneurysms and acute aortic dissections (TAADs) that affect young patients result primarily from genetic mutations.² The vulnerability of the aortic wall is mainly due to its poor ability to appropriately accommodate hemodynamic changes. The aortic wall, particularly in the thoracic aorta, is able to distend without requiring subsequent contraction of vascular smooth muscle cells (VSMCs) because of the elastic recoil provided by the layers of elastin lamellae.³ These mechanical properties depend on the intimate physical and mechanical connections of differentiated VSMCs with the extracellular matrix (ECM, mostly elastin and collagen) that they produce and organize, connections that are established through force-dependent adhesion proteins (integrins) and the cytoskeleton (actin and myosin).³ During aortic development, VSMCs differentiate from neural crest and second heart field progenitors, and also from mesenchymal progenitors recruited to the nascent endothelial tube; during this process proper interaction needs to be established between VSMCs and the ECM.⁴ Detailed analysis of pulmonary artery development demonstrated that formation of the vessel wall involves the induction of successive layers of VSMCs and the invasion of the outer layers through the reorientation and radial migration of the inner ones.⁵ Transforming growth factor (TGF) β has been extensively studied as an inducer of VSMC maturation, and more recent studies have identified gradients of platelet-derived growth factor (PDGF) β and other not-yet identified signals as regulators of VSMC differentiation, providing new insights into artery wall development.⁵

This intimate connection between VSMCs and the ECM ensures that alterations to one impact the other, and can have similar effects on the overall mechanical behavior of the vessel. Thus TAADs can be caused by mutations that affect VSMC function or that alter ECM composition and assembly.² For example Marfan syndrome (MFS), a genetic syndrome that predisposes to TAAD, is caused by mutations in the fibrillin-1 (*FBN1*) gene, which encodes an ECM protein necessary for proper elastin formation,⁶ whereas in Loeys-Dietz syndrome (LDS) TGF β receptors type 1 and 2 (*TGFBR1* and *TGFBR2*) are mutated,⁷ resulting in impeded VSMC differentiation.⁸ Predisposition to TAAD is also conferred by mutations predicted to disrupt the ability of the VSMC to contract. Nonetheless, as many as 75% of patients with a family history of aortic aneurysms do not have an identified genetic syndrome.⁹ Recent efforts to identify novel cellular processes and molecular pathways relevant to these disorders have focused on the application of large-scale omics technologies in mouse models of aortic disease. The availability of whole exome sequence (WES) data allows the genes identified in these analyses to be assessed for mutations in patients with inherited TAAD.^{9,10} Matrix metalloproteinases (MMPs), part of the metzincin family of proteases, are able to cleave all ECM components and can also process transmembrane receptors and matrix-bound soluble factors.¹¹ MMPs are proposed to actively participate in vessel wall remodeling,¹² either through direct degradation of elastin, for example by the elastase Mmp12, or by promoting dedifferentiation and activation of VSMC, for example by Mmp14 (Mt1-mmp).¹³⁻¹⁵ Several MMPs are expressed in mouse embryonic aorta;¹⁶ however, their potential role in arterial vessel wall development and function has not been addressed.

Here we report that Mmp17 (also called Mt4-mmp, membrane-type 4-matrix metalloproteinase), is essential for VSMC maturation and function in the arterial vessel wall. Mmp17, which anchors to the plasma membrane through a glycosylphosphatidylinositol (GPI) link, is expressed in adult aortic VSMCs¹⁷ but its substrates and function are poorly characterized.¹⁸ By genomic analysis we have identified a missense mutation in *MMP17* in a patient with TAAD. A genetic model of Mmp17 loss-of-function in mice demonstrated the requirement of Mmp17 activity for VSMC maturation and arterial wall function in vivo and predisposition to thoracic aortic aneurysm in its absence. We also show that osteopontin (Opn) is a required Mmp17 substrate during embryonic development of the aorta. Expression of active Mmp17 or the N-terminal Opn fragment rescued several phenotypic features in Mmp17-null aortas suggesting avenues for therapeutic intervention in TAADs.

METHODS

Mouse line.

Mmp17^{-/-} mice are in the C57BL/6 background.¹⁷ Mice were handled under pathogen-free conditions in accordance with CNIC institutional guidelines. Experiments were performed in accordance with Spanish legislation on animal protection and were approved by the local governmental animal care committee. Experiments were conducted on mice in three age groups: embryos (E10.5 to E18.5), neonates (P0 to P30), and adults (8-to-16 weeks old).

A detailed methods section is provided in the Online Data Supplement.

RESULTS

Genetic analysis of patients affected by TAAD identified an MMP17 missense mutation.

Previous analysis of the relationship of *MMP17* mRNA levels with aortic aneurysms and other arterial pathologies yielded inconclusive results.^{8, 19-21} This prompted us to directly investigate genetic mutations in *MMP17* in individuals with acute aortic dissection involving the ascending or descending aorta. We performed WES in samples from 58 probands from families with an inherited predisposition to TAAD. This analysis identified the missense mutation R373H (p.Arg373His) in the *MMP17* gene (Figure 1A) of a European American male who had a type A aortic dissection (ascending aorta) at the age of 43 years with an aortic root diameter of 5.5 cm and who also suffered a stable chronic type B dissection (non-ascending aorta). Unfortunately no DNA samples were available from the proband's family to determine segregation of the R373H variant with disease. However, two out of three of the proband's siblings developed ascending aortic aneurysm and his father had a type A dissection. Polyphen analysis indicated that the identified mutation was likely to be deleterious, and *in silico* modeling predicted that the R373H mutation in human *MMP17* would cause a conformational change in the C-terminal region (Figure 1B); such a change would presumably impede GPI-tail binding by transamidases during synthesis of the *MMP17* variant on the endoplasmic reticulum, and therefore likely compromise its expression at the plasma membrane. Because *MMP17* forms functional dimers at the plasma membrane,²² we modeled the *MMP17* homodimer conformation *in silico*, finding that the R373H mutation might also affect the arrangement of the catalytic center of the homodimer (Figure 1B). *In silico* modeling of a heterodimer formed by wild-type *MMP17* and R373H mutant monomers yielded no energetically stable conformation, suggesting that the mutation in heterozygosity might behave as a functional homozygous loss.

To test the impact of the R373H mutation on *MMP17* expression, we transfected human embryonic kidney (HEK) 293 cells with wild-type or R373H mutant *MMP17*. Levels of *MMP17* mRNA were similar in wild-type- and R373H-transfected HEK293 cells (Figure 1C), but the mutant *MMP17* protein was undetectable by western-blot or immunostaining (Figure 1D and 1E). Mutant protein was, however, observed in intracellular vesicles upon treatment of R373H-*MMP17*-transfected HEK293 cells with the proteasome inhibitor bortezomib (Figure 1E), suggesting that the mutant *MMP17* gets degraded during its synthesis in the endoplasmic reticulum.

Mmp17-deficient mice are more susceptible to thoracic aortic aneurysm.

These data suggested the possibility that the *MMP17* mutation might predispose to aortic pathology; however since no DNA samples were available from the family to determine segregation of the R373H variant with disease and the co-existence of other pathogenic gene mutations was not thoroughly ruled out, we decided to directly analyze the impact of *MMP17* absence on the arterial vasculature *in vivo* in a loss-of-function

animal model, *Mmp17* knock-out/lacZ knock-in mice (*Mmp17^{lacZ/lacZ}*, referred to here as *Mmp17^{-/-}*).¹⁷ After confirming the expression of *Mmp17* in the smooth muscle cells of different arterial vascular beds of adult wild-type mice (Online Figure I),¹⁷ we explored the effect of its absence on arterial parameters in *Mmp17^{-/-}* mice. Magnetic resonance imaging of live mice revealed that the diameter of the lumen of the descending aorta was 14% larger in *Mmp17^{-/-}* mice (1.076 ± 0.026 mm in wild-type *versus* 1.159 ± 0.018 mm in *Mmp17^{-/-}*) (Figure 2A). The ascending aorta transverse area was slightly but not significantly larger in histological sections, as this was similarly observed by ultrasound analysis, which also revealed an altered movement in the ascending aortas of *Mmp17^{-/-}* mice with respect to wild-types (Online Figure II; Online Movies I and II). Moreover, *Mmp17^{-/-}* mice became hypotensive 8 weeks after birth without showing differences in heart rate (Figure 2B).

Susceptibility to aneurysm in mice can be masked by hypotension; therefore to analyze this susceptibility we treated 16-week-old *Mmp17^{-/-}* and wild-type mice with angiotensin II and monitored blood pressure and aortic diameter in the aortic arch and the abdominal area. Angiotensin II increased blood pressure in both groups (unpublished data). Three out of 14 *Mmp17^{-/-}* mice died by aortic rupture or dissection (21.43%), whereas no deaths were registered in the wild-type group. Consistent with this finding, *Mmp17*-null mice developed TAA at a higher incidence than wild-types (42.86% in *Mmp17*-null mice vs 7.14% in wild-type; $p=0.0384$ by one-tailed Fisher's exact test); thoracic aortas in *Mmp17*-deficient mice were also significantly more dilated after 4 weeks treatment with angiotensin II (Figures 2C, 2D, and 2E). Although *Mmp17^{-/-}* mice showed no overall increased incidence of abdominal aortic aneurysm (AAA) in response to angiotensin II (33.33% in *Mmp17^{-/-}* mice vs 28.54% in wild-type; $p=0.5629$ by one-tailed Fisher's exact test), abdominal aortic diameter was significantly larger than in wild-types (Figures 2F, 2G and 2H).

We next analyzed the response of *Mmp17^{-/-}* vasculature to another model of vascular injury, triggered by ligation of the carotid artery. The carotid vessel of *Mmp17*-null mice displayed outward remodeling, contrasting with inward remodeling in wild-type carotid arteries (Online Figure IIIA and IIIC). Moreover, after 4 weeks of ligation, neointima formation was more-prominent in *Mmp17^{-/-}* carotid arteries, correlating with greater numbers of proliferative VSMCs (Online Figure IIIB and IIID). These data confirm the pathological response of *Mmp17*-null vasculature to injury.

Mmp17 absence affects VSMC orientation and function.

Transmission electron microscopy (TEM) of transverse and longitudinal sections of the aortic vessel wall revealed an aberrant phenotype in the VSMCs of *Mmp17*-null aortas in basal conditions (Figure 3A).²³ These VSMCs were rounder, disconnected from the elastin lamellae, multilayered between elastin lamellae, and helically/radially oriented in contrast to wild-types (Figure 3A). Similar VSMC and ECM alterations were observed in the aortas of heterozygous mice (unpublished data).

These changes were accompanied by altered distributions of the VSMC markers calponin and smooth muscle myosin heavy chain (SM-MHC, also called Myh11) in *Mmp17^{-/-}* aortas (Figure 3B), and the rounded morphology and increased size were confirmed in VSMCs freshly isolated from *Mmp17^{-/-}* aortas (Online Figure IV). Histological analysis of vessel wall structure in the descending aortas of *Mmp17^{-/-}* mice also revealed higher density of VSMC nuclei than found in wild-type counterparts (Figure 3C), a finding confirmed by counting isolated aortic VSMCs (Figure 3D). However, the number of elastin lamellae was unaltered, and immunostaining of phosphorylated histone H3 (pH3) or Ki67 (protein encoded by MKI67 gene) showed no proliferation in *Mmp17^{-/-}* adult aorta (unpublished data).

Mmp17^{-/-} aortas also showed more abundant fibrillar ECM deposits and frayed elastin lamellae (Figure 3A). Verhoeff-van Gieson and Alcian blue staining showed no major differences in the abundance of elastin or glucosaminoglycans (Online Figure VA). However, picrosirius red and second harmonic generation multi-photon microscopy revealed a greater abundance of collagen fibers in *Mmp17*-null aortas, particularly

in the adventitia (Online Figure VB). Analysis of non-pressure-fixed aortas revealed a significantly thicker vessel wall in *Mmp17*^{-/-} mice that was not apparent in pressure-fixed vessels (Figure 3E), indicating a different vessel-wall structure and behavior in response to pressure, in line with the angiotensin II experiment. Consistently, *Mmp17*^{-/-} mesenteric arteries, which showed similar VSMC and ECM features in TEM analysis to those seen in aorta, underwent higher stress under pressure in *ex vivo* assays and contained a below-normal fenestra area in the internal elastic lamina, indicative of altered structure (Online Figure VI).²⁴

Early postnatal onset of the arterial phenotype in Mmp17-deficient mice.

TEM analysis of *Mmp17*-null neonatal aortas revealed rounder and differently distributed VSMCs as early as postnatal day 0 (P0) in transverse and longitudinal sections (Figure 4A). Compared with stage-matched wild-type VSMCs, *Mmp17*^{-/-} VSMCs contained fewer contractile filaments, more rough endoplasmic reticulum and were disconnected from the elastin lamellae (Figure 4A). Moreover, immunostaining for pH3 revealed significantly more VSMCs proliferating in the aortic media layer in *Mmp17*^{-/-} mice at P0 to P7 (Figures 4B and 4C). Analysis of *Tgfb2* and *Tgfb1*, master regulators of VSMC differentiation,^{1,25} also revealed below normal levels of *Tgfb2* mRNA in aorta extracts from *Mmp17*^{-/-} P7 mice, with no alteration in the levels of *Tgfb1* mRNA (Figure 4D).

Consistent with the early (P0) phenotype of *Mmp17*-null mice, LacZ/ β -galactosidase expression (indicating *Mmp17* promoter activation) in developing embryos was evident in peri-aortic VSMC progenitors of heterozygotes (*Mmp17*^{+/-}/lacZ) at E10.5-11.5, with the highest number of β -galactosidase-positive VSMCs detected in the developing aortic media layer at E14.5. (Online Figure VII). *Mmp17* promoter activation subsequently declined at later embryonic stages (E16.5 and E18.5, Online Figure VII).

Proteome analysis of the early and late aortic phenotype in Mmp17-deficient mice.

To understand the molecular mechanisms affected in the absence of *Mmp17*, we performed a multiplexed quantitative proteomics analysis of protein extracts from neonatal (P7) and adult (8-week-old) aortas obtained from *Mmp17*^{-/-} and wild-type mice. We determined the relative abundance between the null and wild-type mice of 2096 proteins in neonates and 2767 proteins in adults. Significant abundance differences between the two genotypes were found for 219 proteins in neonates and 207 proteins in adults. Functional category analysis (Online Table I) identified alterations related to improper VSMC maturation (increased ribonucleoprotein complex/protein synthesis and decreased muscle contraction and intermediate filaments) as the early event in neonatal *Mmp17*-null aortas (Figure 5A), whereas adult *Mmp17*-null aortas were characterized by an overrepresentation of categories related to ECM (in particular collagen) and cellular shape and adhesion (Figure 5B). Notably, neonatal and adult *Mmp17*^{-/-} aortas both had a below normal representation of the mitochondrion category.

Lentivirus-based gene therapy rescues the arterial phenotype of Mmp17-null mice.

We next tested whether the arterial phenotype of *Mmp17*^{-/-} mice could be rescued by lentivirus-driven restoration of *Mmp17* function in VSMCs. Lentivirus encoding wild-type mouse *Mmp17* (Figure 6A) was injected into *Mmp17*^{-/-} mice on postnatal day 1 (P1). After confirming lentivirus-derived *Mmp17* protein expression and corresponding *Mmp17* mRNA levels in aortic VSMCs 7 days after injection (Online Figure VIIIA and VIIIB),²⁶ we analyzed early (P8) and late (8 weeks) phenotypic features (Figure 6B). Expression of catalytically active *Mmp17* from P1 restored VSMC proliferation to normal levels at P8 (Figure 6C) and prevented aortic wall alterations in adult *Mmp17*^{-/-} mice, including diastolic pressure, density of VSMC nuclei, wall thickness in non-pressure-fixed aortas, VSMC morphology and orientation and ECM organization, and distribution of the contractility marker calponin (Figures 6D to 6H). No recovery of phenotypic features was observed in *Mmp17*-null aortas expressing lentivirus encoding the catalytically inactive E248A *Mmp17* mutant, demonstrating that *Mmp17* catalytic activity is necessary for its function in the vessel wall.

To analyze the possible benefit of this strategy in already established disease, we injected lentivirus into adult mice (8-week-old) and analyzed aortas 8 weeks later. Reexpression of catalytically active Mmp17 in adult *Mmp17^{-/-}* mice rescued some of the aortic features, in particular density of nuclei, while the inactive E248A Mmp17 had no effect (Online Figures VIIIC, VIIID and VIIIE and unpublished data).

Mmp17-mediated cleavage of Opn during aorta development is required for c-Jun N-terminal kinase (JNK) signaling in VSMCs.

MMP17 substrates are poorly characterized, with no vascular substrate proposed so far. The dependence of the vascular action of Mmp17 on its catalytic activity prompted us to conduct a SILAC (stable isotope labeling of amino acids in culture) screen for possible substrates in supernatants of cultured cells derived from wild-type or null mice. From a list of putative substrates including osteopontin (Opn), thrombospondin 4 (Thbs4) and cartilage oligomeric matrix protein (Comp), we selected Opn, a matricellular protein expressed in the vessel wall—including embryonic aorta—and associated with aortic aneurysm and VSMC migration and differentiation.²⁷⁻³⁰ We validated human MMP17-mediated OPN cleavage by *in vitro* digestion (Figure 7A), and N-terminal sequencing determined the cleavage site in human OPN to be between Asp²¹⁰ and Leu²¹¹ (Figure 7B). We next modeled the possible apposition of OPN to dimeric MMP17 by *in silico* docking, obtaining a stable model of human OPN in the catalytic center of the MMP17 dimer (Figure 7C).

We next analyzed the putative relevance of Mmp17-mediated Opn cleavage in mouse aorta. Opn expression was detected by immunostaining in embryo aortas, with particularly strong expression at E14.5, correlating with the observed *Mmp17* expression by lacZ and anti- β -galactosidase staining (Figure 7D; Online Figure VII). More intense Opn immunostaining was observed in Mmp17-null aortas at E14.5 (Figure 7D) and western-blot showed accumulation of full length Opn in E14.5 aorta extracts from Mmp17-null embryos with no changes in *Opn* mRNA levels (Figure 7E and 7F). Opn accumulation was also observed in E14.5 cartilage extracts, a tissue in which Mmp17 is also expressed, but not in aortas or cartilage from P7 Mmp17-null neonates (unpublished data). Moreover, the N-terminal Opn fragment was significantly less abundant in Mmp17-null E14.5 aortas (Figure 7E). This N-terminal Opn fragment generated by Mmp17 cleavage in the aorta at E14.5 would contain an active RGD (arginine (R), glycine (G), aspartic acid (D)) site for binding to $\alpha\beta 3$ integrin, known to regulate VSMC adhesion and migration.³¹ Immunostaining analysis of several signaling pathways potentially triggered by this Opn fragment showed selectively fewer phospho-JNK-positive VSMCs in E14.5 Mmp17-null aortas (Figure 7G). These data suggest that regulated and timely cleavage of Opn by Mmp17 is required for proper activation of JNK signaling in the VSMCs of the developing aortic vessel wall.

To investigate the possible link between the reduction of Opn processing and the aortic wall phenotype of Mmp17-null mice, we generated lentiviruses encoding full length Opn and the predicted cleaved N-terminal Opn fragment (Figure 8A) and injected them into P1 Mmp17-null neonates. Production and secretion of Opn protein forms was confirmed *in vitro* by infection of HEK293 and western-blot of culture supernatants (Online Figure IXA). On day 7 after lentivirus injection, GFP signal was detected in the aortas of neonatal *Mmp17^{-/-}* mice (Online Figure IXB). Expression of the N-terminal Opn fragment, but not full length Opn, in Mmp17-null mice restored normal proliferation of VSMCs (pH3-positive cells) in the aortic vessel wall 7 days after injection (Figures 8B and 8C). Immunostaining of aortas from neonate null mice injected with the N-terminal Opn fragment lentivirus also showed significantly increased phospho-JNK in the arterial media (Figure 8D and 8E), indicating that the N-terminal Opn fragment is required for proper activation of JNK signaling in the vessel wall. Finally, as shown in Online Figure IXC, overexpression of the N-terminal Opn fragment rescued the area and roundness in cultured Mmp17-null aortic VSMC, reinforcing the role of N-terminal Opn-mediated signaling in determining a normal VSMC phenotype.

DISCUSSION

Despite the identification and characterization of several mutations responsible for familial TAAD, as many as 75% of inherited syndromes have no known origin. Although *MMP17* mRNA levels have been analyzed in tissue samples and VSMCs from patients with aortic aneurysms and other arterial pathologies, these previous studies yielded inconsistent results regarding a pathogenic effect of altered *MMP17* levels in these disorders.^{8, 19-21} Our exome sequencing data point to missense mutations in human *MMP17* gene as a predisposing factor for some of these cases; however, larger population samples, segregation of the mutation with the disease, and coexistence with other mutations should be analyzed in order to estimate the pathogenic relevance of mutations in this gene and the percentage of TAAD patients affected by them.

In this study we demonstrate the causative role of *Mmp17* in aortic pathology through the use of a loss-of-function genetic mouse model. *Mmp17*-null mice had dilated aortas, with VSMCs rendered dysfunctional by altered morphology and distribution and associated changes to the ECM. These animals were hypotensive and displayed an adaptive adventitial fibrosis, as described in other mouse models of aortic aneurysm and dissection.³² Unlike other mouse models with reported human TAAD mutations, no spontaneous aneurysm was observed in the *Mmp17*-deficient mice, a finding likely related to the mild hypotension in these animals. However, increased vessel wall stress induced by infusion of angiotensin II increased the susceptibility of *Mmp17*-null mice to thoracic (but not abdominal) aortic aneurysm. In several mouse models of aortic aneurysm, although VSMC are dedifferentiated or have synthetic-like phenotype, no significant effects are found on the protein or mRNA expression of true VSMC differentiation markers such as SM-MHC or calponin.³² Likewise, we found no significant effect on the expression levels of these markers in *Mmp17*-null VSMCs, in spite of their striking alterations revealed by TEM. Our data demonstrate that VSMCs in the mouse aorta can express normal levels of contractile markers and yet be dysfunctional due to their mis-orientation within the arterial vessel wall, thus impacting VSMC-ECM mechanical coupling. Mechano-sensing defects in the aortic wall have recently been proposed as a common mechanism to explain the variety of genetic mutations leading to similar pathological outcomes in aortic pathology,³ and findings in *Mmp17*-null arteries in fact indicate a defective elastic recoil/compliance. Impaired VSMC differentiation in *Mmp17*^{-/-} mice could also be related to the altered ECM organization, which might directly decrease *Tgfb1* availability.³³ Proteome analysis did not reveal changes in the levels of the contractile proteins SM-MHC or calponin, but did indicate an important contribution to the phenotype from alterations to actomyosin and cell-adhesion pathways likely related to matrix/force-dependent responses. Proteomics analysis also identified mitochondrial dysfunction in the de-differentiated phenotype of *Mmp17*-null aortic VSMCs, both in neonates and adults. Given the links between mitochondrial function and TGF β signaling in arterial tortuosity syndrome,³⁴ the putative contribution of impaired mitochondrial fitness to aortic aneurysms deserves further investigation.

MMPs are often found expressed at high levels in aneurysms, and are proposed to contribute to disease progression by direct cleavage of ECM components or by affecting VSMC phenotype.¹² A well-established example is *Mmp12* (elastase), which is directly related to aneurysm formation in mouse models.¹⁵ Also, the membrane-type MMP *Mmp14* (Mt1-mmp) is upregulated during pathological vascular remodeling and contributes to PDFGB/PDGFR β -dependent VSMC de-differentiation.^{13, 14, 35} *MMP17* overexpression in tumor cells affects the covering of vascular endothelial cells by pericytes, perivascular cells related to VSMC,³⁶ and the zebrafish homolog *Mmp17b* is required for migration of neural crest cells, which contribute to VSMCs in certain aortic regions.³⁷ Despite these findings and the reported expression of several MMPs during mouse aorta development,¹⁶ no other MMP mutations or MMP-deficient mouse models have been shown to produce aortic aneurysm.^{1, 38} Moreover, we observed no major changes in other MMP family members (*Mmp2*, *Mmp3*, *Mmp7*, *Mmp14*, *Mmp19*, and *Mmp25*) or in tissue inhibitors of MMPs (TIMPs) in *Mmp17*-null aortas at E14.5, P0, or P7, indicating that the lack of *Mmp17* activity is not compensated by related proteases (unpublished data).

Our lentivirus rescue experiments showed that Mmp17 function in the arterial wall required its catalytic activity. This action occurred mainly during embryonic development and involved the spatiotemporal orchestration of signals through the cleavage of Opn, a matricellular protein that can bind cell receptors such as integrins and matrix proteins.²⁷ The role of OPN in the vessel wall has mainly been recognized in the context of vascular pathologies such as aneurysm, atherosclerosis and vascular calcification.²⁷ Opn-null and Opn-overexpressing transgenic mice have vascular phenotypes that resemble those of Mmp17-null aortas: pressure-induced increased lumen diameter and low blood pressure in Opn-null mice and media thickening and high numbers of VSMCs without injury in Opn-transgenic mice.^{28, 39} Despite these observations and the reported expression of Opn in embryonic rat aorta,³⁰ its function in vessel wall development has remained unclear. We detected Opn mainly in the peripheral layer of the embryonic mouse aorta from E14.5 to E18.5, where scattered Mmp17 positive cells are also found. N-terminal and C-terminal Opn fragments modulate migration and proliferation via distinct signaling pathways and in fact we observed below-normal JNK activation in Mmp17-null embryonic VSMCs.^{27, 40} The rescue in neonates, by lentiviral expression of the N-terminal Opn fragment, of JNK signaling and normal VSMC proliferation, demonstrated that spatiotemporally defined cleavage of Opn by Mmp17 is required for proper VSMC migration and distribution during aorta development. The cellular events required for the formation of a multilayered arterial vessel wall are proposed to be regulated by a gradient of soluble signals including PDGFB.⁵ Since PDGFB-induced migration of arterial VSMCs requires Opn secretion,⁴¹ our data are consistent with a regulatory circuit in which PDGFB stimulates Opn production in embryonic VSMCs, followed by Mmp17-dependent Opn cleavage to ensure proper VSMC migration and reorientation. Binding of $\alpha v \beta 3$ integrin to the Opn N-terminal RGD site will lead to mechanical stretch stimulation of JNK;⁴² in this regard, inhibition of phospho-JNK has been shown to decrease Opn-induced VSMC migration.⁴³

Genetic understanding of TAAD etiology is shifting therapies toward gene-tailored management by interfering either with the angiotensin/TGFB axis or the non-canonical TGFB signaling with ERK (extracellular signal-regulated kinases) or mTOR (mammalian target of rapamycin) inhibitors.^{1, 32} In addition, gene therapy for human disease was recently approved, and gene therapy-based interventions are being considered as a viable alternative for treatment of certain cardiovascular diseases.^{44, 45} The present study shows the therapeutic potential of reexpressing Mmp17 or the Opn N-terminal fragment in Mmp17-null VSMCs both as an early intervention and also in established lesions in mice and the possible application in TAAD patients with mutations in *MMP17*. The use of a loss-of-function mouse model and lentiviral-rescue approaches provide evidence of direct contributions by Mmp17 and Opn to arterial vessel wall development and function, and it is possible that Mmp17-dependent processing of undetectable amounts of Opn, or other potential substrates such as Thbs4 (unpublished data), would be sufficient to partially recover the structure and function of the adult vasculature, resulting in reestablishment of vessel wall properties after lentiviral injection. In addition, we propose that diagnosis of *MMP17* mutations could help to identify patients who might eventually benefit from such tailored-gene therapy approaches.

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DISCLOSURES

None.

AUTHOR CONTRIBUTIONS

M.M-A. designed experiments, performed research and wrote the paper; A.B.G-R. and M.S. performed myography studies; D.G. and D.M. performed human genetic analysis; N.M-B. provided technical support in angiotensin II experiments; A.P. provided technical support; C.S-C. performed embryo LacZ staining; F.M. performed *in silico* modeling; E.C. and J.V. performed proteomics analysis; A.A. and J.M.R. helped with the lentiviral approach; and A.G.A. designed the research and wrote the paper.

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FIGURE LEGENDS

Figure 1. R373H mutation in MMP17 in human TAAD impairs protein expression. **A**, Protein domain structure of human MMP17. The arrow marks the mutation found in a TAAD patient at Arg373. **B**, 3D tertiary protein structures of the lowest energy models for human wild-type MMP17 (left panels) and the R373H mutant (right). Monomers (upper panels) and homodimers (lower panels) are shown. The same colors used for the domain structure (**A**) are used in the 3D models (orange, catalytic center; red, C-terminal residue). Domains with a different orientation in the wild-type and mutant versions are shown in blue. **C**, Quantitative-reverse transcriptase-PCR (Q-RT-PCR) analysis of *MMP17* mRNA levels in HEK293 cells non-transfected (control) or transfected with wild-type or R373H mutated human MMP17, presented as calibrated normalized relative quantity (CNRQ) obtained in qBase analysis; $n = 4$ independent experiments, mean $\pm$ s.e.m. **D**, Representative western-blot of MMP17 protein expression in HEK293 cells transfected with wild-type or R373H mutated human MMP17. **E**, Representative confocal microscope images of transfected HEK293 cells with or without treatment with bortezomib. Cells were stained with anti-MMP17 antibody (green) and Hoechst (blue). Scale bar 20 μ m. $n = 5$ independent experiments.

Figure 2. *Mmp17*^{-/-} mice are more susceptible to thoracic aortic aneurysm in response to angiotensin II. **A**, Representative magnetic resonance images of thoracic descending aorta (left) and lumen diameter quantification (right) in wild-type or *Mmp17*^{-/-} adult mice (12 weeks old; $n = 8$ mice per genotype). **A**, aorta lumen; scale bar 1 mm. **B**, Systolic and diastolic blood pressure and heart rate in 8-week-old wild-type and *Mmp17*^{-/-} mice (representative data are shown from one of 4 independent experiments with similar results; $n = 10$ mice per genotype). **C**, Ultrasound-measured lumen diameter of thoracic ascending aorta (aortic arch) ($n = 14$ mice per genotype tested in two independent experiments). **D**, Representative pictures of thoracic aortas from wild-type and *Mmp17*^{-/-} mice treated with angiotensin II for 28 days (left, wild-type; right, *Mmp17*^{-/-}). Scale bar 2000 μ m. **E**, Histological transverse cuts of ascending thoracic aortas (aortic arch) from angiotensin II-treated wild-type (left) and *Mmp17*^{-/-} mice (right). Scale bar 500 μ m. **F**, Ultrasound-measured lumen diameter of abdominal aorta ($n = 14$ mice per genotype tested in two independent experiments). **G**, Representative pictures of abdominal aortas from wild-type and *Mmp17*^{-/-} mice treated with angiotensin II for 28 days (left, wild-type; right, *Mmp17*^{-/-}). Scale bar 2000 μ m. **H**, Histological transverse cuts of abdominal aortas from angiotensin II-treated wild-type (left) and *Mmp17*^{-/-} mice (right). Scale bar 500 μ m. Numerical data are means $\pm$ s.e.m. Data in **A** and **B** were tested by Student's *t*-test (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$) and data in **C** and **F** were compared by two-way ANOVA followed by Bonferroni post-test.

Figure 3. Arteries from *Mmp17*^{-/-} mice contain aberrant and mis-oriented VSMCs. **A**, Representative TEM images of ultrathin transverse (top) and longitudinal (bottom) sections of thoracic aorta. Note the differences in VSMC morphology, cell-ECM connections (arrows), and cell-cell connections (arrowheads) between wild-type and *Mmp17*^{-/-} aortas. *Mmp17*^{-/-} mice also showed excess ECM (asterisks) and frayed elastin layers (inset, right panel). Scale bar 4 μ m. $n = 10$ mice per genotype. IEL, internal elastic lamina; N, nuclei. **B**, Representative confocal microscopy images of SM-MHC and calponin staining (white), elastin auto-fluorescence (green) and nuclear Hoechst staining (blue) in transverse aortic sections from wild-type or *Mmp17*^{-/-} mice. Scale bar 20 μ m. $n = 7$ mice per genotype. **C**, Density of cell nuclei in transverse sections of wild-type and *Mmp17*^{-/-} aorta stained with Hoechst and elastin auto-fluorescence (nuclei from endothelial and adventitial cells were excluded) ($n = 30$ mice per genotype analyzed in 5 independent experiments). **D**, Numbers of VSMCs freshly isolated from wild-type or *Mmp17*^{-/-} aortas ($n = 8$ aortas per experiment and genotype in 7 independent experiments). **E**, Representative images of transverse sections of thoracic aorta from wild-type and *Mmp17*^{-/-} mice stained with hematoxylin and eosin (left) (scale bar 50 μ m) fixed under pressure (top) or fixed after perfusion (bottom) and media layer thickness (right) and its quantification; $n = 15$ mice per genotype analyzed in 3 independent experiments. Numerical data are means $\pm$ s.e.m., and were tested by unpaired Student's *t*-test (* $p < 0.05$, ** $p < 0.01$).

Figure 4. Perinatal onset of the arterial phenotype of *Mmp17*^{-/-} mice. **A**, Representative TEM images of ultrathin transverse (top) and longitudinal (bottom) aortic sections from neonate (P0) wild-type and *Mmp17*^{-/-} mice. Note the cell-ECM connections (arrows) in wild-type tissue, contrasting with the abundance of microfibril bundles (arrows) and cellular debris (asterisks) in *Mmp17*^{-/-} aortas. Scale bars, 5 and 0.5 μ m for transverse and 5 and 2 μ m for longitudinal sections (n = 3 mice per genotype). **B**, Representative confocal microscope images of aortas from 7-day-old (P7) wild-type and *Mmp17*^{-/-} mice, showing anti-pH3 immunostaining (red), elastin auto-fluorescence (green) and Hoechst nuclear staining (blue). Scale bar 20 μ m. White arrowheads highlight pH3 positive nuclei. **C**, Numbers of pH3-positive nuclei in the media layer of aortas from P0 to P30; n = 15-17 mice per genotype and time point analyzed in 3 independent experiments. **D**, Q-RT-PCR analysis of *Tgfb2* mRNA levels in P7 total aorta extracts, presented as fold change from calibrated normalized relative quantity (CNRQ) obtained in qBase analysis; n = 21 mice per genotype analyzed in 3 independent experiments. Numerical data are means $\pm$ s.e.m., and were tested by one-way ANOVA in **C** (***) p<0.001) and one-sample t-test in **D** (** p<0.01).

Figure 5. Quantitative proteomics comparison of the proteomes of aortas from wild-type and *Mmp17*^{-/-} neonatal (A) and adult (B) mice. Proteins were extracted from 7 pooled aortas per genotype at P7 and from 3 pooled aortas per genotype in adults. Protein pools were digested, and the resulting peptides were subjected to relative quantification by mass spectrometry in multiplexed mode using isobaric tag for relative and absolute quantification (iTRAQ) labeling. The quantitative protein data were grouped into gene ontology (GO) functional categories and the data were analyzed to determine significant category changes. Cumulative frequency distributions of standardized log2 ratios of proteins (Zq) were plotted to show the coordinated alterations (up or down) in proteins belonging to the changing categories. These functional categories showed an abundance decrease (Zq > 0, right shift of sigmoidal curves, blue) or an abundance increase (Zq < 0, left shift of curves, red) in *Mmp17*-null mice relative to the wild-type mice. The dashed lines represent the null-hypothesis distribution, and the black lines show the distribution of all proteins quantified in each experiment.

Figure 6. Expression of catalytically active *Mmp17* in *Mmp17*^{-/-} mice prevents aortic phenotype. **A**, Design of the lentiviral (LV) vector. The vector directs SFFV (spleen focus-forming virus)-driven *Mmp17* expression and IRES (internal ribosome entry site)-driven expression of GFP. **B**, Lentiviral rescue strategy. Lentivirus was injected one day after birth (P1) and mice were sacrificed and analyzed for different parameters 7 days or 8 weeks later. **C**, Numbers of pH3-positive VSMCs 7 days after lentiviral injection of mock (empty vector encoding GFP), wild-type *Mmp17* or E248A mutant *Mmp17* into wild-type or *Mmp17*^{-/-} mice (n = 10-19 mice per condition analyzed in 3 independent experiments). **D-F**, Diastolic blood pressure, density of cell nuclei, and media thickness in non-pressure fixed aortas 8 weeks after injection with mock, wild-type *Mmp17* or E248A mutant *Mmp17* lentivirus (n = 12-20 mice per condition analyzed in 4 independent experiments). **G**, Representative TEM images of thoracic aortic sections 8 weeks after injection with mock, wild-type *Mmp17* or E248A mutant *Mmp17* lentivirus (n = 4 mice per condition analyzed in 3 independent experiments). Scale bar 5 μ m. **H**, Representative confocal microscopy images of calponin immunostaining (white), elastin auto-fluorescence (green), and Hoechst nuclear staining (blue) in thoracic aortic sections 8 weeks after injection with mock, wild-type *Mmp17* or E248A mutant *Mmp17* lentivirus (n = 10 mice per condition analyzed in 3 independent experiments). Scale bar 20 μ m. Data in **C-F** are presented as means $\pm$ s.e.m., and were tested by one-way ANOVA followed by Tukey's multiple comparison test (* p<0.05, ** p<0.01, *** p<0.001).

Figure 7. Osteopontin (Opn) cleavage by *Mmp17* is required for JNK activation in VSMC during aorta development. **A**, Representative western-blot of human OPN after in vitro digestion by human recombinant MMP17. Full length OPN and its C-terminal fragment are detected with the OPN antibody anti-C-terminal (1H3F7). n = 7 independent experiments. **B**, Scheme of human OPN protein. The cleavage site for human MMP17 is localized between 210 and 211 residues (arrow). **C**, *In silico* model of OPN (purple) bound to human MMP17 homodimer (green). Note the location of the OPN cleavage site (yellow) close to the MMP17 catalytic center (orange). **D**, Representative confocal microscopy images of E14.5 *Mmp17*-null aortas stained

for *Opn* (red), with nuclear Hoechst staining in blue. Scale bar 20 μ m. (n = 5-7 embryos per genotype). **E**, Representative western-blot of *Opn* in aortic extracts from E14.5 wild-type (+/+) and *Mmp17*^{-/-} (-/-) embryos (pool of 8-10 embryonic aortas or sternal cartilage pieces per genotype). The chart shows average fold-change of the quantification of the bands corresponding to full length (FL) and the N-terminal *Opn* fragment (N-term) as indicated in the western-blot; n = 3 independent experiments. **F**, Graph shows quantification (fold change) of *Opn* mRNA levels by Q-RT-PCR in aortic extracts from E14.5 wild-type (+/+) and *Mmp17*^{-/-} (-/-) embryos (pool of 4-10 embryonic aortas; n = 4 independent experiments). **G**, Representative confocal microscopy images of E14.5 wild-type and *Mmp17*-null aortas stained for phospho-JNK (red) and CD31 (white), with nuclear Hoechst staining in blue (n = 5-7 embryos per genotype). Scale bar 50 μ m (left) and 20 μ m (right). Numerical data in **E** and **F** are means $\pm$ s.e.m. and were tested by one-sample t-test.

Figure 8. Lentiviral injection of N-terminal *Opn* fragment rescues VSMC proliferation and JNK signaling in *Mmp17*^{-/-} neonatal aortas. **A**, LV design showing full length and N-terminal mouse *Opn* constructs. **B**, Representative confocal images of pH3 staining (red) in P8 aortas from *Mmp17*-null mice injected at P1 with N-terminal (N-term), full length (FL) *Opn* or control LV (left) and quantification of pH3-positive cells (right). (n = 16 to 20 mice per condition, analyzed in two independent experiments). **D**, Representative confocal images of P8 aortas from null mice injected with LV as in **B**, stained for phospho-JNK (green) (left) and quantification of average fluorescence intensity in the arterial media (right); nuclear Hoechst staining in blue. (n = 16 to 20 mice were analyzed per condition in two independent experiments). Numerical data are means $\pm$ s.e.m. and were tested by one-way ANOVA followed by Tukey's multiple comparison test (** p<0.01, *** p<0.001).

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Novelty and Significance

What Is Known?

- Aortic aneurysms result from alterations to extracellular matrix (ECM) assembly and/or vascular smooth muscle cell (VSMC) maturation in the aortic vessel wall.
- Matrix metalloproteinases (MMP) are considered active players in the progression of pathological vascular remodeling.
- Osteopontin (OPN) is a matricellular protein with recognized functions in vascular pathology.

What New Information Does This Article Contribute?

- The absence of the matrix metalloproteinase Mmp17 affects the vascular smooth muscle cell phenotype in the aorta and results in increased predisposition to thoracic aortic aneurysms.
- A novel molecular axis involving Mmp17/Opn cleavage and phospho-JNK signaling is shown to be required for normal VSMC maturation and distribution during aorta development.
- Lentiviral-based expression of active Mmp17 or the N-terminal OPN fragment rescues the aortic VSMC phenotype in Mmp17-null mice.

Aortic aneurysms are associated with high mortality due to increased risk of aorta dissection and rupture. These disorders are often associated with mutations in genes that impact VSMC differentiation and contractility or ECM composition and assembly, thus affecting the mechanics of the vessel wall. Novel therapies are mostly focused on the inhibition of components of the angiotensin II/ TGFbeta signaling pathway. In this study we identify the protease Mmp17 as required for proper VSMC maturation and distribution in the aortic wall. Mutations found in the *MMP17* gene in thoracic aortic aneurysm patients suggested that the absence of MMP17 increases predisposition to TAA, and this was confirmed in a genetic loss-of-function model in mice. We have also delineated a novel molecular pathway in which Mmp17-dependent cleavage of the matricellular protein OPN is required for activation of phospho-JNK in VSMC, regulating their normal maturation and distribution in the aorta during embryonic development. Lentiviral-based expression of active Mmp17 or the N-terminal fragment of Opn rescues the VSMC phenotype in the aortas of MMP17-deficient mice, opening potential options for personalized gene therapy in these life-threatening disorders.

Figure 1-R3

Figure 2-R3

Figure 3-R3

Figure 4-R3

Figure 5R3

Figure 6-R3

Figure 7-R3

Figure 8-R3

Supplemental Material

Supplemental Methods

Exome sequencing. The study protocol was approved by the Committee for the Protection of Human Subjects at the University of Texas Health Science Center at Houston, and the study participants gave informed consent. Genomic DNA was extracted from peripheral blood lymphocytes using standard protocols. Five µg samples of DNA from probands were used for construction of the shotgun sequencing library using adaptors for paired-end sequencing.¹ Exome sequences were captured with SeqCap EZ. Exome probes version 1.0 (Roche, Basilea, Switzerland) and recovered according to manufacturer's directions. Enriched libraries were then sequenced on an Illumina (San Diego, USA) GAIIX. Reads were mapped to the reference human genome (UCSC hg19, Santa Cruz, USA) with BWA (Burrows-Wheeler Aligner),² and variants called with SAMtools.³

MMP17 *in silico* modeling. A theoretical model of the MMP17 protein was calculated using the *de novo* prediction method with the structural homologs comparison approach. The Fasta sequence (603 aminoacids (aa)) of the MMP17 protein precursor (UniProtKB: Q9ULZ9.4) was processed to eliminate the signal peptide and pro-peptide sequences and yield a new sequence for the mature wild-type protein (440 aa: positions 126 to 565 of the precursor protein). A similar process was used with a point mutation (R373H) in the precursor protein sequence. Both MMP17 sequences were submitted to the iTASSER server (<http://zhanglab.ccmb.med.umich.edu/I-TASSER/>).⁴ We selected the PDB (Protein Data Bank) model with highest probability and minimal energy compatible with biochemical properties (di-S intrachain, accessible and exposed glycosylation sites and accessible active region [active site and neighboring zinc binding sites] C-score= -0.43 for wild-type (WT) and C-score= -0.18 for R373H-mutant). Both models were aligned, visualized and decorated using PyMol v1.6.0.0. *In silico* models of wild-type and R373H-mut MMP17 homodimers were calculated by submitting PDB models of monomeric MMP17 or monomeric MMP17-R373H to Hex server v 6.9 (<http://hexserver.loria.fr/>).⁵ Docking in dimer mode was predicted with shape and electrostatic restrictions to select the best (minimal energy) model of each

dimer type compatible with biochemical properties (di-S interchain).⁶ Docking predictions for the MMP17 dimer (WT) as receptor and OPN as ligand were submitted to the ClusPro server (<http://cluspro.bu.edu>),⁷ and the best model compatible with the biological topology of the MMP17 binding site was selected. The model was then refined by closer pre-alignment of the MMP17 dimer to the binding site using PyMol v 1.6.0.0, and this refined preliminary model was submitted to the docking application of the ROSIE server (<http://rosie.rosettacommons.org>) with default values. From the ten models with the lowest energy, we selected the model with best topology (and smallest binding distance, score = -770.875).

MMP17 R373H generation and HEK293 transfection. The human *MMP17*-PG6 vector was mutated with the QuikChange Site-Directed Mutagenesis Kit (Agilent Technologies, Santa Clara, USA) to yield the hMMP17 R373H mutant. The following primers were used: Fw 5'-GGCACAGATGCACCACTTCTGGCGGG-3' and Rv 5'-CCCGCCAGAAGTGGTGCATCTGTGCC-3'. HEK293 cells (80% confluence) were transfected over 3 hours with wild-type or R373H-mutated *MMP17* vectors using Lipofectamine 2000 (Invitrogen, Waltham, USA), and expression was analyzed during the subsequent 24 hours. The transfected cells were treated with 100 µg/ml bortezomib (Sigma-Aldrich, St. Louis, USA) for 24 hours. Protein and RNA were extracted as described later. For immunofluorescence assay, HEK293 cells were fixed for 10 minutes in 4% paraformaldehyde (PFA) in PBS and permeabilized with 0.1% Triton X-100 for 5 minutes. The anti-human MMP17 antibody (M3684, Sigma-Aldrich) was used at 1:100 dilution followed by secondary anti-rabbit antibody and cells were visualized under a Zeiss LSM 700 microscope. Figure panels show maximal projections of confocal images.

Mouse Line. *Mmp17*^{-/-} mice in the C57BL/6 background have been described previously.⁸ Mice were handled under pathogen-free conditions in accordance with CNIC institutional guidelines. Experiments were performed in accordance with Spanish legislation on animal protection and were approved by the local governmental animal care committee. All mice were genotyped by PCR of tail samples using the following primers: *Mmp17* SK1 5'-TCAGACACAGCCAGATCAGG-3'

SK2 5'-AGCAACACGGCATCCACTAC-3' and SK3 5'-AATATGCGAAGTGGACCTGG-3'.

Experiments were conducted on mice in three age groups: embryos (E10.5 to E18.5), neonates (P0 to P30), or adults (8- to 16-weeks old).

Magnetic resonance imaging. Magnetic resonance images were obtained in anesthetized adult mice (12 weeks old) using a Bruker Biospec 47/40 instrument (60 mm gradient, 35 mm internal diameter quadrature coil). Images were taken every millimeter in the descending thoracic and abdominal aorta and the lumen area was measured using Image J (NIH, <http://imagej.nih.gov/ij/>),⁹ and OsiriX software (Geneva, Switzerland).

Hemodynamic measurements. Tail cuff measurements of blood pressure were taken in groups of 10 mice per genotype and condition, using BP2000 (Visitech Systems, Apex, USA). Ten recordings of each conscious mouse were obtained after one week of training over 5 consecutive days at the same hour of the day. Average values were calculated for each mouse from the measurements recorded over the 5 days.

Angiotensin II infusion by miniosmotic pump implantation. 16-week-old mice were administered with angiotensin II by subcutaneous osmotic minipump infusion (Alzet DURECT Corporation, Cupertino, USA) as described previously.¹⁰ Angiotensin II (Sigma-Aldrich) was administered at 1 µg/kg/min during 28 days and blood pressure was monitored once a week by tail cuff. Aortic lumen diameter of ascending thoracic aorta and abdominal aorta was analyzed by high-frequency ultrasound with the VEVO770 system (VisualSonics, Toronto, Canada). TAA was defined as $\geq 25\%$ increase in aortic arch intraluminal diameter together with the presence of the following histological features: breakage and loss of elastin fibers, inflammatory infiltrate in the adventitia and/or media, VSMC loss, and thickening of the media on one side and thinning on the opposite site of the aortic section.¹¹ AAA was defined by intraluminal diameter of the abdominal aorta (suprarenal area) ≥ 1.3 mm together with the presence of

pronounced ECM remodeling and thrombus.¹² After perfusion with 4% PFA and 2% sucrose in PBS, aortas were embedded in paraffin for histological analysis.

Histological, LacZ and immunohistochemical studies. Aortas were excised after perfusion under constant pressure with 4% PFA, 2% sucrose in PBS (pressure-fixed aortas) or perfusion with PBS alone (non-pressure-fixed aortas). Aortas were then either embedded directly in OCT or further fixed for 12 hours and embedded in paraffin. Paraffin-embedded aorta cross-sections (7 μ m) were stained with H&E, picrosirius red, alcian blue or Verhoeff-van Gieson stain. Aortic medial thickness, density of nucleus, lumen area, and elastin lamellae number were measured independently by two researchers blinded to sample identity, and were quantified using MetaMorph software (Molecular Devices LLC, Sunnyvale, California). Endothelial and adventitial cells were excluded from the analysis. For LacZ analysis, OCT frozen sections (5 μ m) of vessels and embryos were fixed in 0.125% glutaraldehyde in PBS for 5 minutes, rinsed in PBS and incubated at 37°C overnight in X-gal buffer (5 mM potassium ferrocyanide, 5 mM potassium ferricyanate, 2 mM MgCl₂ and 0.1% X-gal in PBS). Immunohistochemical staining for Mmp17 (PAB4785, Abnova, Taipei, Taiwan) was performed on OCT sections fixed in 4% PFA, 2% sucrose for 7 minutes; for SM-MHC (BT-562, Biomedical Technologies Inc., Alfa Aesar, Ward Hill, USA), calponin (E798Y clone, ab46794, Abcam, Cambridge, UK), and anti- pH3 (06-570, Millipore, Billerica, USA), OCT sections were first permeabilized with 0.1% Triton X-100 for 5 minutes. Sections were then processed for incubation with specific secondary antibody and Hoechst stain. pH3-positive medial aortic cells were quantified by counting the number of positive VSMCs per transverse section. One to five sections were analyzed per mouse. For GFP analysis, overnight fixed (4% PFA) aortas were embedded in OCT and sections were stained with anti-GFP antibody (ab13970, Abcam). For analysis of aortas in embryos, E14.5 embryos were perfused and fixed overnight in 4% PFA, 2% sucrose solution followed by 30% sucrose solution for 3 hours. OCT sections were stained for Opn (AF808 polyclonal antibody, R&D, Minneapolis, USA), β -galactosidase (ab4761, Abcam), phospho-JNK (9255, Cell signaling, Danvers, USA) and CD31 (MAB1398Z, Millipore) followed by the specific secondary antibody (Alexa Fluor, Invitrogen).

Preparations were mounted in Fluoromount G imaging medium (4958-02, Affymetrix eBioscience, San Diego, USA). Images were acquired with Zeiss LSM 700 confocal microscope at 21-23°C using 25X (LD LCI Plan Apo 25X/0.8) and 63X (Plan Apo 63X/1.4 oil DICII) objectives. Images were analyzed using Zen 2011 software (Zeiss, Jena, Germany) and maximal projections are shown (25X magnification). Quantification of phospho-JNK was performed using MetaMorph software.

RNA purification and quantitative reverse transcriptase PCR (Q-RT-PCR). Total RNA was isolated from E14.5 embryonic aortas, neonate or adult descending aortas, or cultured cells with the RNeasy® Mini Kit (Qiagen, Venlo, Netherlands). Aortas were first placed in lysis buffer and disrupted with sterile ceramic beads using a MagNA Lyser (Roche), with two rounds of 6500 rpm for 30 seconds each, with care taken to maintain the sample cold. RNA was quantified by spectrophotometry (ND1000 Spectrophotometer, NanoDrop, (Thermo Scientific, Wilmington, USA)) and RNA integrity was monitored by ethidium bromide staining after agarose gel electrophoresis. cDNA was synthesized from 1 µg of total RNA using the Qiagen Omniscript RT Kit (Qiagen). Q-RT-PCR was performed using TaqMan probes for mouse *Mmp17* (Mm00449292), human *MMP17* (Hs00211734) and mouse *Tgfb2* (Mm00436955) in an ABI PRISM® 7900HT FAST Q-RT-PCR System. All samples were analyzed in triplicate, and RNA levels (CNRQ; calibrated normalized relative quantity) were obtained with Biogazelle qBase PLUS software. For human analysis, *hTFRC* (00951083_m1), *hHMBS* (00609297) and *hTBP* (00427621) housekeeping genes were used. For mouse analysis, *mGapdh* (99999915), *mTbp* (00446973) and *mHprt* (00446968) probes were used for normalization (Taqman). SYBR green (Applied Biosystems, Carlsbad, USA) was used in *mOpn* mRNA analysis. *mOpn* probes were as follow: FW 5'-AGCAAGAACTCTTCCAAGCAA-3'; RV 5'-GTGAGATTCGTCAGATTCATCCG-3'. *mGapdh* and *mTbp* were used for normalization (*mGapdh*: FW 5'-AATGCATCCTGCACCACCAA-3'; RV 5'-GTGGCAGTGATGGCATGGA-3' and *mTbp*: FW 5'-GCTCTGGAATTGTACCGCAG-3'; RV 5'-CTGGCTCATAGCTCTTGGCTC-3').

Protein extraction and western-blot analysis. Protein extracts were obtained from cell cultures as described.⁶ Briefly, cell monolayers were covered with cold lysis buffer (25 mM Tris-HCl [pH 8.0], 100 mM NaCl, 1% IGEPAL CA-630 and 60 mM Octyl glucoside) supplemented with 20 mM N-ethylmaleimide (NEM, Sigma-Aldrich) and protease inhibitors (Complete, Mini, EDTA-free, Roche). Descending aortas were disrupted with MagNA Lyser (Roche) in cold regular RIPA buffer or the specific Tris-based lysis buffer described above. Proteins (50 to 150 µg) were resolved by 7-12% SDS-PAGE in reducing or non-reducing conditions and transferred onto nitrocellulose membranes (0.45 µm, Bio-Rad, Hercules, California). Antibodies against MMP17 (EP1270Y clone, ab51075, Abcam.), tubulin (ab6160, Abcam.) and β-actin (A5441, Sigma-Aldrich,) were used at 1:1000 dilution. For Opn analysis in E14.5 embryos a pool of 8-to-10 aortas or a piece of cartilage were disrupted as before and resolved on 4-20% gradient gels (Bio-Rad). Antibodies to Opn (18621, IBL, Fujioka, Japan) and calponin (E798Y clone, ab46794, Abcam) were used at a 1:1000 dilution overnight. Immunoreactive proteins were visualized with corresponding fluorochrome-conjugated secondary antibodies (680 or 800 ODYSSEY IRDye®) and recorded by Licor Odyssey technology. Quantification of western-blot bands was performed using ODYSSEY software (LI-COR Biosciences, Lincoln, USA).

Transmission electron microscopy. Male mice were anesthetized and trans-cardially perfused with Sörensen solution [pH 7.3] at 100 mmHg pressure (50 ml) followed by fixation solution (50 ml PBS containing 4% PFA and 1% glutaraldehyde) using a peristaltic pump (Dynamax, Rainin RP1, Mettler Toledo, Greifensee, Switzerland). Dissected arteries were additionally fixed in the same solution for 16 hours. Arteries were then embedded in resin (Durcupan ACM Fluka, Sigma-Aldrich) for transverse or longitudinal sectioning, and ultrathin sections were cut and counterstained by the Electron Microscopy core (SIdI service) at the Universidad Autónoma de Madrid (Madrid). Sections were imaged using a transmission electron microscope (Jeol Jem 1010, 80Kv, Jeol Ltd. Tokyo, Japan) and recorded with a Gatan camera (Orius, SC200, Pleasanton, California) at the indicated magnifications. VSMC phenotype was determined according to reported criteria.¹³ Thoracic descending aortas and mesenteric arteries of adults or neonatal mice of

each genotype and condition were visualized and used for morphological and ultrastructural analysis and for quantification of medial thickness with MetaMorph software.

VSMC isolation and culture. Six to eight aortas from 8-week-old male mice were pooled to obtain a cell suspension.¹⁴ Briefly, after fat removal under a microscope, aortas were incubated in collagenase solution (collagenase type I, 3.33 mg/ml, Worthington, Lakewood, USA) for 5 minutes at 37°C, allowing the removal of the adventitia with forceps. The aortas were then cut into small pieces and a cell suspension was obtained by incubation for 45 minutes at 37°C in 6 mg/ml type I collagenase and 2.5 mg/ml elastase (Worthington) diluted in DMEM. VSMCs were counted in a Neubauer chamber and cultured on 0.02% gelatin-coated plates in DMEM supplemented with 20% fetal bovine serum (FBS) (Gibco, Invitrogen), 2 mM L-glutamine (Lonza, BioWhittaker, Basel, Switzerland), 0.1 mM nonessential amino acids (Sigma-Aldrich) and penicillin (50 UI/ml), streptomycin (50 µg/ml) (P/S) (Lonza, BioWhittaker). Endothelial cells (mouse aortic endothelial cells, MAEC) were positively selected from the VSMC culture with an antibody to intercellular adhesion molecule 2 (anti-ICAM-2; 553325 BD Biosciences, Franklin Lakes, USA) coupled to magnetic beads, and were cultured as indicated.¹⁵ Macrophages were differentiated from bone marrow cells by treatment for 7 days with interleukin-3 (IL-3, PeproTech, Rocky Hill, USA), granulocyte macrophage colony-stimulating factor (GM-CSF, PeproTech) and stem cell factor (SCF, PeproTech) (20 ng/ml) in IMDM medium (Lonza) supplemented with 10% FBS, followed by incubation for 5 days with M-CSF (PeproTech) (10 ng/ml) in the same medium. VSMC morphology was analyzed at passage 0 by fixing cultures in 4% PFA, 2% sucrose for 10 minutes and staining with Texas Red®-X-phalloidin (1:200; Invitrogen). Total cell area and shape factor or roundness ($4\pi\text{Area}/\text{Perimeter}^2$) were calculated by masking with MetaMorph software. Lentiviruses encoding GFP (Mock), N-term Opn or full-length Opn (see below) were incubated for 5 hours at 1-10 MOI (multiplicity of infection) with cultured VSMC (passage 0). After virus removal, GFP signal was analyzed at 24 h and 48 h (maximum of protein generation) after infection. Cells were fixed 48 h after virus infection in 4% PFA for 10 min and washed with PBS. VSMC area and shape factor were evaluated in GFP-positive cells by analysis of confocal maximal

projections (Zeiss LSM 700 confocal microscope) with Image J (NIH, <http://imagej.nih.gov/ij/>)⁹. Shape factor (or roundness) values close to 1 indicate a circular form, whereas values closer to 0 indicate an elongated object.

Myography experiments. The structural and mechanical properties of mesenteric resistance arteries were studied with a pressure myograph (Danish Myo Tech, Model P100, J.P. Trading I/S, Aarhus, Denmark).¹⁶ Briefly, the vessel was placed on two glass microcannulae and secured with a nylon surgical suture. After tying off any small branches, vessel length was adjusted so that the vessel walls were parallel without stretch. Intraluminal pressure was then raised to 120 mmHg and the artery was unbuckled by adjusting the cannula. The segment was then set to a pressure of 70 mmHg and allowed to equilibrate for 30 minutes at 37°C in calcium-free KHS (0Ca²⁺-KHS, prepared by omitting calcium and adding 10 mM EGTA). Intraluminal pressure was reduced to 3 mmHg. A pressure-diameter curve was obtained by increasing intraluminal pressure in 20 mmHg steps between 3 and 120 mmHg. Internal and external diameters were continuously measured under passive conditions (D_{i0Ca} , D_{e0Ca}) for 3 minutes at each intraluminal pressure. The final value used was the mean of the measurements taken during the last 30 seconds, when the measurements reached a steady state. Finally, the artery was set to 70 mmHg in 0Ca²⁺-KHS, pressure-fixed with 4% PFA in 0.2 mM phosphate buffer [pH 7.2-7.4] at 37°C for 60 minutes, and kept in 4% PFA at 4°C for confocal microscopy studies. Passive structural and mechanical parameters were calculated from internal and external diameter measurements in passive conditions as follows: Wall thickness, $WT = (D_{e0Ca} - D_{i0Ca})/2$ and Circumferential wall stress ($\sigma = (P \times D_{i0Ca})/(2WT)$, where P is the intraluminal pressure (1 mmHg = 1.334×10^3 dynes/cm²) and WT is wall thickness at each intraluminal pressure in 0Ca²⁺-KHS. The content and organization of elastin and the number of VSMCs in mesenteric arteries were studied in pressure-fixed (70 mmHg), maximally relaxed intact segments using a confocal microscope.¹⁶ Briefly, stacks of images from the adventitia to the lumen (z step= 0.5 μ m) were captured using the 488-nm line of the confocal microscope. A minimum of 2 image stacks from different regions was captured in each arterial segment. All the images were taken under identical conditions of laser intensity, brightness and contrast. Quantitative analysis

was performed with MetaMorph image analysis software.¹⁶ Internal elastic lamina (IEL) thickness was measured from each stack of serial images. Thereafter, individual projections of the IEL were reconstructed and total fenestrae area was measured.

Second harmonic generation multi-photon microscopy. Autofluorescence of organized collagen (425-465 nm filter) and elastin auto-fluorescence (478-573 nm filter) was visualized in fresh aortic sections from wild-type or *Mmp17*^{-/-} adult mice with a Zeiss LSM 780 microscope (Spectra-Physics Mai Tai DS [pulse<70 ps] Laser). 3D rendering reconstruction of aorta thickness (Z stack between 35 and 54 μ m) was performed using Imaris software (Bitplane, Switzerland).

Carotid artery ligation. The left carotid artery was ligated as described previously.¹⁷ Twenty-eight days later, mice were anesthetized and perfused with PBS (5 ml) followed by 4% PFA (5 ml, for 3 minutes). Left and right carotid arteries were excised, further fixed overnight and embedded in paraffin or in OCT. Ligated vessels were sectioned from the aortic arch to the beginning of the ligature, and morphometric analysis was performed along the whole vessel length (approximately 9 mm). H&E-stained paraffin-embedded sections were quantified for neointima or external area (external elastic layer area) using MetaMorph software. OCT sections were stained for Ki67 (ab16667, Abcam) proliferation marker at 1:100 dilution, followed by a fluorescent anti-Rabbit secondary antibody.

Proteomic analysis based on isobaric tags for relative and absolute quantitation (iTRAQ).

Samples (200 μ g) were trypsin-digested separately using the whole proteome in-gel digestion protocol.¹⁸ Peptide iTRAQ labeling was performed essentially according to the manufacturer's instructions. After labeling, the samples were vacuum-dried and redissolved in 1% trifluoroacetic acid for both desalting and removal of excess labeling reagent in reversed-phase C-18 extraction cartridges (Oasis, Waters Corporation, Milford, MA, USA). High-resolution analysis of iTRAQ-labeled peptides was carried out on an Easy nLC 1000 nano-HPLC apparatus (Thermo Scientific, San Jose, CA, USA) coupled to a linear ion trap Orbitrap mass spectrometer (Orbitrap Elite,

Thermo Scientific). Peptides were suspended in 0.1% formic acid and then loaded onto a home-made C-18 reversed-phase nano-column (100 μ m I.D., 45 cm) and separated in a continuous gradient consisting of 8-31% B for 180 min and 31-90% B for 2 min (B = 90% acetonitrile, 0.1% formic acid) at 300 nL/min. Peptides were ionized using a Picotip emitter nanospray needle (New Objective, Woburn, MA, USA). Each MS run consisted of enhanced FT-resolution spectra (120,000 resolution) in the 390–1,200 m/z range followed by data-dependent MS/MS spectra of the 20 most intense parent ions acquired during the chromatographic run. The AGC target value in the Orbitrap for the survey scan was set to 1,000,000. Fragmentation in the linear ion trap was performed at 32% normalized collision energy with a target value of 10,000 ions. The full target was set to 30,000, with 1 microscan and a 100 ms injection time, and the dynamic exclusion was set to 0.5 min. For peptide identification the MS/MS spectra were searched with the Sequest algorithm implemented in Proteome Discoverer 1.3 (Thermo Scientific). The results were analyzed using the probability ratio method,¹⁹ and a false discovery rate (FDR) for peptide identification was calculated based on the search results against a decoy database using the refined method.²⁰ The iTRAQ reporter ion intensities were retrieved from MS/MS scans by QuiXoT software,^{21, 22} and used as inputs to the weighted spectrum, peptide and protein statistical (WSPP) model,²⁰ to obtain peptide and protein abundance changes. In a further step, proteins were classified into ontological categories according to the GO database, and abundance changes at the protein function level were analyzed as described.²⁰ Protein or functional abundance changes were considered statistically significant when they had an FDR below 5%.

Proteomic analysis based on stable isotope labeling by amino acids in cell culture (SILAC).

SILAC assay was performed as previously described,¹⁵ in highly proliferative cells. Briefly, bone-marrow-derived macrophages from wild-type or *Mmp17*^{-/-} mice were cultured in p100 plates (10 plates per genotype; pool of 3 mice per genotype) by seeding 6.5x10⁶ cells per plate in SILAC medium (Invitrogen) supplemented with penicillin/streptomycin, L-glutamine, Hepes and 10% bovine fetal serum, and isotopic amino acids (heavy Lysine and Arginine in wild-type, and light in *Mmp17*^{-/-}). Supernatants (SN) were collected and processed as per the manufacturer's instructions.

In brief, the SN of both genotypes were mixed 1:1 and enriched for glycosylated proteins by incubation with lectin WGA beads. Proteins were then reduced and alkylated, resolved by SDS-PAGE, and stained with colloidal Coomassie, and 20 bands were cut. Bands were processed at the Vall d'Hebron Research Institute (Barcelona, Spain), where proteins were digested with trypsin and the obtained peptides analyzed by mass spectrometry. The data obtained were analyzed with Protein Scape 2.1 and WARP-LC 1.2 software platform (Bruker, Billerica, USA).

In vitro digestion assay and N-terminal sequencing. Human recombinant OPN (500 to 2 µg; hrOPN, R&D, 1433-OP/CF) were incubated with 500 ng of the catalytic domain of human recombinant MMP17 (hrMMP17, 475940, Calbiochem, Billerica, USA) in digestion buffer (50 mM Tris-HCl, 10 mM CaCl₂, 80 mM NaCl, [pH7.4]) for 2 hours at 37°C. Samples were separated by 12% SDS-PAGE and transferred to nitrocellulose membranes (Bio-Rad 45 µm). Full-length OPN and fragments were detected with anti-C-terminal OPN antibody recognizing aminoacids 234 to 240 of the human OPN sequence (1H3F7).²³ An anti-mouse secondary antibody was used. N-terminal sequencing was performed according to Alphalyse guidelines (www.alphalyse.com/nterm_preparation_guideline.html, Palo Alto, USA). Briefly, 6 µg of hrOPN and 3 µg of hrMMP17 catalytic domain were incubated as described and the digestion mixture separated on a 4-16% Tricine gel (Mini-Protean® Tris-Tricine precast gel; Bio-Rad). Proteins were transferred to a PVDF membrane (Immobilon-PSQ, Millipore), and the obtained OPN C-terminal cleavage-derived band in the membrane was visualized by Coomassie staining and used for N-terminal sequencing.

Lentiviral vector generation and infection. Lentiviral vectors were generated using the mouse full-length *Mmp17* vector (ID 5716458, Invitrogen) or the E248A mutant, which was created using the QuikChange Site-Directed mutagenesis Kit (Agilent Technologies, Santa Clara, USA) with the following primers: Fw 5'-GTGGCCGTCCATGCGTTTGGTCATGCC-3' and RV 5'-GGCATGACCAAACGCATGGACGGCCAC-3'. Vectors were cloned into the SFFV-IRES-GFP lentiviral backbone and sequenced to check proper sequence mutation. Lentiviruses

expressing Mock-GFP, Mmp17-GFP or Mmp17 E248A-GFP were prepared and titered as previously described.²⁴ Mouse full length *Opn* was obtained from Sino Biological Inc. (MG50116-M), and subcloned into the same lentivirus backbone. N-terminal *Opn* were obtained with the following primers: FW 5' GGATCCGCATGAGATTGGCAGTGA 3', RV 5' CTAAAGCTGGGGAACAG 3'. Analysis of lentivirus-driven protein production was first analyzed by infection in HEK293 cells. Lentiviruses were injected intravenously at approximately 1×10^8 pfu/ml. P1-stage mice were injected with ~10 μ l of virus solution into the jugular vein after ice anesthesia, using a Hamilton syringe inserted through the neck skin. Mice were sacrificed 1 week (P8) or 8 weeks after injection. For injection into adult mice (8 weeks-old), 100 μ l of virus solution (1×10^8 pfu/ml) was injected into the jugular vein after skin excision, and mice were sacrificed 8 weeks later. Aortas were collected and processed for protein extraction, RNA extraction, microscopy or electron microscopy analysis according to the protocols described above.

Statistical analysis. The statistical analysis performed in each case is explained in detail in the corresponding figure legend. Data were analyzed by two-tailed Student's *t*-test or by one- or two-way ANOVA followed by the indicated comparison test for data with Gaussian normal distribution. Non-normal distributions were analyzed by Wilcoxon test or by one sample *t*-test for fold-induction comparisons. The one-tailed Fisher's exact test was used to analyze the incidence of aneurysm. For comparison of different groups or conditions, one- or two-way ANOVA was used, followed by the indicated comparison test in each case (Bonferroni or Tukey multiple comparison tests). Statistical tests were conducted with Prism 5 software (GraphPad Software, Inc., La Jolla, USA). Data are presented as mean $\pm$ s.e.m. and differences were considered statistically significant at $p < 0.05$: * p value < 0.05 , ** p value < 0.01 , and *** p value < 0.001 .

Supplemental References

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Online Figures

Online Figure I. *Mmp17* is expressed in VSMCs of several arteries. **A**, Representative images of transverse sections of aortas, mesenteric arteries and coronary arterioles from wild-type and *Mmp17*^{-/-} mice stained for LacZ (n = 5-10 mice per genotype in 3 independent experiments). Scale bar 50 μm. **B-D**, *Mmp17* mRNA levels (Q-RT-PCR), protein expression (western-blot) and immunostaining in aortas from wild-type and *Mmp17*^{-/-} mice (n = 30 mice per genotype in 9 independent experiments in **B** and **C**; n = 5 mice in **D**). Scale bar 20 μm. **E**, *Mmp17* mRNA levels in VSMCs, endothelial cells (ECs) and macrophages from wild-type and *Mmp17*-null mice (n = 24 mice per genotype in 3 independent experiments). Bars in **B** and **E** are means ± s.e.m of calibrated relative normalized quantity (CRNQ) of RNA, obtained with qBase software. One representative experiment is shown in **B** and **E**.

Online Figure II. Analysis of ascending aortas of *Mmp17^{-/-}* mice. **A**, Representative images of ascending aortas in transverse cut. The graph shows lumen area (right). $n = 5$ mice per genotype. Scale bar $200\ \mu\text{m}$. **B**, Echocardiography in adult mice showing larger aortic arch diameter in basal conditions in the *Mmp17*-null animal. **C**, Quantification of aortic arch diameter ($n = 8$ mice per genotype). Data are means $\pm$ s.e.m. and were tested by unpaired Student *t*-test in **A** ($p=0.3070$) and **C** ($p=0.1609$).

Online Figure III. Carotid ligation induces outward remodeling and formation of a larger neointima in *Mmp17^{-/-}* mice. **A**, Representative images of sections stained with H&E from right non-ligated (upper panel) and left ligated carotid arteries (lower panel) 28 days after ligation. Scale bar 100 μm . **B**, Representative confocal images of carotid arteries 28 days after ligation immunostained with anti-Ki67 (green). Elastin (auto-fluorescence, green) and nuclei (Hoechst, blue) are also shown. Scale bar 100 μm . **C**, External elastic lamina (EEL) area in wild-type and *Mmp17^{-/-}* carotid arteries and **D**, neointima area quantified along the carotid artery from the aortic arch to the ligation site. One representative experiment is shown of representative of 2 independent experiments. $n = 10$ mice per genotype. Numerical data in **C** and **D** are presented as means $\pm$ s.e.m. and were tested by one-way ANOVA (***) $p < 0.001$) followed by Tukey's multiple comparison, (* $p < 0.05$, *** $p < 0.001$) in **C** and two-way ANOVA (***) $p < 0.001$) in **D**.

Online Figure IV. *Mmp17*^{-/-} VSMCs display increased size and rounder morphology. **A**, Representative epifluorescence microscopy images from cultured VSMCs stained for F-actin (phalloidin, red). Scale bar 10 μ m. **B-C**, Cellular area and roundness (cellular shape factor) quantified in cultured VSMCs isolated from wild-type and *Mmp17*-null aortas (A.U., arbitrary units). Data are presented as means of $\pm$ s.e.m.; and were tested by unpaired Student's *t*-test (* $p < 0.5$, ** $p < 0.01$) ($n = 5$ independent experiments performed; 100 cells quantified per genotype).

Online Figure V. ECM composition and distribution in *Mmp17^{-/-}* aortas. **A**, Representative images of transverse sections of thoracic aortas from wild-type and *Mmp17^{-/-}* mice stained for elastin (Verhoeff-van Gieson) and proteoglycans (Alcian blue) (n = 8 to 12 mice per genotype analyzed in 2 independent experiments). Scale bar 50 µm. **B**, Representative images of transverse sections of thoracic aortas from wild-type and *Mmp17^{-/-}* mice stained for collagen (picrosirius red). Scale bar 50 µm. 3D-rendering reconstruction of second harmonic generation multi-photon microscopy images from wild-type and *Mmp17^{-/-}* aortas (SHG fibrillar collagen in red, and auto-fluorescent elastin in green). Arrows point to collagen deposits in the adventitia of null mice (n = 4 mice per genotype analyzed in 3 independent experiments). Scale bar 30 µm.

Online Figure VI. Mesenteric artery phenotype in *Mmp17*^{-/-} mice. **A**, Lumen and external diameter of mesenteric artery in wild-type and *Mmp17*^{-/-} mice in response to intraluminal pressures applied *ex vivo* between 0 and 120 mmHg (n = 9 mice per genotype). **B**, Vessel wall stress in response to intraluminal pressure in mesenteric arteries from wild-type and *Mmp17*-null mice and **C**, fenestra area in the internal elastic lamina (n = 9 mice per genotype analyzed in 3 independent experiments). **D**, Representative TEM images of mesenteric artery transverse sections from wild-type and *Mmp17*^{-/-} mice. IEL, internal elastic lamina. n = 5 mice per genotype. Scale bar 5 μm and 0.5 μm in inset (bottom). **E-F**, Vessel wall thickness and VSMC nuclear density in mesenteric arteries from wild-type or *Mmp17*-null mice. n = 3 mice per genotype (thickness) and 9 mice per genotype analyzed in 4 independent experiments (VSMC nuclear density). Data are means $\pm$ s.e.m. and were tested by unpaired Student *t*-test in **C**, **E** and **F** (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$) and by two-way ANOVA (***) $p < 0.001$) in **A** and **B**.

A*Mmp17*^{+/LacZ} **B**

Online Figure VII. *Mmp17* expression during embryonic aorta development. **A**, Representative images of LacZ staining in aortas from E10.5, E11.5, E14.5, E16.5 and E18.5 *Mmp17*^{+/LacZ} embryos. n = 4 mice per time point. Scale bar 20 μ m (E10.5 and E11.5) and 50 μ m (E14.5 to 18.5). **B**, Representative confocal microscopy images of E14.5, E16.5 and E18.5 *Mmp17*^{+/LacZ} embryo aortas showing anti- β -galactosidase nuclear immunostaining (white) and nuclei Hoechst (blue). Note abundant positive cells in the E14.5 medial layer compared to the few positive cells in E18.5 aorta. Scale bar 50 μ m. n = 2 to 3 mice per genotype.

Online Figure VIII. Expression of catalytically active *Mmp17* in *Mmp17*-null VSMCs of adult mice ameliorates the vascular phenotype. **A**, Representative immunofluorescence images of aortic sections stained for *Mmp17* (white) 8 weeks after lentiviral injection of mock vector (SFFV-driven, IRES-GFP), *Mmp17*-WT or *Mmp17*-E248A vector at P1. $n = 19$ to 21 mice in 3 independent experiments. Scale bar $20\ \mu\text{m}$. Auto-fluorescent elastin, green. **B**, *Mmp17* mRNA levels 8 weeks after injection at P1 of lentivirus encoding for *Mmp17* ($n = 12$ mice per genotype analyzed in 3 independent experiments). **C-E**, Diastolic pressure, VSMC nucleus density and media thickness, 8 weeks after lentiviral injection in adults (8-week-old). $n = 9$ to 11 mice per condition in 3 independent experiments. Numerical data are means $\pm$ s.e.m. of mRNA levels obtained in qBase analysis in **B**. Data in **C-E** were tested by one-way ANOVA (**C**, ** $p < 0.01$, **D**, *** $p < 0.001$) followed by Tukey's multiple comparison test (* $p < 0.05$, ** $p < 0.01$).

Online Figure IX. Expression of N-terminal Opn fragment in *Mmp17*-null VSMCs rescues VSMC morphological alterations. **A**, Western-blot of cell lysates and supernatants (SN) of HEK293 cells infected with mock, N-term or FL Opn lentivirus. **B**, Confocal images of anti-GFP immunostaining (green) of transverse aortic sections from P8 neonates 1 week after injection with mock, N-term or FL Opn lentivirus. Scale bar 20 μm . **C**, Representative pictures of wild-type and null VSMC infected with mock, N-term or FL Opn lentivirus showing GFP-positive-infected cells. Scale bar 50 μm . Quantification of area and roundness are depicted. (n= 2 independent experiments. One representative experiment is shown with 35 to 50 cells quantified per condition). Data are means $\pm$ s.e.m. and were analyzed by one-way ANOVA (***) $p < 0.001$) followed by Bonferroni post-test (** $p < 0.01$, *** $p < 0.001$).

Online Movies I and II. Movies show echocardiography recording of the aortic arch of wild-type (Movie I) and Mmp17-null (Movie II) mice.

Online Table I

Neonate (P7) and adult protein components of the GO categories found significantly altered in the iTRAQ proteomics experiment. Proteins were classified into GO categories and statistically significant differences at the protein function level were determined as explained in Supplemental Methods. Proteins are sorted according to Zq, the standardized log2-ratio of protein abundance, which describes the variation of protein log2-ratio around the grand mean of the experiment in units of standard deviation, according to the formulation of the WSPP model.

Neonate (P7) iTRAQ proteins in categories

Adult iTRAQ proteins in categories

Actin filament binding GO:0051015			Collagen GO:0005581		
Protein identification	Zq	rank/N	Protein identification	Zq	rank/N
>sp Q61879 MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-2.659	0.015	>sp P28481 CO2A1_MOUSE Collagen alpha-1(II) chain OS=Mus musculus GN=Col2a1 PE=	-3.672	0.025
>sp O88990 ACTN3_MOUSE Alpha-actinin-3 OS=Mus musculus GN=Actn3 PE=2 SV=1	-2.598	0.044	>sp Q3U962 CO5A2_MOUSE Collagen alpha-2(V) chain OS=Mus musculus GN=Col5a2 PE=	-3.301	0.075
>sp Q8VDD5 MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-2.481	0.074	>tr B1AVK5 B1AVK5_MOUSE Procollagen type IV alpha 6 OS=Mus musculus GN=Col4a6	-3.035	0.125
>sp Q9JI91 ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	-2.471	0.103	>sp P39061 CO1A1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1	-2.832	0.175
>sp O89053 COR1A_MOUSE Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	-2.163	0.132	>sp P28301 LYOX_MOUSE Protein-lysine 6-oxidase OS=Mus musculus GN=Lox PE=1 SV=	-2.625	0.225
>sp Q8BTM8 FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	-1.903	0.162	>sp P11087 CO1A1_MOUSE Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1	-2.341	0.275
>tr A1BN54 A1BN54_MOUSE Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=2 SV=1	-1.873	0.191	>sp O88207 CO5A1_MOUSE Collagen alpha-1(V) chain OS=Mus musculus GN=Col5a1 PE=	-2.086	0.325
>sp Q01279 EGFR_MOUSE Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=	-1.839	0.221	>sp Q01149 CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=	-2.071	0.375
>sp P26040 EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	-1.714	0.250	>sp Q04857 CO6A1_MOUSE Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=	-1.838	0.425
>sp Q7TMB8 CYFP1_MOUSE Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfp	-1.485	0.279	>sp Q80X19 COEA1_MOUSE Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1	-1.625	0.475
>sp P57780 ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	-1.441	0.309	>sp Q8C6K9 CO6A6_MOUSE Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=	-1.617	0.525
>sp Q61233 PLSL_MOUSE Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	-1.265	0.338	>sp A6H584 CO6A5_MOUSE Collagen alpha-5(VI) chain OS=Mus musculus GN=Col6a5 PE=	-1.559	0.575
>sp P28650 PURA1_MOUSE Adenylosuccinate synthetase isozyme 1 OS=Mus musculus GN=Adss1 F	-1.133	0.368	>sp O35206 COFA1_MOUSE Collagen alpha-1(XV) chain OS=Mus musculus GN=Col15a1 I	-1.486	0.625
>sp Q9WUM4 COR1C_MOUSE Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-1.090	0.397	>sp P08122 CO4A2_MOUSE Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2 PE=	-1.401	0.675
>sp P26231 CTNA1_MOUSE Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	-1.026	0.426	>sp Q99K41 EMIL1_MOUSE EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1	-1.307	0.725
>sp Q9QYC0 ADDA_MOUSE Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2	-0.981	0.456	>sp P02463 CO4A1_MOUSE Collagen alpha-1(IV) chain OS=Mus musculus GN=Col4a1 PE=	-1.034	0.775
>sp Q6PB66 LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musc	-0.883	0.485	>sp Q02788 CO6A2_MOUSE Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=	-0.863	0.825
>sp Q7TPR4 ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	-0.667	0.515	>tr B7ZNH7 B7ZNH7_MOUSE Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a	-0.770	0.875
>sp A2ALU4 SHRM2_MOUSE Protein Shroom2 OS=Mus musculus GN=Shroom2 PE=1 SV=1	-0.588	0.544	>sp Q60847 COCA1_MOUSE Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 I	0.294	0.925
>sp Q9WUM3 COR1B_MOUSE Coronin-1B OS=Mus musculus GN=Coro1b PE=1 SV=1	-0.573	0.574	>sp Q60994 ADIPO_MOUSE Adiponectin OS=Mus musculus GN=Adipoq PE=1 SV=2	0.829	0.975
>sp Q62418 DBNL_MOUSE Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2	-0.323	0.603	Myosin complex GO:0016459		
>sp Q9QYB8 ADDB_MOUSE Beta-adducin OS=Mus musculus GN=Add2 PE=1 SV=4	-0.152	0.632			
>sp Q8K4L3 SVIL_MOUSE Supervillin OS=Mus musculus GN=Silv PE=1 SV=1	-0.101	0.662	Protein identification	Zq	rank/N
>sp Q6ZWR6 SYNE1_MOUSE Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2	-0.067	0.691	>sp Q64331 MYO6_MOUSE Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1	-3.068	0.024
>sp Q61553 FSCN1_MOUSE Fascin OS=Mus musculus GN=Fscn1 PE=1 SV=4	-0.020	0.721	>tr Q69ZX3 Q69ZX3_MOUSE MKIAA0866 protein (Fragment) OS=Mus musculus GN=Myh	-3.047	0.071
>sp Q9ERGO LIMA1_MOUSE LIM domain and actin-binding protein 1 OS=Mus musculus GN=Lima1	0.000	0.750	>sp Q5SX40 MYH1_MOUSE Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1	-2.997	0.119
>sp P47757 CAPZB_MOUSE F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1	0.099	0.779	>sp Q5SYD0 MYO1D_MOUSE Unconventional myosin-Id OS=Mus musculus GN=Myo1d P	-2.771	0.167
>sp Q64331 MYO6_MOUSE Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1	0.103	0.809	>sp Q6URW6 MYH14_MOUSE Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-2.680	0.214
>sp Q7TPW1 NEXN_MOUSE Nexilin OS=Mus musculus GN=Nexn PE=1 SV=3	0.219	0.838	>tr Q3UFT0 Q3UFT0_MOUSE Putative uncharacterized protein (Fragment) OS=Mus muscul	-2.267	0.262
>sp Q6URW6 MYH14_MOUSE Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	0.273	0.868	>sp Q8VDD5 MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-2.160	0.310
>sp P47753 CAZA1_MOUSE F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 I	0.345	0.897	>sp Q3THE2 ML12B_MOUSE Myosin regulatory light chain 12B OS=Mus musculus GN=M	-1.838	0.357
>sp Q91XC0 AJUBA_MOUSE LIM domain-containing protein ajuba OS=Mus musculus GN=Ajuba PE=	0.459	0.926	>sp Q5SX39 MYH4_MOUSE Myosin-4 OS=Mus musculus GN=Myh4 PE=1 SV=1	-1.783	0.405
>tr Q3TN34 Q3TN34_MOUSE JRAB OS=Mus musculus GN=Micall2 PE=2 SV=1	1.137	0.956	>sp Q60605 MYL6_MOUSE Myosin light polypeptide 6 OS=Mus musculus GN=My16 PE=1	-1.760	0.452
>sp Q61792 LASP1_MOUSE LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1 PE=1 SV=	1.596	0.985	>sp Q9CQ19 MYL9_MOUSE Myosin regulatory light polypeptide 9 OS=Mus musculus GN=	-1.587	0.500
			>sp Q8CI43 MYL6B_MOUSE Myosin light chain 6B OS=Mus musculus GN=My16b PE=2 S	-1.483	0.548
			>sp Q61879 MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-1.350	0.595

Ribonucleoprotein complex GO:0030529

Protein identification	Zq	rank/N			
>tr Q5FWB6 Q5FWB6_MOUSE MCG17387, isoform CRA_a OS=Mus musculus GN=Rplp0 PE=2 SV=	-4.122	0.003	>sp P46735 MYO1B_MOUSE Unconventional myosin-Ib OS=Mus musculus GN=Myo1b PE=	-1.122	0.643
>sp P62702 RS4X_MOUSE 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2	-3.903	0.009	>tr Q8BWY8 Q8BWY8_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musc	-0.997	0.690
>sp Q9J18 RL38_MOUSE 60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	-3.675	0.016	>sp Q9WTI7 MYO1C_MOUSE Unconventional myosin-Ic OS=Mus musculus GN=Myo1c PE=	-0.969	0.738
>sp Q6ZWV3 RL10_MOUSE 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-3.197	0.022	>sp O08638 MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	-0.965	0.786
>sp Q8BP67 RL24_MOUSE 60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	-2.545	0.028	>sp Q6AW69 CGNL1_MOUSE Cingulin-like protein 1 OS=Mus musculus GN=Cgnl1 PE=1 S	-0.084	0.833
>tr Q3TPD2 Q3TPD2_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Iq	-2.211	0.035	>sp P59242 CING_MOUSE Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1	0.379	0.881
>sp P60122 RUVB1_MOUSE RuvB-like 1 OS=Mus musculus GN=Ruvb1 PE=1 SV=1	-2.159	0.041	>sp Q9DOM5 DYL2_MOUSE Dynein light chain 2, cytoplasmic OS=Mus musculus GN=Dyn	0.403	0.929
>sp P62862 RS30_MOUSE 40S ribosomal protein S30 OS=Mus musculus GN=Fau PE=3 SV=1	-2.137	0.047	>sp Q02566 MYH6_MOUSE Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	3.701	0.976
>sp P62900 RL31_MOUSE 60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	-2.042	0.053	Extracellular matrix GO:0031012		
>sp Q8CGC7 SYEP_MOUSE Bifunctional glutamate--tRNA ligase OS=Mus musculus GN=Epr	-2.025	0.060	Protein identification	Zq	rank/N
>sp P62082 RS7_MOUSE 40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-1.846	0.066	>sp Q61282 PGCA_MOUSE Aggrecan core protein OS=Mus musculus GN=Acan PE=1 SV=	-4.710	0.006
>sp O70133 DHX9_MOUSE ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=	-1.830	0.072	>sp P28481 CO2A1_MOUSE Collagen alpha-1(II) chain OS=Mus musculus GN=Col2a1 PE=	-3.672	0.019
>sp P62849 RS24_MOUSE 40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	-1.829	0.079	>sp Q9QZZ6 DERM_MOUSE Dermatopontin OS=Mus musculus GN=Dpt PE=2 SV=1	-3.617	0.031
>tr Q80UW7 Q80UW7_MOUSE IQ motif containing GTPase activating protein 1 OS=Mus musculus G	-1.810	0.085	>sp Q8BPB5 FBLN3_MOUSE EGF-containing fibulin-like extracellular matrix protein 1 OS=	-3.415	0.043
>sp P62830 RL23_MOUSE 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-1.682	0.091	>sp Q06890 CLUS_MOUSE Clusterin OS=Mus musculus GN=Clu PE=1 SV=1	-3.265	0.056
>sp Q9CQI7 RU2B_MOUSE U2 small nuclear ribonucleoprotein B" OS=Mus musculus GN=Snrpb2 PE	-1.656	0.097	>sp P29788 VTNC_MOUSE Vitronectin OS=Mus musculus GN=Vtn PE=1 SV=2	-3.072	0.068
>sp Q6ZWY3 RS27L_MOUSE 40S ribosomal protein S27-like OS=Mus musculus GN=Rps271 PE=2 S	-1.622	0.104	>sp Q91V88 NPNT_MOUSE Nephronectin OS=Mus musculus GN=Npnt PE=1 SV=1	-3.021	0.080
>sp P97351 RS3A_MOUSE 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	-1.590	0.110	>sp Q3UTY6 THSD4_MOUSE Thrombospondin type-1 domain-containing protein 4 OS=Mus	-3.002	0.093
>sp Q9Z204 HNRPC_MOUSE Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN	-1.588	0.116	>sp P39061 COIA1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1	-2.832	0.105
>sp P62267 RS23_MOUSE 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	-1.512	0.123	>sp P11276 FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4	-2.610	0.117
>sp P62281 RS11_MOUSE 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	-1.505	0.129	>sp Q8C4U3 SFRP1_MOUSE Secreted frizzled-related protein 1 OS=Mus musculus GN=Sfrp	-2.608	0.130
>tr Q8CDT3 Q8CDT3_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Iq	-1.465	0.135	>sp O09164 SODE_MOUSE Extracellular superoxide dismutase [Cu-Zn] OS=Mus musculus C	-2.564	0.142
>sp Q6P5F9 XPO1_MOUSE Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1	-1.461	0.142	>sp Q8K4G1 LTBP4_MOUSE Latent-transforming growth factor beta-binding protein 4 OS=	-2.490	0.154
>sp Q3UEB3 PUF60_MOUSE Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Puf60 P	-1.457	0.148	>tr Q3UHH3 Q3UHH3_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Hs	-2.457	0.167
>sp P62855 RS26_MOUSE 40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=2 SV=3	-1.453	0.154	>sp Q99JR5 TINAL_MOUSE Tubulointerstitial nephritis antigen-like OS=Mus musculus GN=	-2.434	0.179
>sp P57780 ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	-1.441	0.160	>sp P11087 CO1A1_MOUSE Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1	-2.341	0.191
>sp P27048 RSMB_MOUSE Small nuclear ribonucleoprotein-associated protein B OS=Mus musculus C	-1.434	0.167	>sp P97873 LOXL1_MOUSE Lysyl oxidase homolog 1 OS=Mus musculus GN=Loxl1 PE=2 S	-2.209	0.204
>sp Q61656 DDX5_MOUSE Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=D	-1.424	0.173	>sp Q9R118 HTRA1_MOUSE Serine protease HTRA1 OS=Mus musculus GN=Htra1 PE=1 S	-2.193	0.216
>sp P57784 RU2A_MOUSE U2 small nuclear ribonucleoprotein A' OS=Mus musculus GN=Snrpa1 PE=	-1.423	0.179	>sp P21956 MFGM_MOUSE Lactadherin OS=Mus musculus GN=Mfge8 PE=1 SV=3	-2.184	0.228
>sp Q6ZWV7 RL35_MOUSE 60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=2 SV=1	-1.361	0.186	>sp O88207 CO5A1_MOUSE Collagen alpha-1(V) chain OS=Mus musculus GN=Col5a1 PE=	-2.086	0.241
>sp P62301 RS13_MOUSE 40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-1.341	0.192	>sp P50608 FMOD_MOUSE Fibromodulin OS=Mus musculus GN=Fmod PE=2 SV=1	-2.085	0.253
>sp P32067 LA_MOUSE Lupus La protein homolog OS=Mus musculus GN=Ssb PE=2 SV=1	-1.326	0.198	>sp Q05793 PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core	-2.073	0.265
>sp P62751 RL23A_MOUSE 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1	-1.272	0.204	>sp Q01339 APOH_MOUSE Beta-2-glycoprotein 1 OS=Mus musculus GN=ApoH PE=1 SV=	-2.071	0.278
>sp P09405 NUCL_MOUSE Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	-1.270	0.211	>sp Q01149 CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=	-2.071	0.290
>sp Q9CPR4 RL17_MOUSE 60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	-1.257	0.217	>sp Q61001 LAMA5_MOUSE Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1	-1.923	0.302
>sp Q9D1R9 RL34_MOUSE 60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-1.220	0.223	>sp P21844 CMA1_MOUSE Chymase OS=Mus musculus GN=Cma1 PE=1 SV=2	-1.887	0.315
>sp P14115 RL27A_MOUSE 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5	-1.139	0.230	>tr B1B0C7 B1B0C7_MOUSE Basement membrane-specific heparan sulfate proteoglycan cor	-1.887	0.327
>sp P29341 PABP1_MOUSE Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV	-1.106	0.236	>sp Q04857 CO6A1_MOUSE Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE	-1.838	0.340
>sp Q61937 NPM_MOUSE Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	-1.084	0.242	>tr Q3TAF9 Q3TAF9_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Bgn	-1.782	0.352
>sp Q8VDM6 HNRLL_MOUSE Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Mus mu	-1.067	0.248	>sp Q8C6K9 CO6A6_MOUSE Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE	-1.617	0.364
>sp Q921F4 HNRLL_MOUSE Heterogeneous nuclear ribonucleoprotein L-like OS=Mus musculus GN=	-1.045	0.255	>sp P28654 PGS2_MOUSE Decorin OS=Mus musculus GN=Den PE=2 SV=1	-1.615	0.377
>sp P51410 RL9_MOUSE 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-1.036	0.261	>sp Q640N1 AEBP1_MOUSE Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=	-1.583	0.389
>sp Q9CXW4 RL11_MOUSE 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	-1.029	0.267	>sp Q9JK53 PRELP_MOUSE Prolargin OS=Mus musculus GN=Prelp PE=2 SV=2	-1.559	0.401
>sp Q7TMK9 HNRPQ_MOUSE Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Sy	-1.009	0.274	>sp Q62000 MIME_MOUSE Mimecan OS=Mus musculus GN=Ogn PE=2 SV=1	-1.550	0.414
>sp P19253 RL13A_MOUSE 60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	-0.910	0.280	>tr A2AQ53 A2AQ53_MOUSE Fibrillin 1 OS=Mus musculus GN=Fbn1 PE=4 SV=1	-1.539	0.426
>sp P62717 RL18A_MOUSE 60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	-0.901	0.286	>sp O35206 COFA1_MOUSE Collagen alpha-1(XV) chain OS=Mus musculus GN=Col15a1 I	-1.486	0.438
>sp Q8CCS6 PABP2_MOUSE Polyadenylate-binding protein 2 OS=Mus musculus GN=Pabpn1 PE=2 S	-0.898	0.292	>sp Q61508 ECM1_MOUSE Extracellular matrix protein 1 OS=Mus musculus GN=Ecm1 PE=	-1.437	0.451
>sp Q6PB66 LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musc	-0.883	0.299	>sp Q07235 GDN_MOUSE Glia-derived nexin OS=Mus musculus GN=Serpine2 PE=2 SV=2	-1.422	0.463

>sp P47964 RL36_MOUSE 60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=2 SV=2	-0.866	0.305	>sp P08122 CO4A2_MOUSE Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2 PE=2 SV=2	-1.401	0.475
>sp P12970 RL7A_MOUSE 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	-0.863	0.311	>sp Q62009 POSTN_MOUSE Periostin OS=Mus musculus GN=Postn PE=1 SV=2	-1.372	0.488
>sp Q91VR5 DDX1_MOUSE ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=2 SV=2	-0.850	0.318	>tr J3QQ16 J3QQ16_MOUSE Protein Col6a3 OS=Mus musculus GN=Col6a3 PE=4 SV=1	-1.313	0.500
>sp P62245 RS15A_MOUSE 40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-0.848	0.324	>sp Q99K41 EMIL1_MOUSE EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1	-1.307	0.512
>sp Q9D0E1 HNRPM_MOUSE Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=HnRpm PE=1 SV=1	-0.755	0.330	>tr Q8BP04 Q8BP04_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Loxl1 PE=1 SV=1	-1.261	0.525
>sp P63017 HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	-0.723	0.336	>sp O88322 NID2_MOUSE Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	-1.257	0.537
>sp P62754 RS6_MOUSE 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	-0.720	0.343	>sp Q08879 FBLN1_MOUSE Fibulin-1 OS=Mus musculus GN=Fbln1 PE=1 SV=2	-1.197	0.549
>sp P62313 LSM6_MOUSE U6 snRNA-associated Sm-like protein LSm6 OS=Mus musculus GN=Lsm6 PE=1 SV=1	-0.637	0.349	>sp Q9DCT8 CRIP2_MOUSE Cysteine-rich protein 2 OS=Mus musculus GN=Crip2 PE=1 SV=1	-1.158	0.562
>tr Q3TT41 Q3TT41_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Ncl PE=2 SV=1	-0.632	0.355	>tr D3YWD1 D3YWD1_MOUSE Protein Col6a3 (Fragment) OS=Mus musculus GN=Col6a3 PE=1 SV=1	-1.103	0.574
>sp P62320 SMD3_MOUSE Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	-0.583	0.362	>sp Q8VEE1 LMCD1_MOUSE LIM and cysteine-rich domains protein 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=1	-1.019	0.586
>sp P47915 RL29_MOUSE 60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	-0.579	0.368	>sp Q61292 LAMB2_MOUSE Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=2 SV=1	-0.875	0.599
>tr Q91V55 Q91V55_MOUSE 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=2 SV=1	-0.559	0.374	>sp Q02788 CO6A2_MOUSE Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=2 SV=1	-0.863	0.611
>sp P62274 RS29_MOUSE 40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=2 SV=2	-0.557	0.381	>sp Q80YX1 TENA_MOUSE Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	-0.836	0.623
>sp Q6NVF9 CPSF6_MOUSE Cleavage and polyadenylation specificity factor subunit 6 OS=Mus musculus GN=Cpsf6 PE=1 SV=1	-0.555	0.387	>sp Q8CG19 LTBP1_MOUSE Latent-transforming growth factor beta-binding protein 1 OS=Mus musculus GN=Ltbp1 PE=1 SV=1	-0.808	0.636
>sp P97461 RS5_MOUSE 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=2 SV=3	-0.546	0.393	>sp Q9WVH9 FBLN5_MOUSE Fibulin-5 OS=Mus musculus GN=Fbln5 PE=2 SV=1	-0.800	0.648
>tr Q3TF92 Q3TF92_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Dhxf1 PE=1 SV=1	-0.532	0.399	>sp P20352 TF_MOUSE Tissue factor OS=Mus musculus GN=TF3 PE=1 SV=2	-0.784	0.660
>sp P47962 RL5_MOUSE 60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	-0.527	0.406	>tr B7ZNH7 B7ZNH7_MOUSE Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1 PE=1 SV=1	-0.770	0.673
>sp P62317 SMD2_MOUSE Small nuclear ribonucleoprotein Sm D2 OS=Mus musculus GN=Snrpd2 PE=1 SV=1	-0.521	0.412	>tr P691W6 Q591W6_MOUSE Protein Abi3bp OS=Mus musculus GN=Abi3bp PE=2 SV=1	-0.766	0.685
>sp Q60668 HNRPD_MOUSE Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=HnRpd1 PE=1 SV=1	-0.496	0.418	>tr B9EHT6 B9EHT6_MOUSE Fn1 protein OS=Mus musculus GN=Fn1 PE=2 SV=1	-0.756	0.698
>sp Q921S7 RM37_MOUSE 39S ribosomal protein L37, mitochondrial OS=Mus musculus GN=Mmrpl37 PE=1 SV=1	-0.493	0.425	>tr F8VQJ3 F8VQJ3_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=1	-0.750	0.710
>sp P53026 RL10A_MOUSE 60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	-0.491	0.431	>sp P51885 LUM_MOUSE Lumican OS=Mus musculus GN=Lum PE=1 SV=2	-0.735	0.722
>sp P62305 RUXE_MOUSE Small nuclear ribonucleoprotein E OS=Mus musculus GN=Snrpe PE=2 SV=1	-0.488	0.437	>sp Q62219 TGFI1_MOUSE Transforming growth factor beta-1-induced transcript 1 protein C OS=Mus musculus GN=Tgfi1 PE=1 SV=1	-0.636	0.735
>sp Q9CXY6 ILF2_MOUSE Interleukin enhancer-binding factor 2 OS=Mus musculus GN=Ilf2 PE=1 SV=1	-0.484	0.443	>sp P28653 PGS1_MOUSE Biglycan OS=Mus musculus GN=Bgn PE=2 SV=1	-0.631	0.747
>sp P14148 RL7_MOUSE 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	-0.476	0.450	>sp Q8CIZ8 VWF_MOUSE von Willebrand factor OS=Mus musculus GN=Vwf PE=1 SV=2	-0.628	0.759
>sp P62264 RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	-0.465	0.456	>sp P97298 PEDF_MOUSE Pigment epithelium-derived factor OS=Mus musculus GN=Serp1 PE=1 SV=1	-0.588	0.772
>sp P99027 RLA2_MOUSE 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=1	-0.457	0.462	>sp O70503 DHB12_MOUSE Estradiol 17-beta-dehydrogenase 12 OS=Mus musculus GN=Dhb12 PE=1 SV=1	-0.501	0.784
>sp P58252 EF2_MOUSE Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	-0.437	0.469	>sp Q61543 GSLG1_MOUSE Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	-0.482	0.796
>sp P62918 RL8_MOUSE 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.436	0.475	>sp Q9QUP5 HPLN1_MOUSE Hyaluronan and proteoglycan link protein 1 OS=Mus musculus GN=Hpln1 PE=1 SV=1	-0.434	0.809
>sp Q8R081 HNRPL_MOUSE Heterogeneous nuclear ribonucleoprotein L OS=Mus musculus GN=HnRpl1 PE=1 SV=1	-0.429	0.481	>sp P08228 SODC_MOUSE Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=1	-0.301	0.821
>sp P62852 RS25_MOUSE 40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1	-0.414	0.487	>sp Q9D1H9 MFAP4_MOUSE Microfibril-associated glycoprotein 4 OS=Mus musculus GN=MFAP4 PE=1 SV=1	-0.237	0.833
>sp P62960 YBOX1_MOUSE Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybox1 PE=1 SV=1	-0.410	0.494	>sp P09242 PPBT_MOUSE Alkaline phosphatase, tissue-nonspecific isozyme OS=Mus musculus GN=Alp PE=1 SV=1	-0.209	0.846
>sp Q8VEK3 HNRPU_MOUSE Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=HnRpu PE=1 SV=1	-0.404	0.500	>sp Q61554 FBN1_MOUSE Fibrillin-1 OS=Mus musculus GN=Fbn1 PE=1 SV=1	-0.142	0.858
>tr A2AW41 A2AW41_MOUSE Heterogeneous nuclear ribonucleoprotein R (Fragment) OS=Mus musculus GN=HnRnp1 PE=1 SV=1	-0.387	0.506	>sp P16045 LEG1_MOUSE Galectin-1 OS=Mus musculus GN=Lgals1 PE=1 SV=3	0.035	0.870
>tr Q6P4T2 Q6P4T2_MOUSE Activating signal cointegrator 1 complex subunit 3-like 1 OS=Mus musculus GN=Aspc1 PE=1 SV=1	-0.375	0.513	>sp P82198 BGH3_MOUSE Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Bgh3 PE=1 SV=1	0.160	0.883
>sp Q61990 PCBP2_MOUSE Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	-0.374	0.519	>sp P97857 ATSI1_MOUSE A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Mus musculus GN=Atsi1 PE=1 SV=1	0.209	0.895
>sp Q9EQK5 MVP_MOUSE Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4	-0.320	0.525	>sp Q60847 COCA1_MOUSE Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 PE=1 SV=1	0.294	0.907
>sp Q9WTM5 RUVB2_MOUSE RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=2 SV=3	-0.307	0.531	>sp P18242 CATD_MOUSE Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	0.378	0.920
>sp P35980 RL18_MOUSE 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	-0.298	0.538	>sp P14211 CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	0.603	0.932
>sp Q6ZWN5 RS9_MOUSE 40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	-0.295	0.544	>sp P10493 NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	0.631	0.944
>sp Q99020 ROAA_MOUSE Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=HnRaa1 PE=1 SV=1	-0.292	0.550	>sp Q99MQ4 ASPN_MOUSE Asporin OS=Mus musculus GN=Aspn PE=1 SV=1	0.657	0.957
>sp P63276 RS17_MOUSE 40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	-0.248	0.557	>sp P07901 HSP90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90 PE=1 SV=1	1.222	0.969
>sp O09167 RL21_MOUSE 60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-0.228	0.563	>sp P07214 SPRC_MOUSE SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	1.547	0.981
>sp Q62376 RU17_MOUSE U1 small nuclear ribonucleoprotein 70 kDa OS=Mus musculus GN=Snrnp17 PE=1 SV=1	-0.227	0.569	>sp Q5FW85 ECM2_MOUSE Extracellular matrix protein 2 OS=Mus musculus GN=Ecm2 PE=1 SV=1	1.723	0.994
>tr E9QNN1 E9QNN1_MOUSE ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=4 SV=1	-0.224	0.575			
>sp P97499 TEP1_MOUSE Telomerase protein component 1 OS=Mus musculus GN=Tep1 PE=1 SV=1	-0.175	0.582	Focal adhesion GO:0005925		
>sp Q9CR57 RL14_MOUSE 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	-0.151	0.588			
>sp P27659 RL3_MOUSE 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.131	0.594			
>sp P62984 RL40_MOUSE Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=1	-0.067	0.601	>sp Q6ZWQ0 SYNE2_MOUSE Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=2	-3.369	0.010
>sp Q99PV0 PRP8_MOUSE Pre-mRNA-processing-splicing factor 8 OS=Mus musculus GN=Prpf8 PE=1 SV=1	-0.046	0.607	>sp Q5SX40 MYH1_MOUSE Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1	-2.997	0.031
			>sp Q62523 ZYX_MOUSE Zyxin OS=Mus musculus GN=Zyx PE=1 SV=2	-2.059	0.052

>sp P62270 RS18_MOUSE 40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=1 SV=3	-0.041	0.613	>sp Q5SX39 MYH4_MOUSE Myosin-4 OS=Mus musculus GN=Myh4 PE=1 SV=1	-1.783	0.073
>tr E9Q3T0 E9Q3T0_MOUSE Uncharacterized protein OS=Mus musculus GN=Gm10073 PE=4 SV=1	-0.029	0.619	>sp Q03173 ENAH_MOUSE Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=1	-1.771	0.094
>sp P61358 RL27_MOUSE 60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-0.024	0.626	>sp Q91XD2 LIMS2_MOUSE LIM and senescent cell antigen-like-containing domain protein	-1.394	0.115
>sp Q91VM5 RMXL1_MOUSE RNA binding motif protein, X-linked-like-1 OS=Mus musculus GN=R	-0.022	0.632	>sp P11688 ITA5_MOUSE Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=3	-1.370	0.135
>sp O35737 HNRH1_MOUSE Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnr	-0.009	0.638	>sp Q8CGB6 TENC1_MOUSE Tensin-like C1 domain-containing phosphatase OS=Mus musc	-1.350	0.156
>sp P62843 RS15_MOUSE 40S ribosomal protein S15 OS=Mus musculus GN=Rps15 PE=2 SV=2	-0.008	0.645	>sp P26039 TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	-1.208	0.177
>sp Q6ZWM4 NAA38_MOUSE N-alpha-acetyltransferase 38, NatC auxiliary subunit OS=Mus muscult	0.004	0.651	>sp P09055 ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	-1.132	0.198
>sp P86048 RL10L_MOUSE 60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=	0.006	0.657	>sp Q7TPR4 ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	-1.092	0.219
>sp Q9D823 RL37_MOUSE 60S ribosomal protein L37 OS=Mus musculus GN=Rpl37 PE=2 SV=3	0.056	0.664	>sp Q99JW4 LIMS1_MOUSE LIM and senescent cell antigen-like-containing domain protein	-1.035	0.240
>tr Q3U1C4 Q3U1C4_MOUSE MCG1271 OS=Mus musculus GN=Secisbp2 PE=2 SV=1	0.056	0.670	>sp Q9R1Z8 VINEX_MOUSE Vinexin OS=Mus musculus GN=Sorbs3 PE=1 SV=1	-0.898	0.260
>sp P14131 RS16_MOUSE 40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	0.066	0.676	>sp P26041 MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	-0.880	0.281
>sp Q9CZM2 RL15_MOUSE 60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	0.072	0.682	>sp Q8V136 PAXI_MOUSE Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1	-0.879	0.302
>sp P62309 RUXG_MOUSE Small nuclear ribonucleoprotein G OS=Mus musculus GN=Snrgp PE=1 S'	0.074	0.689	>tr E9Q0S6 E9Q0S6_MOUSE Protein Tns1 OS=Mus musculus GN=Tns1 PE=4 SV=1	-0.795	0.323
>sp P14206 RSSA_MOUSE 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	0.076	0.695	>sp P26040 EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	-0.782	0.344
>sp P62311 LSM3_MOUSE U6 snRNA-associated Sm-like protein LSm3 OS=Mus musculus GN=Lsm	0.101	0.701	>sp Q9JJ28 FLII_MOUSE Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV	-0.738	0.365
>sp Q64012 RALY_MOUSE RNA-binding protein Raly OS=Mus musculus GN=Raly PE=1 SV=3	0.126	0.708	>sp P70460 VASP_MOUSE Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=V	-0.715	0.385
>sp P61255 RL26_MOUSE 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	0.153	0.714	>sp P26043 RADI_MOUSE Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	-0.706	0.406
>sp Q9CXW2 RT22_MOUSE 28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrps2	0.174	0.720	>sp Q9EPC1 PARVA_MOUSE Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	-0.690	0.427
>sp Q9D0T1 NH2L1_MOUSE NHP2-like protein 1 OS=Mus musculus GN=Nhp2l1 PE=2 SV=4	0.186	0.726	>sp Q61792 LASP1_MOUSE LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1	-0.652	0.448
>sp P62908 RS3_MOUSE 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	0.190	0.733	>sp Q3UTJ2 SRBS2_MOUSE Sorbin and SH3 domain-containing protein 2 OS=Mus musculu	-0.651	0.469
>sp O35900 LSM2_MOUSE U6 snRNA-associated Sm-like protein LSm2 OS=Mus musculus GN=Lsm	0.193	0.739	>sp Q8BFW7 LPP_MOUSE Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp	-0.638	0.490
>sp Q9Z2X1 HNRPF_MOUSE Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnr	0.205	0.745	>sp Q62219 TGFBI_MOUSE Transforming growth factor beta-1-induced transcript 1 protein C	-0.636	0.510
>sp P35550 FBRL_MOUSE rRNA 2'-O-methyltransferase fibrillarin OS=Mus musculus GN=Fbl PE=1	0.207	0.752	>sp Q71FD7 FBLI1_MOUSE Filamin-binding LIM protein 1 OS=Mus musculus GN=Fblim1	-0.561	0.531
>sp P84099 RL19_MOUSE 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	0.211	0.758	>sp Q62422 SRBS1_MOUSE Sorbin and SH3 domain-containing protein 1 OS=Mus musculus	-0.448	0.552
>sp P14869 RLA0_MOUSE 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=	0.212	0.764	>sp P63085 MK01_MOUSE Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapl	-0.428	0.573
>sp P62242 RS8_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	0.212	0.770	>sp Q9JI91 ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	-0.396	0.594
>sp P47911 RL6_MOUSE 60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	0.219	0.777	>sp O70309 ITB5_MOUSE Integrin beta-5 OS=Mus musculus GN=Itgb5 PE=1 SV=2	-0.368	0.615
>tr Q6ZWZ6 Q6ZWZ6_MOUSE 40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=2 SV=1	0.219	0.783	>sp Q64727 VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	-0.368	0.635
>sp P67984 RL22_MOUSE 60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=2 SV=2	0.224	0.789	>sp Q01768 NDKB_MOUSE Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2	-0.363	0.656
>sp Q9Z1X4 ILF3_MOUSE Interleukin enhancer-binding factor 3 OS=Mus musculus GN=Ilf3 PE=1 SV	0.261	0.796	>tr Q3U0Q9 Q3U0Q9_MOUSE Putative uncharacterized protein (Fragment) OS=Mus muscul	-0.211	0.677
>sp P25444 RS2_MOUSE 40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	0.266	0.802	>sp Q3TJD7 PDLI7_MOUSE PDZ and LIM domain protein 7 OS=Mus musculus GN=Pdlim7	-0.173	0.698
>sp Q5SSK3 TEFM_MOUSE Transcription elongation factor, mitochondrial OS=Mus musculus GN=Te	0.267	0.808	>sp Q8BZF8 PGM5_MOUSE Phosphoglucosyltransferase-like protein 5 OS=Mus musculus GN=Pgr	-0.154	0.719
>sp P47955 RLA1_MOUSE 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=	0.303	0.814	>sp Q62165 DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	0.131	0.740
>sp P49962 SRP09_MOUSE Signal recognition particle 9 kDa protein OS=Mus musculus GN=Srp9 PE	0.365	0.821	>sp Q80X90 FLNB_MOUSE Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	0.136	0.760
>tr Q8VHM5 Q8VHM5_MOUSE Heterogeneous nuclear ribonucleoprotein R OS=Mus musculus GN=I	0.412	0.827	>sp Q55222 ILK_MOUSE Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV	0.239	0.781
>sp P63325 RS10_MOUSE 40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	0.416	0.833	>sp P34914 HYES_MOUSE Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2	0.367	0.802
>sp P35979 RL12_MOUSE 60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	0.457	0.840	>sp Q63844 MK03_MOUSE Mitogen-activated protein kinase 3 OS=Mus musculus GN=Map	0.484	0.823
>sp P49312 ROA1_MOUSE Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnr	0.474	0.846	>sp Q8CIB5 FERM2_MOUSE Fermitin family homolog 2 OS=Mus musculus GN=Ferm2 PE	0.503	0.844
>sp Q9CX86 ROA0_MOUSE Heterogeneous nuclear ribonucleoprotein A0 OS=Mus musculus GN=Hnr	0.550	0.852	>sp Q9CVB6 ARPC2_MOUSE Actin-related protein 2/3 complex subunit 2 OS=Mus musculu	0.521	0.865
>sp Q9D8E6 RL4_MOUSE 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	0.573	0.858	>sp P47226 TES_MOUSE Testin OS=Mus musculus GN=Tes PE=1 SV=1	0.549	0.885
>sp Q8BG05 ROA3_MOUSE Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnr	0.587	0.865	>sp Q9ET54 PALLD_MOUSE Palladin OS=Mus musculus GN=Palld PE=1 SV=2	0.701	0.906
>sp O88569 ROA2_MOUSE Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=	0.603	0.871	>sp P31938 MP2K1_MOUSE Dual specificity mitogen-activated protein kinase kinase 1 OS=I	1.227	0.927
>sp P60335 PCBP1_MOUSE Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	0.679	0.877	>sp Q71LX4 TLN2_MOUSE Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.251	0.948
>sp P62889 RL30_MOUSE 60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=2 SV=2	0.711	0.884	>tr Q3TN69 Q3TN69_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculu	1.263	0.969
>sp P70333 HNRH2_MOUSE Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hn	0.712	0.890	>sp Q02566 MYH6_MOUSE Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	3.701	0.990
>sp Q9JIK9 RT34_MOUSE 28S ribosomal protein S34, mitochondrial OS=Mus musculus GN=Mrps34	0.773	0.896			
>sp P61979 HNRPK_MOUSE Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnr	0.783	0.903	Regulation of cell shape GO:0008360		
>sp P60710 ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	0.902	0.909	Protein identification	Zq	rank/N
>sp P50580 PA2G4_MOUSE Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1	0.942	0.915	>tr Q6ZWQ9 Q6ZWQ9_MOUSE MCG5400 OS=Mus musculus GN=Myl12a PE=2 SV=1	-3.282	0.020

>sp O55142 RL35A_MOUSE 60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=2 SV=2	0.975	0.92	>sp Q6URW6 MYH14_MOUSE Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-2.680	0.060
>sp Q9ESX5 DKC1_MOUSE H/ACA ribonucleoprotein complex subunit 4 OS=Mus musculus GN=Dkc1 OS=Mus musculus GN=DKC1 PE=1 SV=1	0.983	0.928	>sp P11276 FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4	-2.610	0.100
>sp P47963 RL13_MOUSE 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	1.052	0.934	>tr Q3UFT0 Q3UFT0_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Q3UFT0 PE=1 SV=1	-2.267	0.140
>sp P83882 RL36A_MOUSE 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=3 SV=2	1.110	0.940	>sp Q8VDD5 MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-2.160	0.180
>sp Q8CJG0 AGO2_MOUSE Protein argonaute-2 OS=Mus musculus GN=Eif2c2 PE=1 SV=3	1.195	0.947	>sp Q3THE2 ML12B_MOUSE Myosin regulatory light chain 12B OS=Mus musculus GN=Myh9 PE=1 SV=4	-1.838	0.220
>sp Q9CQR2 RS21_MOUSE 40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	1.221	0.953	>sp P08032 SPTA1_MOUSE Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Sptalpha1 PE=1 SV=1	-1.687	0.260
>sp P62315 SMD1_MOUSE Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrpd1 PE=1 SV=1	1.222	0.959	>sp Q61879 MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-1.350	0.300
>sp P60867 RS20_MOUSE 40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	1.321	0.965	>sp Q07076 ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=2	-1.013	0.340
>sp Q8CJG1 AGO1_MOUSE Protein argonaute-1 OS=Mus musculus GN=Eif2c1 PE=1 SV=2	1.327	0.972	>sp Q8V136 PAXI_MOUSE Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1	-0.879	0.380
>sp P62858 RS28_MOUSE 40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=2 SV=1	1.365	0.978	>sp P26040 EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	-0.782	0.420
>sp P63323 RS12_MOUSE 40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	1.528	0.984	>sp P19221 THRB_MOUSE Prothrombin OS=Mus musculus GN=F2 PE=1 SV=1	-0.765	0.460
>sp P41105 RL28_MOUSE 60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	2.092	0.991	>sp Q9EPC1 PARVA_MOUSE Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	-0.690	0.500
>sp Q9CZX8 RS19_MOUSE 40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	3.059	0.997	>sp Q71FD7 FBLI1_MOUSE Filamin-binding LIM protein 1 OS=Mus musculus GN=Fblim1 OS=Mus musculus GN=FBLI1 PE=1 SV=1	-0.561	0.540
			>sp Q9Z0P4 PALM_MOUSE Paralemmin-1 OS=Mus musculus GN=Palm PE=1 SV=1	-0.416	0.580
			>sp Q08808 DIAP1_MOUSE Protein diaphanous homolog 1 OS=Mus musculus GN=Diaph1 OS=Mus musculus GN=DIAP1 PE=1 SV=1	-0.107	0.620
			>sp Q7TMB8 CYFP1_MOUSE Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfp1 OS=Mus musculus GN=CYP1 PE=1 SV=1	-0.098	0.660
			>sp P27601 GNA13_MOUSE Guanine nucleotide-binding protein subunit alpha-13 OS=Mus musculus GN=Gna13 OS=Mus musculus GN=GNA13 PE=1 SV=1	0.300	0.700
			>sp Q8BR92 PALM2_MOUSE Paralemmin-2 OS=Mus musculus GN=Palm2 PE=1 SV=1	0.392	0.740
			>sp P39688 FYN_MOUSE Tyrosine-protein kinase Fyn OS=Mus musculus GN=Fyn PE=1 SV=1	0.499	0.780
			>sp Q8CIB5 FERM2_MOUSE Fermitin family homolog 2 OS=Mus musculus GN=Ferm2 OS=Mus musculus GN=FERM2 PE=1 SV=1	0.503	0.820
			>sp Q70243 E41L2_MOUSE Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 OS=Mus musculus GN=E41L2 PE=1 SV=1	0.704	0.860
			>sp Q80953 COR1A_MOUSE Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	1.348	0.900
			>sp Q61738 ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=3	1.587	0.940
			>sp Q9JM96 BORG4_MOUSE Cdc42 effector protein 4 OS=Mus musculus GN=Cdc42ep4 OS=Mus musculus GN=BORG4 PE=1 SV=1	2.568	0.980
Mitochondrion GO:0005739					
Protein identification			Zq	rank/N	
>sp Q9CZT5 VASN_MOUSE Vasorin OS=Mus musculus GN=Vasn PE=2 SV=2	-3.778	0.001			
>sp Q9R257 HEBP1_MOUSE Heme-binding protein 1 OS=Mus musculus GN=Hebp1 PE=1 SV=2	-3.281	0.004			
>sp Q80U23 SNPH_MOUSE Syntaphilin OS=Mus musculus GN=Snph PE=1 SV=3	-3.068	0.006			
>sp P00329 ADH1_MOUSE Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2	-2.654	0.009			
>sp Q924X2 CPT1B_MOUSE Carnitine O-palmitoyltransferase 1, muscle isoform OS=Mus musculus GN=Cpt1b OS=Mus musculus GN=CPT1B PE=1 SV=1	-2.619	0.011			
>sp Q8R2Y8 PTH2_MOUSE Peptidyl-tRNA hydrolase 2, mitochondrial OS=Mus musculus GN=Pth2 OS=Mus musculus GN=PTH2 PE=1 SV=1	-2.188	0.014			
>sp O35459 ECH1_MOUSE Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Mus musculus GN=Ech1 OS=Mus musculus GN=ECH1 PE=1 SV=1	-2.026	0.016			
>sp Q791T5 MTCH1_MOUSE Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1 PE=1 SV=1	-2.016	0.019			
>sp O35658 C1QBP_MOUSE Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Mus musculus GN=C1qbp OS=Mus musculus GN=C1QBP PE=1 SV=1	-1.916	0.021			
>sp P98083 SHC1_MOUSE SHC-transforming protein 1 OS=Mus musculus GN=Shc1 PE=1 SV=3	-1.855	0.023			
>sp Q9CRD2 EMC2_MOUSE ER membrane protein complex subunit 2 OS=Mus musculus GN=Emc2 OS=Mus musculus GN=EMC2 PE=1 SV=1	-1.837	0.026			
>sp P32020 NLTP_MOUSE Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=1	-1.807	0.028			
>sp Q8CG76 ARK72_MOUSE Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus GN=Akr72 OS=Mus musculus GN=ARK72 PE=1 SV=1	-1.800	0.031			
>sp Q8QZS1 HIBCH_MOUSE 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus musculus GN=Hibch OS=Mus musculus GN=HIBCH PE=1 SV=1	-1.718	0.033			
>sp O09164 SODE_MOUSE Extracellular superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod3 OS=Mus musculus GN=SODE PE=1 SV=1	-1.698	0.036			
>sp Q9ERU9 RBP2_MOUSE E3 SUMO-protein ligase RanBP2 OS=Mus musculus GN=Ranbp2 PE=1 SV=1	-1.674	0.038			
>sp Q9QX60 DGUOK_MOUSE Deoxyguanosine kinase, mitochondrial OS=Mus musculus GN=Dguok OS=Mus musculus GN=DGUOK PE=1 SV=1	-1.673	0.041			
>sp P19157 GSTP1_MOUSE Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2	-1.621	0.043			
>sp P46638 RB11B_MOUSE Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	-1.605	0.046			
>sp Q8BMP6 GCP60_MOUSE Golgi resident protein GCP60 OS=Mus musculus GN=Acbd3 PE=1 SV=1	-1.545	0.048			
>sp O008756 HCD2_MOUSE 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17 OS=Mus musculus GN=HCD2 PE=1 SV=1	-1.530	0.051			
>sp O55137 ACOT1_MOUSE Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1 PE=1 SV=1	-1.468	0.053			
>sp Q9Z1Q9 SYVC_MOUSE Valine--tRNA ligase OS=Mus musculus GN=Vars PE=2 SV=1	-1.426	0.056			
>sp P23927 CRYAB_MOUSE Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	-1.419	0.058			
>sp P59017 B2L13_MOUSE Bcl-2-like protein 13 OS=Mus musculus GN=Bcl2l13 PE=1 SV=2	-1.411	0.060			
>sp Q8BWM0 PGES2_MOUSE Prostaglandin E synthase 2 OS=Mus musculus GN=Ptges2 PE=1 SV=3	-1.377	0.063			
>sp Q8BMD8 SCMC1_MOUSE Calcium-binding mitochondrial carrier protein SCaMC1 OS=Mus musculus GN=Scmc1 OS=Mus musculus GN=SCMC1 PE=1 SV=1	-1.342	0.065			
>sp P97807 FUMH_MOUSE Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=1	-1.326	0.068			
>sp P41216 ACSL1_MOUSE Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1 PE=1 SV=1	-1.322	0.070			
>sp Q99LB6 MAT2B_MOUSE Methionine adenosyltransferase 2 subunit beta OS=Mus musculus GN=Mat2b OS=Mus musculus GN=MAT2B PE=1 SV=1	-1.296	0.073			
>sp P61222 ABCE1_MOUSE ATP-binding cassette sub-family E member 1 OS=Mus musculus GN=Abce1 OS=Mus musculus GN=ABCE1 PE=1 SV=1	-1.283	0.075			
>sp Q8R0Y6 AL1L1_MOUSE Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Al1l1 OS=Mus musculus GN=Q8R0Y6 PE=1 SV=1	-1.282	0.078			
>sp Q9D0K2 SCOT1_MOUSE Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Scot1 OS=Mus musculus GN=Q9D0K2 PE=1 SV=1	-1.268	0.080			
			>sp P26645 MARCS_MOUSE Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcs OS=Mus musculus GN=MARCS PE=1 SV=1	-1.626	0.169
			>sp Q6ZWWQ0 SYNE2_MOUSE Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=2	-3.369	0.004
			>sp P20065-2 TYB4_MOUSE Isoform Short of Thymosin beta-4 OS=Mus musculus GN=Tmsb4 OS=Mus musculus GN=TYB4 PE=1 SV=1	-3.090	0.012
			>sp Q64331 MYO6_MOUSE Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1	-3.068	0.020
			>tr Q69ZX3 Q69ZX3_MOUSE MKIAA0866 protein (Fragment) OS=Mus musculus GN=Myh14 PE=1 SV=1	-3.047	0.028
			>sp Q5SX40 MYH1_MOUSE Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1	-2.997	0.035
			>sp Q5SYD0 MYO1D_MOUSE Unconventional myosin-Id OS=Mus musculus GN=Myo1d OS=Mus musculus GN=MYO1D PE=1 SV=1	-2.771	0.043
			>sp Q6URW6 MYH14_MOUSE Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-2.680	0.051
			>sp P13020 GELS_MOUSE Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	-2.602	0.059
			>sp Q9DAW9 CNN3_MOUSE Calponin-3 OS=Mus musculus GN=Cnn3 PE=2 SV=1	-2.489	0.067
			>sp Q070373 XIRP1_MOUSE Xirap actin-binding repeat-containing protein 1 OS=Mus musculus GN=Xirp1 OS=Mus musculus GN=Q070373 PE=1 SV=1	-2.202	0.075
			>sp Q8BVA4 LMOD1_MOUSE Leiomodion-1 OS=Mus musculus GN=Lmod1 PE=2 SV=1	-2.191	0.083
			>sp Q8VDD5 MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-2.160	0.091
			>sp Q08093 CNN2_MOUSE Calponin-2 OS=Mus musculus GN=Cnn2 PE=2 SV=1	-2.036	0.098
			>sp Q6PDN3 MYLK_MOUSE Myosin light chain kinase, smooth muscle OS=Mus musculus GN=Mylk OS=Mus musculus GN=Q6PDN3 PE=1 SV=1	-2.023	0.106
			>sp Q9WUM4 COR1C_MOUSE Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-1.975	0.114
			>sp P04919 B3AT_MOUSE Band 3 anion transport protein OS=Mus musculus GN=Slc4a1 OS=Mus musculus GN=B3AT PE=1 SV=1	-1.923	0.122
			>sp Q5SX39 MYH4_MOUSE Myosin-4 OS=Mus musculus GN=Myh4 PE=1 SV=1	-1.783	0.130
			>sp Q03173 ENAH_MOUSE Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=1	-1.771	0.138
			>tr Q8VCQ8 Q8VCQ8_MOUSE Caldesmon 1 OS=Mus musculus GN=Cald1 PE=2 SV=1	-1.720	0.146
			>sp Q9R0Q6 ARCA1_MOUSE Actin-related protein 2/3 complex subunit 1A OS=Mus musculus GN=Arca1 OS=Mus musculus GN=Q9R0Q6 PE=1 SV=1	-1.690	0.154
			>sp P08032 SPTA1_MOUSE Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Sptalpha1 OS=Mus musculus GN=SPTA1 PE=1 SV=1	-1.687	0.161

>sp P05202 AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 F	-1.231	0.083	>sp Q9JHJ0 TMOD3_MOUSE Tropomodulin-3 OS=Mus musculus GN=Tmod3 PE=1 SV=1	-1.626	0.177
>sp P39688 FYN_MOUSE Tyrosine-protein kinase Fyn OS=Mus musculus GN=Fyn PE=1 SV=3	-1.212	0.085	>sp Q62418 DBNL_MOUSE Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2	-1.613	0.185
>sp P54869 HMCS2_MOUSE Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus	-1.189	0.088	>tr D3YVV9 D3YVV9_MOUSE Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=4 SV=	-1.567	0.193
>sp Q9DCW4 ETFB_MOUSE Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb I	-1.157	0.090	>sp P57780 ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	-1.556	0.201
>sp Q9DCT2 NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondria	-1.139	0.093	>sp Q7TPW1 NEXN_MOUSE Nexilin OS=Mus musculus GN=Nexn PE=1 SV=3	-1.518	0.209
>sp Q920E5 FPPS_MOUSE Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1	-1.132	0.095	>sp P24452 CAPG_MOUSE Macrophage-capping protein OS=Mus musculus GN=Capg PE=1	-1.478	0.217
>sp Q64133 AOFA_MOUSE Amine oxidase [flavin-containing] A OS=Mus musculus GN=Maoa PE=1	-1.120	0.098	>sp P21614 VTDB_MOUSE Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV	-1.428	0.224
>sp P56375 ACYP2_MOUSE Acylphosphatase-2 OS=Mus musculus GN=Acyp2 PE=2 SV=2	-1.115	0.100	>sp P40124 CAP1_MOUSE Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Ca	-1.394	0.232
>sp P63328 PP2BA_MOUSE Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform C	-1.108	0.102	>sp Q91YE8 SYNP2_MOUSE Synaptopodin-2 OS=Mus musculus GN=Synpo2 PE=1 SV=2	-1.353	0.240
>sp P62897 CYC_MOUSE Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2	-1.106	0.105	>sp Q61879 MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-1.350	0.248
>sp Q8BWT1 THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 F	-1.099	0.107	>sp Q9QXS6 DREB_MOUSE Drebrin OS=Mus musculus GN=Dbn1 PE=1 SV=4	-1.288	0.256
>sp Q04447 KCRB_MOUSE Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	-1.094	0.110	>sp P11531 DMD_MOUSE Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=3	-1.252	0.264
>sp Q8BH95 ECHM_MOUSE Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=	-1.064	0.112	>sp Q8VHX6 FLNC_MOUSE Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	-1.237	0.272
>sp P97478 COQ7_MOUSE Ubiquinone biosynthesis protein COQ7 homolog OS=Mus musculus GN=C	-1.055	0.115	>sp Q3V0K9 PLS1_MOUSE Plastin-1 OS=Mus musculus GN=Pls1 PE=2 SV=1	-1.220	0.280
>sp Q8K009 AL1L2_MOUSE Mitochondrial 10-formyltetrahydrofolate dehydrogenase OS=Mus muscu	-1.051	0.117	>sp P47754 CAZA2_MOUSE F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=	-1.220	0.287
>sp P54071 IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Id	-1.047	0.120	>sp P26039 TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	-1.208	0.295
>sp Q62465 VAT1_MOUSE Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus G	-1.014	0.122	>sp P09055 ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	-1.132	0.303
>sp Q8CGK3 LONM_MOUSE Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE	-0.976	0.125	>sp P46735 MYO1B_MOUSE Unconventional myosin-Ib OS=Mus musculus GN=Myo1b PE	-1.122	0.311
>sp Q8BMS1 ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus G	-0.975	0.127	>tr E9Q6R7 E9Q6R7_MOUSE Protein Utrn OS=Mus musculus GN=Utrn PE=4 SV=1	-1.104	0.319
>sp Q99JB2 STML2_MOUSE Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 SV=1	-0.966	0.130	>sp Q8BTM8 FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	-1.103	0.327
>sp Q9JM14 NT5C_MOUSE 5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus GN=Nt5c	-0.952	0.132	>sp Q91YR1 TWF1_MOUSE Twinfilin-1 OS=Mus musculus GN=Twf1 PE=1 SV=2	-1.096	0.335
>sp Q78PY7 SND1_MOUSE Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus C	-0.947	0.135	>sp Q7TPR4 ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	-1.092	0.343
>sp Q9D2G2 ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxogluta	-0.930	0.137	>sp P45591 COF2_MOUSE Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	-1.087	0.350
>sp P58281 OPA1_MOUSE Dynamin-like 120 kDa protein, mitochondrial OS=Mus musculus GN=Opa	-0.927	0.140	>sp P47753 CAZA1_MOUSE F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=	-1.079	0.358
>sp Q99L13 3HIDH_MOUSE 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus musculus C	-0.923	0.142	>sp Q9CYT6 CAP2_MOUSE Adenylyl cyclase-associated protein 2 OS=Mus musculus GN=C	-1.048	0.366
>sp Q8BX02 KANK2_MOUSE KN motif and ankyrin repeat domain-containing protein 2 OS=Mus mus	-0.916	0.144	>sp Q08091 CNN1_MOUSE Calponin-1 OS=Mus musculus GN=Cnn1 PE=2 SV=1	-1.048	0.374
>tr Q99K87 Q99K87_MOUSE Serine hydroxymethyltransferase OS=Mus musculus GN=Shmt2 PE=2 S	-0.915	0.147	>tr Q99LB4 Q99LB4_MOUSE Capping protein (Actin filament), gelsolin-like OS=Mus muscu	-1.045	0.382
>tr Q3U2G2 Q3U2G2_MOUSE Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=2 SV=	-0.915	0.149	>tr Q3TR59 Q3TR59_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus	-0.993	0.390
>sp Q9D1G1 RAB1B_MOUSE Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-0.911	0.152	>sp Q9DWT7 MYO1C_MOUSE Unconventional myosin-Ic OS=Mus musculus GN=Myo1c PE	-0.969	0.398
>sp Q91ZP3-2 LPIN1_MOUSE Isoform 2 of Phosphatidate phosphatase LPIN1 OS=Mus musculus GN=	-0.909	0.154	>sp Q008638 MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	-0.965	0.406
>sp P47738 ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 I	-0.897	0.157	>sp P26041 MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	-0.880	0.413
>sp Q6PB66 LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musc	-0.883	0.159	>sp Q99K51 PLST_MOUSE Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	-0.849	0.421
>sp Q99JY0 ECHB_MOUSE Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=	-0.879	0.162	>sp Q8VD75 HIP1_MOUSE Huntingtin-interacting protein 1 OS=Mus musculus GN=Hip1 PE	-0.827	0.429
>sp P09671 SODM_MOUSE Superoxide dismutase [Mn], mitochondrial OS=Mus musculus GN=Sod2 I	-0.851	0.164	>tr E9Q0S6 E9Q0S6_MOUSE Protein Tns1 OS=Mus musculus GN=Tns1 PE=4 SV=1	-0.795	0.437
>sp Q99MN9 PCCB_MOUSE Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus	-0.848	0.167	>sp P58774 TPM2_MOUSE Tropomyosin beta chain OS=Mus musculus GN=TPm2 PE=1 SV	-0.784	0.445
>sp Q8BU85 MSRB3_MOUSE Methionine-R-sulfoxide reductase B3, mitochondrial OS=Mus musculus	-0.846	0.169	>sp P26040 EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	-0.782	0.453
>sp Q8QZT1 THIL_MOUSE Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Aca	-0.836	0.172	>sp P07091 S10A4_MOUSE Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	-0.747	0.461
>sp Q05920 PYC_MOUSE Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc PE=1 SV=	-0.824	0.174	>sp Q9JJ28 FLII_MOUSE Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV	-0.738	0.469
>sp Q9CZD3 SYG_MOUSE Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1	-0.824	0.177	>sp P70460 VASP_MOUSE Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=V	-0.715	0.476
>sp Q61191 HCF1_MOUSE Host cell factor 1 OS=Mus musculus GN=Hcfc1 PE=1 SV=2	-0.815	0.179	>sp P26043 RADI_MOUSE Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	-0.706	0.484
>sp Q07813 BAX_MOUSE Apoptosis regulator BAX OS=Mus musculus GN=Bax PE=1 SV=1	-0.808	0.181	>sp Q9EPC1 PARVA_MOUSE Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	-0.690	0.492
>sp Q3ULD5 MCCB_MOUSE Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Mus m	-0.807	0.184	>sp Q61792 LASP1_MOUSE LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1 I	-0.652	0.500
>sp Q9JH15 IVD_MOUSE Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Ivd P	-0.793	0.186	>sp Q99JY9 ARP3_MOUSE Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=	-0.649	0.508
>sp P10639 THIO_MOUSE Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	-0.789	0.189	>sp P15508 SPTB1_MOUSE Spectrin beta chain, erythrocytic OS=Mus musculus GN=Sptb P	-0.628	0.516
>sp Q63932 MP2K2_MOUSE Dual specificity mitogen-activated protein kinase kinase 2 OS=Mus musc	-0.769	0.191	>sp P61161 ARP2_MOUSE Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	-0.572	0.524
>sp Q9JLN9 MTOR_MOUSE Serine/threonine-protein kinase mTOR OS=Mus musculus GN=Mtor PE=	-0.769	0.194	>sp Q91235 SNTB2_MOUSE Beta-2-syntrophin OS=Mus musculus GN=Sntb2 PE=1 SV=2	-0.463	0.531
>sp P50516 VATA_MOUSE V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1	-0.755	0.196	>sp P47757-2 CAPZB_MOUSE Isoform 2 of F-actin-capping protein subunit beta OS=Mus m	-0.458	0.539
>sp Q5U458 DJC11_MOUSE DnaJ homolog subfamily C member 11 OS=Mus musculus GN=Dnajc11	-0.740	0.199	>sp Q9J191 ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	-0.396	0.547
>sp Q9D880 TIM50_MOUSE Mitochondrial import inner membrane translocase subunit TIM50 OS=M	-0.722	0.201	>sp Q8K4L3 SVIL_MOUSE Supervillin OS=Mus musculus GN=Svil PE=1 SV=1	-0.384	0.555

>sp O55126 NIPS2_MOUSE Protein NipSnap homolog 2 OS=Mus musculus GN=Gbas PE=2 SV=1	-0.661	0.204	>sp O08579 EMD_MOUSE Emerin OS=Mus musculus GN=Emd PE=1 SV=1	-0.381	0.563
>sp Q99MN1 SYK_MOUSE Lysine--tRNA ligase OS=Mus musculus GN=Kars PE=1 SV=1	-0.659	0.206	>sp Q64727 VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	-0.368	0.571
>sp Q99KI0 ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.657	0.209	>sp Q9D898 ARP5L_MOUSE Actin-related protein 2/3 complex subunit 5-like protein OS=M	-0.363	0.579
>sp Q8BP47 SYNC_MOUSE Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Nars PE=	-0.656	0.211	>sp Q61233 PLSL_MOUSE Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	-0.313	0.587
>sp O54724 PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=	-0.648	0.214	>sp Q9WV32 ARC1B_MOUSE Actin-related protein 2/3 complex subunit 1B OS=Mus muscu	-0.285	0.594
>sp P38060 HMGCL_MOUSE Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus G	-0.646	0.216	>sp Q8CC35 SYNPO_MOUSE Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2	-0.262	0.602
>sp P11499 HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1	-0.643	0.219	>sp P18760 COF1_MOUSE Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	-0.262	0.610
>sp Q9JMH6 TRXR1_MOUSE Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 P	-0.637	0.221	>sp Q9CPW4 ARPC5_MOUSE Actin-related protein 2/3 complex subunit 5 OS=Mus musculu	-0.261	0.618
>sp Q9JHW2 NIT2_MOUSE Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1	-0.631	0.223	>sp Q0GNC1 INF2_MOUSE Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1	-0.251	0.626
>sp P45952 ACADM_MOUSE Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=M	-0.623	0.226	>sp P49813 TMOD1_MOUSE Tropomodulin-1 OS=Mus musculus GN=Tmod1 PE=2 SV=2	-0.238	0.634
>sp Q8K1J6 TRNT1_MOUSE CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus musculus C	-0.617	0.228	>sp P21107 TPM3_MOUSE Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1	-0.230	0.642
>sp Q9QXB9 DRG2_MOUSE Developmentally-regulated GTP-binding protein 2 OS=Mus musculus G	-0.615	0.231	>tr Q3U0Q9 Q3U0Q9_MOUSE Putative uncharacterized protein (Fragment) OS=Mus muscul	-0.211	0.650
>sp Q8BYC6 TAOK3_MOUSE Serine/threonine-protein kinase TAO3 OS=Mus musculus GN=Taok3 F	-0.610	0.233	>sp Q8CI51 PDL15_MOUSE PDZ and LIM domain protein 5 OS=Mus musculus GN=Pdlim5	-0.156	0.657
>sp P07901 HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=	-0.586	0.236	>tr A1BN54 A1BN54_MOUSE Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=2 SV=1	-0.131	0.665
>sp Q9D0S9 HINT2_MOUSE Histidine triad nucleotide-binding protein 2, mitochondrial OS=Mus mus	-0.562	0.238	>sp Q9R0P5 DEST_MOUSE Destrin OS=Mus musculus GN=Dstn PE=1 SV=3	-0.107	0.673
>sp Q6X893 CTL1_MOUSE Choline transporter-like protein 1 OS=Mus musculus GN=Slc44a1 PE=1 S	-0.554	0.241	>sp O08808 DIAP1_MOUSE Protein diaphanous homolog 1 OS=Mus musculus GN=Diaph1 1	-0.107	0.681
>sp P97742 CPT1A_MOUSE Carnitine O-palmitoyltransferase 1, liver isoform OS=Mus musculus GN=	-0.552	0.243	>sp Q7TMB8 CYFP1_MOUSE Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus C	-0.098	0.689
>sp Q91VR2 ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp	-0.542	0.246	>sp P97434 MPRIIP_MOUSE Myosin phosphatase Rho-interacting protein OS=Mus musculus	-0.059	0.697
>sp Q8K4Z3 NNRE_MOUSE NAD(P)H-hydrate epimerase OS=Mus musculus GN=Apoa1bp PE=1 SV	-0.536	0.248	>sp P59999 ARPC4_MOUSE Actin-related protein 2/3 complex subunit 4 OS=Mus musculus	-0.047	0.705
>sp P24270 CATA_MOUSE Catalase OS=Mus musculus GN=Cat PE=1 SV=4	-0.530	0.251	>sp O70566 DIAP2_MOUSE Protein diaphanous homolog 2 OS=Mus musculus GN=Diaph2 1	-0.045	0.713
>sp Q9CWJ9 PUR9_MOUSE Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=	-0.528	0.253	>sp Q8VDP3 MICA1_MOUSE Protein-methionine sulfoxide oxidase MICAL1 OS=Mus musc	-0.020	0.720
>sp Q9Z210 LETM1_MOUSE LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=M	-0.527	0.256	>sp Q9EPK2 XRP2_MOUSE Protein XRP2 OS=Mus musculus GN=Rp2 PE=1 SV=3	-0.016	0.728
>sp Q922E6 FAKD2_MOUSE Fast kinase domain-containing protein 2 OS=Mus musculus GN=Fa	-0.524	0.258	>sp Q99KW3 TARA_MOUSE TRIO and F-actin-binding protein OS=Mus musculus GN=Tric	0.082	0.736
>sp Q922D8 C1TC_MOUSE C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd	-0.523	0.260	>sp Q7TSE6 ST38L_MOUSE Serine/threonine-protein kinase 38-like OS=Mus musculus GN=	0.112	0.744
>sp P05132 KAPCA_MOUSE cAMP-dependent protein kinase catalytic subunit alpha OS=Mus muscul	-0.513	0.263	>tr Q3TNK2 Q3TNK2_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Wd	0.121	0.752
>sp Q921S7 RM37_MOUSE 39S ribosomal protein L37, mitochondrial OS=Mus musculus GN=Mrpl37	-0.493	0.265	>sp Q62165 DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	0.131	0.760
>sp P53026 RL10A_MOUSE 60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	-0.491	0.268	>sp O88342 WDR1_MOUSE WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 F	0.131	0.768
>sp O08553 DPYL2_MOUSE Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpyl2 P	-0.477	0.270	>sp Q80X90 FLNB_MOUSE Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	0.136	0.776
>sp P62264 RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	-0.465	0.273	>sp Q9JM76 ARPC3_MOUSE Actin-related protein 2/3 complex subunit 3 OS=Mus musculus	0.152	0.783
>sp P54320 ELN_MOUSE Elastin OS=Mus musculus GN=Eln PE=2 SV=2	-0.458	0.275	>sp Q9QYC0 ADDA_MOUSE Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2	0.182	0.791
>sp P70404 IDHG1_MOUSE Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial OS=M	-0.455	0.278	>sp Q8BH43 WASF2_MOUSE Wiskott-Aldrich syndrome protein family member 2 OS=Mus	0.209	0.799
>sp P63038 CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 P	-0.452	0.280	>sp Q61234 SNTA1_MOUSE Alpha-1-syntrophin OS=Mus musculus GN=Snta1 PE=1 SV=1	0.352	0.807
>sp P08249 MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=	-0.451	0.283	>sp P59242 CING_MOUSE Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1	0.379	0.815
>sp Q9EQ20 MMSA_MOUSE Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	-0.450	0.285	>sp Q9CVB6 ARPC2_MOUSE Actin-related protein 2/3 complex subunit 2 OS=Mus musculu	0.521	0.823
>sp P70296 PEBP1_MOUSE Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pe	-0.447	0.288	>sp P58771 TPM1_MOUSE Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1	0.584	0.831
>sp Q3UV70 PDP1_MOUSE [Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondr	-0.437	0.290	>sp Q9CQI3 GMFB_MOUSE Glia maturation factor beta OS=Mus musculus GN=Gmfb PE=1	0.679	0.839
>sp Q5SWU9 ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-0.436	0.293	>sp Q9ET54 PALLD_MOUSE Palladin OS=Mus musculus GN=Palld PE=1 SV=2	0.701	0.846
>sp Q9Z219 SUCB1_MOUSE Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=M	-0.422	0.295	>sp O70318 E4IL2_MOUSE Band 4.1-like protein 2 OS=Mus musculus GN=Epb4112 PE=1 S	0.704	0.854
>sp Q91VM9-2 IPYR2_MOUSE Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial OS=Mus mu	-0.420	0.298	>sp Q9QXS1 PLEC_MOUSE Plectin OS=Mus musculus GN=Plec PE=1 SV=2	0.743	0.862
>sp P17156 HSP72_MOUSE Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1	-0.419	0.300	>sp Q3UH68 LIMC1_MOUSE LIM and calponin homology domains-containing protein 1 OS	0.756	0.870
>sp O55028 BCKD_MOUSE [3-methyl-2-oxobutanoate dehydrogenase [lipamide]] kinase, mitochondr	-0.414	0.302	>sp Q62261 SPTB2_MOUSE Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=	0.786	0.878
>sp P35235 PTN11_MOUSE Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN	-0.407	0.305	>tr F6T2Z7 F6T2Z7_MOUSE Protein Cald1 (Fragment) OS=Mus musculus GN=Cald1 PE=4	0.853	0.886
>sp Q9QUJ7 ACSL4_MOUSE Long-chain-fatty-acid--CoA ligase 4 OS=Mus musculus GN=Acsl4 PE=	-0.399	0.307	>sp Q9QYB5 ADDG_MOUSE Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=2	1.040	0.894
>sp P51660 DHB4_MOUSE Peroxisomal multifunctional enzyme type 2 OS=Mus musculus GN=Hsd17	-0.394	0.310	>sp P16546 SPTN1_MOUSE Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=	1.067	0.902
>sp P85094 ISC2A_MOUSE Ischorismatase domain-containing protein 2A, mitochondrial OS=Mus m	-0.390	0.312	>sp P61982 I433G_MOUSE 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV	1.152	0.909
>sp P51175 PPOX_MOUSE Protoporphyrinogen oxidase OS=Mus musculus GN=Ppox PE=2 SV=1	-0.380	0.315	>sp P62962 PROF1_MOUSE Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	1.237	0.917
>sp Q64433 CH10_MOUSE 10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 P	-0.369	0.317	>sp Q641P0 ARP3B_MOUSE Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2	1.243	0.925
>sp Q61462 CY24A_MOUSE Cytochrome b-245 light chain OS=Mus musculus GN=Cyba PE=1 SV=3	-0.366	0.320	>sp Q71LX4 TLN2_MOUSE Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.251	0.933
>sp Q9D051 ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=N	-0.366	0.322	>tr Q3TN69 Q3TN69_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculu	1.263	0.941

>sp P35486 ODPA_MOUSE Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitoc	-0.349	0.325	>sp Q6IRU2 TPM4_MOUSE Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=2	1.292	0.949
>sp P50544 ACADV_MOUSE Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=M	-0.340	0.327	>sp O89053 COR1A_MOUSE Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	1.348	0.957
>sp P26638 SYSC_MOUSE Serine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Sars PE=2 SV=1	-0.338	0.330	>sp P84075 HPCA_MOUSE Neuron-specific calcium-binding protein hippocalcin OS=Mus m	1.554	0.965
>sp O35855 BCAT2_MOUSE Branched-chain-amino-acid aminotransferase, mitochondrial OS=Mus m	-0.328	0.332	>sp Q9CQI6 COTL1_MOUSE Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=1	1.566	0.972
>sp P56382 ATP5E_MOUSE ATP synthase subunit epsilon, mitochondrial OS=Mus musculus GN=Atp	-0.325	0.335	>sp P68510 I433F_MOUSE 14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	1.750	0.980
>sp Q3U9G9 LBR_MOUSE Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-0.324	0.337	>sp Q99L88 SNTB1_MOUSE Beta-1-syntrophin OS=Mus musculus GN=Sntb1 PE=1 SV=4	1.751	0.988
>sp Q2TPA8 HSDL2_MOUSE Hydroxysteroid dehydrogenase-like protein 2 OS=Mus musculus GN=H	-0.322	0.340	>sp Q02566 MYH6_MOUSE Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	3.701	0.996
>sp Q9CZW5 TOM70_MOUSE Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=	-0.314	0.342			
>sp Q8C0V9 FRMD6_MOUSE FERM domain-containing protein 6 OS=Mus musculus GN=Frmd6 PE=	-0.312	0.344	Cell adhesion GO:0007155		
>sp Q8BHC4 DCAKD_MOUSE Dephospho-CoA kinase domain-containing protein OS=Mus musculus	-0.310	0.347	Protein identification	Zq	rank/N
>sp Q9DBF1 AL7A1_MOUSE Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=	-0.310	0.349	>sp Q61282 PGCA_MOUSE Aggrecan core protein OS=Mus musculus GN=Acan PE=1 SV=1	-4.710	0.005
>sp Q9DAR7 DCPS_MOUSE m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=1	-0.297	0.352	>sp Q62059 CSPG2_MOUSE Versican core protein OS=Mus musculus GN=Vcan PE=1 SV=1	-3.806	0.015
>sp P84091 AP2M1_MOUSE AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	-0.294	0.354	>sp Q9QZZ6 DERM_MOUSE Dermatopontin OS=Mus musculus GN=Dpt PE=2 SV=1	-3.617	0.026
>sp Q99LC5 ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musc	-0.293	0.357	>sp Q61581 IBP7_MOUSE Insulin-like growth factor-binding protein 7 OS=Mus musculus GN=	-3.596	0.036
>sp O88587 COMT_MOUSE Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2	-0.286	0.359	>sp P29788 VTNC_MOUSE Vitronectin OS=Mus musculus GN=Vtn PE=1 SV=2	-3.072	0.046
>sp Q9JK48 SHLB1_MOUSE Endophilin-B1 OS=Mus musculus GN=Sh3glb1 PE=1 SV=1	-0.272	0.362	>sp Q91V88 NPNT_MOUSE Nephronectin OS=Mus musculus GN=Npnt PE=1 SV=1	-3.021	0.056
>sp Q8K1M6 DNM1L_MOUSE Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=2	-0.265	0.364	>sp P39061 COIA1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1	-2.832	0.066
>sp Q99LD8 DDAH2_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Mus musc	-0.232	0.367	>sp P11276 FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4	-2.610	0.077
>sp Q9D8B4 NDUAB_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=	-0.215	0.369	>tr Q3UFT0 Q3UFT0_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculu	-2.267	0.087
>sp P28271 ACOC_MOUSE Cytoplasmic aconitate hydratase OS=Mus musculus GN=Aco1 PE=1 SV=	-0.207	0.372	>sp P21956 MFGM_MOUSE Lactadherin OS=Mus musculus GN=Mfge8 PE=1 SV=3	-2.184	0.097
>sp O35857 TIM44_MOUSE Mitochondrial import inner membrane translocase subunit TIM44 OS=M	-0.195	0.374	>sp Q8VDD5 MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-2.160	0.107
>sp Q9Z1J3 NFS1_MOUSE Cysteine desulfurase, mitochondrial OS=Mus musculus GN=Nfs1 PE=2 SV	-0.195	0.377	>sp O88207 CO5A1_MOUSE Collagen alpha-1(V) chain OS=Mus musculus GN=Col5a1 PE=	-2.086	0.117
>sp P16460 ASSY_MOUSE Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	-0.191	0.379	>sp Q62523 ZYX_MOUSE Zyxin OS=Mus musculus GN=Zyx PE=1 SV=2	-2.059	0.128
>sp O35683 NDUA1_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1 OS=M	-0.182	0.381	>sp Q64314 CD34_MOUSE Hematopoietic progenitor cell antigen CD34 OS=Mus musculus GN=	-1.933	0.138
>sp Q9JHR7 IDE_MOUSE Insulin-degrading enzyme OS=Mus musculus GN=Ide PE=1 SV=1	-0.165	0.384	>sp Q61001 LAMA5_MOUSE Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1	-1.923	0.148
>sp Q99LX0 PARK7_MOUSE Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-0.160	0.386	>sp Q04857 CO6A1_MOUSE Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=	-1.838	0.158
>sp Q8CHT0 AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Mus	-0.158	0.389	>sp A2ARA8 ITA8_MOUSE Integrin alpha-8 OS=Mus musculus GN=Itga8 PE=1 SV=1	-1.758	0.168
>sp Q9CZU6 CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	-0.158	0.391	>sp Q9R069 BCAM_MOUSE Basal cell adhesion molecule OS=Mus musculus GN=Bcam PE=	-1.640	0.179
>sp P03930 ATP8_MOUSE ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=1	-0.151	0.394	>sp Q80X19 COEA1_MOUSE Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1	-1.625	0.189
>sp Q9DCC8 TOM20_MOUSE Mitochondrial import receptor subunit TOM20 homolog OS=Mus musc	-0.149	0.396	>sp Q8C6K9 CO6A6_MOUSE Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=	-1.617	0.199
>sp Q60936 ADCK3_MOUSE Chaperone activity of bc1 complex-like, mitochondrial OS=Mus muscul	-0.147	0.399	>sp Q640N1 AEBP1_MOUSE Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=	-1.583	0.209
>sp Q9Z2Y8 PROSC_MOUSE Proline synthase co-transcribed bacterial homolog protein OS=Mus mus	-0.134	0.401	>sp P12023 A4_MOUSE Amyloid beta A4 protein OS=Mus musculus GN=App PE=1 SV=3	-1.581	0.219
>sp A2ARZ3 FSIP2_MOUSE Fibrous sheath-interacting protein 2 OS=Mus musculus GN=Fsp2 PE=1	-0.113	0.404	>sp A6H584 CO6A5_MOUSE Collagen alpha-5(VI) chain OS=Mus musculus GN=Col6a5 PE=	-1.559	0.230
>sp Q91XE0 GLYAT_MOUSE Glycine N-acyltransferase OS=Mus musculus GN=Glyat PE=1 SV=1	-0.112	0.406	>sp O35206 COFA1_MOUSE Collagen alpha-1(XV) chain OS=Mus musculus GN=Col15a1	-1.486	0.240
>sp Q9QZD8 DIC_MOUSE Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=	-0.108	0.409	>sp Q62009 POSTN_MOUSE Periostin OS=Mus musculus GN=Postn PE=1 SV=2	-1.372	0.250
>sp P11352 GPX1_MOUSE Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2	-0.100	0.411	>sp P11688 ITA5_MOUSE Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=3	-1.370	0.260
>sp P06801 MAOX_MOUSE NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=	-0.091	0.414	>sp Q61879 MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-1.350	0.270
>sp P47740 AL3A2_MOUSE Fatty aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2 PE=2 SV	-0.069	0.416	>sp Q99K41 EMIL1_MOUSE EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1	-1.307	0.281
>sp Q60597 ODO1_MOUSE 2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogc	-0.068	0.419	>sp O88322 NID2_MOUSE Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	-1.257	0.291
>sp Q9CWS0 DDAH1_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Mus mus	-0.058	0.421	>sp P26039 TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	-1.208	0.301
>sp Q9QZ18 SUCB2_MOUSE Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=M	-0.056	0.423	>tr Q8BS97 Q8BS97_MOUSE Versican core protein OS=Mus musculus GN=Vcan PE=2 SV=	-1.198	0.311
>sp P42859 HD_MOUSE Huntingtin OS=Mus musculus GN=Htt PE=1 SV=2	-0.055	0.426	>sp Q62470 ITA3_MOUSE Integrin alpha-3 OS=Mus musculus GN=Itga3 PE=1 SV=1	-1.156	0.321
>sp Q9CZ42 NNRD_MOUSE ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus G	-0.050	0.428	>sp Q61490 CD166_MOUSE CD166 antigen OS=Mus musculus GN=Alcam PE=1 SV=3	-1.151	0.332
>sp Q9Z1Q5 CLIC1_MOUSE Chloride intracellular channel protein 1 OS=Mus musculus GN=Clc1 PE	-0.038	0.431	>sp P43406 ITAV_MOUSE Integrin alpha-V OS=Mus musculus GN=Itgav PE=1 SV=2	-1.139	0.342
>sp P55096 ABCD3_MOUSE ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=A	-0.035	0.433	>sp P09055 ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	-1.132	0.352
>sp P16125 LDHB_MOUSE L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhd PE=1 SV=	-0.031	0.436	>sp P97927 LAMA4_MOUSE Laminin subunit alpha-4 OS=Mus musculus GN=Lama4 PE=1	-1.085	0.362
>sp Q9QUI0 RHOA_MOUSE Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1 SV=1	-0.026	0.438	>sp Q9R1V7 ADA23_MOUSE Disintegrin and metalloproteinase domain-containing protein 2	-1.060	0.372
>sp O70325 GPX41_MOUSE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=N	-0.019	0.441	>sp Q9R1Z8 VINEX_MOUSE Vinexin OS=Mus musculus GN=Sorbs3 PE=1 SV=1	-0.898	0.383
>sp P63085 MKO1_MOUSE Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 S	-0.018	0.443	>sp Q8V136 PAXI_MOUSE Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1	-0.879	0.393

>sp P50431 GLYC_MOUSE Serine hydroxymethyltransferase, cytosolic OS=Mus musculus GN=Shmt1	-0.015	0.446	>sp Q61292 LAMB2_MOUSE Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=2	-0.875	0.403
>sp Q9QUM9 PSA6_MOUSE Proteasome subunit alpha type-6 OS=Mus musculus GN=Pma6 PE=1 S'	-0.011	0.448	>sp Q02788 CO6A2_MOUSE Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE	-0.863	0.413
>sp P31750 AKT1_MOUSE RAC-alpha serine/threonine-protein kinase OS=Mus musculus GN=Akt1 P	-0.009	0.451	>tr Q91XX7 Q91XX7_MOUSE Protocadherin gamma B2 OS=Mus musculus GN=Pcdhgb2 P	-0.843	0.423
>sp Q8BVI4 DHPR_MOUSE Dihydropteridine reductase OS=Mus musculus GN=Qdpr PE=1 SV=2	-0.001	0.453	>sp Q80YX1 TENA_MOUSE Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	-0.836	0.434
>sp Q9CQW1 YKT6_MOUSE Synaptobrevin homolog YKT6 OS=Mus musculus GN=Ykt6 PE=2 SV=	0.009	0.456	>sp Q9WVH9 FBLN5_MOUSE Fibulin-5 OS=Mus musculus GN=Fbln5 PE=2 SV=1	-0.800	0.444
>sp P56380 AP4A_MOUSE Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Mus musculus GN=	0.010	0.458	>tr B8JK39 B8JK39_MOUSE Integrin alpha 9 OS=Mus musculus GN=Itga9 PE=3 SV=1	-0.781	0.454
>sp Q07417 ACADS_MOUSE Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus n	0.012	0.460	>tr B9EHT6 B9EHT6_MOUSE Fn1 protein OS=Mus musculus GN=Fn1 PE=2 SV=1	-0.756	0.464
>sp Q61425 HCDH_MOUSE Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mus muscu	0.013	0.463	>tr F8VQJ3 F8VQJ3_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=	-0.750	0.474
>sp Q9D0I9 SYRC_MOUSE Arginine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Rars PE=2 S	0.015	0.465	>sp P62746 RHOB_MOUSE Rho-related GTP-binding protein RhoB OS=Mus musculus GN=	-0.722	0.485
>sp Q8BMF4 ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase component of pyruvate deh	0.016	0.468	>sp Q9EPC1 PARVA_MOUSE Alpha-parvin OS=Mus musculus GN=Parva PE=1 SV=1	-0.690	0.495
>sp Q8BGB8 COQ4_MOUSE Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial OS=Mus	0.024	0.470	>sp P26231 CTNA1_MOUSE Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	-0.663	0.505
>sp Q91VD9 NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=	0.040	0.473	>sp Q3UTJ2 SRBS2_MOUSE Sorbin and SH3 domain-containing protein 2 OS=Mus muscu	-0.651	0.515
>sp Q9CRB9 CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitoch	0.043	0.475	>sp Q8BFW7 LPP_MOUSE Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp1	-0.638	0.526
>tr Q3U1C4 Q3U1C4_MOUSE MCG1271 OS=Mus musculus GN=Secisbp2 PE=2 SV=1	0.056	0.478	>sp Q8CIZ8 VWF_MOUSE von Willebrand factor OS=Mus musculus GN=Vwf PE=1 SV=2	-0.628	0.536
>sp Q9DCX2 ATP5H_MOUSE ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h 1	0.072	0.480	>sp Q9Z0M6 CD97_MOUSE CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	-0.620	0.546
>tr Q99N15 Q99N15_MOUSE 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxya	0.073	0.483	>sp Q71FD7 FBLI1_MOUSE Filamin-binding LIM protein 1 OS=Mus musculus GN=Fblim1	-0.561	0.556
>sp Q9D6J5 NDUB8_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitoc	0.078	0.485	>sp Q9QUP5 HPLN1_MOUSE Hyaluronan and proteoglycan link protein 1 OS=Mus muscu	-0.434	0.566
>sp Q8BKZ9 ODP3_MOUSE Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus n	0.084	0.488	>sp Q9WTR5 CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=1 SV=2	-0.425	0.577
>sp Q8BGT8 PHIPL_MOUSE Phytanoyl-CoA hydroxylase-interacting protein-like OS=Mus musculus	0.088	0.490	>sp Q070309 ITB5_MOUSE Integrin beta-5 OS=Mus musculus GN=Itgb5 PE=1 SV=2	-0.368	0.587
>sp Q91WD5 NDUS2_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondria	0.095	0.493	>sp Q64727 VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	-0.368	0.597
>sp Q8CAY6 THIC_MOUSE Acetyl-CoA acetyltransferase, cytosolic OS=Mus musculus GN=Acat2 PI	0.096	0.495	>sp P02468 LAMC1_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=	-0.350	0.607
>sp Q8BIJ6 SYIM_MOUSE Isoleucine--tRNA ligase, mitochondrial OS=Mus musculus GN=Iars2 PE=	0.099	0.498	>sp Q8R2Y2 MUC18_MOUSE Cell surface glycoprotein MUC18 OS=Mus musculus GN=Muc	-0.318	0.617
>sp P51174 ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus m	0.102	0.500	>tr A2RS43 A2RS43_MOUSE Protein Pcdh7 OS=Mus musculus GN=Pcdh7 PE=2 SV=1	-0.284	0.628
>sp P08228 SODC_MOUSE Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2	0.115	0.502	>sp Q61735 CD47_MOUSE Leukocyte surface antigen CD47 OS=Mus musculus GN=Cd47 P	-0.238	0.638
>sp Q99LP6 GRPE1_MOUSE GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 1	0.126	0.505	>sp Q9D1H9 MFAP4_MOUSE Microfibril-associated glycoprotein 4 OS=Mus musculus GN=	-0.237	0.648
>sp P80313 TCPH_MOUSE T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	0.127	0.507	>sp Q8BZF8 PGM5_MOUSE Phosphoglucosyltransferase-like protein 5 OS=Mus musculus GN=Pgm	-0.154	0.658
>sp P38647 GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=	0.147	0.510	>sp P97300 NPTN_MOUSE Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3	-0.099	0.668
>sp P63168 DYL1_MOUSE Dynein light chain 1, cytoplasmic OS=Mus musculus GN=Dynll1 PE=1 SV=	0.157	0.512	>sp Q08481 PECA1_MOUSE Platelet endothelial cell adhesion molecule OS=Mus musculus	-0.094	0.679
>sp Q9DBM2 ECHP_MOUSE Peroxisomal bifunctional enzyme OS=Mus musculus GN=Ehhadh PE=1	0.165	0.515	>sp P14206 RSSA_MOUSE 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=	-0.062	0.689
>sp P43024 CX6A1_MOUSE Cytochrome c oxidase subunit 6A1, mitochondrial OS=Mus musculus GN=	0.169	0.517	>sp P29533 VCAM1_MOUSE Vascular cell adhesion protein 1 OS=Mus musculus GN=Vcam	-0.025	0.699
>sp Q9CXW2 RT22_MOUSE 28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrps2	0.174	0.520	>tr E9QB01 E9QB01_MOUSE Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncan	0.000	0.709
>sp Q9DC70 NDUS7_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	0.175	0.522	>sp P30999 CTND1_MOUSE Catenin delta-1 OS=Mus musculus GN=Ctnd1 PE=1 SV=2	0.095	0.719
>sp Q9Z1Z2 STRAP_MOUSE Serine-threonine kinase receptor-associated protein OS=Mus musculus C	0.176	0.525	>sp P35441 TSP1_MOUSE Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1	0.104	0.730
>sp P52825 CPT2_MOUSE Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musculus GN=	0.176	0.527	>sp Q99JY8 LPP3_MOUSE Lipid phosphate phosphohydrolase 3 OS=Mus musculus GN=Ppa	0.143	0.740
>sp P47934 CACP_MOUSE Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=1 SV=3	0.179	0.530	>sp P82198 BGH3_MOUSE Transforming growth factor-beta-induced protein ig-h3 OS=Mus	0.160	0.750
>sp Q9CQH3 NDUB5_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mito	0.185	0.532	>sp Q61330 CNTN2_MOUSE Contactin-2 OS=Mus musculus GN=Cntn2 PE=2 SV=2	0.247	0.760
>sp P56480 ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b F	0.200	0.535	>sp O70423 AOC3_MOUSE Membrane primary amine oxidase OS=Mus musculus GN=Aoc3	0.258	0.770
>sp Q63844 MK03_MOUSE Mitogen-activated protein kinase 3 OS=Mus musculus GN=Mapk3 PE=1 S'	0.207	0.537	>sp Q9QUI0 RHOA_MOUSE Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=	0.275	0.781
>sp P53395 ODB2_MOUSE Lipamide acyltransferase component of branched-chain alpha-keto acid de	0.210	0.540	>sp Q60847 COCA1_MOUSE Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 1	0.294	0.791
>sp P28352 APEX1_MOUSE DNA-(apurinic or apyrimidinic site) lyase OS=Mus musculus GN=Ape1	0.221	0.542	>sp P35330 ICAM2_MOUSE Intercellular adhesion molecule 2 OS=Mus musculus GN=Icam2	0.459	0.801
>sp Q64521 GPDH_MOUSE Glyceral-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus C	0.227	0.544	>sp Q8CIB5 FERM2_MOUSE Fermitin family homolog 2 OS=Mus musculus GN=Fermt2 PE	0.503	0.811
>sp Q8VCL2 SCO2_MOUSE Protein SCO2 homolog, mitochondrial OS=Mus musculus GN=Sco2 PE=	0.228	0.547	>sp Q8VCC9 SPON1_MOUSE Spondin-1 OS=Mus musculus GN=Spon1 PE=2 SV=1	0.552	0.821
>sp Q8BFR5 EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1	0.229	0.549	>sp O54890 ITB3_MOUSE Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=1 SV=2	0.585	0.832
>sp P62492 RB11A_MOUSE Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=	0.232	0.552	>sp P10493 NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	0.631	0.842
>sp Q9D855 QCR7_MOUSE Cytochrome b-c1 complex subunit 7 OS=Mus musculus GN=Uqcrcb P	0.234	0.554	>sp Q60634 FLOT2_MOUSE Flotillin-2 OS=Mus musculus GN=Flot2 PE=1 SV=2	0.671	0.852
>sp O70378 EMC8_MOUSE ER membrane protein complex subunit 8 OS=Mus musculus GN=Emc8 P	0.236	0.557	>sp P13595 NCAM1_MOUSE Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam	0.864	0.862
>sp Q9Z0X1 AIFM1_MOUSE Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifi	0.244	0.559	>sp P40240 CD9_MOUSE CD9 antigen OS=Mus musculus GN=Cd9 PE=1 SV=2	0.942	0.872
>sp P54775 PRS6B_MOUSE 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1	0.245	0.562	>tr G3UW60 G3UW60_MOUSE MCG14773 OS=Mus musculus GN=Susd5 PE=4 SV=1	0.992	0.883
>sp Q9CPV4 GLOD4_MOUSE Glyoxalase domain-containing protein 4 OS=Mus musculus GN=Glod4	0.249	0.564	>sp Q60675 LAMA2_MOUSE Laminin subunit alpha-2 OS=Mus musculus GN=Lama2 PE=1	1.083	0.893

>tr Q8JZU2 Q8JZU2_MOUSE Protein Slc25a1 OS=Mus musculus GN=Slc25a1 PE=2 SV=1	0.257	0.567	>sp Q71LX4 TLN2_MOUSE Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.251	0.903
>sp Q9Z1X4 ILF3_MOUSE Interleukin enhancer-binding factor 3 OS=Mus musculus GN=Ilf3 PE=1 SV=1	0.261	0.569	>sp P63001 RAC1_MOUSE Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	1.328	0.913
>sp Q5SSK3 TEFM_MOUSE Transcription elongation factor, mitochondrial OS=Mus musculus GN=TEFM PE=1 SV=1	0.267	0.572	>sp Q02248 CTNNB1_MOUSE Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1	1.411	0.923
>tr Q924B0 Q924B0_MOUSE Inositol (Myo)-1(Or 4)-monophosphatase 1 OS=Mus musculus GN=Imp1 PE=1 SV=1	0.271	0.574	>sp Q61738 ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=3	1.587	0.934
>sp Q9QYB1 CLIC4_MOUSE Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=1	0.271	0.577	>sp Q035114 SCRB2_MOUSE Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=1	1.649	0.944
>sp Q6ZWQ0 SYNE2_MOUSE Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=2	0.274	0.579	>sp Q3V3R4 ITA1_MOUSE Integrin alpha-1 OS=Mus musculus GN=Itga1 PE=2 SV=2	2.446	0.954
>sp P25688 URIC_MOUSE Uricase OS=Mus musculus GN=Uox PE=1 SV=2	0.286	0.581	>sp Q08857 CD36_MOUSE Platelet glycoprotein 4 OS=Mus musculus GN=CD36 PE=1 SV=2	2.737	0.964
>sp Q9DCM0 ETHE1_MOUSE Protein ETHE1, mitochondrial OS=Mus musculus GN=Ethe1 PE=1 SV=1	0.302	0.584	>sp P14094 AT1B1_MOUSE Sodium/potassium-transporting ATPase subunit beta-1 OS=Mus musculus GN=AT1B1 PE=1 SV=1	5.091	0.974
>sp Q91V92 ACLY_MOUSE ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	0.325	0.586	>sp P02469 LAMB1_MOUSE Laminin subunit beta-1 OS=Mus musculus GN=Lamb1 PE=1 SV=1	5.615	0.985
>sp P52480 KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm PE=1 SV=1	0.327	0.589	>sp Q2UY11 COL1A1_MOUSE Collagen alpha-1(XXVIII) chain OS=Mus musculus GN=Col1A1 PE=1 SV=1	12.820	0.995
>sp Q99JR1 SFXN1_MOUSE Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	0.329	0.591			
>sp O08749 DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dldh PE=1 SV=1	0.330	0.594	Calcium ion binding GO:0005509		
>sp Q8VEM8 MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a1 PE=1 SV=1	0.336	0.596	Protein identification	Zq	rank/N
>sp Q922W5 P5CR1_MOUSE Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Mus musculus GN=P5CR1 PE=1 SV=1	0.342	0.599	>sp P70663 SPRL1_MOUSE SPARC-like protein 1 OS=Mus musculus GN=Sparcl1 PE=1 SV=1	-7.129	0.005
>sp Q8CH40 NUDT6_MOUSE Nucleoside diphosphate-linked moiety X motif 6 OS=Mus musculus GN=NUDT6 PE=1 SV=1	0.349	0.601	>sp Q62059 CSGP2_MOUSE Versican core protein OS=Mus musculus GN=Vcan PE=1 SV=1	-3.806	0.014
>sp Q9D3D9 ATPD_MOUSE ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	0.368	0.604	>sp Q8BPP5 FBLN3_MOUSE EGF-containing fibulin-like extracellular matrix protein 1 OS=Mus musculus GN=Fbln3 PE=1 SV=1	-3.415	0.023
>sp P56395 CYB5_MOUSE Cytochrome b5 OS=Mus musculus GN=Cyb5a PE=1 SV=2	0.370	0.606	>tr Q6ZWQ9 Q6ZWQ9_MOUSE MCG5400 OS=Mus musculus GN=Myl12a PE=2 SV=1	-3.282	0.032
>sp Q9WTP6 KAD2_MOUSE Adenylate kinase 2, mitochondrial OS=Mus musculus GN=Ak2 PE=1 SV=1	0.376	0.609	>sp Q91V88 NPNT_MOUSE Nephronectin OS=Mus musculus GN=Npnt PE=1 SV=1	-3.021	0.041
>sp Q99J99 THTM_MOUSE 3-mercaptopyruvate sulfurtransferase OS=Mus musculus GN=Mpst PE=1 SV=1	0.383	0.611	>sp Q8K4G1 LTBP4_MOUSE Latent-transforming growth factor beta-binding protein 4 OS=Mus musculus GN=Ltbp4 PE=1 SV=1	-2.490	0.050
>sp Q921H8 THIKA_MOUSE 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1c PE=1 SV=1	0.390	0.614	>tr F8WIT2 F8WIT2_MOUSE Annexin OS=Mus musculus GN=Anxa6 PE=3 SV=1	-1.915	0.059
>sp P17665 COX7C_MOUSE Cytochrome c oxidase subunit 7C, mitochondrial OS=Mus musculus GN=Cox7c PE=1 SV=1	0.413	0.616	>sp Q3THE2 ML12B_MOUSE Myosin regulatory light chain 12B OS=Mus musculus GN=Myo12b PE=1 SV=1	-1.838	0.068
>sp Q9D3P8 PLRKT_MOUSE Plasminogen receptor (KT) OS=Mus musculus GN=Plgrkt PE=1 SV=1	0.414	0.619	>sp Q9D2N4 DTNA_MOUSE Dystrobrevin alpha OS=Mus musculus GN=Dtna PE=1 SV=2	-1.804	0.077
>sp Q8BH04 PCKGM_MOUSE Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pckgm PE=1 SV=1	0.426	0.621	>sp Q60605 MYL6_MOUSE Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=1	-1.760	0.086
>sp P28474 ADHX_MOUSE Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3	0.439	0.623	>sp P08032 SPTA1_MOUSE Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Spta1 PE=1 SV=1	-1.687	0.095
>sp P62259 1433E_MOUSE 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	0.441	0.626	>sp Q9R0K7 AT2B2_MOUSE Plasma membrane calcium-transporting ATPase 2 OS=Mus musculus GN=ATP2B2 PE=1 SV=1	-1.621	0.104
>sp Q9D6K8 FUND2_MOUSE FUN14 domain-containing protein 2 OS=Mus musculus GN=Fundc2 PE=1 SV=1	0.455	0.628	>sp Q9CQ19 MYL9_MOUSE Myosin regulatory light polypeptide 9 OS=Mus musculus GN=Myl9 PE=1 SV=1	-1.587	0.113
>sp Q9R112 SQRD_MOUSE Sulfide:quinone oxidoreductase, mitochondrial OS=Mus musculus GN=SQRD PE=1 SV=1	0.483	0.631	>sp P57780 ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	-1.536	0.122
>sp P19096 FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	0.490	0.633	>tr A2AQ53 A2AQ53_MOUSE Fibrillin 1 OS=Mus musculus GN=Fbn1 PE=4 SV=1	-1.539	0.131
>sp Q9CQX2 CYB5B_MOUSE Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 SV=1	0.490	0.636	>sp Q8C143 MYL6B_MOUSE Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=2 SV=1	-1.483	0.140
>sp Q64105 SPRE_MOUSE Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1	0.498	0.638	>tr Q61636 Q61636_MOUSE G-utrophin (Predicted protein) OS=Mus musculus GN=Utrn PE=1 SV=1	-1.294	0.149
>sp Q8VHJ7 PRGC2_MOUSE Peroxisome proliferator-activated receptor gamma coactivator 1-beta OS=Mus musculus GN=Prp12 PE=1 SV=1	0.512	0.641	>sp O88322 NID2_MOUSE Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	-1.257	0.158
>sp Q9WUM5 SUCA_MOUSE Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Suca1 PE=1 SV=1	0.512	0.643	>tr Q8C845 Q8C845_MOUSE EF hand domain containing 2 OS=Mus musculus GN=Efh2d2 PE=1 SV=1	-1.255	0.167
>tr Q91VA7 Q91VA7_MOUSE Isocitrate dehydrogenase 3 (NAD+) beta OS=Mus musculus GN=Idh3b PE=1 SV=1	0.517	0.646	>sp P11531 DMD_MOUSE Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=3	-1.252	0.176
>sp P26443 DHE3_MOUSE Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	0.522	0.648	>sp Q3V0K9 PLS1_MOUSE Plastin 1 OS=Mus musculus GN=Pls1 PE=2 SV=1	-1.220	0.185
>sp Q9QZH6 ECSIT_MOUSE Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial OS=Mus musculus GN=Ecsit PE=1 SV=1	0.524	0.651	>sp Q08879 FBLN1_MOUSE Fibulin-1 OS=Mus musculus GN=Fbln1 PE=1 SV=2	-1.197	0.194
>sp P37040 NCPR_MOUSE NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=1	0.537	0.653	>sp O08795 GLU2B_MOUSE Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1	-1.195	0.203
>sp O09005 DEGS1_MOUSE Sphingolipid delta(4)-desaturase DES1 OS=Mus musculus GN=Degs1 PE=1 SV=1	0.537	0.656	>sp P21981 TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=TGM2 PE=1 SV=1	-1.193	0.212
>sp P08074 CBR2_MOUSE Carbonyl reductase [NADPH] 2 OS=Mus musculus GN=Cbr2 PE=1 SV=1	0.539	0.658	>sp O08529 CAN2_MOUSE Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=2 SV=1	-1.151	0.221
>sp Q9D7B6 ACAD8_MOUSE Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=ACAD8 PE=1 SV=1	0.553	0.660	>sp P37889 FBLN2_MOUSE Fibulin-2 OS=Mus musculus GN=Fbln2 PE=1 SV=2	-1.150	0.230
>sp P35700 PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	0.567	0.663	>tr E9Q6R7 E9Q6R7_MOUSE Protein Utrn OS=Mus musculus GN=Utrn PE=4 SV=1	-1.104	0.239
>sp Q3YYR9 ACOT2_MOUSE Acyl-coenzyme A thioesterase 2, mitochondrial OS=Mus musculus GN=ACOT2 PE=1 SV=1	0.567	0.665	>sp Q7TPR4 ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	-1.092	0.248
>sp Q9D6R2 IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=IDH3A PE=1 SV=1	0.579	0.668	>sp A2ASQ1 AGRIN_MOUSE Agrin OS=Mus musculus GN=Agrn PE=1 SV=1	-1.088	0.257
>sp O89023 TPP1_MOUSE Tripeptidyl-peptidase 1 OS=Mus musculus GN=Tppl1 PE=1 SV=2	0.588	0.670	>sp P10107 ANXA1_MOUSE Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	-1.077	0.266
>sp Q60932 VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=VDAC1 PE=1 SV=1	0.607	0.673	>sp Q07076 ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=2	-1.013	0.275
>sp Q9CPY7 AMPL_MOUSE Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	0.610	0.675	>sp P14069 S10A6_MOUSE Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3	-0.894	0.284
>sp P36552 HEM6_MOUSE Coproporphyrinogen-III oxidase, mitochondrial OS=Mus musculus GN=CHEM6 PE=1 SV=1	0.639	0.678	>sp Q99K51 PLST_MOUSE Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	-0.849	0.293
>sp Q9CQN1 TRAP1_MOUSE Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1	0.641	0.680	>tr Q91XX7 Q91XX7_MOUSE Protocadherin gamma B2 OS=Mus musculus GN=Pcdhgb2 PE=1 SV=1	-0.843	0.302
>sp Q60930 VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=VDAC2 PE=1 SV=1	0.642	0.683	>sp Q9D4J1 EFHD1_MOUSE EF-hand domain-containing protein D1 OS=Mus musculus GN=EFHD1 PE=1 SV=1	-0.817	0.311
>sp Q8C196 CPSM_MOUSE Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=CPSM PE=1 SV=1	0.642	0.685	>sp Q8CG19 LTBP1_MOUSE Latent-transforming growth factor beta-binding protein 1 OS=Mus musculus GN=Ltbp1 PE=1 SV=1	-0.808	0.320

>sp P46471 PR57_MOUSE 26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=	0.645	0.688	>sp Q9VWH9 FBLN5_MOUSE Fibulin-5 OS=Mus musculus GN=Fbln5 PE=2 SV=1	-0.800	0.329
>sp P33434 MMP2_MOUSE 72 kDa type IV collagenase OS=Mus musculus GN=Mmp2 PE=2 SV=1	0.653	0.690	>sp Q05186 RCN1_MOUSE Reticulocalbin-1 OS=Mus musculus GN=Rcn1 PE=1 SV=1	-0.767	0.338
>sp E9Q557 DESP_MOUSE Desmoplakin OS=Mus musculus GN=Dsp PE=3 SV=1	0.664	0.693	>sp P19221 THRB_MOUSE Prothrombin OS=Mus musculus GN=F2 PE=1 SV=1	-0.765	0.347
>sp P06151 LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=	0.665	0.695	>sp P07091 S10A4_MOUSE Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	-0.747	0.356
>sp Q9CR61 NDUB7_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=	0.672	0.698	>sp Q62356 FSTL1_MOUSE Follistatin-related protein 1 OS=Mus musculus GN=Fstl1 PE=1	-0.724	0.365
>sp P21981 TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=	0.673	0.700	>sp P62204 CALM_MOUSE Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2	-0.716	0.374
>sp Q641K1 CBPC1_MOUSE Cytosolic carboxypeptidase 1 OS=Mus musculus GN=Agtpbp1 PE=1 SV	0.675	0.702	>sp Q61592 GAS6_MOUSE Growth arrest-specific protein 6 OS=Mus musculus GN=Gas6 PE=	-0.623	0.383
>sp Q921G7 ETFD_MOUSE Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial C	0.678	0.705	>sp Q9Z0M6 CD97_MOUSE CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	-0.620	0.392
>sp Q8BTZ7 GMPPB_MOUSE Mannose-1-phosphate guanylttransferase beta OS=Mus musculus GN=C	0.686	0.707	>sp P97352 S10AD_MOUSE Protein S100-A13 OS=Mus musculus GN=S100a13 PE=1 SV=1	-0.591	0.401
>sp O08709 PRDX6_MOUSE Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	0.692	0.710	>sp P70302 STIM1_MOUSE Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=	-0.562	0.410
>sp Q9CQZ5 NDUA6_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=	0.702	0.712	>sp Q9EQP2 EHD4_MOUSE EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=	-0.554	0.419
>sp Q9WTP7 KAD3_MOUSE GTP:AMP phosphotransferase, mitochondrial OS=Mus musculus GN=A	0.745	0.715	>sp O35887 CALU_MOUSE Calumenin OS=Mus musculus GN=Calu PE=1 SV=1	-0.543	0.428
>sp Q9CR21 ACPM_MOUSE Acyl carrier protein, mitochondrial OS=Mus musculus GN=Ndufab1 PE=	0.761	0.717	>sp Q9ESD7 DYSF_MOUSE Dysferlin OS=Mus musculus GN=Dysf PE=1 SV=3	-0.542	0.437
>sp Q9JLJ2 AL9A1_MOUSE 4-trimethylaminobutyaldehyde dehydrogenase OS=Mus musculus GN=A	0.763	0.720	>sp Q60902 EP15R_MOUSE Epidermal growth factor receptor substrate 15-like 1 OS=Mus m	-0.502	0.446
>sp Q9JIK9 RT34_MOUSE 28S ribosomal protein S34, mitochondrial OS=Mus musculus GN=Mrps34	0.773	0.722	>sp Q9D8Y0 EFHD2_MOUSE EF-hand domain-containing protein D2 OS=Mus musculus GN=	-0.500	0.455
>sp Q8VCM4 LIPT_MOUSE Lipoyltransferase 1, mitochondrial OS=Mus musculus GN=Lipt1 PE=2 SV=	0.774	0.725	>sp P12815 PDCD6_MOUSE Programmed cell death protein 6 OS=Mus musculus GN=Pcdcf	-0.469	0.464
>sp Q9D6U8 F162A_MOUSE Protein FAM162A OS=Mus musculus GN=Fam162a PE=2 SV=1	0.778	0.727	>sp P97347 RPTN_MOUSE Repetin OS=Mus musculus GN=Rptn PE=1 SV=1	-0.458	0.473
>sp P99029 PRDX5_MOUSE Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=	0.783	0.730	>sp Q9WVJ9 FBLN4_MOUSE EGF-containing fibulin-like extracellular matrix protein 2 OS=	-0.449	0.482
>sp Q791V5 MTCH2_MOUSE Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1 SV=	0.786	0.732	>sp Q06138 CAB39_MOUSE Calcium-binding protein 39 OS=Mus musculus GN=Cab39 PE=	-0.437	0.491
>sp Q9CQJ8 NDUB9_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=N	0.795	0.735	>sp Q9WTR5 CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=1 SV=2	-0.425	0.500
>sp Q9CQ54 NDUC2_MOUSE NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus musculus G	0.797	0.737	>sp Q9JI91 ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	-0.396	0.509
>sp Q68FD5 CLH1_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	0.801	0.740	>sp Q61233 PLSL_MOUSE Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	-0.313	0.518
>sp Q9CZW4 ACSL3_MOUSE Long-chain-fatty-acid--CoA ligase 3 OS=Mus musculus GN=Acsl3 PE=	0.806	0.742	>sp Q8R3B1 PLCD1_MOUSE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase del	-0.295	0.527
>sp Q9CQ62 DECR_MOUSE 2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus GN=Decr1	0.823	0.744	>tr A2RS43 A2RS43_MOUSE Protein Pcdh7 OS=Mus musculus GN=Pcdh7 PE=2 SV=1	-0.284	0.536
>sp P18242 CATD_MOUSE Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	0.824	0.747	>sp Q8BLY1 SMOC1_MOUSE SPARC-related modular calcium-binding protein 1 OS=Mus m	-0.263	0.545
>sp Q9CXZ1 NDUS4_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondria	0.853	0.749	>sp P43025 TETN_MOUSE Tetranectin OS=Mus musculus GN=Clec3b PE=1 SV=2	-0.257	0.554
>sp Q62425 NDUA4_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=N	0.855	0.752	>sp Q8BP92 RCN2_MOUSE Reticulocalbin-2 OS=Mus musculus GN=Rcn2 PE=2 SV=1	-0.227	0.563
>sp P47791 GSHR_MOUSE Glutathione reductase, mitochondrial OS=Mus musculus GN=Gsr PE=2 SV=	0.894	0.754	>sp O88456 CPNS1_MOUSE Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=2 SV=	-0.194	0.572
>sp Q9Z2Z6 MCAT_MOUSE Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus	0.902	0.757	>tr A3KGU7 A3KGU7_MOUSE Protein Spna2 OS=Mus musculus GN=Spna2 PE=4 SV=1	-0.148	0.581
>sp Q9C3265 ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a	0.909	0.759	>sp O35639 ANXA3_MOUSE Annexin A3 OS=Mus musculus GN=Anxa3 PE=1 SV=4	-0.144	0.590
>sp P63101 1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	0.912	0.762	>sp Q61554 FBN1_MOUSE Fibrillin-1 OS=Mus musculus GN=Fbn1 PE=1 SV=1	-0.142	0.599
>sp Q06890 CLUS_MOUSE Clusterin OS=Mus musculus GN=Clu PE=1 SV=1	0.943	0.764	>tr A1BN54 A1BN54_MOUSE Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=2 SV=1	-0.131	0.608
>sp Q61171 PRDX2_MOUSE Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	0.952	0.767	>sp Q8R429 AT2A1_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=M	-0.054	0.617
>sp P00405 COX2_MOUSE Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=	0.970	0.769	>sp P52430 PON1_MOUSE Serum paraoxonase/arylesterase 1 OS=Mus musculus GN=Pon1 PE=	-0.033	0.626
>sp O88844 IDHC_MOUSE Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh	0.992	0.772	>sp P52633 STAT6_MOUSE Signal transducer and transcription activator 6 OS=Mus muscul	0.004	0.635
>sp Q9WVL0 MAAI_MOUSE Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=	1.000	0.774	>sp P07356 ANXA2_MOUSE Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.027	0.644
>sp Q9CYW4 HDHD3_MOUSE Haloacid dehalogenase-like hydrolase domain-containing protein 3 OS	1.026	0.777	>tr Q91UZ1 Q91UZ1_MOUSE Phospholipase C beta 4 OS=Mus musculus GN=Plcb4 PE=2 SV=	0.102	0.653
>sp P42125 ECI1_MOUSE Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus GN=Eci1 PE=	1.030	0.779	>sp P35441 TSP1_MOUSE Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1	0.104	0.662
>sp P10605 CATB_MOUSE Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	1.037	0.781	>sp Q62165 DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	0.131	0.671
>sp P15532 NDKA_MOUSE Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV	1.037	0.784	>sp P97384 ANX11_MOUSE Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=2	0.139	0.680
>sp P29758 OAT_MOUSE Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=	1.039	0.786	>sp P63028 TCTP_MOUSE Translationally-controlled tumor protein OS=Mus musculus GN=	0.162	0.689
>sp Q8CI78 RMND1_MOUSE Required for meiotic nuclear division protein 1 homolog OS=Mus muscu	1.047	0.789	>sp Q8BH59 CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus	0.184	0.698
>sp Q9DCN2 NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=	1.047	0.791	>sp Q91ZX7 LRP1_MOUSE Prolow-density lipoprotein receptor-related protein 1 OS=Mus m	0.228	0.707
>sp Q8R404 QIL1_MOUSE Protein QIL1 OS=Mus musculus GN=Qi1 PE=2 SV=1	1.060	0.794	>tr Q6XLQ8 Q6XLQ8_MOUSE Calumenin OS=Mus musculus GN=Calu PE=2 SV=1	0.253	0.716
>sp Q9QYA2 TOM40_MOUSE Mitochondrial import receptor subunit TOM40 homolog OS=Mus musc	1.067	0.796	>sp O70423 AOC3_MOUSE Membrane primary amine oxidase OS=Mus musculus GN=Aoc3 PE=	0.258	0.725
>sp Q8VCW8 ACSF2_MOUSE Acyl-CoA synthetase family member 2, mitochondrial OS=Mus muscul	1.067	0.799	>sp O35350 CAN1_MOUSE Calpain-1 catalytic subunit OS=Mus musculus GN=Capn1 PE=2	0.289	0.734
>sp Q9CQC7 NDUB4_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=N	1.083	0.801	>sp P08207 S10AA_MOUSE Protein S100-A10 OS=Mus musculus GN=S100a10 PE=2 SV=2	0.345	0.743
>sp P56135 ATPK_MOUSE ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=	1.089	0.804	>sp Q9WVK4 EHD1_MOUSE EH domain-containing protein 1 OS=Mus musculus GN=Ehd1	0.413	0.752
>sp Q06185 ATP5I_MOUSE ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=	1.098	0.806	>sp P61022 CHP1_MOUSE Calcineurin B homologous protein 1 OS=Mus musculus GN=Chp	0.478	0.761

>sp P14152 MDHC_MOUSE Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1	1.100	0.809	>sp P14824 ANXA6_MOUSE Annexin A6 OS=Mus musculus GN=Anxa6 PE=1 SV=3	0.481	0.770
>sp Q01768 NDKB_MOUSE Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2 PE=1 SV=	1.117	0.811	>sp O70258 SGCE_MOUSE Epsilon-sarcoglycan OS=Mus musculus GN=Sgce PE=2 SV=2	0.551	0.779
>sp Q9CXT8 MPPB_MOUSE Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=	1.118	0.814	>sp P14211 CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	0.603	0.788
>sp P16675 PPGB_MOUSE Lysosomal protective protein OS=Mus musculus GN=Ctsa PE=1 SV=1	1.125	0.816	>sp Q8BH97 RCN3_MOUSE Reticulocalbin-3 OS=Mus musculus GN=Rcn3 PE=2 SV=1	0.607	0.797
>sp P12787 COX5A_MOUSE Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=	1.129	0.819	>sp P10493 NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2	0.631	0.806
>sp Q8K2B3 DHSA_MOUSE Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondri	1.153	0.821	>sp Q99MQ4 ASPN_MOUSE Asporin OS=Mus musculus GN=Aspn PE=1 SV=1	0.657	0.815
>sp Q99LC3 NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mi	1.161	0.823	>sp Q61576 FKB10_MOUSE Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Mus musculus	0.701	0.824
>sp Q9DCS3 MECR_MOUSE Trans-2-enoyl-CoA reductase, mitochondrial OS=Mus musculus GN=Me	1.207	0.826	>sp Q9QXY6 EHD3_MOUSE EH domain-containing protein 3 OS=Mus musculus GN=Ehd3	0.731	0.833
>sp Q60715 P4HA1_MOUSE Prolyl 4-hydroxylase subunit alpha-1 OS=Mus musculus GN=P4ha1 PE=	1.226	0.828	>sp P62748 HPCL1_MOUSE Hippocalcin-like protein 1 OS=Mus musculus GN=Hpcal1 PE=	0.833	0.842
>sp Q9DC69 NDUA9_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mit	1.266	0.831	>sp P50543 S10AB_MOUSE Protein S100-A11 OS=Mus musculus GN=S100a11 PE=2 SV=1	0.870	0.851
>sp Q9CR62 M2OM_MOUSE Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus C	1.298	0.833	>sp P47713 PA24A_MOUSE Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE	0.886	0.860
>sp Q9WTQ8 TIM23_MOUSE Mitochondrial import inner membrane translocase subunit Tim23 OS=M	1.311	0.836	>sp Q9Z247 FKBP9_MOUSE Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Mus musculus	0.982	0.869
>sp Q91Y70 NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=M	1.335	0.838	>sp P42225 STAT1_MOUSE Signal transducer and activator of transcription 1 OS=Mus musc	0.987	0.878
>sp P19536 COX5B_MOUSE Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus musculus GN=	1.339	0.841	>sp Q02819 NUCB1_MOUSE Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	1.003	0.887
>sp P54310 LIPS_MOUSE Hormone-sensitive lipase OS=Mus musculus GN=Lipe PE=1 SV=2	1.340	0.843	>sp P82350 SGCA_MOUSE Alpha-sarcoglycan OS=Mus musculus GN=Sgca PE=1 SV=1	1.013	0.896
>sp Q7TMF3 NDUAC_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 O	1.340	0.846	>sp P16546 SPTN1_MOUSE Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=	1.067	0.905
>sp Q60575-3 KIF1B_MOUSE Isoform 3 of Kinesin-like protein KIF1B OS=Mus musculus GN=Kif1b	1.353	0.848	>sp Q8BH64 EHD2_MOUSE EH domain-containing protein 2 OS=Mus musculus GN=Ehd2	1.143	0.914
>sp P56392 CX7A1_MOUSE Cytochrome c oxidase subunit 7A1, mitochondrial OS=Mus musculus GN=	1.376	0.851	>sp Q3UYK3 TBGD9_MOUSE TBC1 domain family member 9 OS=Mus musculus GN=Tbc1	1.231	0.923
>sp Q60931 VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus musculus	1.378	0.853	>sp Q99M71 EPDR1_MOUSE Mammalian ependymin-related protein 1 OS=Mus musculus G	1.259	0.932
>sp P17710 HXXK1_MOUSE Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	1.392	0.856	>sp P35564 CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	1.466	0.941
>sp P18572 BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	1.419	0.858	>sp Q64521 GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus m	1.487	0.950
>sp Q9DCJ5 NDUA8_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=	1.436	0.860	>sp P07214 SPRC_MOUSE SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	1.547	0.959
>sp Q92511 ATAD3_MOUSE ATPase family AAA domain-containing protein 3 OS=Mus musculus GN=	1.444	0.863	>sp P84075 HPCA_MOUSE Neuron-specific calcium-binding protein hippocalcin OS=Mus m	1.554	0.968
>sp P00397 COX1_MOUSE Cytochrome c oxidase subunit 1 OS=Mus musculus GN=Mtc1 PE=3 SV=	1.446	0.865	>sp P97429 ANXA4_MOUSE Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=4	1.588	0.977
>sp Q99KK9 SYHM_MOUSE Probable histidine--tRNA ligase, mitochondrial OS=Mus musculus GN=	1.463	0.868	>sp P48036 ANXA5_MOUSE Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	1.906	0.986
>sp Q9CR68 UCRI_MOUSE Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus muscul	1.464	0.870	>sp Q9Z184 PADI3_MOUSE Protein-arginine deiminase type-3 OS=Mus musculus GN=Padi	3.369	0.995
>sp P99028 QCR6_MOUSE Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus musculus GN=	1.523	0.873			
>sp A6H611 MIPEP_MOUSE Mitochondrial intermediate peptidase OS=Mus musculus GN=Mipep PE=	1.525	0.875	Lipid metabolic process GO:0006629		
>sp Q9Z110 P5CS_MOUSE Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a	1.525	0.878			
>sp P31938 MP2K1_MOUSE Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musc	1.539	0.880	>sp P33622 APOC3_MOUSE Apolipoprotein C-III OS=Mus musculus GN=Apoc3 PE=2 SV=	-2.513	0.006
>sp Q9CPQ3 TOM22_MOUSE Mitochondrial import receptor subunit TOM22 homolog OS=Mus musc	1.539	0.883	>sp Q00623 APOA1_MOUSE Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=2	-2.316	0.019
>sp Q8BH59 CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculu	1.565	0.885	>sp P01027 CO3_MOUSE Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	-1.640	0.031
>sp Q62167 DDX3X_MOUSE ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x I	1.592	0.888	>sp Q9Z2V4 PCKGC_MOUSE Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=M	-1.170	0.044
>sp Q99L04 DHRS1_MOUSE Dehydrogenase/reductase SDR family member 1 OS=Mus musculus GN=	1.620	0.890	>tr O35452 O35452_MOUSE Protein Tnxb OS=Mus musculus GN=Tnxb PE=2 SV=1	-0.794	0.056
>sp P31786 ACBP_MOUSE Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2	1.621	0.893	>sp P08226 APOE_MOUSE Apolipoprotein E OS=Mus musculus GN=ApoE PE=1 SV=2	-0.785	0.069
>sp Q91V61 SFXN3_MOUSE Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	1.633	0.895	>sp Q62264 THRSP_MOUSE Thyroid hormone-inducible hepatic protein OS=Mus musculus	-0.749	0.081
>sp Q9CPP6 NDUA5_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=	1.637	0.898	>sp E9Q414 APOB_MOUSE Apolipoprotein B-100 OS=Mus musculus GN=ApoB PE=1 SV=	-0.651	0.094
>sp Q64442 DHSO_MOUSE Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3	1.643	0.900	>sp O35074 PTGIS_MOUSE Prostacyclin synthase OS=Mus musculus GN=Ptgis PE=2 SV=1	-0.603	0.106
>sp Q8BGC4 ZADH2_MOUSE Zinc-binding alcohol dehydrogenase domain-containing protein 2 OS=	1.657	0.902	>sp P19096 FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	-0.597	0.119
>sp Q8BGH2 SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=Mus mus	1.672	0.905	>sp Q921H8 THIKA_MOUSE 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus G	-0.566	0.131
>sp Q9CPQ1 COX6C_MOUSE Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c PE=1	1.696	0.907	>sp Q9DCN2 NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=C	-0.564	0.144
>tr Q91WX5 Q91WX5_MOUSE Bak1 protein OS=Mus musculus GN=Bak1 PE=2 SV=1	1.719	0.910	>sp O70503 DHB12_MOUSE Estradiol 17-beta-dehydrogenase 12 OS=Mus musculus GN=H	-0.501	0.156
>tr Q8R5L1 Q8R5L1_MOUSE Complement component 1 Q subcomponent-binding protein, mitochond	1.728	0.912	>sp Q8VCW8 ACSF2_MOUSE Acyl-CoA synthetase family member 2, mitochondrial OS=M	-0.423	0.169
>sp P54822 PUR8_MOUSE Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=2 SV=2	1.752	0.915	>sp P22437 PGH1_MOUSE Prostaglandin G/H synthase 1 OS=Mus musculus GN=Ptgs1 PE=	-0.418	0.181
>sp Q9CZ13 QCR1_MOUSE Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus G	1.774	0.917	>sp Q9R0Q7 TEBP_MOUSE Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=	-0.337	0.194
>sp Q9ERS2 NDUAD_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS	1.778	0.920	>sp Q8R3B1 PLCD1_MOUSE 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase del	-0.295	0.206
>sp P67778 PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	1.791	0.922	>sp Q9JHU9 INO1_MOUSE Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 I	-0.290	0.219
>sp Q9CQ75 NDUA2_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=	1.951	0.925	>sp P51174 ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial O	-0.240	0.231
>sp Q922Q1 MOSC2_MOUSE MOSC domain-containing protein 2, mitochondrial OS=Mus musculus C	1.978	0.927	>sp Q9DBL1 ACDSB_MOUSE Short/branched chain specific acyl-CoA dehydrogenase, mitoc	-0.225	0.244

>sp Q61398 PCOC1_MOUSE Procollagen C-endopeptidase enhancer 1 OS=Mus musculus GN=Pcolce	-0.618	0.197	>sp Q8VDJ3 VIGLN_MOUSE Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	1.223	0.869
>sp P07901 HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=	-0.586	0.208	>sp O35678 MGLL_MOUSE Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1	1.317	0.881
>sp Q9D2L5 CPXM2_MOUSE Inactive carboxypeptidase-like protein X2 OS=Mus musculus GN=Cpxi	-0.562	0.219	>sp Q8JZK9 HMCS1_MOUSE Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Mus m	1.331	0.894
>sp Q8CIZ8 VWF_MOUSE von Willebrand factor OS=Mus musculus GN=Vwf PE=1 SV=2	-0.545	0.230	>sp Q9DBL9 ABHD5_MOUSE 1-acylglycerol-3-phosphate O-acyltransferase ABHD5 OS=M	1.404	0.906
>tr Q3TAF9 Q3TAF9_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Bgn PE=2 SV	-0.500	0.242	>sp Q9CY27 TECR_MOUSE Very-long-chain enoyl-CoA reductase OS=Mus musculus GN=	1.541	0.919
>sp Q99K41 EMIL1_MOUSE EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1	-0.439	0.253	>sp Q9EQ06 DHB11_MOUSE Estradiol 17-beta-dehydrogenase 11 OS=Mus musculus GN=H	1.835	0.931
>sp Q640N1 AEBP1_MOUSE Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=Aebp1 PE	-0.423	0.264	>sp Q8BMS1 ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=M m	1.908	0.944
>sp P11087 CO1A1_MOUSE Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1 SV=4	-0.333	0.275	>sp P51910 APOD_MOUSE Apolipoprotein D OS=Mus musculus GN=Apod PE=2 SV=1	2.042	0.956
>sp Q00780 CO8A1_MOUSE Collagen alpha-1(VIII) chain OS=Mus musculus GN=Col8a1 PE=1 SV=	-0.328	0.287	>sp P50172 DHI1_MOUSE Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Mus muscu	2.437	0.969
>tr Q99K31 Q99K31_MOUSE Col6a3 protein (Fragment) OS=Mus musculus GN=Col6a3 PE=2 SV=1	-0.324	0.298	>sp Q07417 ACADS_MOUSE Short-chain specific acyl-CoA dehydrogenase, mitochondrial C	2.528	0.981
>sp P08121 CO3A1_MOUSE Collagen alpha-1(III) chain OS=Mus musculus GN=Col3a1 PE=2 SV=4	-0.263	0.309	>sp Q8CGN5 PLIN1_MOUSE Perilipin-1 OS=Mus musculus GN=Plin1 PE=1 SV=2	3.179	0.994
>sp Q80YX1 TENA_MOUSE Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	-0.156	0.320			
>sp O88232 NID2_MOUSE Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	-0.137	0.331	Mitochondrion GO:0005739		
>sp P28653 PGS1_MOUSE Biglycan OS=Mus musculus GN=Bgn PE=2 SV=1	-0.137	0.343	Protein identification	Zq	rank/N
>sp Q61554 FBN1_MOUSE Fibrillin-1 OS=Mus musculus GN=Fbn1 PE=1 SV=1	-0.136	0.354	>sp O55028 BCKD_MOUSE [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, n	-5.942	0.001
>sp Q3UQ28 PXDN_MOUSE Peroxidasin homolog OS=Mus musculus GN=Pxdn PE=2 SV=2	-0.134	0.365	>sp Q8K1Z0 COQ9_MOUSE Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mus	-3.581	0.004
>sp Q8CD91 SMOC2_MOUSE SPARC-related modular calcium-binding protein 2 OS=Mus musculus	-0.074	0.376	>sp Q6ZWQ0 SYNE2_MOUSE Nesprin-2 OS=Mus musculus GN=Syne2 PE=1 SV=2	-3.369	0.006
>sp Q8CG19 LTBP1_MOUSE Latent-transforming growth factor beta-binding protein 1 OS=Mus muscu	-0.012	0.388	>sp Q06890 CLUS_MOUSE Clusterin OS=Mus musculus GN=Clu PE=1 SV=1	-3.265	0.009
>sp Q01149 CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=2 SV=2	0.035	0.399	>sp Q8BGC4 ZADH2_MOUSE Zinc-binding alcohol dehydrogenase domain-containing prote	-2.928	0.011
>tr O88493 O88493_MOUSE Type VI collagen alpha 3 subunit OS=Mus musculus GN=Col6a3 PE=2 S	0.036	0.410	>sp O09164 SODE_MOUSE Extracellular superoxide dismutase [Cu-Zn] OS=Mus musculus	-2.564	0.014
>sp P97873 LOXL1_MOUSE Lysyl oxidase homolog 1 OS=Mus musculus GN=Loxl1 PE=2 SV=3	0.046	0.421	>sp Q920A7 AFG31_MOUSE AFG3-like protein 1 OS=Mus musculus GN=Afg31 PE=2 SV=	-2.471	0.016
>tr Q9Z0I9 Q9Z0I9_MOUSE Collagen alpha3(VI) (Fragment) OS=Mus musculus GN=Col6a3 PE=2 SV	0.065	0.433	>sp Q8BP47 SYNC_MOUSE Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus GN=	-2.422	0.019
>sp P08228 SODC_MOUSE Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2	0.115	0.444	>sp Q60931 VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus	-1.962	0.021
>sp Q8R2G6 CCD80_MOUSE Coiled-coil domain-containing protein 80 OS=Mus musculus GN=Ccdc8	0.146	0.455	>tr Q8R5L1 Q8R5L1_MOUSE Complement component 1 Q subcomponent-binding protein, n	-1.881	0.024
>tr Q3UZF9 Q3UZF9_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Fn	0.187	0.466	>sp Q91V61 SFXN3_MOUSE Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	-1.866	0.026
>sp Q9QZZ6 DERM_MOUSE Dermatopontin OS=Mus musculus GN=Dpt PE=2 SV=1	0.210	0.478	>sp Q61171 PRDX2_MOUSE Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	-1.808	0.029
>sp Q08879-2 FBLN1_MOUSE Isoform C of Fibulin-1 OS=Mus musculus GN=Fbln1	0.229	0.489	>sp Q9Z2Y8 PROSC_MOUSE Proline synthase co-transcribed bacterial homolog protein OS=	-1.636	0.031
>tr B1B0C7 B1B0C7_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein	0.293	0.500	>sp Q9DC29 ABCB6_MOUSE ATP-binding cassette sub-family B member 6, mitochondrial	-1.606	0.034
>sp Q62005 ZP1_MOUSE Zona pellucida sperm-binding protein 1 OS=Mus musculus GN=Zp1 PE=1 S	0.294	0.511	>sp Q9J1M14 NT5C_MOUSE 5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus	-1.507	0.036
>sp Q8C4U3 SFRP1_MOUSE Secreted frizzled-related protein 1 OS=Mus musculus GN=Sfrp1 PE=1 S	0.328	0.522	>sp Q8CH40 NUDT6_MOUSE Nucleoside diphosphate-linked moiety X motif 6 OS=Mus mu	-1.485	0.039
>tr B7ZNH7 B7ZNH7_MOUSE Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1 PE=2 S	0.332	0.534	>sp Q3THF9 CQ10B_MOUSE Coenzyme Q-binding protein COQ10 homolog B, mitochondri	-1.473	0.041
>sp P97298 PEDF_MOUSE Pigment epithelium-derived factor OS=Mus musculus GN=Serpinf1 PE=1 :	0.339	0.545	>sp Q8VFC0 MAVS_MOUSE Mitochondrial antiviral-signaling protein OS=Mus musculus G	-1.433	0.044
>sp P27090 TGFB2_MOUSE Transforming growth factor beta-2 OS=Mus musculus GN=Tgfb2 PE=1 S	0.361	0.556	>sp O35658 C1QBP_MOUSE Complement component 1 Q subcomponent-binding protein, m	-1.377	0.046
>tr A2AQ53 A2AQ53_MOUSE Fibrillin 1 OS=Mus musculus GN=Fbn1 PE=4 SV=1	0.365	0.567	>tr Q3U2G2 Q3U2G2_MOUSE Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 F	-1.311	0.049
>sp P28654 PGS2_MOUSE Decorin OS=Mus musculus GN=Dcn PE=2 SV=1	0.392	0.579	>sp P13707 GPDA_MOUSE Glyceral-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS	-1.267	0.052
>sp Q61001 LAMA5_MOUSE Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1 SV=4	0.404	0.590	>tr D3Z7C8 D3Z7C8_MOUSE Branched-chain-amino-acid aminotransferase OS=Mus muscu	-1.244	0.054
>tr Q3UHH3 Q3UHH3_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Hspg2 PE=2	0.445	0.601	>sp P21981 TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus muscu	-1.193	0.057
>sp P82198 BGH3_MOUSE Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus	0.446	0.612	>sp Q9DCS9 NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subu	-1.158	0.059
>sp P21844 CMA1_MOUSE Chymase OS=Mus musculus GN=Cma1 PE=1 SV=2	0.514	0.624	>sp Q8BGB8 COQ4_MOUSE Ubiquinone biosynthesis protein COQ4 homolog, mitochondria	-1.137	0.062
>sp Q62219 TGF1_MOUSE Transforming growth factor beta-1-induced transcript 1 protein OS=Mus n	0.529	0.635	>sp O08756 HCD2_MOUSE 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus G	-1.123	0.064
>sp P50608 FMOD_MOUSE Fibromodulin OS=Mus musculus GN=Fmod PE=2 SV=1	0.643	0.646	>tr B1AWZ3 B1AWZ3_MOUSE Novel protein (1700054F22Rik) OS=Mus musculus GN=Nij	-1.082	0.067
>sp P33434 MMP2_MOUSE 72 kDa type IV collagenase OS=Mus musculus GN=Mmp2 PE=2 SV=1	0.653	0.657	>sp Q99JR1 SFXN1_MOUSE Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	-1.071	0.069
>sp Q62009-2 POSTN_MOUSE Isoform 2 of Periostin OS=Mus musculus GN=Postn	0.670	0.669	>sp P56395 CYB5_MOUSE Cytochrome b5 OS=Mus musculus GN=Cyb5a PE=1 SV=2	-1.040	0.072
>sp Q61292 LAMB2_MOUSE Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=2 SV=2	0.737	0.680	>sp P23927 CRYAB_MOUSE Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 :	-1.032	0.074
>sp P18242 CATD_MOUSE Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	0.824	0.691	>sp O70325 GPX4_MOUSE Phospholipid hydroperoxide glutathione peroxidase, mitochond	-1.030	0.077
>sp P14211 CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	0.890	0.702	>sp Q9CZW5 TOM70_MOUSE Mitochondrial import receptor subunit TOM70 OS=Mus mus	-0.966	0.079
>sp Q04857 CO6A1_MOUSE Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=2 SV=1	0.914	0.713	>sp Q9WTP7 KAD3_MOUSE GTP:AMP phosphotransferase, mitochondrial OS=Mus muscu	-0.947	0.082
>sp Q06890 CLUS_MOUSE Clusterin OS=Mus musculus GN=Clu PE=1 SV=1	0.943	0.725	>sp P56391 CX6B1_MOUSE Cytochrome c oxidase subunit 6B1 OS=Mus musculus GN=Cox	-0.940	0.084
>sp Q02788 CO6A2_MOUSE Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=2 SV=3	1.038	0.736	>sp O08807 PRDX4_MOUSE Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	-0.918	0.087

>sp Q8VEE1 LMCD1_MOUSE LIM and cysteine-rich domains protein 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=2	1.104	0.747	>sp Q9Z1Q5 CLIC1_MOUSE Chloride intracellular channel protein 1 OS=Mus musculus GN=Clc1 PE=1 SV=2	-0.915	0.089
>sp O70503 DHB12_MOUSE Estradiol 17-beta-dehydrogenase 12 OS=Mus musculus GN=Hsd17b12 PE=1 SV=2	1.125	0.758	>sp P08074 CBR2_MOUSE Carbonyl reductase [NADPH] 2 OS=Mus musculus GN=Cbr2 PE=1 SV=2	-0.896	0.092
>sp P51885 LUM_MOUSE Lumican OS=Mus musculus GN=Lum PE=1 SV=2	1.147	0.770	>sp Q8BVI4 DHPR_MOUSE Dihydropteridine reductase OS=Mus musculus GN=Qdpr PE=1 SV=2	-0.883	0.094
>sp P07214 SPRC_MOUSE SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	1.160	0.781	>sp Q791V5 MTCH2_MOUSE Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtcl2 PE=1 SV=2	-0.860	0.097
>sp Q05793 PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Pgbm PE=1 SV=2	1.258	0.792	>sp Q8BW75 AOFB_MOUSE Amine oxidase [flavin-containing] B OS=Mus musculus GN=Aofb PE=1 SV=2	-0.855	0.099
>sp Q01339 APOH_MOUSE Beta-2-glycoprotein 1 OS=Mus musculus GN=ApoH PE=1 SV=1	1.264	0.803	>sp P14152 MDHC_MOUSE Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdch PE=1 SV=2	-0.852	0.102
>sp P11276 FNC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4	1.283	0.815	>sp Q8BU85 MSRB3_MOUSE Methionine-R-sulfoxide reductase B3, mitochondrial OS=Mus musculus GN=Msrb3 PE=1 SV=2	-0.830	0.104
>sp Q8C6K9 CO6A6_MOUSE Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=1 SV=2	1.306	0.826	>sp Q9DBF1 AL7A1_MOUSE Alpha-aminoacidic semialdehyde dehydrogenase OS=Mus musculus GN=Al7a1 PE=1 SV=2	-0.818	0.107
>tr B9EHT6 B9EHT6_MOUSE Fn1 protein OS=Mus musculus GN=Fn1 PE=2 SV=1	1.391	0.837	>sp Q9D4J1 EFHD1_MOUSE EF-hand domain-containing protein D1 OS=Mus musculus GN=Efhd1 PE=1 SV=2	-0.817	0.109
>sp Q9WVH9 FBLN5_MOUSE Fibulin-5 OS=Mus musculus GN=Fbln5 PE=2 SV=1	1.433	0.848	>sp Q9DCM2 GSTK1_MOUSE Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1 PE=1 SV=2	-0.777	0.112
>sp Q62000 MIME_MOUSE Mimecan OS=Mus musculus GN=Ogn PE=2 SV=1	1.441	0.860	>sp P35700 PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	-0.776	0.114
>sp Q9R118 HTRA1_MOUSE Serine protease HTRA1 OS=Mus musculus GN=Htra1 PE=1 SV=2	1.540	0.871	>sp Q9CYG7 TOM34_MOUSE Mitochondrial import receptor subunit TOM34 OS=Mus musculus GN=Tom34 PE=1 SV=2	-0.770	0.117
>sp P16045 LEG1_MOUSE Galectin-1 OS=Mus musculus GN=Lgals1 PE=1 SV=3	1.550	0.882	>sp Q7TMF3 NDUAC_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3 OS=Mus musculus GN=Nduac3 PE=1 SV=2	-0.766	0.119
>sp Q8K4G1 LTBP4_MOUSE Latent-transforming growth factor beta-binding protein 4 OS=Mus musculus GN=Ltbp4 PE=1 SV=2	1.580	0.893	>sp P12242 UCP1_MOUSE Mitochondrial brown fat uncoupling protein 1 OS=Mus musculus GN=Ucp1 PE=1 SV=2	-0.764	0.122
>sp Q3UTY6 THSD4_MOUSE Thrombospondin type-1 domain-containing protein 4 OS=Mus musculus GN=Thsd4 PE=1 SV=2	1.586	0.904	>sp Q8K2B3 DHSA_MOUSE Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Dhsa PE=1 SV=2	-0.762	0.124
>sp Q99JR5 TINAL_MOUSE Tubulointerstitial nephritis antigen-like OS=Mus musculus GN=Tinagl1 PE=1 SV=2	1.630	0.916	>sp Q99LB2 DHRS4_MOUSE Dehydrogenase/reductase SDR family member 4 OS=Mus musculus GN=Dhrs4 PE=1 SV=2	-0.741	0.127
>sp P08122 CO4A2_MOUSE Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2 PE=2 SV=4	1.646	0.927	>tr Q924B0 Q924B0_MOUSE Inositol (Myo)-1(Or 4)-monophosphatase 1 OS=Mus musculus GN=Ino1 PE=1 SV=2	-0.717	0.129
>sp P39061 CO1A1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1 PE=1 SV=2	1.773	0.938	>sp Q9Z2I0 LETM1_MOUSE LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Mus musculus GN=Letm1 PE=1 SV=2	-0.716	0.132
>sp Q8BPP5 FBLN3_MOUSE EGF-containing fibulin-like extracellular matrix protein 1 OS=Mus musculus GN=Fbln3 PE=1 SV=2	1.960	0.949	>sp Q9CZW7 SNAG_MOUSE Gamma-soluble NSF attachment protein OS=Mus musculus GN=Snag PE=1 SV=2	-0.716	0.134
>sp Q61282 PGCA_MOUSE Aggrecan core protein OS=Mus musculus GN=Acan PE=1 SV=2	2.130	0.961	>sp Q9Z0X1 AIFM1_MOUSE Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=2	-0.703	0.137
>sp Q9D1H9 MFAP4_MOUSE Microfibril-associated glycoprotein 4 OS=Mus musculus GN=Mfap4 PE=1 SV=2	2.663	0.972	>sp Q9CQK7 AT5F1_MOUSE ATP synthase subunit b, mitochondrial OS=Mus musculus GN=At5f1 PE=1 SV=2	-0.692	0.139
>sp Q61245 COBA1_MOUSE Collagen alpha-1(XI) chain OS=Mus musculus GN=Col11a1 PE=1 SV=2	3.066	0.983	>sp Q2TPA8 HSDL2_MOUSE Hydroxysteroid dehydrogenase-like protein 2 OS=Mus musculus GN=Hsdl2 PE=1 SV=2	-0.685	0.142
>sp O35206 COFA1_MOUSE Collagen alpha-1(XV) chain OS=Mus musculus GN=Col15a1 PE=1 SV=2	3.784	0.994	>sp Q7TNF8 RIMB1_MOUSE Peripheral-type benzodiazepine receptor-associated protein 1 C OS=Mus musculus GN=Rimb1 PE=1 SV=2	-0.677	0.144
Intermediate filament GO:0005882			>sp Q60932 VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=2	-0.675	0.149
Protein identification	Zq	rank/N	>sp Q78PY7 SND1_MOUSE Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=2	-0.675	0.152
>sp P46660 AINX_MOUSE Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	-0.172	0.036	>sp P51881 ADT2_MOUSE ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=2	-0.656	0.155
>sp O55135 IF6_MOUSE Eukaryotic translation initiation factor 6 OS=Mus musculus GN=Eif6 PE=1 SV=2	-0.004	0.107	>sp Q91ZR1 RAB4B_MOUSE Ras-related protein Rab-4B OS=Mus musculus GN=Rab4b PE=1 SV=2	-0.638	0.157
>sp P08551 NFL_MOUSE Neurofilament light polypeptide OS=Mus musculus GN=Nefl PE=1 SV=5	0.273	0.179	>sp P56375 ACYP2_MOUSE Acylphosphatase 2 OS=Mus musculus GN=Acyp2 PE=2 SV=2	-0.607	0.160
>sp P14733 LMNB1_MOUSE Lamin-B1 OS=Mus musculus GN=Lmnb1 PE=1 SV=3	0.427	0.250	>sp P19096 FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	-0.597	0.162
>sp P15331 PERI_MOUSE Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	0.563	0.321	>sp P46471 PRS7_MOUSE 26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=2	-0.581	0.165
>sp E9Q557 DESP_MOUSE Desmoplakin OS=Mus musculus GN=Dsp PE=3 SV=1	0.664	0.393	>sp Q9DCM0 ETHE1_MOUSE Protein ETHE1, mitochondrial OS=Mus musculus GN=Ethe1 PE=1 SV=2	-0.574	0.167
>sp P48678 LMNA_MOUSE Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	0.855	0.464	>sp Q921H8 THIKA_MOUSE 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Thika PE=1 SV=2	-0.566	0.170
>sp P21619 LMNB2_MOUSE Lamin-B2 OS=Mus musculus GN=Lmnb2 PE=1 SV=2	0.922	0.536	>sp Q9DCN2 NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Ci3 PE=1 SV=2	-0.564	0.172
>tr Q3TFD9 Q3TFD9_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Vim PE=2 SV=2	0.979	0.607	>sp P15105 GLNA_MOUSE Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	-0.554	0.175
>sp P31001 DESM_MOUSE Desmin OS=Mus musculus GN=Des PE=1 SV=3	1.047	0.679	>sp P06151 LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=2	-0.554	0.177
>sp Q6P5H2 NEST_MOUSE Nestin OS=Mus musculus GN=Nes PE=1 SV=1	1.222	0.750	>sp Q8BX02 KANK2_MOUSE KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Kank2 PE=1 SV=2	-0.549	0.180
>sp P03995 GFAP_MOUSE Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	1.428	0.821	>sp Q9D3P8 PLRKT_MOUSE Plasminogen receptor (KT) OS=Mus musculus GN=Plgrkt PE=1 SV=2	-0.536	0.182
>sp Q91ZU6 DYST_MOUSE Dystonin OS=Mus musculus GN=Dst PE=1 SV=1	1.995	0.893	>sp P58281 OPA1_MOUSE Dynamin-like 120 kDa protein, mitochondrial OS=Mus musculus GN=Opa1 PE=1 SV=2	-0.528	0.185
>sp P20152 VIME_MOUSE Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	2.667	0.964	>sp Q8BTZ7 GMPBP_MOUSE Mannose-1-phosphate guanylyltransferase beta OS=Mus musculus GN=Gmpbp PE=1 SV=2	-0.497	0.187
Muscle contraction GO:0006936			>sp Q3UIU2 NDUB6_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Mus musculus GN=Nduab6 PE=1 SV=2	-0.477	0.190
Protein identification	Zq	rank/N	>sp O70591 PFD2_MOUSE Prefoldin subunit 2 OS=Mus musculus GN=Pfdn2 PE=2 SV=2	-0.456	0.192
>sp Q60605 MYL6_MOUSE Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3	-0.430	-0.036	>sp Q9DAR7 DCPS_MOUSE m7GpppX diphosphatase OS=Mus musculus GN=Dcps PE=1 SV=2	-0.451	0.195
>sp A2ASS6 TITN_MOUSE Titin OS=Mus musculus GN=Ttn PE=1 SV=1	0.138	0.012	>sp Q9CQW1 YKT6_MOUSE Synaptobrevin homolog YKT6 OS=Mus musculus GN=Ykt6 PE=1 SV=2	-0.438	0.197
>sp Q64018 GLRA1_MOUSE Glucocorticoid receptor subunit alpha-1 OS=Mus musculus GN=Glra1 PE=1 SV=2	0.673	0.056	>sp P63085 MKO1_MOUSE Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=2	-0.428	0.200
>sp P58774-2 TPM2_MOUSE Isoform 2 of Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=2	0.737	0.061	>sp Q8VCW8 ACSF2_MOUSE Acyl-CoA synthetase family member 2, mitochondrial OS=Mus musculus GN=Acsf2 PE=1 SV=2	-0.423	0.202
>tr Q8VCQ8 Q8VCQ8_MOUSE Caldesmon 1 OS=Mus musculus GN=Cald1 PE=2 SV=1	1.453	0.121	>sp Q9CRB9 CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3 OS=Mus musculus GN=Chch3 PE=1 SV=2	-0.422	0.205
>tr F6T2Z7 F6T2Z7_MOUSE Protein Cald1 (Fragment) OS=Mus musculus GN=Cald1 PE=4 SV=1	1.640	0.137	>sp Q60930 VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	-0.416	0.207
			>sp Q62167 DDX3X_MOUSE ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=2	-0.396	0.210

>sp E9PZQ0 RYR1_MOUSE Ryanodine receptor 1 OS=Mus musculus GN=Ryr1 PE=1 SV=1	1.944	0.162	>sp Q99KR3 LACB2_MOUSE Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2	-0.394	0.212
>sp Q8CI43 MYL6B_MOUSE Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=2 SV=1	1.978	0.165	>sp Q922B1 MACD1_MOUSE O-acetyl-ADP-ribose deacetylase MACROD1 OS=Mus muscu	-0.377	0.215
>sp P26883 FKB1A_MOUSE Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkb	2.168	0.181	>sp Q8CAQ8 IMMT_MOUSE Mitochondrial inner membrane protein OS=Mus musculus GN:	-0.376	0.217
>sp Q5SX39 MYH4_MOUSE Myosin-4 OS=Mus musculus GN=Myh4 PE=1 SV=1	4.217	0.351	>sp P52196 THTR_MOUSE Thiosulfate sulfurtransferase OS=Mus musculus GN=Tst PE=1 S	-0.373	0.220
>sp Q02566 MYH6_MOUSE Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	12.556	1.046	>sp P30416 FKBP4_MOUSE Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus C	-0.372	0.222
>sp Q5SX40 MYH1_MOUSE Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1	15.231	1.269	>sp Q01768 NDKB_MOUSE Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2	-0.363	0.225
			>sp P99028 QCR6_MOUSE Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus mu	-0.360	0.227
			>sp Q921G7 ETFD_MOUSE Electron transfer flavoprotein-ubiquinone oxidoreductase, mitoc	-0.359	0.230
			>sp Q8QZT1 THIL_MOUSE Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus	-0.357	0.232
			>sp Q8K4Z3 NNRE_MOUSE NAD(P)H-hydrate epimerase OS=Mus musculus GN=Apoa1bp	-0.356	0.235
			>sp Q9JHW2 NIT2_MOUSE Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1	-0.348	0.237
			>sp P05132 KAPCA_MOUSE cAMP-dependent protein kinase catalytic subunit alpha OS=Mt	-0.346	0.240
			>sp Q99LX0 PARK7_MOUSE Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-0.338	0.242
			>sp Q6PHN9 RAB35_MOUSE Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE	-0.322	0.245
			>tr G5E895 G5E895_MOUSE MCG142264, isoform CRA_b OS=Mus musculus GN=Akr1b1	-0.320	0.247
			>sp P62264 RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 S	-0.308	0.250
			>sp P46638 RB11B_MOUSE Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PI	-0.303	0.253
			>sp P08228 SODC_MOUSE Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE:	-0.301	0.255
			>sp Q9CQA3 DHSB_MOUSE Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitc	-0.298	0.258
			>sp P52503 NDUS6_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitoc	-0.292	0.260
			>sp Q8CG76 ARK72_MOUSE Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus	-0.291	0.263
			>sp Q64105 SPRE_MOUSE Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1	-0.291	0.265
			>sp Q64516 GLPK_MOUSE Glycerol kinase OS=Mus musculus GN=Gk PE=2 SV=2	-0.276	0.268
			>sp P03930 ATP8_MOUSE ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV	-0.260	0.270
			>sp P28271 ACOC_MOUSE Cytoplasmic aconitate hydratase OS=Mus musculus GN=Aco1 F	-0.242	0.273
			>sp P51174 ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial O	-0.240	0.275
			>sp Q9QX60 DGUOK_MOUSE Deoxyguanosine kinase, mitochondrial OS=Mus musculus G	-0.234	0.278
			>sp Q9DBL1 ACDSB_MOUSE Short/branched chain specific acyl-CoA dehydrogenase, mitoc	-0.225	0.280
			>sp Q8BMF3 MAON_MOUSE NADP-dependent malic enzyme, mitochondrial OS=Mus mus	-0.210	0.283
			>sp Q9DCT2 NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mit	-0.209	0.285
			>sp Q8R2Y8 PTH2_MOUSE Peptidyl-tRNA hydrolase 2, mitochondrial OS=Mus musculus G	-0.198	0.288
			>sp Q9Z1Q9 SYVC_MOUSE Valine--tRNA ligase OS=Mus musculus GN=Vars PE=2 SV=1	-0.189	0.290
			>sp P28474 ADHX_MOUSE Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PI	-0.187	0.293
			>sp Q9JLJ2 AL9A1_MOUSE 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus muscu	-0.174	0.295
			>sp P35385 HSPB7_MOUSE Heat shock protein beta-7 OS=Mus musculus GN=Hspb7 PE=1	-0.173	0.298
			>sp Q8BH04 PCKGM_MOUSE Phosphoenolpyruvate carboxykinase [GTP], mitochondrial O	-0.152	0.300
			>sp P37040 NCPR_MOUSE NADPH--cytochrome P450 reductase OS=Mus musculus GN=Pc	-0.146	0.303
			>sp Q9CZB0 C560_MOUSE Succinate dehydrogenase cytochrome b560 subunit, mitochondri	-0.137	0.305
			>sp Q9DCS3 MECR_MOUSE Trans-2-enoyl-CoA reductase, mitochondrial OS=Mus muscul	-0.133	0.308
			>sp Q6P8J7 KCRS_MOUSE Creatine kinase S-type, mitochondrial OS=Mus musculus GN=C	-0.129	0.310
			>sp Q8C3X2 CC90B_MOUSE Coiled-coil domain-containing protein 90B, mitochondrial OS=	-0.126	0.313
			>sp O70378 EMC8_MOUSE ER membrane protein complex subunit 8 OS=Mus musculus GN	-0.108	0.315
			>sp Q922D8 C1TC_MOUSE C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus C	-0.106	0.318
			>sp Q9D0S9 HINT2_MOUSE Histidine triad nucleotide-binding protein 2, mitochondrial OS=	-0.104	0.320
			>sp Q9CR21 ACPM_MOUSE Acyl carrier protein, mitochondrial OS=Mus musculus GN=Nd	-0.096	0.323
			>sp Q3V132 ADT4_MOUSE ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2	-0.092	0.325
			>sp Q9QYB1 CLIC4_MOUSE Chloride intracellular channel protein 4 OS=Mus musculus GN	-0.083	0.328
			>sp Q8BGH2 SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=	-0.082	0.330
			>sp Q9CQX2 CYB5B_MOUSE Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 :	-0.080	0.333

>sp P56392 CX7A1_MOUSE Cytochrome c oxidase subunit 7A1, mitochondrial OS=Mus mu	-0.078	0.335
>sp Q99L43 CDS2_MOUSE Phosphatidate cytidyltransferase 2 OS=Mus musculus GN=Cds	-0.078	0.338
>sp O35857 TIM44_MOUSE Mitochondrial import inner membrane translocase subunit TIM4	-0.077	0.340
>sp Q8K1M6 DNM1L_MOUSE Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=	-0.057	0.343
>sp Q9CR61 NDUB7_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subun	-0.056	0.345
>sp P00158 CYB_MOUSE Cytochrome b OS=Mus musculus GN=Mt-Cyb PE=2 SV=1	-0.046	0.348
>sp Q9DCJ5 NDUA8_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	-0.023	0.351
>sp Q9Z2I8 SUCB2_MOUSE Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondria	-0.022	0.353
>sp Q9WUM5 SUCA_MOUSE Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mito	-0.022	0.356
>sp P62897 CYC_MOUSE Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2	-0.007	0.358
>sp Q9Z110 P5CS_MOUSE Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=	0.000	0.361
>sp P15532 NDKA_MOUSE Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1	0.008	0.363
>sp P19783 COX41_MOUSE Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=N	0.020	0.366
>sp Q9DCV4 RMD1_MOUSE Regulator of microtubule dynamics protein 1 OS=Mus muscul	0.025	0.368
>sp Q91V92 ACLY_MOUSE ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	0.029	0.371
>sp Q9QZ23 NFU1_MOUSE NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=N	0.034	0.373
>sp Q9R0H0 ACOX1_MOUSE Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus C	0.051	0.376
>sp Q8C0V9 FRMD6_MOUSE FERM domain-containing protein 6 OS=Mus musculus GN=F	0.055	0.378
>sp Q06185 ATP5I_MOUSE ATP synthase subunit e, mitochondrial OS=Mus musculus GN=	0.056	0.381
>sp P11352 GPX1_MOUSE Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV	0.068	0.383
>sp Q5SWU9 ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PI	0.081	0.386
>sp P19157 GSTP1_MOUSE Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=	0.084	0.388
>sp P31786 ACBP_MOUSE Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV	0.098	0.391
>sp P47791 GSHR_MOUSE Glutathione reductase, mitochondrial OS=Mus musculus GN=G	0.101	0.393
>sp P06801 MAOX_MOUSE NADP-dependent malic enzyme OS=Mus musculus GN=Me1 P	0.128	0.396
>sp P28867 KPCD_MOUSE Protein kinase C delta type OS=Mus musculus GN=Prkcd PE=1 :	0.134	0.398
>sp Q9CQ75 NDUA2_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	0.136	0.401
>sp Q5U458 DJC11_MOUSE DnaJ homolog subfamily C member 11 OS=Mus musculus GN=	0.154	0.403
>sp Q9JK48 SHLB1_MOUSE Endophilin-B1 OS=Mus musculus GN=Sh3glb1 PE=1 SV=1	0.154	0.406
>sp Q9R112 SQRD_MOUSE Sulfide:quinone oxidoreductase, mitochondrial OS=Mus muscul	0.160	0.408
>sp Q99MN9 PCCB_MOUSE Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus	0.163	0.411
>sp Q8BIJ6 SYIM_MOUSE Isoleucine--tRNA ligase, mitochondrial OS=Mus musculus GN=I	0.165	0.413
>sp Q91WS0 CISD1_MOUSE CDGSH iron-sulfur domain-containing protein 1 OS=Mus mus	0.175	0.416
>sp Q99LC3 NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	0.179	0.418
>tr A2AFQ2 A2AFQ2_MOUSE 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus	0.181	0.421
>sp Q8K1R7 NEK9_MOUSE Serine/threonine-protein kinase Nek9 OS=Mus musculus GN=N	0.183	0.423
>sp Q8BH59 CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus	0.184	0.426
>sp Q99MN1 SYK_MOUSE Lysine--tRNA ligase OS=Mus musculus GN=Kars PE=1 SV=1	0.205	0.428
>sp Q9Z1Z2 STRAP_MOUSE Serine-threonine kinase receptor-associated protein OS=Mus m	0.214	0.431
>tr Q5XJF6 Q5XJF6_MOUSE Ribosomal protein OS=Mus musculus GN=Rpl10a PE=2 SV=1	0.214	0.433
>sp Q99JB2 STML2_MOUSE Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 S	0.216	0.436
>sp O35129 PHB2_MOUSE Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	0.219	0.438
>tr Q91VA7 Q91VA7_MOUSE Isocitrate dehydrogenase 3 (NAD+) beta OS=Mus musculus C	0.231	0.441
>sp Q8R4N0 CLYBL_MOUSE Citrate lyase subunit beta-like protein, mitochondrial OS=Mus	0.237	0.443
>sp P62259 I433E_MOUSE 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=	0.253	0.446
>sp Q920E5 FPPS_MOUSE Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps P	0.263	0.448
>sp Q9WV85 NDK3_MOUSE Nucleoside diphosphate kinase 3 OS=Mus musculus GN=Nme	0.265	0.451
>sp E9Q557 DESP_MOUSE Desmoplakin OS=Mus musculus GN=Dsp PE=3 SV=1	0.266	0.454
>sp Q91WK5 GCSH_MOUSE Glycine cleavage system H protein, mitochondrial OS=Mus m	0.267	0.456

>sp P52480 KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm	0.267	0.459
>sp P05202 AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus G	0.273	0.461
>sp Q9QUI0 RHOA_MOUSE Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=	0.275	0.464
>sp P47738 ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN	0.275	0.466
>sp O55137 ACOT1_MOUSE Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1	0.279	0.469
>sp O70571 PDK4_MOUSE [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitoch	0.289	0.471
>sp Q60936 ADCK3_MOUSE Chaperone activity of bc1 complex-like, mitochondrial OS=M	0.293	0.474
>sp Q9CPY7 AMPL_MOUSE Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 S'	0.294	0.476
>sp Q9D6K8 FUND2_MOUSE FUN14 domain-containing protein 2 OS=Mus musculus GN=	0.301	0.479
>sp Q9CPV4 GLOD4_MOUSE Glyoxalase domain-containing protein 4 OS=Mus musculus G	0.325	0.481
>sp O35459 ECH1_MOUSE Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=	0.326	0.484
>sp P61922 GABT_MOUSE 4-aminobutyrate aminotransferase, mitochondrial OS=Mus musc	0.327	0.486
>sp Q9ZZZ6 MCAT_MOUSE Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus n	0.327	0.489
>sp O35855 BCAT2_MOUSE Branched-chain-amino-acid aminotransferase, mitochondrial O	0.330	0.491
>sp Q9JIQ3 DBLOH_MOUSE Diablo homolog, mitochondrial OS=Mus musculus GN=Diabl	0.331	0.494
>sp Q8CHT0 AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	0.336	0.496
>sp Q99L13 3HIDH_MOUSE 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus n	0.356	0.499
>sp P45952 ACADM_MOUSE Medium-chain specific acyl-CoA dehydrogenase, mitochondri	0.357	0.501
>sp P03911 NU4M_MOUSE NADH-ubiquinone oxidoreductase chain 4 OS=Mus musculus G	0.367	0.504
>sp Q3TL44 NLRX1_MOUSE NLR family member X1 OS=Mus musculus GN=NlrX1 PE=2	0.369	0.506
>sp P18242 CATD_MOUSE Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1	0.378	0.509
>sp P84091 AP2M1_MOUSE AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=	0.384	0.511
>sp Q99J99 THTM_MOUSE 3-mercaptopyruvate sulfurtransferase OS=Mus musculus GN=M	0.390	0.514
>sp P80313 TCPH_MOUSE T-complex protein 1 subunit eta OS=Mus musculus GN=Cet7 PE	0.392	0.516
>sp Q9CPQ3 TOM22_MOUSE Mitochondrial import receptor subunit TOM22 homolog OS=	0.398	0.519
>sp Q922W5 P5CR1_MOUSE Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Mus m	0.401	0.521
>sp Q9DCX2 ATP5H_MOUSE ATP synthase subunit d, mitochondrial OS=Mus musculus GN	0.405	0.524
>sp Q68FD5 CLH1_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	0.411	0.526
>sp P10605 CATB_MOUSE Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	0.411	0.529
>sp P70404 IDHG1_MOUSE Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondri	0.412	0.531
>sp P16332 MUTA_MOUSE Methylmalonyl-CoA mutase, mitochondrial OS=Mus musculus	0.417	0.534
>sp P50136 ODBA_MOUSE 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS	0.419	0.536
>sp Q8C5H8 NAKD1_MOUSE NAD kinase domain-containing protein 1 OS=Mus musculus	0.426	0.539
>sp P48962 ADT1_MOUSE ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 S	0.439	0.541
>sp Q9CZD3 SYG_MOUSE Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1	0.441	0.544
>sp Q9CQ69 QCR8_MOUSE Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uc	0.444	0.546
>sp O88844 IDHC_MOUSE Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus muscul	0.447	0.549
>sp Q9ROX4 ACOT9_MOUSE Acyl-coenzyme A thioesterase 9, mitochondrial OS=Mus mus	0.453	0.552
>sp Q9CR62 M2OM_MOUSE Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus n	0.459	0.554
>tr E9QPQ8 E9QPQ8_MOUSE 39S ribosomal protein L48, mitochondrial OS=Mus musculus	0.466	0.557
>sp O08749 DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus	0.468	0.559
>sp Q99LD8 DDAH2_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=	0.475	0.562
>sp Q9D6Y7 MSRA_MOUSE Mitochondrial peptide methionine sulfoxide reductase OS=Mus	0.484	0.564
>sp Q63844 MK03_MOUSE Mitogen-activated protein kinase 3 OS=Mus musculus GN=Map	0.484	0.567
>sp Q99LB6 MAT2B_MOUSE Methionine adenosyltransferase 2 subunit beta OS=Mus musc	0.489	0.569
>sp P52825 CPT2_MOUSE Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musc	0.497	0.572
>sp P39688 FYN_MOUSE Tyrosine-protein kinase Fyn OS=Mus musculus GN=Fyn PE=1 SV	0.499	0.574
>sp Q9CWJ9 PUR9_MOUSE Bifunctional purine biosynthesis protein PURH OS=Mus muscu	0.510	0.577
>sp P10639 THIO_MOUSE Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	0.515	0.579

>sp Q8R0N6 HOT_MOUSE Hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Mus	0.517	0.582
>sp Q99KB8 GLO2_MOUSE Hydroxyacylglutathione hydrolase, mitochondrial OS=Mus mus	0.543	0.584
>sp P12787 COX5A_MOUSE Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus mus	0.555	0.587
>sp P41216 ACSL1_MOUSE Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Ac	0.561	0.589
>sp Q9CZ42 NNRD_MOUSE ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus m	0.562	0.592
>sp Q8R164 BPHL_MOUSE Valacyclovir hydrolase OS=Mus musculus GN=Bphl PE=2 SV=	0.564	0.594
>sp Q9JK42 PDK2_MOUSE [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitocho	0.565	0.597
>sp Q3ULD5 MCCB_MOUSE Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial C	0.578	0.599
>sp Q91VS7 MGST1_MOUSE Microsomal glutathione S-transferase 1 OS=Mus musculus GN=	0.580	0.602
>sp Q9D0I9 SYRC_MOUSE Arginine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Rai	0.586	0.604
>sp Q9QUM9 PSA6_MOUSE Proteasome subunit alpha type-6 OS=Mus musculus GN=Psma	0.592	0.607
>sp P70296 PEBP1_MOUSE Phosphatidylethanolamine-binding protein 1 OS=Mus musculus	0.594	0.609
>sp Q8BFR5 EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tu	0.597	0.612
>sp P00329 ADH1_MOUSE Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=	0.604	0.614
>sp Q9D023 MPC2_MOUSE Mitochondrial pyruvate carrier 2 OS=Mus musculus GN=Mpc2	0.606	0.617
>sp P16125 LDHB_MOUSE L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb F	0.613	0.619
>sp Q9D0M3 CY1_MOUSE Cytochrome c1, heme protein, mitochondrial OS=Mus musculus	0.614	0.622
>sp Q61425 HCDH_MOUSE Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=M	0.615	0.624
>sp Q8K1J6 TRNT1_MOUSE CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus m	0.619	0.627
>sp P50544 ACADV_MOUSE Very long-chain specific acyl-CoA dehydrogenase, mitochondi	0.622	0.629
>sp P51660 DHB4_MOUSE Peroxisomal multifunctional enzyme type 2 OS=Mus musculus C	0.644	0.632
>sp Q9CQ62 DECR_MOUSE 2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus C	0.664	0.634
>sp Q9QYA2 TOM40_MOUSE Mitochondrial import receptor subunit TOM40 homolog OS=	0.667	0.637
>sp Q32MW3 ACO10_MOUSE Acyl-coenzyme A thioesterase 10, mitochondrial OS=Mus m	0.669	0.639
>sp P97742 CPT1A_MOUSE Carnitine O-palmitoyltransferase 1, liver isoform OS=Mus musc	0.683	0.642
>sp Q8BH95 ECHM_MOUSE Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=E	0.686	0.644
>sp P08249 MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=M	0.687	0.647
>sp O08528 HXX2_MOUSE Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	0.707	0.649
>sp Q9JLZ3 AUHM_MOUSE Methylglutaconyl-CoA hydratase, mitochondrial OS=Mus mus	0.712	0.652
>sp P29758 OAT_MOUSE Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=	0.714	0.655
>sp P20108 PRDX3_MOUSE Thioredoxin-dependent peroxide reductase, mitochondrial OS=M	0.714	0.657
>sp Q9CQN6 TM14C_MOUSE Transmembrane protein 14C OS=Mus musculus GN=Tmem1	0.718	0.660
>sp Q91WD5 NDUS2_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mit	0.720	0.662
>sp Q07813 BAX_MOUSE Apoptosis regulator BAX OS=Mus musculus GN=Bax PE=1 SV=	0.722	0.665
>sp Q8JZN5 ACAD9_MOUSE Acyl-CoA dehydrogenase family member 9, mitochondrial OS	0.746	0.667
>sp Q9QYR9 ACOT2_MOUSE Acyl-coenzyme A thioesterase 2, mitochondrial OS=Mus mus	0.746	0.670
>sp P09671 SODM_MOUSE Superoxide dismutase [Mn], mitochondrial OS=Mus musculus C	0.747	0.672
>sp Q05920 PYC_MOUSE Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc P	0.749	0.675
>sp P63101 I433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 S	0.762	0.677
>sp Q91VR2 ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus	0.762	0.680
>sp P99029 PRDX5_MOUSE Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 I	0.763	0.682
>sp P58044 IDI1_MOUSE Isopentenyl-diphosphate Delta-isomerase 1 OS=Mus musculus GN	0.776	0.685
>sp Q6PB66 LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=	0.776	0.687
>sp P67778 PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	0.781	0.690
>sp Q9D1G1 RAB1B_MOUSE Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE	0.798	0.692
>sp Q9CRD0 OCAD1_MOUSE OCIA domain-containing protein 1 OS=Mus musculus GN=C	0.807	0.695
>sp P47934 CACP_MOUSE Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=1	0.812	0.697
>sp P18572 BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	0.813	0.700
>sp Q99JY0 ECHB_MOUSE Trifunctional enzyme subunit beta, mitochondrial OS=Mus musc	0.815	0.702

>sp Q91W97 HKDC1_MOUSE Putative hexokinase HKDC1 OS=Mus musculus GN=Hkdc1	0.817	0.705
>sp Q8BWT1 THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN	0.817	0.707
>sp P54310 LIPS_MOUSE Hormone-sensitive lipase OS=Mus musculus GN=Lipe PE=1 SV=	0.820	0.710
>sp Q8JZQ2 AFG32_MOUSE AFG3-like protein 2 OS=Mus musculus GN=Afg3l2 PE=1 SV=	0.824	0.712
>sp Q99L04 DHRS1_MOUSE Dehydrogenase/reductase SDR family member 1 OS=Mus mus	0.824	0.715
>sp Q99LB7 SARDH_MOUSE Sarcosine dehydrogenase, mitochondrial OS=Mus musculus C	0.826	0.717
>sp P54071 IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus muscu	0.832	0.720
>sp P56480 ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN	0.835	0.722
>sp Q99K10 ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Acc	0.838	0.725
>sp Q9DC70 NDUS7_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitc	0.845	0.727
>sp Q9WUR2 ECI2_MOUSE Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculus	0.847	0.730
>sp Q9DCB8 ISCA2_MOUSE Iron-sulfur cluster assembly 2 homolog, mitochondrial OS=Mus	0.851	0.732
>sp P42125 ECI1_MOUSE Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus G	0.854	0.735
>sp P11499 HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90	0.864	0.737
>sp Q9CQ54 NDUC2_MOUSE NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus m	0.881	0.740
>sp P35235 PTN11_MOUSE Tyrosine-protein phosphatase non-receptor type 11 OS=Mus mu	0.881	0.742
>sp Q99MR8 MCCA_MOUSE Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondri	0.887	0.745
>sp P56135 ATPK_MOUSE ATP synthase subunit f, mitochondrial OS=Mus musculus GN=A	0.892	0.747
>sp Q9JHR7 IDE_MOUSE Insulin-degrading enzyme OS=Mus musculus GN=Ide PE=1 SV=	0.896	0.750
>sp Q9CXZ1 NDUS4_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mit	0.904	0.753
>sp Q91ZA3 PCCA_MOUSE Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus	0.904	0.755
>sp Q04447 KCRB_MOUSE Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	0.912	0.758
>sp Q8BMP6 GCP60_MOUSE Golgi resident protein GCP60 OS=Mus musculus GN=Acbd3	0.914	0.760
>sp P63328 PP2BA_MOUSE Serine/threonine-protein phosphatase 2B catalytic subunit alpha	0.916	0.763
>sp Q03265 ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus C	0.917	0.765
>sp Q9CZU6 CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=	0.927	0.768
>sp P24270 CATA_MOUSE Catalase OS=Mus musculus GN=Cat PE=1 SV=4	0.930	0.770
>sp Q91VD9 NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondr	0.931	0.773
>sp Q8CGK3 LONM_MOUSE Lon protease homolog, mitochondrial OS=Mus musculus GN=	0.933	0.775
>sp P59017 B2L13_MOUSE Bcl-2-like protein 13 OS=Mus musculus GN=Bcl2l13 PE=1 SV=	0.934	0.778
>sp Q9CQZ5 NDUA6_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	0.935	0.780
>sp Q64373 B2CL1_MOUSE Bcl-2-like protein 1 OS=Mus musculus GN=Bcl2l1 PE=1 SV=1	0.942	0.783
>sp Q9JHI5 IVD_MOUSE Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculus	0.953	0.785
>sp O08709 PRDX6_MOUSE Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	0.953	0.788
>sp Q8VEM8 MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus G	0.970	0.790
>sp Q9D3D9 ATPD_MOUSE ATP synthase subunit delta, mitochondrial OS=Mus musculus	0.975	0.793
>sp P38647 GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9	0.977	0.795
>sp Q9EQ20 MMSA_MOUSE Methylmalonate-semialdehyde dehydrogenase [acylating], mit	0.981	0.798
>sp Q60597 ODO1_MOUSE 2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus	0.985	0.800
>sp P54775 PRS6B_MOUSE 26S protease regulatory subunit 6B OS=Mus musculus GN=Psm	0.989	0.803
>sp Q9DB77 QCR2_MOUSE Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus m	0.995	0.805
>sp P26638 SYSC_MOUSE Serine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Sars P	1.013	0.808
>sp Q9WTP6 KAD2_MOUSE Adenylate kinase 2, mitochondrial OS=Mus musculus GN=Ak	1.017	0.810
>sp Q9CZ13 QCR1_MOUSE Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus m	1.018	0.813
>sp Q9CPQ8 ATP5L_MOUSE ATP synthase subunit g, mitochondrial OS=Mus musculus GN	1.022	0.815
>sp Q62465 VAT1_MOUSE Synaptic vesicle membrane protein VAT-1 homolog OS=Mus m	1.034	0.818
>sp Q9DB20 ATPO_MOUSE ATP synthase subunit O, mitochondrial OS=Mus musculus GN=	1.046	0.820
>sp Q9D0K2 SCOT1_MOUSE Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochon	1.048	0.823
>sp Q9D172 ES1_MOUSE ES1 protein homolog, mitochondrial OS=Mus musculus GN=D10	1.066	0.825

>sp Q8R0Y6 AL1L1_MOUSE Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus n	1.067	0.828
>sp Q9D8S4 ORN_MOUSE Oligoribonuclease, mitochondrial OS=Mus musculus GN=Rexo2	1.096	0.830
>sp Q99LC5 ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial OS=l	1.114	0.833
>sp P50171 DHB8_MOUSE Estradiol 17-beta-dehydrogenase 8 OS=Mus musculus GN=Hsd1	1.118	0.835
>sp Q9WVL0 MAAI_MOUSE Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 P	1.127	0.838
>sp Q8BWF0 SSDH_MOUSE Succinate-semialdehyde dehydrogenase, mitochondrial OS=Mt	1.155	0.840
>sp P53395 ODB2_MOUSE Lipoamide acyltransferase component of branched-chain alpha-k	1.157	0.843
>sp P25799 NFKB1_MOUSE Nuclear factor NF-kappa-B p105 subunit OS=Mus musculus Gf	1.158	0.845
>sp Q9D6R2 IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (	1.168	0.848
>sp Q91VM9 IPYR2_MOUSE Inorganic pyrophosphatase 2, mitochondrial OS=Mus muscul	1.174	0.851
>sp Q8BKZ9 ODPX_MOUSE Pyruvate dehydrogenase protein X component, mitochondrial C	1.177	0.853
>sp Q3UJU9 RMD3_MOUSE Regulator of microtubule dynamics protein 3 OS=Mus muscul	1.179	0.856
>sp Q9ZZ19 SUCB1_MOUSE Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondri	1.185	0.858
>sp P26443 DHE3_MOUSE Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus G	1.188	0.861
>sp Q91YT0 NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochon	1.207	0.863
>sp Q9D855 QCR7_MOUSE Cytochrome b-c1 complex subunit 7 OS=Mus musculus GN=Uc	1.213	0.866
>sp P07901 HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp9	1.222	0.868
>sp P31938 MP2K1_MOUSE Dual specificity mitogen-activated protein kinase 1 OS=l	1.227	0.871
>sp O54724 PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN	1.249	0.873
>sp P63168 DYL1_MOUSE Dynein light chain 1, cytoplasmic OS=Mus musculus GN=Dynl1	1.258	0.876
>sp Q9CYH2 F213A_MOUSE Redox-regulatory protein FAM213A OS=Mus musculus GN=I	1.308	0.878
>sp O08553 DPYL2_MOUSE Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=	1.323	0.881
>sp Q64442 DHSO_MOUSE Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=	1.324	0.883
>sp P54822 PUR8_MOUSE Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=2 SV=	1.329	0.886
>sp Q9D051 ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochond	1.358	0.888
>sp Q9DCW4 ETFB_MOUSE Electron transfer flavoprotein subunit beta OS=Mus musculus (	1.373	0.891
>sp Q9CR68 UCRI_MOUSE Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=M	1.378	0.893
>sp P35486 ODPA_MOUSE Pyruvate dehydrogenase E1 component subunit alpha, somatic fo	1.379	0.896
>sp Q9ERS2 NDUAD_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub	1.431	0.898
>sp O89023 TPP1_MOUSE Tripeptidyl-peptidase 1 OS=Mus musculus GN=Tpp1 PE=1 SV=	1.441	0.901
>sp P63038 CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=	1.452	0.903
>sp Q9CQR4 ACO13_MOUSE Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Ac	1.471	0.906
>sp Q64433 CH10_MOUSE 10 kDa heat shock protein, mitochondrial OS=Mus musculus GN	1.472	0.908
>sp Q64521 GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus n	1.487	0.911
>sp P19536 COX5B_MOUSE Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus mus	1.488	0.913
>sp Q9CQ92 FIS1_MOUSE Mitochondrial fission 1 protein OS=Mus musculus GN=Fis1 PE=	1.497	0.916
>sp Q9D2G2 ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2	1.506	0.918
>sp P62492 RB11A_MOUSE Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a Pl	1.512	0.921
>sp Q9CQH3 NDUB5_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subu	1.581	0.923
>tr Q3UKH3 Q3UKH3_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Ac	1.614	0.926
>sp Q8QZS1 HIBCH_MOUSE 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus r	1.643	0.928
>sp P85094 ISC2A_MOUSE Isochorismatase domain-containing protein 2A, mitochondrial O	1.646	0.931
>sp Q9D6U8 F162A_MOUSE Protein FAM162A OS=Mus musculus GN=Fam162a PE=2 SV	1.688	0.933
>sp Q8BMF4 ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase component of py	1.713	0.936
>sp Q9CWS0 DDAH1_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=	1.721	0.938
>sp P17710 HXK1_MOUSE Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	1.726	0.941
>sp P97807 FUMH_MOUSE Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh P	1.778	0.943
>sp P00405 COX2_MOUSE Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 I	1.827	0.946
>sp P32020 NLTP_MOUSE Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 l	1.893	0.948

>sp Q8BMS1 ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=Mus m	1.908	0.951
>sp P50516 VATA_MOUSE V-type proton ATPase catalytic subunit A OS=Mus musculus GN=	1.934	0.954
>sp Q922Q1 MOSC2_MOUSE MOSC domain-containing protein 2, mitochondrial OS=Mus r	1.964	0.956
>tr Q8JZU2 Q8JZU2_MOUSE Protein Slc25a1 OS=Mus musculus GN=Slc25a1 PE=2 SV=1	1.983	0.959
>sp O08599 STXB1_MOUSE Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=	2.123	0.961
>sp Q05421 CP2E1_MOUSE Cytochrome P450 2E1 OS=Mus musculus GN=Cyp2e1 PE=1 S	2.193	0.964
>sp P00397 COX1_MOUSE Cytochrome c oxidase subunit 1 OS=Mus musculus GN=Mtco1 I	2.371	0.966
>sp Q07417 ACADS_MOUSE Short-chain specific acyl-CoA dehydrogenase, mitochondrial C	2.528	0.969
>sp Q62425 NDUA4_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	2.537	0.971
>sp Q8R1I1 QCR9_MOUSE Cytochrome b-c1 complex subunit 9 OS=Mus musculus GN=Uq	2.764	0.974
>sp Q9DC69 NDUA9_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	2.928	0.976
>sp Q9JMH6 TRXR1_MOUSE Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=	3.500	0.979
>sp P50518 VATE1_MOUSE V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp	4.363	0.981
>sp Q64133 AOFA_MOUSE Amine oxidase [flavin-containing] A OS=Mus musculus GN=M	4.437	0.984
>sp Q8VCL2 SCO2_MOUSE Protein SCO2 homolog, mitochondrial OS=Mus musculus GN=	4.665	0.986
>tr D3YZ32 D3YZ32_MOUSE Mitochondrial fission 1 protein OS=Mus musculus GN=Fis1 F	4.786	0.989
>tr Q80X68 Q80X68_MOUSE Citrate synthase OS=Mus musculus GN=Csl PE=1 SV=1	4.863	0.991
>sp A2ARZ3 FSIP2_MOUSE Fibrous sheath-interacting protein 2 OS=Mus musculus GN=Fsi	9.179	0.994
>tr Q3TCI7 Q3TCI7_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Ldha	9.691	0.996
>sp P24529 TY3H_MOUSE Tyrosine 3-monooxygenase OS=Mus musculus GN=Th PE=1 SV	13.622	0.999