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The VE-cadherin/AmotL2 mechanosensory pathway suppresses aortic inflammation and the formation of abdominal aortic aneurysms

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Abstract

Arterial endothelial cells (ECs) have the ability to respond to mechanical forces exerted by fluid shear stress. This response is of importance, as it is protective against vascular diseases such as atherosclerosis and aortic aneurysms. Mechanical forces are transmitted at the sites of adhesion to the basal membrane as well as cell-cell junctions where protein complexes connect to the cellular cytoskeleton to relay force into the cell. Here we present a novel protein complex that connects junctional VE-cadherin and radial actin filaments to the LINC complex in the nuclear membrane. We show that the scaffold protein AmotL2 is essential for the formation of radial actin filaments and the flow-induced alignment of aortic and arterial ECs. The deletion of endothelial AmotL2 alters nuclear shape as well as subcellular positioning. Molecular analysis shows that VE-cadherin is mechanically associated with the nuclear membrane via binding to AmotL2 and Actin. Furthermore, the deletion of AmotL2 in ECs provokes a pro-inflammatory response and abdominal aortic aneurysms (AAA) in the aorta of mice on a normal diet. Remarkably, transcriptome analysis of AAA samples from human patients revealed a negative correlation between AmotL2 expression and aneurysm diameters, as well as a positive correlation between AmotL2 and YAP expression. These findings provide a conceptual framework regarding how mechanotransduction in the junctions is coupled with vascular disease.

Introduction

The blood vessel wall is lined with a thin layer of vascular endothelial cells (ECs), which form a barrier between the blood and tissues. These cells differ in biochemical characteristics depending on their localization in arteries or veins, as well as on the organ in which they reside. The endothelium is continuously exposed to the shear stress exerted by the blood flow. Understanding how ECs respond to shear stress is of importance as it has implications for the development of vascular diseases. Indeed, since the 1870's it has been postulated that mechanical stress exerted on the blood vessel wall may be a trigger of atherosclerosis. Also, low wall shear stress has been associated with abdominal aortic aneurysm (AAA) rupture¹. AAA is characterized by localized medial and adventitial inflammation and dilatation of the abdominal aorta and is prevalent in men over 65 with significant morbidity and mortality². By contrast, areas of laminar flow appeared relatively protected against the development of the inflammatory disease³.

To explore how the mechanotransductive pathways mediate protection or activation of the vascular disease is of clear importance⁴⁻¹⁸. To date, several mechanosensory pathways have been identified that relay external mechanical forces to the endothelial lining¹⁹. *In vitro*, flow-induced endothelial alignment is dependent on the activation of GTPases and consequent actin reorganization. *In vivo*, it has been shown that endothelial junctional protein complexes including PECAM-1, VE-cadherin, and VEGFR2 play an important role in the adaptive response to shear stress¹⁸. However, it is still not clear how mechanical forces exerted by the blood flow are transmitted from the junctions via the cytoskeleton into the cell.

Studies of the (Angiomotin) Amot protein family may provide important insights into this aspect. This is a family of scaffold proteins that link membrane receptors to the actin cytoskeleton, polarity proteins, and are implicated in modulating the Hippo pathway²⁰⁻²⁶.

We have recently shown that one of its members, AmotL2 (p100 isoform), is associated with the VE-cadherin complex in ECs and E-cadherin in epithelial cells^{25,27}. Silencing of AmotL2 in zebrafish, mouse or cells *in vitro* results in a loss of radial actin filaments that run perpendicular to the outer cell membrane. These actin filaments mechanically connect cells via binding to junctional cadherins, and thereby transmit force. Conditional silencing of AmotL2 in the endothelial lineage of mice inhibits expansion of the aorta during the onset of circulation resulting in death *in utero* at embryonic day 10²⁵. In this report, we have analyzed the role of AmotL2 in controlling junctional and cytoskeletal components during the alignment of arterial ECs exposed to laminar flow. Here we present a novel mechanical transduction pathway active in arteries that is protective against vascular inflammation as well as the formation of AAAs.

Results

Amotl2 is essential for arterial alignment.

We analyzed the expression pattern of AmotL2 in mouse descending aorta (DA) and the inferior vena cava (IVC) as shown in **Fig. 1a,b**. ECs of the DA were typically elongated and aligned with the direction of blood circulation and contained radial actin filaments that were connected to the cellular junctions (**Fig. 1c**). AmotL2 localized to EC junctions as previously reported²⁵. In contrast, ECs of the IVC exhibited a more rounded cellular shape with no or few detectable radial actin filaments as well as a significantly lower expression level of AmotL2. Box plots in **Fig. 1d-f** represents the statistically significant difference between the DA and IVC with regards to AmotL2 expression, cellular shape and the presence of radial actin filaments. In addition, we mapped AmotL2 expression in mouse retinal vasculature at different ages (**Supplementary Fig. 1**). AmotL2 was expressed at similar levels in arteries and veins of post-natal day 6 mice, whereas in mature mice (three months) Amotl2 was primarily expressed in retinal arteries. Interestingly, AmotL2 was barely detectable in blood vessels of mice older than 15 months.

We have previously shown that AmotL2 is required for the formation of radial actin filaments both in epithelial and endothelial cells^{25,27}. The preferential expression of AmotL2 in EC of the aorta raised the possibility that AmotL2 controlled arterial EC shape via the formation of radial actin fibers. To address this question, we used a genetic deletion approach to silence *amotl2* gene expression specifically in the endothelial lineage as previously reported²⁸. In this model system, *amotl2*^{flox/flox} mice were crossed with Cdh5(PAC)^{CreERT2} transgenics as well as ROSA26-EYFP reporter mice²⁵, from now on referred to as *amotl2*^{ec/ec}. This crossing enables efficient inducible conditional recombinase expression and subsequent *amotl2* knockout in ECs (*amotl2*^{ec-/ec-}) after tamoxifen injections as well as quantification of recombination efficiency by YFP expression (**Supplementary**

Fig. 2a,b). Adult mice (7-9 months old) were euthanized one month after tamoxifen injections, and aortae were dissected and analyzed by whole-mount immunostaining. Inactivation of AmotL2 in the DA resulted in the loss of radial actin filaments and altered cell shape (**Fig. 2a**, quantification in **2b,c**). No detectable changes in the actin cytoskeleton and cellular shape were observed in the endothelium of the IVC of *amotl2^{ec-/ec-}* mice. This observed phenotype change appeared to be arterial-specific as similar effects were observed in arterial, but not venous ECs of other organs such as the urinary bladder (**Fig. 2d**, quantification in **2e,f**).

The nucleus is the largest organelle of the EC. As such it is exposed to the hemodynamic drag by the blood flow. In response to shear stress, EC as well as EC nuclei elongate, and nuclei orient themselves relative to the direction of flow. Nuclear positioning as well as alignment has previously been shown to be dependent on the association to microfilaments as well as the tubulin network²⁹. In *amotl2^{ec+/ec+}* mice, nuclei of ECs of the DA were elongated and orientated in parallel with cell alignment in the direction of blood flow. However, in AmotL2 deficient ECs, the nuclei were more rounded with irregular shapes and positioned close to the cell edge downstream of the flow direction (**Fig. 2g**, quantification in **2h,i**). These changes in nuclear shape and positioning were again not observed in the IVC (**Fig. 2j**, quantification in **2k,l**). Taken together, these data showed that AmotL2 is required for EC elongation as well as positioning of the EC nucleus.

AmotL2 expression is required for arterial response to flow.

Next we investigated whether AmotL2 is required for arterial endothelial compliance to laminar flow *in vitro*. For this purpose, we used a short hair-pin Lentiviral approach to deplete AmotL2 in Human Aortic ECs (HAoEC, **Fig. 3a**). No differences between control and AmotL2 depleted cells in cellular and nuclear shape were detectable under static

conditions (**Fig. 3b-d**). To recapitulate arterial flow conditions, cells were exposed to 14dynes/cm² for 48h in a flow chamber as described in materials and methods. Control HAoECs exhibited an elongated phenotype and aligned in the direction of flow; however, the depletion of AmotL2 resulted in failure to elongate and align in the direction of flow (**Fig. 3b**, quantification in **3e,f**). We could further show that AmotL2 was required for controlling nuclear shape and positioning. Consistent with the cellular shape change, nuclei also exhibited a rounder shape and could not maintain the positioning at the center of the cells when compared to control HAoECs (**Fig. 3g,h**).

AmotL2 couples VE-cadherin to the nuclear lamina.

Actin filaments are coupled to the nuclear membrane through the LINC complex²⁹⁻³². This complex consisting of Sun-domain proteins (SUN-1 and -2) and KASH domain proteins (Nesprin-2) connects to Lamin A/C of the nuclear lamina. Therefore, we next investigated a possible connection between VE-cadherin, AmotL2, actin and the LINC complex.

We used a Co-IP approach to obtain AmotL2 associated immunocomplexes from both murine endothelial cell line (MS1) and primary Bovine Aortic Endothelial (BAE) cells. By spectrometry analysis (raw data in **Supplementary Table 1,2**), we identified cellular membrane protein VE-cadherin and α -, β -, δ -catenin, as well as the nuclear laminal proteins such as SUN2 and Lamin A, in all triplicate IP samples from MS1 cells (**Fig. 4a**). Consistently, the majority of key membrane proteins were recognized in BAE AmotL2 immunoprecipitates (**Supplementary Fig. 3a**). Mouse lungs consist of approximately 10-20% ECs. We performed immunoprecipitation using AmotL2 antibodies and could verify that AmotL2 associates with VE-cadherin, B-catenin, actin, and Lamin A also in the murine lung tissue *in vivo* (**Fig. 4b**). It was not possible to analyze Nesprin-2 by western blot due to its high molecular mass (<800 kDa). The association of AmotL2 was dependent on

myosin contraction and actin filaments as treatment with the myosin II inhibitor blebbistatin or the actin polymerization inhibitor cytochalasin D both decreased the association of AmotL2 to Lamin A/C and SUN2 (**Fig. 4c**). In addition, immunoprecipitation of VE-cadherin confirmed the association to AmotL2 and Lamin A in HAoECs (**Fig. 4d**). Interestingly, shRNA depletion of AmotL2 protein in ECs abrogated the association of VE-cadherin to both actin and Lamin A (**Fig. 4d**).

The higher expression levels of AmotL2 detected in the DA as compared to the IVC *in vivo* raised the question of whether AmotL2 associated complex is shear stress responsive. We placed primary Human Umbilical Venous ECs (HUVECs) in a 15cm culture dish on an orbital shaker to apply the circulatory flow to the cells (schematic in **Supplementary Fig. 3b**). As previously described³³, the alignment of the cells at the periphery area was observed after 96h (**Supplementary Fig. 3c,d**). Analyses of the AmotL2 IP revealed a dramatically increased binding with VE-cadherin, actin and nuclear membrane proteins compared to the static condition (**Fig. 4e**).

Taken together, MS and IP data suggest a model where VE-cadherin/AmotL2 forms a complex that is connected to the nuclear LINC complex via actin filaments (schematic in **Fig.4f**).

Deletion of AmotL2 promotes vascular inflammation.

EC alignment and cytoskeletal reorganization in response to laminar blood flow is protective against inflammation³. The change in the mechano-response of *amotl2*^{ec-/ec} EC raised the question whether this was accompanied by a pro-inflammatory phenotype. The aortic arch is exposed to turbulent blood flow and the descending aorta is exposed to laminar flow. For this reason, we analyzed these areas of the aorta separately (**Fig. 5a**). mRNA isolated from DAs in both *amotl2*^{ec+/ec+} (n=3) and *amotl2*^{ec-/ec-} (n=5) mice were analyzed by

mRNA-seq. Due to high variability between individual mice, only 65 genes were identified to be differentially expressed (*adjusted p value* < 0.05) between *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* groups (**Supplementary Table 3**). However, those genes were obviously enriched to immuno-related GO terms, such as “Neutrophil activation involved in immune response”, “inflammatory response” and “regulation of immune effector process” (**Fig. 5b**). Gene expression profile analysis on MS1 cells *in vitro* treated with control or AmotL2 siRNA was also performed by RNA-seq. Interestingly, we did not observe any up-regulation of inflammatory gene signatures *in vitro* (**Supplementary Fig. 4a** and **Supplementary Table 4**), indicating that the *in vivo* environment was required for this to occur. We therefore performed whole-mount immunostaining to analyze the presence of CD45⁺ inflammatory cells in the aortic arch. The whole mount immunofluorescence staining showed the presence of spindle-like CD45⁺ cells in the inner curvature of the aortic arch in wild-type animals and in arterial bifurcations (**Fig. 5c,d**). Analyses of the *amotl2^{ec-/ec-}* mice 1-month post-injection of tamoxifen revealed the infiltration of CD45⁺ round monocytes in the outer curvature of the aortic arch (**Fig. 5c,d**). The CD45⁺ monocyte-like cells were detected in the sub-endothelial compartment of the aorta (**Fig. 5e,f**). In total, 45% (9/20) *amotl2^{ec-/ec-}* arches contained more than one CD45⁺ lesion.

Inflammatory markers are up-regulated in *amotl2^{ec-/ec-}* mouse aortae.

Next, we quantified mRNA expression of inflammatory markers in DAs. The mRNA expression level analyzed by TaqMan qRT-PCR showed a significant increase of inflammatory markers, such as *Il6*, *Tnf*, and *Cd68a* in *amotl2^{ec-/ec-}* DA, suggesting a provocation of a general immune response. Interestingly, up-regulation of pro-inflammatory markers was more pronounced in male animals (**Fig. 5g-j**).

In response to pathogenic stimuli, expression of various leukocyte adhesion molecules can be augmented as the initial sign of vascular inflammation, such as ICAM-1 and VCAM-1. Indeed, in *amotl2^{ec-/ec}* DA, an increase in *Vcam-1* expression on transcriptional level was detected by qPCR, but the change of *Icam-1* was less obvious (**Supplementary Fig. 4b,c**), revealing the activation of endothelium of the DAs in the absence of AmotL2. Remarkably, *Vcam-1* up-regulation was also more profound in male mice (**Supplementary Fig. 4b**).

Once leukocytes attach and migrate into underlying intima, the process of lesion formation begins. This requires the participation of chemoattractant cytokines such as *Ccl2*, also known as monocyte chemoattractant protein-1 (MCP-1), which is especially important for the recruitment of mononuclear immune cells. Compared to the *amotl2^{ec+/ec+}* aortic tissues, *amotl2* deletion caused an increase of *Ccl2* expression in the descending regions (**Fig. 5j**), as well as *Cxcl10*, which is able to selectively attract NK cells as well as T and B lymphocytes. (**Supplementary Fig. 4d**). However, other chemokines such as *Ccl5* had no significant changes (**Supplementary Fig. 4e**), suggesting that the induced inflammatory response was mainly affecting innate immune cells.

By contrast, the T and B cell markers *Cd4*, *Cd8*, and *Cd19*, as adaptive immune markers, showed no differences in expression level of these markers on average was detected in the DAs with or without AmotL2 (**Supplementary Fig. 4f-h**).

In conclusion, the expression profile of inflammatory-related genes indicates that AmotL2 depletion results in an innate immune response rather than an activation of adaptive immunity. Of note is the preferential upregulation of pro-inflammatory markers in *amotl2^{ec-/ec-}* males.

AmotL2 depletion promotes the formation of abdominal aortic aneurysms in male mice.

Aortic inflammation is a predictor of the development of arterial aneurysm³⁴. Inflammatory aortic aneurysms account for up to 10% of all AAA cases³⁵. After dissection of the aorta, we could detect the formation of abdominal aortic aneurysms (AAA, dilatation>1.5 times normal size) in the proximity of the renal arterial branch (**Fig. 6a**), but not in ascending or thoracic aortae. Interestingly, 20 % of male *amotl2*^{ec-/ec-} (5/25) mice developed an AAA; however, no aneurysm was detected in the females (0/20). Furthermore, no aneurysms were observed in the *amotl2*^{ec+/ec+} mice (36 mice, 20 male and 16 female).

Imaging analysis of a typical AAA revealed damage to the endothelium as well as the vessel wall (**Fig. 6b,c**). The insult to the vessel wall was further verified by histological sectioning. The intima of the vessel wall was infiltrated by CD45+ leukocytes (**Fig. 6d**) and elastin fibers were degraded (**Fig. 6e**).

AmotL2/YAP correlation in human AAA samples.

Next, we assessed whether AmotL2 gene expression could be correlated to disease progression in human AAA patients. We analyzed mRNA expression in surgically resected materials from both healthy donors and patients diagnosed with AAA and undergoing aneurysm repair at the Karolinska University Hospital. mRNA samples were taken from both medial and adventitial layers of the intact aorta (13 donors) or AAA tissues (35 patients). Interestingly, AmotL2 expression level in the media tissue (containing endothelial cells, schematic in **Fig. 7a**) in AAA samples was significantly down regulated compared to the intact aortic media, which was not found in adventitia tissues (**Fig. 7b**). The expression pattern of the first exon of AmotL2 was specifically analyzed since this exon is specific for the p100-AmotL2 isoform that we have previously shown interacts with VE-cadherin²⁵. In line with the studies in mice, there was an inverse correlation between the expression of the first exon of AMOTL2 and the luminal/external diameter of AAA (**Fig. 7c**).

YAP (Yes Associated Protein 1) has been reported to act as a rheostat of external mechanical force³⁶. Of interest is that YAP binds to the AmotL2 promoter and thus activates its transcription³⁷. Consistent with these findings, a significant positive correlation was detected between AMOTL2 and YAP mRNA levels ($r = 0.800$, $P < 0.0001$) in media tissues containing endothelium in AAA patients of both genders (**Fig. 7d**). We also found a weaker positive correlation of AMOTL2/YAP in adventitia tissues that did not contain ECs ($r=0.592$, $p=0.0002$). A robust correlation of the well-established YAP target genes CTGF and CYR61 with AMOTL2 was also observed, as shown in **Fig. 7e** and **7f**, respectively. C-FOS has been reported to bind to the promoter and drive expression of the p60 AMOTL2 isoform. This isoform is primarily activated by severe hypoxia in ischemic tissues²⁵. However, no correlation between AMOTL2 and C-FOS mRNA expression could be detected (**Supplementary Fig. 5a**). YAP and TAZ are paralogs with overlapping function as transcriptional regulators of the Hippo pathway. However, there was no significant correlation between AMOTL2 and TAZ expression, suggesting that YAP is primarily driving AMOTL2 expression in the human aortic tissues (**Supplementary Fig. 5b**). In addition, there was no correlation of AmotL2 with gender (**Supplementary Fig. 5c-g**).

Discussion

The vascular endothelium plays an important role in the biomechanical response to hemodynamic forces. Understanding the pathways involved in this response is of importance to comprehend the pathogenesis of vascular disease. In this report we show for the first time that the cellular junctions of arterial ECs are connected via AmotL2 and microfilaments to the nuclear lamina. Interference with this pathway impairs EC alignment in response to shear stress and abrogates nuclear positioning resulting in inflammation and formation of abdominal aortic aneurysms.

We have used an inducible mouse model to target AmotL2 in the EC lineage. In our previous publication, we could show that Amotl2 silencing in ECs *in utero* resulted in impaired aortic expansion and death at embryonic day 10. Silencing of AmotL2 in adult mice, however, did not affect overall survival or had any obvious negative effects up to six months after AmotL2 depletion. The defect in adult mice was clearly more subtle as it was restricted to ECs exposed to arterial flow. We demonstrated not only that AmotL2 is required for cellular alignment in areas of shear stress, but also provided novel insights into how VE-cadherin is mechanically coupled to the cytoskeleton and thereby controls cell shape. AmotL2 triggers the formation of radial actin filaments that mediate junctional tension between neighboring cells. These radial actin filaments were detected in arterial, but not or at least at lower levels in venous endothelium. AmotL2 is a scaffold protein and as such brings together protein complexes of different functions such as Par3, MAGI-1b, Merlin, Actin, VE-cadherin. Of interest is that, in HUVECs of the venous origin, AmotL2 is sufficient to induce radial actin filaments when the cells aligned under flow condition. Our data are consistent with the notion that VE-cadherin is part of a mechanosensory complex with VEGFR2 and PECAM-1 as previously described³⁸. The present data show that the VE-cadherin/AmotL2 protein complex is responsible for the actual cell shape

modulation in arterial ECs. These most recent investigations together with our previous findings have shown that the VE-cadherin AmotL2 complex mediates mechanical forces between ECs, suggesting that AmotL2 may also relay mechanical forces not only from circulatory shear stress, but also transfers mechanical signals between cells. Of particular interest is the observation that AmotL2 is required for nuclear shape and subcellular positioning. Ingber and coworkers showed early on that there is a direct linkage between the cytoskeleton and the cell nucleus opening up the possibility of a novel mechanical signaling pathway from the exterior to the nucleus³⁹. Actin filaments are directly associated with the nuclear lamina by binding to Nesprin2, SUN-1 and -2, and Lamin A that form the LINC complex. The actin filaments are anchored to the nuclear lamina via the LINC complex to form linear punctae called TAN lines. In this report we present evidence for a novel mechanical pathway that mechanically links junctional proteins to the nuclear LINC complex. We show that concomitant with the loss of AmotL2 and radial actin filaments, nuclei lose their central position and translocate to a polarized position in the cell, downstream of the exerted flow direction. Arterial nuclei not only lose their sub-cellular positioning, but the integrity of the nuclear lamina is perturbed. Measurement of forces exerted on the LINC proteins suggest that nuclear positioning is a result of the dynamic interactions of the cytoskeleton where nuclei are exposed to constant actomyosin forces⁴⁰. Depletion of AmotL2 also had consequences for the integrity of the nuclear lamina. The nuclear lamina is an intermediate filament meshwork composed of two types of lamin proteins, the B type (Lamin B1 and B2) and the A type (Lamin A/C) and associated inner nuclear membrane proteins⁴¹. This network determines the mechanical properties and morphology of the nucleus⁴². In particular, Lamin A has been proposed to be responsive to mechanical cues from the extracellular matrix. Reduction of Lamin A in the nuclear membrane also results in a less rigid nuclear membrane.

The lack of alignment and the consequent irregular shapes of the arterial endothelium concomitant with the loss of nuclear positioning had direct consequences for the endothelial function. We could show that AmotL2 deficient cells acquire a pro-inflammatory phenotype with ensuing formation of areas of vascular inflammation characterized by the presence of CD45⁺ monocytes. Quantitative PCR-analysis indicated a gender-specific difference in inflammatory response. The underlying reason is unclear but may relate to levels of estrogen as shown by other reports. Of clinical importance is the formation of AAA in the *amotl2^{ec-/ec-}* male mice. This is of interest as AAA has a relatively high prevalence in males between 65-79 years of age and the rupture of AAA is the cause of over 15 000 deaths/year in the USA alone and 175 000 globally^{2,43,44}. Our data indicate a lower expression of AmotL2 in AAA from patients as compared to healthy aortae. Furthermore, the expression levels of AmotL2 were negatively correlated with the diameter of the aneurysms. Several mouse models of AAA have been established for developing therapies for AAA. However, so far these models have failed to reliably predict results in clinical trials. Here we suggest a model where AmotL2 deficiency activates pro-inflammatory markers such as VCAM-1 and ICAM-1 on the EC surface. This promotes the extravasation of CD45⁺ inflammatory cells. The presence of inflammatory cells in the tunica media promotes the degradation of the extracellular matrix such as elastin, and thus weakens the physical strength of the aortic wall. The weakened area of the artery then bulges out and poses an increased risk of blood vessel rupture and hemorrhage (as shown in the schematic **Fig. 7g**). The possibility that lower levels of AmotL2 could increase the risk of developing vascular inflammation, opens up the potential to therapeutically restore the AmotL2 mechano-transductory pathway and thereby increase the resilience of the arterial wall to shear stress.

Methods

Human material

Aortic samples from AAA patients were obtained from the surgery performed at Karolinska Hospital in Stockholm. Control samples were taken from the abdominal aorta of beating-heart, solid organ transplant donors. Ethical permit (2009/1098-32) was granted by Regionala etikprövningsnämnden (Regional ethical review boards) in Stockholm. RNA was extracted from both medial and adventitia layer of the aortic wall and subsequently sequenced on HTA 2.0 (Human Transcriptome Array 2.0 - Affymetrix) platform.

Mice and tamoxifen injections

The *amotl2^{lox/lox}* mice, carrying a loxP-flanked *amotl2* gene, were crossed to *Cdh5(PAC)^{CreERT2}* and *ROSA26-EYFP* double transgenic mice. To induce endothelial-specific *amotl2* gene inactivation, tamoxifen was administered by intraperitoneal (IP) injection for 5 continuous days. For adult mice over 6 weeks old, 100µl of tamoxifen (20mg/ml) was administered at each injection site. Analysis of mice samples was performed four to six weeks after injections. All mice in this report were in C57BL/6 background, and both females and males were included. Ethical permits were obtained from North Stockholm Animal Ethical Committee and all experiments were carried out in accordance with the guidelines of the Swedish Board of Agriculture.

Tissue preparation

Mice were euthanized using carbon dioxide. Thoracic cavity was rapidly opened, and the heart was exposed while still beating. Cold PBS was injected through a cannula for perfusion for 1 minute and then changed to 4% paraformaldehyde (PFA) for another 1-minute perfusion. Aorta from root to aortic-common iliac bifurcation was dissected followed by careful removal of the connective tissues. After 1h extra fixation in 4% PFA,

the entire aorta was opened longitudinally. For the aortic arch part, using spring scissors, the inner curvature was cut along anteriorly, while the outer curvature of the aorta was opened from the aortic root through innominate, carotid, and subclavian arteries until the aortic arch resembled a Y shaped split. The whole flattened-out aorta was pinned onto the wax mold and prepared for immunostaining.

For RNA isolation, the aorta was perfused with cold PBS for 2 minutes before careful dissection. Thoracic and abdominal aorta were taken out and frozen in -80°C for subsequent RNA extraction.

To isolate the urinary bladder, the mice were handled especially gently before sacrifice, which prevented urine leakage. Full bladders were immersed in fixative for 2 hours (2h) and pinned on the wax mold in an open flower shape for whole-mount staining.

Mouse eyeballs were taken out at postnatal day 6 (P6) and month 6 (week 24). After a 2h fixation in 4% PFA, the retinas were dissected out and prepared for immunofluorescence staining for analysis of vasculature.

Cell culture

MS1 cells were cultured in RPMI-1640 medium (GIBCO, 21875-034) supplemented with 10% FBS (GIBCO, 10270-106) and 1% penicillin/streptomycin (P/S, GIBCO, 15140-122). BAE cells (Bovine Aortic Endothelial cell) purchased from Sigma-Aldrich (B304-05) were cultured in Bovine Endothelial Cell Growth Medium (Sigma, B211-500). Human Umbilical Vein Endothelial Cells (HUVEC) purchased from ScienCell (#8000) were cultured in Endothelial cell Medium (ScienCell, #1001). Human Aortic Endothelial Cell (HAoEC) were purchased from PromoCell (C-12271) and cultured with Endothelial Cell Growth Medium MV (C-22020). To note, the batch of HAoEC used for this study was from a 55-year-old male donor with a Caucasian background.

Lentiviral induced knock-down

For knockdown studies, HAoECs (PromoCell) were infected with customized AmotL2 shRNA Lentiviral particles (Sigma) or scrambled shRNA control virus in complete endothelial cell medium with 5 µg/mL polybrene (Vector Builder). The Lentivirus-containing medium was removed after overnight incubation and fresh medium was added. Further analyses of confluent cells (WB, IF, Ibidi flow) were performed at ≥ 72 h after infection.

Flow experiments

Ibidi flow system: Flow chamber slides (Ibidi µ-Slides VI 0,4 Ibidi-treated) with a volume of 30 µl per parallel channel were coated with fibronectin (Sigma). HAoECs/HUVECs were grown on the slides for 24h until 30-50% confluency followed by infection with Lentivirus or control treatment. 96h after that cells were subjected to 14 dyn/cm² laminar flow using the Ibidi pump system and pump control software or kept at static conditions and cultured for 48h at 37°C 5% CO₂. Cells were then harvested and processed for further analysis.

Orbital shaker: The Rotamax 120 (Heidolph) complies well with cell incubator and generates circular motion with the maximum speed of 300rpm. HUVECs on a 15cm culture dish with 16ml medium were placed on the shaker for 96h before the harvesting the cell lysates.

Immunofluorescence (IF) staining

Immunofluorescence staining on MS1 cells, HAoEC, and HUVECs was performed as previously described²⁵. To stain open aorta pinned on wax, endothelium exposed on the top layer was carefully treated using the same protocol as for cell staining, with the exception that the aorta was permeabilized for 20 minutes with 0.1% Tween 20 in PBS.

Retinas and bladders were blocked and permeabilized in 1% BSA and 0.3% Triton-X100 in PBS overnight. Pblec buffer (1.0% Triton X-100 plus 0.1M MgCl₂, 0.1M CaCl₂, 0.01M MnCl₂ in PBS) was used for washing and incubating one or more primary antibodies. Then

fluorophore-conjugated antibodies were added in blocking buffer, followed by 5 x 20-minutes wash with blocking buffer at 1:1 dilution in PBS. The cells/whole tissue was finally mounted with Fluoroshield™ with DAPI (Sigma, F6057). For a list of primary and secondary antibodies used see *Supplementary Table 5*.

Western blot (WB)

Cells were scraped directly from the culture dish in lysis buffer (50 mM Hepes buffer, 150 mM NaCl, 1.5 mM MgCl₂, 1 mM EGTA, 10% Glycerol, 1% TritonX-100), with 1 x protease inhibitor (Roche, 04693159001) and optionally with Phosphatase Inhibitor Cocktail 1 (Sigma, P2850). Lysates were prepared with SDS sample buffer (Novex, 1225644) containing 10 % sample reducing agent (Novex, 1176192), separated in a polyacrylamide gel with 4-12% gradient (Novex, NP0322BOX), and transferred to a nitrocellulose membrane (Whatman, 10401396). The membrane was blocked in 5% non-fat milk PBS with 0.1% Tween 20 and sequentially incubated with the primary antibody at 4°C overnight. Horseradish peroxidase (HRP) conjugated secondary antibody was added in order for labelled proteins to be detected by Western Lightning Plus-ECL (PerkinElmer, 203-170071). Primary and secondary antibodies used are listed in *Supplementary Table 5*.

Co-immunoprecipitation (Co-IP) analysis

Mouse lung tissues were cut into small pieces before transferring into lysis buffer for western blot. Tissue homogenizer was gently applied for better protein extraction. Cell/tissue lysates were incubated with protein G sepharose beads (GE, 17-0618-01) for 1.5 hours at 4°C as pre-cleaning. Afterwards 2µg Amotl2, Lamin A/C, VE-cadherin antibody or control IgG were added in the lysates overnight at 4°C. The next morning, the immunocomplexes were enriched by protein G beads for 2h at 4°C, followed by five-time washing with lysis buffer. The final protein samples were fractionated by polyacrylamide gel and fractions were western blotted for evaluation of IP protein input level.

Mass spectrometry (MS) analysis

IP samples were dissolved in 200 μ L lysis buffer (4 % SDS, 50 mM HEPES pH 7.6, 1 mM DTT). After heating at 95°C for 5 min and centrifugation at 14,000g for 15 min, the supernatant was transferred to new tubes. Protein digestion was performed using a modified SP3-protocol. In brief, each sample was alkylated with 40 mM chloroacetamide and Sera-Mag SP3 bead mix (20 μ l) was transferred into the protein sample together with 100 % acetonitrile to a final concentration of 70 %. The mix was incubated under rotation at room temperature for 20 min. The mixture was placed on the magnetic rack and the supernatant was discarded, followed by two washes with 70 % ethanol and one with 100 % acetonitrile. The beads-protein-complex was reconstituted in 100 μ l trypsin buffer (50 mM HEPES pH 7.6 and 0.8 μ g trypsin) and incubated overnight at 37°C. The eluted samples were dried in a SpeedVac. Approximately 10 μ g was suspended in LC mobile phase A and 1 μ g was injected on the LC-MS/MS system.

Online LC-MS was performed using a Dionex UltiMate™ 3000 RSLCnano System coupled to a Q-Exactive-HF mass spectrometer (Thermo Scientific). IP samples were trapped on a C18 guard-desalting column (Acclaim PepMap 100, 75 μ m x 2cm, nanoViper, C18, 5 μ m, 100 Å), and separated on a 50cm long C18 column (Easy spray PepMap RSLC, C18, 2 μ m, 100 Å, 75 μ m x 50cm). The nano capillary solvent A was 95% water, 5% DMSO, 0.1% formic acid; and solvent B was 5% water, 5% DMSO, 95% acetonitrile, 0.1% formic acid. At a constant flow of 0.25 μ l min⁻¹, the curved gradient went from 2% B up to 40 % B in 240 min, followed by a steep increase to 100% B in 5 min.

FTMS master scans with 70,000 resolution (and mass range 300-1700 m/z) were followed by data-dependent MS/MS (35,000 resolution) on the top 5 ions using higher-energy collision dissociation (HCD) at 30-40 % normalized collision energy. Precursors were isolated with a 2m/z window. Automatic gain control (AGC) targets were 1e⁶ for MS1 and

1e⁵ for MS2. Maximum injection times were 100ms for MS1 and 150-200 ms for MS2. The entire duty cycle lasted ~2.5s. Dynamic exclusion was used with 60s duration. Precursors with unassigned charge state or charge state 1 were excluded and an underfill ratio of 1% was used.

Quantitative real-time RT-PCR (qRT-PCR)

To extract RNA from dissected aorta from *amotl2*^{ec+/ec+} (n=3) and *amotl2*^{ec-/ec-} mice (n=3) was immersed in TRIzol and homogenised by TissueLyser (Qiagen) in TRIzol. Chloroform addition allowed the homogenate to separate into the lower organic phase and the upper clear aqueous phase (containing RNA). MS1 cells were scraped directly from culture dish in RLT buffer. Total RNA purification was carried out using RNeasy Plus Mini Kit (Qiagen), after which RNA concentrations were measured by Nanodrop spectrophotometer (ThermoFisher Scientific). cDNA synthesis was performed using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Quantitative real-time PCR was performed on a 7900HT Fast Real-Time PCR system (Perkin-Elmer Applied Biosystems) using TaqMan Assay-on-Demand (Applied Biosystems). Results were calculated as 2^{-ΔCT} obtained by comparing the threshold cycle (CT) for the genes of interest with that obtained for housekeeping gene hypoxanthine guanine phosphoribosyltransferase (HPRT). All TaqMan probes involved were purchased from Thermo Fisher Scientific and detailed information can be found in *Supplementary Table 5*.

RNA-seq

Total RNA purified from full-length aorta (thoracic and abdominal aorta) of *amotl2*^{ec+/ec+} (n=3) and *amotl2*^{ec-/ec-} mice (n=3) were sent for RNA-seq analysis (Novogene, Beijing, China). Libraries were prepared from 4-5μg of total RNA. PolyA RNA was purified using the Dynabeads mRNA purification kit (Ambion) and fragmented using Fragmentation Reagent (Ambion). First strand cDNA was synthesized from polyA RNA using the

SuperScript III Reverse Transcriptase Kit with random primers (Life Technologies). Second strand cDNA synthesis was performed using Second Strand Synthesis buffer, DNA Pol I, and RNase H (Life Technologies). cDNA libraries were prepared for sequencing using the mRNA TruSeq protocol (Illumina).

The genes with significantly differential expression were input to online Enrichr (Ma'ayan Laboratory, Computational systems biology) for GO term analysis (Biological process 2018)^{45,46}.

Statistical analysis

All statistical figures and analyses were performed using GraphPad Prism software, with the exception of the gene correlation graphs, which were generated using R (<https://www.r-project.org/index.html>). Statistical analysis of *in vivo* results was based on at least three animals per group. Comparisons between two groups with similar variances were analyzed by the standard unpaired two-tailed Student t-test, while comparisons between multiple groups were analyzed by Kruskal–Wallis test. The correlation between two genes were analyzed by Pearson Correlation and pearson correlation coefficient is referred to *r*. A value of $P < 0.05$ was considered as statistically significant (*n.s.* not significant, $*P < 0.05$, $**P < 0.01$ and $***P < 0.001$). No statistical method was used to predetermine sample size in animal studies and the experiments were not randomized. The investigators were not blinded to allocation during experiments and outcome assessment.

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Author contributions

Y.Z. performed *in vivo* experiments using the AmotL2 transgenic model, performed *in vitro* experiments, finalized all figures, and wrote the manuscript. E.H. performed Lenti-virus based transfection *in vitro* and Ibidi flow experiment with data analysis. S.H. performed *in vivo* experiments on the Amotl2 mouse model and summarized data. O.B. and P.E. performed bio-informatical analysis on human aortic samples. J.R. contributed with human samples from clinical surgery. D.K. designed the experiments to investigate inflammation and M.F. performed the TaqMan qPCR on RNA from murine aortic samples. Z.A. performed flow experiment with orbital shaker. L.H developed the theory, designed experiments and wrote the manuscript. All authors reviewed the manuscript prior to submission.

Competing financial interests

The authors declare no competing financial interests.

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Figure 1. AmotL2 is primarily expressed in DA rather than IVC. **a**, Schematic of major blood vessels connected to the heart. DA indicates descending aorta leaving from the heart and IVC is for inferior vena cava. **b**, Anatomical images of the DA and IVC under microscopy during dissection process. DA image was taken after PFA perfusion. **c**, Representative images of DA and IVC used for whole-mount staining. Both vessels were stained with immunoaffinity purified AmotL2 antibodies (in green), VE-cadherin (in red) and phalloidin (in gray scale). **d**, Graph of box plot showing quantification of fluorescence intensity of AmotL2 in co-localization with CD31 in *amotl2^{ec+/ec+}* DA, using ImageJ. **e**, Box plot depicting the difference of cell length/width ratio in *amotl2^{ec+/ec+}* DA and IVC. **f**, Quantification of macroscopic radial actin filaments per EC in the DA and IVC. At least 4 images per mouse (n>3) were analyzed for each group. ****P*<0.001. Scale bars, 20 μ m.

Figure 2. Deletion of AmotL2 resulted in aortic endothelial cellular and nuclear shape change. **a**, Whole-mount IF staining of *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* DA with phalloidin and TO-PRO-3 showing F-actin and nuclei (in gray scale), respectively. **b**, Box plot showing quantification of radial actin filaments per EC in DAs from *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* mice (n=6 in each group). **c**, Quantification of cell length/width ratio in *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* DAs (n=6 in each group). **d**, IF staining of bladder vasculature in *amotl2^{ec+/ec+}* (n=6) and *amotl2^{ec-/ec-}* (n=6) mice, with PECAM-1 indicating ECs (in green). Quantification of EC shape in bladder arteries and veins were presented in **e** and **f**, respectively. Boxed area in the left panel was magnified in the middle and right panels. White character V and A were abbreviations of vein and artery respectively. **g**, Whole-mount IF staining of *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* DAs with VE-cadherin (in green) and TO-PRO-3 showing nuclei (in blue,). **h**, Quantification of nuclear length/width ratio in *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* DAs (n ≥ 6 in each group). Along with the long axis of the EC, the closest distance between nuclei to one end of the cell was measured and normalized to the full cell length. The ratio was depicted in box plot **i**. **j**, Representative images on IVC of *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* mice with VE-cadherin (in green) and TO-PRO-3 (in blue). Quantification of nuclear shape and nuclear positioning of ECs in IVC were presented in **k** and **l** (n=5 in each group). *n.s.*, not significant. ****P*<0.001. Scale bars: **(a)**, **(g)** and **(j)** are 10 μm, **(d)** is 20 μm.

Figure 3. Effect of AmotL2 knockdown on HAoEC *in vitro*. **a**, WB analysis of whole cell lysates of confluent HAoEC cells treated with scrambled control or AmotL2 shRNA Lentivirus probed for AmotL2 and GAPDH. **b**, IF staining for VE-cadherin (in green) and DAPI (in blue) of HAoEC cells infected with scrambled control or AmotL2 shRNA Lentivirus under static or flow (14 dyn/cm²) conditions. Flow direction is indicated below the images. **c**, Quantification of cellular length/width ratio and **d**, nuclear length/width ratio in scrambled control and AmotL2 shRNA Lentivirus of HAoEC cells under static conditions. Representative quantification analysis of cell length/width ratio (**e**, n>80 cells), cell alignment (**f**, n>250 cells), nuclear length/width ratio (**g**, n>60) and nuclear positioning (**h**, n>55 cells) were performed in both control and KD HAoEC cells. Scale bars: (**b**) 100 μ m. *n.s.*, not significant. ****P*<0.001.

Figure 4. AmotL2 links VE-cadherin to nuclear membrane protein Lamin A/C through F-actin. **a**, AmotL2, together with cellular membrane proteins (framed in green box) and nuclear membrane proteins (framed in red box) were identified from AmotL2 immunoprecipitates from MS1 cells analyzed by MS. The data was displayed with fold change ($\log_{10}$) as compared to control immunoprecipitate samples. **b**, Mouse lung tissues from two randomly picked *amotl2^{ec+/ec+}* mice were lysed, subjected to IP with rabbit IgG or AmotL2 antibody and analyzed by WB. **c**, Murine endothelial cells (MS1) either treated with 25 μ M blebbistatin for 2h or 1 μ M cytochalasin D for 1h. Cell immunoprecipitates with rabbit IgG or AmotL2 antibody were analyzed by WB. **d**, Immunoblotting (IB) of VE-cadherin associated protein complexes in HAoEC with either Lenti-Control or Lenti-shAmotL2. Whole lysate harvested from those cells were used as positive input. **e**, WB analysis of AmotL2 IP samples in HUVECs, either under the static condition or 96h after orbital shaking (300 rpm). Only the cells that grew at the periphery (6cm to the edge) of a 15cm dish were harvested. **f**, Hypothetical schematic of AmotL2 associated mechano-responsive complex forming under flow condition.

Figure 5. Absence of AmotL2 resulted in pro-inflammatory phenotype of aorta. **a**, Schematic of the full-length aorta. mRNA was isolated from “DA” indicating descending aorta (including part of thoracic aorta and whole abdominal aorta). **b**, Enriched GO terms (Biological process 2018) analyzed by Enrichr (**Supplementary Table 3**) and presented in the graph ranking by $-\log_{10}$ adjusted *P* value. mRNA isolated from DAs of *amotl2*^{ec+/ec+} (n=3) and *amotl2*^{ec-/ec-} (n=5) mice were sent for RNA-sequencing analysis. 65 significant genes which were differentially expressed were subjected to GO terms matching. **c**, Whole-mount staining on aortic arch of *amotl2*^{ec+/ec+} and *amotl2*^{ec-/ec-} mice, stained with CD45 (in green) and phalloidin (in red). White arrows are pointing at the cluster of CD45 positive cells, which indicates the endothelial lesions. **d**, Representative images of CD45 positive cell clusters (in green) in *amotl2*^{ec-/ec-} aortic arches within the area outlined by white dash line, which were not present in the *amotl2*^{ec+/ec+} arch. **e**, Orthogonal view of *amotl2*^{ec+/ec+} arch and *amotl2*^{ec-/ec-} lesion area stained with CD45 (in green), phalloidin (in red) and TO-PRO-3 (in blue). The luminal cells are on the top layer in the images. **f**, 3D-projection view of CD45+ (in red) cells invading in the endothelium (in green) in *amotl2*^{ec-/ec-} arch. The image was processed in ImageJ. **g-j**, The relative mRNA expression levels of *Il6*, *Tnf*, *Cd68*, and *Ccl2* were determined with TaqMan probes. The mRNA was isolated from DA (**g-j**) tissues of 13 *amotl2*^{ec+/ec+} mice (in black dots, male n=7, female n=4-9) and 15 *amotl2*^{ec-/ec-} mice (in red dots, male n=8-10 and female n=5-6). Relative expression levels were normalized versus *Hprt*. Fold-changes are quantified, and data shown are mean $\pm$ S.E. Scale bars: **(c)** 1000 μ m, **(d)** 100 μ m, and **(e)** 20 μ m. **P*<0.05. ****P*<0.001.

Figure 6. Aortic aneurysms were induced in male *amotl2^{ec-/ec-}* mice. **a**, The dissected full-length aorta from *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* mice. White arrow indicates the abdominal aortic aneurysm (AAA), which occurred close to the renal artery bifurcations. **b**, Representative images of *amotl2^{ec+/ec+}* DA and aneurysm in *amotl2^{ec-/ec-}* mice (VE-cadherin in green, phalloidin in red and TO-PRO-3 in blue). Selective area (boxed) was magnified and presented in **c**. The red box shows wild-type EC morphology in *amotl2^{ec+/ec+}* DA, while the blue box, orange box, white box, and yellow box sequentially outlined in aneurysm reveal the impact on endothelium during aneurysm formation. In orange box, endothelium was damaged and regressed, indicated by white arrows. The DAs from *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* mice with aneurysm were fixed and embedded by paraffin. H&E (upper and middle panel) and CD45 (lower panel) staining was applied on the paraffin sections in **d**. Additionally, aneurysm section was stained by CD45 and showed in the bottom panel. Boxed areas are magnified and placed on the right. In the aneurysm section, abnormal nuclei penetrated were observed along the lumen side indicated by black arrows. **e**, Elastin structure visualized by auto-fluorescence captured under UV light. Layers of elastin were presented in magnified images in white boxes on the right. White arrows indicate normal elastin structure in *amotl2^{ec+/ec+}* DA and discontinuation in *amotl2^{ec-/ec-}* aneurysm, respectively. Scale bars: 1000 μ m (**a**), 25 μ m (**c**) and 100 μ m (**d** and **e**).

a **b** **c** **d** **e** **f** **g**

Hypothetical schematic of aneurysm formation

Figure 7. YAP1 and AMOTL2 correlates in human AAA patients. AAA samples of intima/media region of aortic wall not covered by an intraluminal thrombus i.e., aneurysm wall covered by an EC layer were obtained at open AAA surgery, and mRNA were isolated from both media and adventitia. **a**, Schematic depicting anatomical view of the media and adventitia tissue in the aorta. **b**, Quantification of AmotL2 mRNA expression in medial and adventitial tissues from both intact aortae (13 healthy donors) and dilated aortae (35 AAA patients). * $P < 0.05$. ** $P < 0.01$. **c**, The correlations between AMOTL2 mRNA level of expression and the luminal (upper panel) / external (lower panel) diameter of aneurysms in AAA patients (n=35). AMOTL2 expression level was based on the expression of the first exon from 3' end, detected by specific exon probe, which represents the full-length isoform of AMOTL2. AMOTL2 correlation with YAP1, CTGF and CYR61 of mRNA level of expression were shown in **d-f**, respectively. AMOTL2 expression level was calculated with mean value of every exon expression detected. For each correlation analysis, samples from media were present on top while samples from adventitia on bottom. Correlation coefficient r and p -value are labelled in each individual figure. 21 male and 10 female patients were analyzed in **c**, while 25 male and 10 female patients were enrolled in **d-f**. **g**, Hypothetical schematic of the formation of an AAA. The step-by-step formation of an AAA includes EC activation, immune cell rolling and attachment, leukocyte extravasation, macrophage differentiation, thrombus formation, and finally, lumen dilation (aneurysm).

Supplementary Figure 1. AmotL2 expression pattern in mouse retina of different ages.

amotl2^{ec+/ec+} mice retinas were stained with IB4 (in red) and AmotL2 (in gray) at the age of postnatal day 6, month 3 and month 15, which are placed in the left, middle and right panel, respectively. Both representative images of vasculature in arteries and veins are shown for each time point. Scale bars: 25 μ m (left panel) and 50 μ m (middle/right panel).

Supplementary Figure 2. Recombination efficiency in *amotl2^{flox/flox}* Cdh5(PAC)^{CreERT2} ROSA26-EYFP mice. **a**, GFP immunofluorescence staining (in green) was performed to visualize the YFP reporter, as a marker for Cre-recombinase expression of DAs in *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* Cdh5(PAC)^{CreERT2} ROSA26-EYFP mice. **b**, Quantification of the percentage YFP⁺/YFP⁻ of 3 representative *amotl2^{ec+/ec+}* and *amotl2^{ec-/ec-}* DAs. Size bars: 100 μ m.

a

b

c

Supplementary Figure 3

Supplementary Figure 3. AmotL2 links VE-cadherin to LINC complex through actin. a, Catenins in cellular membrane proteins (framed in green box) and nuclear membrane proteins (framed in red box) were identified from AmotL2 immunoprecipitates from BAE cells analyzed by MS. The data was displayed with fold change ($\log_{10}$) as compared to control IP samples. **b,** Schematic describing how circulatory flow was applied to HUVECs cultured in 15cm dish (300rpm, 96h). The peripheral area with a width of 6cm (pink area) is where the cells were harvested for CO-IP experiments. **c,** Bright field images of HUVECs located in the pink area indicated in **b**, illustrating the cell morphology in both static and one post-flow conditions (96h on orbital shaker). Polar bar chart depicting the angle of cell orientation are presented on the right side. The mean of the actual angular value was normalized to 0° in both conditions. Size bars: 5 μm .

a GO terms-Biological process (Amotl2 knockdown vs control in MS-1 cells)

Supplementary Figure 4. Absence of AmotL2 provokes immune response in the aorta. **a**, Enriched GO terms (Biological process 2018) analyzed by Enrichr (**Supplementary Table 4**) and presented in the graph ranking by $-\log_{10}$ *adjusted P* value. mRNA isolated from MS1 cells treated by control or AmotL2 siRNA (n=3) mice were sent for RNA-sequencing analysis. Top 500 differentially expressed genes with the lowest *adjusted-P* value were subjected to GO terms matching. **b-h**, mRNA was isolated separately from descending aorta (DA, in red), and analyzed by TaqMan qRT-PCR. Relative expression levels of *Vcam-1* (**b**), *Icam-1* (**c**), *Cxcl10* (**d**), *Ccl5* (**e**), *Cd4* (**f**), *Cd8* (**g**), and *Cd19* (**h**) were normalized versus *Hprt*. mRNA was obtained from about 10 *amotl2*^{ec+/ec+} mice (in black dots, male n=5-7, female n=4-5) and 14 *amotl2*^{ec-/ec-} mice (in red dots, male n=7-9 and female n=6). Fold-changes are quantified, and data shown are mean $\pm$ S.E. **P*<0.05. ****P*<0.001. To note that, all *the p-values* unlabelled in the graphs indicate “not statistically significant”.

Supplementary Figure 5

Supplementary Figure 5. The AmotL2 correlation with Hippo pathway in AAA samples from human patients. mRNA expression level correlations of AmotL2 with C-FOS in **a**, and TAZ in **b** were analyzed separately in media (left panel) and adventitia (right panel) tissues. 25 male and 10 female patients were enrolled. Aortic media tissues from male and female of AAA patients were analyzed separately for AmotL2 mRNA expression correlation with YAP1 (**c**), CTGF (**d**), CYR61 (**e**), C-FOS (**f**) and TAZ (**g**). Correlation coefficient r and p -value are labelled in each individual figure.

Figure 3a

Figure 4b

Supplementary Figure 6. Full length blots to Figure 3a and 4b.

Figure 4c

All in MS1 cells

Supplementary Figure 7. Full length blots to Figure 4c.

Figure 4d

All in HAoEC

Supplementary Figure 8. Full length blots to Figure 4d.

Figure 4e

All in HUVEC

Supplementary Figure 9. Full length blots to Figure 4e.

Supplementary Table 1. Mass-spec analysis of AmodL2 immunoprecipitation in MS1 cells

Accession	Description	Area_Ctrl_1	Area_Ctrl_2	Area_Ctrl_3	Area_AmodL2_1	Area_AmodL2_2	Area_AmodL2_3	Gene name
P99027	60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3 - [RLA2_MOUSE]	1,197E7	0,000E0	0,000E0	1,025E8	1,555E8	5,822E8	Rplp2
P62204	Calmodulin OS=Mus musculus GN=Calml1 PE=1 SV=2 - [CALM_MOUSE]	7,282E7	0,000E0	8,936E7	1,808E9	4,501E9	9,019E9	Calml1
P58771-2	Isoform 2 of Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 - [TPM1_MOUSE]	0,000E0	0,000E0	1,752E9	2,736E9		4,298E9	Tpm1
P60710	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 - [ACTB_MOUSE]	9,315E8	8,508E5	2,323E8	1,154E10	2,141E10	1,591E10	Actb
Q60605	Myosin light polypeptide 6 OS=Mus musculus GN=Myf6 PE=1 SV=3 - [MYL6_MOUSE]	3,418E8	0,000E0	1,038E8	7,357E9	1,214E10	1,374E10	Myf6
Q60605-2	Isoform Smooth muscle of Myosin light polypeptide 6 OS=Mus musculus GN=Myf6 - [MYL6_MOUSE]	3,354E8	0,000E0	1,038E8	7,357E9	1,214E10	1,374E10	Myf6
Q93J08	SH3 domain-binding glutamic acid-rich-like protein OS=Mus musculus GN=Sh3bgr1 PE=1 SV=1 - [SH3L1_MOUSE]	0,000E0	0,000E0	0,000E0	2,505E6	1,384E7	7,620E7	Sh3bgr1
P20152	Vimentin OS=Mus musculus GN=Vim PE=1 SV=3 - [VIME_MOUSE]	6,052E7	0,000E0	4,966E7	1,116E8	2,178E8	1,545E9	Vim
P63168	Dynein light chain 1, cytoplasmic OS=Mus musculus GN=Dynl1l1 PE=1 SV=1 - [DYL1_MOUSE]	0,000E0	0,000E0	9,000E5	6,575E7	3,637E6	2,389E6	Dynl1l1
P62908	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 - [RS3_MOUSE]	2,511E7	0,000E0	1,247E7	5,806E8	1,105E9	2,353E9	Rps3
P18760	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3 - [COF1_MOUSE]	0,000E0	0,000E0	1,219E7	2,350E8	6,076E8	5,269E8	Cfl1
Q61RU2	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=1 SV=3 - [TPM4_MOUSE]	0,000E0	0,000E0	1,218E7	7,452E8	6,204E8	9,875E8	Tpm4
Q3TH2E	Myosin regulatory light chain 12B OS=Mus musculus GN=My1l2b PE=1 SV=2 - [ML12B_MOUSE]	1,647E8	0,000E0	1,331E8	5,052E9	8,498E9	1,342E10	My1l2b
Q8VD05	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4 - [MYH9_MOUSE]	7,800E8	0,000E0	3,751E8	1,395E10	2,268E10	1,618E10	Myh9
P63101	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1 - [1433Z_MOUSE]	0,000E0	0,000E0	5,426E6	1,197E8	2,066E8	3,279E8	Ywhaz
Q9WT17-3	Isoform 3 of Unconventional myosin-Ic OS=Mus musculus GN=Myo1c - [MYO1C_MOUSE]	5,544E7	0,000E0	4,243E7	1,796E9	4,341E9	1,165E10	Myo1c
Q9WT17	Unconventional myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2 - [MYO1C_MOUSE]	5,544E7	0,000E0	4,243E7	1,796E9	4,341E9	1,165E10	Myo1c
Q9WWK4	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1 - [EHD1_MOUSE]	0,000E0	0,000E0	1,740E8	2,243E8	3,243E8	3,573E8	Ehd1
P21107-2	Isoform 2 of Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 - [TPM3_MOUSE]	2,921E7	0,000E0	1,212E7	2,040E9	3,139E9	4,747E9	Tpm3
P62259	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 - [1433E_MOUSE]	0,000E0	0,000E0	4,263E6	1,606E8	3,051E8	5,462E8	Ywhae
P47757-2	Isoform 2 of F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb - [CAPZB_MOUSE]	0,000E0	0,000E0	2,392E8	5,000E8	5,788E8	8,469E8	Capzb
P62702	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=1 SV=2 - [RS4X_MOUSE]	0,000E0	0,000E0	0,000E0	4,817E8	8,993E8	1,160E9	Rps4x
P59999	Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3 - [ARPC4_MOUSE]	0,000E0	0,000E0	0,000E0	1,485E8	3,042E8	4,275E8	Arpc4
P47754	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3 - [CAZA2_MOUSE]	0,000E0	0,000E0	2,214E5	1,560E8	3,100E8	2,515E8	Capza2
Q9D0M5	Dynein light chain 2, cytoplasmic OS=Mus musculus GN=Dynl1l2 PE=1 SV=1 - [DYL2_MOUSE]	0,000E0	0,000E0	1,134E6	3,076E7	4,492E6	2,203E6	Dynl1l2
Q61879	Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2 - [MYH10_MOUSE]	1,848E8	0,000E0	7,692E7	5,644E9	9,609E9	6,899E9	Myh10
P68040	Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 - [RACK1_MOUSE]	0,000E0	0,000E0	7,614E6	2,549E8	4,560E8	1,075E9	Rack1
P47757	F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3 - [CAPZB_MOUSE]	0,000E0	0,000E0	2,392E8	5,000E8	5,788E8	8,469E8	Capzb
P57780	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1 - [ACTN4_MOUSE]	0,000E0	0,000E0	3,995E7	6,351E7	2,203E8	3,475E8	Actn4
Q9CQV8-2	Isoform Short of 14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab - [1433B_MOUSE]	0,000E0	0,000E0	3,951E6	8,622E7	9,673E7	1,169E8	Ywhab
P10854	Histone H2B type 1-M OS=Mus musculus GN=Hist1h2bm PE=1 SV=2 - [H2BM_MOUSE]	0,000E0	0,000E0	3,713E6	5,988E7	5,647E7	2,447E8	Hist1h2bm
P14131	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=1 SV=4 - [RS16_MOUSE]	0,000E0	0,000E0	3,807E6	3,581E8	6,287E8	1,211E9	Rps16
P62889	60S ribosomal protein L30 OS=Mus musculus GN=Rpl30 PE=1 SV=2 - [RL30_MOUSE]	0,000E0	0,000E0	3,622E6	1,217E8	3,463E8	4,716E8	Rpl30
P62962	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2 - [PROFL_MOUSE]	0,000E0	0,000E0	0,000E0	6,477E7	5,550E7	1,591E8	Pfn1
P26041	Moesin OS=Mus musculus GN=Msn PE=1 SV=3 - [MOES_MOUSE]	0,000E0	0,000E0	8,796E5	1,725E8	6,499E8	8,865E8	Msn
Q9W1X5	S-phase kinase-associated protein 1 OS=Mus musculus GN=Skp1 PE=1 SV=3 - [SKP1_MOUSE]	0,000E0	0,000E0	3,377E6	1,064E7	4,061E7	7,292E7	Skp1
Q9QXS1-3	Isoform PLEC-1A of Plectin OS=Mus musculus GN=Plec - [PLEC_MOUSE]	0,000E0	0,000E0	3,966E6	3,329E8	7,844E8	1,021E9	Plec
P39447	Tight junction protein ZO-1 OS=Mus musculus GN=Tjp1 PE=1 SV=2 - [ZO1_MOUSE]	0,000E0	0,000E0	1,395E5	5,906E8	1,169E9	7,026E8	Tjp1
Q9CPW4	Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=1 SV=3 - [ARPC5_MOUSE]	0,000E0	0,000E0	0,000E0	3,182E7	5,002E7	1,035E8	Arpc5
Q9WVA4	Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4 - [TAGL2_MOUSE]	0,000E0	0,000E0	0,000E0	1,844E7	5,034E7	9,225E7	Tagln2
Q9EQP2	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1 - [EHD4_MOUSE]	0,000E0	0,000E0	2,279E8	1,218E6	2,279E8	4,719E8	Ehd4
P62830	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1 - [RL23_MOUSE]	0,000E0	0,000E0	1,581E7	1,267E8	2,247E8	2,290E8	Rpl23
P45591	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1 - [COF2_MOUSE]	0,000E0	0,000E0	1,310E7	2,582E8	3,874E8	2,411E8	Cfl2
Q77PR4	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1 - [ACTN1_MOUSE]	0,000E0	0,000E0	3,995E7	6,662E7	2,352E8	3,566E8	Actn1
Q9QXS1-2	Isoform PLEC-1 of Plectin OS=Mus musculus GN=Plec - [PLEC_MOUSE]	0,000E0	0,000E0	3,986E6	3,329E8	7,844E8	1,021E9	Plec
P30999	Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2 - [CTND1_MOUSE]	0,000E0	0,000E0	3,219E6	1,240E8	3,330E8	4,168E8	Ctnnd1
Q8BH64	EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1 - [EHD2_MOUSE]	0,000E0	0,000E0	0,000E0	9,033E7	1,842E8	2,833E8	Ehd2
P26231	Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1 - [CTNA1_MOUSE]	0,000E0	0,000E0	0,000E0	2,894E8	4,583E8	5,492E8	Ctnna1
P51410	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2 - [RL9_MOUSE]	0,000E0	0,000E0	0,000E0	1,632E8	2,751E8	2,248E8	Rpl9
P62264	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=1 SV=3 - [RS14_MOUSE]	0,000E0	0,000E0	8,814E6	3,426E8	1,848E8	1,001E9	Rps14
Q68FD5	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3 - [CLH1_MOUSE]	0,000E0	0,000E0	5,093E6	9,943E8	1,302E9	1,989E9	Cltc
P35979	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2 - [RL12_MOUSE]	1,348E7	0,000E0	3,911E6	2,635E8	5,822E8	9,416E8	Rpl12
P60843	Eukaryotic initiation factor 4A-1 OS=Mus musculus GN=Eif4a1 PE=1 SV=1 - [IF4A1_MOUSE]	0,000E0	0,000E0	3,565E5	7,572E7	1,578E8	2,085E8	Eif4a1
Q91WK0	Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfp2 PE=1 SV=1 - [LRRF2_MOUSE]	0,000E0	0,000E0	1,370E6	1,962E8	3,153E8	2,418E8	Lrrfp2
P17182	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3 - [ENO4_MOUSE]	0,000E0	0,000E0	3,821E6	4,461E7	1,095E8	1,119E8	Eno1
P84228	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2 - [H32_MOUSE]	0,000E0	0,000E0	6,932E6	5,171E7	9,432E7	5,068E8	Hist1h3b
P63242	Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=2 - [IF5A1_MOUSE]	0,000E0	0,000E0	0,000E0	1,968E7	8,325E7	9,981E7	Eif5a
P21107	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=3 - [TPM3_MOUSE]	1,721E7	0,000E0	8,255E6	1,895E9	2,603E9	4,298E9	Tpm3
Q99JY9	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3 - [ARP3_MOUSE]	0,000E0	0,000E0	2,151E6	9,174E7	2,808E8	3,414E8	Actr3
Q8BQ30	Phostensin OS=Mus musculus GN=Ppp1r18 PE=1 SV=1 - [PPR18_MOUSE]	0,000E0	0,000E0	0,000E0	8,519E7	2,448E8	5,048E8	Ppp1r18
E9Q634	Unconventional myosin-Ie OS=Mus musculus GN=Myo1e PE=1 SV=1 - [MYO1E_MOUSE]	0,000E0	0,000E0	2,601E6	2,534E8	4,588E8	8,539E8	Myo1e
P97351	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3 - [RS3A_MOUSE]	0,000E0	0,000E0	3,947E6	2,516E8	4,956E8	9,725E8	Rps3a
P62245	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=1 SV=2 - [RS15A_MOUSE]	0,000E0	0,000E0	0,000E0	2,970E8	5,802E8	7,716E8	Rps15a
P23506	Protein-L-isaspartate(D-aspartate) O-methyltransferase OS=Mus musculus GN=Pomt1 PE=1 SV=3 - [PIMT_MOUSE]	0,000E0	0,000E0	3,447E5	4,734E7	5,273E7	4,213E7	Pcm1
P16546-2	Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 - [SPTN1_MOUSE]	0,000E0	0,000E0	0,000E0	7,210E7	1,351E8	1,963E8	Sptan1
Q9CVB6	Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3 - [ARPC2_MOUSE]	0,000E0	0,000E0	0,000E0	9,702E7	3,457E8	5,493E8	Arpc2
Q9JKB3-2	Isoform 2 of Y-box-binding protein 3 OS=Mus musculus GN=Ybx3 - [YBOX3_MOUSE]	0,000E0	0,000E0	1,701E8	3,202E8	3,202E8	7,399E8	Ybx3
P16546	Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=4 - [SPTN1_MOUSE]	0,000E0	0,000E0	0,000E0	7,210E7	1,351E8	1,963E8	Sptan1
P63017	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1 - [HSP7C_MOUSE]	3,744E7	0,000E0	1,198E7	6,088E8	1,368E9	2,139E9	Hspa8
P61750	ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2 - [ARF4_MOUSE]	0,000E0	0,000E0	7,116E5	2,373E7	5,966E7	9,349E7	Arf4
Q9Z0U1	Tight junction protein ZO-2 OS=Mus musculus GN=Tjp2 PE=1 SV=2 - [ZO2_MOUSE]	0,000E0	0,000E0	2,474E6	5,557E8	1,315E9	1,020E9	Tjp2
O54962	Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1 - [BAF_MOUSE]	0,000E0	0,000E0	0,000E0	4,798E6	7,358E7	1,607E8	Banf1
Q9JH30	Tropomodulin-3 OS=Mus musculus GN=Tmod3 PE=1 SV=1 - [TMOD3_MOUSE]	0,000E0	0,000E0	1,356E6	3,738E8	7,196E8	9,605E8	Tmod3
P14869	60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3 - [RLA0_MOUSE]	4,904E7	0,000E0	0,000E0	1,401E8	3,082E8	8,169E8	Rplp0
Q9CZJ8	40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3 - [RS19_MOUSE]	0,000E0	0,000E0	1,201E7	2,159E8	3,365E8	7,448E8	Rps19
Q64337	Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1 - [SQSTM_MOUSE]	0,000E0	0,000E0	0,000E0	1,741E7	1,819E8	1,250E8	Sqstm1
P62806	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2 - [H4_MOUSE]	3,548E7	0,000E0	2,100E6	4,491E7	1,256E8	1,525E9	Hist1h4a
P14148	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2 - [RL7_MOUSE]	0,000E0	0,000E0	8,463E5	1,918E8	3,841E8	1,158E9	Rpl7
Q62261	Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2 - [SPTB2_MOUSE]	0,000E0	0,000E0	2,966E6	5,610E7	1,701E8	2,578E8	Sptbn1
Q61937	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1 - [NPM_MOUSE]	0,000E0	0,000E0	1,406E7	4,148E8	3,164E8	3,566E8	Npm1
P68254	14-3-3 protein theta OS=Mus musculus GN=Ywhag PE=1 SV=1 - [1433T_MOUSE]	0,000E0	0,000E0	5,736E6	6,738E7	8,793E7	1,954E8	Ywhag
Q9JWU7	Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdc6ip PE=1 SV=3 - [PDC6I_MOUSE]	0,000E0	0,000E0	2,031E5	1,063E8	2,196E8	3,132E8	Pdc6ip
Q62261-2	Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptbn1 - [SPTB2_MOUSE]	0,000E0	0,000E0	2,966E6	5,538E7	1,701E8	2,578E8	Sptbn1
P61255	60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=1 SV=1 - [RL26_MOUSE]	0,000E0	0,000E0	0,000E0	2,152E8	2,489E8	7,882E8	Rpl26
P61982	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2 - [1433G_MOUSE]	0,000E0	0,000E0	0,000E0	1,573E8	1,448E8	1,471E8	Ywhag
P97434-2	Isoform 2 of Myosin phosphatase Rho-interacting protein OS=Mus musculus GN=Mrip - [MPRIIP_MOUSE]	0,000E0	0,000E0	0,000E0	1,158E8	1,846E8	2,425E8	Mrip
P62082	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1 - [RS7_MOUSE]	0,000E0	0,000E0	1,346E7	1,913E8	1,777E8	3,225E8	Rps7
P62270	40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=1 SV=3 - [RS18_MOUSE]	0,000E0	0,000E0	5,188E6	2,852E8	2,371E8	9,919E8	Rps18
Q9EP71	Ankyrin OS=Mus musculus GN=Rai14 PE=1 SV=1 - [RAI14_MOUSE]	0,000E0	0,000E0	0,000E0	1,024E8	1,644E8	2,120E8	Rai14
Q62WV3	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=1 SV=3 - [RL10_MOUSE]	0,000E0	0,000E0	3,303E6	1,397E8	3,848E8	7,309E8	Rpl10

Q62167	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3 - [DDX3X_MOUSE]	1,704E6	0,000E0	2,060E6	1,659E8	3,520E8	4,797E8	Ddx3x
Q9CPR4	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=3 - [RL17_MOUSE]	0,000E0	0,000E0	0,000E0	2,699E8	5,729E8	7,944E8	Rpl17
Q8C143	Myosin light chain 6B OS=Mus musculus GN=MyI6b PE=1 SV=1 - [MYL6B_MOUSE]	7,368E8	0,000E0	1,897E8	4,242E9	5,319E9	5,089E9	MyI6b
Q2KN98	Cytosin-A OS=Mus musculus GN=Specc11 PE=1 SV=1 - [CYTSA_MOUSE]	0,000E0	0,000E0	0,000E0	1,569E8	2,118E8	1,865E8	Specc11
P16858	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 - [G3P_MOUSE]	8,286E7	0,000E0	3,409E6	4,568E8	9,609E8	1,120E9	Gapdh
Q9QYB1	Chloride intracellular channel protein 4 OS=Mus musculus GN=Clc4 PE=1 SV=3 - [CLIC4_MOUSE]	0,000E0	0,000E0	2,973E6	1,351E7	5,759E7	1,109E8	Clc4
Q8CGP6	Histone H2A type 1-H OS=Mus musculus GN=Hist1H2ah PE=1 SV=3 - [H2A1H_MOUSE]	1,458E7	9,648E6	2,742E7	5,055E7	9,659E7	7,366E8	Hist1h2ah
P47753	F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4 - [CAZA1_MOUSE]	0,000E0	0,000E0	0,000E0	1,417E8	2,442E8	2,328E8	Capza1
P35700	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1 - [PRDX1_MOUSE]	0,000E0	0,000E0	0,000E0	1,399E8	2,938E8	4,122E8	Prdx1
P52480	Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4 - [KPYM_MOUSE]	0,000E0	0,000E0	1,563E7	3,242E7	6,608E7	8,367E7	Pkm
Q9JHL1-2	Isoform 2 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Mus musculus GN=Slc9a3r2 - [NHRF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,469E7	7,123E7	9,701E7	Slc9a3r2
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1 - [PP1A_MOUSE]	0,000E0	0,000E0	2,353E6	8,782E7	1,568E8	3,225E8	Ppp1ca
P63276	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2 - [RS17_MOUSE]	0,000E0	0,000E0	0,000E0	1,737E8	1,680E8	1,554E8	Rps17
Q9R1K9	Centrin-2 OS=Mus musculus GN=Cetn2 PE=1 SV=1 - [CETN2_MOUSE]	0,000E0	0,000E0	0,000E0	5,634E6	1,292E7	1,475E7	Cetn2
Q9DBJ1	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3 - [PGAM1_MOUSE]	0,000E0	0,000E0	0,000E0	2,791E7	3,348E7	7,829E7	Pgam1
P27659	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3 - [RL3_MOUSE]	0,000E0	0,000E0	3,066E6	9,362E7	2,469E8	8,279E8	Rpl3
P38647	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hsp9a PE=1 SV=3 - [GRP75_MOUSE]	6,017E7	0,000E0	2,130E7	2,372E8	2,735E8	3,258E8	Hsp9a
P68510	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2 - [143F_MOUSE]	0,000E0	0,000E0	7,196E5	1,335E8	1,491E8	1,981E8	Ywhah
P62242	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 - [RS8_MOUSE]	0,000E0	0,000E0	1,222E6	3,501E8	6,842E8	3,991E8	Rps8
P61358	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 SV=2 - [RL27_MOUSE]	0,000E0	0,000E0	0,000E0	3,338E8	7,779E8	1,012E9	Rpl27
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5 - [GNAI2_MOUSE]	0,000E0	0,000E0	7,794E4	5,374E7	2,147E8	3,711E8	Gnai2
P62869	Elongin-B OS=Mus musculus GN=Elob PE=1 SV=1 - [ELOB_MOUSE]	0,000E0	0,000E0	0,000E0	1,002E7	1,568E7	3,827E7	Elob
P54823	Probable ATP-dependent RNA helicase DDX6 OS=Mus musculus GN=Ddx6 PE=1 SV=1 - [DDX6_MOUSE]	0,000E0	0,000E0	0,000E0	4,259E7	5,714E7	7,585E7	Ddx6
P62918	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=1 SV=2 - [RL8_MOUSE]	0,000E0	0,000E0	0,000E0	1,063E8	3,000E8	8,066E8	Rpl8
Q8BKX1	Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Mus musculus GN=Baiap2 PE=1 SV=2 - [BAIP2_MOUSE]	0,000E0	0,000E0	0,000E0	1,514E7	3,729E7	7,650E7	Baiap2
Q88569	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnmpa2b1 PE=1 SV=2 - [ROA2_MOUSE]	0,000E0	0,000E0	0,000E0	4,976E7	4,955E7	1,864E8	Hnmpa2b1
Q09044	Synaptosomal-associated protein 23 OS=Mus musculus GN=Snap23 PE=1 SV=1 - [SNP23_MOUSE]	0,000E0	0,000E0	0,000E0	1,280E7	8,024E7	8,525E7	Snap23
P61205	ADP-ribosylation factor 3 OS=Mus musculus GN=Arf3 PE=2 SV=2 - [ARF3_MOUSE]	0,000E0	0,000E0	0,000E0	5,665E7	1,137E8	9,176E7	Arf3
Q02248	Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1 - [CTNNB1_MOUSE]	0,000E0	0,000E0	3,246E6	3,082E8	4,62E8	5,499E8	Ctnnb1
Q5SYD0	Unconventional myosin-1d OS=Mus musculus GN=Myo1d PE=1 SV=1 - [MYO1D_MOUSE]	2,735E6	0,000E0	6,818E6	1,427E8	3,484E8	8,994E8	Myo1d
P62281	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3 - [RS11_MOUSE]	0,000E0	0,000E0	4,261E6	1,330E8	3,233E8	4,583E8	Rps11
Q64523	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3 - [H2A2C_MOUSE]	0,000E0	0,000E0	1,828E7	4,055E7	8,789E7	7,541E8	Hist2h2ac
P83940	Elongin-C OS=Mus musculus GN=Eloc PE=1 SV=1 - [ELOC_MOUSE]	0,000E0	0,000E0	0,000E0	1,346E7	2,038E7	2,708E7	Eloc
P29391	Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2 - [FRIL1_MOUSE]	0,000E0	0,000E0	0,000E0	2,343E7	2,971E7	5,841E7	Ftl1
P97855	Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1 - [G3BP1_MOUSE]	8,322E6	0,000E0	0,000E0	1,364E8	2,011E8	6,557E8	G3bp1
P68037	Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1 - [UBZL3_MOUSE]	0,000E0	0,000E0	0,000E0	8,416E6	7,511E6	5,615E6	Ube2l3
Q9D8E6	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3 - [RL4_MOUSE]	0,000E0	0,000E0	1,238E6	2,018E8	3,842E8	8,158E8	Rpl4
P68372	Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1 - [TB4B_MOUSE]	7,924E6	0,000E0	5,484E6	1,362E8	2,937E8	3,976E8	Tubb4b
Q8BT07	Centrosomal protein of 55 kDa OS=Mus musculus GN=Cep55 PE=1 SV=2 - [CEP55_MOUSE]	0,000E0	0,000E0	0,000E0	7,690E7	1,616E8	2,430E8	Cep55
P17426-2	Isoform B of AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 - [AP2A1_MOUSE]	0,000E0	0,000E0	0,000E0	1,427E8	2,388E8	3,233E8	Ap2a1
P98078	Disabled homolog 2 OS=Mus musculus GN=Dab2 PE=1 SV=2 - [DAB2_MOUSE]	0,000E0	0,000E0	0,000E0	6,229E8	3,975E8	6,565E8	Dab2
P12970	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=1 SV=2 - [RL7A_MOUSE]	0,000E0	0,000E0	9,615E5	2,438E8	4,138E8	1,418E9	Rpl7a
P62983	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2 - [RS27A_MOUSE]	2,631E7	0,000E0	2,882E7	7,431E8	9,040E8	9,846E7	Rps27a
Q8BF23	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1 - [ACTBL_MOUSE]	6,609E8	0,000E0	1,502E8	5,101E9	1,354E10	1,337E10	Actbl2
Q9CY58-2	Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 - [PAIRB_MOUSE]	0,000E0	0,000E0	1,047E7	1,214E8	2,512E8	5,693E8	Serbp1
P20029	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3 - [GRP78_MOUSE]	6,100E7	0,000E0	1,220E7	1,944E8	2,001E8	4,070E8	Hspa5
Q61584-3	Isoform B of Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 - [FXR1_MOUSE]	0,000E0	0,000E0	3,780E5	9,430E7	1,716E8	3,955E8	Fxr1
P62960	Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3 - [YBOX1_MOUSE]	1,609E7	0,000E0	8,242E5	2,920E8	6,613E8	1,151E9	Ybx1
P61161	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1 - [ARP2_MOUSE]	0,000E0	0,000E0	2,837E6	1,061E8	2,855E8	5,562E8	Actr2
P68033	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1 - [ACTC_MOUSE]	7,491E8	1,763E8	9,328E9	2,030E10	1,500E10	1,500E10	Actc1
Q9CQ19	Myosin regulatory light polypeptide 9 OS=Mus musculus GN=My9 PE=1 SV=3 - [MYL9_MOUSE]	1,440E8	0,000E0	1,331E8	5,016E9	8,498E9	1,152E10	My9
P67871	Casein kinase II subunit beta OS=Mus musculus GN=Csnk2b PE=1 SV=1 - [CSK2B_MOUSE]	0,000E0	0,000E0	0,000E0	8,717E6	2,380E7	3,732E7	Csnk2b
P80318	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1 - [TCPG_MOUSE]	0,000E0	0,000E0	0,000E0	2,080E7	4,257E7	4,939E7	Cct3
P14206	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4 - [RSSA_MOUSE]	0,000E0	0,000E0	0,000E0	4,752E8	8,327E8	1,754E9	Rpsa
P29341	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2 - [PABP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,375E8	2,779E8	5,690E8	Pabpc1
Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Mus musculus GN=Slc9a3r2 PE=1 SV=2 - [NHRF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,469E7	7,123E7	9,769E7	Slc9a3r2
P62751	60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1 - [RL23A_MOUSE]	0,000E0	0,000E0	1,154E7	2,928E8	5,583E8	1,436E9	Rpl23a
P51881	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3 - [ADT2_MOUSE]	3,742E5	0,000E0	1,161E7	1,170E8	2,168E8	2,044E8	Slc25a5
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmmpo PE=1 SV=4 - [LAP2A_MOUSE]	0,000E0	0,000E0	7,435E5	8,448E7	2,430E8	4,506E8	Tmmpo
Q9D8B3	Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=1 SV=2 - [CHM4B_MOUSE]	0,000E0	0,000E0	0,000E0	1,016E8	2,077E8	3,188E8	Chmp4b
P62301	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2 - [RS13_MOUSE]	0,000E0	0,000E0	3,325E6	1,528E8	3,612E8	7,062E8	Rps13
P99024	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1 - [TB5_MOUSE]	7,924E6	0,000E0	5,484E6	1,705E8	4,630E8	3,976E8	Tubb5
P84104-2	Isoform Short of Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 - [SRSF3_MOUSE]	0,000E0	0,000E0	0,000E0	6,099E7	7,007E7	1,265E8	Srsf3
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 PE=1 SV=2 - [PDXD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,205E8	9,430E7	9,452E7	Pdxdc1
P63325	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1 - [RS10_MOUSE]	0,000E0	0,000E0	1,503E8	1,726E8	3,338E8	7,850E8	Rps10
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Mus musculus GN=Ppp1cb PE=1 SV=3 - [PP1B_MOUSE]	0,000E0	0,000E0	2,535E6	5,939E7	1,204E8	2,192E8	Ppp1cb
P47911	60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3 - [RL6_MOUSE]	0,000E0	0,000E0	2,927E6	1,822E8	4,127E8	9,566E8	Rpl6
Q99K01-2	Isoform 2 of Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 - [PDXD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,547E8	9,430E7	1,446E8	Pdxdc1
P17742	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 - [PPIA_MOUSE]	0,000E0	0,000E0	9,673E5	1,240E8	2,344E8	2,885E8	Ppia
Q6ZWN5	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=1 SV=3 - [RS9_MOUSE]	0,000E0	0,000E0	4,221E6	1,742E8	2,236E8	4,800E8	Rps9
Q3U056	Ras-interacting protein 1 OS=Mus musculus GN=Rasip1 PE=1 SV=3 - [RAIN_MOUSE]	5,784E6	0,000E0	1,974E6	2,222E8	5,526E8	1,186E9	Rasip1
P68373	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 - [TBA1C_MOUSE]	1,425E7	0,000E0	7,585E6	7,937E7	4,307E8	4,357E8	Tuba1c
P63037	DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dnaj1 PE=1 SV=1 - [DNAJ1_MOUSE]	0,000E0	0,000E0	0,000E0	2,998E7	4,294E7	8,657E7	Dnaj1
Q91KB3	Y-box-binding protein 3 OS=Mus musculus GN=Ybx3 PE=1 SV=2 - [YBOX3_MOUSE]	0,000E0	0,000E0	0,000E0	1,701E8	3,202E8	7,389E8	Ybx3
Q60598	Src substrate cortactin OS=Mus musculus GN=Ctn PE=1 SV=2 - [SRCB_MOUSE]	0,000E0	0,000E0	0,000E0	9,379E7	1,714E8	2,807E8	Ctnn
R07356	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2 - [ANXA2_MOUSE]	0,000E0	0,000E0	1,418E6	4,466E7	1,027E8	1,429E8	Anxa2
Q9JJ18	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=1 SV=3 - [RL38_MOUSE]	0,000E0	0,000E0	0,000E0	6,069E7	1,067E8	1,839E8	Rpl38
Q8K371	Angiomotin-like protein 2 OS=Mus musculus GN=Amotl2 PE=1 SV=1 - [AMOL2_MOUSE]	0,000E0	0,000E0	0,000E0	2,745E8	2,477E8	2,037E8	Amotl2
P10126	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 - [EFA1A_MOUSE]	4,552E6	0,000E0	2,176E6	4,168E8	7,622E8	9,864E8	Eef1a1
Q9D1G1	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1 - [RAB1B_MOUSE]	0,000E0	0,000E0	3,456E5	6,625E7	1,481E8	2,129E8	Rab1b
P42208	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2 - [SEPT2_MOUSE]	0,000E0	0,000E0	0,000E0	2,179E7	4,498E7	2,781E7	SEPT2
Q9JJ28	Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV=1 - [FLI1_MOUSE]	0,000E0	0,000E0	0,000E0	1,469E8	2,788E8	3,289E8	Flii
Q99104	Unconventional myosin-Va OS=Mus musculus GN=Myo5a PE=1 SV=1 - [MYO5A_MOUSE]	2,735E6	0,000E0	6,683E5	8,479E7	1,585E8	5,972E8	Myo5a
Q9DBG3	AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1 SV=1 - [AP2B1_MOUSE]	0,000E0	0,000E0	0,000E0	2,544E8	4,341E8	4,493E8	Ap2b1
P63323	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2 - [RS12_MOUSE]	0,000E0	0,000E0	1,701E5	1,409E8	3,121E8	7,002E8	Rps12
Q8K4L3-3	Isoform 2 of Supervillin OS=Mus musculus GN=Svil - [SVIL_MOUSE]	0,000E0	0,000E0	4,058E5	9,909E7	1,704E8	2,919E8	Svil
P62858	40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=1 SV=1 - [RS28_MOUSE]	1,014E7	0,000E0	9,284E6	5,536E7	3,534E7	2,064E7	Rps28
Q4ACU6	SH3 and multiple ankyrin repeat domains protein 3 OS=Mus musculus GN=Shank3 PE=1 SV=3 - [SHAN3_MOUSE]	0,000E0	0,000E0	0,000E0	7,759E7	1,981E8	3,177E8	Shank3
Q8QX90	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3 - [FLNB_MOUSE]	0,000E0	0,000E0	1,416E6	3,471E7	1,033E8	1,361E8	Flnb
Q99LF4	tRNA-splicing ligase RtcB homolog OS=Mus musculus GN=Rtcb PE=1 SV=1 - [RTCB_MOUSE]	0,000E0	0,000E0	0,000E0	2,398E7	5,221E7	5,902E7	Rtcb
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1 - [EIF3B_MOUSE]	0,000E0	0,000E0	0,000E0	3,702E7	6,414E7	1,069E8	Eif3b
P68134	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1 - [ACTS_MOUSE]	7,491E8	0,000E0	1,507E8	9,328E9	2,030E10	1,500E10	Acta1
Q60737	Casein kinase II subunit alpha OS=Mus musculus GN=Csnk2a1 PE=1 SV=2 - [CSK21_MOUSE]	0,000E0	0,000E0	0,000E0	3,069E7	3,592E7	4,701E7	Csnk2a1

P53026	60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3 - [RL10A_MOUSE]	0,000E0	0,000E0	1,121E6	2,194E8	4,647E8	7,238E8	Rpl10a
Q9C2M2	60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4 - [RL15_MOUSE]	0,000E0	0,000E0	0,000E0	1,410E8	2,356E8	6,112E8	Rpl15
Q9JMH9	Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2 - [MY18A_MOUSE]	0,000E0	0,000E0	0,000E0	6,613E7	1,364E8	1,946E8	Myo18a
Q04736	Tyrosine-protein kinase Yes OS=Mus musculus GN=Yes1 PE=1 SV=3 - [YES_MOUSE]	0,000E0	0,000E0	2,114E5	2,150E7	6,777E7	7,664E7	Yes1
P60867	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1 - [RS20_MOUSE]	0,000E0	0,000E0	1,652E6	4,106E8	8,724E8	1,511E9	Rps20
Q3UZ39	Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfp1 PE=1 SV=2 - [LRRF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,787E7	7,631E7	9,605E7	Lrrfp1
P62843	40S ribosomal protein S15 OS=Mus musculus GN=Rps15 PE=1 SV=2 - [RS15_MOUSE]	0,000E0	0,000E0	1,279E6	2,102E8	3,951E8	1,292E9	Rps15
Q8BP67	60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=1 SV=2 - [RL24_MOUSE]	0,000E0	0,000E0	0,000E0	1,450E8	3,722E8	2,636E8	Rpl24
OS5142	60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=1 SV=2 - [RL35A_MOUSE]	0,000E0	0,000E0	6,178E6	1,554E8	1,967E8	3,439E8	Rpl35a
Q9Z0F4	Calcium and integrin-binding protein 1 OS=Mus musculus GN=Cib1 PE=1 SV=3 - [CIB1_MOUSE]	0,000E0	0,000E0	0,000E0	7,585E6	1,559E7	2,096E7	Cib1
Q64331	Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1 - [MYO6_MOUSE]	0,000E0	0,000E0	3,053E6	3,372E8	4,575E8	5,465E8	Myo6
Q61584-7	Isform G of Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus GN=Fxr1 - [FXR1_MOUSE]	0,000E0	0,000E0	3,780E5	8,816E7	1,716E8	3,689E8	Fxr1
P84084	ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2 - [ARF5_MOUSE]	0,000E0	0,000E0	0,000E0	2,539E7	3,693E7	5,111E7	Arf5
Q99KW3-1	Isform 1 of TRIO and F-actin-binding protein OS=Mus musculus GN=Triobp - [TARA_MOUSE]	0,000E0	0,000E0	0,000E0	2,693E7	5,169E7	6,085E7	Triobp
P25444	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3 - [RS2_MOUSE]	0,000E0	0,000E0	8,204E6	1,941E8	4,589E8	1,303E9	Rps2
Q9JW9	Ras-related protein Rab-B OS=Mus musculus GN=Rab PE=1 SV=1 - [RALB_MOUSE]	0,000E0	0,000E0	0,000E0	1,527E7	3,698E7	7,532E7	Ralb
P11499	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 - [H90B_MOUSE]	0,000E0	0,000E0	1,205E7	1,597E8	3,718E8	5,243E8	Hsp90ab1
P62821	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3 - [RAB1A_MOUSE]	0,000E0	0,000E0	3,456E5	6,625E7	1,481E8	2,129E8	Rab1A
P09528	Ferritin heavy chain OS=Mus musculus GN=Fth1 PE=1 SV=2 - [FRIH_MOUSE]	0,000E0	0,000E0	0,000E0	2,738E7	3,287E7	7,222E7	Fth1
P68368	Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 - [TBA4A_MOUSE]	1,425E7	0,000E0	1,199E6	7,937E7	3,125E8	2,375E8	Tuba4a
Q61599	Rho GDP-dissociation inhibitor 2 OS=Mus musculus GN=Arhgdib PE=1 SV=3 - [GDIR2_MOUSE]	0,000E0	0,000E0	0,000E0	1,438E7	1,430E7	2,190E7	Arhgdib
Q9CQR2	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=1 SV=1 - [RS21_MOUSE]	0,000E0	0,000E0	0,000E0	8,197E7	1,348E8	2,985E8	Rps21
P19253	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4 - [RL13A_MOUSE]	0,000E0	0,000E0	0,000E0	1,611E8	2,253E8	7,323E8	Rpl13a
Q9WUM4	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2 - [COR1C_MOUSE]	0,000E0	0,000E0	1,502E6	1,097E8	1,440E8	1,489E8	Coro1c
P80317	T-complex protein 1 subunit zeta OS=Mus musculus GN=Ctcf6 PE=1 SV=3 - [TCPZ_MOUSE]	0,000E0	0,000E0	0,000E0	3,232E7	5,697E7	4,656E7	Ctcf6
Q9FWH6	Rho guanine nucleotide exchange factor 15 OS=Mus musculus GN=Arhgef15 PE=1 SV=1 - [ARHG_F_MOUSE]	0,000E0	0,000E0	7,429E5	4,489E7	1,085E8	1,937E8	Arhgef15
P99029-2	Isform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 - [PRDX5_MOUSE]	0,000E0	0,000E0	0,000E0	2,649E6	1,180E7	1,535E7	Prdx5
Q8BMK4	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=1 SV=2 - [CKAP4_MOUSE]	0,000E0	0,000E0	0,000E0	3,904E7	8,981E7	1,947E8	Ckap4
Q4ACU6-10	Isform 9 of SH3 and multiple ankyrin repeat domains protein 3 OS=Mus musculus GN=Shank3 - [SHAN3_MOUSE]	0,000E0	0,000E0	0,000E0	6,440E7	1,816E8	2,818E8	Shank3
Q922F4	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1 - [TBB6_MOUSE]	0,000E0	0,000E0	4,329E6	2,256E7	9,625E7	1,470E8	Tubb6
Q7TPV4	Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2 - [MBB1A_MOUSE]	0,000E0	0,000E0	8,014E5	5,727E7	1,472E8	2,763E8	Mybbp1a
P09411	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4 - [PGK1_MOUSE]	0,000E0	0,000E0	4,676E6	3,787E7	9,668E7	1,492E8	Pgk1
O09167	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=1 SV=3 - [RL21_MOUSE]	0,000E0	0,000E0	4,561E5	1,193E8	2,589E8	2,638E7	Rpl21
Q02257	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3 - [PLAK_MOUSE]	0,000E0	0,000E0	6,011E6	7,841E7	8,065E7	6,165E7	Jup
Q8BX10	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Mus musculus GN=Pgam5 PE=1 SV=1 - [PGAM5_MOUSE]	0,000E0	0,000E0	0,000E0	1,269E7	3,446E7	5,267E7	Pgam5
Q63918	Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3 - [SDPR_MOUSE]	0,000E0	0,000E0	0,000E0	1,519E7	3,899E7	3,75E7	Sdpr
Q8BX10-2	Isform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Mus musculus GN=Pgam5 - [PGAM5_MOUSE]	0,000E0	0,000E0	0,000E0	1,269E7	3,446E7	5,267E7	Pgam5
Q99PL5	Ribosome-binding protein 1 OS=Mus musculus GN=Rbp1 PE=1 SV=2 - [RRBP1_MOUSE]	0,000E0	0,000E0	0,000E0	7,835E5	3,909E7	1,697E8	Rbp1
Q9PDM2	Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3 - [SRSF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,573E7	1,008E8	1,991E8	Srsf1
Q9CQ69	Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uqcrc PE=1 SV=3 - [QCR8_MOUSE]	0,000E0	0,000E0	0,000E0	1,865E7	2,823E7	7,016E7	Uqcrc
Q64152	Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=1 SV=3 - [BTF3_MOUSE]	0,000E0	0,000E0	0,000E0	4,684E6	2,488E7	7,617E7	Btf3
Q9R0P3	S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 - [ESTD_MOUSE]	0,000E0	0,000E0	0,000E0	6,329E6	2,115E7	3,230E7	Esd
Q01853	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4 - [TERA_MOUSE]	0,000E0	0,000E0	9,011E6	2,354E7	4,093E7	7,549E7	Vcp
Q9JL8	Serine--tRNA ligase, mitochondrial OS=Mus musculus GN=Sars2 PE=1 SV=2 - [SYSM_MOUSE]	0,000E0	0,000E0	0,000E0	8,537E7	1,164E8	6,457E7	Sars2
P06151	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3 - [LDHA_MOUSE]	0,000E0	0,000E0	1,621E6	1,657E7	2,224E7	3,302E7	Ldha
Q7TSJ2-3	Isform 3 of Microtubule-associated protein 6 OS=Mus musculus GN=Map6 - [MAP6_MOUSE]	0,000E0	0,000E0	0,000E0	4,323E6	1,328E7	1,689E7	Map6
Q9ER60	LIM domain and actin-binding protein 1 OS=Mus musculus GN=Lima1 PE=1 SV=3 - [LIMA1_MOUSE]	0,000E0	0,000E0	2,209E6	5,855E7	1,755E8	3,073E8	Lima1
Q7TMM9	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1 - [TBB2A_MOUSE]	7,924E6	0,000E0	5,484E6	1,259E8	3,918E8	3,976E8	Tubb2a
OS4724	Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1 - [PTRF_MOUSE]	0,000E0	0,000E0	0,000E0	9,998E7	2,089E8	4,354E8	Ptrf
P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE=1 SV=3 - [GBB2_MOUSE]	0,000E0	0,000E0	2,238E6	8,151E7	1,019E8	1,458E8	Gnb2
OS4931-2	Isform 2 of A-kinase anchor protein 2 OS=Mus musculus GN=Akap2 - [AKAP2_MOUSE]	0,000E0	0,000E0	0,000E0	7,483E7	1,794E8	2,695E8	Akap2
P05064	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2 - [ALDOA_MOUSE]	0,000E0	0,000E0	3,110E6	1,479E7	4,467E7	6,221E7	Aldoa
Q8K4L3	Supervillin OS=Mus musculus GN=Svil PE=1 SV=1 - [SVIL_MOUSE]	0,000E0	0,000E0	4,058E5	9,909E7	1,704E8	2,919E8	Svil
Q9JKF1	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=2 - [IQGA1_MOUSE]	0,000E0	0,000E0	0,000E0	3,865E7	1,035E8	1,009E8	Iqgap1
Q8K0D0	Cyclin-dependent kinase 17 OS=Mus musculus GN=Cdk17 PE=1 SV=2 - [CDK17_MOUSE]	0,000E0	0,000E0	0,000E0	2,189E7	5,107E7	7,426E7	Cdk17
P70372	ELAV-like protein 1 OS=Mus musculus GN=Elavl1 PE=1 SV=2 - [ELAV1_MOUSE]	0,000E0	0,000E0	0,000E0	2,757E7	3,517E7	7,062E7	Elavl1
FRVQB6	Unconventional myosin-X OS=Mus musculus GN=Myo10 PE=1 SV=1 - [MYO10_MOUSE]	0,000E0	0,000E0	9,589E5	7,241E7	1,355E8	3,570E8	Myo10
Q91YR1	Twirlin-1 OS=Mus musculus GN=Twf1 PE=1 SV=2 - [TWIF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,734E7	5,632E7	5,271E7	Twf1
P58774-2	Isform 2 of Tropomyosin beta chain OS=Mus musculus GN=Tpm2 - [TPM2_MOUSE]	0,000E0	0,000E0	1,208E7	1,533E9	2,676E9	4,035E9	Tpm2
P17427	AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a PE=1 SV=2 - [AP2A_MOUSE]	0,000E0	0,000E0	0,000E0	8,722E7	1,468E8	1,521E8	Ap2a
Q61553	Fascin OS=Mus musculus GN=Fscn1 PE=1 SV=4 - [FSCN1_MOUSE]	0,000E0	0,000E0	0,000E0	2,980E7	1,009E8	1,233E8	Fscn1
Q8VD75	Huntingtin-interacting protein 1 OS=Mus musculus GN=Hip1 PE=1 SV=2 - [HIP1_MOUSE]	0,000E0	0,000E0	0,000E0	9,588E7	1,233E8	1,739E8	Hip1
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2 - [PAIRB_MOUSE]	0,000E0	0,000E0	1,047E7	1,214E8	2,632E8	5,693E8	Serbp1
Q62036	Centrosomal protein of 131 kDa OS=Mus musculus GN=Cep131 PE=1 SV=2 - [CP131_MOUSE]	0,000E0	0,000E0	0,000E0	2,516E7	3,654E7	4,793E7	Cep131
Q8CFI0-3	Isform 3 of E3 ubiquitin-protein ligase NEDD4-like OS=Mus musculus GN=Nedd4 - [NED4_MOUSE]	0,000E0	0,000E0	0,000E0	3,146E7	6,150E7	8,335E7	Nedd4
Q9D0E1-2	Isform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrm - [HNRPM_MOUSE]	0,000E0	0,000E0	2,753E6	3,202E7	7,252E7	8,884E7	Hnrm
P84096	Rho-related GTP-binding protein RhoG OS=Mus musculus GN=Rhog PE=1 SV=1 - [RHOG_MOUSE]	0,000E0	0,000E0	0,000E0	1,246E7	3,793E7	2,480E7	Rhog
Q62419	Endophilin-A2 OS=Mus musculus GN=Sh3gl1 PE=1 SV=1 - [SH3GL1_MOUSE]	0,000E0	0,000E0	0,000E0	1,292E7	3,795E7	5,374E7	Sh3gl1
O08583	THO complex subunit 4 OS=Mus musculus GN=Alyrf PE=1 SV=3 - [THOC4_MOUSE]	0,000E0	0,000E0	1,665E6	2,366E7	5,814E7	7,797E7	Alyrf
Q9DA59	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3 - [GBG12_MOUSE]	0,000E0	0,000E0	0,000E0	1,868E7	2,397E7	4,152E7	Gng12
P47962	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3 - [RL5_MOUSE]	0,000E0	0,000E0	7,551E6	2,499E8	5,103E8	1,052E9	Rpl5
O35887	Calumenin OS=Mus musculus GN=Calu PE=1 SV=1 - [CALU_MOUSE]	0,000E0	0,000E0	2,708E5	1,610E7	1,348E7	3,112E7	Calu
P48962	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4 - [ADT1_MOUSE]	3,742E5	0,000E0	1,161E7	4,647E7	8,723E7	9,796E7	Slc25a4
P62900	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=1 SV=1 - [RL31_MOUSE]	0,000E0	0,000E0	0,000E0	2,845E8	2,459E8	2,062E8	Rpl31
P47963	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=1 SV=3 - [RL13_MOUSE]	0,000E0	0,000E0	3,828E5	1,670E8	3,233E8	9,822E8	Rpl13
Q9CYL5	Golgi-associated plant pathogenesis-related protein 1 OS=Mus musculus GN=Glpr2 PE=1 SV=3 - [GAPR1_MOUSE]	0,000E0	0,000E0	0,000E0	1,357E7	7,178E6	7,037E7	Glpr2
Q9D757-2	Isform 2 of 60S ribosomal protein L22-like 1 OS=Mus musculus GN=Rpl22l1 - [RL22L_MOUSE]	0,000E0	0,000E0	3,909E6	1,340E8	1,938E8	5,866E8	Rpl22l1
P70333	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrmh2 PE=1 SV=1 - [HNRH2_MOUSE]	0,000E0	0,000E0	0,000E0	3,742E7	1,043E8	1,349E8	Hnrmh2
Q9QYB5-2	Isform 1 of Gamma-adducin OS=Mus musculus GN=Add3 - [ADDG_MOUSE]	0,000E0	0,000E0	0,000E0	4,894E7	8,614E7	8,715E7	Add3
P80315	T-complex protein 1 subunit delta OS=Mus musculus GN=Cttd PE=1 SV=3 - [CTPD_MOUSE]	0,000E0	0,000E0	0,000E0	2,245E7	4,479E7	3,445E7	Cttd
P16045	Galectin-1 OS=Mus musculus GN=Lgals1 PE=1 SV=3 - [LEG1_MOUSE]	0,000E0	0,000E0	0,000E0	2,196E7	1,144E8	1,585E8	Lgals1
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3 - [IF2A_MOUSE]	0,000E0	0,000E0	0,000E0	2,257E7	1,515E7	5,969E7	Eif2s1
Q8BTM8	Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5 - [FLNA_MOUSE]	0,000E0	0,000E0	6,534E6	4,699E7	1,089E8	1,788E8	Flna
Q8VHX6-2	Isform 2 of Filamin-C OS=Mus musculus GN=Finc - [FLNC_MOUSE]	0,000E0	0,000E0	0,000E0	3,769E7	8,105E7	1,164E8	Finc
O35658	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Mus musculus GN=C1qb PE=1 SV=1 - [C1QBP_MOUSE]	0,000E0	0,000E0	1,830E7	1,081E7	8,232E7	1,538E8	C1qb
Q91VN6	Probable ATP-dependent RNA helicase DDX41 OS=Mus musculus GN=Ddx41 PE=1 SV=2 - [DDX41_MOUSE]	0,000E0	0,000E0	1,932E7	3,780E7	1,380E7	1,113E8	Ddx41
Q6ZQ58	La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=3 - [LARP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,993E7	3,441E7	1,043E8	Larp1
O88342	WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3 - [WDR1_MOUSE]	0,000E0	0,000E0	0,000E0	3,821E7	8,776E7	1,533E8	Wdr1
Q9JXK1	Syntaxin-6 OS=Mus musculus GN=Stx6 PE=1 SV=1 - [STX6_MOUSE]	0,000E0	0,000E0	0,000E0	5,035E6	5,487E6	1,000E7	Stx6
P9405	Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2 - [NUCL_MOUSE]	0,000E0	0,000E0	1,477E6	9,349E7	1,382E8	4,549E8	Ncl
P32883-2	Isform 2B of GTPase Kras OS=Mus musculus GN=Kras - [RASK_MOUSE]	0,000E0	0,000E0	5,661E6	2,507E7	3,621E7	3,621E7	Kras
Q9WV32	Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arpc1b PE=1 SV=4 - [ARPC1B_MOUSE]	0,000E0	0,000E0	0,000E0	1,711E8	3,299E8	4,938E8	Arpc1b
Q8BJL1	F-box only protein 30 OS=Mus musculus GN=Fbxo30 PE=1 SV=2 - [FBX30_MOUSE]	0,000E0	0,000E0	0,000E0	7,762E7	6,969E7	7,297E7	Fbxo30

P17751	Triosephosphate isomerase OS=Mus musculus GN=Tip1 PE=1 SV=4 - [TPIS_MOUSE]	0,000E0	0,000E0	0,000E0	4,244E7	1,087E8	9,983E7	Tpi1
Q61029	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4 - [LAP2B_MOUSE]	0,000E0	0,000E0	9,723E5	3,714E7	2,430E8	4,506E8	Tmpo
P08556	GTase Nras OS=Mus musculus GN=Nras PE=1 SV=1 - [RASN_MOUSE]	0,000E0	0,000E0	0,000E0	5,964E6	1,781E7	2,239E7	Nras
Q6PCF5-2	Isomform 2 of Mitochondrial fission factor OS=Mus musculus GN=Mif - [MFF_MOUSE]	0,000E0	0,000E0	0,000E0	1,152E7	3,571E7	5,104E7	Mff
Q61029-3	Isomform Epsilon of Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo - [LAP2B_MOUSE]	0,000E0	0,000E0	9,723E5	3,714E7	2,430E8	4,506E8	Tmpo
P62071	Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1 - [RRAS2_MOUSE]	0,000E0	0,000E0	0,000E0	7,704E7	1,746E8	2,174E8	Rras2
Q6PCF5-3	Isomform 3 of Mitochondrial fission factor OS=Mus musculus GN=Mif - [MFF_MOUSE]	0,000E0	0,000E0	0,000E0	1,152E7	2,788E7	5,104E7	Mff
P50580-2	Isomform 2 of Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 - [PA2G4_MOUSE]	0,000E0	0,000E0	0,000E0	1,663E7	9,169E7	2,356E8	Pa2g4
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I OS=Mus musculus GN=Eif3i PE=1 SV=1 - [EIF3I_MOUSE]	0,000E0	0,000E0	0,000E0	3,220E7	5,741E7	6,133E7	Eif3i
P80314	T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4 - [TCPB_MOUSE]	0,000E0	0,000E0	0,000E0	2,422E7	4,273E7	6,022E7	Cct2
P48678	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2 - [LMNA_MOUSE]	0,000E0	0,000E0	0,000E0	6,761E6	9,536E6	4,185E7	Lmna
Q9MWC3	Caveolin-2 OS=Mus musculus GN=Cav2 PE=1 SV=1 - [CAV2_MOUSE]	0,000E0	0,000E0	0,000E0	1,301E7	5,749E6	2,362E8	Cav2
P62717	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1 - [RL18A_MOUSE]	0,000E0	0,000E0	0,000E0	1,130E8	2,777E8	6,537E8	Rpl18a
Q91V41	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3 - [RAB14_MOUSE]	0,000E0	0,000E0	3,456E5	1,027E8	8,942E7	1,245E8	Rab14
Q61656	Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=2 - [DDX5_MOUSE]	0,000E0	0,000E0	0,000E0	1,638E8	3,091E8	4,592E8	Ddx5
Q08509	Epidermal growth factor receptor kinase substrate 8 OS=Mus musculus GN=Egfr PE=1 SV=2 - [EPFR_MOUSE]	0,000E0	0,000E0	0,000E0	5,863E7	1,229E8	2,265E8	Egfr
Q921Q5	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3 - [CLIC1_MOUSE]	0,000E0	0,000E0	0,000E0	7,145E7	1,471E8	1,639E8	Clic1
Q9DBR7	Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2 - [MYPT1_MOUSE]	0,000E0	0,000E0	0,000E0	7,218E7	1,219E8	1,762E8	Ppp1r12a
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial OS=Mus musculus GN=Ssbp1 PE=1 SV=1 - [SSBP_MOUSE]	0,000E0	0,000E0	9,309E5	6,492E6	1,066E7	1,504E7	Ssbp1
Q9WUD1	STP1 homology and U box-containing protein 1 OS=Mus musculus GN=Stub1 PE=1 SV=1 - [CHIP_MOUSE]	0,000E0	0,000E0	0,000E0	1,338E7	2,392E7	3,369E7	Stub1
Q61194	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Mus musculus GN=Plk3c2a PE=1 SV=2 - [P3C2A_MOUSE]	0,000E0	0,000E0	0,000E0	1,325E8	2,152E8	2,174E8	Plk3c2a
Q9WUK4	Replication factor C subunit 2 OS=Mus musculus GN=Rfc2 PE=1 SV=1 - [RFC2_MOUSE]	0,000E0	0,000E0	0,000E0	1,233E7	2,693E7	7,828E7	Rfc2
P70460	Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4 - [VASP_MOUSE]	0,000E0	0,000E0	0,000E0	2,338E7	4,614E7	5,160E7	Vasp
P35980	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=1 SV=3 - [RL18_MOUSE]	0,000E0	0,000E0	9,509E5	1,395E8	2,471E8	4,872E8	Rpl18
Q6R891	Neurabin-2 OS=Mus musculus GN=Ppp1r9b PE=1 SV=1 - [NER2_MOUSE]	0,000E0	0,000E0	0,000E0	2,384E7	5,639E7	4,791E7	Ppp1r9b
Q8BGS2	Bola-like protein 2 OS=Mus musculus GN=Bola2 PE=1 SV=1 - [BOLA2_MOUSE]	0,000E0	0,000E0	0,000E0	8,013E6	1,473E7	1,713E7	Bola2
Q61699-2	Isomform HSP105-beta of Heat shock protein 105 kDa OS=Mus musculus GN=Hsp1 - [HS105_MOUSE]	0,000E0	0,000E0	0,000E0	2,281E7	4,287E7	6,099E7	Hsp1
P51150	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2 - [RAB7A_MOUSE]	0,000E0	0,000E0	0,000E0	1,686E7	2,573E7	4,079E7	Rab7a
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog OS=Mus musculus GN=Vps28 PE=1 SV=1 - [VPS28_MOUSE]	0,000E0	0,000E0	0,000E0	9,550E6	1,693E7	2,457E7	Vps28
Q6AW69-5	Isomform 5 of Cingulin-like protein 1 OS=Mus musculus GN=Cgn1 - [CGN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,233E7	2,225E7	4,436E7	Cgn1
P0C056	Histone H2A.2 OS=Mus musculus GN=H2afz PE=1 SV=2 - [H2AZ_MOUSE]	0,000E0	0,000E0	1,349E7	3,580E7	1,246E8	7,278E8	H2afz
Q61598	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1 - [GDIIB_MOUSE]	0,000E0	0,000E0	0,000E0	1,071E7	1,674E7	2,722E7	Gdi2
O08709	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3 - [PRDX6_MOUSE]	0,000E0	0,000E0	0,000E0	5,746E6	9,588E6	8,522E6	Prdx6
Q921U8-2	Isomform L2 of Smoothelin OS=Mus musculus GN=Smtn - [SMTN_MOUSE]	0,000E0	0,000E0	0,000E0	1,817E7	1,588E7	2,681E7	Smtn
P11440	Cyclin-dependent kinase 1 OS=Mus musculus GN=Cdk1 PE=1 SV=3 - [CDK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,447E7	3,150E7	4,251E7	Cdk1
P97461	40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=3 - [RSS_MOUSE]	0,000E0	0,000E0	0,000E0	5,890E7	1,996E8	2,289E8	Rps5
Q91WK2	Eukaryotic translation initiation factor 3 subunit H OS=Mus musculus GN=Eif3h PE=1 SV=1 - [EIF3H_MOUSE]	0,000E0	0,000E0	1,755E7	1,304E7	4,705E7	4,705E7	Eif3h
P11031	Activated RNA polymerase II transcriptional coactivator p15 OS=Mus musculus GN=Sub1 PE=1 SV=3 - [TCP4_MOUSE]	0,000E0	0,000E0	7,455E5	8,276E6	3,919E7	1,363E8	Sub1
O88746	Target of Myb protein 1 OS=Mus musculus GN=Tom1 PE=1 SV=1 - [TOM1_MOUSE]	0,000E0	0,000E0	0,000E0	6,818E6	9,103E6	2,581E7	Tom1
Q99J96	Homer protein homology 3 OS=Mus musculus GN=Homer3 PE=1 SV=2 - [HOME3_MOUSE]	0,000E0	0,000E0	0,000E0	8,433E6	2,793E7	3,148E7	Homer3
P61979-3	Isomform 3 of Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk - [HNRPK_MOUSE]	0,000E0	0,000E0	5,493E6	7,494E7	1,383E8	1,478E8	Hnrnpk
O88952	Protein lin-7 homolog C OS=Mus musculus GN=Linc7c PE=1 SV=2 - [LIN7C_MOUSE]	0,000E0	0,000E0	0,000E0	1,219E7	1,148E7	2,671E7	Lin7c
P63094	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Mus musculus GN=Gnas PE=1 SV=1 - [GNAS2_MOUSE]	0,000E0	0,000E0	9,807E4	4,359E7	1,460E8	1,327E8	Gnas
O35737	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnh1 PE=1 SV=3 - [HNRH1_MOUSE]	0,000E0	0,000E0	0,000E0	6,189E7	1,034E8	1,349E8	Hnrnhp1
P46062	Signal-induced proliferation-associated protein 1 OS=Mus musculus GN=Sipa1 PE=1 SV=2 - [SIPA1_MOUSE]	0,000E0	0,000E0	0,000E0	9,330E7	2,101E8	2,001E8	Sipa1
Q03141-2	Isomform 2 of MAP/microtubule affinity-regulating kinase 3 OS=Mus musculus GN=Mark3 - [MARK3_MOUSE]	0,000E0	0,000E0	0,000E0	7,830E6	1,999E7	3,415E7	Mark3
Q8BFR5	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufrm PE=1 SV=1 - [EFTU_MOUSE]	0,000E0	0,000E0	0,000E0	1,445E7	4,087E7	3,940E7	Tufrm
Q8D0W7	Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1 - [LYRIC_MOUSE]	0,000E0	0,000E0	0,000E0	1,880E7	2,869E7	5,753E7	Mtdh
Q9CQH7	Transcription factor BTF3 homolog 4 OS=Mus musculus GN=Btf3h PE=1 SV=1 - [BT3L4_MOUSE]	0,000E0	0,000E0	0,000E0	8,981E6	5,634E6	2,506E7	Btf3h
Q9R0L6	Pericentriolar material 1 protein OS=Mus musculus GN=Pcm1 PE=1 SV=2 - [PCM1_MOUSE]	0,000E0	0,000E0	0,000E0	3,804E7	5,684E7	7,729E7	Pcm1
Q9W1T5	RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=1 SV=3 - [RUVB2_MOUSE]	0,000E0	0,000E0	7,090E6	5,668E6	1,560E7	1,195E7	Ruvbl2
Q9ESZ8-5	Isomform 5 of General transcription factor II-1 OS=Mus musculus GN=Gtf2 - [GTF2I_MOUSE]	0,000E0	0,000E0	0,000E0	2,469E7	4,671E7	5,957E7	Gtf2i
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1 - [EIF3L_MOUSE]	0,000E0	0,000E0	0,000E0	1,678E7	4,144E7	7,162E7	Eif3l
Q6ZWV7	60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=1 SV=1 - [RL35_MOUSE]	0,000E0	0,000E0	0,000E0	1,505E8	3,069E8	3,144E8	Rpl35
P23116	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5 - [EIF3A_MOUSE]	0,000E0	0,000E0	0,000E0	3,221E7	9,439E7	1,025E8	Eif3a
Q9JLQ0	CD2-associated protein OS=Mus musculus GN=Cd2ap PE=1 SV=3 - [CD2AP_MOUSE]	0,000E0	0,000E0	0,000E0	9,052E6	2,508E7	3,529E7	Cd2ap
Q922Y1	UBX domain-containing protein 1 OS=Mus musculus GN=Ubxn1 PE=1 SV=1 - [UBXN1_MOUSE]	0,000E0	0,000E0	0,000E0	6,038E6	5,523E6	1,906E7	Ubxn1
Q8BL97-3	Isomform 3 of Serine/arginine-rich splicing factor 7 OS=Mus musculus GN=Srsf7 - [SRSF7_MOUSE]	0,000E0	0,000E0	0,000E0	3,855E7	8,333E7	7,202E7	Srsf7
P84099	60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1 - [RL19_MOUSE]	0,000E0	0,000E0	0,000E0	1,113E8	1,560E8	4,269E8	Rpl19
P60335	Poly(C)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 - [PCBP1_MOUSE]	0,000E0	0,000E0	6,208E5	1,724E7	4,032E7	8,903E7	Pcbp1
P46638	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3 - [RB11B_MOUSE]	0,000E0	0,000E0	0,000E0	1,056E7	1,009E7	3,102E7	Rab11b
P58252	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 - [EF2_MOUSE]	0,000E0	0,000E0	0,000E0	4,746E7	1,351E8	1,998E8	Eef2
Q6PIF6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Mus musculus GN=Ppp2r2a PE=1 SV=1 - [ZABA_MOUSE]	0,000E0	0,000E0	0,000E0	1,087E7	2,245E7	3,175E7	Ppp2r2a
Q9QYQ0	Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2 - [ADDA_MOUSE]	0,000E0	0,000E0	0,000E0	1,140E8	1,436E8	1,348E8	Add1
P62274	40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=3 SV=2 - [RS29_MOUSE]	0,000E0	0,000E0	0,000E0	1,264E7	1,214E8	3,232E8	Rps29
Q8BU31	Ras-related protein Rap-2c OS=Mus musculus GN=Rap2c PE=1 SV=1 - [RAP2C_MOUSE]	0,000E0	0,000E0	0,000E0	5,651E6	1,716E7	1,418E7	Rap2c
P63087-2	Isomform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Mus musculus GN=Ppp1cc - [PP1G_MOUSE]	0,000E0	0,000E0	2,353E6	5,878E7	1,101E8	2,064E8	Ppp1cc
P84091	AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1 - [AP2M1_MOUSE]	0,000E0	0,000E0	0,000E0	2,087E8	2,792E8	3,114E8	Ap2m1
Q61187	Tumor susceptibility gene 101 protein OS=Mus musculus GN=Tsg101 PE=1 SV=2 - [TS101_MOUSE]	0,000E0	0,000E0	0,000E0	1,464E7	2,686E7	6,469E7	Tsg101
P42932	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3 - [TCPQ_MOUSE]	0,000E0	0,000E0	6,390E5	2,318E7	4,541E7	5,123E7	Cct8
P62849-2	Isomform 2 of 40S ribosomal protein S24 OS=Mus musculus GN=Rps24 - [RS24_MOUSE]	0,000E0	0,000E0	0,000E0	1,181E8	1,024E8	1,444E8	Rps24
P97379-2	Isomform B of Ras GTPase-activating protein-binding protein 2 OS=Mus musculus GN=G3bp2 - [G3BP2_MOUSE]	0,000E0	0,000E0	5,026E6	3,650E7	7,730E7	1,353E8	G3bp2
Q3TN34	MICAL-like protein 2 OS=Mus musculus GN=Mical2 PE=1 SV=1 - [MILK2_MOUSE]	0,000E0	0,000E0	1,204E7	2,860E7	4,201E7		Mical2
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3 - [KAP0_MOUSE]	0,000E0	0,000E0	0,000E0	2,393E7	5,342E7	6,425E7	Prkar1a
P67984	60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=1 SV=2 - [RL22_MOUSE]	0,000E0	0,000E0	2,391E6	1,809E8	3,362E8	7,719E8	Rpl22
Q8BGO5	Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnmpa3 PE=1 SV=1 - [ROA3_MOUSE]	0,000E0	0,000E0	6,529E5	9,406E7	1,311E8	2,374E8	Hnmpa3
Q6ZWY3	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=1 SV=3 - [RS27L_MOUSE]	0,000E0	0,000E0	1,094E7	2,132E8	2,594E8	8,226E8	Rps27l
Q6ZWI9	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3 - [RS27_MOUSE]	0,000E0	0,000E0	1,094E7	2,519E8	4,230E8	8,883E8	Rps27
P05480	Neuronal proto-oncogene tyrosine-protein kinase Src OS=Mus musculus GN=Src PE=1 SV=4 - [SRC_MOUSE]	0,000E0	0,000E0	0,000E0	2,114E5	1,340E7	6,219E7	Src
Q8BGB1	Polymerase delta-interacting protein 3 OS=Mus musculus GN=Poldip3 PE=1 SV=1 - [PDIP3_MOUSE]	0,000E0	0,000E0	0,000E0	1,115E7	2,284E7	3,877E7	Poldip3
Q8BDS05	SH2 domain-containing adapter protein E OS=Mus musculus GN=She PE=1 SV=1 - [SHE_MOUSE]	0,000E0	0,000E0	0,000E0	1,152E7	3,268E7	1,414E7	She
Q01320	DNA topoisomerase 2-alpha OS=Mus musculus GN=Top2a PE=1 SV=2 - [TOP2A_MOUSE]	0,000E0	0,000E0	0,000E0	2,889E7	6,027E7	1,207E8	Top2a
Q8CC35	Synaptotagmin OS=Mus musculus GN=Synpo PE=1 SV=2 - [SYNPO_MOUSE]	0,000E0	0,000E0	0,000E0	8,920E6	3,404E7	5,640E7	Synpo
Q9CQE8	UPF0568 protein C14orf166 homolog OS=Mus musculus PE=1 SV=1 - [CN166_MOUSE]	0,000E0	0,000E0	0,000E0	1,244E7	2,785E7	4,335E7	CN166
Q8VHG2	Angiotensin OS=Mus musculus GN=Amot PE=1 SV=3 - [AMOT_MOUSE]	0,000E0	0,000E0	0,000E0	1,728E7	9,856E6	1,533E7	Amot
Q78PY7	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1 - [SND1_MOUSE]	0,000E0	0,000E0	0,000E0	2,632E7	4,073E7	8,755E7	Snd1
P62911	60S ribosomal protein L32 OS=Mus musculus GN=Rpl32 PE=1 SV=2 - [RL32_MOUSE]	0,000E0	0,000E0	0,000E0	2,833E7	7,406E7	1,433E8	Rpl32
P62855	40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=1 SV=3 - [RS26_MOUSE]	0,000E0	0,000E0	0,000E0	1,540E8	4,089E8	4,789E8	Rps26
Q99K48	Non-POU domain-containing octamer-binding protein OS=Mus musculus GN=Nono PE=1 SV=3 - [NONO_MOUSE]	0,000E0	0,000E0	0,000E0	3,121E7	4,880E7	1,454E8	Nono
Q9Z2U0	Proteasome subunit alpha type-7 OS=Mus musculus GN=Psmat7 PE=1 SV=1 - [PSA7_MOUSE]	0,000E0	0,000E0	0,000E0	5,100E6	5,638E6	9,853E6	Psmat7
P27661	Histone H2AX OS=Mus musculus GN=H2afx PE=1 SV=2 - [H2AX_MOUSE]	1,458E7	9,648E5	2,742E7	5,055E7	9,659E7	7,366E8	H2afx
P48036	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1 - [ANKA5_MOUSE]	0,000E0	0,000E0	3,591E6	8,024E6	6,314E6	9,419E6	Anxa5
Q3V038	Tetratricopeptide repeat protein 9A OS=Mus musculus GN=Ttr9 PE=1 SV=1 - [TTC9A_MOUSE]	0,000E0	0,000E0	0,000E0	8,639E6	2,000E7	3,373E7	Ttr9

Q9QZQ1-2	Isoform 1 of Afadin OS=Mus musculus GN=Afdn - [AFAD_MOUSE]	0,000E0	0,000E0	0,000E0	3,317E7	5,627E7	7,192E7	Afdn
Q3UKC1	Tax1-binding protein 1 homolog OS=Mus musculus GN=Tax1bp1 PE=1 SV=2 - [TAXB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,523E7	4,905E7	7,367E7	Tax1bp1
Q8BH0	Proline-rich protein 11 OS=Mus musculus GN=Prr11 PE=2 SV=1 - [PRR1_MOUSE]	0,000E0	0,000E0	0,000E0	1,001E7	2,125E7	5,087E7	Prr11
P63085	Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3 - [MK01_MOUSE]	0,000E0	0,000E0	0,000E0	1,495E7	2,924E7	2,626E7	Mapk1
Q9EPU0-2	Isoform 2 of Regulator of nonsense transcripts 1 OS=Mus musculus GN=Uprf1 - [RENT1_MOUSE]	0,000E0	0,000E0	0,000E0	1,840E7	3,985E7	6,251E7	Uprf1
P26043	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3 - [RAD1_MOUSE]	0,000E0	0,000E0	2,157E5	1,246E8	4,352E8	7,129E8	Rdx
Q99LE6	ATP-binding cassette sub-family F member 2 OS=Mus musculus GN=Abcf2 PE=1 SV=1 - [ABCF2_MOUSE]	0,000E0	0,000E0	0,000E0	4,174E7	7,807E7	1,309E8	Abcf2
O70194	Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2 - [EIF3D_MOUSE]	0,000E0	0,000E0	0,000E0	1,504E7	4,491E7	7,632E7	Eif3d
P35278	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2 - [RAB5C_MOUSE]	0,000E0	0,000E0	0,000E0	4,074E6	2,691E7	1,939E7	Rab5c
Q8R323	Replication factor C subunit 3 OS=Mus musculus GN=Rfc3 PE=1 SV=1 - [RFC3_MOUSE]	0,000E0	0,000E0	2,006E6	1,036E7	8,776E6	3,592E7	Rfc3
Q8BFW7	Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp PE=1 SV=1 - [LPP_MOUSE]	0,000E0	0,000E0	0,000E0	1,323E7	2,344E7	6,516E7	Lpp
P07901	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4 - [HS90A_MOUSE]	1,255E7	0,000E0	5,594E6	1,376E8	3,170E8	4,339E8	Hsp90aa1
Q692N7	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2 - [MYOF_MOUSE]	0,000E0	0,000E0	0,000E0	2,787E7	5,833E7	9,810E7	Myof
P62317	Small nuclear ribonucleoprotein Sm D2 OS=Mus musculus GN=Snrp2 PE=1 SV=1 - [SMD2_MOUSE]	0,000E0	0,000E0	0,000E0	2,805E6	4,126E6	8,124E6	Snrp2
P32233	Developmentally-regulated GTP-binding protein 1 OS=Mus musculus GN=Drg1 PE=1 SV=1 - [DRG1_MOUSE]	0,000E0	0,000E0	0,000E0	6,982E6	7,431E6	1,208E7	Drg1
Q8R105	Vacuolar protein sorting-associated protein 37C OS=Mus musculus GN=Vps37c PE=1 SV=1 - [VP37C_MOUSE]	0,000E0	0,000E0	0,000E0	1,138E7	1,580E7	6,983E6	Vps37c
P62331	ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2 - [ARF6_MOUSE]	0,000E0	0,000E0	0,000E0	1,985E7	1,674E7	5,163E7	Arf6
Q61235	Beta-2-syntrophin OS=Mus musculus GN=Sntb2 PE=1 SV=2 - [SNTB2_MOUSE]	0,000E0	0,000E0	0,000E0	1,425E7	3,066E7	6,413E7	Sntb2
Q99JY3	GTPase IMAP family member 4 OS=Mus musculus GN=Gimap4 PE=1 SV=1 - [GIMAA_MOUSE]	0,000E0	0,000E0	0,000E0	1,139E7	2,714E7	1,689E7	Gimap4
Q3UEB3-2	Isoform 2 of Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Pu6f0 - [PUF60_MOUSE]	0,000E0	0,000E0	0,000E0	1,578E7	3,409E7	4,270E7	Puf60
Q61316	Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1 - [HSP74_MOUSE]	0,000E0	0,000E0	0,000E0	1,679E7	3,326E7	5,921E7	Hspa4
Q922Q4	Pyroline-5-carboxylate reductase 2 OS=Mus musculus GN=Pycr2 PE=1 SV=1 - [PSCR2_MOUSE]	0,000E0	0,000E0	0,000E0	4,318E7	5,612E7	1,792E8	Pycr2
O70551	SRSF protein kinase 1 OS=Mus musculus GN=Sprk1 PE=1 SV=2 - [SRPK1_MOUSE]	0,000E0	0,000E0	0,000E0	8,180E6	1,890E7	4,935E7	Sprk1
P35922-9	Isoform 9 of Synaptic functional regulator FMR1 OS=Mus musculus GN=Fmr1 - [FMR1_MOUSE]	0,000E0	0,000E0	1,048E6	6,566E7	1,602E8	3,140E8	Fmr1
P63001	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1 - [RAC1_MOUSE]	0,000E0	0,000E0	0,000E0	3,428E7	8,787E7	1,288E8	Rac1
P80316	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1 - [TCPE_MOUSE]	0,000E0	0,000E0	2,663E5	6,466E7	3,368E7	2,674E7	Cct5
P26040	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3 - [EZRI_MOUSE]	0,000E0	0,000E0	6,577E5	1,246E8	4,352E8	7,129E8	Ezr
Q91VR2	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1 - [ATPG_MOUSE]	0,000E0	0,000E0	0,000E0	1,589E7	2,744E7	3,222E7	Atp5c1
Q60902	Epidermal growth factor receptor substrate 15-like 1 OS=Mus musculus GN=Eps15l1 PE=1 SV=3 - [EP15R_MOUSE]	0,000E0	0,000E0	0,000E0	1,358E7	2,052E7	2,776E7	Eps15l1
Q05512-3	Isoform 3 of Serine/threonine-protein kinase MARK2 OS=Mus musculus GN=Mark2 - [MARK2_MOUSE]	0,000E0	0,000E0	0,000E0	1,491E7	3,665E7	5,667E7	Mark2
P60229	Eukaryotic translation initiation factor 3 subunit E OS=Mus musculus GN=Eif3e PE=1 SV=1 - [EIF3E_MOUSE]	0,000E0	0,000E0	0,000E0	1,019E7	4,321E7	5,216E7	Eif3e
P14069	Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3 - [S10A6_MOUSE]	0,000E0	0,000E0	0,000E0	1,257E6	2,975E7	4,743E7	S100a6
P49817	Caveolin-1 OS=Mus musculus GN=Cav1 PE=1 SV=1 - [CAV1_MOUSE]	0,000E0	0,000E0	0,000E0	1,334E8	2,111E8	3,995E8	Cav1
Q55F07	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Mus musculus GN=Igf2bp2 PE=1 SV=1 - [IF2B2_MOUSE]	0,000E0	0,000E0	0,000E0	2,192E7	4,628E7	7,923E7	Igf2bp2
P17225	Polypyrimidine tract-binding protein 1 OS=Mus musculus GN=Ptbp1 PE=1 SV=2 - [PTBP1_MOUSE]	0,000E0	0,000E0	5,409E4	7,832E7	1,331E8	2,944E8	Ptbp1
Q91VR5	ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=1 SV=1 - [DDX1_MOUSE]	0,000E0	0,000E0	0,000E0	2,905E7	4,032E7	9,545E7	Ddx1
Q60854	Serpin B6 OS=Mus musculus GN=Serpinb6 PE=1 SV=1 - [SPB6_MOUSE]	0,000E0	0,000E0	0,000E0	3,046E7	3,197E7	6,054E7	Serpinb6
P57776	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3 - [EF1D_MOUSE]	0,000E0	0,000E0	0,000E0	7,344E7	4,998E7	1,104E8	Eef1d
Q99J16	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=1 SV=2 - [RAP1B_MOUSE]	0,000E0	0,000E0	0,000E0	1,082E7	4,667E7	7,742E7	Rap1b
P35279	Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4 - [RAB6A_MOUSE]	0,000E0	0,000E0	3,456E5	3,992E7	1,305E8	1,415E8	Rab6a
Q9D4H4-2	Isoform 2 of Angiomotin-like protein 1 OS=Mus musculus GN=Amotl1 - [AMOL1_MOUSE]	0,000E0	0,000E0	0,000E0	3,518E7	3,733E7	4,278E7	Amotl1
Q9CWX8	Sorting nexin-2 OS=Mus musculus GN=Snx2 PE=1 SV=2 - [SNX2_MOUSE]	0,000E0	0,000E0	2,776E6	1,623E6	5,511E6	1,081E7	Snx2
P23242	Gap junction alpha-1 protein OS=Mus musculus GN=Gja1 PE=1 SV=2 - [CXA1_MOUSE]	0,000E0	0,000E0	0,000E0	7,979E7	1,158E8	1,664E8	Gja1
Q9D898	Actin-related protein 2/3 complex subunit 5-like protein OS=Mus musculus GN=Arpc5l PE=1 SV=1 - [ARPSL_MOUSE]	0,000E0	0,000E0	0,000E0	2,921E7	8,950E7	1,197E8	Arpc5l
P63321	Ras-related protein Raf-A OS=Mus musculus GN=Rala PE=1 SV=1 - [RALA_MOUSE]	0,000E0	0,000E0	0,000E0	9,094E6	9,536E6	2,875E7	Rala
P11983	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3 - [TCPA_MOUSE]	0,000E0	0,000E0	2,616E6	3,239E7	5,712E7	6,535E7	Tcp1
Q60875-5	Isoform 5 of Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 - [ARHG2_MOUSE]	0,000E0	0,000E0	0,000E0	1,999E7	3,828E7	3,560E7	Arhgef2
Q99PT1	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdla PE=1 SV=3 - [GDIR1_MOUSE]	0,000E0	0,000E0	0,000E0	2,653E7	5,288E7	1,434E8	Arhgdla
P61027	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1 - [RAB10_MOUSE]	0,000E0	0,000E0	3,456E5	5,919E7	1,322E8	1,924E8	Rab10
Q9DCT8	Cysteine-rich protein 2 OS=Mus musculus GN=Crip2 PE=1 SV=1 - [CRIP2_MOUSE]	0,000E0	0,000E0	6,090E7	5,476E7	5,476E7	1,094E6	Crip2
Q5SRX1	TOM1-like protein 2 OS=Mus musculus GN=Tom1l2 PE=1 SV=1 - [TM1L2_MOUSE]	0,000E0	0,000E0	0,000E0	6,885E6	2,888E7	3,616E7	Tom1l2
Q92XZ1-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrfp - [HNRPF_MOUSE]	0,000E0	0,000E0	1,777E6	5,494E7	8,067E7	4,935E7	Hnrfp
E9Q5G3	Kinesin-like protein KIF23 OS=Mus musculus GN=Kif23 PE=1 SV=1 - [KIF23_MOUSE]	0,000E0	0,000E0	0,000E0	1,194E7	3,136E7	9,652E7	Kif23
O08529	Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=1 SV=4 - [CAN2_MOUSE]	0,000E0	0,000E0	0,000E0	1,254E7	2,816E7	4,059E7	Capn2
Q8C1B7-3	Isoform 3 of Septin-11 OS=Mus musculus GN=Sept11 - [SEP11_MOUSE]	0,000E0	0,000E0	4,405E6	1,720E7	3,815E7	1,994E7	SEP11
P42669	Transcriptional activator protein Pur-alpha OS=Mus musculus GN=Pura PE=1 SV=1 - [PURA_MOUSE]	0,000E0	0,000E0	0,000E0	8,450E6	2,327E7	4,283E7	Pura
P80313	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1 - [TCPH_MOUSE]	0,000E0	0,000E0	8,568E6	2,270E7	4,153E7	5,233E7	Cct7
P60122	RuvB-like 1 OS=Mus musculus GN=Ruvb1 PE=1 SV=1 - [RUVB1_MOUSE]	0,000E0	0,000E0	0,000E0	6,639E6	1,183E7	2,234E7	Ruvb1
Q5F2E7	Nuclear fragile X mental retardation-interacting protein 2 OS=Mus musculus GN=Nufip2 PE=1 SV=1 - [NUFP2_MOUSE]	0,000E0	0,000E0	1,339E6	1,442E7	4,056E7	8,343E7	Nufip2
Q9D116	39S ribosomal protein L14, mitochondrial OS=Mus musculus GN=Mrlp14 PE=1 SV=1 - [RM14_MOUSE]	0,000E0	0,000E0	0,000E0	8,072E6	2,486E7	1,484E7	Mrlp14
P70698	CTP synthase 1 OS=Mus musculus GN=Ctps1 PE=1 SV=2 - [PYRG1_MOUSE]	0,000E0	0,000E0	0,000E0	1,140E7	1,289E7	4,524E7	Ctps1
Q8BK63-2	Isoform 2 of Casein kinase 1 isoform alpha OS=Mus musculus GN=Csk1a1 - [KC1A_MOUSE]	0,000E0	0,000E0	0,000E0	5,485E6	1,552E7	1,259E7	Csk1a1
Q99L45	Eukaryotic translation initiation factor 2 subunit 2 OS=Mus musculus GN=Eif2s2 PE=1 SV=1 - [IF2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,279E7	1,732E7	1,940E7	Eif2s2
P62315	Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrp1 PE=1 SV=1 - [SMD1_MOUSE]	0,000E0	0,000E0	2,089E6	9,435E6	1,590E7	2,582E7	Snrp1
P62192	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1 - [PRS4_MOUSE]	0,000E0	0,000E0	0,000E0	5,738E6	1,003E7	1,440E7	Psmc1
P17918	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2 - [PCNA_MOUSE]	0,000E0	0,000E0	8,188E5	1,183E7	1,534E7	2,127E7	Pcna
Q3JUQ2	F-BAR domain only protein 2 OS=Mus musculus GN=Fcho2 PE=1 SV=1 - [FCHO2_MOUSE]	0,000E0	0,000E0	0,000E0	3,931E7	6,535E7	6,284E7	Fcho2
Q99K51	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 - [PLST_MOUSE]	0,000E0	0,000E0	0,000E0	8,897E6	2,724E7	3,385E7	Pls3
Q9DB05	Alpha-soluble NSF attachment protein OS=Mus musculus GN=Napa PE=1 SV=1 - [SNAA_MOUSE]	0,000E0	0,000E0	0,000E0	7,134E6	8,855E6	1,656E7	Napa
P57776-2	Isoform 2 of Elongation factor 1-delta OS=Mus musculus GN=Eef1d - [EF1D_MOUSE]	0,000E0	0,000E0	0,000E0	2,851E7	2,366E7	9,933E7	Eef1d
Q9DC14	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2 - [EIF3F_MOUSE]	0,000E0	0,000E0	0,000E0	2,204E7	3,839E7	9,736E7	Eif3f
Q8C7U1	NEDD4-binding protein 3 OS=Mus musculus GN=Nbp3 PE=1 SV=1 - [NBP3_MOUSE]	0,000E0	0,000E0	0,000E0	1,985E7	4,326E7	4,841E7	N4bp3
P40124	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4 - [CAP1_MOUSE]	0,000E0	0,000E0	0,000E0	3,900E6	8,752E6	9,536E6	Cap1
P14115	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=1 SV=5 - [RL27A_MOUSE]	0,000E0	0,000E0	3,543E5	1,074E8	2,647E8	4,072E8	Rpl27a
Q6A065	Centrosomal protein of 170 kDa OS=Mus musculus GN=Cep170 PE=1 SV=2 - [CE170_MOUSE]	0,000E0	0,000E0	2,926E5	3,143E7	3,321E7	3,629E7	Cep170
P25911-2	Isoform 2 of Tyrosine-protein kinase Lyn OS=Mus musculus GN=Lyn - [LYN_MOUSE]	0,000E0	0,000E0	0,000E0	1,185E7	2,666E7	6,034E7	Lyn
P35293	Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=1 SV=2 - [RAB18_MOUSE]	0,000E0	0,000E0	0,000E0	3,896E6	2,097E7	1,646E7	Rab18
P26039	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2 - [TLN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,185E7	3,566E7	6,755E7	Tln1
Q9D6Z1	Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2 - [NOP56_MOUSE]	0,000E0	0,000E0	0,000E0	5,334E6	1,353E7	3,920E7	Nop56
Q9R0P5	Destrin OS=Mus musculus GN=Dstrn PE=1 SV=3 - [DEST_MOUSE]	0,000E0	0,000E0	0,000E0	7,401E6	4,813E7	5,375E7	Dstrn
Q922B2	Aspartate--tRNA ligase, cytoplasmic OS=Mus musculus GN=Dars PE=1 SV=2 - [SYDC_MOUSE]	0,000E0	0,000E0	0,000E0	8,969E6	2,554E7	5,697E7	Dars
Q7TMK9-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncr1 - [HNRPQ_MOUSE]	0,000E0	0,000E0	0,000E0	3,354E7	6,045E7	1,287E8	Syncr1
Q8R361	Rab11 family-interacting protein 5 OS=Mus musculus GN=Rab11fp5 PE=1 SV=2 - [RFIP5_MOUSE]	0,000E0	0,000E0	0,000E0	1,404E7	3,032E7	5,150E7	Rab11fp5
P46935	E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3 - [NEDD4_MOUSE]	0,000E0	0,000E0	0,000E0	1,561E7	2,262E7	2,872E7	Nedd4
Q61166	Microtubule-associated protein RP/EB family member 1 OS=Mus musculus GN=Mapre1 PE=1 SV=3 - [MARE1_MOUSE]	0,000E0	0,000E0	0,000E0	4,351E6	1,225E7	1,624E7	Mapre1
Q8R411	Myc target protein 1 OS=Mus musculus GN=Myct1 PE=1 SV=1 - [MYCT1_MOUSE]	0,000E0	0,000E0	1,124E5	1,514E8	3,331E8	2,796E8	Myct1
Q9QYQ0	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1 - [DNAJ2_MOUSE]	0,000E0	0,000E0	0,000E0	2,477E7	5,809E7	8,467E7	Dnaja2
P35922-3	Isoform 3 of Synaptic functional regulator FMR1 OS=Mus musculus GN=Fmr1 - [FMR1_MOUSE]	0,000E0	0,000E0	1,048E6	6,566E7	1,602E8	3,140E8	Fmr1
Q9D8N0	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 - [EF1G_MOUSE]	0,000E0	0,000E0	1,369E6	5,285E7	9,319E7	1,575E8	Eef1g
Q9DC51	Guanine nucleotide-binding protein G(k) subunit alpha OS=Mus musculus GN=Gnai3 PE=1 SV=3 - [GNAI3_MOUSE]	0,000E0	0,000E0	7,794E4	3,831E7	1,634E8	7,500E7	Gnai3
P49312	Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnmpa1 PE=1 SV=2 - [ROA1_MOUSE]	0,000E0	0,000E0	2,262E6	6,352E7	6,110E7	1,429E8	Hnmpa1
Q91W92	Cdc42 effector protein 1 OS=Mus musculus GN=Cdc42ep1 PE=1 SV=1 - [BORGS_MOUSE]	0,000E0	0,000E0	0,000E0	1,837E7	3,988E7	4,361E7	Cdc42ep1
P97379	Ras GTPase-activating protein-binding protein 2 OS=Mus musculus GN=G3bp2 PE=1 SV=2 - [G3BP2_MOUSE]	0,000E0	0,000E0	5,026E6	3,650E7	7,730E7	1,353E8	G3bp2

P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3 - [GBB1_MOUSE]	0,000E0	0,000E0	2,238E6	8,151E7	1,097E8	1,052E8	Gnb1
Q9QZ06	Toll-interacting protein OS=Mus musculus GN=ToIip PE=1 SV=1 - [TOLIP_MOUSE]	0,000E0	0,000E0	0,000E0	8,920E6	3,551E7	4,536E7	Tollip
Q50136	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=1 SV=1 - [DDX17_MOUSE]	0,000E0	0,000E0	0,000E0	1,227E8	3,091E8	3,813E8	Ddx17
P56873	Sjogren syndrome/scleroderma autoantigen 1 homolog OS=Mus musculus GN=Ssca1 PE=1 SV=1 - [SSA27_MOUSE]	0,000E0	0,000E0	0,000E0	4,624E6	8,224E6	8,401E6	Ssca1
Q91267	SLIT-ROBO Rho GTPase-activating protein 2 OS=Mus musculus GN=Srgap2 PE=1 SV=2 - [SRGP2_MOUSE]	0,000E0	0,000E0	3,662E5	3,400E7	5,991E7	5,075E7	Srgap2
Q6PGB6-3	Isoform 3 of N-alpha-acetyltransferase 50 OS=Mus musculus GN=Naa50 - [NAA50_MOUSE]	0,000E0	0,000E0	0,000E0	6,866E5	2,613E6	5,084E6	Naa50
Q60865	Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2 - [CAPR1_MOUSE]	0,000E0	0,000E0	6,825E4	2,103E8	4,260E8	9,731E8	Caprin1
Q8CHP5-2	Isoform 2 of Partner of Y14 and mago OS=Mus musculus GN=Pym1 - [PYM1_MOUSE]	0,000E0	0,000E0	1,961E5	2,149E6	4,501E6	1,344E7	Pym1
Q9QX56-3	Isoform E2 of Drebrin OS=Mus musculus GN=Dbrn1 - [DREB_MOUSE]	0,000E0	0,000E0	5,168E7	1,054E8	2,197E8	2,197E8	Dbrn1
Q8R1A4-2	Isoform 2 of Dedicator of cytokinesis protein 7 OS=Mus musculus GN=Dock7 - [DOCK7_MOUSE]	0,000E0	0,000E0	0,000E0	3,671E7	8,172E7	8,590E7	Dock7
P48024	Eukaryotic translation initiation factor 1 OS=Mus musculus GN=Eif1 PE=1 SV=2 - [EIF1_MOUSE]	0,000E0	0,000E0	0,000E0	3,642E5	1,994E6	6,159E6	Eif1
Q9D086	Protein PBDC1 OS=Mus musculus GN=Pbdc1 PE=1 SV=1 - [PBDC1_MOUSE]	0,000E0	0,000E0	0,000E0	4,026E5	3,951E6	7,323E6	Pbdc1
P62754	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 - [RS6_MOUSE]	0,000E0	0,000E0	2,070E6	6,530E7	2,832E8	7,990E8	Rps6
Q35295	Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3 - [PURB_MOUSE]	0,000E0	0,000E0	4,627E6	1,351E7	5,019E7	5,019E7	Purb
P25911	Tyrosine-protein kinase Lyn OS=Mus musculus GN=Lyn PE=1 SV=4 - [LYN_MOUSE]	0,000E0	0,000E0	0,000E0	1,185E7	2,666E7	6,034E7	Lyn
P58468	Protein FAM207A OS=Mus musculus GN=Fam207a PE=1 SV=1 - [F207A_MOUSE]	0,000E0	0,000E0	0,000E0	6,126E6	7,327E6	5,908E7	Fam207a
O08992	Syntenin-1 OS=Mus musculus GN=Sdcbp PE=1 SV=1 - [SDCB1_MOUSE]	0,000E0	0,000E0	0,000E0	4,975E7	1,798E7	8,151E7	Sdcbp
Q8K1N2	Pleckstrin homology-like domain family B member 2 OS=Mus musculus GN=Phldb2 PE=1 SV=2 - [PHLB2_MOUSE]	0,000E0	0,000E0	0,000E0	1,612E7	1,964E7	3,291E7	Phldb2
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha Isoform OS=Mus musculus GN=Ppp2ca PE=1 SV=1 - [PP2AA_MOUSE]	0,000E0	0,000E0	0,000E0	1,422E7	1,728E7	1,129E7	Ppp2ca
P83882	60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=2 - [RL36A_MOUSE]	0,000E0	0,000E0	3,401E6	1,254E8	2,063E8	5,486E8	Rpl36a
O54824-2	Isoform 2 of Pro-interleukin-16 OS=Mus musculus GN=Il16 - [IL16_MOUSE]	0,000E0	0,000E0	0,000E0	5,722E7	5,224E7	5,908E7	Il16
O70325-2	Isoform Cytoplasmic of Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Mus musculus GN=Gpx4 - [GPX4_MOUSE]	0,000E0	0,000E0	0,000E0	5,742E6	1,710E6	1,312E7	Gpx4
O89086	RNA-binding protein 3 OS=Mus musculus GN=Rbm3 PE=1 SV=1 - [RBM3_MOUSE]	0,000E0	0,000E0	0,000E0	2,435E7	4,328E7	7,787E7	Rbm3
Q8CC35-2	Isoform 2 of Synaptopodin OS=Mus musculus GN=Synpo - [SYNPO_MOUSE]	0,000E0	0,000E0	0,000E0	8,920E6	1,585E7	3,134E7	Synpo
Q9QC65	S-methyl-5'-thiodenosine phosphorylase OS=Mus musculus GN=Mtap PE=1 SV=1 - [MTAP_MOUSE]	0,000E0	0,000E0	0,000E0	1,504E7	2,064E7	1,153E7	Mtap
Q9DBV8	Nuclear valosin-containing protein-like OS=Mus musculus GN=Nvl PE=1 SV=1 - [NVL_MOUSE]	0,000E0	0,000E0	0,000E0	7,359E6	1,504E7	3,411E7	Nvl
O54833	Casein kinase II subunit alpha' OS=Mus musculus GN=Csk2a2 PE=1 SV=1 - [CSK22_MOUSE]	0,000E0	0,000E0	6,999E6	7,068E6	2,742E7	2,742E7	Cskn2a2
P55284	Cadherin-5 OS=Mus musculus GN=Cdh5 PE=1 SV=2 - [CADH5_MOUSE]	0,000E0	0,000E0	0,000E0	1,798E8	2,365E8	1,645E8	Cdh5
Q9QUR7	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Mus musculus GN=Pin1 PE=1 SV=1 - [PIN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,972E6	1,882E6	1,479E6	Pin1
Q9Z108	Double-stranded RNA-binding protein Staufin homolog 1 OS=Mus musculus GN=Stau1 PE=1 SV=1 - [STAU1_MOUSE]	0,000E0	0,000E0	0,000E0	1,767E7	3,046E7	5,957E7	Stau1
P27546-3	Isoform 3 of Microtubule-associated protein 4 OS=Mus musculus GN=Map4 - [MAP4_MOUSE]	0,000E0	0,000E0	0,000E0	6,365E6	2,015E7	2,944E7	Map4
Q9J3A9	General receptor for phosphoinositides 1-associated scaffold protein OS=Mus musculus GN=Grasp PE=1 SV=2 - [GRASP_MOUSE]	0,000E0	0,000E0	0,000E0	5,810E6	8,331E6	2,913E7	Grasp
Q3UTJ2-3	Isoform 3 of Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 - [SRBS2_MOUSE]	0,000E0	0,000E0	0,000E0	3,852E6	1,294E7	1,957E7	Sorbs2
Q9D0T1	NHP2-like protein 1 OS=Mus musculus GN=Snu13 PE=1 SV=4 - [NH2L1_MOUSE]	0,000E0	0,000E0	0,000E0	3,638E6	5,437E6	1,946E7	Snu13
P12399	Protein CTLA-2 alpha OS=Mus musculus GN=Ctla2a PE=2 SV=2 - [CTLA2_MOUSE]	0,000E0	0,000E0	0,000E0	1,371E7	2,130E7	2,974E6	Ctla2a
Q9WXT6	Cullin-1 OS=Mus musculus GN=Cul1 PE=1 SV=1 - [CULL1_MOUSE]	0,000E0	0,000E0	0,000E0	2,746E7	2,275E7	3,225E7	Cul1
P62267	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=1 SV=3 - [RS23_MOUSE]	0,000E0	0,000E0	0,000E0	1,824E8	3,247E8	6,382E8	Rps23
Q9Z1M7	Protein FAM49B OS=Mus musculus GN=Fam49b PE=1 SV=1 - [FA49B_MOUSE]	0,000E0	0,000E0	0,000E0	5,147E6	1,069E7	1,774E7	Fam49b
Q8BFY7	Protein FAM64A OS=Mus musculus GN=Fam64a PE=1 SV=1 - [FA64A_MOUSE]	0,000E0	0,000E0	0,000E0	8,115E6	1,556E7	1,863E7	Fam64a
Q9WUM3	Coronin-1B OS=Mus musculus GN=Coro1b PE=1 SV=1 - [COR1B_MOUSE]	0,000E0	0,000E0	0,000E0	7,533E6	3,962E7	7,708E7	Coro1b
Q91Z96	BMP-2-inducible protein kinase OS=Mus musculus GN=Bmp2k PE=1 SV=1 - [BMP2K_MOUSE]	0,000E0	0,000E0	0,000E0	4,933E7	9,379E7	8,089E7	Bmp2k
Q8CGB3	Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Mus musculus GN=Uaca PE=1 SV=2 - [UACA_MOUSE]	0,000E0	0,000E0	0,000E0	3,024E7	5,798E7	6,492E7	Uaca
Q9QCQ1	Ras-related protein Rab-5A OS=Mus musculus GN=Rab5a PE=1 SV=1 - [RAB5A_MOUSE]	0,000E0	0,000E0	0,000E0	1,978E6	2,563E7	3,682E7	Rab5a
P62867	40S ribosomal protein S30 OS=Mus spicilegus GN=Fau PE=3 SV=1 - [RS30_MUSST]	0,000E0	0,000E0	0,000E0	3,120E7	2,086E8	2,241E8	Fau
P70313	Nitric oxide synthase, endothelial OS=Mus musculus GN=Nos3 PE=1 SV=4 - [NOS3_MOUSE]	0,000E0	0,000E0	0,000E0	5,605E7	1,240E8	1,950E8	Nos3
Q6PHN9	Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE=1 SV=1 - [RAB35_MOUSE]	0,000E0	0,000E0	3,456E3	6,493E7	1,449E8	2,096E8	Rab35
Q8C863	E3 ubiquitin-protein ligase Itchy OS=Mus musculus GN=Itch PE=1 SV=2 - [ITCH_MOUSE]	0,000E0	0,000E0	0,000E0	1,676E7	5,431E7	5,098E7	Itch
Q9JLB2	MAGUK p55 subfamily member 5 OS=Mus musculus GN=Mpp5 PE=1 SV=1 - [MPP5_MOUSE]	0,000E0	0,000E0	0,000E0	1,155E7	1,314E7	6,369E6	Mpp5
Q6PAM1	Alpha-taxilin OS=Mus musculus GN=Tlxna PE=1 SV=1 - [TXLNA_MOUSE]	0,000E0	0,000E0	0,000E0	1,945E7	2,437E7	4,189E7	Tlxna
Q99020	Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnnpab PE=1 SV=1 - [ROAA_MOUSE]	0,000E0	0,000E0	1,457E6	1,603E7	6,814E7	1,107E8	Hnnpab
Q9Z511	ATPase family AAA domain-containing protein 3 OS=Mus musculus GN=Atad3 PE=1 SV=1 - [ATAD3_MOUSE]	0,000E0	0,000E0	0,000E0	1,707E7	3,857E7	4,622E7	Atad3
P15864	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2 - [H12_MOUSE]	0,000E0	0,000E0	6,982E5	6,443E7	1,356E8	3,936E8	Hist1h1c
Q8QX85	28S ribosomal protein S7, mitochondrial OS=Mus musculus GN=Mps7 PE=1 SV=1 - [RT07_MOUSE]	0,000E0	0,000E0	0,000E0	2,532E6	4,189E6	6,744E6	Mps7
Q9D824-4	Isoform 4 of Pre-mRNA 3'-end-processing factor FIP1 OS=Mus musculus GN=Fip1l1 - [FIP1_MOUSE]	0,000E0	0,000E0	0,000E0	5,832E6	1,672E7	8,311E6	Fip1l1
Q3JUZ2-2	Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfip1 - [LRRF1_MOUSE]	0,000E0	0,000E0	0,000E0	4,588E7	9,723E7	1,245E8	Lrrfip1
O35643	AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=2 - [APB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,272E8	3,054E8	3,824E8	Ap1b1
Q9CSN1	SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3 - [SNW1_MOUSE]	0,000E0	0,000E0	0,000E0	3,256E6	5,669E6	1,096E7	Snw1
Q8C111	Guanine nucleotide-binding protein-like 3 OS=Mus musculus GN=Gnl3 PE=1 SV=2 - [GNL3_MOUSE]	0,000E0	0,000E0	0,000E0	1,329E7	2,000E7	4,750E7	Gnl3
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnnpu PE=1 SV=1 - [HNRPU_MOUSE]	0,000E0	0,000E0	0,000E0	5,206E7	1,019E8	9,049E7	Hnnpu
P34022	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2 - [RANG_MOUSE]	0,000E0	0,000E0	0,000E0	5,821E6	2,511E7	1,554E7	Ranbp1
Q8CBW3-5	Isoform 5 of Abl interactor 1 OS=Mus musculus GN=Abi1 - [ABI1_MOUSE]	0,000E0	0,000E0	0,000E0	1,595E7	5,288E7	6,136E7	Abi1
Q9Z315	U4/U6.U5 tri-snRNP-associated protein 1 OS=Mus musculus GN=Sart1 PE=1 SV=1 - [SNUT1_MOUSE]	0,000E0	0,000E0	0,000E0	4,632E6	7,366E6	1,288E7	Sart1
Q3JUB9-2	Isoform 2 of Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 - [EDC4_MOUSE]	0,000E0	0,000E0	0,000E0	1,246E7	3,479E7	5,171E7	Edc4
Q60631	Growth factor receptor-bound protein 2 OS=Mus musculus GN=Grb2 PE=1 SV=1 - [GRB2_MOUSE]	0,000E0	0,000E0	0,000E0	6,084E6	2,165E7	6,661E6	Grb2
Q91VH2	Sorting nexin-9 OS=Mus musculus GN=Snx9 PE=1 SV=1 - [SNX9_MOUSE]	0,000E0	0,000E0	0,000E0	4,403E7	6,422E7	1,053E8	Snx9
Q9QY13	DnaJ homolog subfamily C member 7 OS=Mus musculus GN=Dnajc7 PE=1 SV=2 - [DNJC7_MOUSE]	0,000E0	0,000E0	0,000E0	3,884E6	1,192E7	9,746E6	Dnajc7
Q9JM76	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=3 - [ARPC3_MOUSE]	0,000E0	0,000E0	7,380E5	9,633E7	1,244E8	4,962E7	Arpc3
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1 - [AT1A1_MOUSE]	0,000E0	0,000E0	1,542E7	3,807E7	5,302E7	5,302E7	Atp1a1
Q5SV80	Unconventional myosin-XIX OS=Mus musculus GN=Myo19 PE=2 SV=1 - [MYO19_MOUSE]	0,000E0	0,000E0	0,000E0	1,546E7	4,680E7	1,137E8	Myo19
Q8BP92	Reticulocalbin-2 OS=Mus musculus GN=Rcn2 PE=1 SV=1 - [RCN2_MOUSE]	0,000E0	0,000E0	0,000E0	6,868E6	7,837E6	9,801E6	Rcn2
Q3JUP5	Zinc finger CCOH-type antiviral protein 1 OS=Mus musculus GN=Zc3hav1 PE=1 SV=1 - [ZCCH_MOUSE]	0,000E0	0,000E0	0,000E0	1,162E7	3,385E7	5,499E7	Zc3hav1
Q9D7X3	Dual specificity protein phosphatase 3 OS=Mus musculus GN=Dusp3 PE=1 SV=1 - [DUS3_MOUSE]	0,000E0	0,000E0	0,000E0	5,026E6	1,652E7	1,630E7	Dusp3
Q8BGD9	Eukaryotic translation initiation factor 4B OS=Mus musculus GN=Eif4b PE=1 SV=1 - [IF4B_MOUSE]	0,000E0	0,000E0	0,000E0	2,896E7	7,821E7	1,342E8	Eif4b
P19324	Serpin H1 OS=Mus musculus GN=Serpinh1 PE=1 SV=3 - [SERPH_MOUSE]	0,000E0	0,000E0	0,000E0	1,283E7	2,961E7	6,453E7	Serpinh1
Q99JK4	Eukaryotic translation initiation factor 3 subunit M OS=Mus musculus GN=Eif3m PE=1 SV=1 - [EIF3M_MOUSE]	0,000E0	0,000E0	0,000E0	2,294E6	1,269E7	2,249E7	Eif3m
Q99K43	Protein regulator of cytokinesis 1 OS=Mus musculus GN=Prc1 PE=1 SV=2 - [PRC1_MOUSE]	0,000E0	0,000E0	0,000E0	9,965E6	2,177E7	5,021E7	Prc1
Q61510	E3 ubiquitin/ISG15 ligase TRIM25 OS=Mus musculus GN=Trim25 PE=1 SV=2 - [TRIZ5_MOUSE]	0,000E0	0,000E0	0,000E0	3,692E6	9,474E6	1,924E7	Trim25
P27773	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2 - [PDIA3_MOUSE]	0,000E0	0,000E0	0,000E0	7,711E6	1,708E7	2,700E7	Pdia3
Q9JMB0	G kinase-anchoring protein 1 OS=Mus musculus GN=Gkap1 PE=1 SV=1 - [GKAP1_MOUSE]	0,000E0	0,000E0	0,000E0	4,392E6	8,445E6	2,065E7	Gkap1
Q9CQW9	Interferon-induced transmembrane protein 3 OS=Mus musculus GN=Ifitm3 PE=1 SV=1 - [IFM3_MOUSE]	0,000E0	0,000E0	0,000E0	5,875E7	1,817E8	3,251E8	Ifitm3
P49710	Hematopoietic lineage cell-specific protein OS=Mus musculus GN=Hcls1 PE=1 SV=2 - [HCLSL_MOUSE]	0,000E0	0,000E0	0,000E0	5,149E6	3,039E7	4,934E7	Hcls1
P63024	Vesicle-associated membrane protein 3 OS=Mus musculus GN=Vamp3 PE=1 SV=1 - [VAMP3_MOUSE]	0,000E0	0,000E0	0,000E0	8,104E6	2,040E7	3,192E7	Vamp3
Q61990-2	Isoform 2 of Poly(C)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=2 - [PCBP2_MOUSE]	0,000E0	0,000E0	0,000E0	2,185E7	4,015E7	1,195E8	Pcbp2
Q99KN9	Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=2 - [EPN4_MOUSE]	0,000E0	0,000E0	0,000E0	5,761E7	1,243E8	1,776E8	Clint1
Q9WV95	Pleckstrin homology-like domain family A member 3 OS=Mus musculus GN=Phlda3 PE=1 SV=1 - [PHLA3_MOUSE]	0,000E0	0,000E0	0,000E0	8,774E6	9,073E6	2,023E7	Phlda3
P98083-2	Isoform p52Shc of SHC-transforming protein 1 OS=Mus musculus GN=Shc1 - [SHC1_MOUSE]	0,000E0	0,000E0	0,000E0	2,970E5	9,397E6	8,707E6	Shc1
Q6A0D4	Raftlin OS=Mus musculus GN=Rftn1 PE=1 SV=4 - [RFTN1_MOUSE]	0,000E0	0,000E0	2,147E5	3,394E6	1,906E7	2,461E7	Rftn1
P24369	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=PpiB PE=1 SV=2 - [PPIB_MOUSE]	0,000E0	0,000E0	0,000E0	2,723E6	4,032E6	9,577E6	PpiB
Q7TM88	Cytoplasmic FMRI-interacting protein 1 OS=Mus musculus GN=Cyfp1 PE=1 SV=1 - [CYFP1_MOUSE]	0,000E0	0,000E0	1,055E4	3,183E7	7,211E7	1,079E8	Cyfp1
Q8CGB6-2	Isoform 2 of Tensin-2 OS=Mus musculus GN=Tns2 - [TNS2_MOUSE]	0,000E0	0,000E0	0,000E0	1,830E7	2,899E7	6,879E7	Tns2
Q8OUG5-3	Isoform 3 of Septin-9 OS=Mus musculus GN=Sept9 - [SEPT9_MOUSE]	0,000E0	0,000E0	9,735E6	3,039E7	4,188E7	4,188E7	SEPT9
Q8BIE6	FERM domain-containing protein 4A OS=Mus musculus GN=Frm4a PE=1 SV=2 - [FRM4A_MOUSE]	0,000E0	0,000E0	0,000E0	1,217E7	2,155E7	3,558E7	Frm4a
P21279	Guanine nucleotide-binding protein G(q) subunit alpha OS=Mus musculus GN=Gnaq PE=1 SV=4 - [GNAQ_MOUSE]	0,000E0	0,000E0	0,000E0	7,952E6	1,498E7	6,855E7	Gnaq

Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog OS=Mus musculus GN=Vta1 PE=1 SV=1 - [VTA1_MOUSE]	0,000E0	0,000E0	0,000E0	7,016E6	2,514E7	2,132E7	Vta1
Q8CGC4	Protein LSM14 homolog B OS=Mus musculus GN=Lsm14b PE=1 SV=3 - [LS14B_MOUSE]	0,000E0	0,000E0	0,000E0	5,806E6	1,099E7	2,024E7	Lsm14b
Q09131	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2 - [GSTO1_MOUSE]	0,000E0	0,000E0	0,000E0	2,292E6	6,208E6	3,993E6	Gsto1
Q8C8U-3	Isomform 3 of Liprin-beta-1 OS=Mus musculus GN=Ppfbp1 - [LIPB1_MOUSE]	0,000E0	0,000E0	0,000E0	6,686E6	2,453E7	2,451E7	Ppfbp1
Q5Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked OS=Mus musculus GN=EIF2s3x PE=1 SV=2 - [IF2G_MOUSE]	0,000E0	0,000E0	0,000E0	2,187E7	4,219E7	1,079E8	Elf2s3x
Q3TWW8	Serine/arginine-rich splicing factor 6 OS=Mus musculus GN=Srsf6 PE=1 SV=1 - [SRSF6_MOUSE]	0,000E0	0,000E0	0,000E0	6,749E7	9,168E7	1,266E8	Srsf6
Q9DC2B-2	Isomform 2 of Casein kinase I isomform delta OS=Mus musculus GN=Csnk1d - [KC1D_MOUSE]	0,000E0	0,000E0	0,000E0	1,802E7	1,701E7	5,040E7	Csnk1d
Q9Z122	Serine-threonine kinase receptor-associated protein OS=Mus musculus GN=Strap PE=1 SV=2 - [STRAP_MOUSE]	0,000E0	0,000E0	0,000E0	2,811E6	9,091E6	1,280E7	Strap
Q9D019	Arginine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Rars PE=1 SV=2 - [SYRC_MOUSE]	0,000E0	0,000E0	0,000E0	1,698E7	4,400E7	4,834E7	Rars
Q7T7SC1	Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1 - [PRC2A_MOUSE]	0,000E0	0,000E0	0,000E0	1,548E7	2,932E7	5,129E7	Prrc2a
Q9Z1X4-2	Isomform 2 of Interleukin enhancer-binding factor 3 OS=Mus musculus GN=Ilf3 - [ILF3_MOUSE]	0,000E0	0,000E0	0,000E0	1,067E7	2,008E7	3,246E7	Ilf3
P08032	Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Spta1 PE=1 SV=3 - [SPTA1_MOUSE]	0,000E0	0,000E0	0,000E0	5,728E6	3,475E7	1,557E7	Spta1
P59325	Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Elf5 PE=1 SV=1 - [IF5_MOUSE]	0,000E0	0,000E0	0,000E0	1,703E7	1,619E7	1,360E7	Elf5
Q9QX04	Calcium-binding mitochondrial carrier protein Arala2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1 - [CMC2_MOUSE]	0,000E0	0,000E0	0,000E0	4,422E6	6,795E6	1,149E7	Slc25a13
P70452	Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1 - [STX4_MOUSE]	0,000E0	0,000E0	0,000E0	1,853E7	3,916E7	6,333E7	Stx4
Q9D735	Uncharacterized protein C19orf43 homolog OS=Mus musculus PE=1 SV=1 - [CS043_MOUSE]	0,000E0	0,000E0	0,000E0	2,063E6	1,013E7	2,284E6	CS043
Q91VC3	Eukaryotic initiation factor 4A-III OS=Mus musculus GN=Elf4a3 PE=1 SV=3 - [IF4A3_MOUSE]	0,000E0	0,000E0	0,000E0	1,511E7	9,340E7	6,129E7	Elf4a3
Q7M6Y3-6	Isomform 6 of Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm - [PICAL_MOUSE]	0,000E0	0,000E0	0,000E0	5,366E7	5,766E7	8,626E7	Picalm
Q08553	Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2 - [DPYL2_MOUSE]	0,000E0	0,000E0	0,000E0	3,094E6	5,656E6	2,043E7	Dpysl2
Q9J72-4	Isomform 4 of DNA c->du-editing enzyme APOBEC3 OS=Mus musculus GN=Apobec3 - [ABEC3_MOUSE]	0,000E0	0,000E0	0,000E0	1,687E7	3,229E7	6,607E7	Apobec3
PE2835	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1 - [RAP1A_MOUSE]	0,000E0	0,000E0	0,000E0	1,164E7	4,687E7	6,988E7	Rap1a
Q6PH22-2	Isomform 2 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Mus musculus GN=Camk2d - [KCC2D_MOUSE]	0,000E0	0,000E0	0,000E0	1,122E7	2,205E7	5,066E7	Camk2d
Q3UMF0-3	Isomform 3 of Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobl1 - [COBL1_MOUSE]	0,000E0	0,000E0	0,000E0	5,329E6	8,762E6	1,537E7	Cobl1
P4693B-2	Isomform 2 of Transcriptional coactivator YAP1 OS=Mus musculus GN=Yap1 - [YAP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,125E7	2,034E7	2,711E7	Yap1
D08664	B-cell CLL/lymphoma 7 protein family member C OS=Mus musculus GN=Bcl7c PE=1 SV=1 - [BCL7C_MOUSE]	0,000E0	0,000E0	0,000E0	4,896E6	1,098E7	2,133E7	Bcl7c
Q9JLJ0	CTTNBP2 N-terminal-like protein OS=Mus musculus GN=Ctnb2nl PE=1 SV=1 - [CT2NL_MOUSE]	0,000E0	0,000E0	0,000E0	4,181E6	1,498E7	1,145E7	Ctnb2nl
Q9CZT6	Protein CMISS1 OS=Mus musculus GN=Cmiss1 PE=2 SV=1 - [CMS1_MOUSE]	0,000E0	0,000E0	0,000E0	4,121E6	6,794E6	6,962E6	Cmiss1
O55131	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1 - [SEPT7_MOUSE]	0,000E0	0,000E0	0,000E0	2,813E7	6,631E7	6,870E7	SEPT7
Q8CAQ8-2	Isomform 2 of MICOS complex subunit Mic60 OS=Mus musculus GN=Immt - [MIC60_MOUSE]	0,000E0	0,000E0	1,006E6	7,826E6	2,905E7	4,285E7	Immt
O35608	Angiotensin-2 OS=Mus musculus GN=Angpt2 PE=2 SV=2 - [ANGP2_MOUSE]	0,000E0	0,000E0	0,000E0	1,818E7	1,822E7	4,407E7	Angpt2
Q8BHL4	Retinoic acid-induced protein 3 OS=Mus musculus GN=Gprc3a PE=1 SV=1 - [RAI3_MOUSE]	0,000E0	0,000E0	0,000E0	3,834E7	9,301E7	1,499E8	Gprc3a
Q9CQ22	Regulator complex protein LAMTOR1 OS=Mus musculus GN=Lamtor1 PE=1 SV=1 - [LTOR1_MOUSE]	0,000E0	0,000E0	0,000E0	5,700E6	2,655E6	1,469E7	Lamtor1
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Elf3c PE=1 SV=1 - [EIF3C_MOUSE]	0,000E0	0,000E0	1,214E6	3,060E7	4,183E7	8,884E7	Elf3c
Q9CR57	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 SV=3 - [RL14_MOUSE]	0,000E0	0,000E0	2,375E5	9,775E7	1,658E8	3,495E8	Rpl14
Q9R0Y5	Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1 - [KAD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,613E6	2,610E6	3,376E6	Ak1
Q99PU8-2	Isomform 2 of Putative ATP-dependent RNA helicase DHX30 OS=Mus musculus GN=Dhx30 - [DHX30_MOUSE]	0,000E0	0,000E0	0,000E0	6,139E6	1,251E7	2,627E7	Dhx30
Q8BK67	Protein RCC2 OS=Mus musculus GN=Rcc2 PE=1 SV=1 - [RCC2_MOUSE]	0,000E0	0,000E0	0,000E0	1,435E6	7,118E6	1,014E7	Rcc2
Q9DC28	Casein kinase I isoform delta OS=Mus musculus GN=Csnk1d PE=1 SV=2 - [KC1D_MOUSE]	0,000E0	0,000E0	0,000E0	1,802E7	1,827E7	5,035E7	Csnk1d
P21278	Guanine nucleotide-binding protein subunit alpha-11 OS=Mus musculus GN=Gna11 PE=1 SV=1 - [GNA11_MOUSE]	0,000E0	0,000E0	0,000E0	1,313E7	2,392E7	5,427E7	Gna11
P35601-2	Isomform 2 of Replication factor C subunit 1 OS=Mus musculus GN=Rfc1 - [RFC1_MOUSE]	0,000E0	0,000E0	5,241E5	1,702E7	3,416E7	4,237E7	Rfc1
Q08481	Platelet endothelial cell adhesion molecule OS=Mus musculus GN=Pecam1 PE=1 SV=1 - [PECA1_MOUSE]	0,000E0	0,000E0	0,000E0	1,680E7	1,080E8	1,578E8	Pecam1
Q9WVM1	Rac GTPase-activating protein 1 OS=Mus musculus GN=Racgap1 PE=1 SV=1 - [RGAP1_MOUSE]	0,000E0	0,000E0	0,000E0	6,677E6	1,981E7	7,133E7	Racgap1
P13020-2	Isomform 2 of Gelsolin OS=Mus musculus GN=Gen - [GELS_MOUSE]	0,000E0	0,000E0	9,668E6	1,955E7	4,489E7	8,300E7	Gsn
Q7M6Y3-5	Isomform 5 of Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm - [PICAL_MOUSE]	0,000E0	0,000E0	0,000E0	6,471E7	1,028E8	1,098E8	Picalm
PE3028	Translationally-controlled tumor protein OS=Mus musculus GN=Tpt1 PE=1 SV=1 - [TCTP_MOUSE]	0,000E0	0,000E0	0,000E0	6,326E6	3,679E7	9,994E6	Tpt1
Q99J62	Replication factor C subunit 4 OS=Mus musculus GN=Rfc4 PE=1 SV=1 - [RFC4_MOUSE]	0,000E0	0,000E0	0,000E0	3,254E6	2,363E7	4,087E7	Rfc4
Q6P542	ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1 - [ABCF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,163E7	3,402E7	6,852E7	Abcf1
Q9W7X2	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1 - [PRKRA_MOUSE]	0,000E0	0,000E0	0,000E0	8,709E6	7,977E6	3,095E7	Prkra
P19157	Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 - [GSTP1_MOUSE]	0,000E0	0,000E0	0,000E0	6,291E6	2,846E7	1,988E7	Gstp1
Q1W617	Protein Shroom4 OS=Mus musculus GN=Shroom4 PE=1 SV=1 - [SHRM4_MOUSE]	0,000E0	0,000E0	0,000E0	1,488E7	4,474E7	7,397E7	Shroom4
Q8K298	Anillin OS=Mus musculus GN=Anln PE=1 SV=2 - [ANLN_MOUSE]	0,000E0	0,000E0	0,000E0	6,823E6	1,148E7	1,416E7	Anln
Q8VH51-2	Isomform 2 of RNA-binding protein 39 OS=Mus musculus GN=Rbm39 - [RBM39_MOUSE]	1,010E7	0,000E0	2,877E6	6,717E7	1,269E8	2,173E8	Rbm39
Q8VD89	Dedicator of cytokinesis protein 6 OS=Mus musculus GN=Dock6 PE=1 SV=4 - [DOCK6_MOUSE]	0,000E0	0,000E0	0,000E0	2,811E7	5,121E7	6,504E7	Dock6
Q6A028	Switch-associated protein 70 OS=Mus musculus GN=Swap70 PE=1 SV=2 - [SWP70_MOUSE]	0,000E0	0,000E0	0,000E0	7,522E6	1,159E7	2,236E7	Swap70
Q9D1R9	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=1 SV=2 - [RL34_MOUSE]	0,000E0	0,000E0	0,000E0	9,653E7	3,124E8	6,352E8	Rpl34
Q9ESD7-2	Isomform 2 of Dysferlin OS=Mus musculus GN=Dysf - [DYSF_MOUSE]	0,000E0	0,000E0	0,000E0	1,472E7	2,247E7	1,128E8	Dysf
P54775	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2 - [PRS6B_MOUSE]	0,000E0	0,000E0	9,752E5	3,711E6	6,896E6	2,076E6	Psmc4
Q64010-2	Isomform Crk-1 of Adapter molecule crk OS=Mus musculus GN=Crk - [CRK_MOUSE]	0,000E0	0,000E0	0,000E0	1,024E6	3,410E6	6,294E6	Crk
Q60864	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1 - [STIP1_MOUSE]	0,000E0	0,000E0	0,000E0	5,908E6	1,515E7	1,678E7	Stip1
Q62465	Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=1 SV=3 - [VAT1_MOUSE]	0,000E0	0,000E0	0,000E0	1,740E7	3,133E7	3,327E7	Vat1
Q9D0F6	Replication factor C subunit 5 OS=Mus musculus GN=Rfc5 PE=1 SV=1 - [RFC5_MOUSE]	0,000E0	0,000E0	0,000E0	6,434E6	1,869E7	3,372E7	Rfc5
Q8BMA3	Connector enhancer of kinase suppressor of ras 3 OS=Mus musculus GN=Cnksr3 PE=1 SV=1 - [CNKR3_MOUSE]	0,000E0	0,000E0	0,000E0	3,575E6	3,502E7	1,434E7	Cnksr3
Q76M23	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3 - [ZAAA_MOUSE]	0,000E0	0,000E0	0,000E0	2,808E7	6,379E7	7,992E7	Ppp2r1a
Q9ESD07	Dysferlin OS=Mus musculus GN=Dysf PE=1 SV=3 - [DYSF_MOUSE]	0,000E0	0,000E0	0,000E0	1,472E7	2,225E7	1,128E8	Dysf
P52927	High mobility group protein HMGB2 OS=Mus musculus GN=Hmga2 PE=1 SV=1 - [HMG2_MOUSE]	0,000E0	0,000E0	0,000E0	4,944E7	8,353E7	2,038E8	Hmga2
O70492	Sorting nexin-3 OS=Mus musculus GN=Snx3 PE=1 SV=3 - [SNX3_MOUSE]	0,000E0	0,000E0	0,000E0	7,197E5	1,315E7	2,166E7	Snx3
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2 - [FKB1A_MOUSE]	0,000E0	0,000E0	0,000E0	1,798E5	2,116E7	4,437E7	Fkbp1a
PE2852	40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 SV=1 - [RS25_MOUSE]	0,000E0	0,000E0	0,000E0	4,270E8	4,491E8	9,905E8	Rps25
PE2743	AP-2 complex subunit sigma OS=Mus musculus GN=Ap2s1 PE=1 SV=1 - [AP2S1_MOUSE]	0,000E0	0,000E0	0,000E0	1,235E8	9,021E7	8,276E7	Ap2s1
Q6NZK5	Protein hinderin OS=Mus musculus GN=Klaa1328 PE=1 SV=2 - [K1328_MOUSE]	0,000E0	0,000E0	0,000E0	5,606E6	4,169E6	6,911E6	Klaa1328
Q8R4U7	Leucine zipper protein 1 OS=Mus musculus GN=Luzp1 PE=1 SV=2 - [LUZP1_MOUSE]	0,000E0	0,000E0	0,000E0	5,260E6	1,013E7	1,647E7	Luzp1
Q99K85	Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=1 SV=1 - [SERC_MOUSE]	0,000E0	0,000E0	0,000E0	7,764E6	2,652E7	4,732E7	Psat1
Q9E528-4	Isomform D of Rho guanine nucleotide exchange factor 7 OS=Mus musculus GN=Arhgef7 - [ARHG7_MOUSE]	0,000E0	0,000E0	0,000E0	7,933E6	1,967E7	2,425E7	Arhgef7
Q9Z1Y4	Thyroid receptor-interacting protein 6 OS=Mus musculus GN=Trip6 PE=1 SV=1 - [TRIP6_MOUSE]	0,000E0	0,000E0	0,000E0	4,312E6	1,240E7	5,904E6	Trip6
Q9D0I8	mRNA turnover protein 4 homolog OS=Mus musculus GN=Mrto4 PE=1 SV=1 - [MRT4_MOUSE]	0,000E0	0,000E0	0,000E0	2,490E6	1,134E7	2,526E7	Mrto4
Q9D937	Uncharacterized protein C11orf98 homolog OS=Mus musculus PE=1 SV=1 - [CK098_MOUSE]	0,000E0	0,000E0	0,000E0	2,049E7	1,145E7	7,374E7	CK098
Q9CYZ3	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1 - [UBZV1_MOUSE]	0,000E0	0,000E0	0,000E0	5,127E6	1,410E7	2,524E7	Ube2v1
Q99J88	Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1 - [PACN3_MOUSE]	0,000E0	0,000E0	0,000E0	1,013E7	2,183E7	1,543E7	Pacsin3
P43274	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2 - [H14_MOUSE]	0,000E0	0,000E0	6,982E5	5,100E7	1,359E8	3,077E8	Hist1h1e
Q99J93	Interferon-induced transmembrane protein 2 OS=Mus musculus GN=Ifitm2 PE=1 SV=1 - [IFM2_MOUSE]	0,000E0	0,000E0	0,000E0	3,591E6	1,890E8	2,051E8	Ifitm2
Q62188	Dihydropyrimidinase-related protein 3 OS=Mus musculus GN=Dpyls3 PE=1 SV=1 - [DPYL3_MOUSE]	0,000E0	0,000E0	0,000E0	4,926E6	1,162E7	2,964E7	Dpyls3
Q04750	DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2 - [TOP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,463E7	1,640E7	8,076E7	Top1
Q7TQH0-2	Isomform 2 of Ataxin-2-like protein OS=Mus musculus GN=Atxn2l - [ATXL2_MOUSE]	0,000E0	0,000E0	2,775E5	2,831E7	4,559E7	1,007E8	Atxn2l
Q99KY4	Cyclin-G-associated kinase OS=Mus musculus GN=Gak PE=1 SV=2 - [GAK_MOUSE]	0,000E0	0,000E0	0,000E0	3,046E7	2,869E7	4,032E7	Gak
Q6244B-2	Isomform 2 of Eukaryotic translation initiation factor 4 gamma 2 OS=Mus musculus GN=Elf4g2 - [IF4G2_MOUSE]	0,000E0	0,000E0	0,000E0	1,365E7	2,158E7	2,428E7	Elf4g2
Q60634-3	Isomform 3 of Fliotilin-2 OS=Mus musculus GN=Fliot2 - [FLOT2_MOUSE]	0,000E0	0,000E0	0,000E0	7,771E5	6,085E6	3,056E7	Fliot2
P70441	Na ⁺ /H ⁺ exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc3a3r1 PE=1 SV=3 - [NHRF1_MOUSE]	0,000E0	0,000E0	0,000E0	3,953E6	1,152E7	2,282E7	Slc3a3r1
P47955	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1 - [RLP1_MOUSE]	0,000E0	0,000E0	0,000E0	8,722E7	6,232E7	2,633E8	Rplp1
P97479-2	Isomform 2 of Unconventional myosin-VIIa OS=Mus musculus GN=Myo7a - [MYO7A_MOUSE]	2,735E6	0,000E0	0,000E0	1,253E7	2,377E7	4,692E7	Myo7a
Q9WV55	Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2 - [VAPA_MOUSE]	0,000E0	0,000E0	0,000E0	1,038E7	1,461E7	2,391E7	Vapa
Q6472Z	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4 - [VINC_MOUSE]	0,000E0	0,000E0	6,575E5	6,419E6	5,994E6	1,489E7	Vcl
Q8C310	Roundabout homolog 4 OS=Mus musculus GN=Robo4 PE=1 SV=2 - [ROBO4_MOUSE]	0,000E0	0,000E0	0,000E0	1,506E7	3,265E7	4,558E7	Robo4
Q60817	Nascent polypeptide-associated complex subunit alpha OS=Mus musculus GN=Naca PE=1 SV=1 - [NACA_MOUSE]	0,000E0	0,000E0	0,000E0	1,286E8	1,393E8	3,863E8	Naca

Q9WVR4	Fragile X mental retardation syndrome-related protein 2 OS=Mus musculus GN=Fx2 PE=1 SV=1 - [FXR2_MOUSE]	0,000E0	0,000E0	0,000E0	6,711E7	1,504E8	3,104E8	Fxr2
P45377	Alkose reductase-related protein 2 OS=Mus musculus GN=Akr1b8 PE=1 SV=2 - [ALD2_MOUSE]	0,000E0	0,000E0	0,000E0	6,907E6	8,907E6	1,044E7	Akr1b8
Q9CQW1	Synaptobrevin homolog YKT6 OS=Mus musculus GN=Ykt6 PE=1 SV=1 - [YKT6_MOUSE]	0,000E0	0,000E0	0,000E0	2,513E6	6,558E6	1,345E7	Ykt6
Q8C1Q6	Small integral membrane protein 4 OS=Mus musculus GN=Smim4 PE=1 SV=2 - [SMIM4_MOUSE]	0,000E0	0,000E0	0,000E0	5,398E6	4,131E6	2,890E6	Smim4
Q8BVU0	Leucine-rich repeat and calponin homology domain-containing protein 3 OS=Mus musculus GN=Lrch3 PE=1 SV=3 - [LRCH3_MOUSE]	0,000E0	0,000E0	0,000E0	2,790E7	6,295E7	5,882E7	Lrch3
P11103	Poly [ADP-ribose] polymerase 1 OS=Mus musculus GN=Parp1 PE=1 SV=1 - [PARP1_MOUSE]	0,000E0	0,000E0	0,000E0	3,326E7	5,602E7	1,078E8	Parp1
A2A758-2	Isoform 2 of Uncharacterized protein KIAA1522 OS=Mus musculus GN=Kiaa1522 - [K1522_MOUSE]	0,000E0	0,000E0	0,000E0	4,083E6	8,124E6	1,459E7	Kiaa1522
O08967	Cytohesin-3 OS=Mus musculus GN=Cyth3 PE=1 SV=1 - [CYH3_MOUSE]	0,000E0	0,000E0	0,000E0	9,632E6	1,203E7	1,007E7	Cyth3
Q0GNC1	Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1 - [INF2_MOUSE]	0,000E0	0,000E0	0,000E0	1,073E7	2,623E7	3,561E7	Inf2
P55258	Ras-related protein Rab-8A OS=Mus musculus GN=Rab8a PE=1 SV=2 - [RAB8A_MOUSE]	0,000E0	0,000E0	3,456E5	8,538E7	1,285E8	1,853E8	Rab8a
P61028	Ras-related protein Rab-8B OS=Mus musculus GN=Rab8b PE=1 SV=1 - [RAB8B_MOUSE]	0,000E0	0,000E0	3,456E5	8,538E7	1,285E8	1,853E8	Rab8b
P10833	Ras-related protein R-Ras OS=Mus musculus GN=Rras PE=1 SV=1 - [RRAS_MOUSE]	0,000E0	0,000E0	0,000E0	5,125E7	1,417E8	2,087E8	Rras
Q99KP6	Pre-miRNA-processing factor 19 OS=Mus musculus GN=Prpf19 PE=1 SV=1 - [PRP19_MOUSE]	0,000E0	0,000E0	0,000E0	1,126E7	1,887E7	4,198E7	Prpf19
Q8C310-2	Isoform 2 of Roundabout homolog 4 OS=Mus musculus GN=Robo4 - [ROBO4_MOUSE]	0,000E0	0,000E0	0,000E0	1,233E7	3,040E7	3,519E7	Robo4
Q99JF8	PC4 and SFRS1-interacting protein OS=Mus musculus GN=Psp1 PE=1 SV=1 - [PSP1_MOUSE]	0,000E0	0,000E0	0,000E0	4,153E6	1,615E7	3,209E7	Psp1
Q70318	Band 4.1-like protein 2 OS=Mus musculus GN=Epb41f2 PE=1 SV=2 - [E41f2_MOUSE]	0,000E0	0,000E0	0,000E0	1,023E7	3,099E7	3,963E7	Epb41f2
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=2 - [EIF3G_MOUSE]	0,000E0	0,000E0	0,000E0	1,971E7	3,817E7	6,295E7	Eif3g
Q9JIK5	Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3 - [DDX21_MOUSE]	0,000E0	0,000E0	0,000E0	3,983E6	8,756E6	3,872E7	Ddx21
Q8R077	Vacuolar protein sorting-associated protein 37B OS=Mus musculus GN=Vps37b PE=1 SV=1 - [VP37B_MOUSE]	0,000E0	0,000E0	0,000E0	6,840E6	8,000E6	2,561E7	Vps37b
Q62425	Cytochrome c oxidase subunit NDUF4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2 - [NDUA4_MOUSE]	0,000E0	0,000E0	0,000E0	1,639E7	2,127E7	4,603E7	Ndufa4
Q5DTX6	Junctional protein associated with coronary artery disease OS=Mus musculus GN=Jcad PE=1 SV=2 - [JCAD_MOUSE]	0,000E0	0,000E0	0,000E0	2,165E6	1,951E7	4,623E7	Jcad
Q912J6-3	Isoform 3 of Dystonin OS=Mus musculus GN=Dst - [DYST_MOUSE]	0,000E0	0,000E0	0,000E0	1,372E7	2,283E7	1,736E7	Dst
Q9DBY0	EF-hand domain-containing protein D2 OS=Mus musculus GN=Efh2d2 PE=1 SV=1 - [EFHD2_MOUSE]	0,000E0	0,000E0	0,000E0	1,699E6	2,151E7	4,016E7	Efh2d2
Q80X50-2	Isoform 2 of Ubiquitin-associated protein 2-like OS=Mus musculus GN=Ubpap2l - [UBP2L_MOUSE]	0,000E0	0,000E0	0,000E0	2,248E7	2,929E7	5,600E7	Ubpap2l
D0QMC3	Myeloid cell nuclear differentiation antigen-like protein OS=Mus musculus GN=Mndal PE=1 SV=1 - [MNDAL_MOUSE]	0,000E0	0,000E0	0,000E0	1,867E5	9,720E6	1,238E7	Mndal
K3X930	Signal-induced proliferation-associated 1-like protein 3 OS=Mus musculus GN=Spa13 PE=1 SV=1 - [S113_MOUSE]	0,000E0	0,000E0	0,000E0	1,902E7	1,497E7	5,078E7	Spa13
P08207	Protein S100-A10 OS=Mus musculus GN=S100a10 PE=1 SV=2 - [S10AA_MOUSE]	0,000E0	0,000E0	0,000E0	9,947E6	7,128E6	1,307E7	S100a10
Q9CR16	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3 - [PPID_MOUSE]	0,000E0	0,000E0	0,000E0	2,557E6	2,588E6	5,581E6	Ppid
P35550	rRNA 2'-O-methyltransferase fibrillarin OS=Mus musculus GN=Fbl PE=1 SV=2 - [FBL_MOUSE]	0,000E0	0,000E0	0,000E0	9,037E6	2,221E7	5,299E7	Fbl
P56480	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2 - [ATPb_MOUSE]	0,000E0	0,000E0	0,000E0	2,061E6	6,927E6	4,275E6	Atp5b
Q8R1F1	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2 - [NIBL1_MOUSE]	0,000E0	0,000E0	0,000E0	7,346E6	1,495E7	2,254E7	Fam129b
P10630	Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=1 SV=2 - [IF4A2_MOUSE]	0,000E0	0,000E0	0,000E0	3,511E7	9,17E7	7,502E7	Eif4a2
P97863	Nuclear factor 1 B-type OS=Mus musculus GN=Nf1b PE=1 SV=2 - [NFB_MOUSE]	0,000E0	0,000E0	0,000E0	1,739E7	4,045E7	4,062E7	Nf1b
O08585	Clathrin light chain A OS=Mus musculus GN=Cla PE=1 SV=2 - [CLCA_MOUSE]	0,000E0	0,000E0	0,000E0	1,618E8	2,524E8	1,907E8	Cla
PE1089	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1 - [UBE2N_MOUSE]	0,000E0	0,000E0	0,000E0	4,490E6	8,080E6	1,842E7	Ube2n
A2ALU4	Protein Shroom2 OS=Mus musculus GN=Shroom2 PE=1 SV=1 - [SHRM2_MOUSE]	0,000E0	0,000E0	0,000E0	3,672E6	1,142E7	1,142E7	Shroom2
P52293	Importin subunit alpha-1 OS=Mus musculus GN=Kpna2 PE=1 SV=2 - [IMAI_MOUSE]	0,000E0	0,000E0	0,000E0	6,294E6	1,788E7	5,973E7	Kpna2
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1 - [QCR2_MOUSE]	0,000E0	0,000E0	0,000E0	1,047E7	1,787E7	2,301E7	Uqcrc2
Q7T750	Serine/threonine-protein kinase MRCK beta OS=Mus musculus GN=Cdc42bpb PE=1 SV=2 - [MRCKB_MOUSE]	0,000E0	0,000E0	0,000E0	3,322E7	3,905E7	5,367E7	Cdc42bpb
P14685	26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psm3d3 PE=1 SV=3 - [PSMD3_MOUSE]	0,000E0	0,000E0	0,000E0	3,528E6	6,222E6	2,676E6	Psmd3
P16460	Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 - [ASSY_MOUSE]	0,000E0	0,000E0	0,000E0	1,045E6	7,049E6	7,550E6	Ass1
P56389	Cytidine deaminase OS=Mus musculus GN=Cda PE=1 SV=2 - [CDD_MOUSE]	0,000E0	0,000E0	0,000E0	1,768E6	3,275E6	5,216E6	Cda
P25976-2	Isoform UBF2 of Nucleolar transcription factor 1 OS=Mus musculus GN=Ubf1 - [UBF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,807E7	4,107E7	7,156E7	Ubf1
PE1226	Ras-related protein Rap-2b OS=Mus musculus GN=Rap2b PE=1 SV=1 - [RAP2B_MOUSE]	0,000E0	0,000E0	0,000E0	6,647E6	1,636E7	1,418E7	Rap2b
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5 OS=Mus musculus GN=Nudt21 PE=1 SV=1 - [CPSF5_MOUSE]	0,000E0	0,000E0	0,000E0	8,429E6	4,930E6	8,752E6	Nudt21
Q8C132	BAG family molecular chaperone regulator 5 OS=Mus musculus GN=Bag5 PE=1 SV=1 - [BAG5_MOUSE]	0,000E0	0,000E0	0,000E0	1,632E6	5,031E6	7,844E6	Bag5
Q8V136	Paxillin OS=Mus musculus GN=Pxn PE=1 SV=1 - [PAXI_MOUSE]	0,000E0	0,000E0	0,000E0	8,372E6	1,208E7	2,223E7	Pxn
Q9JL15	Galectin-8 OS=Mus musculus GN=Lgals8 PE=1 SV=1 - [LG8_MOUSE]	0,000E0	0,000E0	0,000E0	8,521E6	6,596E6	1,544E7	Lgals8
P42567	Epidermal growth factor receptor substrate 15 OS=Mus musculus GN=Eps15 PE=1 SV=1 - [EPS15_MOUSE]	0,000E0	0,000E0	0,000E0	5,288E6	1,221E7	2,108E6	Eps15
Q9E528-3	Isoform C of Rho guanine nucleotide exchange factor 7 OS=Mus musculus GN=Arhgef7 - [ARHG7_MOUSE]	0,000E0	0,000E0	0,000E0	7,933E6	1,967E7	2,425E7	Arhgef7
Q03963	Interferon-induced, double-stranded RNA-activated protein kinase OS=Mus musculus GN=Eif2ak2 PE=1 SV=2 - [E2AK2_MOUSE]	0,000E0	0,000E0	0,000E0	1,825E7	1,189E7	4,821E7	Eif2ak2
Q3JT26	Protein FAM98A OS=Mus musculus GN=Fam98a PE=1 SV=1 - [FA98A_MOUSE]	0,000E0	0,000E0	0,000E0	1,311E7	3,298E7	5,471E7	Fam98a
Q9CPQ8	ATP synthase subunit g, mitochondrial OS=Mus musculus GN=Atpsl PE=1 SV=1 - [ATPSL_MOUSE]	0,000E0	0,000E0	0,000E0	7,494E6	1,746E6	2,020E6	Atp5l
Q9DBR1	5'-3' exonuclease 2 OS=Mus musculus GN=Xrn2 PE=1 SV=1 - [XRN2_MOUSE]	0,000E0	0,000E0	0,000E0	1,271E7	2,706E7	1,111E7	Xrn2
Q8BMU3	Eukaryotic translation initiation factor 1A, X-chromosomal OS=Mus musculus GN=Eif1ax PE=2 SV=3 - [IF1AX_MOUSE]	0,000E0	0,000E0	0,000E0	5,414E6	2,123E7	5,076E7	Eif1ax
Q5F2E8	Serine/threonine-protein kinase TAO1 OS=Mus musculus GN=Taok1 PE=1 SV=1 - [TAOK1_MOUSE]	0,000E0	0,000E0	8,146E5	7,558E6	3,267E7	9,395E7	Taok1
Q921F4	Heterogeneous nuclear ribonucleoprotein L-like OS=Mus musculus GN=Hnrppl PE=1 SV=3 - [HNRLL_MOUSE]	0,000E0	0,000E0	0,000E0	7,243E6	1,012E7	1,466E7	Hnrppl
Q9DB34	Charged multivesicular body protein 2a OS=Mus musculus GN=Chmp2a PE=1 SV=1 - [CHM2A_MOUSE]	0,000E0	0,000E0	0,000E0	1,985E7	4,101E7	5,862E7	Chmp2a
P49718	DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=1 SV=1 - [MCM5_MOUSE]	0,000E0	0,000E0	0,000E0	1,051E7	2,035E7	2,451E7	Mcm5
P25206	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=1 - [MCM3_MOUSE]	0,000E0	0,000E0	0,000E0	6,610E6	1,312E7	1,015E7	Mcm3
O55135	Eukaryotic translation initiation factor 6 OS=Mus musculus GN=Eif6 PE=1 SV=2 - [IF6_MOUSE]	0,000E0	0,000E0	0,000E0	1,485E7	2,684E7	1,696E7	Eif6
P28660-2	Isoform 2 of Nck-associated protein 1 OS=Mus musculus GN=Nckap1 - [NCKP1_MOUSE]	0,000E0	0,000E0	6,061E5	2,268E7	5,553E7	5,784E7	Nckap1
Q8VJ36	Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1 - [SFPQ_MOUSE]	0,000E0	0,000E0	0,000E0	3,941E7	7,024E7	1,793E8	Sfpq
Q99J38	Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3 - [DCTN2_MOUSE]	0,000E0	0,000E0	0,000E0	1,506E6	5,075E6	3,515E6	Dctn2
Q8C8Y8-2	Isoform 2 of Dynactin subunit 4 OS=Mus musculus GN=Dctn4 - [DCTN4_MOUSE]	0,000E0	0,000E0	0,000E0	3,898E6	4,745E6	1,342E7	Dctn4
Q64012-2	Isoform 1 of RNA-binding protein Raly OS=Mus musculus GN=Raly - [RALY_MOUSE]	0,000E0	0,000E0	0,000E0	1,885E6	1,563E7	2,233E7	Raly
Q91VR8	Protein BRICK1 OS=Mus musculus GN=Brk1 PE=1 SV=1 - [BRK1_MOUSE]	0,000E0	0,000E0	0,000E0	5,373E6	1,025E7	1,071E7	Brk1
Q9Z204-2	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrnpc - [HNRPC_MOUSE]	0,000E0	0,000E0	0,000E0	5,070E6	9,824E5	1,648E7	Hnrnpc
Q8VEE4	Replication protein A 70 kDa DNA-binding subunit OS=Mus musculus GN=Rpa1 PE=1 SV=1 - [RFA1_MOUSE]	0,000E0	0,000E0	0,000E0	4,744E6	8,574E6	3,292E6	Rpa1
Q8R080	G2 and S phase-expressed protein 1 OS=Mus musculus GN=Gtse1 PE=1 SV=2 - [GTSE1_MOUSE]	0,000E0	0,000E0	0,000E0	8,248E6	1,316E7	2,286E7	Gtse1
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0 OS=Mus musculus GN=Hnrpao PE=1 SV=1 - [ROA0_MOUSE]	0,000E0	0,000E0	0,000E0	1,633E7	3,586E7	5,517E7	Hnrnpao
P58137	Acyl-coenzyme A thioesterase 8 OS=Mus musculus GN=Aco8 PE=1 SV=1 - [ACOT8_MOUSE]	0,000E0	0,000E0	0,000E0	4,770E6	3,566E6	1,936E7	Aco8
P27601	Guanine nucleotide-binding protein subunit alpha-13 OS=Mus musculus GN=Gna13 PE=1 SV=1 - [GNA13_MOUSE]	0,000E0	0,000E0	0,000E0	2,341E7	1,140E8	4,388E6	Gna13
Q80XC3	USP6 N-terminal-like protein OS=Mus musculus GN=Usp6nl PE=1 SV=2 - [US6NL_MOUSE]	0,000E0	0,000E0	0,000E0	4,142E6	7,592E6	3,751E7	Usp6nl
Q8VDJ3	Viglin OS=Mus musculus GN=Hdlbp PE=1 SV=1 - [VIGLN_MOUSE]	0,000E0	0,000E0	0,000E0	5,970E6	7,004E6	2,054E7	Hdlbp
Q8CGU1	Calcium-binding and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Calcoo1 PE=1 SV=2 - [CACO1_MOUSE]	0,000E0	0,000E0	0,000E0	1,143E7	1,697E7	2,881E7	Calcoo1
Q66GT5	Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Mus musculus GN=Ptpmt1 PE=1 SV=1 - [PTPM1_MOUSE]	0,000E0	0,000E0	0,000E0	3,818E6	7,785E6	9,755E6	Ptpmt1
G5E829	Plasma membrane calcium-transporting ATPase 1 OS=Mus musculus GN=Atp2b1 PE=1 SV=1 - [AT2B1_MOUSE]	0,000E0	0,000E0	0,000E0	8,901E6	2,316E7	2,315E7	Atp2b1
Q60872	Eukaryotic translation initiation factor 1A OS=Mus musculus GN=Eif1a PE=2 SV=3 - [IF1A_MOUSE]	0,000E0	0,000E0	0,000E0	8,348E6	2,123E7	5,076E7	Eif1a
Q9DB20	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1 - [ATPO_MOUSE]	0,000E0	0,000E0	0,000E0	1,631E6	4,673E6	4,143E6	Atp5o
Q8K124	Pleckstrin homology domain-containing family O member 2 OS=Mus musculus GN=Plekh2 PE=1 SV=1 - [PKHO2_MOUSE]	0,000E0	0,000E0	0,000E0	2,216E6	5,138E6	6,130E6	Plekh2
Q03265	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 - [ATPA_MOUSE]	0,000E0	0,000E0	1,105E6	8,822E6	6,280E6	1,502E7	Atp5a1
Q60766-2	Isoform 2 of Immunity-related GTPase family M protein 1 OS=Mus musculus GN=Irgm1 - [IRGM1_MOUSE]	0,000E0	0,000E0	0,000E0	9,248E6	2,004E7	3,084E7	Irgm1
P56135	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5f2 PE=1 SV=3 - [ATPK_MOUSE]	0,000E0	0,000E0	0,000E0	5,203E6	2,964E7	4,474E7	Atp5f2
Q9NVA3	Mitotic checkpoint protein Bub3 OS=Mus musculus GN=Bub3 PE=1 SV=2 - [BUB3_MOUSE]	0,000E0	0,000E0	0,000E0	6,979E6	1,265E7	2,698E7	Bub3
P54116	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3 - [STOM_MOUSE]	0,000E0	0,000E0	3,789E5	2,246E6	5,342E6	1,535E7	Stom
P10107	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2 - [ANXA1_MOUSE]	0,000E0	0,000E0	0,000E0	1,019E7	1,799E7	1,162E7	Anxa1
P25976	Nucleolar transcription factor 1 OS=Mus musculus GN=Ubf1 PE=1 SV=1 - [UBF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,807E7	4,107E7	7,156E7	Ubf1
Q8BYK6-3	Isoform 3 of YTH domain-containing family protein 3 OS=Mus musculus GN=Ythdf3 - [YTHD3_MOUSE]	0,000E0	0,000E0	5,369E6	1,804E7	1,525E7	1,924E7	Ythdf3
Q9CRB9	MICOS complex subunit Mic19 OS=Mus musculus GN=Chchd3 PE=1 SV=1 - [MIC19_MOUSE]	0,000E0	0,000E0	5,868E5	8,755E6	1,533E7	2,797E7	Chchd3
Q9Z0R6	Intersectin-2 OS=Mus musculus GN=Itsn2 PE=1 SV=2 - [ITSN2_MOUSE]	0,000E0	0,000E0	0,000E0	1,868E7	2,768E7	5,085E7	Itsn2
Q9D1C2	Protein chibby homolog 1 OS=Mus musculus GN=Cby1 PE=1 SV=1 - [CBY1_MOUSE]	0,000E0	0,000E0	0,000E0	1,215E6	3,119E6	4,995E6	Cby1
Q91W59-2	Isoform 2 of RNA-binding motif, single-stranded-interacting protein 1 OS=Mus musculus GN=Rbms1 - [RBMS1_MOUSE]	0,000E0	0,000E0	0,000E0	2,295E6	1,371E7	5,239E7	Rbms1

Q8BP80	MOB kinase activator 1B OS=Mus musculus GN=Mob1b PE=1 SV=3 - [MOB1B_MOUSE]	0,000E0	0,000E0	0,000E0	1,913E7	4,068E7	3,950E7	Mob1b
P62827	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3 - [RAN_MOUSE]	0,000E0	0,000E0	0,000E0	3,064E7	1,239E9	1,129E8	Ran
P26645	Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2 - [MARCS_MOUSE]	0,000E0	0,000E0	0,000E0	4,771E6	6,669E6	9,817E6	Marcks
O08579	Emerin OS=Mus musculus GN=Emd PE=1 SV=1 - [EMD_MOUSE]	0,000E0	0,000E0	0,000E0	3,630E6	9,661E6	1,267E7	Emd
Q8VD24	Palmitoyltransferase ZDHHC5 OS=Mus musculus GN=Zdhhc5 PE=1 SV=1 - [ZDHCS_MOUSE]	0,000E0	0,000E0	0,000E0	3,212E6	6,478E6	1,889E7	Zdhhc5
Q8C2Q3	RNA-binding protein 14 OS=Mus musculus GN=Rbm14 PE=1 SV=1 - [RBM14_MOUSE]	0,000E0	0,000E0	0,000E0	1,986E7	3,339E7	5,818E7	Rbm14
Q4VAA2-2	Isform 2 of Protein CDV3 OS=Mus musculus GN=Cdv3 - [CDV3_MOUSE]	0,000E0	0,000E0	0,000E0	1,485E6	1,485E6	6,074E6	Cdv3
P97477	Aurora kinase A OS=Mus musculus GN=Aurka PE=1 SV=1 - [AURKA_MOUSE]	0,000E0	0,000E0	0,000E0	1,045E6	4,874E6	4,838E6	Aurka
Q9CQM9	Glutaredoxin-3 OS=Mus musculus GN=Glx3 PE=1 SV=1 - [GLRX3_MOUSE]	0,000E0	0,000E0	0,000E0	9,684E6	2,899E7	2,885E7	Glrx3
P35831	Tyrosine-protein phosphatase non-receptor type 12 OS=Mus musculus GN=Ptpn12 PE=1 SV=3 - [PTN12_MOUSE]	0,000E0	0,000E0	0,000E0	3,444E6	1,364E7	1,241E7	Ptpn12
Q62418-3	Isform 3 of Drebrin-like protein OS=Mus musculus GN=Dbrn1 - [DBNL_MOUSE]	0,000E0	0,000E0	0,000E0	8,414E6	1,922E7	3,395E7	Dbrn1
O54916	RaiBP1-associated Eps domain-containing protein 1 OS=Mus musculus GN=Reps1 PE=1 SV=2 - [REPS1_MOUSE]	0,000E0	0,000E0	0,000E0	1,497E7	4,671E7	3,297E7	Reps1
Q91V17	Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 - [RINI_MOUSE]	0,000E0	0,000E0	0,000E0	1,471E7	3,332E7	3,525E7	Rnh1
P47915	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2 - [RL29_MOUSE]	5,786E6	0,000E0	0,000E0	1,387E8	2,903E8	3,218E8	Rpl29
P32067	Lupus La protein homolog OS=Mus musculus GN=Ssb PE=1 SV=1 - [LA_MOUSE]	0,000E0	0,000E0	0,000E0	7,627E6	1,431E7	3,148E7	Ssb
Q9QWT9	Kinesin-like protein KIFC1 OS=Mus musculus GN=Kifc1 PE=1 SV=2 - [KIFC1_MOUSE]	0,000E0	0,000E0	0,000E0	6,150E6	1,388E7	2,053E7	Kifc1
Q02053	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1 - [UBA1_MOUSE]	0,000E0	0,000E0	0,000E0	1,124E7	2,029E7	2,900E7	Uba1
Q8BX02	KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Kank2 PE=1 SV=1 - [KANK2_MOUSE]	0,000E0	0,000E0	0,000E0	3,546E6	1,385E7	2,069E7	Kank2
E9Q682	Coiled-coil domain-containing protein 85C OS=Mus musculus GN=Ccdc85c PE=1 SV=1 - [CC85C_MOUSE]	0,000E0	0,000E0	0,000E0	1,008E7	1,893E7	2,081E7	Ccdc85c
Q69Z38	Pseudopodium-enriched atypical kinase 1 OS=Mus musculus GN=Peak1 PE=1 SV=4 - [PEAK1_MOUSE]	0,000E0	0,000E0	0,000E0	8,664E6	2,644E7	3,621E7	Peak1
P01942	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2 - [HBA_MOUSE]	8,540E7	0,000E0	0,000E0	3,162E6	1,324E6	1,836E6	Hba
Q99KD5	Protein unc-45 homolog A OS=Mus musculus GN=Unc45a PE=1 SV=2 - [UNH5A_MOUSE]	0,000E0	0,000E0	0,000E0	1,333E7	3,343E7	4,808E7	Unc45a
O33526	Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=2 - [SRSF5_MOUSE]	0,000E0	0,000E0	0,000E0	5,935E7	1,001E8	1,434E8	Srsf5
Q8R081	Heterogeneous nuclear ribonucleoprotein L OS=Mus musculus GN=Hnrppl PE=1 SV=2 - [HNRPL_MOUSE]	0,000E0	0,000E0	0,000E0	5,301E6	6,986E6	3,423E7	Hnrppl
Q8K4G5-2	Isform 2 of Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 - [ABLIM1_MOUSE]	0,000E0	0,000E0	0,000E0	1,459E7	2,145E7	2,120E7	Ablim1
Q9D6T0	Nitric oxide synthase-interacting protein OS=Mus musculus GN=Nosip PE=1 SV=1 - [NOSIP_MOUSE]	0,000E0	0,000E0	0,000E0	2,716E6	1,921E6	3,403E6	Nosip
Q3JUH8	Trinucleotide repeat-containing gene 6A protein OS=Mus musculus GN=Trnca PE=2 SV=1 - [TNRGA_MOUSE]	0,000E0	0,000E0	0,000E0	1,113E7	1,839E7	2,129E7	Trnca
Q5NBX1-3	Isform 3 of Protein cordon-bleu OS=Mus musculus GN=Cobl - [COBL_MOUSE]	0,000E0	0,000E0	0,000E0	3,065E6	1,138E7	1,383E7	Cobl
Q9Z0P5-2	Isform 2 of Twirlin-2 OS=Mus musculus GN=Twf2 - [TWIF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,270E6	1,763E7	2,147E7	Twf2
P81270-4	Isform 5 of Transcriptional regulator ERG OS=Mus musculus GN=Erg - [ERG_MOUSE]	0,000E0	0,000E0	0,000E0	1,590E7	3,929E7	4,297E7	Erg
Q9DCI5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Mus musculus GN=Ndufa8 PE=1 SV=3 - [NDUAR_MOUSE]	0,000E0	0,000E0	0,000E0	5,153E6	1,979E7	3,327E7	Ndufa8
Q9CX84	Regulator of G-protein signaling 19 OS=Mus musculus GN=Rgs19 PE=1 SV=1 - [RGS19_MOUSE]	0,000E0	0,000E0	0,000E0	2,998E6	5,032E6	1,203E7	Rgs19
P24552	Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2 - [CAPG_MOUSE]	0,000E0	0,000E0	0,000E0	1,727E7	1,524E7	5,665E7	Capg
P17156	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2 - [HSP72_MOUSE]	3,628E7	0,000E0	9,603E6	5,026E8	1,340E9	1,698E9	Hspa2
Q8BT18-3	Isform 3 of Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 - [SRRM2_MOUSE]	0,000E0	0,000E0	0,000E0	6,293E7	1,057E8	3,756E7	Srrm2
Q99JR5	Tubulointerstitial nephritis antigen-like OS=Mus musculus GN=Timag1 PE=1 SV=1 - [TINAL_MOUSE]	0,000E0	0,000E0	0,000E0	2,047E7	3,463E7	6,051E7	Timag1
Q8CHU3-2	Isform 2 of Epsin-2 OS=Mus musculus GN=Epn2 - [EPN2_MOUSE]	0,000E0	0,000E0	0,000E0	1,593E7	3,361E7	4,295E7	Epn2
Q9R0P4	Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1 - [SMAP_MOUSE]	0,000E0	0,000E0	0,000E0	1,453E7	2,317E7	2,234E7	Smap
Q8K2Q7	BRO1 domain-containing protein BROX OS=Mus musculus GN=Brox PE=1 SV=1 - [BROX_MOUSE]	0,000E0	0,000E0	0,000E0	1,442E7	2,271E7	1,951E7	Brox
Q8CIN4	Serine/threonine-protein kinase PAK 2 OS=Mus musculus GN=Pa2 PE=1 SV=1 - [PAK2_MOUSE]	0,000E0	0,000E0	0,000E0	2,749E6	6,116E6	6,800E6	Pa2
O35286	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Mus musculus GN=Dhx15 PE=1 SV=2 - [DHX15_MOUSE]	0,000E0	0,000E0	0,000E0	1,157E7	2,387E7	4,372E7	Dhx15
Q63844	Mitogen-activated protein kinase 3 OS=Mus musculus GN=Mapk3 PE=1 SV=5 - [MK03_MOUSE]	0,000E0	0,000E0	0,000E0	7,220E6	2,158E7	1,576E7	Mapk3
Q3JUL8	Arginine and glutamate-rich protein 1 OS=Mus musculus GN=Arglu1 PE=1 SV=2 - [ARGL1_MOUSE]	0,000E0	0,000E0	0,000E0	2,188E7	5,139E7	1,013E8	Arglu1
Q9NVV6	Protein kinase C and casein kinase substrate in neurons protein 2 OS=Mus musculus GN=Pascin2 PE=1 SV=1 - [PACN2_MOUSE]	0,000E0	0,000E0	0,000E0	8,708E6	1,935E7	2,479E7	Pascin2
O35682	Myeloid-associated differentiation marker OS=Mus musculus GN=Myadm PE=1 SV=2 - [MYADM_MOUSE]	0,000E0	0,000E0	0,000E0	1,847E7	3,261E7	6,739E7	Myadm
O70251	Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5 - [EF1B_MOUSE]	0,000E0	0,000E0	0,000E0	8,634E6	1,486E7	2,198E7	Eef1b
Q922Q8	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=1 SV=1 - [LRC59_MOUSE]	0,000E0	0,000E0	0,000E0	1,407E7	1,216E7	1,421E7	Lrrc59
Q8CIB5	Fermitin family homolog 2 OS=Mus musculus GN=Fermt2 PE=1 SV=1 - [FERM2_MOUSE]	0,000E0	0,000E0	0,000E0	5,421E6	1,288E7	1,880E7	Fermt2
Q8BRV5	Uncharacterized protein KIAA1671 OS=Mus musculus GN=Kiaa1671 PE=2 SV=1 - [K1671_MOUSE]	0,000E0	0,000E0	0,000E0	3,164E6	9,524E6	1,937E7	Kiaa1671
Q3JUV16	Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 OS=Mus musculus GN=Itprlp2 PE=2 SV=1 - [IPL2_MOUSE]	0,000E0	0,000E0	0,000E0	7,271E6	1,156E7	1,591E7	Itprlp2
Q8CD15	Bifunctional lysine-specific demethylase and histidyl-hydroxylase MINA OS=Mus musculus GN=Mina PE=1 SV=2 - [MINA_MOUSE]	0,000E0	0,000E0	0,000E0	6,348E6	1,140E7	2,259E7	Mina
Q99M87-2	Isform 2 of Dnal homolog subfamily A member 3, mitochondrial OS=Mus musculus GN=Dnaja3 - [DNJA3_MOUSE]	0,000E0	0,000E0	0,000E0	4,330E6	4,381E6	2,074E6	Dnaja3
Q3TLH4	Protein PRRC2c OS=Mus musculus GN=Prrc2c PE=1 SV=3 - [PRC2C_MOUSE]	0,000E0	0,000E0	0,000E0	2,502E7	4,852E7	1,051E8	Prrc2c
Q6PGC1	ATP-dependent RNA helicase DHX29 OS=Mus musculus GN=Dhx29 PE=1 SV=1 - [DHX29_MOUSE]	0,000E0	0,000E0	0,000E0	7,366E6	1,401E7	3,320E7	Dhx29
Q8BZ10	Actin filament-associated protein 1-like 1 OS=Mus musculus GN=Afp1l1 PE=1 SV=1 - [AF1L1_MOUSE]	0,000E0	0,000E0	0,000E0	2,343E6	8,594E6	1,284E7	Afp1l1
Q91W53	Golgin subfamily A member 7 OS=Mus musculus GN=Golg7 PE=1 SV=1 - [GOGA7_MOUSE]	0,000E0	0,000E0	0,000E0	5,104E6	3,380E6	3,987E6	Golg7
Q811D0-2	Isform 2 of Disks large homolog 1 OS=Mus musculus GN=Dlg1 - [DLG1_MOUSE]	0,000E0	0,000E0	0,000E0	5,706E6	1,062E7	1,638E7	Dlg1
O08917	Flotillin-1 OS=Mus musculus GN=Flot1 PE=1 SV=1 - [FLOT1_MOUSE]	0,000E0	0,000E0	0,000E0	6,363E6	1,408E7	3,919E7	Flot1
Q05793	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1 - [PGBM_MOUSE]	0,000E0	0,000E0	2,843E5	4,050E7	4,860E7	1,022E8	Hspg2
Q04899	Cyclin-dependent kinase 18 OS=Mus musculus GN=Cdk18 PE=1 SV=1 - [CDK18_MOUSE]	0,000E0	0,000E0	0,000E0	1,843E7	4,135E7	6,772E7	Cdk18
Q9R1P4	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psm1 PE=1 SV=1 - [PSA1_MOUSE]	0,000E0	0,000E0	0,000E0	2,894E6	1,458E6	3,993E6	Psm1
P97762	Retinitis pigmentosa 9 protein homolog OS=Mus musculus GN=rp9 PE=1 SV=1 - [RP9_MOUSE]	0,000E0	0,000E0	0,000E0	1,814E7	6,423E6	8,916E7	rp9
Q61024	Asparagine synthetase [glutamine-hydrolyzing] OS=Mus musculus GN=Asns PE=1 SV=3 - [ASNS_MOUSE]	0,000E0	0,000E0	0,000E0	4,585E6	1,146E7	1,541E7	Asns
Q60780-2	Isform 2 of Growth arrest-specific protein 7 OS=Mus musculus GN=Gas7 - [GAS7_MOUSE]	0,000E0	0,000E0	0,000E0	4,506E6	1,638E7	1,713E7	Gas7
P47964	60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=3 SV=2 - [RL36_MOUSE]	0,000E0	0,000E0	0,000E0	5,638E7	2,324E8	8,175E8	Rpl36
Q9EQK5	Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4 - [MVP_MOUSE]	0,000E0	0,000E0	0,000E0	5,282E6	8,100E6	1,092E7	Mvp
P23249	Putative helicase MOV-10 OS=Mus musculus GN=Mov10 PE=1 SV=2 - [MOV10_MOUSE]	0,000E0	0,000E0	0,000E0	9,086E6	1,693E7	3,938E7	Mov10
O08784	Treacle protein OS=Mus musculus GN=Tcof1 PE=1 SV=1 - [TCOF_MOUSE]	0,000E0	0,000E0	0,000E0	9,476E6	1,466E7	7,132E7	Tcof1
O88456	Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=1 SV=1 - [CPNS1_MOUSE]	0,000E0	0,000E0	0,000E0	1,073E7	3,470E7	4,177E7	Capns1
Q9QZ53-4	Isform 4 of Protein numb homolog OS=Mus musculus GN=Numb - [NUMB_MOUSE]	0,000E0	0,000E0	0,000E0	1,424E7	2,309E7	3,875E7	Numb
Q6NZ36	Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1 - [IF4G1_MOUSE]	0,000E0	0,000E0	0,000E0	2,752E7	6,198E7	9,263E7	Eif4g1
Q80X41-2	Isform 2 of Serine/threonine-protein kinase VRK1 OS=Mus musculus GN=Vrk1 - [VRK1_MOUSE]	0,000E0	0,000E0	0,000E0	3,237E6	9,328E5	1,020E7	Vrk1
Q62130	Tyrosine-protein phosphatase non-receptor type 14 OS=Mus musculus GN=Ptpn14 PE=1 SV=2 - [PTN14_MOUSE]	0,000E0	0,000E0	0,000E0	4,449E6	1,381E7	1,150E7	Ptpn14
O55222	Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2 - [ILK_MOUSE]	0,000E0	0,000E0	0,000E0	6,128E6	2,165E7	2,143E7	Ilk
Q9JMS2-3	Isform 3 of Mischapen-like kinase 1 OS=Mus musculus GN=Mink1 - [MINK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,194E7	2,380E7	2,645E7	Mink1
Q05D44	Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2 - [IF2P_MOUSE]	0,000E0	0,000E0	0,000E0	1,555E7	1,733E7	3,988E7	Eif5b
Q61792	LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1 PE=1 SV=1 - [LASP1_MOUSE]	0,000E0	0,000E0	1,221E5	1,556E7	3,632E7	4,679E7	Lasp1
Q03975	IgE-binding protein OS=Mus musculus GN=Iap PE=2 SV=1 - [IGEB_MOUSE]	0,000E0	0,000E0	0,000E0	2,446E7	5,838E7	3,430E7	Iap
Q9Z0P4	Paralemm-1 OS=Mus musculus GN=Paln PE=1 SV=1 - [PALM_MOUSE]	0,000E0	0,000E0	0,000E0	1,697E6	4,314E6	1,275E7	Paln
P0C0A3	Charged multivesicular body protein 6 OS=Mus musculus GN=Chmp6 PE=1 SV=2 - [CHMP6_MOUSE]	0,000E0	0,000E0	0,000E0	3,477E6	8,921E6	7,572E6	Chmp6
P06745	Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4 - [G6PI_MOUSE]	0,000E0	0,000E0	0,000E0	1,591E6	5,944E6	1,402E7	Gpi
O70152	Dolichol-phosphate mannosyltransferase subunit 1 OS=Mus musculus GN=Dpm1 PE=1 SV=1 - [DPM1_MOUSE]	0,000E0	0,000E0	0,000E0	3,099E6	7,989E6	8,095E6	Dpm1
P44647	Vacuolar protein sorting-associated protein 4B OS=Mus musculus GN=Vps4b PE=1 SV=2 - [VPS4B_MOUSE]	0,000E0	0,000E0	0,000E0	1,535E7	3,574E7	2,822E7	Vps4b
Q9WV12	26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psm13 PE=1 SV=1 - [PSD13_MOUSE]	0,000E0	0,000E0	0,000E0	1,557E6	4,578E6	6,930E6	Psm13
P58871	182 kDa tankyase-1-binding protein OS=Mus musculus GN=Trks1bp1 PE=1 SV=2 - [TB182_MOUSE]	0,000E0	0,000E0	0,000E0	8,133E6	1,472E7	2,318E7	Trks1bp1
Q8R154-2	Isform 2 of Metastasis suppressor protein 1 OS=Mus musculus GN=Mtss1 - [MTSS1_MOUSE]	0,000E0	0,000E0	0,000E0	5,823E6	5,977E6	1,087E7	Mtss1
Q9D083-3	Isform 3 of Kinetochore protein Spc24 OS=Mus musculus GN=Spc24 - [SPC24_MOUSE]	0,000E0	0,000E0	0,000E0	8,734E5	2,966E6	1,288E6	Spc24
P17095	High mobility group protein HMG-1/HMG-Y OS=Mus musculus GN=Hmg1 PE=1 SV=4 - [HMG1_MOUSE]	0,000E0	0,000E0	0,000E0	7,616E6	7,656E6	5,975E7	Hmg1
P70168	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2 - [IMB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,376E7	2,902E7	7,291E7	Kpnb1
Q8BWW4	La-related protein 4 OS=Mus musculus GN=Larp4 PE=1 SV=2 - [LARP4_MOUSE]	0,000E0	0,000E0	0,000E0	2,113E7	4,057E7	6,761E7	Larp4
Q8V194	2'-5'-oligoadenylate synthase-like protein 1 OS=Mus musculus GN=Oasl1 PE=2 SV=1 - [OASL1_MOUSE]	0,000E0	0,000E0	0,000E0	7,767E6	3,928E7	6,882E7	Oasl1
Q8BJS4-3	Isform 3 of SUN domain-containing protein 2 OS=Mus musculus GN=Sun2 - [SUN2_MOUSE]	0,000E0	0,000E0	0,000E0	2,530E6	7,310E6	1,358E7	Sun2
O70493	Sorting nexin-12 OS=Mus musculus GN=Snx12 PE=1 SV=1 - [SNX12_MOUSE]	0,000E0	0,000E0	0,000E0	1,689E6	9,900E6	1,219E7	Snx12

Q80UM3	N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Mus musculus GN=Naa15 PE=1 SV=1 - [NAA15_MOUSE]	0,000E0	0,000E0	0,000E0	9,395E6	1,095E7	2,746E7	Naa15
A2ASZ6	E3 ubiquitin-protein ligase SMURF2 OS=Mus musculus GN=Smurf2 PE=1 SV=1 - [SMURF2_MOUSE]	0,000E0	0,000E0	0,000E0	9,907E6	2,289E7	2,499E7	Smurf2
Q8K1M4	Spermatogenesis-associated serine-rich protein 2 OS=Mus musculus GN=Spats2 PE=1 SV=1 - [SPAS2_MOUSE]	0,000E0	0,000E0	0,000E0	4,632E6	3,355E6	1,913E7	Spats2
Q76N33	AMSH-like protease OS=Mus musculus GN=Stampb1 PE=1 SV=1 - [STALP_MOUSE]	0,000E0	0,000E0	0,000E0	4,477E6	1,332E7	1,458E7	Stampb1
P62196	26S protease regulatory subunit 8 OS=Mus musculus GN=Pamc5 PE=1 SV=1 - [PR58_MOUSE]	0,000E0	0,000E0	0,000E0	6,374E5	3,117E6	4,484E6	Psmc5
P11352	Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 - [GPX1_MOUSE]	0,000E0	0,000E0	0,000E0	1,390E6	2,417E6	7,535E6	Gpx1
Q61753	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3 - [SERA_MOUSE]	0,000E0	0,000E0	0,000E0	1,120E7	2,966E7	3,892E7	Phgdh
Q9J1I7	AN1-type zinc finger protein 2A OS=Mus musculus GN=Zfand2a PE=2 SV=1 - [ZF2A_MOUSE]	0,000E0	0,000E0	0,000E0	2,063E6	1,942E7	1,404E7	Zfand2a
P97820	Mitogen-activated protein kinase kinase kinase kinase 4 OS=Mus musculus GN=Map4k4 PE=1 SV=1 - [MK4_MOUSE]	0,000E0	0,000E0	7,335E5	1,709E7	3,924E7	5,588E7	Map4k4
P63280	SUMO-conjugating enzyme UBC9 OS=Mus musculus GN=Ube2f PE=1 SV=1 - [UBC9_MOUSE]	0,000E0	0,000E0	0,000E0	3,191E5	5,271E6	5,223E6	Ube2i
Q9J1I0-2	Isoform 2 of Serine/threonine-protein kinase 3 OS=Mus musculus GN=Stk3 - [STK3_MOUSE]	0,000E0	0,000E0	0,000E0	2,199E6	3,381E6	2,556E6	Stk3
Q3UH02	28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdpap1 PE=1 SV=1 - [HAP28_MOUSE]	0,000E0	0,000E0	0,000E0	3,005E7	4,895E7	7,068E7	Pdap1
P61211	ADP-ribosylation factor-like protein 1 OS=Mus musculus GN=Ar1f PE=1 SV=1 - [ARL1_MOUSE]	0,000E0	0,000E0	0,000E0	5,809E6	8,103E6	1,017E7	Ar1f
P46061	Ran GTPase-activating protein 1 OS=Mus musculus GN=Rangap1 PE=1 SV=2 - [RAGP1_MOUSE]	0,000E0	0,000E0	0,000E0	8,310E5	9,599E6	2,210E7	Rangap1
A2A699-2	Isoform 2 of Protein FAM171A2 OS=Mus musculus GN=Fam171a2 - [F1712_MOUSE]	0,000E0	0,000E0	0,000E0	3,642E6	6,221E6	7,218E6	Fam171a2
Q3UH60	Disco-interacting protein 2 homolog B OS=Mus musculus GN=Dip2b PE=1 SV=1 - [DIP2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,078E7	2,206E7	3,748E7	Dip2b
Q8VBK6-2	Isoform 2 of Multiple PDZ domain protein OS=Mus musculus GN=Mpdz - [MPDZ_MOUSE]	0,000E0	0,000E0	0,000E0	1,728E7	2,365E7	2,371E7	Mpdz
Q8CFE2	Histone PARylation factor 1 OS=Mus musculus GN=Hpf1 PE=1 SV=1 - [HPF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,220E6	2,362E6	4,225E6	Hpf1
Q8CHC4	Synaptotagmin-1 OS=Mus musculus GN=Synj1 PE=1 SV=3 - [SYNJ1_MOUSE]	0,000E0	0,000E0	0,000E0	4,993E6	8,975E6	9,989E6	Synj1
Q6A049	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus GN=FAM120A PE=1 SV=2 - [F120A_MOUSE]	0,000E0	0,000E0	0,000E0	5,463E6	2,658E7	5,671E7	FAM120A
O88384	Vesicle transport through interaction with t-SNAREs homolog 1B OS=Mus musculus GN=Vti1b PE=1 SV=1 - [VT11B_MOUSE]	0,000E0	0,000E0	0,000E0	4,794E6	8,905E6	2,242E6	Vti1b
P06869	Urokinase-type plasminogen activator OS=Mus musculus GN=Plau PE=1 SV=1 - [UROK_MOUSE]	0,000E0	0,000E0	0,000E0	5,666E6	8,101E6	3,151E7	Plau
A2A6T1	Cerebellar degeneration-related protein 2-like OS=Mus musculus GN=Cdr2l PE=1 SV=1 - [CDR2L_MOUSE]	0,000E0	0,000E0	0,000E0	3,174E6	1,327E7	1,679E7	Cdr2l
Q92258	Kinesin-like protein KIF2C OS=Mus musculus GN=Kif2c PE=1 SV=1 - [KIF2C_MOUSE]	0,000E0	0,000E0	0,000E0	1,088E7	1,58E7	1,737E7	Kif2c
Q3UH0-2	Isoform 2 of AP2-associated protein kinase 1 OS=Mus musculus GN=Aak1 - [AAK1_MOUSE]	0,000E0	0,000E0	0,000E0	6,965E6	1,404E7	1,939E7	Aak1
Q9CQ71	Replication protein A 14 kDa subunit OS=Mus musculus GN=Rpa3 PE=1 SV=1 - [RFA3_MOUSE]	0,000E0	0,000E0	0,000E0	3,372E6	3,016E6	4,829E6	Rpa3
Q6NXY1	TBC1 domain family member 31 OS=Mus musculus GN=Tbc1d31 PE=1 SV=1 - [TBC31_MOUSE]	0,000E0	0,000E0	0,000E0	2,719E6	4,502E6	6,390E6	Tbc1d31
Q92112	GTP-binding protein Rheb OS=Mus musculus GN=Rheb PE=1 SV=1 - [RHEB_MOUSE]	0,000E0	0,000E0	0,000E0	1,711E6	7,163E6	9,167E6	Rheb
Q80Z96	Vang-like protein 1 OS=Mus musculus GN=Vangl1 PE=1 SV=2 - [VANG1_MOUSE]	0,000E0	0,000E0	0,000E0	8,226E6	1,761E7	2,405E7	Vangl1
Q923T9-3	Isoform 3 of Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Mus musculus GN=Camk2g - [KCC2G_MOUSE]	0,000E0	0,000E0	0,000E0	2,093E7	1,749E7	4,232E7	Camk2g
Q920G0	PDZ domain-containing protein GIPC1 OS=Mus musculus GN=Gipc1 PE=1 SV=1 - [GIPC1_MOUSE]	0,000E0	0,000E0	0,000E0	2,849E6	2,383E6	3,256E6	Gipc1
Q9JLV1	BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=2 - [BAG3_MOUSE]	0,000E0	0,000E0	0,000E0	2,944E6	5,236E6	6,464E6	Bag3
O88685	26S protease regulatory subunit 6A OS=Mus musculus GN=Psmc3 PE=1 SV=2 - [PR56A_MOUSE]	0,000E0	0,000E0	0,000E0	2,886E6	2,997E6	7,228E6	Psmc3
Q61081	Hsp90 co-chaperone Cdc37 OS=Mus musculus GN=Cdc37 PE=1 SV=1 - [CDC37_MOUSE]	0,000E0	0,000E0	0,000E0	9,211E6	6,998E6	2,902E7	Cdc37
Q9DCL9	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4 - [PUR6_MOUSE]	0,000E0	0,000E0	0,000E0	9,520E6	9,746E6	2,651E7	Paics
Q8VDF2-2	Isoform 2 of E3 ubiquitin-protein ligase UHRF1 OS=Mus musculus GN=Uhrf1 - [UHRF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,050E6	6,417E6	1,313E7	Uhrf1
Q8CB04	Spindle and centriole-associated protein 1 OS=Mus musculus GN=Spice1 PE=1 SV=2 - [SPICE_MOUSE]	0,000E0	0,000E0	0,000E0	2,627E6	4,366E6	1,290E6	Spice1
Q805Y4	E3 ubiquitin-protein ligase MIB1 OS=Mus musculus GN=Mib1 PE=1 SV=1 - [MIB1_MOUSE]	0,000E0	0,000E0	0,000E0	9,291E6	1,315E7	1,944E7	Mib1
Q9D0B0	Serine/arginine-rich splicing factor 9 OS=Mus musculus GN=Srsf9 PE=1 SV=1 - [SRSF9_MOUSE]	0,000E0	0,000E0	0,000E0	7,898E6	1,969E7	2,276E7	Srsf9
Q91YU6	Leucine zipper putative tumor suppressor 2 OS=Mus musculus GN=Lzts2 PE=1 SV=3 - [LZTS2_MOUSE]	0,000E0	0,000E0	0,000E0	5,866E6	8,866E6	1,170E7	Lzts2
Q6P9Q6	FK506-binding protein 15 OS=Mus musculus GN=Fkbp15 PE=1 SV=2 - [FKB15_MOUSE]	0,000E0	0,000E0	0,000E0	1,176E7	2,349E7	3,190E7	Fkbp15
P59326	YTH domain-containing family protein 1 OS=Mus musculus GN=Ythdf1 PE=1 SV=1 - [YTHD1_MOUSE]	0,000E0	0,000E0	5,369E6	1,748E6	8,622E6	2,171E7	Ythdf1
Q8CKG0	Protein argonaute-2 OS=Mus musculus GN=Ago2 PE=1 SV=3 - [AGO2_MOUSE]	0,000E0	0,000E0	0,000E0	9,572E6	2,013E7	2,308E7	Ago2
Q92239	Fatty acyl-CoA reductase 1 OS=Mus musculus GN=Far1 PE=1 SV=1 - [FACR1_MOUSE]	0,000E0	0,000E0	0,000E0	4,808E6	1,573E7	2,175E7	Far1
P46471	26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5 - [PR57_MOUSE]	0,000E0	0,000E0	0,000E0	3,186E6	4,674E6	1,178E7	Psmc2
Q91VJ2	Protein kinase C delta-binding protein OS=Mus musculus GN=Prkcdpb PE=1 SV=1 - [PRDBP_MOUSE]	0,000E0	0,000E0	0,000E0	1,960E7	2,419E7	1,155E8	Prkcdbp
Q9CQW4	60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4 - [RL11_MOUSE]	3,381E7	0,000E0	1,574E7	2,628E8	4,519E8	8,359E8	Rpl11
P70336	Rho-associated protein kinase 2 OS=Mus musculus GN=Rock2 PE=1 SV=1 - [ROCK2_MOUSE]	0,000E0	0,000E0	1,352E5	8,759E6	1,528E7	2,314E7	Rock2
P63034-3	Isoform 3 of Cytohesin-2 OS=Mus musculus GN=Cyth2 - [CYH2_MOUSE]	0,000E0	0,000E0	0,000E0	6,002E6	1,902E7	1,211E7	Cyth2
P97427	Dihydropyrimidine-related protein 1 OS=Mus musculus GN=Crmpp1 PE=1 SV=1 - [DPYL1_MOUSE]	0,000E0	0,000E0	0,000E0	3,092E6	3,970E6	2,221E7	Crmpp1
Q3JUGC7	Eukaryotic translation initiation factor 3 subunit J-A OS=Mus musculus GN=Eif3j PE=2 SV=1 - [EIF3JA_MOUSE]	0,000E0	0,000E0	0,000E0	2,092E6	1,031E7	1,266E7	Eif3j1
Q6DFW4	Nucleolar protein 58 OS=Mus musculus GN=Nop58 PE=1 SV=1 - [NOP58_MOUSE]	0,000E0	0,000E0	0,000E0	2,212E6	7,008E6	2,353E7	Nop58
O70503	Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus GN=Hsd17b12 PE=1 SV=1 - [DHB12_MOUSE]	0,000E0	0,000E0	0,000E0	6,565E6	3,142E7	3,408E7	Hsd17b12
Q9CYK6	Interleukin enhancer-binding factor 2 OS=Mus musculus GN=Ilf2 PE=1 SV=1 - [ILF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,362E6	6,579E5	4,972E6	Ilf2
Q8K2J7-2	Isoform 2 of RELT-like protein 1 OS=Mus musculus GN=Relt1 - [RELT1_MOUSE]	0,000E0	0,000E0	0,000E0	2,517E6	4,497E6	1,202E7	Relt1
Q9DD03	Ras-related protein Rab-13 OS=Mus musculus GN=Rab13 PE=1 SV=1 - [RAB13_MOUSE]	0,000E0	0,000E0	0,000E0	3,615E7	6,702E7	6,617E7	Rab13
Q3UFY8	Mitochondrial ribonuclease P protein 1 OS=Mus musculus GN=Trmt10c PE=1 SV=2 - [MRRP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,560E6	1,396E7	1,870E7	Trmt10c
O70311	Glycylpeptide N-tetradecanoyltransferase 2 OS=Mus musculus GN=Nmt2 PE=1 SV=1 - [NMT2_MOUSE]	0,000E0	0,000E0	0,000E0	5,967E6	1,059E7	1,900E7	Nmt2
P11276	Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=4 - [FINC_MOUSE]	0,000E0	0,000E0	0,000E0	1,421E7	3,555E7	6,967E7	Fn1
Q07832	Serine/threonine-protein kinase PLK1 OS=Mus musculus GN=Plk1 PE=1 SV=2 - [PLK1_MOUSE]	0,000E0	0,000E0	0,000E0	3,303E6	6,068E6	1,424E7	Plk1
P63038	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 - [CH60_MOUSE]	0,000E0	0,000E0	2,327E6	1,869E6	3,667E6	6,890E6	Hspd1
Q8J2X3-3	Isoform 3 of POC1 centriolar protein homolog A OS=Mus musculus GN=Poc1a - [POCIA_MOUSE]	0,000E0	0,000E0	0,000E0	1,943E6	2,016E6	3,526E6	Poc1a
P00493	Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus GN=Hprt1 PE=1 SV=3 - [HPRT_MOUSE]	0,000E0	0,000E0	0,000E0	1,010E6	3,314E6	4,216E6	Hprt1
Q9DBU6	Serine/Arginine-related protein 53 OS=Mus musculus GN=Rsrc1 PE=1 SV=1 - [RSRC1_MOUSE]	0,000E0	0,000E0	0,000E0	7,670E6	7,425E6	2,003E7	Rsrc1
Q0VGY8	Protein TANC1 OS=Mus musculus GN=Tanc1 PE=1 SV=2 - [TANC1_MOUSE]	0,000E0	0,000E0	0,000E0	4,532E6	1,065E7	9,495E6	Tanc1
O55029	Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=1 SV=2 - [COPB2_MOUSE]	0,000E0	0,000E0	0,000E0	3,313E6	5,361E6	5,242E6	Copb2
Q9EPK2-3	Isoform 3 of Protein XRP2 OS=Mus musculus GN=Rp2 - [XRP2_MOUSE]	0,000E0	0,000E0	0,000E0	6,839E6	2,917E6	4,658E7	Rp2
A2AJI0	MAP7 domain-containing protein 1 OS=Mus musculus GN=Map7d1 PE=1 SV=1 - [MA7D1_MOUSE]	0,000E0	0,000E0	0,000E0	2,432E6	9,492E6	3,072E7	Map7d1
B2RY56	RNA-binding protein 25 OS=Mus musculus GN=Rbm25 PE=1 SV=2 - [RBM25_MOUSE]	0,000E0	0,000E0	0,000E0	7,150E6	1,567E7	3,457E7	Rbm25
Q9JJK2	LanC-like protein 2 OS=Mus musculus GN=Lanc2 PE=1 SV=1 - [LANC2_MOUSE]	0,000E0	0,000E0	0,000E0	2,190E7	1,958E7	1,622E7	Lanc2
P14602-2	Isoform B of Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 - [HSPB1_MOUSE]	0,000E0	0,000E0	6,467E6	7,573E6	1,754E7	8,848E6	Hspb1
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap1l1 PE=1 SV=1 - [UAP1L_MOUSE]	0,000E0	0,000E0	0,000E0	3,531E6	9,751E6	1,701E7	Uap1l1
Q3UIA2	Rho GTPase-activating protein 17 OS=Mus musculus GN=Arhgap17 PE=1 SV=1 - [RHG17_MOUSE]	0,000E0	0,000E0	0,000E0	2,402E6	7,691E6	6,211E6	Arhgap17
Q99JN2	Kelch-like protein 22 OS=Mus musculus GN=Klh22 PE=1 SV=1 - [KLH22_MOUSE]	0,000E0	0,000E0	0,000E0	3,111E6	5,413E6	1,810E6	Klh22
Q88MA6	Signal recognition particle subunit SRP68 OS=Mus musculus GN=Srp68 PE=1 SV=2 - [SRP68_MOUSE]	0,000E0	0,000E0	0,000E0	4,619E6	4,176E6	9,298E6	Srp68
P30285	Cyclin-dependent kinase 4 OS=Mus musculus GN=Cdk4 PE=1 SV=1 - [CDK4_MOUSE]	0,000E0	0,000E0	0,000E0	9,391E6	2,088E7	3,528E7	Cdk4
Q91YD3	mRNA-decapping enzyme 1A OS=Mus musculus GN=Dcp1a PE=1 SV=1 - [DCP1A_MOUSE]	0,000E0	0,000E0	0,000E0	3,234E6	4,938E6	1,499E7	Dcp1a
Q55XY1-3	Isoform 4 of Cytosin-B OS=Mus musculus GN=Specc1 - [CYTSB_MOUSE]	0,000E0	0,000E0	0,000E0	3,509E6	1,006E7	1,905E7	Specc1
Q9ET54-4	Isoform 4 of Palladin OS=Mus musculus GN=Palld - [PALLD_MOUSE]	0,000E0	0,000E0	0,000E0	1,035E7	2,581E7	2,404E7	Palld
P61963	DDB1- and CUL4-associated factor 7 OS=Mus musculus GN=Dcaf7 PE=1 SV=1 - [DCAF7_MOUSE]	0,000E0	0,000E0	0,000E0	2,564E6	5,953E6	8,447E6	Dcaf7
Q8VEH3	ADP-ribosylation factor-like protein 8A OS=Mus musculus GN=Ar1ba PE=1 SV=1 - [ARL8A_MOUSE]	0,000E0	0,000E0	0,000E0	3,034E6	4,126E6	3,245E6	Ar1ba
P61759	Prefoldin subunit 3 OS=Mus musculus GN=Vbp1 PE=1 SV=2 - [PFD3_MOUSE]	0,000E0	0,000E0	0,000E0	1,069E6	2,875E6	2,854E6	Vbp1
Q9JMK2	Casein kinase I isoform epsilon OS=Mus musculus GN=Cnck1e PE=1 SV=2 - [KCIE_MOUSE]	0,000E0	0,000E0	0,000E0	1,802E7	1,414E7	3,542E7	Cnck1e
Q6Y7W8	PERQ amino acid-rich with GYF domain-containing protein 2 OS=Mus musculus GN=Gigyf2 PE=1 SV=2 - [PERQ2_MOUSE]	0,000E0	0,000E0	0,000E0	6,806E6	1,734E7	5,043E7	Gigyf2
Q62318	Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3 - [TIF1B_MOUSE]	0,000E0	0,000E0	0,000E0	4,817E6	1,123E7	1,715E7	Trim28
P21981	Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=4 - [TGM2_MOUSE]	0,000E0	0,000E0	0,000E0	4,802E6	9,148E6	2,607E7	Tgm2
Q9ESX5	H/ACA ribonucleoprotein complex subunit 4 OS=Mus musculus GN=Dkc1 PE=1 SV=4 - [DKC1_MOUSE]	0,000E0	0,000E0	0,000E0	3,347E6	5,017E6	9,911E6	Dkc1
Q9CZ44	NSFL1 cofactor p47 OS=Mus musculus GN=Nsf11c PE=1 SV=1 - [NSF1C_MOUSE]	0,000E0	0,000E0	0,000E0	1,622E6	5,938E6	9,900E6	Nsf11c
P47941	Crk-like protein OS=Mus musculus GN=Crkl PE=1 SV=2 - [CRKL_MOUSE]	0,000E0	0,000E0	0,000E0	1,295E6	1,866E6	4,185E6	Crkl
P61270-3	Isoform 1 of Transcriptional regulator ERG OS=Mus musculus GN=Erg - [ERG_MOUSE]	0,000E0	0,000E0	0,000E0	1,590E7	3,929E7	4,297E7	Erg
Q91VX2	Ubiquitin-associated protein 2 OS=Mus musculus GN=Ubaip2 PE=1 SV=1 - [UBAP2_MOUSE]	0,000E0	0,000E0	0,000E0	2,538E7	3,871E7	5,953E7	Ubaip2
P56959	RNA-binding protein FUS OS=Mus musculus GN=Fus PE=1 SV=1 - [FUS_MOUSE]	0,000E0	0,000E0	0,000E0	1,050E8	7,401E7	1,250E8	Fus
Q8C570	mRNA export factor OS=Mus musculus GN=Rae1 PE=1 SV=1 - [RAE1_MOUSE]	0,000E0	0,000E0	0,000E0	4,069E6	7,391E6	5,248E6	Rae1

Q7TNC4-2	Isoform 2 of Putative RNA-binding protein Luc7-like 2 OS=Mus musculus GN=Luc7i2 - [LC7L2_MOUSE]	0,000E0	0,000E0	0,000E0	1,859E7	1,285E7	1,522E7	Luc7i2
Q8C650-2	Isoform 2 of Septin-10 OS=Mus musculus GN=Septi10 - [SEP10_MOUSE]	0,000E0	0,000E0	0,000E0	1,377E7	2,659E7	1,836E7	SEP10
Q70479	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 2 OS=Mus musculus GN=Trnfp1 PE=2 SV=1 - [BACD2_MOUSE]	0,000E0	0,000E0	0,000E0	1,470E6	1,089E6	5,919E6	Trnfp1
P97376	Protein FRG1 OS=Mus musculus GN=Frq1 PE=1 SV=2 - [FRG1_MOUSE]	0,000E0	0,000E0	0,000E0	5,329E6	8,235E6	2,307E7	Frq1
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=1 - [CMC1_MOUSE]	0,000E0	0,000E0	0,000E0	3,337E6	6,330E6	1,401E7	Slc25a12
Q80VP1	Epsin-1 OS=Mus musculus GN=Epn1 PE=1 SV=3 - [EPN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,231E7	1,602E7	1,741E7	Epn1
Q60770	Syntaxin-binding protein 3 OS=Mus musculus GN=Stxbp3 PE=1 SV=1 - [STXB3_MOUSE]	0,000E0	0,000E0	0,000E0	5,633E6	1,007E7	2,380E7	Stxbp3
Q9DBF7	Pre-mRNA-splicing factor CWC25 homolog OS=Mus musculus GN=Cwc25 PE=2 SV=2 - [CWC25_MOUSE]	0,000E0	0,000E0	0,000E0	8,290E6	2,534E7	5,619E7	Cwc25
Q6P939	Anoctamin-6 OS=Mus musculus GN=Ano6 PE=1 SV=1 - [ANO6_MOUSE]	0,000E0	0,000E0	0,000E0	1,782E7	7,361E7	5,032E7	Ano6
P55012	Solute carrier family 12 member 2 OS=Mus musculus GN=Slc12a2 PE=1 SV=2 - [S12A2_MOUSE]	0,000E0	0,000E0	0,000E0	1,428E7	4,314E7	7,206E7	Slc12a2
Q69Z49	Rho GTPase-activating protein 23 OS=Mus musculus GN=Arhgap23 PE=1 SV=2 - [RHG23_MOUSE]	0,000E0	0,000E0	0,000E0	6,428E6	1,428E7	1,929E7	Arhgap23
Q89983	Syntaxin-8 OS=Mus musculus GN=Stx8 PE=1 SV=1 - [STX8_MOUSE]	0,000E0	0,000E0	0,000E0	1,409E6	2,829E6	6,116E6	Stx8
P19096	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 - [FAS_MOUSE]	0,000E0	0,000E0	0,000E0	1,005E7	1,049E8	3,513E7	Fasn
Q61595-3	Isoform 3 of Kinetin OS=Mus musculus GN=Ktn1 - [KTN1_MOUSE]	0,000E0	0,000E0	0,000E0	3,072E6	5,064E6	1,429E7	Ktn1
Q61696	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2 - [H571A_MOUSE]	4,285E7	0,000E0	6,668E6	6,497E8	3,755E8	4,452E8	Hspa1a
Q9NW60	Glycogen synthase kinase-3 beta OS=Mus musculus GN=Gsk3b PE=1 SV=2 - [GSK3B_MOUSE]	0,000E0	0,000E0	0,000E0	7,454E6	2,103E6	1,642E7	Gsk3b
Q9EQH3	Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1 - [VPS35_MOUSE]	0,000E0	0,000E0	4,640E6	3,466E6	1,376E7	1,532E7	Vps35
Q8BP47	Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2 - [SYNC_MOUSE]	0,000E0	0,000E0	0,000E0	2,679E6	9,245E6	2,191E7	Nars
Q80U72	Protein scribble homolog OS=Mus musculus GN=Scrib PE=1 SV=2 - [SCRIB_MOUSE]	0,000E0	0,000E0	0,000E0	4,114E6	1,275E7	1,263E7	Scrib
Q08807	Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1 - [PRDX4_MOUSE]	0,000E0	0,000E0	0,000E0	7,418E7	1,501E8	2,181E8	Prdx4
Q3JUM0	Spermatogenesis-associated protein 5 OS=Mus musculus GN=Spata5 PE=1 SV=2 - [SPAT5_MOUSE]	0,000E0	0,000E0	0,000E0	1,559E6	1,190E7	5,678E6	Spata5
O08638-2	Isoform 2 of Myosin-11 OS=Mus musculus GN=Myh11 - [MYH11_MOUSE]	2,336E8	0,000E0	2,340E8	3,928E9	7,665E9	5,658E9	Myh11
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus GN=Decr1 PE=1 SV=1 - [DECR_MOUSE]	0,000E0	0,000E0	0,000E0	1,257E6	1,499E7	2,072E7	Decr1
P97473	RISC-loading complex subunit TARBP2 OS=Mus musculus GN=Trbp2 PE=1 SV=2 - [TRBP2_MOUSE]	0,000E0	0,000E0	0,000E0	3,365E6	9,437E6	1,787E7	Trbp2
Q78HU3	Multivesicular body subunit 12A OS=Mus musculus GN=Mvb12a PE=1 SV=1 - [MB12A_MOUSE]	0,000E0	0,000E0	0,000E0	8,758E6	1,521E7	2,166E7	Mvb12a
Q9Z110-2	Isoform Short of Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 - [PSCS_MOUSE]	0,000E0	0,000E0	0,000E0	5,133E6	7,406E6	6,006E6	Aldh18a1
Q62093	Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4 - [SRSF2_MOUSE]	0,000E0	0,000E0	0,000E0	5,248E7	1,203E8	1,941E8	Srsf2
Q99JB2	Stomatin-like protein 2, mitochondrial OS=Mus musculus GN=Stoml2 PE=1 SV=1 - [STML2_MOUSE]	0,000E0	0,000E0	0,000E0	4,798E6	3,895E6	7,812E6	Stoml2
Q99M11	ELKS/Rab6-interacting/CAST family member 1 OS=Mus musculus GN=Erc1 PE=1 SV=1 - [RB6I2_MOUSE]	0,000E0	0,000E0	0,000E0	2,984E6	5,782E6	1,285E7	Erc1
P62234	26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 - [PRS10_MOUSE]	0,000E0	0,000E0	0,000E0	3,346E6	6,920E6	9,617E6	Psmc6
Q3JUV1	Coiled-coil domain-containing protein 61 OS=Mus musculus GN=Ccdc61 PE=1 SV=1 - [CCD61_MOUSE]	0,000E0	0,000E0	0,000E0	1,260E7	6,014E6	1,051E7	Ccdc61
P28798	Granulins OS=Mus musculus GN=Grn PE=1 SV=2 - [GRN_MOUSE]	0,000E0	0,000E0	3,374E6	5,539E7	2,659E7	1,343E7	Grn
O08573-3	Isoform 3 of Galectin-9 OS=Mus musculus GN=Lgals9 - [LEG9_MOUSE]	0,000E0	0,000E0	0,000E0	4,338E7	8,750E7	1,411E8	Lgals9
Q6PDN3-2	Isoform 2 of Myosin light chain kinase, smooth muscle OS=Mus musculus GN=Mylk - [MYLK_MOUSE]	0,000E0	0,000E0	0,000E0	3,810E6	5,593E6	4,908E6	Mylk
P11928	Z'-5'-oligoadenylate synthase 1A OS=Mus musculus GN=Oas1a PE=1 SV=2 - [OAS1A_MOUSE]	0,000E0	0,000E0	0,000E0	2,327E6	3,065E6	4,501E6	Oas1a
P45376	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3 - [ALDR_MOUSE]	0,000E0	0,000E0	0,000E0	4,119E6	4,037E6	2,748E6	Akr1b1
P62892	60S ribosomal protein L39 OS=Mus musculus GN=Rpl39 PE=1 SV=2 - [RL39_MOUSE]	0,000E0	0,000E0	5,020E7	1,776E8	2,018E7	2,018E7	Rpl39
P18654	Ribosomal protein S6 kinase alpha-3 OS=Mus musculus GN=Rps6ka3 PE=1 SV=2 - [KS6A3_MOUSE]	0,000E0	0,000E0	0,000E0	8,356E6	8,702E6	9,966E6	Rps6ka3
Q9DM3-2	Isoform 2 of Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cycl1 - [CY1_MOUSE]	0,000E0	0,000E0	0,000E0	3,243E6	5,202E6	3,767E6	Cycl1
Q9JLQ2	ARF GTPase-activating protein GIT2 OS=Mus musculus GN=Git2 PE=1 SV=2 - [GIT2_MOUSE]	0,000E0	0,000E0	0,000E0	2,868E6	8,952E6	3,523E6	Git2
Q9DC53	Copine-8 OS=Mus musculus GN=Cpne8 PE=2 SV=3 - [CPNE8_MOUSE]	0,000E0	0,000E0	0,000E0	1,988E6	5,852E6	6,593E6	Cpne8
Q8K382	DENN domain-containing protein 1A OS=Mus musculus GN=Dennd1a PE=1 SV=2 - [DEN1A_MOUSE]	0,000E0	0,000E0	0,000E0	1,630E7	2,689E7	2,916E7	Dennd1a
Q00547-2	Isoform RHAMM1 of Hyaluronan mediated motility receptor OS=Mus musculus GN=Hmnr - [HMMR_MOUSE]	0,000E0	0,000E0	0,000E0	4,188E6	5,031E6	1,273E7	Hmnr
P26369	Splicing factor U2AF 65 kDa subunit OS=Mus musculus GN=U2af2 PE=1 SV=3 - [U2AF2_MOUSE]	0,000E0	0,000E0	0,000E0	3,688E6	1,219E7	2,900E7	U2af2
Q62433	Protein NDRG1 OS=Mus musculus GN=Ndr1 PE=1 SV=1 - [NDRG1_MOUSE]	0,000E0	0,000E0	0,000E0	1,007E7	1,516E7	1,487E7	Ndr1
P12382	ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkfb1 PE=1 SV=4 - [PFKAL_MOUSE]	0,000E0	0,000E0	0,000E0	7,220E6	1,677E7	9,026E6	Pfkfb1
Q6PIU9	Uncharacterized protein FLJ45252 homolog OS=Mus musculus PE=1 SV=2 - [YJ005_MOUSE]	0,000E0	0,000E0	0,000E0	7,404E6	1,401E7	7,361E6	YJ0051
Q3UHD6-2	Isoform 2 of Sorting nexin-27 OS=Mus musculus GN=Snx27 - [SNX27_MOUSE]	0,000E0	0,000E0	0,000E0	3,634E6	7,773E6	1,341E7	Snx27
P61327	Protein mago nashi homolog OS=Mus musculus GN=Magoh PE=2 SV=1 - [MGN_MOUSE]	0,000E0	0,000E0	0,000E0	6,361E6	9,293E6	1,220E7	Magoh
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psm2 PE=1 SV=1 - [PSMD2_MOUSE]	0,000E0	0,000E0	7,491E5	4,942E6	1,437E7	1,767E7	Psmd2
Q8BYC6	Serine/threonine-protein kinase TAO3 OS=Mus musculus GN=Taok3 PE=1 SV=2 - [TAOK3_MOUSE]	0,000E0	0,000E0	0,000E0	2,401E6	1,906E7	8,089E7	Taok3
Q8R1F0	Leydig cell tumor 10 kDa protein homolog OS=Mus musculus GN=D8Ertd738e PE=3 SV=1 - [L10K_MOUSE]	0,000E0	0,000E0	0,000E0	3,468E6	5,988E6	2,568E7	D8Ertd738e
Q9DAW9	Calponin-3 OS=Mus musculus GN=Cnn3 PE=1 SV=1 - [CNN3_MOUSE]	0,000E0	0,000E0	0,000E0	1,946E6	4,101E6	2,096E7	Cnn3
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2 - [DYH1C1_MOUSE]	0,000E0	0,000E0	2,944E6	5,116E6	7,967E6	1,125E7	Dync1h1
Q3JUMT1	Protein phosphatase 1 regulatory subunit 12C OS=Mus musculus GN=Ppp1r12c PE=1 SV=1 - [PP12C_MOUSE]	0,000E0	0,000E0	0,000E0	4,169E6	7,718E6	7,432E6	Ppp1r12c
Q56926	Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1 - [TR150_MOUSE]	0,000E0	0,000E0	0,000E0	4,365E6	8,336E6	1,974E7	Thrap3
Q4VAA7	Sorting nexin-33 OS=Mus musculus GN=Snx33 PE=1 SV=1 - [SNX33_MOUSE]	0,000E0	0,000E0	0,000E0	9,825E6	1,609E7	3,495E7	Snx33
P70297	Signal transducing adapter molecule 1 OS=Mus musculus GN=Stam PE=1 SV=3 - [STAM1_MOUSE]	0,000E0	0,000E0	0,000E0	1,535E6	1,783E7	7,236E6	Stam
Q70133-2	Isoform 2 of ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 - [DHX9_MOUSE]	0,000E0	0,000E0	0,000E0	1,772E6	4,093E6	1,239E7	Dhx9
Q8C147	Dedicator of cytokinesis protein 8 OS=Mus musculus GN=Dock8 PE=1 SV=4 - [DOCK8_MOUSE]	0,000E0	0,000E0	0,000E0	1,105E7	5,246E7	2,007E7	Dock8
O55143-2	Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 - [AT2A2_MOUSE]	0,000E0	0,000E0	0,000E0	7,180E6	6,207E6	2,255E7	Atp2a2
O88643	Serine/threonine-protein kinase PAK 1 OS=Mus musculus GN=Pak1 PE=1 SV=1 - [PAK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,356E6	1,486E6	5,065E6	Pak1
Q9CWT6	Probable ATP-dependent RNA helicase DDX28 OS=Mus musculus GN=Ddx28 PE=2 SV=2 - [DDX28_MOUSE]	0,000E0	0,000E0	0,000E0	3,404E6	8,764E6	5,939E6	Ddx28
Q9EPL8	Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2 - [IPO7_MOUSE]	0,000E0	0,000E0	0,000E0	1,051E7	1,243E7	3,272E7	Ipo7
P12815	Programmed cell death protein 6 OS=Mus musculus GN=Pdc6 PE=1 SV=2 - [PDCD6_MOUSE]	0,000E0	0,000E0	0,000E0	1,087E6	1,745E6	2,091E5	Pdc6
Q9Z1Q9	Valine--tRNA ligase OS=Mus musculus GN=Vars PE=1 SV=1 - [SYVC_MOUSE]	0,000E0	0,000E0	0,000E0	1,242E7	2,355E7	4,246E7	Vars
Q8BPJ7	Engulfment and cell motility protein 1 OS=Mus musculus GN=Elmo1 PE=1 SV=2 - [ELMO1_MOUSE]	0,000E0	0,000E0	0,000E0	4,423E6	2,429E6	1,424E7	Elmo1
Q9Z1P7	KN motif and ankyrin repeat domain-containing protein 3 OS=Mus musculus GN=Kank3 PE=1 SV=1 - [KANK3_MOUSE]	0,000E0	0,000E0	0,000E0	7,252E6	8,195E6	2,766E7	Kank3
P52332	Tyrosine-protein kinase JAK1 OS=Mus musculus GN=Jak1 PE=1 SV=1 - [JAK1_MOUSE]	0,000E0	0,000E0	0,000E0	5,634E6	1,422E7	1,417E7	Jak1
Q99JX7	Nuclear RNA export factor 1 OS=Mus musculus GN=Nxf1 PE=1 SV=3 - [NXF1_MOUSE]	0,000E0	0,000E0	0,000E0	6,390E6	8,956E6	3,575E7	Nxf1
Q8CIE6	Coatamer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=2 - [COPA_MOUSE]	0,000E0	0,000E0	0,000E0	7,174E6	1,016E7	1,350E7	Copa
Q6A068	Cell division cycle 5-like protein OS=Mus musculus GN=Cdc5l PE=1 SV=2 - [CDC5L_MOUSE]	0,000E0	0,000E0	0,000E0	2,788E6	4,932E6	8,101E6	Cdc5l
P24547	Inosine 5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2 - [IMDH2_MOUSE]	0,000E0	0,000E0	1,492E5	2,540E6	9,987E6	1,309E7	Impdh2
Q9JIF0-3	Isoform 3 of Protein arginine N-methyltransferase 1 OS=Mus musculus GN=Prrmt1 - [ANM1_MOUSE]	0,000E0	0,000E0	0,000E0	2,328E6	1,527E6	8,366E6	Prrmt1
Q810D6	Glutamate-rich WD repeat-containing protein 1 OS=Mus musculus GN=Grwd1 PE=1 SV=2 - [GRWD1_MOUSE]	0,000E0	0,000E0	0,000E0	2,322E6	6,257E6	1,152E7	Grwd1
O70310	Glycylpeptide N-tetradecanoyltransferase 1 OS=Mus musculus GN=Nnt1 PE=1 SV=1 - [NNT1_MOUSE]	0,000E0	0,000E0	0,000E0	5,233E6	1,449E7	1,426E7	Nnt1
Q9D0F4	NF-kappa-B-activating protein OS=Mus musculus GN=Nkap PE=2 SV=1 - [NKAP_MOUSE]	0,000E0	0,000E0	0,000E0	1,025E7	1,824E7	1,192E7	Nkap
Q60668-4	Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnnpd - [HNRPD_MOUSE]	0,000E0	0,000E0	0,000E0	5,570E6	3,767E7	4,084E6	Hnnpd
Q8K045	Serine/threonine-protein kinase N3 OS=Mus musculus GN=Pkn3 PE=1 SV=1 - [PKN3_MOUSE]	0,000E0	0,000E0	0,000E0	2,128E6	5,524E6	3,647E6	Pkn3
Q3U134	DNA damage-binding protein 1 OS=Mus musculus GN=Ddb1 PE=1 SV=2 - [DDB1_MOUSE]	0,000E0	0,000E0	0,000E0	4,267E6	3,772E6	9,233E6	Ddb1
Q3JUQ28	Peroxidase homolog OS=Mus musculus GN=Pxdn PE=1 SV=2 - [PXDN_MOUSE]	0,000E0	0,000E0	0,000E0	9,280E6	1,365E7	2,619E7	Pxdn
Q08288	Cell growth-regulating nucleolar protein OS=Mus musculus GN=Lyar PE=1 SV=2 - [LYAR_MOUSE]	0,000E0	0,000E0	0,000E0	2,423E6	3,167E6	4,356E6	Lyar
Q4FK66	Pre-mRNA-splicing factor 38A OS=Mus musculus GN=Prpf38a PE=1 SV=1 - [PR38A_MOUSE]	0,000E0	0,000E0	2,106E6	1,084E7	3,212E7	3,212E7	Prpf38a
Q07076	Annexin A7 OS=Mus musculus GN=Anxa7 PE=1 SV=2 - [ANXA7_MOUSE]	0,000E0	0,000E0	0,000E0	7,293E6	1,131E7	1,712E7	Anxa7
Q8CIW5	Twinkle protein, mitochondrial OS=Mus musculus GN=Peo1 PE=2 SV=1 - [PEO1_MOUSE]	0,000E0	0,000E0	0,000E0	1,675E6	2,124E6	6,791E6	Peo1
Q61074	Protein phosphatase 1G OS=Mus musculus GN=Ppm1g PE=1 SV=3 - [PPM1G_MOUSE]	0,000E0	0,000E0	0,000E0	1,792E6	4,290E6	2,796E6	Ppm1g
Q5SW75	Protein phosphatase Slingshot homolog 2 OS=Mus musculus GN=Ssh2 PE=1 SV=2 - [SSH2_MOUSE]	0,000E0	0,000E0	0,000E0	1,604E6	2,964E6	7,512E6	Ssh2
Q01730	Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=1 SV=3 - [RSU1_MOUSE]	0,000E0	0,000E0	0,000E0	3,683E6	7,382E6	4,768E6	Rsu1
Q6IRU5-2	Isoform 2 of Clathrin light chain B OS=Mus musculus GN=Cltb - [CLCB_MOUSE]	0,000E0	0,000E0	0,000E0	2,662E7	5,010E7	8,397E7	Cltb
Q9CS00	Cactin OS=Mus musculus GN=Cactin PE=1 SV=2 - [CATIN_MOUSE]	0,000E0	0,000E0	0,000E0	1,148E6	2,699E6	2,574E7	Cactin
P97372	Proteasome activator complex subunit 2 OS=Mus musculus GN=Psme2 PE=1 SV=4 - [PSME2_MOUSE]	0,000E0	0,000E0	0,000E0	1,607E6	4,578E6	1,067E6	Psme2
Q61768	Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3 - [KINH_MOUSE]	0,000E0	0,000E0	0,000E0	3,844E6	7,054E6	7,687E6	Kif5b
P68181	cAMP-dependent protein kinase catalytic subunit beta OS=Mus musculus GN=Prkach PE=1 SV=2 - [KAPCB_MOUSE]	0,000E0	0,000E0	0,000E0	5,456E6	9,244E6	7,668E6	Prkach

Q80TH2-1	Isoform 1 of Erbin OS=Mus musculus GN=Erbin - [ERBIN_MOUSE]	0,000E0	0,000E0	0,000E0	2,347E6	6,759E6	8,371E6	Erbin
Q8VB76	Apolipoprotein B receptor OS=Mus musculus GN=ApoBr PE=1 SV=1 - [APOBR_MOUSE]	0,000E0	0,000E0	0,000E0	3,354E6	6,306E6	7,357E6	ApoBr
Q9CWX9	Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2 - [PUR9_MOUSE]	0,000E0	0,000E0	0,000E0	2,409E6	6,303E6	4,578E6	Atic
A2AQ19	RNA polymerase-associated protein RTF1 homolog OS=Mus musculus GN=RTf1 PE=1 SV=1 - [RTF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,034E6	3,900E6	1,019E7	Rtf1
P39688	Tyrosine-protein kinase Fyn OS=Mus musculus GN=Fyn PE=1 SV=4 - [FYN_MOUSE]	0,000E0	0,000E0	2,114E5	1,442E7	6,131E7	7,532E7	Fyn
Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3 - [M2OM_MOUSE]	0,000E0	0,000E0	0,000E0	6,059E6	1,770E7	1,029E7	Slc25a11
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1 SV=2 - [LIS1_MOUSE]	0,000E0	0,000E0	0,000E0	8,818E6	6,403E6	2,972E7	Pafah1b1
Q9Z2X8	Keich-like ECH-associated protein 1 OS=Mus musculus GN=Keap1 PE=1 SV=1 - [KEAP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,604E6	6,488E6	1,298E7	Keap1
P97386-2	Isoform Beta of DNA ligase 3 OS=Mus musculus GN=Lig3 - [DNLJ3_MOUSE]	0,000E0	0,000E0	0,000E0	3,950E6	2,136E6	1,202E7	Lig3
Q8VHK9	ATP-dependent RNA helicase DHX36 OS=Mus musculus GN=Dhx36 PE=1 SV=2 - [DHX36_MOUSE]	0,000E0	0,000E0	0,000E0	6,937E6	7,944E6	1,198E7	Dhx36
Q61846	Maternal embryonic leucine zipper kinase OS=Mus musculus GN=Melk PE=1 SV=2 - [MELK_MOUSE]	0,000E0	0,000E0	0,000E0	1,905E6	2,942E6	6,697E6	Melk
Q8CHH9	Septin-8 OS=Mus musculus GN=Sept8 PE=1 SV=4 - [SEPT8_MOUSE]	0,000E0	0,000E0	0,000E0	1,802E7	3,045E7	1,040E7	SEPT18
Q8OUF5	Ankyrin repeat domain-containing protein 13A OS=Mus musculus GN=Ankrd13a PE=1 SV=2 - [AN13A_MOUSE]	0,000E0	0,000E0	0,000E0	2,476E6	1,354E6	2,324E6	Ankrd13a
Q8R570	Synaposomal-associated protein 47 OS=Mus musculus GN=Snap47 PE=1 SV=1 - [SNP47_MOUSE]	0,000E0	0,000E0	0,000E0	9,854E5	4,840E6	6,747E6	Snap47
P50516	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2 - [VATA_MOUSE]	0,000E0	0,000E0	0,000E0	2,553E6	1,379E6	5,067E6	Atp6v1a
Q69ZB0-3	Isoform 3 of Leucine-rich repeat and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Lrrcc1 - [LRCC1_MOUSE]	0,000E0	0,000E0	0,000E0	2,347E6	4,735E6	3,274E6	Lrrcc1
Q99KK2	N-acyneuraminase cytidylyltransferase OS=Mus musculus GN=Cmas PE=1 SV=2 - [NEUA_MOUSE]	0,000E0	0,000E0	0,000E0	1,756E6	5,798E6	7,022E6	Cmas
Q62172	RalA-binding protein 1 OS=Mus musculus GN=Ralbp1 PE=1 SV=4 - [RBP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,565E7	1,146E7	1,415E7	Ralbp1
B2RQC6	CAD protein OS=Mus musculus GN=Cad PE=1 SV=1 - [PYR1_MOUSE]	0,000E0	0,000E0	0,000E0	5,483E6	1,615E7	1,448E7	Cad
Q1HFZ0	tRNA (cytosine(34)-C)-5'-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2 - [NSUN2_MOUSE]	0,000E0	0,000E0	0,000E0	2,205E6	2,475E6	7,144E6	Nsun2
Q68FH0	Plakophilin-4 OS=Mus musculus GN=Pkp4 PE=1 SV=1 - [PKP4_MOUSE]	0,000E0	0,000E0	0,000E0	2,776E6	7,408E6	5,875E6	Pkp4
Q3JTG2	Protein FAM107B OS=Mus musculus GN=Fam107b PE=1 SV=2 - [F107B_MOUSE]	0,000E0	0,000E0	0,000E0	2,030E6	9,268E6	1,621E7	Fam107b
Q8BM83	Eukaryotic translation initiation factor 4E type 2 OS=Mus musculus GN=Eif4e2 PE=1 SV=1 - [IF4E2_MOUSE]	0,000E0	0,000E0	0,000E0	8,189E6	6,987E6	3,439E7	Eif4e2
Q80X14	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta OS=Mus musculus GN=Pip4k2b PE=1 SV=1 - [PI42B_MOUSE]	0,000E0	0,000E0	0,000E0	2,082E6	3,995E6	1,697E7	Pip4k2b
Q908W5	26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psmd12 PE=1 SV=4 - [PSD12_MOUSE]	0,000E0	0,000E0	0,000E0	1,880E6	5,001E6	3,952E6	Psmd12
Q8R2Q8	Bone marrow stromal antigen 2 OS=Mus musculus GN=Bst2 PE=1 SV=1 - [BST2_MOUSE]	0,000E0	0,000E0	0,000E0	4,800E7	1,182E8	3,273E8	Bst2
Q9Z3D4	Splicing factor 3B subunit 5 OS=Mus musculus GN=SF3b5 PE=1 SV=1 - [SF3B5_MOUSE]	0,000E0	0,000E0	0,000E0	3,545E6	8,978E6	1,730E7	Sf3b5
P97465	Docking protein 1 OS=Mus musculus GN=Dok1 PE=1 SV=2 - [DOK1_MOUSE]	0,000E0	0,000E0	0,000E0	3,292E6	6,291E6	1,275E7	Dok1
P28656	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap1l1 PE=1 SV=2 - [NP1L1_MOUSE]	0,000E0	0,000E0	0,000E0	8,986E6	3,494E7	3,736E7	Nap1l1
Q9QX11-2	Isoform 2 of Cytohesin-1 OS=Mus musculus GN=Cytl1 - [CYH1_MOUSE]	0,000E0	0,000E0	0,000E0	4,744E6	2,455E7	4,210E6	Cytl1
Q64511	DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2 - [TOP2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,330E7	4,832E7	9,462E7	Top2b
P61164	Alpha-centractin OS=Mus musculus GN=Actr1a PE=1 SV=1 - [ACTZ_MOUSE]	0,000E0	0,000E0	0,000E0	5,285E6	3,488E7	2,330E7	Actr1a
P17257	Protein FAM167B OS=Mus musculus GN=Fam167b PE=2 SV=2 - [F167B_MOUSE]	0,000E0	0,000E0	0,000E0	5,233E6	1,353E7	9,100E6	Fam167b
Q9E5T5	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Mus musculus GN=Anp32b PE=1 SV=1 - [AN32B_MOUSE]	0,000E0	0,000E0	0,000E0	3,187E6	6,358E6	3,465E6	Anp32b
P35235	Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2 - [PTN11_MOUSE]	0,000E0	0,000E0	0,000E0	2,902E6	3,135E6	5,808E6	Ptpn11
Q78IK2	Up-regulated during skeletal muscle growth protein 5 OS=Mus musculus GN=Usmg5 PE=1 SV=1 - [USMG5_MOUSE]	0,000E0	0,000E0	0,000E0	3,272E6	4,998E6	1,352E7	Usmg5
Q8VEHM	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1 - [MPCP_MOUSE]	0,000E0	0,000E0	0,000E0	2,277E7	3,369E7	5,978E7	Slc25a3
Q9R0N0	Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2 - [GALK1_MOUSE]	0,000E0	0,000E0	0,000E0	8,671E6	8,518E6	1,557E7	Galk1
Q99NH2-3	Isoform 3 of Partitioning defective 3 homolog OS=Mus musculus GN=Pard3 - [PARD3_MOUSE]	0,000E0	0,000E0	0,000E0	3,627E6	7,534E6	9,230E6	Pard3
Q6RHR9	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1 OS=Mus musculus GN=Mag1 PE=1 SV=1 - [MAG1_MOUSE]	0,000E0	0,000E0	0,000E0	9,352E6	2,147E7	3,627E7	Mag1
Q9JLV5	Cullin-3 OS=Mus musculus GN=Cul3 PE=1 SV=1 - [CUL3_MOUSE]	0,000E0	0,000E0	0,000E0	5,636E5	4,144E6	5,399E6	Cul3
Q64324	Syntaxin-binding protein 2 OS=Mus musculus GN=Stxbp2 PE=1 SV=1 - [STXB2_MOUSE]	0,000E0	0,000E0	0,000E0	4,569E5	4,727E6	5,283E6	Stxbp2
Q9QZ88	Vacuolar protein sorting-associated protein 29 OS=Mus musculus GN=Vps29 PE=1 SV=1 - [VPS29_MOUSE]	0,000E0	0,000E0	0,000E0	4,303E6	4,444E6	8,343E6	Vps29
Q9CYH6	Ribosome biogenesis regulatory protein homolog OS=Mus musculus GN=Rrs1 PE=1 SV=1 - [RRS1_MOUSE]	0,000E0	0,000E0	0,000E0	7,456E5	2,835E6	3,820E6	Rrs1
Q9WV02-2	Isoform 2 of RNA-binding motif protein, X chromosome OS=Mus musculus GN=RbmX - [RBMX_MOUSE]	0,000E0	0,000E0	0,000E0	4,958E6	3,403E6	2,397E7	RbmX
Q924C6	Lysoyl oxidase homolog 4 OS=Mus musculus GN=LoxH4 PE=2 SV=2 - [LOXL4_MOUSE]	0,000E0	0,000E0	0,000E0	7,417E6	1,448E7	3,724E7	LoxH4
P15379-2	Isoform 13 of CD44 antigen OS=Mus musculus GN=Cd44 - [CD44_MOUSE]	0,000E0	0,000E0	0,000E0	3,270E6	1,960E7	4,612E7	Cd44
Q9CQV6	Microtubule-associated proteins 1A/1B light chain 3B OS=Mus musculus GN=Map1lc3b PE=1 SV=3 - [MLP3B_MOUSE]	0,000E0	0,000E0	0,000E0	9,970E6	2,051E7	2,933E7	Map1lc3b
Q9CZH8-2	Isoform 2 of Coiled-coil domain-containing protein 77 OS=Mus musculus GN=Cdc77 - [CCD77_MOUSE]	0,000E0	0,000E0	0,000E0	2,014E6	8,513E6	5,174E6	Cdc77
Q91WB7	Ubiquitin domain-containing protein 1 OS=Mus musculus GN=UbtD1 PE=2 SV=1 - [UBTD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,787E6	9,254E5	2,288E6	UbtD1
Q99NB9	Splicing factor 3B subunit 1 OS=Mus musculus GN=SF3b1 PE=1 SV=1 - [SF3B1_MOUSE]	0,000E0	0,000E0	0,000E0	2,034E6	1,116E7	1,570E7	Sf3b1
Q60848-2	Isoform 2 of Lymphocyte-specific helicase OS=Mus musculus GN=Hells - [HELLS_MOUSE]	0,000E0	0,000E0	0,000E0	2,855E6	4,705E6	8,351E6	Hells
Q54946	DnaJ homolog subfamily B member 6 OS=Mus musculus GN=DnaJb6 PE=1 SV=4 - [DNUB6_MOUSE]	0,000E0	0,000E0	0,000E0	9,339E6	9,220E6	8,046E6	DnaJb6
Q8K2X3	CST complex subunit STN1 OS=Mus musculus GN=Stn1 PE=1 SV=2 - [STN1_MOUSE]	0,000E0	0,000E0	0,000E0	4,694E6	4,647E6	5,395E6	Stn1
A2RSY6	TRMT1-like protein OS=Mus musculus GN=Trmt1l PE=1 SV=1 - [TRMT1_MOUSE]	0,000E0	0,000E0	0,000E0	5,755E6	7,540E6	1,548E7	Trmt1l
Q3TKT4	Transcription activator BRG1 OS=Mus musculus GN=Smarca4 PE=1 SV=1 - [SMCA4_MOUSE]	0,000E0	0,000E0	0,000E0	5,388E6	4,917E6	6,777E6	Smarca4
P97432	Next to BRCA1 gene 1 protein OS=Mus musculus GN=Nbr1 PE=1 SV=1 - [NBR1_MOUSE]	0,000E0	0,000E0	0,000E0	1,301E7	2,664E7	2,224E7	Nbr1
Q91V92	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1 - [ACLY_MOUSE]	0,000E0	0,000E0	0,000E0	3,734E6	7,970E6	1,037E7	Acly
Q9ETZ6	E3 ubiquitin-protein ligase RNF114 OS=Mus musculus GN=Rnf114 PE=1 SV=2 - [RNF114_MOUSE]	0,000E0	0,000E0	0,000E0	1,559E6	3,166E6	4,096E6	Rnf114
Q62312-2	Isoform RII-1 of TGF-beta receptor type-2 OS=Mus musculus GN=Tgfr2 - [TGFR2_MOUSE]	0,000E0	0,000E0	0,000E0	3,425E6	9,760E6	1,333E7	Tgfr2
Q08788-2	Isoform 2 of Dynactin subunit 1 OS=Mus musculus GN=Dctn1 - [DCTN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,861E6	1,100E7	6,943E6	Dctn1
Q8COC7	Phenylalanine--tRNA ligase alpha subunit OS=Mus musculus GN=Farsa PE=1 SV=1 - [SYFA_MOUSE]	0,000E0	0,000E0	0,000E0	2,208E6	4,154E6	8,435E6	Farsa
Q9Z2D1	Myotubularin-related protein 2 OS=Mus musculus GN=Mtmr2 PE=1 SV=3 - [MTMR2_MOUSE]	0,000E0	0,000E0	0,000E0	8,915E5	4,390E6	6,080E6	Mtmr2
Q9CWX9	Probable ATP-dependent RNA helicase DDX47 OS=Mus musculus GN=Ddx47 PE=2 SV=2 - [DDX47_MOUSE]	0,000E0	0,000E0	0,000E0	3,773E6	4,408E6	7,407E6	Ddx47
Q9Z2B9	Ribosomal protein S6 kinase alpha-4 OS=Mus musculus GN=Rps6ka4 PE=1 SV=2 - [KS6A4_MOUSE]	0,000E0	0,000E0	0,000E0	2,213E6	4,829E6	4,433E6	Rps6ka4
Q9CQU1	Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1 - [MFAP1_MOUSE]	0,000E0	0,000E0	0,000E0	6,425E5	4,287E6	3,922E6	Mfap1
Q80943	FACT complex subunit SSRP1 OS=Mus musculus GN=Sarp1 PE=1 SV=2 - [SSRP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,363E6	2,438E6	2,111E7	Ssrp1
P31324	CAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkar2b PE=1 SV=3 - [KAP3_MOUSE]	0,000E0	0,000E0	0,000E0	2,595E6	3,574E6	9,664E5	Prkar2b
Q9DBE9	pre-rRNA processing protein FTSJ3 OS=Mus musculus GN=Ftsj3 PE=1 SV=1 - [SPB1_MOUSE]	0,000E0	0,000E0	0,000E0	1,958E6	3,378E6	9,315E6	Ftsj3
P62996	Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1 - [TRA2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,430E7	1,984E7	1,334E7	Tra2b
Q80UM7	Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=1 SV=1 - [MOGS_MOUSE]	0,000E0	0,000E0	0,000E0	2,944E6	1,768E6	5,937E6	Mogs
P61021	Ras-related protein Rab-5B OS=Mus musculus GN=Rab5b PE=1 SV=1 - [RAB5B_MOUSE]	0,000E0	0,000E0	0,000E0	1,294E6	2,563E7	5,475E7	Rab5b
Q91X43	SH3 domain-containing protein 19 OS=Mus musculus GN=Sh3d19 PE=1 SV=2 - [SH319_MOUSE]	0,000E0	0,000E0	0,000E0	2,247E6	6,127E6	3,582E6	Sh3d19
P28658	Ataxin-10 OS=Mus musculus GN=Atxn10 PE=1 SV=2 - [ATX10_MOUSE]	0,000E0	0,000E0	0,000E0	3,189E6	2,810E6	1,759E6	Atxn10
Q922W5	Pyroline-5-carboxylate reductase 1, mitochondrial OS=Mus musculus GN=Pycr1 PE=1 SV=1 - [P5CR1_MOUSE]	0,000E0	0,000E0	0,000E0	3,839E6	8,170E6	6,841E7	Pycr1
Q9CWZ3-2	Isoform 2 of RNA-binding protein 8A OS=Mus musculus GN=Rbm8a - [RBM8A_MOUSE]	0,000E0	0,000E0	0,000E0	1,669E6	6,538E6	5,105E6	Rbm8a
Q68FG3	Protein SPT2 homolog OS=Mus musculus GN=Spty2d1 PE=2 SV=1 - [SPT2_MOUSE]	0,000E0	0,000E0	0,000E0	2,451E6	1,018E7	9,001E6	Spty2d1
Q9JX06	ADP-sugar pyrophosphatase OS=Mus musculus GN=Nudt5 PE=1 SV=1 - [NUDT5_MOUSE]	0,000E0	0,000E0	0,000E0	6,197E6	4,715E6	7,611E6	Nudt5
Q909Z1	Small kinetochore-associated protein OS=Mus musculus GN=Knmtr PE=2 SV=2 - [SKAP_MOUSE]	0,000E0	0,000E0	0,000E0	3,112E6	7,991E6	8,356E6	Knmtr
B2RRF7	OTU domain-containing protein 4 OS=Mus musculus GN=Otu4 PE=1 SV=1 - [OTUD4_MOUSE]	0,000E0	0,000E0	0,000E0	7,442E6	6,910E6	1,338E7	Otu4
Q9DZQ3	Uncharacterized protein C10orf88 homolog OS=Mus musculus PE=2 SV=1 - [CJ088_MOUSE]	0,000E0	0,000E0	0,000E0	3,169E6	5,142E6	3,502E6	SKT
A2AQ25-8	Isoform 8 of Sic1e tail protein OS=Mus musculus GN=Skt - [SKT_MOUSE]	0,000E0	0,000E0	0,000E0	1,650E6	5,131E6	2,511E6	Skt
Q7TTF2	3'-5' exoribonuclease 1 OS=Mus musculus GN=Er1l PE=1 SV=2 - [ER11_MOUSE]	0,000E0	0,000E0	0,000E0	1,411E6	7,569E6	8,443E6	Er1l
Q8BG67	Protein EFR3 homolog A OS=Mus musculus GN=Efr3a PE=1 SV=1 - [EFR3A_MOUSE]	0,000E0	0,000E0	0,000E0	3,915E6	1,151E7	1,620E7	Efr3a
Q62415	Apoptosis-stimulating of p53 protein 1 OS=Mus musculus GN=Ppp1r13b PE=1 SV=2 - [ASPP1_MOUSE]	0,000E0	0,000E0	0,000E0	7,092E6	1,296E7	2,250E7	Ppp1r13b
P35441	Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1 - [TSP1_MOUSE]	0,000E0	0,000E0	0,000E0	8,753E6	1,171E7	2,563E7	Thbs1
Q60749	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Mus musculus GN=Khdrbs1 PE=1 SV=2 - [KHDR1_MOUSE]	0,000E0	0,000E0	0,000E0	1,327E7	1,459E7	3,045E7	Khdrbs1
Q91W50	Cold shock domain-containing protein E1 OS=Mus musculus GN=Csd1 PE=1 SV=1 - [CSD1_MOUSE]	0,000E0	0,000E0	0,000E0	3,768E6	7,555E6	1,671E7	Csd1
Q9CR67	Transmembrane protein 33 OS=Mus musculus GN=Tmem33 PE=1 SV=1 - [TMM33_MOUSE]	0,000E0	0,000E0	0,000E0	1,557E6	1,401E6	7,004E6	Tmem33
Q62523	Zyxin OS=Mus musculus GN=Zyx PE=1 SV=2 - [ZYX_MOUSE]	0,000E0	0,000E0	0,000E0	5,576E6	1,209E7	1,797E7	Zyx
Q03958	Prefoldin subunit 6 OS=Mus musculus GN=Pfdn6 PE=1 SV=1 - [PPD6_MOUSE]	0,000E0	0,000E0	0,000E0	1,502E6	2,888E6	4,143E6	Pfdn6
P54822	Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=1 SV=2 - [PUR8_MOUSE]	0,000E0	0,000E0	0,000E0	1,150E6	2,581E6	5,568E6	Adsl
Q64213-2	Isoform CW17E of Splicing factor 1 OS=Mus musculus GN=Sfi - [SF01_MOUSE]	0,000E0	0,000E0	0,000E0	4,830E6	6,298E6	3,930E7	Sfi1

Q80VD1	Protein FAM98B OS=Mus musculus GN=Fam98b PE=1 SV=1 - [FAM98_MOUSE]	0,000E0	0,000E0	0,000E0	1,435E6	5,079E6	2,171E6	Fam98b
Q9WUA2	Phenylalanine-tRNA ligase beta subunit OS=Mus musculus GN=Farsh PE=1 SV=2 - [SYFB_MOUSE]	0,000E0	0,000E0	0,000E0	3,032E6	3,172E6	1,251E7	Farsb
Q3TZZ7	Extended synaptotagmin-2 OS=Mus musculus GN=Esy2 PE=1 SV=1 - [ESYT2_MOUSE]	0,000E0	0,000E0	0,000E0	4,744E6	3,524E6	7,689E6	Esy2t
Q6NVF9	Cleavage and polyadenylation specificity factor subunit 6 OS=Mus musculus GN=Cpsf6 PE=1 SV=1 - [CPSF6_MOUSE]	0,000E0	0,000E0	0,000E0	5,040E6	1,384E7	1,272E7	Cpsf6
P40336	Vacuolar protein sorting-associated protein 26A OS=Mus musculus GN=Vps26a PE=1 SV=1 - [VP26A_MOUSE]	0,000E0	0,000E0	0,000E0	1,322E6	3,810E6	5,425E6	Vps26a
Q99M28-2	Isform 2 of RNA-binding protein with serine-rich domain 1 OS=Mus musculus GN=Rnps1 - [RNPS1_MOUSE]	0,000E0	0,000E0	0,000E0	2,831E6	1,237E7	1,851E7	Rnps1
P27048	Small nuclear ribonucleoprotein-associated protein B OS=Mus musculus GN=Snrbp PE=1 SV=1 - [RSMB_MOUSE]	0,000E0	0,000E0	0,000E0	2,612E6	8,608E6	1,963E7	Snrbp
Q80YK4-2	Isform 2 of Zinc finger protein 598 OS=Mus musculus GN=Znf598 - [ZNS98_MOUSE]	0,000E0	0,000E0	0,000E0	7,897E5	4,384E6	9,729E6	Znf598
Q03145	Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=3 - [EPHA2_MOUSE]	0,000E0	0,000E0	0,000E0	9,608E6	2,018E7	4,015E7	Epha2
E9Q3L2	Phosphatidylinositol 4-kinase alpha OS=Mus musculus GN=P4ka PE=1 SV=2 - [P4KA_MOUSE]	0,000E0	0,000E0	0,000E0	3,502E6	1,026E7	2,568E7	P4ka
Q80V11	E3 ubiquitin-protein ligase TRIM56 OS=Mus musculus GN=Trim56 PE=1 SV=1 - [TRIS6_MOUSE]	0,000E0	0,000E0	0,000E0	4,133E6	4,301E6	1,038E7	Trim56
Q5SURF2	Luc7-like protein 3 OS=Mus musculus GN=Luc73 PE=1 SV=1 - [LC7L3_MOUSE]	0,000E0	0,000E0	0,000E0	1,066E7	1,508E7	2,945E7	Luc7l3
Q8BGJ5-2	Isform 2 of Cyclin-Y OS=Mus musculus GN=Ccnv - [CCNV_MOUSE]	0,000E0	0,000E0	0,000E0	1,658E6	8,696E6	1,143E7	Ccnv
Q6ZPF4	Formin-like protein 3 OS=Mus musculus GN=Fmnl3 PE=1 SV=2 - [FMNL3_MOUSE]	0,000E0	0,000E0	0,000E0	5,625E6	6,977E6	1,567E7	Fmnl3
Q8CH77	Neuron navigator 1 OS=Mus musculus GN=Nav1 PE=1 SV=2 - [NAV1_MOUSE]	0,000E0	0,000E0	0,000E0	3,656E6	6,640E6	1,178E7	Nav1
Q922R8	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3 - [PDIA6_MOUSE]	0,000E0	0,000E0	0,000E0	4,343E6	1,020E7	1,314E7	Pdia6
P28828	Receptor-type tyrosine-protein phosphatase mu OS=Mus musculus GN=Ptpm PE=1 SV=2 - [PTPRM_MOUSE]	0,000E0	0,000E0	0,000E0	1,893E7	2,155E7	5,201E7	Ptpm
Q8BTW9	Serine/threonine-protein kinase PAK 4 OS=Mus musculus GN=Pa4 PE=1 SV=1 - [PAK4_MOUSE]	0,000E0	0,000E0	0,000E0	3,970E6	8,193E6	4,169E6	Pa4
Q8BWT5	Disco-interacting protein 2 homolog A OS=Mus musculus GN=Dip2a PE=1 SV=3 - [DIP2A_MOUSE]	0,000E0	0,000E0	0,000E0	6,147E6	1,695E7	2,390E7	Dip2a
E9Q6P5	Tetratricopeptide repeat protein 7B OS=Mus musculus GN=Ttc7b PE=1 SV=2 - [TTC7B_MOUSE]	0,000E0	0,000E0	0,000E0	1,440E6	5,095E6	3,417E6	Ttc7b
Q60973	Histone-binding protein RBBP7 OS=Mus musculus GN=Rbbp7 PE=1 SV=1 - [RBBP7_MOUSE]	0,000E0	0,000E0	0,000E0	5,163E6	8,607E6	8,965E6	Rbbp7
Q8BHL3	TBC1 domain family member 10B OS=Mus musculus GN=Tbc1d10b PE=1 SV=2 - [TB10B_MOUSE]	0,000E0	0,000E0	0,000E0	3,973E6	3,281E6	6,240E6	Tbc1d10b
Q8VDM6-2	Isform 2 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Mus musculus GN=Hnmpu1 - [HNRL1_MOUSE]	0,000E0	0,000E0	0,000E0	3,663E6	1,010E7	1,069E7	Hnnpu1
Q8C854-2	Isform 4 of Myelin expression factor 2 OS=Mus musculus GN=Myef2 - [MYEF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,791E6	5,703E6	5,880E6	Myef2
Q3UFK8	FERM domain-containing protein 8 OS=Mus musculus GN=Frmd8 PE=1 SV=2 - [FRMD8_MOUSE]	0,000E0	0,000E0	0,000E0	1,696E6	6,759E6	8,161E6	Frmd8
Q5EG47	5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Mus musculus GN=Prkaa1 PE=1 SV=2 - [AAPK1_MOUSE]	0,000E0	0,000E0	0,000E0	3,574E6	6,432E6	8,643E6	Prkaa1
Q78ZAT	Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap14 PE=1 SV=1 - [NP14_MOUSE]	0,000E0	0,000E0	0,000E0	2,814E6	7,931E6	9,935E6	Nap14
Q8C533-4	Isform 4 of Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 - [CIP4_MOUSE]	0,000E0	0,000E0	0,000E0	2,371E6	5,979E6	8,934E6	Trip10
Q9D1E6	Tubulin-folding cofactor B OS=Mus musculus GN=Tbcb PE=1 SV=2 - [TBCB_MOUSE]	0,000E0	0,000E0	0,000E0	1,996E6	5,520E6	1,107E7	Tbcb
Q91V64	Ischorismatase domain-containing protein 1 OS=Mus musculus GN=Isoc1 PE=1 SV=1 - [ISOC1_MOUSE]	0,000E0	0,000E0	0,000E0	6,309E5	9,475E5	1,217E7	Isoc1
Q9CZ30	Obg-like ATPase 1 OS=Mus musculus GN=Ola1 PE=1 SV=1 - [OLA1_MOUSE]	0,000E0	0,000E0	0,000E0	5,487E6	1,013E7	8,356E6	Ola1
008810	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=1 SV=1 - [U5S1_MOUSE]	0,000E0	0,000E0	0,000E0	1,263E6	4,777E6	1,038E7	Eftud2
P70261	Paladin OS=Mus musculus GN=Pald1 PE=1 SV=1 - [PALD_MOUSE]	0,000E0	0,000E0	0,000E0	3,772E6	1,473E7	2,316E7	Pald1
P61620	Protein transport protein Sec61 subunit alpha Isform 1 OS=Mus musculus GN=Sec61a1 PE=1 SV=2 - [S61A1_MOUSE]	0,000E0	0,000E0	0,000E0	8,238E6	1,329E7	1,101E7	Sec61a1
Q3UMJ9-4	Isform 4 of Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgrp2 - [HDGR2_MOUSE]	0,000E0	0,000E0	0,000E0	7,439E6	1,257E7	3,517E7	Hdgrp2
Q8C166	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1 - [CPNE1_MOUSE]	0,000E0	0,000E0	0,000E0	3,143E6	7,466E6	1,485E7	Cpne1
P05532-2	Isform 2 of Mast/stem cell growth factor receptor Kit OS=Mus musculus GN=Kit - [KIT_MOUSE]	0,000E0	0,000E0	0,000E0	6,934E6	1,624E7	1,454E7	Kit
P24788-2	Isform 2 of Cyclin-dependent kinase 11B OS=Mus musculus GN=Cdk11b - [CD11B_MOUSE]	0,000E0	0,000E0	0,000E0	2,265E6	2,024E6	6,840E6	Cdk11b
Q8BTH8	Casein kinase 1 isoform gamma-1 OS=Mus musculus GN=Csnk1g1 PE=1 SV=2 - [KC1G1_MOUSE]	0,000E0	0,000E0	0,000E0	1,557E6	6,473E6	6,647E6	Csnk1g1
Q8BSF4	Phosphatidylserine decarboxylase preenzyme, mitochondrial OS=Mus musculus GN=Psid PE=2 SV=1 - [PSID_MOUSE]	0,000E0	0,000E0	0,000E0	1,467E6	9,084E6	9,000E5	Psid
Q80YV0	Cytohesin-4 OS=Mus musculus GN=Cyht4 PE=1 SV=1 - [CYH4_MOUSE]	0,000E0	0,000E0	0,000E0	6,843E6	2,783E6	1,430E6	Cyht4
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1 - [SYAC_MOUSE]	0,000E0	0,000E0	2,770E6	1,262E6	2,349E6	4,970E6	Aars
P54103	DnaJ homolog subfamily C member 2 OS=Mus musculus GN=Dnajc2 PE=1 SV=2 - [DNJC2_MOUSE]	0,000E0	0,000E0	0,000E0	2,778E6	8,690E6	9,383E6	Dnajc2
Q9Z130	Heterogeneous nuclear ribonucleoprotein D-like OS=Mus musculus GN=Hnmpdl PE=1 SV=1 - [HNRLD_MOUSE]	0,000E0	0,000E0	0,000E0	2,962E6	3,767E7	8,374E5	Hnnpndl
070591	Prefoldin subunit 2 OS=Mus musculus GN=Pfdn2 PE=1 SV=2 - [PFD2_MOUSE]	0,000E0	0,000E0	0,000E0	2,267E6	8,575E6	7,390E6	Pfdn2
Q99MU3-2	Isform 2 of Double-stranded RNA-specific adenosine deaminase OS=Mus musculus GN=Adar - [DSRAD_MOUSE]	0,000E0	0,000E0	0,000E0	1,586E6	4,370E6	7,698E6	Adar
Q922M3	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3 OS=Mus musculus GN=Kctd10 PE=1 SV=1 - [BACD3_MOUSE]	0,000E0	0,000E0	0,000E0	1,638E6	1,853E6	2,809E6	Kctd10
Q922N8	Actin-like protein 6A OS=Mus musculus GN=Actl6a PE=1 SV=2 - [ACL6A_MOUSE]	0,000E0	0,000E0	0,000E0	1,781E6	1,211E6	1,226E7	Actl6a
Q8R052	IQ motif and SEC7 domain-containing protein 1 OS=Mus musculus GN=Iqsec1 PE=1 SV=2 - [IQEC1_MOUSE]	0,000E0	0,000E0	0,000E0	9,196E6	8,235E6	1,536E7	Iqsec1
P63158	High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2 - [HMGb1_MOUSE]	0,000E0	0,000E0	1,350E6	5,490E6	1,748E7	1,527E7	Hmgb1
Q8C4X2	Casein kinase 1 isoform gamma-3 OS=Mus musculus GN=Csnk1g3 PE=1 SV=2 - [KC1G3_MOUSE]	0,000E0	0,000E0	0,000E0	8,887E5	7,405E6	1,273E7	Csnk1g3
Q8C0T5-2	Isform 2 of Signal-induced proliferation-associated 1-like protein 1 OS=Mus musculus GN=Sipa1l1 - [S11L1_MOUSE]	0,000E0	0,000E0	0,000E0	2,472E6	1,051E7	8,639E6	Sipa1l1
054941	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Mus musculus GN=Smrce1 PE=1 SV=1 - [SMCE1_MOUSE]	0,000E0	0,000E0	0,000E0	1,832E6	6,045E6	5,037E6	Smrce1
Q569Z5	Probable ATP-dependent RNA helicase DDX46 OS=Mus musculus GN=Ddx46 PE=1 SV=2 - [DDX46_MOUSE]	0,000E0	0,000E0	0,000E0	1,133E6	4,288E6	1,951E7	Ddx46
Q99L47	Hsc70-interacting protein OS=Mus musculus GN=St13 PE=1 SV=1 - [F10A1_MOUSE]	0,000E0	0,000E0	0,000E0	3,360E6	1,326E7	1,360E7	St13
Q68FF6	ARF GTPase-activating protein GIT1 OS=Mus musculus GN=Gt1 PE=1 SV=1 - [GIT1_MOUSE]	0,000E0	0,000E0	0,000E0	2,866E6	9,406E6	5,909E6	Gt1
Q8C108	SLAIN motif-containing protein 2 OS=Mus musculus GN=Slain2 PE=1 SV=2 - [SLAI2_MOUSE]	0,000E0	0,000E0	0,000E0	1,662E6	6,204E5	1,296E6	Slain2
Q9EQJ5-2	Isform 2 of Protein SET OS=Mus musculus GN=Set - [SET_MOUSE]	0,000E0	0,000E0	0,000E0	1,135E6	2,098E6	1,744E6	Set
P40142	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1 - [TKT_MOUSE]	0,000E0	0,000E0	0,000E0	1,552E6	2,564E6	4,408E6	Tkt
P28740	Kinesin-like protein KIF2A OS=Mus musculus GN=Kif2a PE=1 SV=2 - [KIF2A_MOUSE]	0,000E0	0,000E0	0,000E0	3,446E6	7,067E6	1,070E7	Kif2a
P63073	Eukaryotic translation initiation factor 4E OS=Mus musculus GN=Eif4e PE=1 SV=1 - [EIF4_MOUSE]	0,000E0	0,000E0	0,000E0	1,825E6	1,121E7	1,342E7	Eif4e
Q69ZK2	E3 ubiquitin-protein ligase HECTD1 OS=Mus musculus GN=Hectd1 PE=1 SV=2 - [HECD1_MOUSE]	0,000E0	0,000E0	0,000E0	4,761E6	8,592E6	4,090E7	Hectd1
Q62376	U1 small nuclear ribonucleoprotein 70 kDa OS=Mus musculus GN=Snmp70 PE=1 SV=2 - [RU17_MOUSE]	0,000E0	0,000E0	0,000E0	3,976E6	8,504E6	1,748E7	Snmp70
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Mus musculus GN=Ndufs7 PE=1 SV=1 - [NDUS7_MOUSE]	0,000E0	0,000E0	0,000E0	1,121E6	2,305E6	4,994E6	Ndufs7
009110	Dual specificity mitogen-activated protein kinase kinase 3 OS=Mus musculus GN=Map2k3 PE=1 SV=2 - [MP2K3_MOUSE]	0,000E0	0,000E0	0,000E0	3,822E6	2,368E6	2,177E6	Map2k3
Q3U9G9	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2 - [LBR_MOUSE]	0,000E0	0,000E0	0,000E0	9,738E6	2,503E7	3,335E7	Lbr
Q8CH72	E3 ubiquitin-protein ligase TRIM32 OS=Mus musculus GN=Trim32 PE=1 SV=2 - [TRI32_MOUSE]	0,000E0	0,000E0	0,000E0	6,924E6	4,576E6	1,080E7	Trim32
Q8BNJ2	A disintegrin and metalloproteinase with thrombospondin motifs 4 OS=Mus musculus GN=Adamts4 PE=2 SV=2 - [AT54_MOUSE]	0,000E0	0,000E0	0,000E0	1,303E7	2,145E7	1,972E7	Adamts4
E9Q555	E3 ubiquitin-protein ligase RNF213 OS=Mus musculus GN=Rnf213 PE=1 SV=2 - [RN213_MOUSE]	0,000E0	0,000E0	8,642E5	1,198E7	1,853E7	3,576E7	Rnf213
Q60790	Ras GTPase-activating protein 3 OS=Mus musculus GN=Rasa3 PE=1 SV=2 - [RASA3_MOUSE]	0,000E0	0,000E0	0,000E0	3,180E6	6,456E6	1,620E7	Rasa3
Q8BH07-2	Isform 2 of Polypyrimidine tract-binding protein 3 OS=Mus musculus GN=Ptbp3 - [PTBP3_MOUSE]	0,000E0	0,000E0	0,000E0	3,256E7	5,081E7	1,794E8	Ptbp3
P17095-1	Isform HMG-Y of High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmgal - [HMGAL_MOUSE]	0,000E0	0,000E0	0,000E0	8,704E7	1,389E8	5,081E8	Hmgal
Q8BH88	DEP domain-containing protein 1B OS=Mus musculus GN=Depdc1b PE=2 SV=1 - [DEP1B_MOUSE]	0,000E0	0,000E0	0,000E0	3,815E5	4,607E5	1,198E6	Depdc1b
Q3TIV5	Zinc finger CCHC domain-containing protein 15 OS=Mus musculus GN=Zc3h15 PE=1 SV=2 - [ZC3HF_MOUSE]	0,000E0	0,000E0	0,000E0	5,932E6	2,158E6	4,901E6	Zc3h15
Q8CGC7	Bifunctional glutamate/proline-tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4 - [SYEP_MOUSE]	0,000E0	0,000E0	0,000E0	5,461E6	8,137E6	9,736E6	Eprs
Q64737	Trifunctional purine biosynthetic protein adenosine-3 OS=Mus musculus GN=Gart PE=1 SV=3 - [PUR2_MOUSE]	0,000E0	0,000E0	0,000E0	5,563E6	1,099E7	1,584E7	Gart
Q9Z2D8	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4 - [C1TC_MOUSE]	0,000E0	0,000E0	0,000E0	2,757E6	1,379E7	1,235E7	Mthfd1
Q9ESL4-2	Isform 2 of Mitogen-activated protein kinase kinase kinase MLT OS=Mus musculus GN=Zak - [MLTK_MOUSE]	0,000E0	0,000E0	0,000E0	6,924E6	6,027E6	8,104E6	Zak
Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Mus musculus GN=Plod3 PE=1 SV=1 - [PLOD3_MOUSE]	0,000E0	0,000E0	0,000E0	1,599E6	5,597E6	7,792E6	Plod3
Q60953-2	Isform 2 of Protein PML OS=Mus musculus GN=Pml - [PML_MOUSE]	0,000E0	0,000E0	0,000E0	5,147E6	1,029E7	1,552E7	Pml
Q8BWY3	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Erf1 PE=1 SV=4 - [ERF1_MOUSE]	0,000E0	0,000E0	0,000E0	2,605E6	1,678E6	7,679E6	Erf1
Q9CZ52	Anthrax toxin receptor 1 OS=Mus musculus GN=Anbr1 PE=1 SV=2 - [ANTR1_MOUSE]	0,000E0	0,000E0	0,000E0	5,248E6	1,095E7	1,206E7	Antrx1
P62046	Leucine-rich repeat and calponin homology domain-containing protein 1 OS=Mus musculus GN=Lrch1 PE=1 SV=2 - [LRCH1_MOUSE]	0,000E0	0,000E0	0,000E0	4,710E7	8,244E6	3,222E6	Lrch1
Q8K363	ATP-dependent RNA helicase DDX18 OS=Mus musculus GN=Ddx18 PE=1 SV=1 - [DDX18_MOUSE]	0,000E0	0,000E0	0,000E0	2,499E6	5,402E6	2,078E7	Ddx18
Q9ERU9	E3 SUMO-protein ligase Ranbp2 OS=Mus musculus GN=Ranbp2 PE=1 SV=2 - [RBP2_MOUSE]	0,000E0	0,000E0	0,000E0	3,740E6	6,148E6	2,168E7	Ranbp2
035691	Pinin OS=Mus musculus GN=Pnn PE=1 SV=4 - [PININ_MOUSE]	0,000E0	0,000E0	0,000E0	3,341E6	7,965E6	9,962E6	Pnn
P70255-5	Isform 5 of Nuclear factor 1 C-type OS=Mus musculus GN=Nfic - [NFIC_MOUSE]	0,000E0	0,000E0	0,000E0	8,960E6	4,007E6	7,908E5	Nfic
Q7TN60	Transmembrane channel-like protein 6 OS=Mus musculus GN=Tmc6 PE=1 SV=2 - [TMC6_MOUSE]	0,000E0	0,000E0	0,000E0	4,582E6	8,849E6	8,960E6	Tmc6
Q8CE50	N-alpha-acetyltransferase 30 OS=Mus musculus GN=Naa30 PE=1 SV=2 - [NAA30_MOUSE]	0,000E0	0,000E0	0,000E0	2,084E6	4,505E6	6,319E6	Naa30
P05132-2	Isform 2 of cAMP-dependent protein kinase catalytic subunit alpha OS=Mus musculus GN=Prkaca - [KAPCA_MOUSE]	0,000E0	0,000E0	0,000E0	7,310E6	9,244E6	1,493E7	Prkaca
P70429-2	Isform 1 of Ena/VASP-like protein OS=Mus musculus GN=Evl - [EVL_MOUSE]	0,000E0	0,000E0	0,000E0	1,947E6	5,076E6	3,122E6	Evl
Q3UMG5	Leucine-rich repeat and calponin homology domain-containing protein 2 OS=Mus musculus GN=Lrch2 PE=2 SV=2 - [LRCH2_MOUSE]	0,000E0	0,000E0	0,000E0	2,261E6	4,988E5	3,334E6	Lrch2
Q62432-2	Isform Short of Mothers against decapentaplegic homolog 2 OS=Mus musculus GN=Smad2 - [SMAD2_MOUSE]	0,000E0	0,000E0	0,000E0	1,545E6	1,128E7	7,537E6	Smad2

Q791V5	Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1 SV=1 - [MTCH2_MOUSE]	0,000E0	0,000E0	0,000E0	2,528E6	6,857E6	1,589E7	Mtch2
P28740-2	Isoform 2 of Kinesin-like protein KIF2a OS=Mus musculus GN=Kif2a - [KIF2a_MOUSE]	0,000E0	0,000E0	0,000E0	3,466E6	7,067E6	1,070E7	Kif2a
Q6PGH0	Ubiquitin domain-containing protein 2 OS=Mus musculus GN=Ubtgd2 PE=2 SV=1 - [UBTD2_MOUSE]	0,000E0	0,000E0	0,000E0	1,088E6	9,254E5	2,288E6	Ubtgd2
Q91V26	Stromal membrane-associated protein 1 OS=Mus musculus GN=Smap1 PE=1 SV=1 - [SMAP1_MOUSE]	0,000E0	0,000E0	0,000E0	7,338E6	5,100E6	1,010E7	Smap1
Q8K310	Matrin-3 OS=Mus musculus GN=Matr3 PE=1 SV=1 - [MATR3_MOUSE]	0,000E0	0,000E0	0,000E0	3,095E6	6,647E6	8,931E6	Matr3
Q9R1C7	Pre-mRNA-processing factor 40 homolog A OS=Mus musculus GN=Prpf40a PE=1 SV=1 - [PR40A_MOUSE]	0,000E0	0,000E0	0,000E0	3,490E6	1,286E6	6,385E6	Prpf40a
Q8BP48	Methionine aminopeptidase 1 OS=Mus musculus GN=Metap1 PE=1 SV=1 - [MAP1_MOUSE]	0,000E0	0,000E0	0,000E0	5,609E6	8,226E6	1,541E7	Metap1
Q922H2	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial OS=Mus musculus GN=Pdk3 PE=1 SV=1 - [PKD3_MOUSE]	0,000E0	0,000E0	0,000E0	1,334E6	2,837E6	4,537E6	Pdk3
Q89Q32-3	Isoform 3 of SH3 and PX domain-containing protein 2A OS=Mus musculus GN=Sh3pxd2a - [SPD2A_MOUSE]	0,000E0	0,000E0	0,000E0	1,672E6	2,803E6	7,624E5	Sh3pxd2a
Q77NV0	Protein DEK OS=Mus musculus GN=Dek PE=1 SV=1 - [DEK_MOUSE]	0,000E0	0,000E0	0,000E0	9,174E6	1,565E7	4,193E7	Dek
P58742	Aladin OS=Mus musculus GN=Aas PE=1 SV=1 - [AAAS_MOUSE]	0,000E0	0,000E0	0,000E0	2,053E6	3,132E6	4,919E6	Aas
Q922B9	Sperm-specific antigen 2 homolog OS=Mus musculus GN=Safa2 PE=1 SV=3 - [SSFA2_MOUSE]	0,000E0	0,000E0	0,000E0	1,922E6	7,426E6	1,126E7	Ssfa2
Q9CK56	26S proteasome non-ATPase regulatory subunit 8 OS=Mus musculus GN=Psmd8 PE=1 SV=2 - [PSMD8_MOUSE]	0,000E0	0,000E0	0,000E0	1,638E6	2,575E6	6,820E6	Psmd8
Q9D0R8	Protein LSM12 homolog OS=Mus musculus GN=Lsm12 PE=1 SV=1 - [LSM12_MOUSE]	0,000E0	0,000E0	0,000E0	6,599E6	1,335E7	4,919E7	Lsm12
P52479	Ubiquitin carboxyl-terminal hydrolase 10 OS=Mus musculus GN=Usp10 PE=1 SV=3 - [UBP10_MOUSE]	0,000E0	0,000E0	0,000E0	5,551E6	5,949E6	1,147E7	Usp10
E9QAM5	Helicase with zinc finger domain 2 OS=Mus musculus GN=Helz2 PE=1 SV=1 - [HELZ2_MOUSE]	0,000E0	0,000E0	0,000E0	4,552E6	7,940E6	1,770E7	Helz2
P97857	A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Mus musculus GN=Adamts1 PE=1 SV=4 - [ATSL_MOUSE]	0,000E0	0,000E0	0,000E0	1,311E6	1,522E7	2,013E7	Adamts1
Q91WF3	Adenylate cyclase type 4 OS=Mus musculus GN=Adcy4 PE=1 SV=1 - [ADCY4_MOUSE]	0,000E0	0,000E0	0,000E0	1,978E7	4,084E6	3,966E7	Adcy4
Q9QY06	Unconventional myosin-IXb OS=Mus musculus GN=Myo9b PE=1 SV=2 - [MYO9B_MOUSE]	0,000E0	0,000E0	0,000E0	1,760E7	5,944E6	1,397E7	Myo9b
Q60930	Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2 - [VDAC2_MOUSE]	0,000E0	0,000E0	0,000E0	2,949E6	2,913E6	2,793E7	Vdac2
Q61211	Eukaryotic translation initiation factor 2D OS=Mus musculus GN=Eif2d PE=1 SV=3 - [EIF2D_MOUSE]	0,000E0	0,000E0	0,000E0	1,481E6	3,212E6	3,017E6	Eif2d
P52624	Uridine phosphorylase 1 OS=Mus musculus GN=Upp1 PE=1 SV=2 - [URP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,649E7	1,939E7	3,489E7	Upp1
P31938	Dual specificity mitogen-activated protein kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 - [MP2K1_MOUSE]	0,000E0	0,000E0	0,000E0	2,900E6	5,955E6	5,631E6	Map2k1
Q9QUJ7-2	Isoform Short of Long-chain-fatty-acid-CoA ligase 4 OS=Mus musculus GN=AcsM4 - [ACSL4_MOUSE]	0,000E0	0,000E0	0,000E0	1,513E6	3,519E6	6,474E6	AcsM4
Q8KZY3	Protein eva-1 homolog B OS=Mus musculus GN=Eva1b PE=1 SV=1 - [EVA1B_MOUSE]	0,000E0	0,000E0	0,000E0	7,679E6	1,947E7	2,912E7	Eva1b
P61290	Proteasome activator complex subunit 3 OS=Mus musculus GN=Psm3 PE=1 SV=1 - [PSME3_MOUSE]	0,000E0	0,000E0	0,000E0	9,215E5	2,921E6	2,106E6	Psm3
Q64282	Interferon-induced protein with tetratricopeptide repeats 1 OS=Mus musculus GN=Ifit1 PE=1 SV=2 - [IFIT1_MOUSE]	0,000E0	0,000E0	0,000E0	2,261E6	2,178E6	3,218E6	Ifit1
Q6Q0B8-2	Isoform 2 of CCR4-NOT transcription complex subunit 1 OS=Mus musculus GN=Cnot1 - [CNOT1_MOUSE]	0,000E0	0,000E0	0,000E0	3,243E6	9,629E6	2,528E7	Cnot1
B2RX54	Plexin-B2 OS=Mus musculus GN=Plmb2 PE=1 SV=1 - [PLXB2_MOUSE]	0,000E0	0,000E0	0,000E0	8,971E6	2,376E7	2,615E7	Plxbn2
Q8BY21	ABI gene family member 3 OS=Mus musculus GN=Abi3 PE=1 SV=3 - [ABI3_MOUSE]	0,000E0	0,000E0	0,000E0	1,460E6	1,228E6	1,285E7	Abi3
Q9DB66	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=1 SV=1 - [RPN2_MOUSE]	0,000E0	0,000E0	0,000E0	4,305E6	2,029E6	4,959E6	Rpn2
P70290	55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1 - [EM55_MOUSE]	0,000E0	0,000E0	0,000E0	1,230E6	3,760E6	5,170E6	Mpp1
Q6A0A2-2	Isoform 2 of La-related protein 4B OS=Mus musculus GN=Larp4b - [LAR4B_MOUSE]	0,000E0	0,000E0	0,000E0	2,613E6	4,581E6	7,816E6	Larp4b
Q8BGH2	Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1 - [SAM50_MOUSE]	0,000E0	0,000E0	0,000E0	1,496E6	4,964E6	5,368E6	Samm50
P46662-2	Isoform 2 of Merlin OS=Mus musculus GN=Nf2 - [MERL_MOUSE]	0,000E0	0,000E0	0,000E0	3,500E6	7,885E6	5,335E6	Nf2
Q91X11	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like OS=Mus musculus GN=Dus3l PE=1 SV=1 - [DUS3L_MOUSE]	0,000E0	0,000E0	0,000E0	2,557E6	1,539E6	6,855E6	Dus3l
Q99K41	EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1 - [EMIL1_MOUSE]	0,000E0	0,000E0	0,000E0	3,541E6	7,391E6	1,837E7	Emilin1
P23298	Protein kinase C eta type OS=Mus musculus GN=Prkch PE=1 SV=2 - [KPCL_MOUSE]	0,000E0	0,000E0	0,000E0	1,263E6	4,204E6	5,704E6	Prkch
Q8K297	Procollagen galactosyltransferase 1 OS=Mus musculus GN=Colgalt1 PE=1 SV=2 - [GT2S1_MOUSE]	0,000E0	0,000E0	0,000E0	9,669E5	2,498E6	5,346E6	Colgalt1
P08113	Endoplasmic OS=Mus musculus GN=Hsp90b1 PE=1 SV=2 - [ENPL_MOUSE]	0,000E0	0,000E0	1,544E6	4,372E7	8,485E7	1,170E8	Hsp90b1
P62748	Hippocalcin-like protein 1 OS=Mus musculus GN=Hpcal1 PE=1 SV=2 - [HPCLL_MOUSE]	0,000E0	0,000E0	0,000E0	1,121E6	2,203E6	2,076E6	Hpcal1
P02088	Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1 SV=2 - [HBB1_MOUSE]	0,000E0	0,000E0	0,000E0	1,094E7	6,133E6	5,045E7	Hbb-b1
Q54781	SRF protein kinase 2 OS=Mus musculus GN=Sprk2 PE=1 SV=2 - [SRPK2_MOUSE]	0,000E0	0,000E0	0,000E0	3,952E6	8,114E6	2,294E7	SrpK2
P53811	Phosphatidylinositol transfer protein beta isoform OS=Mus musculus GN=Ptprnb PE=1 SV=2 - [PTPNB_MOUSE]	0,000E0	0,000E0	0,000E0	8,319E5	1,857E6	5,166E6	Ptprnb
Q61286-2	Isoform ALF1A of Transcription factor 12 OS=Mus musculus GN=Tcf12 - [HTF4_MOUSE]	0,000E0	0,000E0	0,000E0	2,336E6	3,253E6	8,158E6	Tcf12
Q99P88	Nuclear pore complex protein Nup155 OS=Mus musculus GN=Nup155 PE=1 SV=1 - [NU155_MOUSE]	0,000E0	0,000E0	0,000E0	4,020E6	4,944E6	3,121E6	Nup155
Q9ESL4	Mitogen-activated protein kinase kinase kinase MLT OS=Mus musculus GN=Zak PE=1 SV=1 - [MLTK_MOUSE]	0,000E0	0,000E0	0,000E0	2,076E6	3,000E6	8,300E6	Zak
P56399	Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus GN=Usp5 PE=1 SV=1 - [UBP5_MOUSE]	0,000E0	0,000E0	0,000E0	1,050E6	4,989E6	6,692E6	Usp5
P47856-2	Isoform 2 of Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 - [GPPT1_MOUSE]	0,000E0	0,000E0	0,000E0	6,250E5	1,727E6	4,308E6	Gfpt1
Q8BH43	Wiskott-Aldrich syndrome protein family member 2 OS=Mus musculus GN=Wasf2 PE=1 SV=1 - [WASF2_MOUSE]	0,000E0	0,000E0	0,000E0	6,262E6	4,034E7	7,108E7	Wasf2
Q99NH0	Ankyrin repeat domain-containing protein 17 OS=Mus musculus GN=Ankrd17 PE=1 SV=2 - [ANR17_MOUSE]	0,000E0	0,000E0	0,000E0	4,666E6	2,623E7	2,195E7	Ankrd17
Q92ZF2	2'-5'-oligoadenylate synthase-like protein 2 OS=Mus musculus GN=Oas2 PE=1 SV=2 - [OASL2_MOUSE]	0,000E0	0,000E0	0,000E0	1,002E6	1,240E7	2,688E7	OasL2
P18052-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase alpha OS=Mus musculus GN=Ptptra - [PTPTRA_MOUSE]	0,000E0	0,000E0	0,000E0	1,240E7	1,291E7	5,005E6	Ptptra
Q9ESW4	Acylglycerol kinase, mitochondrial OS=Mus musculus GN=Agk PE=1 SV=1 - [AGK_MOUSE]	0,000E0	0,000E0	0,000E0	1,982E6	4,453E6	6,674E6	Agk
Q6PBX1	Sorting nexin-6 OS=Mus musculus GN=Snx6 PE=1 SV=2 - [SNX6_MOUSE]	0,000E0	0,000E0	0,000E0	2,933E6	1,510E6	8,915E6	Snx6
Q8VCG3	WD repeat-containing protein 74 OS=Mus musculus GN=Wdr74 PE=2 SV=1 - [WDR74_MOUSE]	0,000E0	0,000E0	0,000E0	8,721E5	3,251E6	5,117E6	Wdr74
Q3TFK5-2	Isoform 2 of G patch domain-containing protein 4 OS=Mus musculus GN=Gpatch4 - [GPTC4_MOUSE]	0,000E0	0,000E0	0,000E0	1,561E6	4,151E6	7,693E6	Gpatch4
Q35344	Importin subunit alpha-4 OS=Mus musculus GN=Kpna3 PE=1 SV=1 - [IMA4_MOUSE]	0,000E0	0,000E0	0,000E0	1,775E6	2,925E6	1,103E6	Kpna3
Q08093	Calponin-2 OS=Mus musculus GN=Cnn2 PE=1 SV=1 - [CNN2_MOUSE]	0,000E0	0,000E0	0,000E0	9,081E5	2,767E6	2,943E7	Cnn2
Q811D2	Ankyrin repeat domain-containing protein 26 OS=Mus musculus GN=Ankrd26 PE=1 SV=2 - [ANR26_MOUSE]	0,000E0	0,000E0	0,000E0	3,144E6	8,723E6	7,694E6	Ankrd26
Q8CQ47	Structural maintenance of chromosomes protein 4 OS=Mus musculus GN=Smc4 PE=1 SV=1 - [SMC4_MOUSE]	0,000E0	0,000E0	0,000E0	1,233E6	5,219E6	1,148E7	Smc4
Q9ROM6	Ras-related protein Rab-9A OS=Mus musculus GN=Rab9a PE=1 SV=1 - [RAB9A_MOUSE]	0,000E0	0,000E0	0,000E0	9,937E5	4,799E6	5,981E6	Rab9a
P01899	H-2 class I histocompatibility antigen, D-B alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=2 - [HA11_MOUSE]	0,000E0	0,000E0	0,000E0	3,338E6	3,956E6	5,133E6	H2-D1
Q60996-2	Isoform 1 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Mus musculus GN=Ppp2r5c - [ZASG_MOUSE]	0,000E0	0,000E0	0,000E0	1,138E6	5,271E6	8,010E6	Ppp2r5c
Q48725-3	Isoform 3 of Pericentrin OS=Mus musculus GN=Pcnt - [PCNT_MOUSE]	0,000E0	0,000E0	0,000E0	4,379E6	6,258E6	1,140E7	Pcnt
Q8VE19	Vacuolar protein sorting-associated protein 4A OS=Mus musculus GN=Vps4a PE=1 SV=1 - [VPS4A_MOUSE]	0,000E0	0,000E0	0,000E0	6,175E6	1,626E7	6,757E6	Vps4a
Q921F2	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 - [TADBP_MOUSE]	0,000E0	0,000E0	0,000E0	1,031E7	7,503E6	1,321E7	Tardbp
Q88967	ATP-dependent zinc metalloprotease YME1L1 OS=Mus musculus GN=Yme1l1 PE=1 SV=1 - [YME1L_MOUSE]	0,000E0	0,000E0	0,000E0	5,834E5	4,008E6	1,804E6	Yme1l1
Q77PM1	Protein PRRC2B OS=Mus musculus GN=Prrc2b PE=1 SV=1 - [PRC2B_MOUSE]	0,000E0	0,000E0	0,000E0	3,412E6	4,394E6	1,053E7	Prrc2b
Q3THK7	GMP synthase [glutamine-hydrolyzing] OS=Mus musculus GN=Gmps PE=1 SV=2 - [GUAA_MOUSE]	0,000E0	0,000E0	0,000E0	2,168E6	4,355E6	1,321E7	Gmps
Q6ZPG2	WD repeat-containing protein 90 OS=Mus musculus GN=Wdr90 PE=1 SV=2 - [WDR90_MOUSE]	0,000E0	0,000E0	0,000E0	2,192E6	3,340E6	2,379E6	Wdr90
Q912R2	Sorting nexin-18 OS=Mus musculus GN=Snx18 PE=1 SV=1 - [SNX18_MOUSE]	0,000E0	0,000E0	0,000E0	5,857E6	1,448E7	2,441E7	Snx18
Q70585-2	Isoform 2 of Dystrobrevin beta OS=Mus musculus GN=Dtnb - [DTNB_MOUSE]	0,000E0	0,000E0	0,000E0	1,979E6	1,019E7	1,152E7	Dtnb
Q99JP0	Mitogen-activated protein kinase kinase kinase 3 OS=Mus musculus GN=Map4k3 PE=1 SV=4 - [M4K3_MOUSE]	0,000E0	0,000E0	0,000E0	9,770E5	4,454E6	5,719E6	Map4k3
Q6A4J8-3	Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 7 OS=Mus musculus GN=Usp7 - [UBP7_MOUSE]	0,000E0	0,000E0	0,000E0	5,889E6	2,984E6	4,744E6	Usp7
Q9CZJ2	Heat shock 70 kDa protein 12B OS=Mus musculus GN=Hspa12b PE=1 SV=1 - [HS12B_MOUSE]	0,000E0	0,000E0	0,000E0	3,971E6	5,995E6	1,628E7	Hspa12b
Q8BZ03	Serine/threonine-protein kinase D2 OS=Mus musculus GN=Prkd2 PE=1 SV=1 - [KPCD2_MOUSE]	0,000E0	0,000E0	0,000E0	5,511E6	1,064E7	1,232E7	Prkd2
Q61210-2	Isoform 2 of Rho guanine nucleotide exchange factor 1 OS=Mus musculus GN=Arhgef1 - [ARHG1_MOUSE]	0,000E0	0,000E0	0,000E0	1,986E6	2,255E6	8,846E6	Arhgef1
Q8CG48	Structural maintenance of chromosomes protein 2 OS=Mus musculus GN=Smc2 PE=1 SV=2 - [SMC2_MOUSE]	0,000E0	0,000E0	0,000E0	3,193E6	3,833E6	5,829E6	Smc2
Q8CI51	PDZ and LIM domain protein 5 OS=Mus musculus GN=Pdlim5 PE=1 SV=4 - [PDLIS_MOUSE]	0,000E0	0,000E0	0,000E0	1,462E6	4,524E6	1,317E7	Pdlim5
P49615	Cyclin-dependent-like kinase 5 OS=Mus musculus GN=Cdk5 PE=1 SV=1 - [CDK5_MOUSE]	0,000E0	0,000E0	0,000E0	2,128E7	1,886E7	8,067E7	Cdk5
Q8K0V4	CCR4-NOT transcription complex subunit 3 OS=Mus musculus GN=Cnot3 PE=1 SV=1 - [CNOT3_MOUSE]	0,000E0	0,000E0	0,000E0	2,547E6	8,552E6	1,123E7	Cnot3
P43406	Integrin alpha-V OS=Mus musculus GN=Itgav PE=1 SV=2 - [ITAV_MOUSE]	0,000E0	0,000E0	0,000E0	4,718E6	5,063E6	7,399E6	Itgav
E9PVX6	Proliferation marker protein Ki-67 OS=Mus musculus GN=Mki67 PE=1 SV=1 - [KI67_MOUSE]	0,000E0	0,000E0	0,000E0	1,850E6	3,812E6	1,244E7	Mki67
Q9DCN2-2	Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 - [NBSR3_MOUSE]	0,000E0	0,000E0	0,000E0	4,026E6	4,921E6	7,402E6	Cyb5r3
P09103	Protein disulfide-isomerase OS=Mus musculus GN=Pthb PE=1 SV=2 - [PDIAL_MOUSE]	0,000E0	0,000E0	0,000E0	4,297E6	3,028E6	3,019E6	Pthb
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5 - [FKBP4_MOUSE]	0,000E0	0,000E0	0,000E0	7,166E5	3,053E6	3,546E6	Fkbp4
Q91Y17	YTH domain-containing family protein 2 OS=Mus musculus GN=Ythdf2 PE=1 SV=1 - [YTHD2_MOUSE]	0,000E0	0,000E0	5,369E6	5,946E6	2,355E6	1,089E7	Ythdf2
Q8BVY0	Ribosomal L1 domain-containing protein 1 OS=Mus musculus GN=Rsl1d1 PE=1 SV=1 - [RL1D1_MOUSE]	0,000E0	0,000E0	0,000E0	1,323E6	2,043E6	1,577E7	Rsl1d1
Q9B883	Splicing factor U2AF 35 kDa subunit OS=Mus musculus GN=U2af1 PE=1 SV=4 - [U2AF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,700E6	6,966E6	6,575E6	U2af1
A2RTL5	Arginine/serine-rich coiled-coil protein 2 OS=Mus musculus GN=Rsrc2 PE=2 SV=1 - [RSRC2_MOUSE]	0,000E0	0,000E0	0,000E0	2,971E6	1,963E6	1,383E7	Rsrc2
Q9CWX2	28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrs22 PE=1 SV=1 - [RT22_MOUSE]	0,000E0	0,000E0	0,000E0	3,939E6	3,983E6	7,501E6	Mrs22
Q70305-2	Isoform 2 of Ataxin-2 OS=Mus musculus GN=Atxn2 - [ATX2_MOUSE]	0,000E0	0,000E0	0,000E0	5,520E6	3,783E6	1,268E7	Atxn2

Q9ERG2	Striatin-3 OS=Mus musculus GN=Strn3 PE=1 SV=1 - [STRN3_MOUSE]	0,000E0	0,000E0	0,000E0	1,089E6	3,985E6	9,441E5	Strn3
Q8BW86	Metalloenductase STEAP2 OS=Mus musculus GN=Steap2 PE=1 SV=1 - [STEAP2_MOUSE]	0,000E0	0,000E0	0,000E0	3,532E6	7,136E6	7,036E6	Steap2
P70248	Unconventional myosin-If OS=Mus musculus GN=MyoIf PE=1 SV=1 - [MYOIf_MOUSE]	0,000E0	0,000E0	2,601E6	1,353E8	1,824E8	1,442E8	Myoif1
054988-2	Isoform 2 of STE20-like serine/threonine-protein kinase OS=Mus musculus GN=Slk - [SLK_MOUSE]	0,000E0	0,000E0	0,000E0	2,328E6	1,076E7	1,029E7	Slk
Q7TN58	Transmembrane channel-like protein 8 OS=Mus musculus GN=Tmc8 PE=1 SV=2 - [TMC8_MOUSE]	0,000E0	0,000E0	0,000E0	5,571E6	8,204E6	1,124E7	Tmc8
Q8JZX4	Splicing factor 45 OS=Mus musculus GN=Rbm17 PE=1 SV=1 - [SPF45_MOUSE]	0,000E0	0,000E0	0,000E0	1,023E6	1,296E6	3,236E6	Rbm17
Q9DC16	39S ribosomal protein L4, mitochondrial OS=Mus musculus GN=Mrp4 PE=1 SV=1 - [RMD4_MOUSE]	0,000E0	0,000E0	0,000E0	1,707E6	3,613E6	1,972E6	Mrp4
P60766	Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2 - [CDC42_MOUSE]	0,000E0	0,000E0	0,000E0	3,260E6	1,599E7	4,871E6	Cdc42
Q92IM3	Splicing factor 3B subunit 3 OS=Mus musculus GN=SF3b3 PE=1 SV=1 - [SF3B3_MOUSE]	0,000E0	0,000E0	0,000E0	2,382E6	5,391E6	1,208E7	Sf3b3
Q8CSQ4	G-rich sequence factor 1 OS=Mus musculus GN=Grsf1 PE=1 SV=2 - [GRSF1_MOUSE]	0,000E0	0,000E0	0,000E0	1,194E6	2,171E6	8,444E5	Grsf1
L0N7N1	Kinesin-like protein KIF14 OS=Mus musculus GN=Kif14 PE=1 SV=1 - [KIF14_MOUSE]	0,000E0	0,000E0	0,000E0	2,803E6	3,500E6	1,129E7	Kif14
Q8CG79	Apoptosis-stimulating of p53 protein 2 OS=Mus musculus GN=Tp53bp2 PE=1 SV=3 - [ASPP2_MOUSE]	0,000E0	0,000E0	0,000E0	4,976E6	6,521E6	1,030E7	Tp53bp2
Q9D0J4	ADP-ribosylation factor-like protein 2 OS=Mus musculus GN=Arl2 PE=1 SV=1 - [ARL2_MOUSE]	0,000E0	0,000E0	0,000E0	3,752E6	7,184E6	4,523E6	Arl2
Q8CB44	GRAM domain-containing protein 4 OS=Mus musculus GN=Gramd4 PE=1 SV=1 - [GRAM4_MOUSE]	0,000E0	0,000E0	0,000E0	1,775E6	2,846E6	3,503E6	Gramd4
Q9DBR4	Amyloid beta A4 precursor protein-binding family B member 2 OS=Mus musculus GN=Appb2 PE=1 SV=2 - [APBB2_MOUSE]	0,000E0	0,000E0	0,000E0	1,942E6	2,801E6	6,187E6	Appb2
P13864	DNA (cytosine-5)-methyltransferase 1 OS=Mus musculus GN=Dnmt1 PE=1 SV=5 - [DNMT1_MOUSE]	0,000E0	0,000E0	0,000E0	2,100E6	7,456E6	1,556E7	Dnmt1
P58660	Caspase recruitment domain-containing protein 10 OS=Mus musculus GN=Card10 PE=1 SV=1 - [CAR10_MOUSE]	0,000E0	0,000E0	0,000E0	1,067E6	2,822E6	6,974E7	Card10
Q9Z0H3-2	Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Mus musculus GN=Smarcb1 - [SNF5_MOUSE]	0,000E0	0,000E0	0,000E0	1,930E6	5,985E6	8,512E6	Smarcb1
Q9CQ10	Charged multivesicular body protein 3 OS=Mus musculus GN=Chmp3 PE=1 SV=3 - [CHMP3_MOUSE]	0,000E0	0,000E0	0,000E0	9,984E6	1,585E7	3,655E7	Chmp3
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial OS=Mus musculus GN=Acot9 PE=1 SV=1 - [ACOT9_MOUSE]	0,000E0	0,000E0	0,000E0	2,974E6	5,397E6	4,126E6	Acot9
Q7TNP2	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Mus musculus GN=Ppp2r1b PE=1 SV=2 - [2AAB_MOUSE]	0,000E0	0,000E0	0,000E0	1,239E7	9,631E6	6,012E6	Ppp2r1b
Q64322	Neural proliferation differentiation and control protein 1 OS=Mus musculus GN=Npdc1 PE=2 SV=2 - [NPDC1_MOUSE]	0,000E0	0,000E0	0,000E0	4,126E6	1,073E7	1,187E7	Npdc1
035379	Multidrug resistance-associated protein 1 OS=Mus musculus GN=Abcc1 PE=1 SV=1 - [MRP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,495E6	5,537E6	7,573E6	Abcc1
Q9QCQ9	GTP-binding protein SAR1B OS=Mus musculus GN=Sar1b PE=1 SV=1 - [SAR1B_MOUSE]	0,000E0	0,000E0	0,000E0	5,084E6	4,001E6	7,373E6	Sar1b
Q9WLW2	Serine/threonine-protein kinase TBK1 OS=Mus musculus GN=Tbk1 PE=1 SV=1 - [TBK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,266E6	5,612E6	1,006E7	Tbk1
Q9QY76	Vesicle-associated membrane protein-associated protein B OS=Mus musculus GN=Vapb PE=1 SV=3 - [VAPB_MOUSE]	0,000E0	0,000E0	0,000E0	2,272E6	7,010E6	1,196E7	Vapb
P70349	Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=3 - [HINT1_MOUSE]	0,000E0	0,000E0	0,000E0	1,951E7	4,461E7	7,495E7	Hint1
Q61292	Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=1 SV=2 - [LAMB2_MOUSE]	0,000E0	0,000E0	0,000E0	1,502E6	4,312E6	1,824E7	Lamb2
Q8BM51	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 - [ECHA_MOUSE]	0,000E0	0,000E0	0,000E0	5,197E6	5,934E6	1,326E7	Hadha
P1D493	Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=2 - [NID1_MOUSE]	0,000E0	0,000E0	0,000E0	2,374E6	1,150E7	2,464E7	Nid1
Q9CZX0	Elongator complex protein 3 OS=Mus musculus GN=Elp3 PE=1 SV=1 - [ELP3_MOUSE]	0,000E0	0,000E0	0,000E0	9,901E5	2,217E6	2,652E6	Elp3
Q6PFQ7	Ras GTPase-activating protein 4 OS=Mus musculus GN=Rasa4 PE=1 SV=1 - [RASL2_MOUSE]	0,000E0	0,000E0	0,000E0	1,237E6	5,838E6	1,404E7	Rasa4
Q8BG02	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B gamma isoform OS=Mus musculus GN=Ppp2r2c PE=1 SV=1 - [2ABG_MOUSE]	0,000E0	0,000E0	0,000E0	2,575E6	1,944E7	1,721E7	Ppp2r2c
05XJY5	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=1 SV=2 - [COPD_MOUSE]	0,000E0	0,000E0	0,000E0	1,114E6	1,134E6	6,827E6	Arcn1
P54761	Ephrin type-B receptor 4 OS=Mus musculus GN=Ephb4 PE=1 SV=2 - [EPHB4_MOUSE]	0,000E0	0,000E0	0,000E0	4,637E6	1,105E7	2,906E7	Ephb4
Q9JIF7	Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1 - [COPB_MOUSE]	0,000E0	0,000E0	0,000E0	4,996E5	7,296E5	5,339E6	Copb1
Q8BJJ2	Tetraspanin-9 OS=Mus musculus GN=Tspan9 PE=1 SV=1 - [TSN9_MOUSE]	0,000E0	0,000E0	0,000E0	2,053E6	6,829E6	9,509E6	Tspan9
Q57114	Tyrosine-protein kinase Sgk223 OS=Mus musculus GN=Sgk223 PE=1 SV=2 - [SG223_MOUSE]	0,000E0	0,000E0	0,000E0	1,445E6	5,808E6	6,616E6	Sgk223
Q5SFM8	RNA-binding protein 27 OS=Mus musculus GN=Rbm27 PE=1 SV=3 - [RBM27_MOUSE]	0,000E0	0,000E0	0,000E0	4,092E6	6,751E6	1,214E7	Rbm27
Q8BRN9	Coiled-coil and C2 domain-containing protein 1B OS=Mus musculus GN=C2d1b PE=1 SV=1 - [C2D1B_MOUSE]	0,000E0	0,000E0	0,000E0	2,454E6	6,912E6	1,554E6	Cc2d1b
Q8BX17	Gem-associated protein 5 OS=Mus musculus GN=Gemin5 PE=1 SV=2 - [GEM15_MOUSE]	0,000E0	0,000E0	0,000E0	2,525E6	3,809E6	9,602E6	Gemin5
Q61545	RNA-binding protein EWS OS=Mus musculus GN=Ewsr1 PE=1 SV=2 - [EWS_MOUSE]	0,000E0	0,000E0	0,000E0	1,766E7	1,874E7	3,023E7	Ewsr1
Q9CZD3	Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1 - [SYG_MOUSE]	0,000E0	0,000E0	0,000E0	2,348E6	3,909E6	9,834E6	Gars
P10922	Histone H1.0 OS=Mus musculus GN=H1f0 PE=2 SV=4 - [H10_MOUSE]	0,000E0	0,000E0	0,000E0	6,867E6	9,401E6	9,565E6	H1f0
Q8R550-5	Isoform 5 of SH3 domain-containing kinase-binding protein 1 OS=Mus musculus GN=Sh3kbp1 - [SH3K1_MOUSE]	0,000E0	0,000E0	0,000E0	1,205E6	2,662E6	1,878E6	Sh3kbp1
Q91YE6	Importin-9 OS=Mus musculus GN=Ipo9 PE=1 SV=3 - [IPO9_MOUSE]	0,000E0	0,000E0	0,000E0	6,400E6	9,136E6	7,160E6	Ipo9
035149	Zinc transporter 4 OS=Mus musculus GN=Slc30a4 PE=1 SV=2 - [ZNT4_MOUSE]	0,000E0	0,000E0	0,000E0	3,931E6	4,028E6	1,718E6	Slc30a4
Q3V1V3	ESF1 homolog OS=Mus musculus GN=Esf1 PE=1 SV=1 - [ESF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,764E6	9,590E6	3,536E6	Esf1
Q6JRW6-2	Isoform 2 of Myosin-14 OS=Mus musculus GN=Myh14 - [MYH14_MOUSE]	2,336E8	0,000E0	5,102E7	2,921E9	6,979E9	5,047E9	Myh14
Q9R1Z8	Vinexin OS=Mus musculus GN=Sorbs3 PE=1 SV=1 - [VINEX_MOUSE]	0,000E0	0,000E0	0,000E0	8,258E6	1,907E7	3,088E7	Sorbs3
P70207	Plexin-A2 OS=Mus musculus GN=Plxna2 PE=1 SV=2 - [PLXA2_MOUSE]	0,000E0	0,000E0	0,000E0	6,187E6	8,567E6	1,411E7	Plxna2
Q32P12-2	Isoform 2 of Uncharacterized protein C17orf53 homolog OS=Mus musculus - [CQ053_MOUSE]	0,000E0	0,000E0	0,000E0	2,390E6	9,890E5	7,516E6	Sep2
Q9CXF4	TBC1 domain family member 15 OS=Mus musculus GN=Tbc1d15 PE=1 SV=1 - [TBC15_MOUSE]	0,000E0	0,000E0	0,000E0	1,078E6	2,489E6	4,261E6	Tbc1d15
088554	Poly [ADP-ribose] polymerase 2 OS=Mus musculus GN=Parp2 PE=1 SV=3 - [PARP2_MOUSE]	0,000E0	0,000E0	0,000E0	9,644E5	3,483E6	8,206E5	Parp2
Q99L0U	Charged multivesicular body protein 1b-1 OS=Mus musculus GN=Chmp1b1 PE=1 SV=1 - [CH1B1_MOUSE]	0,000E0	0,000E0	0,000E0	1,233E7	3,477E7	1,166E7	Chmp1b1
Q9CZV5	PIN2/TERF1-interacting telomerase inhibitor 1 OS=Mus musculus GN=Pinx1 PE=1 SV=2 - [PINX1_MOUSE]	0,000E0	0,000E0	0,000E0	1,479E6	7,902E6	2,114E7	Pinx1
Q8R326-2	Isoform 2 of Paraspeckle component 1 OS=Mus musculus GN=Pspc1 - [PSPC1_MOUSE]	0,000E0	0,000E0	0,000E0	1,780E6	1,248E7	3,724E7	Pspc1
Q9QZM4	Tumor necrosis factor receptor superfamily member 10B OS=Mus musculus GN=Trnfrs10b PE=2 SV=3 - [TR10B_MOUSE]	0,000E0	0,000E0	0,000E0	2,374E6	4,057E6	4,490E6	Tnfrsf10b
Q8BWG8-2	Isoform 1B of Beta-arrestin-1 OS=Mus musculus GN=Arrb1 - [ARRB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,430E6	5,763E6	1,077E7	Arrb1
Q9JLB0-2	Isoform Alpha of MAGUK p55 subfamily member 6 OS=Mus musculus GN=Mpp6 - [MPP6_MOUSE]	0,000E0	0,000E0	0,000E0	1,225E6	5,467E6	7,884E6	Mpp6
Q8OXI6	Mitogen-activated protein kinase kinase kinase 11 OS=Mus musculus GN=Map3k11 PE=1 SV=1 - [M3K11_MOUSE]	0,000E0	0,000E0	0,000E0	4,111E5	4,143E6	5,980E6	Map3k11
Q9DZY4-2	Isoform 2 of Mixed lineage kinase domain-like protein OS=Mus musculus GN=Mkl1 - [MLKL_MOUSE]	0,000E0	0,000E0	0,000E0	1,071E6	2,731E6	2,986E6	Mkl1
P12894	Probable Pol polypeptide OS=Mus musculus intracisternal A-particle IL3 PE=3 SV=1 - [POL_IPMAI]	0,000E0	0,000E0	0,000E0	1,981E6	3,566E6	4,052E6	[POL]
Q8BHFF	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial OS=Mus musculus GN=Pgs1 PE=1 SV=1 - [PGPS1_MOUSE]	0,000E0	0,000E0	0,000E0	3,374E6	1,843E6	1,678E6	Pgs1
Q6PB44-2	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 23 OS=Mus musculus GN=Ptpn23 - [PTN23_MOUSE]	0,000E0	0,000E0	0,000E0	2,543E6	5,850E6	9,455E6	Ptpn23
035368	Interferon-activable protein 203 OS=Mus musculus GN=Ifi203 PE=1 SV=1 - [IFI3_MOUSE]	0,000E0	0,000E0	0,000E0	3,036E6	5,717E6	3,630E6	Ifi203
Q8K019-3	Isoform 3 of Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 - [BCLF1_MOUSE]	0,000E0	0,000E0	0,000E0	6,968E5	1,412E6	6,045E6	Bclaf1
Q8BG95	Protein phosphatase 1 regulatory subunit 12B OS=Mus musculus GN=Ppp1r12b PE=1 SV=2 - [MYPT2_MOUSE]	0,000E0	0,000E0	0,000E0	6,992E7	9,881E7	1,253E8	Ppp1r12b
009172	Glutamate--cysteine ligase regulatory subunit OS=Mus musculus GN=Gclm PE=1 SV=1 - [GSH0_MOUSE]	0,000E0	0,000E0	0,000E0	2,737E6	6,511E6	6,788E6	Gclm
Q9XC00	IST1 homolog OS=Mus musculus GN=Ist1 PE=1 SV=1 - [IST1_MOUSE]	0,000E0	0,000E0	0,000E0	4,093E6	7,738E6	1,106E7	Ist1
009106	Histone deacetylase 1 OS=Mus musculus GN=Hdac1 PE=1 SV=1 - [HDAC1_MOUSE]	0,000E0	0,000E0	0,000E0	4,690E6	8,142E6	1,634E7	Hdac1
Q8BRT1-5	Isoform 2 of CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 - [CLAP2_MOUSE]	0,000E0	0,000E0	0,000E0	4,562E5	3,844E6	1,018E7	Clasp2
Q80UY2-2	Isoform 2 of E3 ubiquitin-protein ligase KCMF1 OS=Mus musculus GN=Kcmf1 - [KCMF1_MOUSE]	0,000E0	0,000E0	0,000E0	5,965E6	9,529E6	2,306E7	Kcmf1
P51912	Neutral amino acid transporter B(0) OS=Mus musculus GN=Slc1a5 PE=1 SV=2 - [AAAT_MOUSE]	0,000E0	0,000E0	0,000E0	2,869E6	8,670E6	1,370E7	Slc1a5
P45640	Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2 - [NSF_MOUSE]	0,000E0	0,000E0	0,000E0	1,126E6	4,179E6	2,901E6	Nsf
Q9D0R4	Probable ATP-dependent RNA helicase DDX56 OS=Mus musculus GN=Ddx56 PE=2 SV=1 - [DDX56_MOUSE]	0,000E0	0,000E0	0,000E0	2,047E6	2,882E6	3,378E6	Ddx56
A2AGT5-2	Isoform 2 of Cytoskeleton-associated protein 5 OS=Mus musculus GN=Ckap5 - [CKAP5_MOUSE]	0,000E0	0,000E0	0,000E0	3,133E6	6,127E6	9,096E6	Ckap5
P70288	Histone deacetylase 2 OS=Mus musculus GN=Hdac2 PE=1 SV=1 - [HDAC2_MOUSE]	0,000E0	0,000E0	0,000E0	2,860E6	8,451E6	1,402E7	Hdac2
035963	Ras-related protein Rab-33B OS=Mus musculus GN=Rab33b PE=1 SV=1 - [RB33B_MOUSE]	0,000E0	0,000E0	0,000E0	3,456E5	1,027E8	2,549E8	Rab33b
P23475	X-ray repair cross-complementing protein 6 OS=Mus musculus GN=Xrcc6 PE=1 SV=5 - [XRCC6_MOUSE]	0,000E0	0,000E0	0,000E0	1,892E6	5,125E6	8,931E6	Xrcc6
Q8VC03	Echinoderm microtubule-associated protein-like 3 OS=Mus musculus GN=Emi3 PE=1 SV=1 - [EMAL3_MOUSE]	0,000E0	0,000E0	0,000E0	2,787E6	3,125E6	8,089E6	Emi3
Q3JDE2	Tubulin--tyrosine ligase-like protein 12 OS=Mus musculus GN=Ttl12 PE=1 SV=1 - [TTL12_MOUSE]	0,000E0	0,000E0	0,000E0	7,815E5	2,796E6	1,890E6	Ttl12
Q6ZP86	Inhibitor of Bruton tyrosine kinase OS=Mus musculus GN=Ibtb PE=1 SV=3 - [IBTK_MOUSE]	0,000E0	0,000E0	0,000E0	1,539E6	3,276E6	6,271E6	Ibtb
Q9CLN6	E3 ubiquitin-protein ligase SMURF1 OS=Mus musculus GN=Smurf1 PE=1 SV=2 - [SMURF1_MOUSE]	0,000E0	0,000E0	0,000E0	9,328E6	1,463E7	1,269E7	Smurf1
P39876	Metalloproteinase inhibitor 3 OS=Mus musculus GN=Timpp3 PE=1 SV=1 - [TIMP3_MOUSE]	0,000E0	0,000E0	0,000E0	4,363E6	7,335E6	1,727E7	Timp3
P34152-3	Isoform 3 of Focal adhesion kinase 1 OS=Mus musculus GN=Prk2 - [FAK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,661E6	6,078E6	1,008E7	Ptk2
P40201	Chromodomain-helicase-DNA-binding protein 1 OS=Mus musculus GN=Chd1 PE=1 SV=3 - [CHD1_MOUSE]	0,000E0	0,000E0	0,000E0	3,349E6	1,313E6	2,135E6	Chd1
P97440	Histone RNA hairpin-binding protein OS=Mus musculus GN=Slbp PE=1 SV=1 - [SLBP_MOUSE]	0,000E0	0,000E0	0,000E0	4,769E6	1,498E6	6,832E5	Slbp
Q8VCL2	Protein SCO2 homolog, mitochondrial OS=Mus musculus GN=Sco2 PE=1 SV=1 - [SCO2_MOUSE]	0,000E0	0,000E0	0,000E0	7,012E5	5,956E6	3,012E6	Sco2
Q6Q477	Plasma membrane calcium-transporting ATPase 4 OS=Mus musculus GN=Atp2b4 PE=1 SV=1 - [AT2B4_MOUSE]	0,000E0	0,000E0	0,000E0	8,105E6	9,547E6	1,788E7	Atp2b4
Q9ER72	Cysteine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2 - [SYCC_MOUSE]	0,000E0	0,000E0	0,000E0	1,499E6	6,499E6	1,030E7	Cars
Q5SWD9	Pre-rRNA-processing protein Tsr1 homolog OS=Mus musculus GN=Tsr1 PE=1 SV=1 - [TSR1_MOUSE]	0,000E0	0,000E0	0,000E0	3,056E6	1,380E6	1,192E7	Tsr1
P0DOV2	Interferon-activable protein 204 OS=Mus musculus GN=Ifi204 PE=1 SV=1 - [IFI4_MOUSE]	0,000E0	0,000E0	0,000E0	2,361E6	2,647E6	3,973E5	Ifi204

Q9ERK4	Exportin-2 OS=Mus musculus GN=Cse1l PE=1 SV=1 - [XPO2_MOUSE]	0,000E0	0,000E0	0,000E0	2,980E6	7,246E6	9,950E6	Cse1l
P11365	Retrovirus-related Gag polyprotein OS=Mouse intracisternal A-particle MIA14 GN=gag PE=4 SV=2 - [GAG_IPMA]	0,000E0	0,000E0	0,000E0	1,226E7	1,761E7	2,545E7	gag
Q80X73	Protein pelota homolog OS=Mus musculus GN=Pelo PE=1 SV=3 - [PELO_MOUSE]	0,000E0	0,000E0	0,000E0	4,291E6	6,583E6	7,123E6	Pelo
Q7TT37	Elongator complex protein 1 OS=Mus musculus GN=Ikkbp PE=1 SV=2 - [ELP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,022E6	3,183E6	3,921E6	Ikkbp
Q6PID5	Inactive rhomboid protein 1 OS=Mus musculus GN=Rhbdf1 PE=1 SV=2 - [RHDF1_MOUSE]	0,000E0	0,000E0	0,000E0	3,128E6	6,078E6	6,945E6	Rhbdf1
Q62191	E3 ubiquitin-protein ligase TRIM21 OS=Mus musculus GN=Trim21 PE=1 SV=1 - [ROS2_MOUSE]	0,000E0	0,000E0	1,073E6	1,027E7	4,860E6	5,318E6	Trim21
P35123	Ubiquitin carboxyl-terminal hydrolase 4 OS=Mus musculus GN=Usp4 PE=1 SV=3 - [UBP4_MOUSE]	0,000E0	0,000E0	0,000E0	3,696E5	1,566E6	3,832E6	Usp4
Q6PGL7-2	Isoform 2 of WASH complex subunit 2 OS=Mus musculus GN=Washc2 - [WASC2_MOUSE]	0,000E0	0,000E0	0,000E0	1,493E6	1,827E6	2,271E6	Washc2
Q99P72	Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2 - [RTN4_MOUSE]	0,000E0	0,000E0	0,000E0	6,569E6	6,637E6	2,184E7	Rtn4
O08919	Numb-like protein OS=Mus musculus GN=Numb1 PE=1 SV=3 - [NUMB1_MOUSE]	0,000E0	0,000E0	0,000E0	7,608E6	9,439E6	1,152E7	Numb1
O08582	GTP-binding protein 1 OS=Mus musculus GN=Gtbp1 PE=1 SV=2 - [GTBP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,521E6	6,914E6	2,708E6	Gtbp1
Q8R381	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Mus musculus GN=Ptkd1 PE=1 SV=2 - [PLCD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,428E6	4,103E6	5,665E6	Plcd1
Q02858	Angiopoietin-1 receptor OS=Mus musculus GN=Tek PE=1 SV=2 - [TIE2_MOUSE]	0,000E0	0,000E0	0,000E0	7,184E6	8,964E6	1,756E7	Tek
Q3TX57	26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psmd1 PE=1 SV=1 - [PSMD1_MOUSE]	0,000E0	0,000E0	0,000E0	8,673E5	5,261E6	5,129E6	Psmd1
P07742	Ribonucleoside-diphosphate reductase large subunit OS=Mus musculus GN=Rrm1 PE=1 SV=2 - [RIR1_MOUSE]	0,000E0	0,000E0	0,000E0	3,894E6	1,027E7	1,104E7	Rrm1
P49962	Signal recognition particle 9 kDa protein OS=Mus musculus GN=Srp9 PE=1 SV=2 - [SRP9_MOUSE]	0,000E0	0,000E0	0,000E0	5,072E6	5,400E6	8,531E6	Srp9
Q9QWY8-2	Isoform 2 of Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Mus musculus GN=Asap1 - [ASAP1_MOUSE]	0,000E0	0,000E0	0,000E0	8,234E5	4,151E6	4,461E6	Asap1
Q3UH93	Plexin-D1 OS=Mus musculus GN=Plxd1 PE=1 SV=1 - [PLXD1_MOUSE]	0,000E0	0,000E0	0,000E0	6,711E6	1,528E7	2,068E7	Plxd1
P32507	Nectin-2 OS=Mus musculus GN=Nectin2 PE=1 SV=2 - [NECT2_MOUSE]	0,000E0	0,000E0	0,000E0	1,861E6	5,041E5	9,776E5	Nectin2
Q8BK63	Inactive tyrosine-protein kinase 7 OS=Mus musculus GN=Ptk7 PE=1 SV=1 - [PTK7_MOUSE]	0,000E0	0,000E0	0,000E0	7,024E6	1,317E7	4,140E7	Ptk7
Q8C7Q4	RNA-binding protein 4 OS=Mus musculus GN=Rbm4 PE=1 SV=1 - [RBM4_MOUSE]	0,000E0	0,000E0	0,000E0	7,181E6	7,197E6	6,225E6	Rbm4
P35283	Ras-related protein Rab-12 OS=Mus musculus GN=Rab12 PE=1 SV=3 - [RAB12_MOUSE]	0,000E0	0,000E0	3,456E5	1,027E8	2,549E8	3,658E8	Rab12
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2 - [LPPRC_MOUSE]	0,000E0	0,000E0	0,000E0	1,442E6	1,610E6	3,796E6	Lrpprc
Q8R3P2	Probable E3 ubiquitin-protein ligase DTX2 OS=Mus musculus GN=Dtx2 PE=1 SV=2 - [DTX2_MOUSE]	0,000E0	0,000E0	0,000E0	2,626E6	3,255E6	8,966E5	Dttx2
A2APV2-2	Isoform 2 of Formin-like protein 2 OS=Mus musculus GN=Fmn12 - [FNLN2_MOUSE]	0,000E0	0,000E0	0,000E0	5,462E6	4,438E6	8,570E6	Fmn12
Q91JA4	Ribosome biogenesis protein WDR12 OS=Mus musculus GN=Wdr12 PE=1 SV=1 - [WDR12_MOUSE]	0,000E0	0,000E0	0,000E0	6,465E5	8,510E5	2,441E6	Wdr12
Q6NSQ7	Protein LTV1 homolog OS=Mus musculus GN=Ltv1 PE=1 SV=2 - [LTV1_MOUSE]	0,000E0	0,000E0	0,000E0	2,306E6	1,807E6	2,956E6	Ltv1
Q8CB77	Elongin-A OS=Mus musculus GN=Eloa PE=1 SV=3 - [ELOA1_MOUSE]	0,000E0	0,000E0	0,000E0	2,946E6	4,660E6	1,078E7	Eloa
Q99L18	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Mus musculus GN=Hgs PE=1 SV=2 - [HGS_MOUSE]	0,000E0	0,000E0	0,000E0	9,902E6	1,667E7	2,330E7	Hgs
Q9D832	DnaJ homolog subfamily B member 4 OS=Mus musculus GN=Dnajb4 PE=1 SV=1 - [DNUB4_MOUSE]	0,000E0	0,000E0	0,000E0	2,647E6	3,081E6	7,481E6	Dnajb4
Q8BR11	CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=1 SV=1 - [CLAP2_MOUSE]	0,000E0	0,000E0	0,000E0	1,931E6	5,136E6	6,954E6	Clasp2
Q8R0A0	General transcription factor IIF subunit 2 OS=Mus musculus GN=Gtf2f2 PE=1 SV=1 - [TF2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,547E6	2,185E6	2,953E6	Gtf2f2
Q9QZES	Cotamount subunit gamma-1 OS=Mus musculus GN=Cogp1 PE=1 SV=1 - [COGP1_MOUSE]	0,000E0	0,000E0	0,000E0	3,576E6	1,021E7	1,051E7	Cogp1
O35593	26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psm14 PE=1 SV=2 - [PSDE_MOUSE]	0,000E0	0,000E0	0,000E0	3,273E6	4,008E6	1,070E7	Psm14
Q52K38-2	Isoform 2 of Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srm1 - [SRRM1_MOUSE]	0,000E0	0,000E0	0,000E0	3,972E6	5,575E5	2,050E7	Srm1
Q6PAJ1	Breakpoint cluster region protein OS=Mus musculus GN=Bcr PE=1 SV=3 - [BCR_MOUSE]	0,000E0	0,000E0	0,000E0	1,494E6	1,814E6	3,458E6	Bcr
P14211	Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1 - [CALR_MOUSE]	0,000E0	0,000E0	0,000E0	2,109E6	9,833E6	1,378E7	Calr
Q9CPP0	Nucleoplasmin-3 OS=Mus musculus GN=Npm3 PE=1 SV=3 - [NPM3_MOUSE]	0,000E0	0,000E0	0,000E0	1,052E7	3,717E7	8,792E7	Npm3
Q8BH19	Pre-mRNA-splicing factor SLU7 OS=Mus musculus GN=Slu7 PE=1 SV=1 - [SLU7_MOUSE]	0,000E0	0,000E0	0,000E0	3,418E6	5,002E6	1,383E6	Slu7
Q5ND28	Scavenger receptor class F member 1 OS=Mus musculus GN=Scarf1 PE=1 SV=1 - [SREC_MOUSE]	0,000E0	0,000E0	0,000E0	1,314E6	9,480E6	1,543E6	Scarf1
Q6NVF0-2	Isoform 2 of Inositol polyphosphate 5-phosphatase OCRL-1 OS=Mus musculus GN=Ocr1 - [OCRL_MOUSE]	0,000E0	0,000E0	0,000E0	1,591E6	5,005E6	3,078E6	Ocr1
Q8CAF4-3	Isoform 3 of NfH-like protein 1 OS=Mus musculus GN=Nhl1 - [NHL1_MOUSE]	0,000E0	0,000E0	0,000E0	2,637E6	5,915E6	2,842E7	Nhl1
O54890	Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=1 SV=2 - [ITB3_MOUSE]	0,000E0	0,000E0	0,000E0	7,201E6	7,933E6	2,257E7	Itgb3
Q640N1	Adipocyte enhancer-binding protein 1 OS=Mus musculus GN=Aebp1 PE=1 SV=1 - [AEBP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,332E6	3,504E6	7,733E6	Aebp1
Q9E552-3	Isoform 3 of Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d - [SHIP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,468E6	2,990E6	3,909E6	Inpp5d
Q9JKP5	Muscleblind-like protein 1 OS=Mus musculus GN=Mbnl1 PE=1 SV=1 - [MBNL1_MOUSE]	0,000E0	0,000E0	0,000E0	9,110E5	9,671E6	7,498E6	Mbnl1
Q8DW68	Kin of IRRE-like protein 1 OS=Mus musculus GN=Kirrel PE=1 SV=1 - [KIRRL_MOUSE]	0,000E0	0,000E0	0,000E0	3,203E6	1,306E7	2,271E7	Kirrel
Q9D662	Protein transport protein Sec23B OS=Mus musculus GN=Sec23b PE=1 SV=1 - [SC23B_MOUSE]	0,000E0	0,000E0	0,000E0	4,185E6	5,073E6	6,851E6	Sec23b
P23949	mRNA decay activator protein ZFP36L2 OS=Mus musculus GN=Zfp36l2 PE=1 SV=2 - [TSD_MOUSE]	0,000E0	0,000E0	0,000E0	2,162E6	1,397E7	5,862E6	Zfp36l2
Q9EPJ9	ADP-ribosylation factor GTPase-activating protein 1 OS=Mus musculus GN=Arfgap1 PE=1 SV=2 - [ARFG1_MOUSE]	0,000E0	0,000E0	0,000E0	1,061E6	2,219E6	4,447E6	Arfgap1
Q9CY27	Very-long-chain enoyl-CoA reductase OS=Mus musculus GN=Tecr PE=1 SV=1 - [TECR_MOUSE]	0,000E0	0,000E0	0,000E0	1,247E7	2,198E7	1,537E7	Tecr
Q8BMJ2	Leucine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Lars PE=1 SV=2 - [SYLC_MOUSE]	0,000E0	0,000E0	0,000E0	7,083E5	3,374E6	6,364E6	Lars
Q9R1Q6	Transmembrane protein 176B OS=Mus musculus GN=Tmem176b PE=1 SV=1 - [T176B_MOUSE]	0,000E0	0,000E0	0,000E0	3,373E6	4,638E6	7,472E6	Tmem176b
E9Q557	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1 - [DESP_MOUSE]	0,000E0	0,000E0	8,274E5	5,286E6	1,965E6	2,370E6	Dsp
Q6ZP23-2	Isoform 2 of Zinc finger CCH domain-containing protein 4 OS=Mus musculus GN=Zc3h4 - [ZC3H4_MOUSE]	0,000E0	0,000E0	0,000E0	2,382E6	3,241E6	1,269E7	Zc3h4
Q76LS9-2	Isoform 2 of Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Mus musculus GN=Fam63a - [FA63A_MOUSE]	0,000E0	0,000E0	0,000E0	4,213E6	1,147E6	6,166E6	Fam63a
Q61214	Dual specificity tyrosine-phosphorylation-regulated kinase 1A OS=Mus musculus GN=Dyrk1a PE=1 SV=1 - [DYRK1A_MOUSE]	0,000E0	0,000E0	0,000E0	1,151E6	4,814E6	9,037E6	Dyrk1a
P35822	Receptor-type tyrosine-protein phosphatase kappa OS=Mus musculus GN=Ptpkr PE=1 SV=1 - [PTPRK_MOUSE]	0,000E0	0,000E0	0,000E0	3,513E6	4,003E6	1,329E7	Ptpkr
Q9JKY5	Huntingtin-interacting protein 1-related protein OS=Mus musculus GN=Hip1r PE=1 SV=2 - [HIP1R_MOUSE]	0,000E0	0,000E0	0,000E0	1,761E7	4,116E7	2,839E6	Hip1r
Q6PFD9	Nuclear pore complex protein Nup98-Nup96 OS=Mus musculus GN=Nup98 PE=1 SV=2 - [NUP98_MOUSE]	0,000E0	0,000E0	0,000E0	1,011E6	3,277E6	6,815E6	Nup98
Q5FWK3	Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1 - [RHG01_MOUSE]	0,000E0	0,000E0	0,000E0	1,877E6	8,360E5	7,619E6	Arhgap1
Q8K3W3	Protein CASC3 OS=Mus musculus GN=Casc3 PE=1 SV=3 - [CASC3_MOUSE]	0,000E0	0,000E0	0,000E0	6,702E6	1,400E7	1,137E7	Casc3
Q60805	Tyrosine-protein kinase Mer OS=Mus musculus GN=Mertk PE=1 SV=1 - [MERTK_MOUSE]	0,000E0	0,000E0	0,000E0	9,170E6	4,119E6	1,162E7	Mertk
Q921Y2	U3 small nuclear ribonucleoprotein protein IMP3 OS=Mus musculus GN=Imp3 PE=2 SV=1 - [IMP3_MOUSE]	0,000E0	0,000E0	0,000E0	4,491E6	1,072E7	1,033E7	Imp3
P02468	Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=2 - [LAMC1_MOUSE]	0,000E0	0,000E0	0,000E0	1,063E6	3,982E6	1,833E7	Lamc1
Q8C1J9	[F-actin]-methionine sulfoxide oxidase MICAL3 OS=Mus musculus GN=Mical3 PE=1 SV=2 - [MICA3_MOUSE]	0,000E0	0,000E0	0,000E0	2,930E6	4,563E6	6,390E6	Mical3
Q8BH8D	Protein-L-isopartate O-methyltransferase domain-containing protein 2 OS=Mus musculus GN=Pcmdt2 PE=2 SV=1 - [PCMD2_MOUSE]	0,000E0	0,000E0	0,000E0	7,963E5	2,480E6	1,124E6	Pcmdt2
Q9CQN1	Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1 - [TRAP1_MOUSE]	0,000E0	0,000E0	0,000E0	9,790E7	1,385E8	2,929E8	Trap1
Q8L0Z0	FYVE, RhoGEF and PH domain-containing protein 5 OS=Mus musculus GN=Fgds PE=1 SV=2 - [FGD5_MOUSE]	0,000E0	0,000E0	0,000E0	4,539E6	7,869E6	4,507E6	Fgds
Q92089	FACT complex subunit SPT16 OS=Mus musculus GN=Supt16h PE=1 SV=2 - [SP16H_MOUSE]	0,000E0	0,000E0	0,000E0	2,583E6	2,788E6	2,679E7	Supt16h
Q91V81	RNA-binding protein 42 OS=Mus musculus GN=Rbm42 PE=1 SV=1 - [RBM42_MOUSE]	0,000E0	0,000E0	0,000E0	1,869E6	1,776E6	2,204E6	Rbm42
Q68FE6	Protein FAM65A OS=Mus musculus GN=Fam65a PE=1 SV=2 - [FA65A_MOUSE]	0,000E0	0,000E0	0,000E0	2,239E6	5,659E6	6,782E6	Fam65a
O55S25-2	Isoform 2 of Tensin-3 OS=Mus musculus GN=Tns3 - [TENS3_MOUSE]	0,000E0	0,000E0	0,000E0	3,158E7	1,846E5	4,529E7	Tns3
P70227	Inositol 1,4,5-trisphosphate receptor type 3 OS=Mus musculus GN=Itrp3 PE=1 SV=3 - [ITPR3_MOUSE]	0,000E0	0,000E0	0,000E0	4,207E6	7,277E6	1,349E7	Itrp3
Q9DAK2	Phospholipid phosphatase 2 OS=Mus musculus GN=Plpp2 PE=1 SV=1 - [PLPP2_MOUSE]	0,000E0	0,000E0	0,000E0	6,375E5	3,376E6	6,159E6	Plpp2
Q00560	Interleukin-6 receptor subunit beta OS=Mus musculus GN=Il6st PE=1 SV=2 - [IL6RB_MOUSE]	0,000E0	0,000E0	0,000E0	1,181E6	3,818E6	5,858E6	Il6st
Q00612	Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3 - [G6PD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,193E6	4,309E6	2,511E6	G6pdx
P51432	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Mus musculus GN=Ptkb3 PE=1 SV=2 - [PLCB3_MOUSE]	0,000E0	0,000E0	0,000E0	2,362E6	4,868E6	7,343E6	Ptkb3
O35680	28S ribosomal protein S12, mitochondrial OS=Mus musculus GN=Mps12 PE=2 SV=1 - [RT12_MOUSE]	0,000E0	0,000E0	0,000E0	5,814E6	9,954E6	7,431E6	Mps12
Q8R5Q7	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 OS=Mus musculus GN=Arap3 PE=1 SV=3 - [ARAP3_MOUSE]	0,000E0	0,000E0	0,000E0	1,388E6	3,386E6	4,623E6	Arap3
A2RT67	DENN domain-containing protein 3 OS=Mus musculus GN=Dennd3 PE=1 SV=2 - [DEND3_MOUSE]	0,000E0	0,000E0	0,000E0	1,304E6	2,968E6	2,659E6	Dennd3
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Mus musculus GN=Aimp2 PE=1 SV=2 - [AIMP2_MOUSE]	0,000E0	0,000E0	0,000E0	4,011E6	2,240E5	4,491E6	Aimp2
Q8R4Y4-2	Isoform 2 of Stablin-1 OS=Mus musculus GN=Stab1 - [STAB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,266E7	2,584E7	4,512E7	Stab1
B1AXH1	NfH-like protein 2 OS=Mus musculus GN=Nhl2 PE=1 SV=1 - [NHL2_MOUSE]	0,000E0	0,000E0	0,000E0	5,183E6	9,820E6	3,006E6	Nhl2
A24P0	ATP-dependent RNA helicase DHX8 OS=Mus musculus GN=Dhx8 PE=2 SV=1 - [DHX8_MOUSE]	0,000E0	0,000E0	0,000E0	4,776E6	7,091E6	1,020E7	Dhx8
Q02105	Complement C1q subcomponent subunit C OS=Mus musculus GN=C1qc PE=1 SV=2 - [C1QC_MOUSE]	0,000E0	0,000E0	0,000E0	1,832E7	3,056E8	1,616E8	C1qc
O54734	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=2 - [DOST_MOUSE]	0,000E0	0,000E0	0,000E0	1,655E6	2,711E6	3,503E6	Ddost
Q3TTA7-2	Isoform 2 of E3 ubiquitin-protein ligase CBL-B OS=Mus musculus GN=Cblb - [CBLB_MOUSE]	0,000E0	0,000E0	0,000E0	1,702E6	2,150E6	2,271E6	Cblb
Q80Z25	Oral-facial-digital syndrome 1 protein homolog OS=Mus musculus GN=Ofd1 PE=1 SV=1 - [OFD1_MOUSE]	0,000E0	0,000E0	0,000E0	6,329E5	1,646E6	4,614E7	Ofd1
Q9J1I5-2	Isoform 2 of DAZ-associated protein 1 OS=Mus musculus GN=Dazap1 - [DAZP1_MOUSE]	0,000E0	0,000E0	0,000E0	5,965E6	7,044E6	1,613E7	Dazap1
Q6DVA0	LEM domain-containing protein 2 OS=Mus musculus GN=Lemd2 PE=1 SV=1 - [LEMD2_MOUSE]	0,000E0	0,000E0	0,000E0	8,142E5	2,401E6	9,327E5	Lemd2
B2RU80	Receptor-type tyrosine-protein phosphatase beta OS=Mus musculus GN=Ptprb PE=1 SV=1 - [PTPRB_MOUSE]	0,000E0	0,000E0	0,000E0	2,030E6	1,113E7	1,904E7	Ptprb
Q9CZD5	Translation initiation factor IF-3, mitochondrial OS=Mus musculus GN=Mif3 PE=1 SV=1 - [IF3M_MOUSE]	0,000E0	0,000E0	0,000E0	2,908E6	7,095E6	1,633E7	Mif3

Q01705-4	Isform 4 of Neurogenic locus notch homolog protein 1 OS=Mus musculus GN=Notch1 - [NOTC1_MOUSE]	0,000E0	0,000E0	0,000E0	1,475E7	2,933E7	1,564E7	Notch1
Q8J2W4	Copine-5 OS=Mus musculus GN=Cpne5 PE=1 SV=1 - [CPNE5_MOUSE]	0,000E0	0,000E0	0,000E0	2,218E6	3,588E6	7,389E6	Cpne5
Q9QX20	Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=2 - [MACF1_MOUSE]	0,000E0	0,000E0	0,000E0	4,223E6	1,297E8	1,338E9	Macf1
Q8OU78-2	Isform 2 of Pumilio homolog 1 OS=Mus musculus GN=Pum1 - [PUM1_MOUSE]	0,000E0	0,000E0	0,000E0	1,253E6	6,252E5	8,476E6	Pum1
Q07139-2	Isform 2 of Protein ECT2 OS=Mus musculus GN=Ect2 - [ECT2_MOUSE]	0,000E0	0,000E0	0,000E0	5,244E5	1,416E6	2,241E6	Ect2
P61079	Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 - [UBE2D3_MOUSE]	0,000E0	0,000E0	0,000E0	1,082E7	3,589E7	5,207E7	Ube2d3
Q8CSL3-3	Isform 3 of CCR4-NOT transcription complex subunit 2 OS=Mus musculus GN=Cnot2 - [CNOT2_MOUSE]	0,000E0	0,000E0	0,000E0	1,973E6	8,405E6	1,798E7	Cnot2
Q91WM1-2	Isform 2 of Spermatid perinuclear RNA-binding protein OS=Mus musculus GN=Strbp - [STRBP_MOUSE]	0,000E0	0,000E0	0,000E0	1,346E7	9,306E6	2,199E7	Strbp
O35660	Glutathione S-transferase Mu 6 OS=Mus musculus GN=Gstm6 PE=1 SV=4 - [GSTM6_MOUSE]	0,000E0	0,000E0	0,000E0	5,973E5	4,301E5	5,492E5	Gstm6
Q99M57	EH domain-binding protein 1-like protein 1 OS=Mus musculus GN=Ehbp111 PE=1 SV=1 - [EH111_MOUSE]	0,000E0	0,000E0	0,000E0	3,964E6	9,571E6	1,144E7	Ehbp111
P23463	Homeobox protein Hox-D8 OS=Mus musculus GN=Hoxd8 PE=3 SV=4 - [HDXD8_MOUSE]	0,000E0	0,000E0	0,000E0	2,880E6	7,146E6	4,389E6	Hoxd8
P83093	Stromal interaction molecule 2 OS=Mus musculus GN=Stim2 PE=1 SV=2 - [STIM2_MOUSE]	0,000E0	0,000E0	0,000E0	1,603E6	2,805E6	2,647E6	Stim2
Q61001	Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1 SV=4 - [LAMA5_MOUSE]	0,000E0	0,000E0	0,000E0	1,300E6	4,150E6	1,434E7	Lama5
P35821	Tyrosine-protein phosphatase non-receptor type 1 OS=Mus musculus GN=Ptpn1 PE=1 SV=2 - [PTN1_MOUSE]	0,000E0	0,000E0	0,000E0	8,743E5	1,694E6	3,833E6	Ptpn1
Q8OSW1	Putative adenosylhomocysteinase 2 OS=Mus musculus GN=Ahcy1 PE=1 SV=1 - [SAH42_MOUSE]	0,000E0	0,000E0	0,000E0	2,795E6	2,412E6	2,775E6	Ahcy1
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Mus musculus GN=Ndufa9 PE=1 SV=2 - [NDUA9_MOUSE]	0,000E0	0,000E0	0,000E0	1,643E6	2,321E6	3,761E6	Ndufa9
Q99KN1-2	Isform 2 of Arrestin domain-containing protein 1 OS=Mus musculus GN=Arrdc1 - [ARRD1_MOUSE]	0,000E0	0,000E0	0,000E0	9,543E5	4,932E6	6,451E6	Arrdc1
Q8QY56	Raberosyn-5 OS=Mus musculus GN=Rbsn PE=1 SV=1 - [RBNS5_MOUSE]	0,000E0	0,000E0	0,000E0	9,590E5	1,130E6	1,492E6	Rbsn
Q64430	Copper-transporting ATPase 1 OS=Mus musculus GN=Atp7a PE=1 SV=3 - [ATP7A_MOUSE]	0,000E0	0,000E0	0,000E0	1,294E6	2,214E6	3,588E6	Atp7a
Q8BG79	CWF19-like protein 2 OS=Mus musculus GN=Cwf19l2 PE=1 SV=1 - [C19L2_MOUSE]	0,000E0	0,000E0	0,000E0	7,675E5	1,405E6	5,503E6	Cwf19l2
P35917	Vascular endothelial growth factor receptor 2 OS=Mus musculus GN=Kdr PE=1 SV=1 - [VGF2_MOUSE]	0,000E0	0,000E0	0,000E0	1,139E7	9,802E6	2,165E7	Kdr
Q8BZK4	Splicing regulatory glutamine/lysine-rich protein 1 OS=Mus musculus GN=Srek1 PE=2 SV=1 - [SREK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,378E6	5,429E5	6,565E6	Srek1
Q63850	Nuclear pore glycoprotein p62 OS=Mus musculus GN=Nup62 PE=1 SV=2 - [NUP62_MOUSE]	0,000E0	0,000E0	0,000E0	1,735E6	2,664E6	3,891E6	Nup62
Q8BK12	Trinucleotide repeat-containing gene 6B protein OS=Mus musculus GN=Tnrc6b PE=1 SV=2 - [TNR6B_MOUSE]	0,000E0	0,000E0	0,000E0	2,376E6	3,406E6	2,598E6	Tnrc6b
P46664	Adenylosuccinate synthetase isozyme 2 OS=Mus musculus GN=Adss PE=1 SV=2 - [PURA2_MOUSE]	0,000E0	0,000E0	0,000E0	2,239E6	3,514E6	7,118E6	Adss
Q8BM55	Transmembrane protein 214 OS=Mus musculus GN=Tmem214 PE=1 SV=1 - [TM214_MOUSE]	0,000E0	0,000E0	0,000E0	2,949E6	3,795E6	5,973E6	Tmem214
Q9D2R0	Acetoacetyl-CoA synthetase OS=Mus musculus GN=Aacs PE=1 SV=1 - [AACS_MOUSE]	0,000E0	0,000E0	0,000E0	1,939E6	1,747E6	4,128E6	Aacs
Q9Z1T1	AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=2 - [AP3B1_MOUSE]	0,000E0	0,000E0	0,000E0	3,649E6	6,259E6	5,274E6	Ap3b1
A2AAY5	SH3 and PX domain-containing protein 2B OS=Mus musculus GN=Sh3pxd2b PE=1 SV=1 - [SPD2B_MOUSE]	0,000E0	0,000E0	0,000E0	1,672E6	3,423E6	4,022E6	Sh3pxd2b
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=SDha PE=1 SV=1 - [SDHA_MOUSE]	0,000E0	0,000E0	0,000E0	3,018E6	4,687E6	2,565E6	SDha
Q3JUFM5	Nucleolar MIF4G domain-containing protein 1 OS=Mus musculus GN=Nom1 PE=1 SV=2 - [NOM1_MOUSE]	0,000E0	0,000E0	0,000E0	4,975E5	5,572E6	6,752E6	Nom1
Q9D706	RNA polymerase II-associated protein 3 OS=Mus musculus GN=Rpap3 PE=1 SV=1 - [RPAP3_MOUSE]	0,000E0	0,000E0	0,000E0	3,438E6	5,609E6	1,368E7	Rpap3
Q511X5	RelA-associated inhibitor OS=Mus musculus GN=Ppp1r13l PE=1 SV=1 - [IASPP_MOUSE]	0,000E0	0,000E0	0,000E0	8,316E5	5,868E5	3,700E6	Ppp1r13l
Q6ZPE2-2	Isform 2 of Myotubularin-related protein 5 OS=Mus musculus GN=Sbf1 - [MTMR5_MOUSE]	0,000E0	0,000E0	0,000E0	1,716E6	1,606E6	3,705E6	Sbf1
Q3JUH7-3	Isform 3 of Rho guanine nucleotide exchange factor 40 OS=Mus musculus GN=Arhgef40 - [ARH40_MOUSE]	0,000E0	0,000E0	0,000E0	2,345E6	6,154E6	8,629E6	Arhgef40
Q8BX57-3	Isform 3 of PX domain-containing protein kinase-like protein OS=Mus musculus GN=Pxx - [PXX_MOUSE]	0,000E0	0,000E0	0,000E0	1,065E6	2,147E6	2,671E6	Pxx
Q8CIP4-2	Isform 2 of MAP/microtubule affinity-regulating kinase 4 OS=Mus musculus GN=Mark4 - [MARK4_MOUSE]	0,000E0	0,000E0	0,000E0	9,286E6	1,155E7	1,407E7	Mark4
Q8OU93	Nuclear pore complex protein Nup214 OS=Mus musculus GN=Nup214 PE=1 SV=2 - [NU214_MOUSE]	0,000E0	0,000E0	0,000E0	5,193E5	2,763E6	5,939E6	Nup214
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=1 SV=2 - [CAND1_MOUSE]	0,000E0	0,000E0	0,000E0	1,241E6	3,688E6	3,377E6	Cand1
Q8OSU7	Interferon-induced very large GTPase 1 OS=Mus musculus GN=Gvin1 PE=1 SV=1 - [GVIN1_MOUSE]	0,000E0	0,000E0	0,000E0	1,487E6	3,487E6	8,673E6	Gvin1
Q99L15	Zinc finger protein 281 OS=Mus musculus GN=Znf281 PE=1 SV=1 - [ZN281_MOUSE]	0,000E0	0,000E0	0,000E0	2,058E6	4,160E6	5,764E6	Znf281
Q9R0U0-3	Isform 3 of Serine/arginine-rich splicing factor 10 OS=Mus musculus GN=Srsf10 - [SRS10_MOUSE]	0,000E0	0,000E0	0,000E0	1,277E6	5,243E6	1,221E7	Srsf10
P47226-2	Isform TES1 of Testin OS=Mus musculus GN=Tes - [TES_MOUSE]	0,000E0	0,000E0	0,000E0	6,851E5	2,694E6	3,421E6	Tes
Q6ZQ73	Cullin-associated NEDD8-dissociated protein 2 OS=Mus musculus GN=Cand2 PE=1 SV=2 - [CAND2_MOUSE]	0,000E0	0,000E0	0,000E0	2,120E6	6,679E6	8,745E6	Cand2
Q8BP22	Protein FAM92A1 OS=Mus musculus GN=Fam92a1 PE=1 SV=1 - [F92A1_MOUSE]	0,000E0	0,000E0	0,000E0	1,141E6	1,944E6	6,828E6	Fam92a1
P14873	Microtubule-associated protein 1B OS=Mus musculus GN=Map1b PE=1 SV=2 - [MAP1B_MOUSE]	0,000E0	0,000E0	2,559E6	2,404E6	4,708E6	5,312E6	Map1b
Q8C0D4	Rho GTPase-activating protein 12 OS=Mus musculus GN=Arhgap12 PE=1 SV=2 - [RHG12_MOUSE]	0,000E0	0,000E0	0,000E0	1,616E6	4,145E6	1,531E7	Arhgap12
Q8BU30	Isoleucine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Iars PE=1 SV=2 - [SYIC_MOUSE]	0,000E0	0,000E0	0,000E0	5,789E5	3,740E6	9,802E6	Iars
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Mus musculus GN=Usp9x PE=1 SV=2 - [USP9X_MOUSE]	0,000E0	0,000E0	8,255E5	2,010E6	1,172E6	3,421E6	Usp9x
Q8K389	CDK5 regulatory subunit-associated protein 2 OS=Mus musculus GN=Cdk5rap2 PE=1 SV=3 - [CKSP2_MOUSE]	0,000E0	0,000E0	8,224E5	3,240E5	3,340E6	2,110E6	Cdk5rap2
Q8K2D3	Enhancer of mRNA-decapping protein 3 OS=Mus musculus GN=Edc3 PE=1 SV=1 - [EDC3_MOUSE]	0,000E0	0,000E0	0,000E0	1,428E6	2,141E7	4,625E6	Edc3
P22777	Plasminogen activator inhibitor 1 OS=Mus musculus GN=Serpine1 PE=1 SV=1 - [PAI1_MOUSE]	0,000E0	0,000E0	0,000E0	4,451E6	4,869E6	1,024E7	Serpine1
F6ZD54	Nucleoprotein TPR OS=Mus musculus GN=Tpr PE=1 SV=1 - [TPR_MOUSE]	0,000E0	0,000E0	0,000E0	7,245E5	3,571E6	5,196E6	Tpr
Q8CSN3-2	Isform 2 of Pre-mRNA-splicing factor CWC22 homolog OS=Mus musculus GN=Cwc22 - [CWC22_MOUSE]	0,000E0	0,000E0	0,000E0	6,254E6	7,502E6	1,230E7	Cwc22
Q9DBH0	NEDD4-like E3 ubiquitin-protein ligase WWP2 OS=Mus musculus GN=Wwp2 PE=1 SV=1 - [WWP2_MOUSE]	0,000E0	0,000E0	0,000E0	2,994E6	4,391E6	1,077E7	Wwp2
P10404	MLV-related proviral Env polyprotein OS=Mus musculus PE=1 SV=3 - [ENV1_MOUSE]	0,000E0	0,000E0	0,000E0	4,281E6	6,622E6	4,626E6	ENV1
P24270	Catalase OS=Mus musculus GN=Cat PE=1 SV=4 - [CATA_MOUSE]	0,000E0	0,000E0	0,000E0	2,870E6	1,661E6	6,442E5	Cat
Q9R1Q9	V-type proton ATPase subunit S1 OS=Mus musculus GN=Atp6ap1 PE=1 SV=1 - [VAS1_MOUSE]	0,000E0	0,000E0	0,000E0	1,220E6	2,027E6	5,582E6	Atp6ap1
Q64343	ATP-binding cassette sub-family G member 1 OS=Mus musculus GN=Abcg1 PE=1 SV=1 - [ABCG1_MOUSE]	0,000E0	0,000E0	0,000E0	5,462E6	1,148E7	6,352E6	Abcg1
Q06806	Tyrosine-protein kinase receptor Tie-1 OS=Mus musculus GN=Tie1 PE=1 SV=3 - [TIE1_MOUSE]	0,000E0	0,000E0	0,000E0	8,554E6	1,148E7	1,662E7	Tie1
Q8BKFI	DNA-directed RNA polymerase, mitochondrial OS=Mus musculus GN=Polmt PE=1 SV=1 - [RPOM_MOUSE]	0,000E0	0,000E0	0,000E0	2,080E6	5,330E6	1,317E8	Polrmt
O54825	Bystin OS=Mus musculus GN=Bysl PE=1 SV=3 - [BYST_MOUSE]	0,000E0	0,000E0	0,000E0	7,798E5	1,247E6	2,392E6	Bysl
Q3JU96	Serine/threonine-protein kinase MRCK alpha OS=Mus musculus GN=Cdc42bpa PE=1 SV=2 - [MRCKA_MOUSE]	0,000E0	0,000E0	0,000E0	2,825E6	1,123E7	2,968E7	Cdc42bpa
Q6DFV3	Rho GTPase-activating protein 21 OS=Mus musculus GN=Arhgap21 PE=1 SV=1 - [RHG21_MOUSE]	0,000E0	0,000E0	0,000E0	2,212E6	2,860E6	3,103E6	Arhgap21
Q8C156	Condensin complex subunit 2 OS=Mus musculus GN=Ncap PE=1 SV=1 - [COND2_MOUSE]	0,000E0	0,000E0	0,000E0	2,078E6	8,302E5	3,655E6	Ncap
R2RX88-2	Isform 2 of Centrosome and spindle pole associated protein 1 OS=Mus musculus GN=Cssp1 - [CSPP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,909E6	2,755E6	1,054E6	Cssp1
Q8BHY3-2	Isform 2 of Anoctamin-1 OS=Mus musculus GN=Ano1 - [ANO1_MOUSE]	0,000E0	0,000E0	0,000E0	1,282E6	3,161E6	1,033E7	Ano1
Q6Z077	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Mus musculus GN=Plcg1 PE=1 SV=2 - [PLCG1_MOUSE]	0,000E0	0,000E0	0,000E0	1,321E6	9,439E5	2,369E6	Plcg1
Q8BPM0-2	Isform 2 of Disheveled-associated activator of morphogenesis 1 OS=Mus musculus GN=Daam1 - [DAAM1_MOUSE]	0,000E0	0,000E0	0,000E0	1,516E6	2,309E6	5,149E6	Daam1
Q3JUV2	Tumor necrosis factor receptor type 1-associated DEATH domain protein OS=Mus musculus GN=Tradd PE=1 SV=1 - [TRADD_MOUSE]	0,000E0	0,000E0	0,000E0	2,135E5	1,301E6	3,664E6	Tradd
Q8QTP3	E3 ubiquitin-protein ligase UBR5 OS=Mus musculus GN=Ubr5 PE=1 SV=2 - [UBR5_MOUSE]	0,000E0	0,000E0	0,000E0	1,013E6	7,372E6	4,983E6	Ubr5
Q61233	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4 - [PLSL_MOUSE]	0,000E0	0,000E0	0,000E0	6,535E6	3,327E7	1,948E7	Lcp1
Q8VE97	Serine/arginine-rich splicing factor 4 OS=Mus musculus GN=Srsf4 PE=2 SV=1 - [SRSF4_MOUSE]	0,000E0	0,000E0	0,000E0	1,028E8	7,600E7	3,874E6	Srsf4
O08911	Mitogen-activated protein kinase 12 OS=Mus musculus GN=Mapk12 PE=1 SV=1 - [MK12_MOUSE]	0,000E0	0,000E0	0,000E0	4,305E6	1,014E7	8,472E6	Mapk12
Q4J2R1	E3 ubiquitin-protein ligase HERC2 OS=Mus musculus GN=Herc2 PE=1 SV=3 - [HERC2_MOUSE]	0,000E0	0,000E0	0,000E0	1,073E6	3,650E6	5,635E6	Herc2
P59764	Dedicator of cytokinesis protein 4 OS=Mus musculus GN=Dock4 PE=1 SV=1 - [DOCK4_MOUSE]	0,000E0	0,000E0	0,000E0	1,700E6	6,895E5	2,725E6	Dock4
P47811-4	Isform 4 of Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 - [MK14_MOUSE]	0,000E0	0,000E0	0,000E0	4,305E6	1,014E7	8,472E6	Mapk14
Q9JMD0-4	Isform 4 of BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Mus musculus GN=Znf207 - [ZN207_MOUSE]	0,000E0	0,000E0	0,000E0	9,455E6	1,236E7	2,380E7	Znf207
Q8CCP0	Nuclear export mediator factor Nrmf OS=Mus musculus GN=Nrmf PE=1 SV=2 - [NEMF_MOUSE]	0,000E0	0,000E0	0,000E0	3,048E6	1,315E6	6,649E6	Nrmf
Q8BT60	Copine-3 OS=Mus musculus GN=Cpne3 PE=1 SV=2 - [CPNE3_MOUSE]	0,000E0	0,000E0	0,000E0	2,218E6	4,070E6	2,504E6	Cpne3
Q6PSF9	Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1 - [XPO1_MOUSE]	0,000E0	0,000E0	0,000E0	2,028E6	4,358E6	3,288E6	Xpo1
P27460	Gag polyprotein OS=Cas-Br-E murine leukemia virus GN=gag PE=3 SV=3 - [GAG_MLVCB]	0,000E0	0,000E0	0,000E0	3,382E6	5,988E6	9,946E6	gag
E9QSK9-3	Isform 3 of YTH domain-containing protein 1 OS=Mus musculus GN=Ythdc1 - [YTDC1_MOUSE]	0,000E0	0,000E0	0,000E0	2,534E6	6,894E6	1,071E7	Ythdc1
Q8K2J0	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3 OS=Mus musculus GN=Plcd3 PE=1 SV=2 - [PLCD3_MOUSE]	0,000E0	0,000E0	0,000E0	9,401E5	2,877E6	4,154E6	Plcd3
Q5SUA5	Unconventional myosin-Ig OS=Mus musculus GN=Myo1g PE=1 SV=1 - [MYO1G_MOUSE]	0,000E0	0,000E0	0,000E0	1,010E7	1,075E8	1,460E8	Myo1g
O55103	Periaxin OS=Mus musculus GN=Prx PE=1 SV=1 - [PRAX_MOUSE]	0,000E0	0,000E0	0,000E0	3,868E6	7,077E6	7,313E6	Prx
O88532	Zinc finger RNA-binding protein OS=Mus musculus GN=Zfr PE=1 SV=2 - [ZFR_MOUSE]	0,000E0	0,000E0	0,000E0	1,465E6	3,810E6	4,531E6	Zfr
Q9CZU3	Superkiller viralicidal activity 2-like 2 OS=Mus musculus GN=Skiv2l2 PE=1 SV=1 - [SKL2_MOUSE]	0,000E0	0,000E0	0,000E0	4,226E5	6,021E5	1,874E6	Skiv2l2
Q9ESV0	ATP-dependent RNA helicase DDX24 OS=Mus musculus GN=Ddx24 PE=1 SV=2 - [DDX24_MOUSE]	0,000E0	0,000E0	0,000E0	1,063E6	1,765E6	4,905E6	Ddx24
Q9D8S3	ADP-ribosylation factor GTPase-activating protein 3 OS=Mus musculus GN=Arfgap3 PE=1 SV=2 - [ARFG3_MOUSE]	0,000E0	0,000E0	0,000E0	1,234E6	2,397E6	5,351E6	Arfgap3
Q70FJ1-3	Isform 3 of A-kinase anchor protein 9 OS=Mus musculus GN=Akap9 - [AKAP9_MOUSE]	0,000E0	0,000E0	0,000E0	1,105E6	2,762E6	3,939E6	Akap9
Q8BFY9-2	Isform 2 of Transportin-1 OS=Mus musculus GN=Tnpo1 - [TNPO1_MOUSE]	0,000E0	0,000E0	0,000E0	2,208E6	3,223E6	3,676E6	Tnpo1
Q8CJ96	Ras association domain-containing protein 8 OS=Mus musculus GN=Rassf8 PE=2 SV=1 - [RASf8_MOUSE]	0,000E0	0,000E0	0,000E0	3,567E6	5,238E6	9,753E6	Rassf8

Q920Q4-2	Isomform 2 of Vacuolar protein sorting-associated protein 16 homolog OS=Mus musculus GN=Vps16 - [VPS16_MOUSE]	0,000E0	0,000E0	0,000E0	1,449E6	2,497E5	4,894E5	Vps16
P97789-3	Isomform 3 of 5'-3' exonuclease 1 OS=Mus musculus GN=Xrn1 - [XRN1_MOUSE]	0,000E0	0,000E0	0,000E0	4,721E7	5,406E7	8,493E7	Xrn1
P97798-5	Isomform 5 of Neogenin OS=Mus musculus GN=Neo1 - [NEO1_MOUSE]	0,000E0	0,000E0	0,000E0	1,446E6	4,804E6	2,924E6	Neo1
Q8JZ59	39S ribosomal protein L48, mitochondrial OS=Mus musculus GN=MprL48 PE=1 SV=1 - [RM48_MOUSE]	0,000E0	0,000E0	0,000E0	1,058E6	2,448E6	1,067E7	MprL48
Q6PDH0	Pleckstrin homology-like domain family B member 1 OS=Mus musculus GN=Phldb1 PE=1 SV=1 - [PHLB1_MOUSE]	0,000E0	0,000E0	0,000E0	6,779E5	2,258E6	3,730E6	Phldb1
Q8R418-2	Isomform 2 of Endoribonuclease Dicer OS=Mus musculus GN=Dicer1 - [DICER_MOUSE]	0,000E0	0,000E0	0,000E0	1,087E6	2,393E6	2,349E6	Dicer1
P58404-2	Isomform 2 of Striatin-4 OS=Mus musculus GN=Strn4 - [STRN4_MOUSE]	0,000E0	0,000E0	0,000E0	5,413E5	2,563E6	4,056E6	Strn4
O54774	AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1 - [AP3D1_MOUSE]	0,000E0	0,000E0	0,000E0	3,698E6	7,873E5	3,980E6	Ap3d1
Q9WVL3	Solute carrier family 12 member 7 OS=Mus musculus GN=Slc12a7 PE=1 SV=1 - [SL12A7_MOUSE]	0,000E0	0,000E0	0,000E0	3,468E6	4,885E6	3,674E6	Slc12a7
Q6PAR5-5	Isomform 5 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Mus musculus GN=Gapvd1 - [GAPD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,895E6	3,290E6	4,345E6	Gapvd1
Q8VE73-3	Isomform 2 of Cullin-7 OS=Mus musculus GN=Cul7 - [CUL7_MOUSE]	0,000E0	0,000E0	0,000E0	1,794E6	2,435E6	5,081E6	Cul7
Q6DFX2	Anthrax toxin receptor 2 OS=Mus musculus GN=Antxr2 PE=1 SV=1 - [ANTR2_MOUSE]	0,000E0	0,000E0	0,000E0	5,963E6	7,414E6	1,849E7	Antxr2
Q6PSE4	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Ugg1t PE=1 SV=4 - [UGGG1_MOUSE]	0,000E0	0,000E0	0,000E0	2,985E6	4,484E6	3,749E6	Ugg1t
Q9DBB4	N-alpha-acetyltransferase 16, NaTA auxiliary subunit OS=Mus musculus GN=Naa16 PE=2 SV=1 - [NAA16_MOUSE]	0,000E0	0,000E0	0,000E0	4,245E6	1,204E7	1,929E7	Naa16
Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4 OS=Mus musculus GN=Chd4 PE=1 SV=1 - [CHD4_MOUSE]	0,000E0	0,000E0	0,000E0	5,787E6	4,604E6	7,235E6	Chd4
Q8C0E3	Tripartite motif-containing protein 47 OS=Mus musculus GN=Trim47 PE=1 SV=2 - [TRI47_MOUSE]	0,000E0	0,000E0	0,000E0	2,201E6	1,115E6	1,048E6	Trim47
Q99MD9-2	Isomform 2 of Nuclear autoantigenic sperm protein OS=Mus musculus GN=Nasp - [NASP_MOUSE]	0,000E0	0,000E0	0,000E0	1,443E6	2,879E6	3,129E6	Nasp
P06795	Multidrug resistance protein 1B OS=Mus musculus GN=Abcb1b PE=1 SV=1 - [MDR1B_MOUSE]	0,000E0	0,000E0	0,000E0	8,525E5	2,665E6	4,124E6	Abcb1b
Q3UYV9	Nuclear cap-binding protein subunit 1 OS=Mus musculus GN=Ncbp1 PE=1 SV=2 - [NCBP1_MOUSE]	0,000E0	0,000E0	0,000E0	3,681E6	5,270E6	1,785E6	Ncbp1
A2AR02	Peptidyl-prolyl cis-trans isomerase G OS=Mus musculus GN=Ppig PE=1 SV=1 - [PPIG_MOUSE]	0,000E0	0,000E0	0,000E0	3,317E6	5,165E6	8,024E6	Ppig
P17809	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4 - [GTR1_MOUSE]	0,000E0	0,000E0	0,000E0	1,538E6	4,671E6	7,468E6	Slc2a1
Q7S1G6	Art-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 OS=Mus musculus GN=Asap2 PE=1 SV=3 - [ASAP2_MOUSE]	0,000E0	0,000E0	0,000E0	7,767E5	3,134E6	1,793E6	Asap2
Q91Z69	SLIT-ROBO Rho GTPase-activating protein 1 OS=Mus musculus GN=Srgap1 PE=1 SV=2 - [SRGP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,599E7	2,463E7	5,061E7	Srgap1
Q640Q5	PAB-dependent poly(A)-specific ribonuclease subunit PAN3 OS=Mus musculus GN=Pan3 PE=1 SV=3 - [PAN3_MOUSE]	0,000E0	0,000E0	0,000E0	1,110E6	2,124E6	1,232E6	Pan3
Q8BUR4	Dedicator of cytokinesis protein 1 OS=Mus musculus GN=Dock1 PE=1 SV=3 - [DOCK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,558E6	4,658E6	4,354E6	Dock1
P18406	Protein CYR61 OS=Mus musculus GN=Cyr61 PE=1 SV=1 - [CYR61_MOUSE]	0,000E0	0,000E0	0,000E0	8,365E5	3,064E6	8,443E6	Cyr61
Q9D5V5	Cullin-5 OS=Mus musculus GN=Cul5 PE=1 SV=3 - [CUL5_MOUSE]	0,000E0	0,000E0	0,000E0	6,775E6	2,137E6	5,404E6	Cul5
Q08297	DNA repair protein RAD51 homolog 1 OS=Mus musculus GN=Rad51 PE=1 SV=1 - [RAD51_MOUSE]	0,000E0	0,000E0	0,000E0	5,634E5	3,666E6	2,870E6	Rad51
Q9W1U6-2	Isomform Alpha-1 of Mitogen-activated protein kinase 9 OS=Mus musculus GN=Mapk9 - [MK09_MOUSE]	0,000E0	0,000E0	0,000E0	4,305E6	6,578E6	8,472E6	Mapk9
Q9D742	AP-5 complex subunit sigma-1 OS=Mus musculus GN=Ap5s1 PE=1 SV=1 - [AP5S1_MOUSE]	0,000E0	0,000E0	0,000E0	1,281E7	4,401E7	9,475E7	Ap5s1
P08122	Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2 PE=1 SV=4 - [CO4A2_MOUSE]	0,000E0	0,000E0	0,000E0	8,132E5	8,923E6	2,293E7	Col4a2
Q14AX6-3	Isomform 3 of Cyclin-dependent kinase 12 OS=Mus musculus GN=Cdk12 - [CDK12_MOUSE]	0,000E0	0,000E0	0,000E0	7,773E6	1,847E7	3,097E7	Cdk12
P48722-2	Isomform 2 of Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l - [H574L_MOUSE]	0,000E0	0,000E0	0,000E0	3,849E6	1,344E7	2,462E7	Hspa4l
Q8K2Z4	Condensin complex subunit 1 OS=Mus musculus GN=Ncapd2 PE=1 SV=2 - [CND1_MOUSE]	0,000E0	0,000E0	0,000E0	3,405E6	4,844E6	3,110E6	Ncapd2
Q9D0G0	28S ribosomal protein S30, mitochondrial OS=Mus musculus GN=Mrsp30 PE=1 SV=1 - [RT30_MOUSE]	0,000E0	0,000E0	0,000E0	1,736E6	6,170E6	5,311E6	Mrsp30
Q9DBR0	A-kinase anchor protein 8 OS=Mus musculus GN=Akap8 PE=1 SV=1 - [AKAP8_MOUSE]	0,000E0	0,000E0	0,000E0	4,310E6	2,684E6	2,331E6	Akap8
Q8K4R9-3	Isomform 3 of Disks large-associated protein 5 OS=Mus musculus GN=Dlgap5 - [DLG5_MOUSE]	0,000E0	0,000E0	0,000E0	7,256E5	1,115E6	6,524E5	Dlgap5
P11881-8	Isomform 8 of Inositol 1,4,5-trisphosphate receptor type 1 OS=Mus musculus GN=Itpr1 - [ITPR1_MOUSE]	0,000E0	0,000E0	0,000E0	3,231E6	6,095E6	9,739E6	Itpr1
Q9DC23	DnaJ homolog subfamily C member 10 OS=Mus musculus GN=Dnajc10 PE=1 SV=2 - [DICI0_MOUSE]	0,000E0	0,000E0	0,000E0	8,297E5	6,589E6	1,239E7	Dnajc10
E9PZJ8	Activating signal cointegrator 1 complex subunit 3 OS=Mus musculus GN=Ascc3 PE=1 SV=1 - [ASCC3_MOUSE]	0,000E0	0,000E0	0,000E0	1,845E6	3,609E6	8,034E6	Ascc3
Q99KQ4	Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1 - [NAMPT_MOUSE]	0,000E0	0,000E0	0,000E0	1,363E6	7,218E5	3,470E6	Nampt
P33174	Chromosome-associated kinesin KIF4 OS=Mus musculus GN=Kif4 PE=1 SV=3 - [KIF4_MOUSE]	0,000E0	0,000E0	0,000E0	1,563E6	2,604E6	4,897E6	Kif4
Q8BQN6	Zinc finger protein QZF OS=Mus musculus GN=Znf146 PE=2 SV=2 - [QZF_MOUSE]	0,000E0	0,000E0	0,000E0	1,770E6	5,388E6	7,491E6	Znf146
P52431	DNA polymerase delta catalytic subunit OS=Mus musculus GN=Pold1 PE=1 SV=2 - [DPDD1_MOUSE]	0,000E0	0,000E0	0,000E0	5,264E5	2,011E6	3,008E6	Pold1
Q9QXD8	LIM domain-containing protein 1 OS=Mus musculus GN=Limd1 PE=1 SV=2 - [LIMD1_MOUSE]	0,000E0	0,000E0	0,000E0	1,322E6	5,519E6	4,380E6	Limd1
P15306	Thrombomodulin OS=Mus musculus GN=Thbd PE=1 SV=1 - [TRBM_MOUSE]	0,000E0	0,000E0	0,000E0	3,583E7	1,059E7	7,472E6	Thbd
Q8CDJ8	Stonin-1 OS=Mus musculus GN=Ston1 PE=1 SV=2 - [STON1_MOUSE]	0,000E0	0,000E0	0,000E0	1,355E6	3,264E6	8,801E6	Ston1
P42225	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1 - [STAT1_MOUSE]	0,000E0	0,000E0	0,000E0	1,240E6	8,767E5	1,237E6	Stat1
Q9Z329-3	Isomform 3 of Inositol 1,4,5-trisphosphate receptor type 2 OS=Mus musculus GN=Itpr2 - [ITPR2_MOUSE]	0,000E0	0,000E0	0,000E0	3,667E6	4,245E6	6,724E6	Itpr2
Q99PV0	Pre-mRNA-processing-splicing factor 8 OS=Mus musculus GN=Prpf8 PE=1 SV=2 - [PRPF_MOUSE]	0,000E0	0,000E0	0,000E0	8,824E5	9,027E5	2,375E6	Prpf8
Q8BFZ2-2	Isomform 2 of Phospholipid phosphatase-related protein type 1 OS=Mus musculus GN=Plppr1 - [PLPR1_MOUSE]	0,000E0	0,000E0	0,000E0	5,935E6	5,969E6	2,766E6	Plppr1
Q99JW4	LIM and senescent cell antigen-like-containing domain protein 1 OS=Mus musculus GN=Lims1 PE=1 SV=3 - [LIMS1_MOUSE]	0,000E0	0,000E0	0,000E0	5,696E6	9,240E6	1,772E7	Lims1
Q7TDP1-3	Isomform 3 of F-box only protein 11 OS=Mus musculus GN=Fbxo11 - [FBX11_MOUSE]	0,000E0	0,000E0	0,000E0	6,609E5	2,284E6	5,642E6	Fbxo11
Q9DCC4	Pyroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr1 PE=1 SV=2 - [P5CR3_MOUSE]	0,000E0	0,000E0	0,000E0	1,854E6	1,452E6	4,737E6	Pycr1
Q9R158	Calpain-7 OS=Mus musculus GN=Capn7 PE=2 SV=1 - [CAN7_MOUSE]	0,000E0	0,000E0	0,000E0	1,762E6	2,080E6	1,511E6	Capn7
Q9WTR2	Mitogen-activated protein kinase kinase kinase 6 OS=Mus musculus GN=Map3k6 PE=1 SV=4 - [M3K6_MOUSE]	0,000E0	0,000E0	0,000E0	7,774E8	1,237E9	1,635E8	Map3k6
Q9QYI3	DnaJ homolog subfamily B member 1 OS=Mus musculus GN=Dnajb1 PE=1 SV=3 - [DNJB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,528E6	1,835E6	4,638E6	Dnajb1
Q71LX4	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3 - [TLN2_MOUSE]	0,000E0	0,000E0	0,000E0	3,980E6	1,115E7	5,270E6	Tln2
F8VPJ2	FERM, RhoGEF and pleckstrin domain-containing protein 1 OS=Mus musculus GN=Farp1 PE=1 SV=1 - [FARP1_MOUSE]	0,000E0	0,000E0	0,000E0	6,273E5	1,829E6	3,045E6	Farp1
P83741-4	Isomform 4 of Serine/threonine-protein kinase WNK1 OS=Mus musculus GN=Wnk1 - [WNK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,033E6	1,671E6	2,138E6	Wnk1
P70206	Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1 - [PLXA1_MOUSE]	0,000E0	0,000E0	0,000E0	2,637E6	3,080E6	8,465E6	Plxna1
P53995	Anaphase-promoting complex subunit 1 OS=Mus musculus GN=Anapc1 PE=1 SV=2 - [APC1_MOUSE]	0,000E0	0,000E0	0,000E0	2,948E6	2,756E6	3,839E6	Anapc1
Q9QY73	Transmembrane protein 59 OS=Mus musculus GN=Tmem59 PE=1 SV=2 - [TMM59_MOUSE]	0,000E0	0,000E0	0,000E0	8,690E6	5,998E6	1,482E6	Tmem59
P00532	Serine/threonine-protein kinase-transforming protein raf OS=Murine sarcoma virus 3611 GN=V-RAF PE=3 SV=1 - [RAF_MSV36]	0,000E0	0,000E0	0,000E0	3,362E6	6,129E6	1,139E7	V-RAF
Q9JIS8	Solute carrier family 12 member 4 OS=Mus musculus GN=Slc12a4 PE=1 SV=2 - [SL12A4_MOUSE]	0,000E0	0,000E0	0,000E0	2,203E6	7,992E6	1,280E7	Slc12a4
Q6P549	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Mus musculus GN=Inpp1 PE=1 SV=1 - [SHIP2_MOUSE]	0,000E0	0,000E0	0,000E0	4,295E6	6,776E6	1,432E7	Inpp1
Q5SSK3	Transcription elongation factor, mitochondrial OS=Mus musculus GN=Tefm PE=1 SV=1 - [TEFM_MOUSE]	0,000E0	0,000E0	0,000E0	5,918E5	1,960E6	3,581E6	Tefm
Q9Z0R4	Intersectin-1 OS=Mus musculus GN=Itsn1 PE=1 SV=2 - [ITSN1_MOUSE]	0,000E0	0,000E0	0,000E0	4,169E6	2,358E6	6,731E6	Itsn1
D3YXK2	Scaffold attachment factor B1 OS=Mus musculus GN=Safb PE=1 SV=2 - [SAFB1_MOUSE]	0,000E0	0,000E0	0,000E0	2,573E6	5,010E6	1,005E7	Safb
P55937-1	Isomform 1 of Golgin subfamily A member 3 OS=Mus musculus GN=Golga3 - [GOGA3_MOUSE]	0,000E0	0,000E0	0,000E0	1,080E6	1,569E6	2,899E6	Golga3
Q9Z280-2	Isomform PLD1B of Phospholipase D1 OS=Mus musculus GN=Pld1 - [PLD1_MOUSE]	0,000E0	0,000E0	0,000E0	2,111E6	2,099E6	3,634E6	Pld1
B1AYV7	Kinesin-like protein KIF16b OS=Mus musculus GN=Kif16b PE=1 SV=1 - [K116b_MOUSE]	0,000E0	0,000E0	0,000E0	1,563E6	2,138E6	4,571E6	Kif16b
Q4JIM5	Abelson tyrosine-protein kinase 2 OS=Mus musculus GN=Abi2 PE=1 SV=1 - [ABL2_MOUSE]	0,000E0	0,000E0	0,000E0	1,355E6	1,597E6	3,912E6	Abi2
Q9R117	Non-receptor tyrosine-protein kinase TYK2 OS=Mus musculus GN=Tyk2 PE=1 SV=2 - [TYK2_MOUSE]	0,000E0	0,000E0	0,000E0	2,786E6	6,157E6	8,241E6	Tyk2
Q8BWY9	Protein CIP2A OS=Mus musculus GN=Kiaa1524 PE=1 SV=3 - [CIP2A_MOUSE]	0,000E0	0,000E0	0,000E0	1,554E6	2,989E6	4,467E6	Kiaa1524
Q88738-3	Isomform 3 of Baculoviral IAP repeat-containing protein 6 OS=Mus musculus GN=Birc6 - [BIRC6_MOUSE]	0,000E0	0,000E0	0,000E0	5,657E6	4,645E6	5,420E6	Birc6
Q80TV1-2	Isomform 2 of CLIP-associating protein 1 OS=Mus musculus GN=Clasp1 - [CLAP1_MOUSE]	0,000E0	0,000E0	0,000E0	1,014E6	1,426E6	5,115E5	Clasp1
P59913	Protein-L isopartate O-methyltransferase domain-containing protein 1 OS=Mus musculus GN=Pcmtd1 PE=1 SV=1 - [PCMD1_MOUSE]	0,000E0	0,000E0	0,000E0	3,097E6	2,367E6	1,530E6	Pcmtd1
P01872	Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2 - [IGHM_MOUSE]	0,000E0	0,000E0	0,000E0	4,839E7	4,957E8	4,273E8	Ighm
Q99M51	Cytoplasmic protein NCK1 OS=Mus musculus GN=Nck1 PE=1 SV=1 - [NCK1_MOUSE]	0,000E0	0,000E0	0,000E0	1,839E6	1,213E6	3,944E6	Nck1
P35917	Vascular endothelial growth factor receptor 3 OS=Mus musculus GN=Flt4 PE=1 SV=1 - [VGRF3_MOUSE]	0,000E0	0,000E0	0,000E0	3,523E6	1,319E7	1,225E7	Flt4
Q8CYG8-2	Isomform 2 of UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Mus musculus GN=Ogt - [OGT1_MOUSE]	0,000E0	0,000E0	0,000E0	1,460E6	3,095E6	5,330E6	Ogt
Q8VDG3	Poly(A)-specific ribonuclease PARN OS=Mus musculus GN=Parn PE=1 SV=1 - [PARN_MOUSE]	0,000E0	0,000E0	0,000E0	1,275E6	3,004E6	3,372E6	Parn
Q7TMY8-4	Isomform 4 of E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 - [HUWE1_MOUSE]	0,000E0	0,000E0	0,000E0	2,401E6	1,430E6	3,032E6	Huwe1
Q3J214	Microtubule-associated serine/threonine-protein kinase 3 OS=Mus musculus GN=Mas3 PE=1 SV=3 - [MAST3_MOUSE]	0,000E0	0,000E0	0,000E0	3,096E6	2,839E6	3,860E6	Mast3
Q640M1	U3 small nuclear RNA-associated protein 14 homolog A OS=Mus musculus GN=Utp14a PE=1 SV=1 - [UT14A_MOUSE]	0,000E0	0,000E0	0,000E0	1,773E6	8,582E5	1,322E6	Utp14a
Q8BZQ7	Anaphase-promoting complex subunit 2 OS=Mus musculus GN=Anapc2 PE=1 SV=2 - [ANPC2_MOUSE]	0,000E0	0,000E0	0,000E0	6,631E6	8,064E6	1,735E7	Anapc2
A2AN08-3	Isomform 3 of E3 ubiquitin-protein ligase UBR4 OS=Mus musculus GN=Ubr4 - [UBR4_MOUSE]	0,000E0	0,000E0	0,000E0	2,192E6	3,358E6	6,423E6	Ubr4
Q99MR1	PERQ amino acid-rich with GYF domain-containing protein 1 OS=Mus musculus GN=Gigyf1 PE=1 SV=2 - [PERQ1_MOUSE]	0,000E0	0,000E0	0,000E0	2,615E6	5,911E6	9,832E6	Gigyf1
Q91ZK7	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1 - [LRP1_MOUSE]	0,000E0	0,000E0	0,000E0	2,824E6	7,341E6	6,997E6	Lrp1
Q80WQ6	Inactive rhomboid protein 2 OS=Mus musculus GN=Rhbf2 PE=1 SV=1 - [RHDF2_MOUSE]	0,000E0	0,000E0	0,000E0	2,015E6	5,360E6	8,553E6	Rhbf2
A2ASS6	Titin OS=Mus musculus GN=Ttn PE=1 SV=1 - [TITIN_MOUSE]	0,000E0	0,000E0	0,000E0	5,187E6	8,800E6	1,166E7	Ttn

Supplementary Table 2. Mass-spec analysis of AmotL2 immunoprecipitation in BAE cells

Accession	Description	Area Ctr1_1	Area Ctr1_2	Area Ctr1_3	Area AmotL2_1	Area AmotL2_2	Area AmotL2_3	Gene name
F1MQ37	Myosin heavy chain 9 OS=Bos taurus OX=9913 GN=MYH9 PE=1 SV=2 - [F1MQ37_BOVIN]	6,020E7	4,102E6	6,816E6	5,610E9	1,448E10	3,618E10	MYH9
E1BF59	Plectin OS=Bos taurus OX=9913 GN=PLEC PE=1 SV=2 - [E1BF59_BOVIN]	0,000E0	0,000E0	0,000E0	2,215E8	1,471E9	1,320E9	PLEC
Q27991	Myosin-10 OS=Bos taurus OX=9913 GN=MYH10 PE=2 SV=2 - [MYH10_BOVIN]	5,663E7	1,987E6	0,000E0	3,047E9	8,568E9	9,278E9	MYH10
B8Y559	Embryo-specific fibronectin 1 transcript variant OS=Bos taurus OX=9913 GN=FN1 PE=2 SV=1 - [B8Y559_BOVIN]	0,000E0	0,000E0	0,000E0	3,601E8	2,960E9	2,496E9	FN1
O02717	Non-muscle myosin heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=2 - [O02717_BOVIN]	5,457E7	0,000E0	7,722E6	4,326E9	1,312E10	2,392E10	O02717
E1BF80	Spectrin alpha, non-erythrocytic 1 OS=Bos taurus OX=9913 GN=SPTAN1 PE=1 SV=2 - [E1BF80_BOVIN]	0,000E0	0,000E0	0,000E0	2,591E7	3,456E8	3,012E9	SPTAN1
E1BK07	Flamin B OS=Bos taurus OX=9913 GN=FLNB PE=1 SV=2 - [E1BK07_BOVIN]	0,000E0	0,000E0	0,000E0	1,752E7	3,028E8	3,291E8	FLNB
F1MYC9	Spectrin beta chain OS=Bos taurus OX=9913 GN=SPTBN1 PE=1 SV=1 - [F1MYC9_BOVIN]	0,000E0	0,000E0	0,000E0	2,334E7	2,665E8	2,825E8	SPTBN1
F1MER7	Heparan sulfate proteoglycan 2 OS=Bos taurus OX=9913 GN=HSPG2 PE=1 SV=1 - [F1MER7_BOVIN]	0,000E0	0,000E0	0,000E0	3,977E7	4,752E8	4,630E8	HSPG2
P48616	Vimentin OS=Bos taurus OX=9913 GN=VIM PE=1 SV=3 - [VIME_BOVIN]	1,773E7	3,057E7	0,000E0	4,604E9	1,087E10	1,784E10	VIM
Q27966-3	Isoform 3 of Unconventional myosin-1c OS=Bos taurus OX=9913 GN=MYO1C - [MYO1C_BOVIN]	1,185E6	0,000E0	0,000E0	5,697E8	4,504E9	4,765E9	MYO1C
F1MH73	Myosin VA OS=Bos taurus OX=9913 GN=MYOSA PE=3 SV=2 - [F1MH73_BOVIN]	0,000E0	0,000E0	0,000E0	7,743E7	5,367E9	3,435E9	MYOSA
A507D1	Alpha-actinin-4 OS=Bos taurus OX=9913 GN=ACTN4 PE=2 SV=1 - [ACTN4_BOVIN]	0,000E0	0,000E0	0,000E0	1,224E8	1,008E9	9,257E8	ACTN4
F1MQ21	Nestin OS=Bos taurus OX=9913 GN=NES PE=3 SV=2 - [F1MQ21_BOVIN]	0,000E0	0,000E0	0,000E0	2,002E8	8,770E8	9,379E8	NES
P60712	Actin, cytoplasmic 1 OS=Bos taurus OX=9913 GN=ACTB PE=1 SV=1 - [ACTB_BOVIN]	2,164E8	2,069E7	0,000E0	2,369E10	1,389E10	9,397E9	ACTB
F1MJ56	Unconventional myosin-1d OS=Bos taurus OX=9913 GN=MYO1D PE=3 SV=1 - [F1MJ56_BOVIN]	0,000E0	0,000E0	0,000E0	2,315E8	8,567E8	5,625E8	MYO1D
F1MQ65	Myosin IE OS=Bos taurus OX=9913 GN=MYO1E PE=3 SV=2 - [F1MQ65_BOVIN]	0,000E0	0,000E0	0,000E0	8,994E7	7,000E8	6,884E8	MYO1E
G5E631	Uncharacterized protein OS=Bos taurus OX=9913 GN=DDX3X PE=1 SV=1 - [G5E631_BOVIN]	1,741E8	5,158E6	0,000E0	8,700E8	3,134E9	4,333E8	DDX3X
F1MRD0	Actin, cytoplasmic 1 OS=Bos taurus OX=9913 GN=ACTB PE=3 SV=2 - [F1MRD0_BOVIN]	2,164E8	2,069E7	0,000E0	1,916E10	9,283E9	9,397E9	ACTB
Q3B7N2	Alpha-actinin-1 OS=Bos taurus OX=9913 GN=ACTN1 PE=2 SV=1 - [ACTN1_BOVIN]	0,000E0	0,000E0	0,000E0	8,213E7	5,927E8	6,215E8	ACTN1
E1BD0F	Nexlin F-actin binding protein OS=Bos taurus OX=9913 GN=NEXN PE=4 SV=2 - [E1BD0F_BOVIN]	0,000E0	0,000E0	0,000E0	1,259E8	7,540E8	1,343E9	NEXN
Q1RMT6	Drebrin 1 OS=Bos taurus OX=9913 GN=DBN1 PE=1 SV=1 - [Q1RMT6_BOVIN]	0,000E0	0,000E0	0,000E0	8,127E8	1,487E9	1,750E9	DBN1
E1BPK6	Myosin VI OS=Bos taurus OX=9913 GN=MYO6 PE=3 SV=2 - [E1BPK6_BOVIN]	0,000E0	0,000E0	0,000E0	5,921E7	3,677E8	5,488E8	MYO6
F1N6K7	Protein transport protein sec1c OS=Bos taurus OX=9913 GN=SEC1CA PE=3 SV=2 - [F1N6K7_BOVIN]	1,024E7	0,000E0	8,998E6	5,670E7	4,123E7	4,923E7	SEC1CA
E1BD0X	LJM domain and actin binding 1 OS=Bos taurus OX=9913 GN=LJMA1 PE=1 SV=2 - [E1BD0X_BOVIN]	0,000E0	0,000E0	0,000E0	8,139E7	1,247E9	1,051E9	LJMA1
F1MY06	Trinucleotide repeat containing 6B OS=Bos taurus OX=9913 GN=TNRC6B PE=4 SV=2 - [F1MY06_BOVIN]	9,599E6	0,000E0	1,379E7	4,931E7	3,929E7	3,542E7	TNRC6B
P19120	Heat shock cognate 71 kDa protein OS=Bos taurus OX=9913 GN=HSPA8 PE=1 SV=2 - [HSP7C_BOVIN]	2,063E7	8,924E6	1,636E7	4,185E8	1,116E9	1,126E9	HSPA8
E1BC59	Protein phosphatase 1 regulatory subunit 12A OS=Bos taurus OX=9913 GN=PPP1R12A PE=4 SV=2 - [E1BC59_BOVIN]	0,000E0	0,000E0	0,000E0	8,072E7	7,197E8	6,971E8	PPP1R12A
A0A1407897	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1 - [A0A1407897_BOVIN]	1,543E8	0,000E0	3,453E7	1,193E8	5,507E7	2,688E7	ALB
G3MWI5	Coronin OS=Bos taurus OX=9913 GN=CORO1C PE=3 SV=1 - [G3MWI5_BOVIN]	0,000E0	0,000E0	0,000E0	1,239E8	9,689E8	5,237E8	CORO1C
E1BK70	Leucine zipper protein 1 OS=Bos taurus OX=9913 GN=LUZP1 PE=4 SV=2 - [E1BK70_BOVIN]	0,000E0	0,000E0	0,000E0	1,877E7	9,483E7	9,462E7	LUZP1
Q3ZCH0	Stress-70 protein, mitochondrial OS=Bos taurus OX=9913 GN=HSPA9 PE=2 SV=1 - [GRP75_BOVIN]	2,855E7	1,100E7	2,041E7	3,600E8	3,932E8	3,923E8	HSPA9
F1N2D3	Tight junction protein 1 OS=Bos taurus OX=9913 GN=TJP1 PE=3 SV=2 - [F1N2D3_BOVIN]	0,000E0	0,000E0	0,000E0	1,086E7	7,229E7	1,165E8	TJP1
P9951	Claudin heavy chain 1 OS=Bos taurus OX=9913 GN=CLTC PE=1 SV=1 - [CLH1_BOVIN]	0,000E0	0,000E0	0,000E0	1,570E7	1,786E8	2,593E8	CLTC
A6QLD6	MYO1B protein OS=Bos taurus OX=9913 GN=MYO1B PE=2 SV=1 - [A6QLD6_BOVIN]	0,000E0	0,000E0	0,000E0	8,800E6	1,984E8	1,939E8	MYO1B
Q5KR49	Tropomyosin alpha-1 chain OS=Bos taurus OX=9913 GN=TPM1 PE=2 SV=1 - [TPM1_BOVIN]	0,000E0	0,000E0	0,000E0	1,441E9	8,777E9	7,273E9	TPM1
A1MF8	Actin, alpha 1, skeletal muscle OS=Bos taurus OX=9913 GN=ACTA1 PE=2 SV=1 - [A1MF8_BOVIN]	2,426E8	2,069E7	0,000E0	1,945E10	1,203E10	7,861E9	ACTA1
F1N365	FLII, actin remodeling protein OS=Bos taurus OX=9913 GN=FLII PE=4 SV=1 - [F1N365_BOVIN]	0,000E0	0,000E0	0,000E0	2,696E7	2,339E8	1,845E8	FLII
Q5KR47-2	Isoform 2 of Tropomyosin alpha-3 chain OS=Bos taurus OX=9913 GN=TPM3 - [TPM3_BOVIN]	0,000E0	0,000E0	0,000E0	1,349E9	9,210E9	8,943E9	TPM3
P61286	Polyadenylate-binding protein 1 OS=Bos taurus OX=9913 GN=PABPC1 PE=2 SV=1 - [PABP1_BOVIN]	1,166E7	0,000E0	0,000E0	2,575E8	1,549E8	1,684E8	PABPC1
Q0V8H6	Putative helicase MOV-10 OS=Bos taurus OX=9913 GN=MOV10 PE=2 SV=1 - [MOV10_BOVIN]	0,000E0	0,000E0	0,000E0	9,763E7	3,227E7	6,965E7	MOV10
F1MDC1	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=2 - [F1MDC1_BOVIN]	0,000E0	0,000E0	0,000E0	1,287E7	4,050E8	4,074E8	F1mdc1
E1BEK9	UPF1, RNA helicase and ATPase OS=Bos taurus OX=9913 GN=UPF1 PE=4 SV=2 - [E1BEK9_BOVIN]	0,000E0	0,000E0	0,000E0	3,604E7	5,350E7	1,193E7	UPF1
F1MBA3	Integrin alpha-2 OS=Bos taurus OX=9913 GN=ITGA2 PE=3 SV=2 - [F1MBA3_BOVIN]	1,531E7	0,000E0	2,417E7	9,388E7	3,219E7	7,963E7	ITGA2
G3X575	Transitional endoplasmic reticulum ATPase OS=Bos taurus OX=9913 GN=VCP PE=3 SV=1 - [G3X575_BOVIN]	0,000E0	0,000E0	0,000E0	3,692E7	9,752E7	1,599E8	VCP
Q0VQK2	Endoplasmic reticulum chaperone BIP OS=Bos taurus OX=9913 GN=HSPA5 PE=2 SV=1 - [BIP_BOVIN]	2,051E7	0,000E0	2,976E7	1,622E8	1,787E8	1,935E8	HSPA5
A4FUC2	HNRNPUL1 protein OS=Bos taurus OX=9913 GN=HNRNPUL1 PE=1 SV=1 - [A4FUC2_BOVIN]	6,245E7	6,810E7	0,000E0	4,349E8	2,130E8	6,945E7	HNRNPUL1
P53712	Integrin beta-1 OS=Bos taurus OX=9913 GN=ITGB1 PE=1 SV=3 - [ITB1_BOVIN]	8,016E7	4,170E7	7,723E7	5,275E8	3,133E8	3,005E8	ITGB1
F1MRK3	Angiomotin-like protein 2 OS=Bos taurus OX=9913 GN=AMOTL2 PE=2 SV=3 - [AMOTL2_BOVIN]	6,080E8	6,000E8	6,308E8	1,919E8	8,611E7	1,499E8	AMOTL2
Q2H060	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Bos taurus OX=9913 GN=HNRNPA2B1 PE=2 SV=1 - [ROA2_BOVIN]	3,004E8	5,764E6	1,665E8	5,180E8	4,291E7	1,664E7	HNRNPA2B1
F1MCL1	Keratin, type I cytoskeletal 14 OS=Bos taurus OX=9913 GN=KRT14 PE=1 SV=2 - [F1MCL1_BOVIN]	4,111E8	6,366E7	2,939E8	6,043E8	3,424E7	1,067E7	KRT14
F1MM57	Myosin heavy chain 14 OS=Bos taurus OX=9913 GN=MYH14 PE=1 SV=2 - [F1MM57_BOVIN]	3,181E7	0,000E0	0,000E0	2,032E9	9,526E9	1,439E10	MYH14
E1BET5	Sperm specific antigen 2 OS=Bos taurus OX=9913 GN=ITPRID2 PE=4 SV=2 - [E1BET5_BOVIN]	0,000E0	0,000E0	0,000E0	1,495E6	1,186E8	7,795E7	ITPRID2
E1BNE7	Caveolae associated protein 1 OS=Bos taurus OX=9913 GN=CAVIN1 PE=1 SV=1 - [E1BNE7_BOVIN]	5,895E6	0,000E0	0,000E0	4,678E8	4,985E9	4,407E9	CAVIN1
Q1RMR3	Cortactin OS=Bos taurus OX=9913 GN=CTTN PE=1 SV=1 - [Q1RMR3_BOVIN]	0,000E0	0,000E0	0,000E0	1,909E8	1,216E9	1,528E9	CTTN
A7MB15	DPYSL3 protein OS=Bos taurus OX=9913 GN=DPYSL3 PE=1 SV=1 - [A7MB15_BOVIN]	0,000E0	1,643E6	7,066E6	6,500E7	4,821E7	4,016E7	DPYSL3
E1BF20	Heterogeneous nuclear ribonucleoprotein H1 OS=Bos taurus OX=9913 GN=HNRNPH1 PE=1 SV=2 - [E1BF20_BOVIN]	3,774E8	3,634E7	1,022E8	1,917E9	7,770E8	9,580E8	HNRNPH1
MQQVZ6	Keratin, type II cytoskeletal 5 OS=Bos taurus OX=9913 GN=KRT5 PE=3 SV=1 - [MQQVZ6_BOVIN]	1,295E9	2,610E7	2,830E7	4,192E8	1,092E7	1,227E7	KRT5
Q5KR47	Tropomyosin alpha-3 chain OS=Bos taurus OX=9913 GN=TPM3 PE=2 SV=1 - [TPM3_BOVIN]	0,000E0	0,000E0	0,000E0	1,349E9	8,165E9	6,151E9	TPM3
A7E307	DDX17 protein OS=Bos taurus OX=9913 GN=DDX17 PE=1 SV=1 - [A7E307_BOVIN]	0,000E0	0,000E0	0,000E0	7,125E7	1,596E8	1,779E8	DDX17
F1MBQ8	DEAD-box helicase 5 OS=Bos taurus OX=9913 GN=DDX5 PE=3 SV=2 - [F1MBQ8_BOVIN]	0,000E0	0,000E0	0,000E0	1,226E8	2,143E8	2,056E8	DDX5
F1N3L7	Dedicator of cytokinesis 7 OS=Bos taurus OX=9913 GN=DOCK7 PE=3 SV=2 - [F1N3L7_BOVIN]	0,000E0	0,000E0	0,000E0	6,523E6	6,343E7	3,671E7	DOCK7
K9ZRL4	Heat shock 70kDa protein 1A OS=Bos indicus x Bos taurus OX=30522 GN=HSPA1A PE=2 SV=1 - [K9ZRL4_BOBOX]	3,446E7	0,000E0	2,976E7	2,943E8	4,032E8	4,354E8	HSPA1A
P19136-2	Isoform Beta-2 of F-actin-capping protein subunit beta OS=Bos taurus OX=9913 GN=CAPZB - [CAPZB_BOVIN]	0,000E0	0,000E0	0,000E0	2,853E8	1,487E9	2,174E9	CAPZB
ABE4L8	LJM domain 7 OS=Bos taurus OX=9913 GN=LMO7 PE=1 SV=1 - [ABE4L8_BOVIN]	0,000E0	0,000E0	0,000E0	5,743E6	7,540E7	1,125E8	LMO7
A6QR15	LOC35277 protein OS=Bos taurus OX=9913 GN=TPM4 PE=1 SV=1 - [A6QR15_BOVIN]	0,000E0	0,000E0	0,000E0	1,049E9	5,247E9	4,464E9	TPM4
E1BKQ6	Myosin XVIIIa OS=Bos taurus OX=9913 GN=MYO18A PE=3 SV=2 - [E1BKQ6_BOVIN]	0,000E0	0,000E0	0,000E0	4,855E6	1,231E8	1,014E8	MYO18A
Q35X36	TFG protein OS=Bos taurus OX=9913 GN=TFG PE=2 SV=1 - [Q35X36_BOVIN]	7,425E8	1,859E8	8,084E7	3,202E9	5,176E8	9,231E8	TFG
F1N3A1	Thrombospondin-1 OS=Bos taurus OX=9913 GN=THBS1 PE=4 SV=1 - [F1N3A1_BOVIN]	9,682E9	0,000E0	0,000E0	1,277E7	1,156E9	1,095E9	THBS1
F1MTP5	WD repeat-containing protein 1 OS=Bos taurus OX=9913 GN=WDR1 PE=4 SV=2 - [F1MTP5_BOVIN]	0,000E0	0,000E0	0,000E0	2,044E7	3,156E8	4,507E8	WDR1
Q3MR47	Actin-related protein 2/3 complex subunit 2 OS=Bos taurus OX=9913 GN=ARPC2 PE=1 SV=1 - [ARPC2_BOVIN]	0,000E0	0,000E0	0,000E0	8,576E7	5,033E8	9,465E8	ARPC2
P61157	Actin-related protein 3 OS=Bos taurus OX=9913 GN=ACTR3 PE=1 SV=3 - [ARP3_BOVIN]	0,000E0	0,000E0	0,000E0	1,341E8	2,483E8	1,186E8	ACTR3
ABE654	COL18A1 protein OS=Bos taurus OX=9913 GN=COL18A1 PE=2 SV=1 - [ABE654_BOVIN]	0,000E0	0,000E0	0,000E0	5,072E7	3,067E8	3,942E8	COL18A1
F1ME65	Cytoskeleton associated protein 4 OS=Bos taurus OX=9913 GN=CKAP4 PE=1 SV=1 - [F1ME65_BOVIN]	0,000E0	0,000E0	0,000E0	1,215E7	9,264E7	1,071E8	CKAP4
Q7YR4V	E3 ubiquitin-protein ligase TRIM21 OS=Bos taurus OX=9913 GN=TRIM21 PE=2 SV=1 - [ROS2_BOVIN]	0,000E0	0,000E0	0,000E0	8,054E7	1,599E8	5,598E7	TRIM21
E1BFW2	ELKS/RAB6-interacting/CAST family member 1 OS=Bos taurus OX=9913 GN=ERC1 PE=4 SV=2 - [E1BFW2_BOVIN]	0,000E0	0,000E0	0,000E0	1,419E7	9,919E6	5,451E6	ERC1
A7MB80	General transcription factor II-1 OS=Bos taurus OX=9913 GN=GTF2I PE=2 SV=1 - [GTF2I_BOVIN]	0,000E0	0,000E0	0,000E0	1,851E7	2,968E7	2,869E7	GTF2I
F1MD77	Laminin subunit gamma 1 OS=Bos taurus OX=9913 GN=LAMC1 PE=1 SV=2 - [F1MD77_BOVIN]	0,000E0	0,000E0	0,000E0	1,297E7	1,487E8	1,619E8	LAMC1
F1MP70	Leucine-rich repeat flightless-interacting protein 2 OS=Bos taurus OX=9913 GN=LRRFIP2 PE=4 SV=1 - [F1MP70_BOVIN]	0,000E0	0,000E0	0,000E0	7,899E7	1,612E8	1,175E8	LRRFIP2
E1BD01	Ras interacting protein 1 OS=Bos taurus OX=9913 GN=RASIP1 PE=4 SV=1 - [E1BD01_BOVIN]	0,000E0	0,000E0	0,000E0	3,113E7	1,703E8	1,564E8	RASIP1
F1MJ47	RNA-binding protein 14 OS=Bos taurus OX=9913 GN=RBM14 PE=4 SV=1 - [F1MJ47_BOVIN]	0,000E0	1,814E7	0,000E0	6,851E7	7,413E7	5,077E7	RBM14
F1MJ29	60 kDa heat shock protein, mitochondrial OS=Bos taurus OX=9913 GN=HSPD1 PE=1 SV=1 - [F1MJ29_BOVIN]	0,000E0	0,000E0	0,000E0	2,846E7	5,329E7	5,990E7	HSPD1
A7YMC4	ATPase family AAA domain-containing protein 3 OS=Bos taurus OX=9913 GN=ATAD3 PE=2 SV=1 - [ATAD3_BOVIN]	0,000E0	0,000E0	0,000E0	2,815E7	4,185E7	5,686E7	ATAD3
A5D9B4	Heterogeneous nuclear ribonucleoprotein H2 OS=Bos taurus OX=9913 GN=HNRNPH2 PE=2 SV=1 - [A5D9B4_BOVIN]	3,774E8	3,634E7	3,481E7	1,917E9	7,770E8	7,314E8	HNRNPH2
E1B1B4	Heterogeneous nuclear ribonucleoprotein L OS=Bos taurus OX=9913 GN=HNRNPL PE=1 SV=2 - [E1B1B4_BOVIN]	0,000E0	0,000E0	0,000E0	9,256E7	2,010E7	3,332E7	HNRNPL
A4IFC3	Polyadenylate-binding protein OS=Bos taurus OX=9913 GN=PABPC4 PE=2 SV=1 - [A4IFC3_BOVIN]	0,000E0	0,000E0	0,000E0	1,461E8	1,343E8	6,130E7	PABPC4
P63243	Receptor of activated protein C kinase 1 OS=Bos taurus OX=9913 GN=RACK1 PE=2 SV=3 - [RACK1_BOVIN]	7,575E6	0,000E0	0,000E0	2,907E8	4,730E8	2,448E8	RACK1
E1BA93	Synaptopodin OS=Bos taurus OX=9913 GN=SYNPO PE=4 SV=2 - [E1BA93_BOVIN]	0,000E0	0,000E0	0,000E0	2,388E7	2,559E8	1,774E8	SYNPO
A7E355	SYNCRIP protein (Fragment) OS=Bos taurus OX=9913 GN=SYNCRIP PE=2 SV=1 - [A7E355_BOVIN]	0,000E0	0,000E0	1				

Q3T169	40S ribosomal protein S3 OS=Bos taurus OX=9913 GN=RP53 PE=2 SV=1 - [RS3_BOVIN]	8,535E6	8,993E6	5,061E6	1,842E8	5,501E8	5,680E8	RPS3
Q56J39	40S ribosomal protein S3a OS=Bos taurus OX=9913 GN=RP53A PE=2 SV=3 - [RS3A_BOVIN]	0,000E0	0,000E0	0,000E0	8,427E7	4,585E8	2,354E8	RPS3A
A7MB62	Actin-related protein 2 OS=Bos taurus OX=9913 GN=ACTR2 PE=1 SV=1 - [ARP2_BOVIN]	0,000E0	0,000E0	0,000E0	2,174E8	1,042E9	8,179E8	ACTR2
Q0ITK5	ATP-dependent RNA helicase DDX1 OS=Bos taurus OX=9913 GN=DDX1 PE=2 SV=1 - [DDX1_BOVIN]	0,000E0	0,000E0	0,000E0	1,787E7	1,344E8	1,009E8	DDX1
A6H7H1	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Bos taurus OX=9913 GN=FAM120A PE=2 SV=1 - [F120A_BOVIN]	0,000E0	0,000E0	0,000E0	7,518E6	2,471E6	4,423E7	FAM120A
Q76LV1	Heat shock protein HSP 90-beta OS=Bos taurus OX=9913 GN=HSP90AB1 PE=2 SV=3 - [HS90B_BOVIN]	1,281E7	0,000E0	0,000E0	3,924E7	2,724E7	1,981E7	HSP90AB1
P09867	Heterogeneous nuclear ribonucleoprotein A1 OS=Bos taurus OX=9913 GN=HNRNP1 PE=1 SV=2 - [ROA1_BOVIN]	8,950E6	0,000E0	0,000E0	7,875E7	1,325E8	1,223E8	HNRNP1
E1BE62	Heterogeneous nuclear ribonucleoprotein A3 OS=Bos taurus OX=9913 GN=HNRNP3 PE=1 SV=2 - [E1BE62_BOVIN]	3,383E7	0,000E0	0,000E0	3,610E8	1,092E7	3,142E8	HNRNP3
E1BB17	Heterogeneous nuclear ribonucleoprotein H3 OS=Bos taurus OX=9913 GN=HNRNP3 PE=1 SV=1 - [E1BB17_BOVIN]	8,945E7	0,000E0	1,443E7	3,082E8	5,168E6	3,529E6	HNRNP3
Q37D00	Heterogeneous nuclear ribonucleoprotein K OS=Bos taurus OX=9913 GN=HNRNPK PE=2 SV=1 - [HNRPK_BOVIN]	1,081E7	0,000E0	0,000E0	1,077E8	4,562E7	6,817E7	HNRNP3
F1MM59	Integrin alpha-3 OS=Bos taurus OX=9913 GN=ITGA3 PE=3 SV=1 - [ITA3_BOVIN]	2,909E7	3,732E7	3,998E7	1,858E8	2,556E7	4,198E7	ITGA3
B07YP5	Protein argonaute-2 OS=Bos taurus OX=9913 GN=AGO2 PE=2 SV=1 - [B07YP5_BOVIN]	0,000E0	0,000E0	0,000E0	4,797E7	7,436E7	4,258E7	AGO2
F1MVW5	Protein transport protein SEC23 OS=Bos taurus OX=9913 GN=SEC23A PE=3 SV=2 - [F1MVWS_BOVIN]	3,039E7	0,000E0	0,000E0	3,944E7	8,283E7	3,504E7	SEC23A
Q5E9T9	tRNA-splicing ligase RtcB homolog OS=Bos taurus OX=9913 GN=RTCB PE=2 SV=1 - [RTCB_BOVIN]	0,000E0	0,000E0	0,000E0	4,540E7	1,468E8	6,082E7	RTCB
F1N6C0	Uncharacterized protein OS=Bos taurus OX=9913 GN=CALM2 PE=4 SV=2 - [F1N6C0_BOVIN]	0,000E0	0,000E0	0,000E0	3,826E8	1,006E9	1,923E9	CALM2
Q32P05	40S ribosomal protein S19 OS=Bos taurus OX=9913 GN=RP519 PE=2 SV=3 - [RS19_BOVIN]	0,000E0	0,000E0	0,000E0	1,928E8	5,144E8	1,205E8	RPS19
Q58D0W	60S ribosomal protein L4 OS=Bos taurus OX=9913 GN=RLP4 PE=2 SV=3 - [RL4_BOVIN]	0,000E0	0,000E0	0,000E0	3,119E7	2,577E8	1,279E8	RLP4
Q1JPK9	Actin related protein 2/3 complex subunit 1B (Fragment) OS=Bos taurus OX=9913 GN=ARPC18 PE=2 SV=1 - [Q1JPK9_BOVIN]	0,000E0	0,000E0	0,000E0	8,267E7	3,873E8	1,994E8	ARPC18
G5ESN3	ATP-dependent RNA helicase A OS=Bos taurus OX=9913 GN=DXH9 PE=4 SV=1 - [G5ESN3_BOVIN]	0,000E0	0,000E0	0,000E0	1,991E7	5,330E7	6,292E7	DXH9
AFU0A8	F-actin-capping protein subunit alpha-1 OS=Bos taurus OX=9913 GN=CAPZA1 PE=2 SV=1 - [CAZA1_BOVIN]	0,000E0	0,000E0	0,000E0	3,232E8	1,746E9	1,373E9	CAPZA1
Q8WMQ6	Flavin A (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q8WMQ6_BOVIN]	0,000E0	0,000E0	0,000E0	1,438E7	1,104E8	3,854E7	FLNA
AZVDN7	Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) OS=Bos taurus OX=9913 GN=HNRNP U PE=2 SV=1 - [AZVDN7_BOVIN]	0,000E0	0,000E0	0,000E0	9,752E7	2,376E8	1,282E8	HNRNP U
AK3K06	HNRNPR protein OS=Bos taurus OX=9913 GN=HNRNPR PE=1 SV=1 - [AK3K06_BOVIN]	0,000E0	0,000E0	1,715E7	4,367E7	3,361E7	1,057E7	HNRNPR
P0661-2	Isomform Smooth muscle of Myosin light polypeptide 6 OS=Bos taurus OX=9913 GN=MYL6 - [MYL6_BOVIN]	7,341E6	1,354E7	0,000E0	3,112E9	1,484E10	1,581E10	MYL6
F1M00D	MICOS complex subunit MIC60 OS=Bos taurus OX=9913 GN=IMMT PE=1 SV=1 - [F1M00D_BOVIN]	0,000E0	0,000E0	0,000E0	6,081E6	1,407E8	1,487E8	IMMT
P06661	Myosin light polypeptide 6 OS=Bos taurus OX=9913 GN=MYL6 PE=2 SV=2 - [MYL6_BOVIN]	7,341E6	1,354E7	0,000E0	3,112E9	1,484E10	1,581E10	MYL6
F1M292	Nuclease-sensitive element-binding protein 1 OS=Bos taurus OX=9913 GN=YBK1 PE=4 SV=2 - [F1M292_BOVIN]	2,620E7	0,000E0	5,410E7	1,238E9	7,883E8	1,185E9	YBK1
AOA1407861	Nuclein-binding protein FUS OS=Bos taurus OX=9913 GN=FUS PE=4 SV=1 - [AOA1407861_BOVIN]	9,088E8	0,000E0	5,559E8	1,321E10	1,780E9	2,558E9	FUS
E1BIU0	SEC24 homolog C, COPII coat complex component OS=Bos taurus OX=9913 GN=SEC24C PE=1 SV=1 - [E1BIU0_BOVIN]	1,279E7	1,198E7	1,106E7	8,100E7	6,415E7	5,408E7	SEC24C
E1BGX1	TATA-box binding protein associated factor 15 OS=Bos taurus OX=9913 GN=TAFI5 PE=4 SV=2 - [E1BGX1_BOVIN]	2,706E8	5,179E6	5,559E8	1,737E8	1,158E9	9,225E8	TAFI5
F224H8	TIA1 cytotoxic granule associated RNA binding protein like 1 OS=Bos taurus OX=9913 GN=TIAL1 PE=4 SV=2 - [F224H8_BOVIN]	3,259E7	0,000E0	6,197E7	1,303E8	5,732E6	6,100E8	TIAL1
E1B1B1	Tubulin beta chain OS=Bos taurus OX=9913 GN=TUBB2A PE=1 SV=1 - [E1B1B1_BOVIN]	2,869E7	0,000E0	0,000E0	6,851E7	1,284E8	1,337E8	TUBB2A
Q3M4M5	Tubulin beta-4B chain OS=Bos taurus OX=9913 GN=TUBB4B PE=2 SV=1 - [TBB4B_BOVIN]	2,869E7	0,000E0	0,000E0	8,312E7	1,406E8	1,337E8	TUBB4B
Q2KJ0D	Tubulin beta-5 chain OS=Bos taurus OX=9913 GN=TUBB5 PE=2 SV=1 - [TBB5_BOVIN]	2,220E7	0,000E0	0,000E0	6,628E7	1,479E8	1,067E8	TUBB5
F1MY12	Uncharacterized protein OS=Bos taurus OX=9913 GN=HNRNPM PE=1 SV=2 - [F1MY12_BOVIN]	0,000E0	0,000E0	0,000E0	2,372E7	4,213E7	4,233E7	HNRNPM
ASD7Q4	CSDA protein OS=Bos taurus OX=9913 GN=YBK3 PE=1 SV=1 - [ASD7Q4_BOVIN]	3,000E7	0,000E0	0,000E0	8,555E8	2,257E8	7,208E8	YBK3
F1MJH1	Gelsolin OS=Bos taurus OX=9913 GN=GSN PE=4 SV=1 - [F1MJH1_BOVIN]	1,209E7	0,000E0	0,000E0	1,101E8	2,819E8	8,336E7	GSN
AOA088Q0F	Heat shock protein 90kDa alpha OS=Bos taurus & Bos grunniens OX=1167295 PE=2 SV=1 - [AOA088Q0F_9CETA]	0,000E0	0,000E0	0,000E0	4,005E7	1,283E7	1,617E7	HSP90AB1
Q5E911	Heterogeneous nuclear ribonucleoprotein F OS=Bos taurus OX=9913 GN=HNRNPF PE=2 SV=3 - [HNRPF_BOVIN]	2,343E8	0,000E0	0,000E0	7,057E8	2,517E7	2,077E7	HNRNPF
F1MTN1	Integrin beta OS=Bos taurus OX=9913 GN=ITGB3 PE=3 SV=1 - [F1MTN1_BOVIN]	0,000E0	0,000E0	0,000E0	3,463E7	1,371E7	1,751E7	ITGB3
F1MNT4	Laminin subunit beta 1 OS=Bos taurus OX=9913 GN=LAMB1 PE=4 SV=2 - [F1MNT4_BOVIN]	0,000E0	0,000E0	0,000E0	6,481E6	3,346E7	1,099E7	LAMB1
A4IF97	Myosin regulatory light chain 12B OS=Bos taurus OX=9913 GN=MYL12B PE=2 SV=1 - [ML12B_BOVIN]	1,003E7	0,000E0	0,000E0	4,282E9	1,172E10	8,380E9	MYL12B
F1MU08	Poly (ADP-ribose) polymerase OS=Bos taurus OX=9913 GN=PARP1 PE=4 SV=2 - [F1MU08_BOVIN]	0,000E0	0,000E0	0,000E0	1,386E7	9,516E7	1,115E8	PARP1
F1N6W6	Sorting nexin OS=Bos taurus OX=9913 GN=SNX9 PE=3 SV=2 - [F1N6W6_BOVIN]	4,182E7	6,389E7	5,097E6	2,603E8	2,083E8	2,120E8	SNX9
F224C1	Tubulin alpha chain OS=Bos taurus OX=9913 GN=TUBA1A PE=3 SV=1 - [F224C1_BOVIN]	2,350E7	0,000E0	0,000E0	1,890E8	1,757E8	9,255E7	TUBA1A
P81947	Tubulin alpha-1B chain OS=Bos taurus OX=9913 PE=1 SV=2 - [TBA1B_BOVIN]	2,350E7	0,000E0	0,000E0	1,890E8	1,757E8	9,255E7	TUBA1B
Q370X6	40S ribosomal protein S16 OS=Bos taurus OX=9913 GN=RP516 PE=2 SV=3 - [RS16_BOVIN]	6,254E6	0,000E0	0,000E0	2,518E7	3,647E7	4,029E7	RPS16
Q58D71	60S ribosomal protein L7 OS=Bos taurus OX=9913 GN=RLP7 PE=2 SV=1 - [RL7_BOVIN]	0,000E0	0,000E0	0,000E0	6,401E7	7,190E8	8,174E8	RLP7
AFV37	Caveolae-associated protein 3 OS=Bos taurus OX=9913 GN=CAVIN3 PE=2 SV=1 - [CAVIN3_BOVIN]	0,000E0	0,000E0	0,000E0	1,970E6	2,871E7	2,432E7	CAVIN3
E1BDM8	DEAD-box helicase 6 OS=Bos taurus OX=9913 GN=DDX6 PE=1 SV=1 - [E1BDM8_BOVIN]	0,000E0	0,000E0	0,000E0	3,633E7	2,172E7	3,322E7	DDX6
A6QKZ7	Keratin 10 (Epidermolytic hyperkeratosis; keratosis palmaris et plantaris) OS=Bos taurus OX=9913 GN=KRT10 PE=2 SV=1 - [A6QKZ7_BOVIN]	5,617E8	5,145E8	2,270E7	3,371E9	9,223E7	5,738E8	KRT10
G36B3	Proline rich coiled-coil 2C OS=Bos taurus OX=9913 GN=PRRC2C PE=4 SV=1 - [G36B3_BOVIN]	0,000E0	0,000E0	0,000E0	2,014E6	1,997E7	1,534E7	PRRC2C
AL15B7	SERPINE1 mRNA binding protein 1 OS=Bos taurus OX=9913 GN=SERBP1 PE=1 SV=1 - [AL15B7_BOVIN]	0,000E0	0,000E0	0,000E0	2,193E7	1,771E7	3,206E7	SERBP1
Q86258	Similar to ribosomal protein S18 (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q86258_BOVIN]	0,000E0	0,000E0	8,945E6	5,566E7	7,652E6	8,803E7	RPS18
Q0V8Z6	TIA1 cytotoxic granule-associated RNA binding protein OS=Bos taurus OX=9913 GN=TIA1 PE=2 SV=1 - [Q0V8Z6_BOVIN]	3,259E7	0,000E0	6,825E7	1,655E8	6,116E7	2,315E8	TIA1
AL1505	Ubiquitin associated protein 2-like OS=Bos taurus OX=9913 GN=UBAP2L PE=2 SV=1 - [AL1505_BOVIN]	8,334E6	0,000E0	0,000E0	6,526E7	3,231E7	3,661E7	UBAP2L
E1B8K6	Uncharacterized protein OS=Bos taurus OX=9913 GN=NCL PE=1 SV=1 - [E1B8K6_BOVIN]	0,000E0	0,000E0	0,000E0	3,799E7	2,301E8	1,156E8	NCL
E1B8P5	Uridine-cytidine kinase OS=Bos taurus OX=9913 GN=UCKL1 PE=3 SV=1 - [E1B8P5_BOVIN]	0,000E0	0,000E0	0,000E0	2,367E7	9,340E6	9,001E6	UCKL1
P26452	40S ribosomal protein SA OS=Bos taurus OX=9913 GN=RP5A PE=2 SV=4 - [R5SA_BOVIN]	0,000E0	0,000E0	0,000E0	3,791E8	1,371E9	4,922E8	RPS1A
Q95140	60S acidic ribosomal protein P0 OS=Bos taurus OX=9913 GN=RLP0 PE=2 SV=3 - [RLA0_BOVIN]	0,000E0	0,000E0	0,000E0	1,084E8	7,248E7	2,108E8	RPLP0
P61284	60S ribosomal protein L12 OS=Bos taurus OX=9913 GN=RLP12 PE=2 SV=1 - [RL12_BOVIN]	0,000E0	0,000E0	0,000E0	2,219E8	3,845E7	3,384E7	RPL12
Q58D0W5	60S ribosomal protein L5 OS=Bos taurus OX=9913 GN=RLP5 PE=2 SV=3 - [RL5_BOVIN]	0,000E0	0,000E0	0,000E0	1,071E8	9,474E8	7,394E8	RPL5
Q4VQ06	Actin (Fragment) OS=Cryptosporidium sp. ex Bos taurus OX=310049 PE=3 SV=1 - [Q4VQ06_9CRYT]	1,203E8	0,000E0	0,000E0	2,143E9	3,818E9	3,586E9	ACTB
Q14836	Actin-related protein 2/3 complex subunit 4 OS=Bos taurus OX=9913 GN=ARPC4 PE=1 SV=3 - [ARPC4_BOVIN]	0,000E0	0,000E0	0,000E0	4,048E7	5,205E8	5,024E8	ARPC4
Q85Q58	ADP/ATP translocase 2 OS=Bos taurus OX=9913 GN=SLC25A5 PE=2 SV=3 - [ADT2_BOVIN]	1,971E7	0,000E0	0,000E0	7,164E7	1,573E7	7,765E7	SLC25A5
P32007	ADP/ATP translocase 3 OS=Bos taurus OX=9913 GN=SLC25A6 PE=1 SV=3 - [ADT3_BOVIN]	1,541E7	0,000E0	0,000E0	3,837E7	1,573E7	7,765E7	SLC25A6
P04272	Annxin A2 OS=Bos taurus OX=9913 GN=ANXA2 PE=1 SV=2 - [ANXA2_BOVIN]	7,341E6	0,000E0	0,000E0	6,681E7	1,021E8	3,280E7	ANXA2
P63009	AP-2 complex subunit beta OS=Bos taurus OX=9913 GN=AP2B1 PE=1 SV=2 - [AP2B1_BOVIN]	0,000E0	0,000E0	0,000E0	1,060E7	1,097E8	7,708E7	AP2B1
F1MBT5	BCR, RhoGEF and GTPase activating protein OS=Bos taurus OX=9913 GN=BCR PE=4 SV=2 - [F1MBT5_BOVIN]	0,000E0	0,000E0	0,000E0	2,689E7	1,963E7	3,703E7	BCR
F1MPH9	Caprin-1 OS=Bos taurus OX=9913 GN=CAPRIN1 PE=4 SV=2 - [F1MPH9_BOVIN]	0,000E0	0,000E0	0,000E0	1,178E8	2,185E8	1,780E8	CAPRIN1
P79132	Caveolin-1 OS=Bos taurus OX=9913 GN=CAV1 PE=2 SV=1 - [CAV1_BOVIN]	0,000E0	0,000E0	0,000E0	5,979E7	3,293E8	2,998E8	CAV1
AOA0F6QNP	Complement component 3 OS=Bos taurus OX=9913 GN=C3 PE=2 SV=1 - [AOA0F6QNP_BOVIN]	9,582E6	0,000E0	0,000E0	7,754E7	5,523E6	2,025E8	C3
P11179	Dihydropyridine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Bos taurus OX=9913 GN=DST PE=1 SV=2 - [ODOO_BOVIN]	0,000E0	2,749E6	0,000E0	3,927E7	4,756E7	4,977E7	DLST
P68103	Elongation factor 1-alpha 1 OS=Bos taurus OX=9913 GN=EEF1A1 PE=1 SV=1 - [EF1A1_BOVIN]	4,290E7	0,000E0	0,000E0	2,024E8	5,449E6	8,357E7	EEF1A1
E1B7R4	Eukaryotic translation initiation factor 3 subunit A OS=Bos taurus OX=9913 GN=EIF3A PE=3 SV=2 - [E1B7R4_BOVIN]	0,000E0	0,000E0	0,000E0	2,726E7	3,690E7	1,037E8	EIF3A
Q35Y1W6	Eukaryotic translation initiation factor 3 subunit C OS=Bos taurus OX=9913 GN=EIF3C PE=2 SV=1 - [EIF3C_BOVIN]	0,000E0	0,000E0	0,000E0	2,069E7	3,997E7	5,894E7	EIF3C
ARE651	EWS RNA binding protein 1 OS=Bos taurus OX=9913 GN=EWSR1 PE=2 SV=1 - [ARE651_BOVIN]	1,273E8	1,041E7	4,251E7	1,902E8	9,836E5	8,826E7	EWSR1
Q32C44	Heterogeneous nuclear ribonucleoprotein A/B OS=Bos taurus OX=9913 GN=HNRNPAB PE=1 SV=1 - [Q32C44_BOVIN]	3,097E7	0,000E0	0,000E0	2,817E8	2,237E8	1,885E8	HNRNPAB
Q5E949	HMT1 hnRNP methyltransferase-like 2 isoform 3 OS=Bos taurus OX=9913 GN=PRMT1 PE=2 SV=1 - [Q5E949_BOVIN]	0,000E0	0,000E0	0,000E0	8,383E7	4,567E7	4,871E7	PRMT1
Q2HJH4	HNRPDL protein (Fragment) OS=Bos taurus OX=9913 GN=HNRPDL PE=2 SV=1 - [Q2HJH4_BOVIN]	4,361E7	0,000E0	0,000E0	4,148E8	1,181E8	1,118E8	HNRPDL
F1MMN6	Integrin subunit alpha 1 OS=Bos taurus OX=9913 GN=ITGA1 PE=3 SV=2 - [F1MMN6_BOVIN]	2,087E7	0,000E0	0,000E0	3,219E7	1,607E6	8,844E5	ITGA1
G3N0V2	Keratin 1 OS=Bos taurus OX=9913 GN=KRT1 PE=1 SV=1 - [G3N0V2_BOVIN]	3,489E8	3,147E7	1,634E7	2,256E9	4,360E7	6,381E7	KRT1
P08728	Keratin, type 1 cytoskeletal 19 OS=Bos taurus OX=9913 GN=KRT19 PE=2 SV=1 - [K1C19_BOVIN]	8,877E7	0,000E0	2,196E6	4,416E8	3,785E7	1,190E7	KRT19
G3MZJ4	Myosin XIX OS=Bos taurus OX=9913 GN=MYO19 PE=3 SV=1 - [G3MZJ4_BOVIN]	0,000E0	0,000E0	0,000E0	4,272E6	2,818E7	5,218E7	MYO19
E1BK63	Ribosomal protein L15 OS=Bos taurus OX=9913 PE=3 SV=1 - [E1BK63_BOVIN]	0,000E0	0,000E0	0,000E0	5,926E7	2,486E8	1,016E8	RPL15
F1MW57	Serine/threonine-protein phosphatase OS=Bos taurus OX=9913 GN=PPP1CB PE=3 SV=2 - [F1MW57_BOVIN]	0,000E0	0,000E0	0,000E0	2,519E7	6,897E7	1,588E8	PPP1CB
Q2HJ81	Tubulin beta-6 chain OS=Bos taurus OX=9913 GN=TUBB6 PE=2 SV=1 - [TBB6_BOVIN]	4,519E7	0,000E0	0,000E0	3,323E7	1,818E8	4,385E7	TUBB6
E1BB71	Uncharacterized protein OS=Bos taurus OX=9913 PE=3 SV=1 - [E1BB71_BOVIN]	0,000E0	0,000E0	0,000E0	1,724E7	2,711E8	6,555E8	E18871
O18789								

Q3ZCE2	ELAV-like protein OS=Bos taurus OX=9913 GN=ELAVL1 PE=2 SV=1 - [Q3ZCE2_BOVIN]	0,000E0	0,000E0	0,000E0	2,994E7	8,460E6	2,082E6	ELAVL1
A7MB16	Eukaryotic translation initiation factor 3 subunit B OS=Bos taurus OX=9913 GN=EIF3B PE=2 SV=1 - [EIF3B_BOVIN]	0,000E0	0,000E0	0,000E0	4,213E7	6,440E7	9,518E7	EIF3B
F1N059	Family with sequence similarity 98 member A OS=Bos taurus OX=9913 GN=FAM98A PE=4 SV=2 - [F1N059_BOVIN]	0,000E0	0,000E0	0,000E0	6,168E7	1,409E7	1,757E7	FAM98A
Q08DC3	KIAA1949 OS=Bos taurus OX=9913 GN=PPP1R18 PE=1 SV=1 - [Q08DC3_BOVIN]	0,000E0	0,000E0	0,000E0	7,644E6	1,611E8	1,026E7	PPP1R18
Q3Z5I2	Lamin A/C OS=Bos taurus OX=9913 GN=LMNA PE=2 SV=1 - [Q3Z5I2_BOVIN]	0,000E0	0,000E0	0,000E0	1,192E7	3,000E7	9,390E6	LMNA
A4IFN6	Sorting nexin OS=Bos taurus OX=9913 GN=SNX18 PE=1 SV=1 - [A4IFN6_BOVIN]	0,000E0	0,000E0	0,000E0	5,663E7	2,641E7	2,466E7	SNX18
Q2B194	Thrombospondin-1 (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q2B194_BOVIN]	9,682E5	0,000E0	0,000E0	1,277E7	1,020E8	7,533E7	THBS1
Q7M2Y2	Tumor-specific transplantation antigen P198 homolog p23 (Fragment) OS=Bos taurus OX=9913 PE=3 SV=1 - [Q7M2Y2_BOVIN]	0,000E0	0,000E0	0,000E0	5,632E7	2,310E8	2,325E8	TSTAP198
A0A140T832	40S ribosomal protein S17 OS=Bos taurus OX=9913 GN=RP517 PE=3 SV=1 - [A0A140T832_BOVIN]	0,000E0	0,000E0	0,000E0	1,104E8	2,705E8	3,804E8	RP517
Q3T0U2	60S ribosomal protein L14 OS=Bos taurus OX=9913 GN=RLP14 PE=2 SV=3 - [RL14_BOVIN]	0,000E0	4,570E6	0,000E0	1,233E7	8,023E6	1,448E8	RPL14
P61356	60S ribosomal protein L27 OS=Bos taurus OX=9913 GN=RLP27 PE=2 SV=2 - [RL27_BOVIN]	0,000E0	0,000E0	0,000E0	9,133E7	7,446E8	7,456E8	RPL27
Q3T0D5	60S ribosomal protein L30 OS=Bos taurus OX=9913 GN=RLP30 PE=3 SV=3 - [RL30_BOVIN]	0,000E0	0,000E0	0,000E0	7,082E7	1,011E8	2,929E7	RPL30
Q3T0S6	60S ribosomal protein L8 OS=Bos taurus OX=9913 GN=RLP8 PE=2 SV=3 - [RL8_BOVIN]	0,000E0	0,000E0	0,000E0	1,140E8	4,068E8	5,003E8	RPL8
Q3SYR7	60S ribosomal protein L9 OS=Bos taurus OX=9913 GN=RLP9 PE=2 SV=1 - [RL9_BOVIN]	0,000E0	0,000E0	0,000E0	1,010E8	3,361E8	6,339E8	RPL9
ASPKK3	ABLIM3 protein OS=Bos taurus OX=9913 GN=ABLIM3 PE=2 SV=1 - [ASPKK3_BOVIN]	0,000E0	0,000E0	0,000E0	5,829E6	4,105E7	1,068E7	ABLIM3
Q1J3P9	Actin-related protein 2/3 complex subunit 1A OS=Bos taurus OX=9913 GN=ARPC1A PE=2 SV=1 - [ARPC1A_BOVIN]	0,000E0	0,000E0	0,000E0	4,172E7	3,177E8	1,981E8	ARPC1A
Q7S1H1	Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=1 SV=2 - [A2MG_BOVIN]	1,137E7	3,013E6	0,000E0	1,317E8	2,180E8	2,171E8	A2M
E1BEQ5	Angiotensin-like protein 1 OS=Bos taurus OX=9913 GN=AMOTL1 PE=3 SV=1 - [AMOL1_BOVIN]	0,000E0	0,000E0	0,000E0	1,295E7	1,455E7	6,657E6	AMOTL1
E1B359	Ataxin 2 like OS=Bos taurus OX=9913 GN=ATXN2L PE=4 SV=1 - [E1B359_BOVIN]	0,000E0	0,000E0	0,000E0	1,875E7	1,501E7	9,010E6	ATXN2L
Q3T0S7	Chromosome 14 open reading frame 166 ortholog OS=Bos taurus OX=9913 GN=RTRAF PE=2 SV=1 - [Q3T0S7_BOVIN]	0,000E0	0,000E0	0,000E0	1,074E7	6,778E7	6,546E7	RTRAF
Q5E9F7	Cofilin-1 OS=Bos taurus OX=9913 GN=CFP1 PE=2 SV=3 - [COF1_BOVIN]	0,000E0	0,000E0	0,000E0	4,595E8	1,277E9	1,616E8	CF1
Q3ZC35	Cysteine rich angiogenic inducer 61 OS=Bos taurus OX=9913 GN=CYR61 PE=2 SV=1 - [Q3ZC35_BOVIN]	0,000E0	0,000E0	0,000E0	6,670E7	1,494E8	4,259E7	CYR61
A0A140T862	Eukaryotic translation initiation factor 2 subunit 2 OS=Bos taurus OX=9913 GN=EIF252 PE=4 SV=1 - [A0A140T862_BOVIN]	0,000E0	0,000E0	0,000E0	1,468E7	2,911E7	3,245E7	EIF252
F1M0Q56	Focadhesin OS=Bos taurus OX=9913 GN=FOCAD PE=4 SV=2 - [F1M0Q56_BOVIN]	0,000E0	0,000E0	0,000E0	8,022E7	5,696E7	5,142E7	FOCAD
F1N4M9	Fragile X mental retardation syndrome-related protein 1 OS=Bos taurus OX=9913 GN=FXR1 PE=4 SV=1 - [F1N4M9_BOVIN]	0,000E0	0,000E0	0,000E0	1,292E7	4,025E7	4,736E7	FXR1
A0A1B02542	Heat shock 27 kDa protein 1 OS=Bos taurus OX=9913 GN=HspB1 PE=3 SV=1 - [A0A1B02542_BOVIN]	0,000E0	0,000E0	0,000E0	8,668E7	8,538E7	1,155E8	HspB1
ASD9H5	Heterogeneous nuclear ribonucleoprotein D OS=Bos taurus OX=9913 GN=HNRNPD PE=1 SV=1 - [ASD9H5_BOVIN]	4,372E7	0,000E0	0,000E0	2,938E8	1,979E8	2,843E8	HNRNPD
Q29KQ2	KH RNA binding domain containing, signal transduction associated 1 OS=Bos taurus OX=9913 GN=KHDRBS1 PE=2 SV=1 - [Q29KQ2_BOVIN]	3,071E7	0,000E0	0,000E0	1,917E7	4,182E6	2,765E7	KHDRBS1
ALL5B0	Myosin regulatory light polypeptide 9 (Fragment) OS=Bos taurus OX=9913 GN=MYL9 PE=2 SV=1 - [ALL5B0_BOVIN]	4,387E6	0,000E0	0,000E0	1,692E9	3,386E9	6,005E9	MYL9
F1M0K2	NUFIP2, FMRI interacting protein 2 OS=Bos taurus OX=9913 GN=NUFIP2 PE=4 SV=1 - [F1M0K2_BOVIN]	0,000E0	0,000E0	0,000E0	1,574E7	4,698E7	4,306E7	NUFIP2
E1BIE7	PGAM family member 5, mitochondrial serine/threonine protein phosphatase OS=Bos taurus OX=9913 GN=PGAM5 PE=4 SV=1 - [E1BIE7_BOVIN]	0,000E0	0,000E0	0,000E0	5,324E7	1,114E8	1,166E7	PGAM5
F15246	Protein-L-isopartate(D-aspartate) O-methyltransferase OS=Bos taurus OX=9913 GN=PCMT1 PE=1 SV=2 - [P1MT_BOVIN]	0,000E0	0,000E0	0,000E0	1,224E7	4,604E7	2,820E7	PCMT1
Q0VCV7	Serine/arginine-rich splicing factor 1 OS=Bos taurus OX=9913 GN=SRSF1 PE=2 SV=1 - [SRSF1_BOVIN]	0,000E0	0,000E0	0,000E0	2,288E7	1,376E8	7,552E7	SRSF1
Q862M4	Similar to ribosomal protein L26 (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q862M4_BOVIN]	0,000E0	0,000E0	0,000E0	1,276E8	4,142E8	3,335E8	RPL26
F1MMJ4	Uncharacterized protein OS=Bos taurus OX=9913 GN=H1FX PE=1 SV=2 - [F1MMJ4_BOVIN]	0,000E0	0,000E0	0,000E0	4,781E7	2,250E8	1,146E8	H1FX
F1MTZ5	Uncharacterized protein OS=Bos taurus OX=9913 GN=HDLBP PE=1 SV=2 - [F1MTZ5_BOVIN]	0,000E0	0,000E0	0,000E0	4,485E6	1,594E7	1,650E7	HDLBP
G5E6K7	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1 - [G5E6K7_BOVIN]	0,000E0	0,000E0	0,000E0	8,792E7	1,212E9	1,192E8	G5E6K7
E1BED8	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=2 - [E1BED8_BOVIN]	4,290E7	0,000E0	0,000E0	2,024E8	5,499E6	8,357E7	E1BED8
Q76I81	40S ribosomal protein S12 OS=Bos taurus OX=9913 GN=RP512 PE=2 SV=1 - [RS12_BOVIN]	0,000E0	0,000E0	0,000E0	1,684E8	6,996E7	2,046E7	RP512
Q56JX8	40S ribosomal protein S13 OS=Bos taurus OX=9913 GN=RP513 PE=2 SV=3 - [RS13_BOVIN]	6,413E6	0,000E0	0,000E0	1,517E8	7,887E8	7,134E6	RP513
Q3ZB8H	40S ribosomal protein S20 OS=Bos taurus OX=9913 GN=RP520 PE=3 SV=1 - [RS20_BOVIN]	0,000E0	0,000E0	0,000E0	2,328E8	3,548E8	4,791E8	RP520
F1MKZ5	40S ribosomal protein S6 OS=Bos taurus OX=9913 PE=3 SV=1 - [F1MKZ5_BOVIN]	0,000E0	0,000E0	0,000E0	8,869E7	5,919E8	6,972E8	RP56
Q56JZ1	60S ribosomal protein L13 OS=Bos taurus OX=9913 GN=RLP13 PE=2 SV=3 - [RL13_BOVIN]	0,000E0	0,000E0	0,000E0	5,088E7	3,066E8	1,328E8	RPL13
Q3T0L7	60S ribosomal protein L28 OS=Bos taurus OX=9913 GN=RLP28 PE=2 SV=3 - [RL28_BOVIN]	0,000E0	0,000E0	0,000E0	3,291E7	2,485E8	2,020E8	RPL28
E1BMD5	Apoptosis and caspase activation inhibitor OS=Bos taurus OX=9913 GN=AVEN PE=4 SV=1 - [E1BMD5_BOVIN]	0,000E0	0,000E0	0,000E0	5,971E7	4,600E7	3,175E7	AVEN
G3X6H0	Centrosomal protein 170B OS=Bos taurus OX=9913 GN=CEP170B PE=4 SV=1 - [G3X6H0_BOVIN]	0,000E0	0,000E0	0,000E0	1,348E7	7,762E6	6,083E6	CEP170B
F1MBG0	Coactivator associated arginine methyltransferase 1 OS=Bos taurus OX=9913 GN=CARM1 PE=3 SV=2 - [F1MBG0_BOVIN]	0,000E0	0,000E0	0,000E0	8,712E7	1,873E7	1,653E7	CARM1
Q3T0B6	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Bos taurus OX=9913 GN=C1QB PE=2 SV=1 - [C1QB_BOVIN]	0,000E0	0,000E0	0,000E0	5,750E7	1,105E8	1,085E8	C1QB
ASD9B9	Elongation factor 1-delta OS=Bos taurus OX=9913 GN=EEF1D PE=2 SV=2 - [EF1D_BOVIN]	0,000E0	0,000E0	0,000E0	2,575E7	1,167E8	8,650E7	EEF1D
Q1JPA2	Eukaryotic translation elongation factor 1 gamma (Fragment) OS=Bos taurus OX=9913 GN=EEF1G PE=2 SV=1 - [Q1JPA2_BOVIN]	0,000E0	0,000E0	0,000E0	1,101E7	3,934E7	3,985E7	EEF1G
Q3ZCK1	Eukaryotic translation initiation factor 3 subunit L OS=Bos taurus OX=9913 GN=EIF3L PE=2 SV=1 - [EIF3L_BOVIN]	0,000E0	0,000E0	0,000E0	3,067E7	9,184E7	3,631E7	EIF3L
F1M0D4	Eukaryotic translation initiation factor 4 gamma 1 OS=Bos taurus OX=9913 GN=EIF4G1 PE=1 SV=2 - [F1M0D4_BOVIN]	0,000E0	0,000E0	0,000E0	1,791E6	9,165E6	1,696E7	EIF4G1
F1M4M0	Interleukin enhancer binding factor 3 OS=Bos taurus OX=9913 GN=ILF3 PE=4 SV=2 - [F1M4M0_BOVIN]	0,000E0	0,000E0	0,000E0	9,194E6	2,612E7	3,575E7	ILF3
F11309	Plasminogen activator inhibitor 1 OS=Bos taurus OX=9913 GN=SERPINE1 PE=1 SV=1 - [PAI1_BOVIN]	0,000E0	0,000E0	0,000E0	1,088E7	1,376E7	1,483E6	SERPINE1
A7E3X0	Plastin-3 OS=Bos taurus OX=9913 GN=PLS3 PE=2 SV=1 - [PLST_BOVIN]	0,000E0	0,000E0	0,000E0	1,804E7	2,058E6	5,515E7	PLS3
Q8WN55	Polypyrimidine tract-binding protein 1 OS=Bos taurus OX=9913 GN=PTBP1 PE=2 SV=1 - [PTBP1_BOVIN]	0,000E0	0,000E0	0,000E0	3,831E7	8,054E7	3,395E7	PTBP1
Q5D808	Pyrolysine-5-carboxylate reductase 3 OS=Bos taurus OX=9913 GN=PYCR3 PE=2 SV=1 - [PYCR3_BOVIN]	0,000E0	0,000E0	0,000E0	1,569E7	1,484E7	1,339E7	PYCR3
Q863B7	Similar to ribosomal protein S14 (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q863B7_BOVIN]	4,964E6	0,000E0	1,138E7	1,135E8	8,427E7	5,332E7	RPL14
A6QNY4	STAU1 protein (Fragment) OS=Bos taurus OX=9913 GN=STAU1 PE=2 SV=1 - [A6QNY4_BOVIN]	0,000E0	0,000E0	0,000E0	1,558E7	1,091E7	1,820E7	STAU1
Q1RMR2	U1 small nuclear ribonucleoprotein 70 kDa OS=Bos taurus OX=9913 GN=SNRNP70 PE=2 SV=1 - [RU17_BOVIN]	0,000E0	0,000E0	0,000E0	5,682E7	1,176E7	6,602E7	SNRNP70
G3MNV5	Uncharacterized protein OS=Bos taurus OX=9913 GN=HIST1H1E PE=3 SV=1 - [G3MNV5_BOVIN]	0,000E0	0,000E0	0,000E0	6,812E6	9,031E7	5,153E7	HIST1H1E
P62261	14-3-3 protein epsilon OS=Bos taurus OX=9913 GN=YWHAE PE=2 SV=1 - [1433E_BOVIN]	0,000E0	0,000E0	0,000E0	4,173E7	4,978E7	3,479E7	YWHAE
Q3ZPB8	40S ribosomal protein S21 OS=Bos taurus OX=9913 GN=RP521 PE=3 SV=1 - [RS21_BOVIN]	0,000E0	0,000E0	0,000E0	2,467E8	1,086E8	4,541E8	RP521
Q2KH77	40S ribosomal protein S27 OS=Bos taurus OX=9913 GN=RP527 PE=3 SV=3 - [RS27_BOVIN]	0,000E0	0,000E0	0,000E0	2,349E8	6,740E8	6,140E8	RP527
Q3T0R7	60S ribosomal protein L11 OS=Bos taurus OX=9913 GN=RLP11 PE=2 SV=3 - [RL11_BOVIN]	1,017E7	0,000E0	0,000E0	4,577E8	1,108E9	9,654E8	RPL11
Q3T171	60S ribosomal protein L36 OS=Bos taurus OX=9913 GN=RLP36 PE=3 SV=3 - [RL36_BOVIN]	0,000E0	0,000E0	0,000E0	7,080E7	2,732E8	1,168E8	RPL36
F1M0X2	Argonaute 1, RISC catalytic component OS=Bos taurus OX=9913 GN=AGO1 PE=3 SV=1 - [F1M0X2_BOVIN]	0,000E0	0,000E0	0,000E0	3,785E7	1,025E8	4,834E7	AGO1
F1MPE1	CD109 molecule OS=Bos taurus OX=9913 GN=CD109 PE=4 SV=2 - [F1MPE1_BOVIN]	3,116E6	0,000E0	0,000E0	6,900E6	2,454E7	2,525E7	CD109
G3X6T9	Flotillin-2 OS=Bos taurus OX=9913 GN=FLTOT2 PE=4 SV=1 - [G3X6T9_BOVIN]	0,000E0	0,000E0	0,000E0	3,018E6	2,113E7	3,457E7	FLTOT2
A7MBH9	G protein subunit alpha i2 OS=Bos taurus OX=9913 GN=GNAI2 PE=2 SV=1 - [A7MBH9_BOVIN]	0,000E0	0,000E0	0,000E0	8,082E6	6,638E7	6,357E7	GNAI2
P18246	Gap junction alpha-1 protein OS=Bos taurus OX=9913 GN=GJA1 PE=2 SV=2 - [CXA1_BOVIN]	0,000E0	0,000E0	0,000E0	5,784E7	9,526E7	3,076E8	GJA1
Q27990	Nonmuscle myosin heavy chain B (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q27990_BOVIN]	0,000E0	0,000E0	0,000E0	1,415E7	1,667E8	2,043E8	MYHCB
Q3ZBHS	Proliferation-associated 2G4, 38kDa OS=Bos taurus OX=9913 GN=PA2G4 PE=1 SV=1 - [Q3ZBHS_BOVIN]	0,000E0	0,000E0	0,000E0	3,003E7	8,378E7	1,121E8	PA2G4
F1MSA5	Protein LSM14 homolog A OS=Bos taurus OX=9913 GN=LSM14A PE=4 SV=1 - [F1MSA5_BOVIN]	0,000E0	0,000E0	0,000E0	1,185E7	1,164E7	1,508E7	LSM14A
Q56JY6	Twirlin-1 OS=Bos taurus OX=9913 GN=TWIF1 PE=2 SV=1 - [TWIF1_BOVIN]	0,000E0	0,000E0	0,000E0	8,981E6	5,799E7	6,810E7	TWIF1
ASPJ56	Ubiquitin carboxyl-terminal hydrolase 10 OS=Bos taurus OX=9913 GN=USP10 PE=2 SV=1 - [UBP10_BOVIN]	0,000E0	0,000E0	0,000E0	4,721E8	2,971E7	1,435E7	USP10
G3X7D5	Uncharacterized protein OS=Bos taurus OX=9913 GN=LOC787803 PE=3 SV=1 - [G3X7D5_BOVIN]	0,000E0	0,000E0	0,000E0	8,109E7	1,198E8	3,586E7	LOC787803
G8JKJ9	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1 - [G8JKJ9_BOVIN]	0,000E0	0,000E0	0,000E0	1,582E8	7,630E8	3,930E8	G8JKJ9
E1B880	YTH N6-methyladenosine RNA binding protein 3 OS=Bos taurus OX=9913 GN=YTHDF3 PE=4 SV=2 - [E1B880_BOVIN]	0,000E0	0,000E0	7,660E5	2,072E7	3,117E6	5,268E6	YTHDF3
P63103	14-3-3 protein zeta/delta OS=Bos taurus OX=9913 GN=YWHAZ PE=1 SV=1 - [1433Z_BOVIN]	0,000E0	0,000E0	0,000E0	6,211E7	5,559E7	2,238E7	YWHAZ
G3N3U9	28S ribosomal protein S22, mitochondrial OS=Bos taurus OX=9913 GN=MRPS22 PE=4 SV=1 - [G3N3U9_BOVIN]	0,000E0	0,000E0	0,000E0	1,821E6	1,326E7	2,570E7	MRPS22
Q3T0F4	40S ribosomal protein S10 OS=Bos taurus OX=9913 GN=RP510 PE=2 SV=1 - [RS10_BOVIN]	0,000E0	0,000E0	0,000E0	1,056E8	6,029E8	3,668E7	RP510
Q3T0E7	40S ribosomal protein S27-like OS=Bos taurus OX=9913 GN=RP527L PE=3 SV=3 - [RS27L_BOVIN]	0,000E0	0,000E0	0,000E0	1,669E8	1,329E9	1,157E9	RP527L
Q3T035	Actin-related protein 2/3 complex subunit 3 OS=Bos taurus OX=9913 GN=ARPC3 PE=1 SV=3 - [ARPC3_BOVIN]	0,000E0	0,000E0	0,000E0	1,183E7	8,006E7	6,936E7	ARPC3
Q66W17	Caveolin-2 OS=Bos taurus OX=9913 GN=CAV2 PE=1 SV=1 - [CAV2_BOVIN]	0,000E0	0,000E0	0,000E0	4,629E7	1,038E9	9,367E8	CAV2
Q5E9D5	Destrin OS=Bos taurus OX=9913 GN=DSN PE=2 SV=3 - [DEST_BOVIN]	0,000E0	0,000E0	0,000E0	2,184E7	1,024E8	8,720E7	DSN
Q3T0V7	Endothelial differentiation-related factor 1 OS=Bos taurus OX=9913 GN=EDF1 PE=2 SV=1 - [EDF1_BOVIN]	0,000E0	0,000E0	0,000E0	1,233E8	7,445E6	5,007E8	EDF1
G8JKV2	Eukaryotic translation initiation factor 3 subunit J OS=Bos taurus OX=9913 GN=EIF3J PE=3 SV=1 - [G8JKV2_BOVIN]	0,000E0	0,000E0	0,00				

Q3SZR8	Serine/arginine-rich splicing factor 3 OS=Bos taurus OX=9913 GN=SRSF3 PE=2 SV=1 - [SRSF3_BOVIN]	0,000E0	0,000E0	0,000E0	1,704E7	4,621E7	4,985E6	SRSF3
Q862R3	Similar to ribosomal protein L18a (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1 - [Q862R3_BOVIN]	0,000E0	0,000E0	0,000E0	3,525E6	1,486E8	5,021E7	RPL18
F1MZ00	Small nuclear ribonucleoprotein Sm D3 OS=Bos taurus OX=9913 GN=SNRPD3 PE=3 SV=2 - [F1MZ00_BOVIN]	0,000E0	0,000E0	0,000E0	5,805E6	9,885E7	5,016E7	SNRPD3
E1BQ37	Splicing factor proline and glutamine rich OS=Bos taurus OX=9913 GN=SFPQ PE=1 SV=1 - [E1BQ37_BOVIN]	0,000E0	0,000E0	0,000E0	1,487E6	1,750E6	2,444E6	SFPQ
A6H7J7	Uncharacterized protein OS=Bos taurus OX=9913 PE=2 SV=1 - [A6H7J7_BOVIN]	1,894E8	0,000E0	0,000E0	2,272E8	8,787E7	1,517E8	A6H7J7
Q56K10	40S ribosomal protein S15 OS=Bos taurus OX=9913 GN=RPS15 PE=2 SV=3 - [RS15_BOVIN]	0,000E0	0,000E0	0,000E0	1,377E8	5,099E8	3,286E8	RPS15
Q3SZQ6	60S ribosomal protein L32 OS=Bos taurus OX=9913 GN=RPL32 PE=2 SV=3 - [RL32_BOVIN]	0,000E0	0,000E0	0,000E0	5,706E7	9,771E7	6,501E7	RPL32
G3NZR1	60S ribosomal protein L6 OS=Bos taurus OX=9913 PE=3 SV=1 - [G3NZR1_BOVIN]	0,000E0	0,000E0	0,000E0	1,007E8	4,719E7	4,830E6	RPL6
F1MLB8	ATP synthase subunit alpha OS=Bos taurus OX=9913 GN=ATP5F1A PE=1 SV=1 - [F1MLB8_BOVIN]	0,000E0	0,000E0	0,000E0	6,084E6	1,694E7	6,376E6	ATP5F1A
Q3ZL92	Calponin-3 OS=Bos taurus OX=9913 GN=CNN3 PE=2 SV=1 - [CNN3_BOVIN]	0,000E0	0,000E0	0,000E0	6,621E6	1,696E6	2,887E6	CNN3
Q3ZBH3	CD151 antigen OS=Bos taurus OX=9913 GN=CD151 PE=2 SV=1 - [CD151_BOVIN]	1,829E7	0,000E0	0,000E0	2,437E8	1,726E8	1,498E8	CD151
Q2K3I4	Elongin-C OS=Bos taurus OX=9913 GN=ELOC PE=3 SV=1 - [ELOC_BOVIN]	1,731E6	0,000E0	0,000E0	2,217E7	4,299E7	5,625E7	ELOC
E1BLZ8	Eukaryotic translation initiation factor 3 subunit F OS=Bos taurus OX=9913 GN=EIF3F PE=1 SV=2 - [E1BLZ8_BOVIN]	0,000E0	0,000E0	0,000E0	3,096E7	1,714E6	4,833E7	EIF3F
ASPK49	IGL@ protein OS=Bos taurus OX=9913 GN=IGL@ PE=2 SV=1 - [ASPK49_BOVIN]	5,852E8	1,489E7	6,150E6	1,867E9	1,979E9	1,824E9	RBM8A
Q3ZCE8-2	Isoform 2 of RNA-binding protein 8A OS=Bos taurus OX=9913 GN=RBM8A - [RBM8A_BOVIN]	0,000E0	0,000E0	0,000E0	8,167E6	4,351E6	8,486E6	RBM8A
P00974	Pancreatic trypsin inhibitor OS=Bos taurus OX=9913 PE=1 SV=2 - [BPT1_BOVIN]	0,000E0	0,000E0	3,765E7	1,766E9	7,076E8	2,062E8	BPT1
ASD9D7	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 (Fragment) OS=Bos taurus OX=9913 GN=PLOD3 PE=2 SV=1 - [ASD9D7_BOVIN]	0,000E0	0,000E0	0,000E0	4,242E6	5,760E6	9,798E6	PLOD3
Q0VCQ9	Protein LSM12 homolog OS=Bos taurus OX=9913 GN=LSM12 PE=2 SV=2 - [LSM12_BOVIN]	0,000E0	0,000E0	0,000E0	2,548E7	4,155E7	5,952E7	LSM12
F1ND01	Uncharacterized protein OS=Bos taurus OX=9913 GN=RPL32 PE=1 SV=2 - [F1ND01_BOVIN]	0,000E0	0,000E0	0,000E0	1,154E8	2,741E8	6,289E8	RPL22
E1BHM9	Uncharacterized protein OS=Bos taurus OX=9913 PE=3 SV=1 - [E1BHM9_BOVIN]	0,000E0	0,000E0	0,000E0	5,423E6	1,843E8	7,843E7	E18HM9
Q2K149	39S ribosomal protein L50, mitochondrial OS=Bos taurus OX=9913 GN=MRPL50 PE=1 SV=1 - [RM50_BOVIN]	0,000E0	0,000E0	0,000E0	1,004E7	6,539E6	5,574E6	MRPL50
Q58DW3	60S ribosomal protein L29 OS=Bos taurus OX=9913 GN=RPL29 PE=2 SV=3 - [RL29_BOVIN]	0,000E0	0,000E0	0,000E0	6,262E7	1,076E8	8,776E7	RPL29
P04973-2	Isoform Non-brain of Clathrin light chain A OS=Bos taurus OX=9913 GN=CLTA - [CLCA_BOVIN]	0,000E0	0,000E0	0,000E0	1,010E7	1,430E8	1,471E8	CLTA
F1MKI2	RAB12, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB12 PE=4 SV=2 - [F1MKI2_BOVIN]	0,000E0	0,000E0	0,000E0	3,911E7	2,651E7	1,653E7	RAB12
Q0VCQ9	Reticulocalbin 2, EF-hand calcium binding domain OS=Bos taurus OX=9913 GN=RCN2 PE=2 SV=1 - [Q0VCQ9_BOVIN]	0,000E0	0,000E0	0,000E0	3,154E6	1,860E7	2,527E6	RCN2
Q3ZPA0	U1 small nuclear ribonucleoprotein C OS=Bos taurus OX=9913 GN=SNRPC PE=2 SV=2 - [RU1C_BOVIN]	0,000E0	0,000E0	0,000E0	8,697E7	1,857E7	4,872E6	SNRPC
F1MI18	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=2 - [F1MI18_BOVIN]	0,000E0	0,000E0	0,000E0	1,437E8	2,459E8	3,093E8	F1MI18

Supplementary Table 3. Differentially expressed genes analyzed (Amlt2 KO vs WT aortae) with enriched GO

Gene_ID	readcount_amlt2 KO aorta	readcount_wt_aorta	log2FoldChange	pvalue	padj	Gene_Name
ENSMUSG00000000290	158.927701543679	59.7030557544915	0.64533	0.00020619	0.047359	Itgb2
ENSMUSG000000002111	216.961569643465	100.502648381335	0.6889	4.0862e-05	0.020194	Spi1
ENSMUSG000000003032	1053.73474574084	664.16622403341	0.53107	0.00014112	0.040633	Klf4
ENSMUSG000000005338	173.756385209253	82.7869817301975	0.67988	4.3562e-05	0.020478	Cadm3
ENSMUSG000000010064	32.5248378550642	69.2139660522236	-0.651	0.0001397	0.040633	Slc38a3
ENSMUSG000000010797	111.874554274348	15.1184535312192	0.70298	1.2295e-05	0.0091597	Wnt2
ENSMUSG000000012705	239.844667429362	52.6885310870578	0.79769	3.1281e-06	0.0065624	Retn
ENSMUSG000000015340	143.040000460753	57.6902339080253	0.65278	0.00017391	0.045604	Cybb
ENSMUSG000000015396	78.5125901989447	29.0719859870467	0.70756	4.74e-05	0.020478	Cd83
ENSMUSG000000018339	2485.71158356384	1233.54481642737	0.74646	9.1359e-07	0.003354	Gpx3
ENSMUSG000000018927	707.295207631469	170.544551968579	0.93728	7.1612e-08	0.00035054	Ccl6
ENSMUSG000000019122	476.329244367314	119.344035032349	1.0472	1.4243e-09	1.0458e-05	Ccl9
ENSMUSG000000020099	345.887697572691	496.115281245493	-0.44752	0.00019136	0.046835	Unc5b
ENSMUSG000000020437	77.1633165981257	22.0118072197688	0.77686	7.6345e-06	0.0091597	Myo1g
ENSMUSG000000020607	538.408993623667	750.953249029995	-0.4257	0.00011525	0.037515	Fam84a
ENSMUSG000000021388	1406.02622944515	673.183669052565	0.71181	1.2079e-05	0.0091597	Aspn
ENSMUSG000000021457	213.973625481079	106.330862475272	0.66452	4.9727e-05	0.020478	Syk
ENSMUSG000000022102	145.695459403768	51.5169124495549	0.78403	6.0794e-06	0.0091597	Dok2
ENSMUSG000000022488	205.41780877786	98.2592233833908	0.64108	0.00015277	0.042328	Nckap1l
ENSMUSG000000022901	66.4110773964363	29.7301164689561	0.68252	5.8594e-05	0.022063	Cd86
ENSMUSG000000023046	2884.24901370756	1480.29003107507	0.61981	0.00018518	0.046835	Igfbp6
ENSMUSG000000024679	76.0534731344345	33.0719080199057	0.66918	0.00010042	0.034294	Msa4a6d
ENSMUSG000000024965	165.823698438286	90.238439882096	0.65277	1.4921e-05	0.010434	Fermt3
ENSMUSG000000026109	428.493277023279	244.168057152686	0.61223	3.7101e-05	0.020179	Tmeff2
ENSMUSG000000026177	252.967326692869	135.598140854474	0.6467	3.0292e-05	0.017794	Slc11a1
ENSMUSG000000026395	120.375597657209	44.8203082114949	0.71883	3.5148e-05	0.019852	Ptpcr
ENSMUSG000000026399	297.856093868171	113.297994385314	0.98022	4.6362e-10	6.8082e-06	Cd55
ENSMUSG000000028581	465.732257990103	238.530901942934	0.65498	4.9404e-05	0.020478	Laptn5
ENSMUSG000000029771	112.314140769318	54.4093371094395	0.71349	9.359e-06	0.0091597	Irf5
ENSMUSG000000030787	542.979717509508	221.284214010384	0.74918	1.1737e-05	0.0091597	Lyve1
ENSMUSG000000031827	420.977724023766	199.139679950657	0.70633	1.7501e-05	0.011682	Cotl1
ENSMUSG000000031906	164.547241376456	84.2907934668227	0.62867	0.00013349	0.040042	Smpd3
ENSMUSG000000032332	349.146794512607	192.498035360874	0.6278	4.1255e-05	0.020194	Col12a1
ENSMUSG000000035095	44.906359424677	4.66152356471479	0.63442	3.904e-05	0.020194	Fam167a
ENSMUSG000000035208	84.8499252503698	29.273182687006	0.78264	6.5017e-06	0.0091597	Slnf8
ENSMUSG000000036887	1888.43045766811	1033.03008726011	0.59504	0.00021974	0.049644	C1qa
ENSMUSG000000036905	1436.86135647427	723.356029904941	0.62421	0.00018833	0.046835	C1qb
ENSMUSG000000037379	88.0293142776631	9.28999489950067	0.7633	2.2044e-06	0.0064744	Spon2
ENSMUSG000000038147	68.1694590534354	23.4935738710137	0.65282	0.00016487	0.04402	Cd84
ENSMUSG000000038642	464.667808327248	211.512395936203	0.686	5.0664e-05	0.020478	Ctss
ENSMUSG000000039109	1503.97106070614	747.972796177522	0.6244	0.00020402	0.047359	F13a1
ENSMUSG000000039476	249.429624873089	141.757473194012	0.63225	1.2475e-05	0.0091597	Prrx2
ENSMUSG000000040552	132.466267916088	65.2414056829882	0.62538	0.0002064	0.047359	C3ar1
ENSMUSG000000040612	229.441118259121	88.319984284168	0.69464	6.4261e-05	0.023592	Ildr2
ENSMUSG000000040950	461.518760323747	205.384453243512	0.6718	8.7349e-05	0.030541	Mgl2
ENSMUSG000000044337	1335.306800426	691.095361709203	0.68272	1.154e-05	0.0091597	Ackr3
ENSMUSG000000045573	284.435378949316	164.418066334223	0.57468	0.00020262	0.047359	Penk
ENSMUSG000000046743	1173.27680614689	1606.07262123916	-0.41348	2.4734e-05	0.015134	Fat4
ENSMUSG000000049130	193.925359200559	93.3120301481718	0.64854	0.00011751	0.037515	C5ar1
ENSMUSG000000052384	161.609513064848	75.5828244406309	0.67969	5.1576e-05	0.020478	Nrros
ENSMUSG000000052688	311.450918170674	175.345615022865	0.59411	0.00013361	0.040042	Rab7b
ENSMUSG000000054203	58.3391527588879	21.2200107598094	0.65648	0.00015872	0.043162	Ifi205
ENSMUSG000000056069	52.0027327519442	21.5993828748247	0.69577	5.2991e-05	0.020478	Fam105a
ENSMUSG000000056938	1667.9772179887	2239.70157240921	-0.3859	0.00012605	0.039383	Acbd4
ENSMUSG000000059412	121.602644876039	36.8721972818891	0.69779	5.2982e-05	0.020478	Fxyd2
ENSMUSG000000059498	404.525738192865	205.145200130876	0.62295	0.00018416	0.046835	Fcgr3
ENSMUSG000000060586	1199.0007722268	444.640925833898	0.65852	0.00015262	0.042328	H2-Eb1
ENSMUSG000000062593	78.9260524892479	28.3739884423478	0.75867	1.2294e-05	0.0091597	Lilrb4a
ENSMUSG000000064372	1173.17730974367	724.65728653727	0.56873	2.1634e-05	0.013813	---
ENSMUSG000000069763	308.731091223443	94.2885701350182	0.81497	2.82e-06	0.0065624	Tmem100
ENSMUSG000000072596	37.6559320129037	5.85817747873321	0.73401	8.3062e-06	0.0091597	Ear2
ENSMUSG000000072620	133.548729536474	52.3537752797979	0.77541	5.7835e-06	0.0091597	Slnf2
ENSMUSG000000073421	1230.3363026074	440.149774472324	0.68531	8.1451e-05	0.029173	H2-Ab1
ENSMUSG000000079018	1618.26627631113	772.609348595751	0.65121	0.00011528	0.037515	Ly6c1
ENSMUSG000000097233	64.9621089152712	135.658897939805	-0.72186	9.947e-06	0.0091597	---

Term	Overlap	P-value	Adjusted P-value	Genes
neutrophil activation involved in immune response (GO:0002283)	12/483	2.9981738632589026E-8	1.7959061440920828E-5	PTPRC;SYK;SLC11A1;ITGB2;C5AR1;COTL1;C3AR1;CYBB;NCKAP1L;RETN;CTSS;CD55
neutrophil degranulation (GO:0043312)	11/479	2.655867971923774E-7	6.252698176770551E-5	PTPRC;SLC11A1;ITGB2;C5AR1;COTL1;C3AR1;CYBB;NCKAP1L;RETN;CTSS;CD55
neutrophil mediated immunity (GO:0002446)	11/487	3.131568369000276E-7	6.252698176770551E-5	PTPRC;SLC11A1;ITGB2;C5AR1;COTL1;C3AR1;CYBB;NCKAP1L;RETN;CTSS;CD55
inflammatory response (GO:0006954)	7/252	1.4068317157358681E-5	0.0021067304943144624	NRROS;SYK;SLC11A1;ITGB2;C5AR1;C3AR1;CYBB
regulation of protein activation cascade (GO:2000257)	5/108	2.291690762006761E-5	0.002227345730811466	C1QB;C1QA;C5AR1;C3AR1;CD55
regulation of complement activation (GO:0030449)	5/109	2.3960804936406545E-5	0.002227345730811466	C1QB;C1QA;C5AR1;C3AR1;CD55
regulation of humoral immune response (GO:0002920)	5/113	2.851149974163726E-5	0.002227345730811466	C1QB;C1QA;C5AR1;C3AR1;CD55
regulation of immune effector process (GO:0002697)	5/114	2.9747522281288362E-5	0.002227345730811466	C1QB;C1QA;C5AR1;C3AR1;CD55
regulation of acute inflammatory response (GO:0002673)	5/121	3.9607990367493474E-5	0.0024421469430699785	C1QB;C1QA;C5AR1;C3AR1;CD55
positive regulation of T cell proliferation (GO:0042102)	4/61	4.0770399717361916E-5	0.0024421469430699785	CD86;PTPRC;SYK;NCKAP1L

ENSMUSG000000030313 628.26428817777 1118.0157037987 -0.8315 5.0124e-26 3.6325e-24 Dnmrd5b
ENSMUSG000000040033 3674.38591647911 2251.42899122146 0.70666 5.1189e-26 3.7005e-24 Stai2
ENSMUSG000000029070 1021.1851800977 568.981487489035 0.84389 5.1713e-26 3.727e-24 Mvra8
ENSMUSG000000036606 9887.71696088441 5983.4280579045 0.72467 5.5224e-26 3.9677e-24 Plmb2
ENSMUSG000000031133 42.752809760298 167.033957779383 -1.9661 7.8832e-26 5.6464e-24 Arhge6
ENSMUSG000000027993 560.71212804223 502.232367958081 0.98992 8.2097e-26 5.8621e-24 Trm2
ENSMUSG00000002598 35.616274560469 0.234413562335488 7.4773 8.4934e-26 6.0406e-24 Psca
ENSMUSG000000028008 2023.56584680507 3301.5128461257 -0.70623 9.8663e-26 7.0018e-24 Fam4a
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ENSMUSG000000031355 790.601852442149 283.77813494801 1.4782 1.1933e-25 8.4167e-24 Arhge6
ENSMUSG000000031126 946.238053151427 521.3852530150788 0.85434 1.2113e-25 8.5303e-24 Trm1
ENSMUSG000000040011 6985.1882542741 6878.1882542741 0.77612 1.2736e-25 8.9258e-24 Dpyl13
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ENSMUSG0000000426

Term	Overlap	P-value	Adjusted P-value	Genes
regulation of cell migration (GO:0030334)	34/316	4.168055490873482E-13	1.0586860946818643E-9	CD151;CSF1;SEMA3C;SEMA3A;PDGFB;PDGFA;PTPRJ;SEMA3E;ADARB1;FGF1;PAK1;FAM110C;PDGFD;DPYSL3;LMNA;KDR;CYP1B1;RAC1;SRGAP3;ARPIN;EDN1;JAG1;ANXA1;ARHGEF39;SEMA4B;TPM1;BST2;TIAM1;DAB2;NAV3;PLXNB2;AMOTL2;SGK1;ENG
extracellular matrix organization (GO:0030198)	21/229	2.1678849334941394E-7	2.753213865537557E-4	VCAM1;ITGA1;PDGFB;PDGFA;LOXL4;LAMC1;COL5A1;CTSL;KDR;SERPINH1;TIMP2;CAPN2;COL4A6;CYP1B1;COL4A5;ITGA7;ADAM8;TIMP1;LCP1;CD44;DDR2
cellular response to type I interferon (GO:0071357)	11/65	4.356552813789541E-7	2.7664110367563584E-4	BST2;RSAD2;IFI27;STAT1;OAS3;STAT2;IRF7;ISG15;IFIT1;XAF1;IFIT3
type I interferon signaling pathway (GO:0060337)	11/65	4.356552813789541E-7	2.7664110367563584E-4	BST2;RSAD2;IFI27;STAT1;OAS3;STAT2;IRF7;ISG15;IFIT1;XAF1;IFIT3
response to cytokine (GO:0034097)	15/138	1.418875327663055E-6	6.344663285074403E-4	CD274;STAT1;ISG15;AFF3;OSMR;SELE;BST2;IRAK2;CASP3;DPYSL3;BCL2;TIMP2;ADAM9;TIMP1;XAF1
negative regulation of cell migration (GO:0030336)	14/121	1.498739358678993E-6	6.344663285074403E-4	JAG1;TPM1;PTPRJ;ADARB1;PTPRG;BST2;NAV3;DPYSL3;CYP1B1;HMOX1;SRGAP3;TIMP1;ARPIN;ENG
positive regulation of cell motility (GO:2000147)	17/179	1.9113769513245516E-6	6.93556779480623E-4	EDN1;CD151;CSF1;SEMA3C;ARHGEF39;SEMA3A;SEMA4B;PDGFB;PDGFA;SEMAE;FGF1;TIAM1;DAB2;PAK1;FAM110C;PDGFD;KDR
positive regulation of fibroblast proliferation (GO:0048146)	07/28	3.693471784353107E-6	0.0011726772915321114	CDK6;PDGFB;S100A6;PDGFA;AQP1;EREG;DDR2
positive regulation of cell proliferation (GO:0008284)	27/424	5.994210083927416E-6	0.001570063310885789	CSF1;PDGFB;PDGFA;LAMC1;FGF1;AQP1;EFNB2;ESM1;PAK1;CCND2;PDGFD;PIM1;KDR;HMOX1;TIMP1;EDN1;STAT1;CNBP;OSMR;PGF;TBX2;EREG;TIAM1;BST1;CDK6;S100A6;DDR2
cytokine-mediated signaling pathway (GO:0019221)	35/633	6.1813516176605865E-6	0.001570063310885789	CSF1;MAOA;PDGFB;PTGS2;IFIT1;FOXO1;IFIT3;PSMD8;PSMB7;RPS6KA5;IRAK2;CASP3;PIM1;HMOX1;TNFRSF8;TIMP1;ANXA1;VCAM1;ANXA2;RSAD2;STAT1;STAT2;ISG15;OSMR;EREG;BST2;IFI27;OAS3;KIT;BCL2;IRF7;LCP1;XAF1;SQSTM1;CD44

Primary Antibodies

Antibody	Full name	Company	Catalog number	Dilution
Isolectin B4	Biotinylated griffonia simplicifolia lectin 1	VECTOR	B-1205	IF 1:300
GFP	Chk pAb to GFP	Abcam	ab13970	IF 1:200
Phalloidin	Texas Red-X-Phalloidin	Life Technologies	T7471	IF 1:300 for cell; 1:200 for retina
Phalloidin	Phalloidin-Atto 647N	Sigma	65906-10nmol	IF 1:300 for cell; 1:200 for retina
TO-PRO-3	TO-PRO- iodide (642/661)	Life Technologies	T3605	IF 1:1000
β -actin	Ms mAb to Actin	Abcam	ab3284	WB-1:2000
VE-cadherin	Purified anti human CD144 (BV9)	Bio-legend	348502	IF 1:300
VE-cadherin	Purified rat anti mouse CD144 (11d4.1)	BD	555289	IF 1:300
VE-cadherin	Rabbit polyclonal VE Cadherin antibody	Abcam	33168	WB 1:500
Lamin A/C	Monocolonal Anti-Lamin A/C ab produced in mouse	Sigma	SAB4200236	WB 1:500
Lamin B	Rb pAb to LaminB1	Abcam	ab16048	WB 1:500
SUN2	Rb mAb to SUN2	Abcam	ab124916	WB 1:500
GAPDH	Monocolonal Anti-GAPDH ab produced in mouse	Sigma	G8795	WB 1:3000
CD31 (Pecam-1)	Purified rat anti mouse CD31	BD	553370	IF 1:300
β -catenin	Purified mouse anti β -catenin	BD	810154	WB 1:500
CD45	Mouse CD45 Antibody	R&D systems	AF-114	IF 1:300
AmotL2	Angiomotin like 2	Innovagen, Lund, Sweden	Purified from rabbit serum	WB-1:500, IP-1:1:200 (v/v) IF/IHC 1:100

Secondary Antibodies

	Secondary Antibody	Conjugation	Catalog number	Company	Dilution
For WB	ECL® Anti-rabbit IgG	HRP linked whole antibody from donkey	NA934V	GE Healthcare	1:10000
	ECL® Anti-mouse IgG	HRP linked whole antibody from donkey	NA931V	GE Healthcare	1:10000
	ECL® Anti-rat IgG	HRP linked whole antibody from donkey	NA935V	GE Healthcare	1:10000
For IF staining	goat anti-Mouse IgG (H+L)	Alexa Fluor® 405 conjugate	A31553	LifeTechnologies	1:500
	goat anti-Rat IgG (H+L)	Alexa Fluor® 488 conjugate	A11006	LifeTechnologies	1:500
	donkey anti-Sheep IgG (H+L)	Alexa Fluor® 488 conjugate	A11015	LifeTechnologies	1:500
	goat anti-Chicken IgG (H+L)	Alexa Fluor® 488 conjugate	A11039	LifeTechnologies	1:500
	donkey anti-Goat IgG (H+L)	Alexa Fluor® 488 conjugate	A11055	LifeTechnologies	1:500
	chicken anti-Rabbit IgG (H+L)	Alexa Fluor® 488 conjugate	A21441	LifeTechnologies	1:500
	donkey anti-Mouse IgG (H+L)	Alexa Fluor® 555 conjugate	A31570	LifeTechnologies	1:500
	donkey anti-Rabbit IgG (H+L)	Alexa Fluor® 555 conjugate	A31572	LifeTechnologies	1:500
	goat anti-Mouse IgG (H+L)	Alexa Fluor® 594 conjugate	A11005	LifeTechnologies	1:500
	goat anti-Rat IgG (H+L)	Alexa Fluor® 594 conjugate	A11007	LifeTechnologies	1:500
	goat anti-Rabbit IgG (H+L)	Alexa Fluor® 594 conjugate	A11037	LifeTechnologies	1:500
	goat anti-Rat IgG (H+L)	Alexa Fluor® 633 conjugate	A21094	LifeTechnologies	1:500
	donkey anti-Mouse IgG (H+L)	Alexa Fluor® 647 conjugate	A31571	LifeTechnologies	1:500
	donkey anti-Rabbit IgG (H+L)	Alexa Fluor® 647 conjugate	A31573	LifeTechnologies	1:500
	goat anti-Mouse IgG (H+L)	Cy3®	A10521	LifeTechnologies	1:500
	goat anti-Rabbit IgG (H+L)	Cy3	A10520	LifeTechnologies	1:500
	Streptavidin	Alexa Fluor® 405 conjugate	S32351	LifeTechnologies	1:500
	Streptavidin	Alexa Fluor® 488 conjugate	S32354	LifeTechnologies	1:500

Reagents

	Reagent	Company	Catalog number
<i>In vivo</i>	Tamoxifen	Sigma	T5648
<i>In vitro</i>	Blebbistatin	Sigma	B0560
	Cytoclaxin D	Sigma	C8273
	Paraformaldehyde solution 4% in PBS	ChemCruz	sc-281692
	Fluoroshield with DAPI	Sigma	F6057
	Western Lightning Plus-ECL	PerkinElmer	203-170071
	Protein G Sepharose 4 fast flow	GE Healthcare	17-0618-01
	IgG from rabbit serum	Sigma	I8140
	IgG from mouse serum	Sigma	I8765
	Polybrene (Hexadimethrine Bromide)	VectorBuilder	provided with lentivirus
	Polybrene (Hexadimethrine Bromide)	Sigma	H9268-5G

Lenti-virus

Name	Company	Sequence if it's customized product
Non-Targeting (scrambled) shRNA Control	Sigma	-
human AmotL2 shRNA virus	Sigma	5'-GCGAGAGAAGGAGGAGCAGATC-3'

TaqMan Probes

Company	Thermo-Fisher
Species	Mouse
Gene	Taqman reference
TNF	Mm00443258_m1
CD68	Mm03047343_m1
Cxcl10	Mm00445235_m1
Icam1	Mm00516023_m1
Vcam1	Mm01320970_m1
Cd8a	Mm01188922_m1
Cd4	Mm01185100_m1
Ccl2	Mm00441242_m1
Ccl5	Mm01302427_m1
Cd19	Mm00515420_m1
IL6	Mm00446190_m1
HPRT	Mm03024075_m1