Autonomous role of Wiskott-Aldrich Syndrome platelet deficiency in inducing autoimmunity and inflammation

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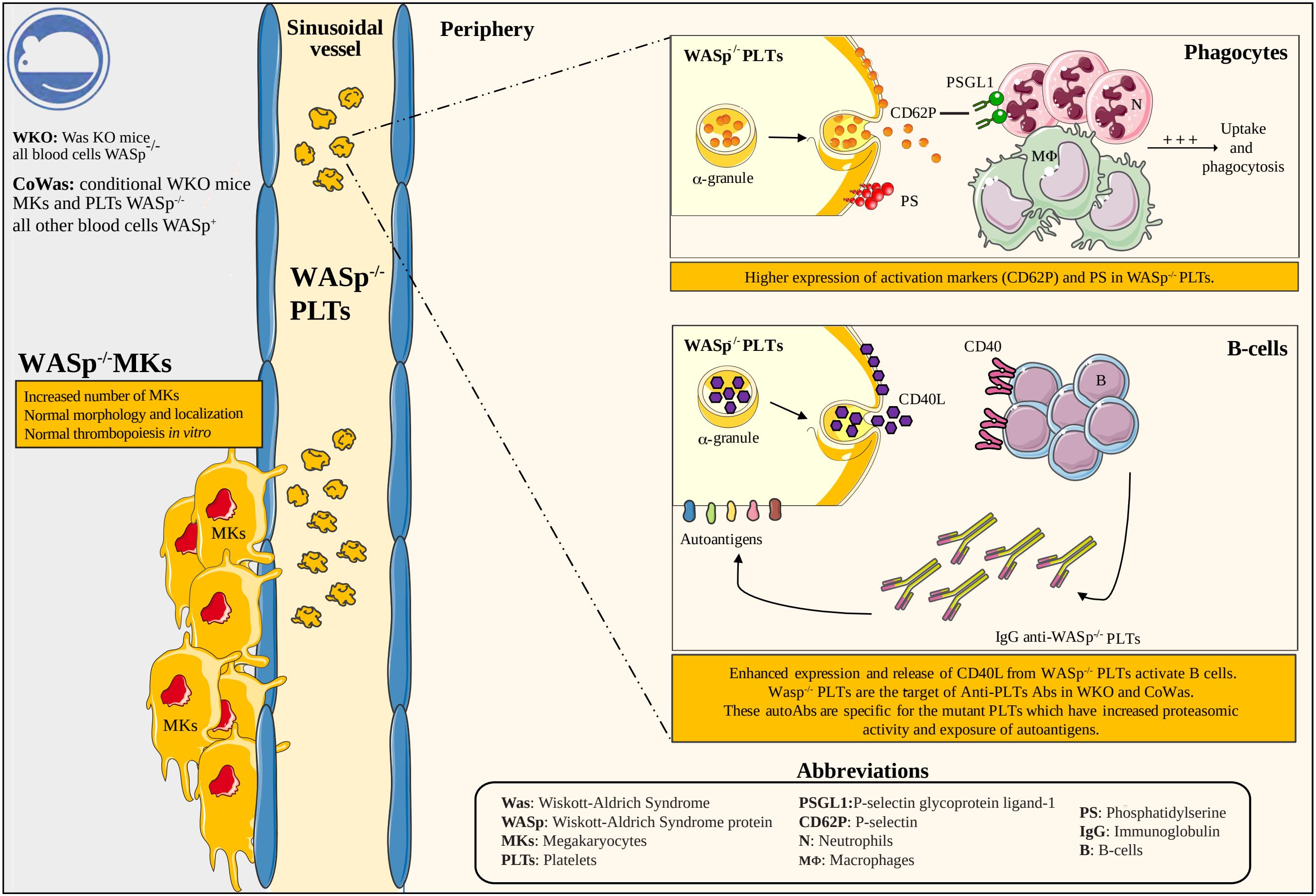
Intrinsic defect of WASp$^{-/-}$ PLTs sustains their peripheral elimination



WKO: Was KO mice
all blood cells WASp$^{-/-}$

CoWas: conditional WKO mice
MKs and PLTs WASp$^{-/-}$
all other blood cells WASp^{+}

WASp$^{-/-}$ MKs

Increased number of MKs
Normal morphology and localization
Normal thrombopoiesis *in vitro*

Higher expression of activation markers (CD62P) and PS in WASp$^{-/-}$ PLTs.

Enhanced expression and release of CD40L from WASp$^{-/-}$ PLTs activate B cells.
Wasp$^{-/-}$ PLTs are the target of Anti-PLTs Abs in WKO and CoWas.
These autoAbs are specific for the mutant PLTs which have increased proteasomic activity and exposure of autoantigens.

Abbreviations

Was: Wiskott-Aldrich Syndrome
WASp: Wiskott-Aldrich Syndrome protein
MKs: Megakaryocytes
PLTs: Platelets
PSGL1:P-selectin glycoprotein ligand-1
CD62P: P-selectin
N: Neutrophils
MΦ: Macrophages
PS: Phosphatidylserine
IgG: Immunoglobulin
B: B-cells

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Abstract

Background: Wiskott-Aldrich Syndrome (WAS) is an X-linked immunodeficiency characterized by eczema, infections and susceptibility to develop autoimmunity and malignancies. Thrombocytopenia is a constant finding, but its pathogenesis remains elusive.

Objective: To dissect the basis of WAS platelet (PLT) defect we used a novel conditional mouse model (CoWas) lacking WASp only in the megakaryocytic lineage in presence of a normal immunological environment and in parallel we analysed samples obtained from WAS patients.

Methods: Phenotypical and functional characterization of megakaryocytes and platelets in mutant CoWas mice and WAS patients with and without autoantibodies were performed. Platelet antigen expression was examined through protein expression profile and cluster proteomic interaction network. Platelet immunogenicity was tested by ELISA assays and B and PLTs co-culture.

Results: CoWas displayed increased MK numbers and normal thrombopoiesis *in vitro* but WASp-deficient PLTs had short lifespan and high expression of activation markers. Proteomic analysis identified signatures compatible with defects in cytoskeletal reorganization and metabolism, yet surprisingly increased antigen-processing capabilities. In addition, WASp-deficient PLTs expressed high levels of surface and soluble CD40L and were capable of inducing B-cell activation *in vitro.* WASp-deficient PLTs were highly immunostimulatory in mice and triggered the generation of antibodies specific for WASp-deficient PLTs even in the context of a normal immune system. WAS patients also showed PLT hyperactivation and elevated plasma soluble CD40L levels correlating with the presence of auto-antibodies.

Conclusion: Overall, these findings suggest that intrinsic defects in WASp-deficient PLTs decrease their lifespan and dysregulate immune responses, corroborating the role of PLTs as modulators of inflammation and immunity.

Key messages:

- Selective WAS absence is dispensable for MK function and thrombopoiesis
- Conditional WAS inactivation in platelets affects peripheral survival leading to phagocytosis and autoantibody elimination via CD40 ligand
- *Was*$^{-/-}$ PLTs have decreased metabolic activity and increased ubiquitination pathways
- Increased platelets activation and CD40 ligand plasma levels are observed in WAS patients

Capsule summary Wiskott-Aldrich Syndrome is an X-linked disease in which immunodeficiency associates with autoimmunity, malignancies and thrombocytopenia. Here we demonstrate platelet-intrinsic defects causing their premature elimination and specific autoimmune induction.

Keywords: Wiskott-Aldrich syndrome, platelet deficiency, CD40 ligand, autoantibodies, autoimmunity

List of abbreviations

α-granules: alpha-granules
Anti-PLTs autoAbs: anti-platelets autoantibodies
aScore: average Score
aSpC: average Spectral Count
BM: Bone Marrow
CoWas: conditional $Was^{-/-}$ mice
CoWas$^{+/-}$: Heterozygous female CoWas mice
CPD: Citrate Phosphate Dextrose Solution
ds-DNA AutoAbs: anti-double strand DNA autoantibodies
δ-granules: dense-granules
HCT: hematocrit
HD: Healthy Donor
HDa: adult Healthy Donor
HDp: pediatric Healthy Donor
IMDM: Iscove's Modified Dulbecco's Medium
ITP: Immune Thrombocytopenia
LDA: Linear Discriminant Analysis
MEP: Megakaryocyte-erythroid progenitors
MFI: Mean Fluorescence Intensity
MK-CFUs: megakaryocytic Colony-Forming Unit
MkPs: megakaryocyte progenitors
MKs: megakaryocytes
MPV: Mean Platelet Volume
MW: Molecular Weight
PB: Peripheral Blood
pI: Isoelectric point
PLTs: platelets
PPP: Platelet Poor Plasma
PRP: Platelet Rich Plasma
PS: phosphatidylserine
RT-PLTs: Reticulated-Platelets

sCD40L: soluble CD40L
sCD62P: soluble CD62P
SD: standard deviation
TCTO: SR-Tiget Clinical Trial Office
TEM: Transmission Electron Microscopy
TO: Thiazole-Orange
vWF: von Willebrand Factor
WAS: Wiskott-Aldrich Syndrome
WASp: Wiskott-Aldrich Syndrome protein
WBCs: White Blood Cells
WKO: Was$^{-/-}$ mice
XLT: X-linked Thrombocytopenia

Introduction

Wiskott-Aldrich syndrome (WAS) is a severe X-linked immunodeficiency caused by mutations in the *WAS* gene encoding the WAS protein (WASp) specifically expressed in hematopoietic cells and involved in actin polymerization [1]. WAS patients have low platelet (PLT) numbers with reduced size, immunodeficiency, eczema and high susceptibility to develop tumours and autoimmune manifestations [2,3]. Thrombocytopenia in the absence of other clinical manifestations is referred to as X-linked thrombocytopenia (XLT) [4–6].

Although bleeding episodes occur in the majority of patients and may cause death in 4 to 10% of the patients [7–9], the pathogenesis of PLTs defect remains elusive [10]. Abnormal PLT shedding from megakaryocytes (MKs) and consequent premature bone marrow (BM) release, in the presence of normal or increased megakaryopoiesis, has been described as a cause of ineffective PLT production [2,11,12]. In contrast, normal megakaryopoiesis and thrombopoiesis associated with increased peripheral elimination were reported by other authors [13–15]. Several studies on PLTs performed in *Was*$^{-/-}$ mouse models (WKO) led to contrasting results. The two mouse models of WAS [16,17] both show reduced PLT counts but normal mean platelet volume (MPV) in the absence of bleeding episodes. Studies carried out in these mutants, demonstrated defective and premature thrombopoiesis [18] and increased peripheral elimination of *Was*$^{-/-}$ PLTs mediated by macrophages and antiplatelet autoantibodies (anti-PLT autoAbs) [19–21]. However, since all previous studies were performed in murine mutants or in patients lacking WASp in all hematopoietic lineages, it remains difficult to discriminate the contribution of the defective immune system to platelet defect. To this end, we generated a conditional *Was*$^{-/-}$ mouse model (CoWas) lacking WASp only in the megakaryocytic lineage. Studies performed in CoWas mice allowed us to identify novel intrinsic defects of *Was*$^{-/-}$ PLTs, which were in part confirmed also in WAS/XLT patients. In conclusion, studies in CoWas mice revealed PLTs intrinsic defects causing their increased peripheral elimination, independently from other immune system abnormalities and contributing to abnormal modulation of immune responses.

Materials and Methods

Mice

C57BL/6J *Was*$^{-/-}$ mice (WKO) were kindly provided by K.A. Siminovitch [17]; WT mice were purchased from Charles River Laboratories Inc. (Calco, Italy); *Rag1*$^{-/-}$*Was*$^{-/-}$ mice were generated by breeding *Rag1*$^{-/-}$ mice (The Jackson Laboratory) with WKO mice. CoWas mice were generated by breeding *Was-floxed* female mice [22] and Pf4-Cre male mice (The Jackson Laboratories). All the mouse models (WT, WKO, WKO-Rag1$^{-/-}$ and *Rag1*$^{-/-}$) were in C57BL/6J background. Mice were genotyped as described in Supplementary Materials.

Flow cytometry of murine and human samples

Cell suspensions were stained in FACS buffer (PBS, 0.3% BSA, 0.1% NaN_3) with antibodies specific for the following markers: anti-CD3 (145-2C11), anti-CD11b (M1/70), anti-B220 (RA3-6B2), anti-Sca1 (D7), anti-CD62P (RB40.34), anti-CD69 (H1.2F3), anti-CD36 (CRF D-2712), anti-CD47 (miap301) and anti-human PAC1 (PAC-1) from BD Pharmingen (San Diego, CA); anti-CD117 (2B8), anti-CD150 (TC15-12F12.2), anti-CD105 (MJ7/18), anti-CD40L (MR1), anti-CD41 (MWReg30), anti-CD16/32 (93), anti-CD61 (2C9.G2), anti-CD38 (90), anti-CD34 (HM34), Lin^{-} cocktail, anti-human CD61 (VI-PL2) from Biolegend (San Diego, CA). Anti-CD42a (Xia.B4) from Emfret Analytics (Eibelstadt, Germany). Anti-human CD62P (Psel.KO2.3) from Invitrogen (MA). Intracellular WASp staining was performed as described in [23]. All the flow cytometry samples were acquired with a FACS Canto II system (BD) and analysed with FlowJo software (Tree Star Inc.).

Platelet collection and surface staining

Blood collected in Citrate Phosphate Dextrose Solution (CPD; Sigma) from retro-orbital sinus was analysed with Sysmex KX-21N hemocytometer (Dasit). To collect Platelet Rich Plasma (PRP) blood was then diluted with the same volume of Tyrode's buffer 1X (5 mM HEPES, 137 mM NaCl, 2.7 mM KCl, 0.4 mM NaH2PO4, 2.8 mM Dextrose, pH 7.4) and centrifuged 7 minutes at 700 rpm. For the analysis of δ-granules, 5 μl of whole blood was stained with 1 μl of anti-mouse CD61 and incubated 10 minutes at RT; next, samples were incubated for 30 minutes at 37°C in the dark with 500 μl of Mepacrine staining solution (10 μM) in PBS or 500 μl of PBS as negative control. For RT-PLTs staining, 5 μl of whole blood was stained with 1 μl of anti-mouse CD61 and incubated 10 minutes at RT. Next, 1 ml of Thiazole Orange solution (50 ng/ml) (Sigma-Aldrich, St Louis, MO) or PBS as negative control was added and incubated for 30 minutes at RT in the dark. To analyse the staining we set the gate on WT mice, considering the percentage of RT-PLTs in normal animals as 3% of total PLTs [24]. For AnnexinV staining, 200.000 PLTs are stained in 100 μl of 1X Binding Buffer with 5 μl of PE-AnnexinV (BD Pharmingen) for 15 minutes at room temperature followed by stopping reaction by 100 μl 1X Binding Buffer addition. To analyse CD40L surface expression, 5 μl of PRP in the presence of 5μl of agonist was stained with anti-mouse CD61 and anti-mouse CD62P. PRP was incubated with Thrombin (1U/ml final concentration) (Sigma-Aldrich, St Louis, MO) for 2 minutes at room temperature. The reaction was stopped by adding 200 μl of FACS Buffer 0.2% PFA and at the end 1 μl of CD40L antibody per sample is added.

TEM analysis

PLT pellets were fixed in 4% paraformaldehyde and 2.5% glutaraldehyde in 125mM cacodylate buffer at 4°C for 30 minutes, and then in 2% OsO_4 in 125mM cacodylate buffer for 1 hour.

Samples were then washed, dehydrated, and embedded in Epon. Sections were examined on a LEO 912AB transmission electron microscope.

In vivo experiments

Platelet depletion was performed by i.v. injection of 0.5 μg/gr of rat purified anti-mouse GPIbα (Emfret Analytics, Europe) in PBS. At different time points after the injection, blood has been collected from the retro-orbital sinus to analyse PLT count by hemogram and RT-PLTs by TO staining. PLT clearance was evaluated by retro-orbital injection of 3 μg of DyLight488-labelled or Alexa647-labelled anti-GPIb-V-IX (Emfret) antibody diluted in PBS [25]. To analyse the percentage of labelled platelets , 10 μl of whole blood was incubated with 2μl of anti-CD61 for 15 minutes followed by the addition of 150 μl of PBS. To perform the adoptive transfer experiment, *Was*$^{-/-}$ PLTs were isolated form WKO or CoWas mice and stained with CellTrace™ Violet Cell Proliferation Kit (Invitrogen) using 1 μl of the dye every 5 x 10^6 of PLTs. PLTs isolated from WT mice were labeled with CellTrace™ FarRed Cell Proliferation Kit (Invitrogen) using 1 μl of the dye every 5 x 10^6 PLTs. PLTs were mixed in a ratio of 30% WT and 70% *Was*$^{-/-}$ in PBS and injected i.v. into WKO mice (using *Was*$^{-/-}$ PLTs isolated form WKO) or into CoWas recipients (*Was*$^{-/-}$ PLTs isolated form CoWas). We injected 33 x 10^6 labelled PLTs into each recipient. Blood was collected 15 minutes later (time 0) and daily for 6 days; the percentage of Violet$^+$ or FarRed$^+$ PLTs was monitored with a FACS Canto II (BD).

To deplete phagocytes, mice were injected i.p. with 100 μl/10 gr mouse weight of Clodronate liposomes (concentration 5 mg/ml) at day 0 and day 4 [26] or PBS Liposomes. Blood was collected at day 0 (pre-injection) and day 7 to evaluate PLT counts.

ELISA assays

Anti–dsDNA antibodies were evaluated by ELISA assay as described in [27]. The presence of anti-PLT autoAbs was assessed as described in [28].

ELISA Kits to evaluate concentrations of murine soluble CD62P (sCD62P) and plasma soluble CD40L (sCD40L) (eBioscience) were used according to manufacturer's instructions.

Megakaryocytes analysis

To analyse the number and frequency of MKs, BM cells have been stained and MKs identified as $CD41^+CD61^+$ cells by flow cytometry; this analysis has been performed in untreated animals of 18 hours after the treatment with anti-GPIbα Ab. Mk-CFU were analysed with MegaCult™-C Complete Kit with Cytokines (StemCell Technologies) according to the manufacture's instructions. Visible Mk-CFU with purple nuclei and brown granules were counted (4x) in wide field microscope. Ploidy Distribution and Reticulated PLTs (RT-PLTs) formation have been evaluated as described in Supplementary materials.

B cell and PLT culture system

$CD43^+$ cells were depleted from the spleen by anti-CD43 microbeads (Miltenyi Biotec) using the AutoMacs Pro separator (Miltenyi Biotec). One hundred µl of PRP containing at least 200.000 PLTs/µl was incubated 1 hour at 37°C in a thermo-mixer (300-350 rpm). Platelet Poor Plasma (PPP) was collected upon double centrifugation at 8000 rcf for 3 minutes. We plated 150.000 CD43 negative cells (resting naïve B-cells) in the presence of 100 µl of PPP supernatants or complete RPMI as negative controls for 72 hours; CD69 expression was analysed by flow cytometry.

Human PLT activation analysis

PRP was collected by centrifuging blood for 10 minutes at 700 rpm. Two hundred thousand PLTs/sample were stained for 10 minutes at RT in FACS buffer and then fixed with 0.2% PFA. The ratio of CD62P/CD61 MFI or PAC1/CD61 Mean Fluorescence Intensity (MFI) [9] was used to normalize the expression level of activation markers for the PLT volume, assigning to the Healthy Donor (HD) unstimulated sample the value of 100.

Sample preparation and proteomic analysis

PRP were centrifuged and lysed through three quick freeze/thaw cycles and then protein extraction was performed by adding RapiGest^{TM} SF at 0.2% (w/w) according to the manufacturer’s protocol (Waters Corporation, Milford, MA, USA). Detailed description of proteomic analysis, data processing and interaction network reconstruction are described in the Supplemental Materials.

Statistical analysis

All results are expressed as mean and standard deviation (SD) if not stated otherwise. To assess significance, we used one-way ANOVA with Bonferroni post-correction or two-way ANOVA analysis of variance when specified. We also used two-tailed Mann-Whitney test where specified. p-values <0.05 were considered significant.

Study approval

Animal procedures were performed according to IACUC 557 and 741 approved by the Italian Institutional Animal Care and OSR Committee. Human studies were performed according to the Helsinki Declaration and the TIGET PERIBLOOD or TIGET08B, TIGET02, TIGET06 clinical protocols approved by the OSR Ethical Committee. The study was also approved by the NIH IRB (protocol 16-I-N139).

Results

CoWas mice selectively lack WASp in platelets

To understand the extent to which the lack of WASp expression affects PLT generation and survival we generated mice lacking WASp only in the megakaryocytic (MK) lineage. We obtained compound heterozygous female (CoWas$^{+/-}$) and CoWas mice, completely null for WASp expression in the megakaryocytic lineage (**Supplemental Figure 1A-C**). The intracellular WASp expression was assessed by flow cytometry on white blood cells (WBCs) and PLTs isolated from the peripheral blood (PB) of age-matched mice. As expected, WKO mice lacked WASp expression both in WBCs and in PLTs, while CoWas mice lacked WASp selectively in PLTs. CoWas$^{+/-}$ showed a double population of WASp^{+} and WASp^{-} PLTs, in the presence of normal WASp expression in WBCs (**Figure 1A**). CoWas$^{+/-}$ female mice showed more than 50% WASp^{+} PLTs suggesting a selective advantage for WASp^{+} PLTs in the periphery (**Figure 1B**). CoWas and WKO mice showed comparably low PLT counts (446,6 ± 69,62 $*10^{6}$ PLTs/ml and 495 ± 105,9 $*10^{6}$ PLTs/ml respectively), while CoWas$^{+/-}$ mice showed intermediate PLT counts between WT and mutant mice (711,2 ± 89,23 $*10^{6}$ PLTs/ml) (**Figure 1C**). No differences in MPV, WBC counts or haematocrit values (HCT) were observed among mutants and control animals (**Figure 1D** and data not shown). Analysis of glycoproteins expressed on PLT surface showed no alterations in mutant mice (**Supplemental Figure 1D**).

To further characterize morphological changes in *Was*$^{-/-}$ PLTs, we analysed the size and granule content by TEM (**Figure 1E**). In contrast to human findings [2,8,29], PLTs from WKO and CoWas mice did not show reduction in size (**Figure 1F**, left panel), as previously reported in WKO models [16,18]. Consistently, the quantity of alpha-granule (α-granule) and dense-granule (δgranule), both containing factors responsible for platelet activation and aggregation, was similar in all three groups of mutant mice (**Figure 1F**, right panel).

Thrombopoiesis in the absence of WASp

To test whether peripheral thrombocytopenia could be due to defective thrombopoiesis, we analysed the megakaryocytic compartment. WKO and CoWas mice showed an increased percentage of MK progenitors (MkPs) ($CD150^{+}CD41^{+}$ on $Lin^{-}cKit^{+}Sca1^{-}$ cells [30]) (**Figure 2A**) and higher number of MK-CFUs (**Figure 2B**). Further analysis to better dissect MK development, showed an increased in MK progenitors from the stage of promegakaryocytes ($CD34^{-}$ $CD38^{+}CD41^{+}CD61^{+}CD42a^{+/-}$ [31]) (**Supplemental Figure 2A**). Of note, no differences in ploidy distribution of MKs were observed in mutant animals compared to controls (**Supplemental Figure 2B**). Analysis of the percentage and absolute number of mature MKs ($CD41^{+}CD61^{+}$) revealed a significant increase in both CoWas and WKO mice, in line with data reported in literature [18,19] (**Figure 2C-D**). All these findings suggest that peripheral thrombocytopenia stimulates megakaryopoiesis to compensate the peripheral defect. To asses the efficiency of thrombopoiesis *in vivo*, we counted reticulated PLTs (RT-PLTs) [24], using Thiazole Orange (TO) staining. WKO and CoWas mice showed a decreased percentage of RT-PLTs (**Figure 2E**), which may suggest impaired thrombopoiesis. However, MKs analysis in the bone marrow of mutant mice assessed by immunohistochemistry using anti-CD31 Ab (depicting sinusoids and MKs) and anti-Factor VIII Ab (von Willebrand Factor - vWF, labelling MKs) did not reveal any mislocalization (data not shown). Also, *Was*$^{-/-}$ MKs showed *in vitro* normal pro-PLTs formation (**Supplemental Figure 2C-E**). To test *in vivo* thrombopoiesis, we depleted PLTs by i.v. injection of anti-GPIbα monoclonal antibody (**Figure 2F**). Daily blood collection demonstrated PLTs recovery to pre-depletion values within 3-4 days in all mice (**Figure 2G**); of note, no effect of anti-GPIbα treatment on MKs number has been found using WT animals (Supplemental Figure 2F); however, we cannot exclude an effect of WASp deficiency on the recovery of the functional megakaryocyte pool after GPIb treatment. Additionally, evaluating the percentage of RT-PLTs after anti-GPIbα treatment, we found that mutant mice RT-PLTs reach an equilibrium with the same kinetics of WT mice (Supplemental Figure 2G). Although these *in vivo* data may suggest normal thrombopoiesis in WKO and CoWas mice, at least in stressed situation, since mutant animals have higher number of MKs in the BM and do not reach an equilibrium of RT-PLTs in a shorter time period, we cannot exclude that thrombopoiesis *per* MK could be affected.

Increased peripheral elimination of hyper-actived *Was*$^{-/-}$ PLTs in CoWas mice

To test the increased peripheral PLT elimination hypothesis, we assessed PLT half-life by *in vivo* injection of DyLight488-anti-GPIb-V-IX antibody selectively labelling circulating PLTs [25] and observed shorter life span in WKO and CoWas mice (**Figure 3A-B**), although we cannot exclude an impact of the antibody on PLT clearance. To further characterize this defect, we transferred a mixed population of differently labelled WASp^{+} (from WT) and WASp^{-} (from WKO or CoWas) PLTs into WKO and CoWas recipients. Specifically, labelled PLTs were mixed in a ratio of 30% WT and 70% CoWas or 30% WT and 70% WKO and i.v. infused into CoWas and WKO, respectively. The proportion of WASp^{+} PLTs increased over time, while WASp^{-} PLTs decreased in all recipients, indicating that WASp^{-} PLT clearance is independent of the host environment (**Figure 3C**) and suggesting an intrinsic PLTs defect.

To test phagocyte contribution in mediating peripheral PLT elimination, we injected clodronate liposomes to deplete macrophages *in vivo* [26,32]. Analysis of the frequency of F4/80 positive cells in the spleens of clodronate liposome-treated mice confirmed macrophage depletion (data not shown). Seven days after administration, WKO and CoWas mice showed a significant increase in PLT numbers indicating a critical contribution of phagocytes to the peripheral elimination of WASp-deficient PLTs (**Figure 3D**). PLT increase was more obvious in WKO than in CoWas mice. We speculate that the defective migratory ability of *Was* $^{-/-}$ macrophages in WKO mice could lead to an increased PLT elimination within tissues, inducing a more substantial increase in PLT counts after phagocytes depletion. Rapid phosphatidylserine (PS) exposure occurring concomitantly to activation is one of main mechanisms mediating PLT phagocytosis. In line with WAS patients data [15], PLTs from both mutant strains showed higher frequency of AnnexinV^{+}-PLTs (**Figure 3E**). Increased levels of sCD62P in the plasma (**Figure 3F**) and surface expression of CD62P (**Figure 3G**) were also found in mutant PLTs as compared to controls. In sum, our data indicate that cell-intrinsic mechanisms cause hyperactivation of WASp-deficient PLTs, which are in turn rapidly removed from the periphery by phagocytic cells.

Proteomics of *Was*$^{-/-}$ platelets reveals perturbed metabolism and enhanced antigen processing

To investigate the intrinsic mechanisms underpinning the enhanced activation and removal of *Was*$^{-/-}$ PLTs, we evaluated their proteomic profile. More than 1400 proteins were identified (**Supplemental Table 1**) and 686 proteins were shared among mutants and WT PLTs (corresponding to >46% of total proteins) **(Figure 4** and **Supplemental Figure 3A-C**).

To identify differentially expressed proteins, Linear Discriminant Analysis (LDA) was applied, and 221 proteins presenting *F* ratio ≥3.5 and *P*-value ≤0.05 were extracted as descriptors (**Supplemental Table 2**). Hierarchical clustering obtained upon processing descriptors showed that CoWas is an intermediate condition between WT e WKO (**Supplemental Figure 3D**). Of note, the majority of extracted descriptors were confirmed by fold change and DAve analyses (see “Proteomics Data Processing” in Materials and Method section). In addition, the effects of WASp deletion were evaluated plotting the selected descriptors into a *Mus musculus* protein-protein interaction network using Cytoscape and STRING db (**Supplemental Figure 4**). The network analysis (19 clusters) confirmed intermediate levels of expression of distinct biological processes/functional classes in CoWas PLTs between WT and WKO PLTs. This finding was more evident focusing on a sub-network of 8 clusters involving metabolic processes, cytoskeleton, ubiquitins, 14-3-3 proteins and immunoglobulins (**Figure 5A**). Specifically, we didn’t find any abnormalities in the total amount of actin-related proteins but relative changes in some proteins related to this pathway. Metabolic profile perturbation with a reduction in lipid, glucose and phosphate metabolism related proteins was also found. On the other hand, ubiquitin-related proteins were upregulated, in line with reduced lifespan and increased antigen processing, which is frequently observed in autoimmune disorders [33]. Proteomic profile also revealed alterations in the Ig content with substantial increase in PLT-associated IgM, IgA and IgG in WKO mice (**Figure 5A**). Of note, the “don’t eat me” signal CD47 molecule decreases in CoWas and WKO mice, as confirmed by flow cytometric analysis (**Figure 5B**).

The proteomic profile suggests a scenario in which absence of WASp (i) decreases PLT lifespan through inhibition of several metabolic pathways and enhancement of ubiquitination and proteasomal activity that (ii) increases antigen processing contributing to trigger autoimmunity.

In addition, our data show that WASp deficient PLTs present intrinsic defects that become more severe in WKO, likely because of the aggravating role of PLT-extrinsic immune dysfunctions.

Was$^{-/-}$ platelets trigger autoimmune responses in CoWas mice

Due to the presence of anti-PLT autoAbs in patients [34] and in WKO mice [20] , we hypothesized that WASp-deficient B-cells may react against PLTs by producing neutralizing antibodies. In line, *Was*$^{-/-}$*Rag1*$^{-/-}$ double knock-out mice (WKO-Rag1$^{-/-}$), lacking T and B cells, showed PLT count values comparable to WT , thus supporting a partial involvement of adaptive immunity in the peripheral elimination of *Was*$^{-/-}$ PLTs (**Figure 6A**) and further supporting data observed in the $\mu MT^{-/-}$ *x Was*$^{-/-}$ model [20].

To test whether the production of anti-PLT autoAbs could be related to B-cell dysregulation [23,35–39] or alternatively could be triggered by the intrinsic immunogenicity of *Was*$^{-/-}$ PLTs PLTs, we measured anti-PLT autoAbs in CoWas mice. To do this, we used an ELISA assay detecting serum anti-PLT IgG more sensitive than the proteomics approach used above. No autoAbs against WT PLTs were detected in WT mice, while autoAbs against *Was*$^{-/-}$ PLTs were present in serum of WKO and CoWas mice. Very importantly, CoWas$^{+/-}$ mice developed autoAbs specifically against *Was*$^{-/-}$ PLTs but not against WT PLTs (**Figure 6B**). Of note, CoWas mice do not show any signs of autoimmunity and the analysis of serum anti-double strand DNA autoantibodies (dsDNA autoAbs) did not detect any positivity (**Figure 6C)**. Because of the presence of autoAbs in CoWas mice despite the normal B-cell compartment, we hypothesized that *Was*$^{-/-}$ PLTs could sustain humoral autoimmunity by producing immunomodulatory factors that trigger B-cell responses. In this context, PLTs have been demonstrated to mediate inflammatory and immune responses by releasing chemokines and cytokines including CD40L, which is highly expressed and released upon activation. PLT-derived CD40L can modulate adaptive immune mechanisms influencing B-cell homeostasis by inducing isotype switching [40–43]. Thus, we evaluated PLTs CD40L surface expression upon *in vitro* activation finding a significant increase in WKO and CoWas mice (**Figure 6D**, left side). Consistently, higher release of sCD40L was retrieved in mutant PPP obtained from unwashed PLTs and maybe reflecting higher activation of *Was*$^{-/-}$ B-cells, which may consume sCD40L (**Figure 6D**, right side).

Next, we tested whether the higher expression and release of CD40L could directly modulate B-cell activation. We cultured B-cells isolated from WT, WKO and CoWas spleens in the presence of PPP from WT, WKO or CoWas mice and analysed B-cell activation. B-cells cultured in the presence of supernatants obtained from PLTs lacking WASp showed a higher proportion of activation marker CD69 (**Figure 6E**). Overall, these findings suggest that, in the absence of WASp, PLTs may contribute to sustain immune dysregulation by expressing and releasing higher levels of CD40L that can induce B-cell activation even in a normal immune environment.

Activated PLTs and increased soluble CD40L in WAS/XLT patients

To corroborate these findings in humans, we evaluated PLT activation and analysed the levels of serum sCD40L in a cohort of WAS patients with various clinical manifestations and presence or absence of auto-antibodies (**Supplemental Table 3**) [37,44]. Human PLT activation was evaluated in adult healthy donors and patients by analyzing the expression of CD62P and PAC1, the activated form of integrin $\alpha_{IIb}\beta_3$ (GPIIbIIIa) [45]. We found that the MFI of both CD62P and PAC1 was significantly increased in patients (**Figure 7A-B**). To support platelets immunomodulatory role, different autoimmune conditions have been associated with increased serum level of sCD40L, of which PLTs are the major source [46–48]. We tested the levels of sCD40L in the plasma of fourteen WAS patients, also at risk of autoimmune complications, and in nineteen pediatric age-matched healthy donors. Higher sCD40L concentration was found in patients with circulating autoAbs than in patients with no autoantibodies **(Figure 7C** and **Supplementary Table 3**).

Overall, in the WAS patients, PLTs are hyperactivated and in turn, this activation may contribute to their peripheral elimination and further sustain inflammation and B-cell activation, predisposing to autoimmune complications.

Discussion

Thrombocytopenia is a common feature present in both XLT and WAS patients [2–6]. Controversial data on PLT defect have been reported but all these studies were performed in patients and murine models lacking WASp in all hematopoietic cells thus preventing a clear dissection of the contribution of intrinsic vs. extrinsic factors. To overcome this issue, we generated CoWas mice lacking WASp only in the megakaryocytic lineage. Although no gross morphological changes were detected in CoWas PLTs, the lower absolute count in a normal immune environment strongly suggested an intrinsic defect.

One of the more controversial issue in WAS-related thrombocytopenia is the analysis of the thrombopoietic activity of deficient MKs and indeed, observations in our mutant models do not completely clarify this complex issue. BM analysis in WKO and CoWas mice showed an increased percentage of MkPs and MKs, suggesting that peripheral thrombocytopenia triggers megakaryopoiesis. *In vitro* pro-PLTs production tests showed that Was$^{-/-}$ MKs are able to produce pro-PLTs at normal rate compared to WT counterpart. Additionally, after *in vivo* PLTs depletion, mutant animals treated with anti-GPIb Ab, restored PLTs count with a kinetics comparable to WT mice. To corroborate our findings, it has been recently demonstrated that human proplatelet formation *in vitro* depends on N-WASp, while WASp is dispensable [49].

Despite these evidences, the RT-PLT number and percentage in PB were reduced in both mutants, similarly to WAS patients [20,50]; these data are in contrast with the work published by Prislovsky and co-workers [19], who showed normal frequency of reticulated PLTs in WKO mice. This discrepancy might be due to the different genetic background and the effect of genetic modifiers present in the various mouse models [16,17]. The reduced frequency and count of RT-PLTs present in WKO and CoWas mice could also suggest a defective thrombopoiesis, although in contrast with our *in vitro* data. However, a reduced half-life of Was$^{-/-}$ RT-PLTs compared to WT RT-PLTs, based on the *in vivo* data of mature PLTs, could be hypothesized . Accelerated kinetics of RT-PLT maturation to compensate the faster mature PLT elimination might be an additional factor. Moreover we cannot exclude the hypothesis that in absence of WASp an important fraction of PLTs could be generated as non-reticulated [19]. Finally, since WKO and CoWas mice have increased MKs number, thrombopoiesis *per* MK could still be affected. Overall, since data reported here are obtained in a stress condition (after severe depletion), defective thrombopoiesis at steady state condition cannot be excluded.

We speculated that despite the normal immune environment, peripheral PLTs destruction in CoWas mice could be the result of an intrinsic PLT defect. In line with this hypothesis, a shorter half-life of *Was*$^{-/-}$ PLTs was observed in CoWas and WKO mice. Moreover, mutant mice showed increased sCD62P levels in the plasma with no increase in sCD62P mRNA (data not shown), indicating that the increased protein expression and serum levels may reflect enhanced α-granules release due to the perturbation of actin polymerization inside the cytosol, consistently with the role of WASp in the regulation of granule release. Thus, WASp deficiency causes a dysregulation in the expression and release of CD62P, which in turn may induce increased uptake of activated PLTs by phagocytes via CD62P/PSGL1 interactions [51–55]. PLT activation also results in the rapid exposure of PS, a well-known "eat-me" signal. In line, the *in vivo* elimination of phagocytes increased PLT counts in WKO and CoWas mice. Additionally, B-cells may produce anti-PLT autoAbs, frequently detected in patients and in WKO mice [20,34]. Remarkably, CoWas mice and even CoWas$^{+/-}$, produce autoAbs selectively against Wasp-deficient PLTs. The increased expression and release of CD40L may contribute to tolerance breakdown by promoting B-cell activation and inducing immunotype switching [23,40,56–59]. Indeed, the difference between sCD40L levels retrieved in the WKO and CoWas PPP may reflect the altered distribution of B-cell subpopulations. In fact, with similar release of sCD40L by *Was*$^{-/-}$ PLTs, CoWas mice have no defects in B-cell compartment and require a lower amount of sCD40L produced by PLTs. On the contrary, WKO mice have hyperactivated B-cells that produce higher levels of circulating IgM and IgG at steady state, thus suggesting that higher consumption of sCD40L occurs to sustain B cell activation and class-switch recombination [22,59–61].

These data were further corroborated in a small cohort of WAS patients. We observed higher expression of activation markers in patients; our observations are in contrast with data reported by Gerrits and colleagues [9] who evaluated PLTs activation on whole blood samples finding no significant difference between patients and HDs. We performed the analyses of PLT activation on PLTs isolated from the peripheral blood. The different type of samples analyzed could explain this discrepancy since in whole blood activated PLTs could bind to leukocytes thus underestimating the P-selectin expression. Patients with detectable autoantibodies also showed increased plasma levels of sCD40L, likely derived from *in vivo* activation of PLTs. In turn, sCD40L increase may sustain inflammation and induce B-cell isotype switching. The proteomic profile of *Was*$^{-/-}$ PLTs isolated from WKO but not from CoWas mice revealed relevant changes in the content of immunoglobulins (IgA, IgG2b, IgG3, IgM), reflecting the perturbation of the B-cell compartment [23,56–59]. In parallel, the proteomic analysis demonstrated that both PLT-intrinsic and extrinsic mechanisms cooperate in the pathogenesis of WAS-related thrombocytopenia. Proteomic alterations shared between WKO and CoWas mice indicate intrinsic PLT defects due to the absence of WASp, while proteins differentially expressed between WKO and CoWas reflect the direct influence of the immune system. *Was*$^{-/-}$ PLTs from both murine models show metabolic dysregulation with lower expression of proteins involved in the lipid metabolism processes such as those involved in electron transport chain or in fatty acids β-oxidation as well as SLC25A24 a mitochondrial Ca-dependent carrier of Mg-ATP/Mg-ADP that protects from oxidative stress [62,63]. Conversely, WKO PLTs upregulated STOM, a lipid-rafts component of α-granules involved in PLT activation [64]. Glucose metabolism, protein kinases, phosphates and relative cascade pathways were downregulated in the absence of WASp. Interestingly CD47, a molecule that when absent leads to mild spontaneous thrombocytopenia [65], progressively decreases from CoWas to WKO, suggesting an additional mechanism contributing to the induction of phagocytosis. Consistently with the frequent bleeding episodes occurring in patients irrespectively to the clinical severity, integrin β3, integrin IIb/IIIa and some 14-3-3 family proteins were downregulated [66]. On the other hand, upregulation of ubiquitin-related proteins was found. All these findings support the intrinsic defect that renders PLTs more prone to apoptosis and concomitantly more capable of processing antigens for presentation to the immune system, a phenomenon that can contribute to the development of autoimmunity [33].

In conclusion, our study provides novel insights into the pathogenesis of WAS, highlighting the intrinsic role of WASp in PLT turnover and peripheral homeostasis. We shed a new light on the mechanisms underlying WAS immune dysregulation showing that in the absence of WASp, PLTs secrete high amount of CD40L, sustaining inflammation and contributing to the altered B-cell function. Overall, our study identifies PLT defects as contributing to both impaired hemostasis and dysregulated immunity, extending the complex scenario of defective cellular processes occurring in WAS.

Author contributions

LS, MCC and AV designed and performed research, analysed data, and wrote the paper; FM, AcAn, MB contribute to the design of the experiments and data interpretation; LDN and AT provided the conditional knock-out mouse model; DDS, SaMo and PLM performed the proteomic analysis and analysed the data; AA, SG, LDN provided human samples and clinical information; ED contributed to animal colony maintenance; StMan performed immunohistochemistry staining.

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Conflict of interest:

GSK is the financial sponsor of an ongoing WAS gene therapy program in which some of the patients listed in this study are participating. AA is the PI of a clinical gene therapy trial sponsored by GSK.

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Figure legends

Fig 1 Characterization of CoWas mice

(A) WASp expression was evaluated in different cell types in peripheral blood of 6 weeks old WT, WKO, CoWas and CoWas$^{+/-}$ mice. (B) Graph shows the percentage of WASp^{+} PLTs in different mouse models at 8-12 weeks of age. Hemogram analysis of WT, WKO, CoWas and CoWas$^{+/-}$ mice shows PLT counts (C) and Mean Platelet Volume (MPV) (D). (E) Representative transmission electron microscopy (TEM) images of PLTs isolated from peripheral blood of WT, WKO and CoWas mice. The perimeter and area were measured by using the ImageJ Software (F, left panel), as well as the number of alpha-granules (F, right panel). Dense-granules were evaluated using mepacrine and analysed by flow cytometry (F, right panel). In graphs B-D each dot represents a different mouse from two independent experiments; in graph F each dot represents the analysis of single platelet within different TEM images. All the graphs report Mean ± SD and the statistical analysis was performed with One-way ANOVA and Bonferroni post-correction test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Fig 2 Phenotypical and functional characterization of megakaryocytic compartment

(A) Evaluation of megakaryocyte progenitors (MkP) identified as CD41^{+}CD150^{+} cells gated on Lin^{-}cKit^{+}Sca1^{-} compartment in WT, WKO and CoWas mice is shown. (B) The number of CFU-Mks colonies was counted at microscope using a 4x objective. (C) Megakaryocytes (CD61^{+}CD41^{+} cells) are expressed as percentage on total BM cells (C) or absolute number (D) and analysed in the bone marrow of age-matched WT, WKO and CoWas mice. (E) The percentage of RT-PLTs is assessed using Thiazole-Orange (TO). (F) Platelet depletion was performed by i.v. injection of anti-mouse GPIb alpha (Emfret) according to the scheme indicated in the figure. (G) PLT counts was monitored daily by blood collection and expressed as percentage of the initial PLT counts at time 0 at different time points.

In all graphs each dot represents a different mouse from one (A), two (G), four (E) or six (B, C and D) independent experiments; all the graphs report Mean ± SD and the statistical analysis was performed with One-way ANOVA (A to E) or with Two-way ANOVA (G) and Bonferroni post-correction test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Fig 3 Peripheral elimination of PLTs

(A) Experimental plan of the *in vivo* PLTs half-life detection. (B) PLTs half-life was analysed as the percentage (%) of GPIb-V-IX^{+}-PLTs 15 minutes after the injection (time 0) and at different time points post-injection. (C) Differentially labelled WT and *Was*$^{-/-}$ PLTs have been mixed in a 30%:70% ratio and injected into recipients. Was$^{-/-}$ PLTs isolated from WKO has been transferred to WKO (left panels) while *Was*$^{-/-}$ PLTs isolated form CoWas have been transferred into CoWas (right panels) (n=5). (D) PLT counts have been evaluated before Clodronate Liposomes injection (T0) and after 7 days (T7). (E) Apoptotic PLTs are expressed as Annexin-V^{+}-PLTs. (F) sCD62P (ng/ml) plasma level is shown (n=10). (G) The graph shows CD62P^{+}-PLTs evaluated by flow cytometry and expressed as percentage of the total PLTs population.

In all graphs each dot represents a different mouse from one (C), two (E and F), three (B and G) or six (D) independent experiments. All graphs report Mean ± SD; graph C reports Mean ± SEM. Statistical analysis has been performed with One-way ANOVA (D to F) or Two-way ANOVA (B and C) and Bonferroni post-correction test. Graph G reports Mean ± SD and has been analysed with Mann-Whitney test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Fig 4 Proteins identified by Proteomic Analysis

Venn diagram of proteins identified in the different PLTs conditions. The number of total proteins identified is 1104 in WT samples, 1017 and 979 in WKO and CoWas samples respectively. Six hundred and eighty-six proteins (corresponding to the 46% of the total protein identified) are shared between mutant and WT animals.

Fig 5 Different proteomic profile between WT and Was$^{-/-}$ platelets

(A) Focus on the main biological processes identified during proteomic analysis. Proposed clusters were selected by BINGO Cytoscape plugin ($P \leq 0.05$) and colour gradient correspond to the normalized average Spectral Count (aSpC) (0-100), where red indicates up-regulated proteins, blue down-regulated and shade between red and blue indicates intermediate level of expression. (B) The graph shows the CD47 MFI on the CD61^{+}-PLTs subpopulation. Statistical analysis has been performed with Unpaired t-test; each dot represents a mouse.

Fig 6 Interaction between platelets and B-cells mediated by CD40L

(A) PLT counts from age matched WT, WKO, Rag1$^{-/-}$ and WKO-Rag1$^{-/-}$ mice is shown. (B) Evaluation of IgG anti-PLTs auto-antibodies. ELISA plates we coated with total protein lysate from WT or *Was*$^{-/-}$ PLTs and incubated with sera according to the grid presented (n=23). (C) The graph represents the percentage of mice positive for the anti-dsDNA autoAbs. (D) The percentage of CD40L^{+} PLTs has been evaluated by flow cytometry before (n=10) and after stimulation (n=12) with thrombin (1U/ml) (left side); the soluble form of CD40L (sCD40L) has been measured in the PPP from unwashed PLTs isolated from WT (n=16), WKO (n=16), CoWAS (n=5) (right side). (E) Resting B-cells (CD43^{-} cells) isolated from the spleen of WT, WKO and CoWas mice have been kept in culture for 72 hours with PPP and analysed by flow cytometry for CD69 expression as activation marker.

In graph A each dot represents a different mouse and Mean ± SD is reported. In graph B, D and E, the Mean ± SD reported is the results of two (B) and 4 (D) independent experiments. The statistic analysis was performed with One-way ANOVA test and Bonferroni post-correction test (A, B, D left panel). In Graph D, sCD40L level (right side of the panel) is analysed with Mann-Whitney test, as well as graph D. Graph C has been analysed statistically with the Chi-square test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Fig 7 Activation profile of Human PLTs

(A-B) Activation profile of human PLTs expressed as Mean Fluorescence Intensity (MFI) ratio of activation markers and CD61 MFI (Fig A for CD62P and Fig B for PAC1). We assigned to the unstimulated adult HD (HDa) a value of 100 and we normalized the patients accordingly. In panel A we analysed 4 patients (3 WAS and 1 XLT) and 7 HDs; in panel B we analysed 3 patients (2 WAS and 1 XLT) and 5 HDs. (C) The level of sCD40L in the plasma of WAS/XLT patients has been analysed by ELISA assay. WAS/XLT patients have been divided according to the presence or absence of autoantibodies or other clinical signs related to autoimmunity (refer to Supplementary Table3). Pediatric HDs (HDp) have been tested as controls.

Graph A and B report Mean and are analysed with Mann-Whitney test; Graph C report Mean ± SD and is analysed with One-way ANOVA test and Bonferroni post-correction test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Fig 1: Characterization of CoWas mice

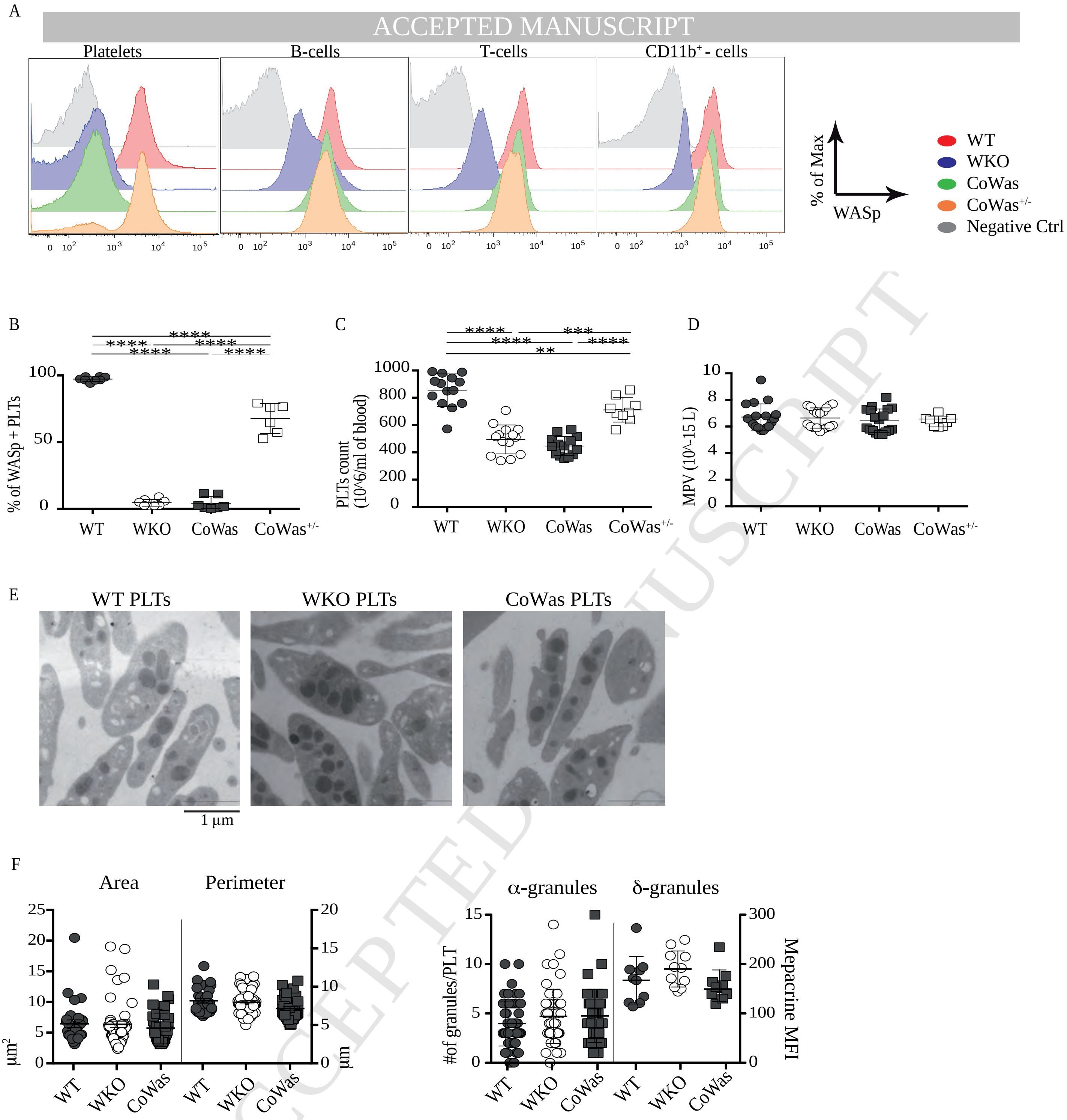


Fig 2: Phenotypical and functional characterization of megakaryocytic compartment

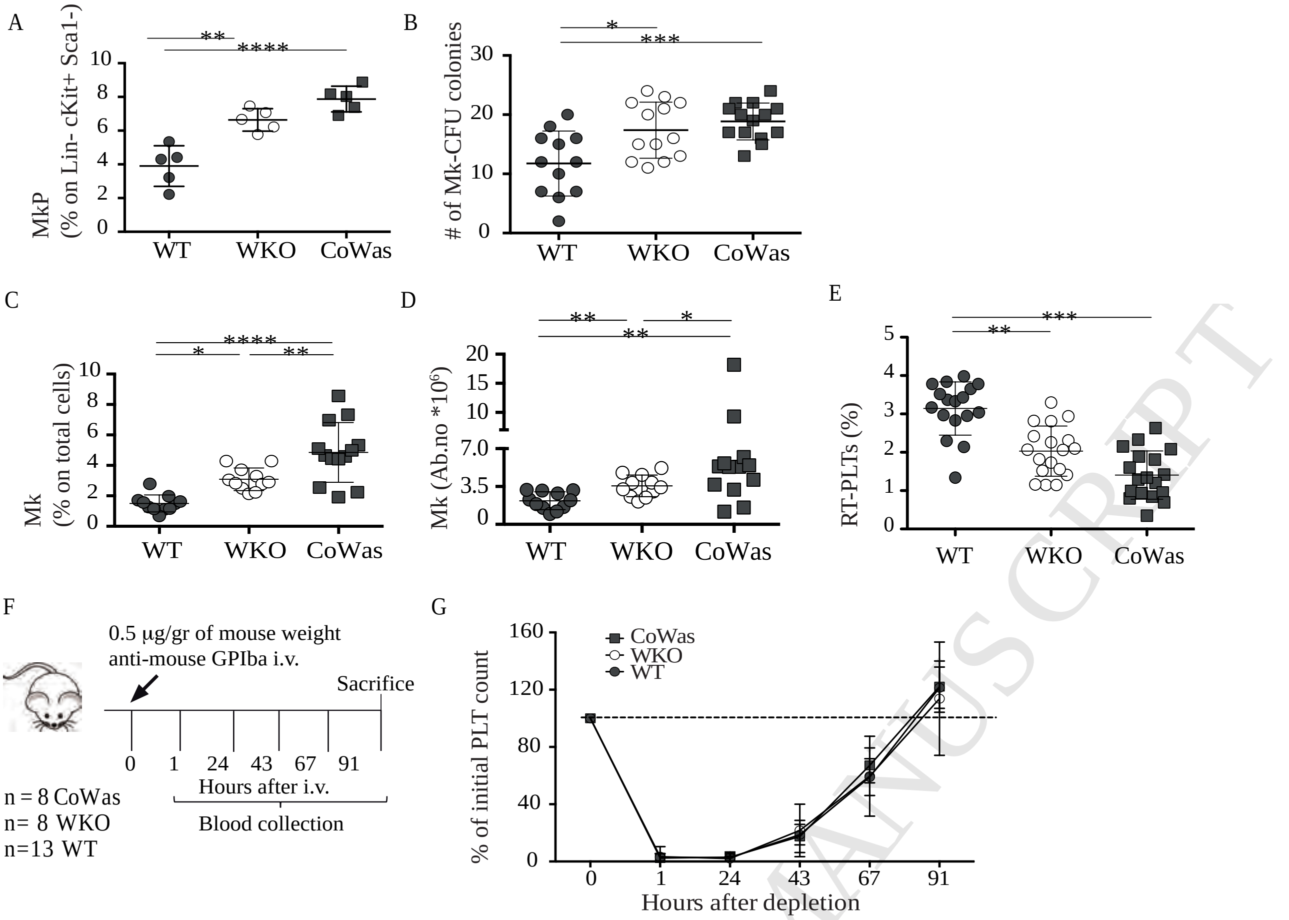


Fig 3: Peripheral elimination of PLTs

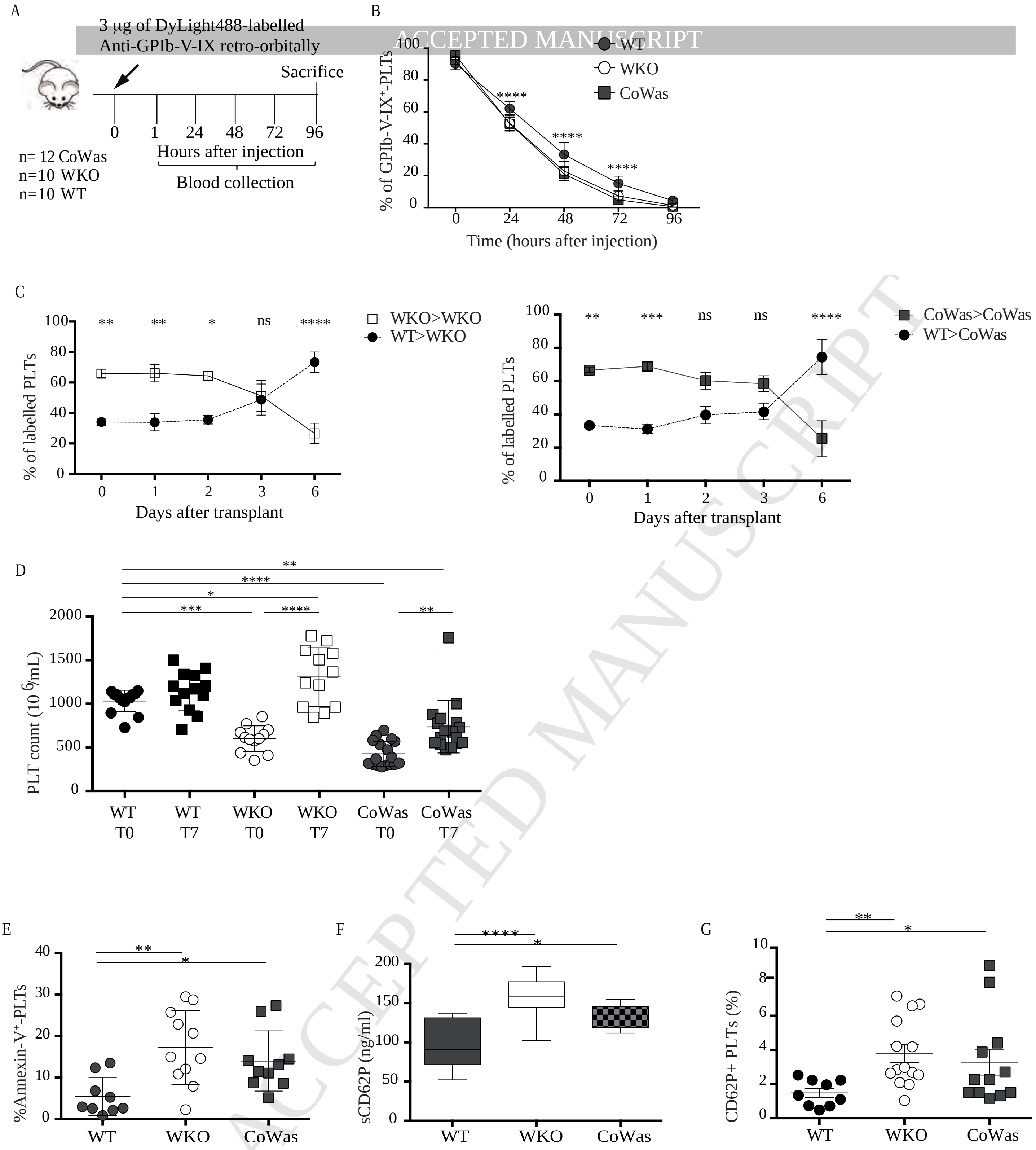


Fig 4: Proteins identified by Proteomic Analysis

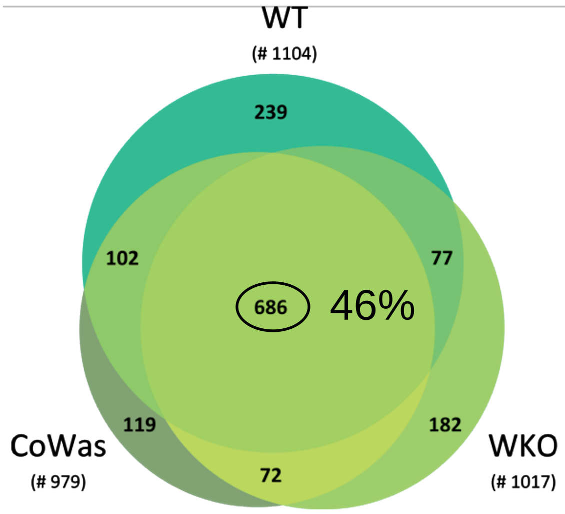


Fig 5: Different proteomic profile between WT and Was-/- platelets

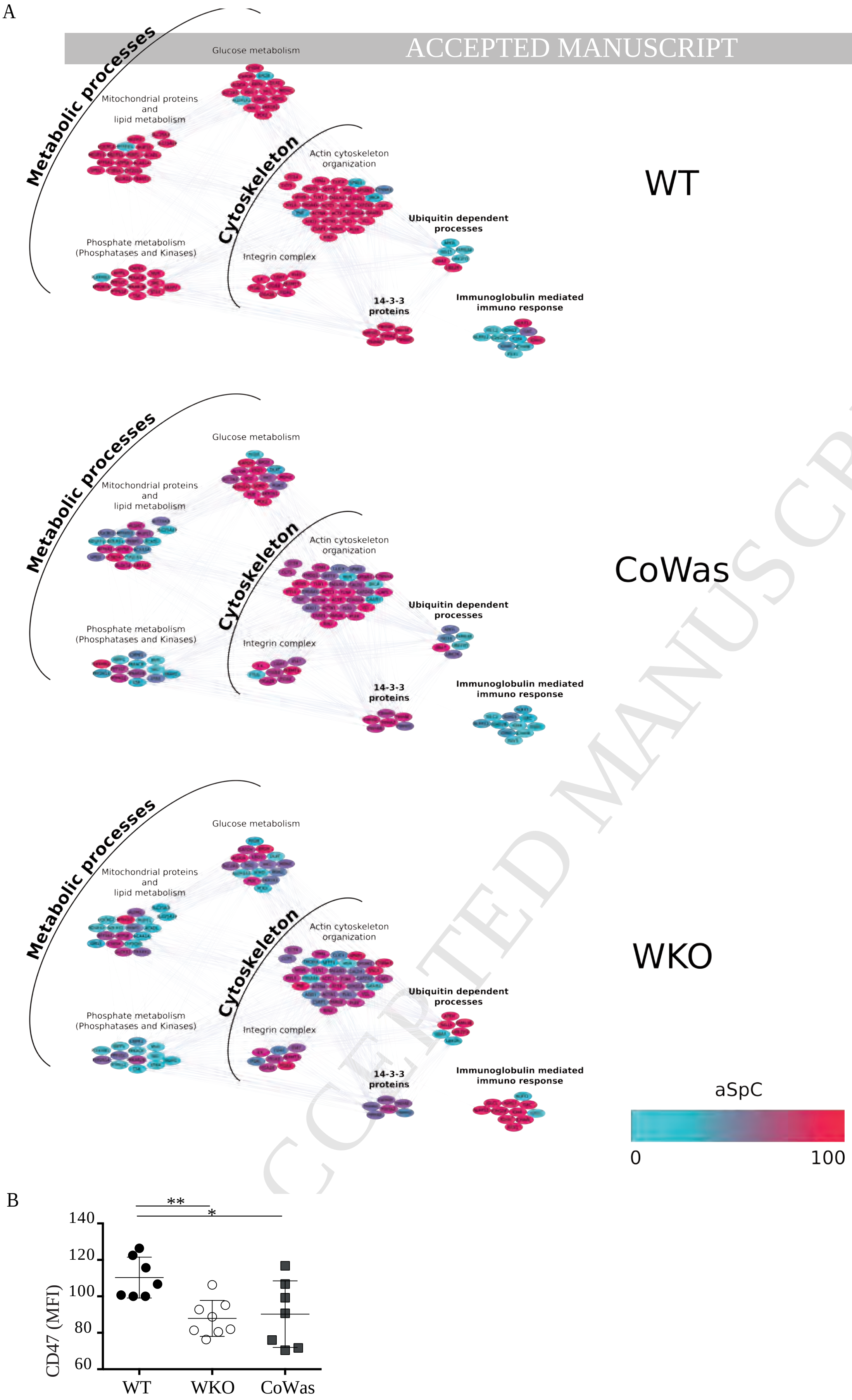
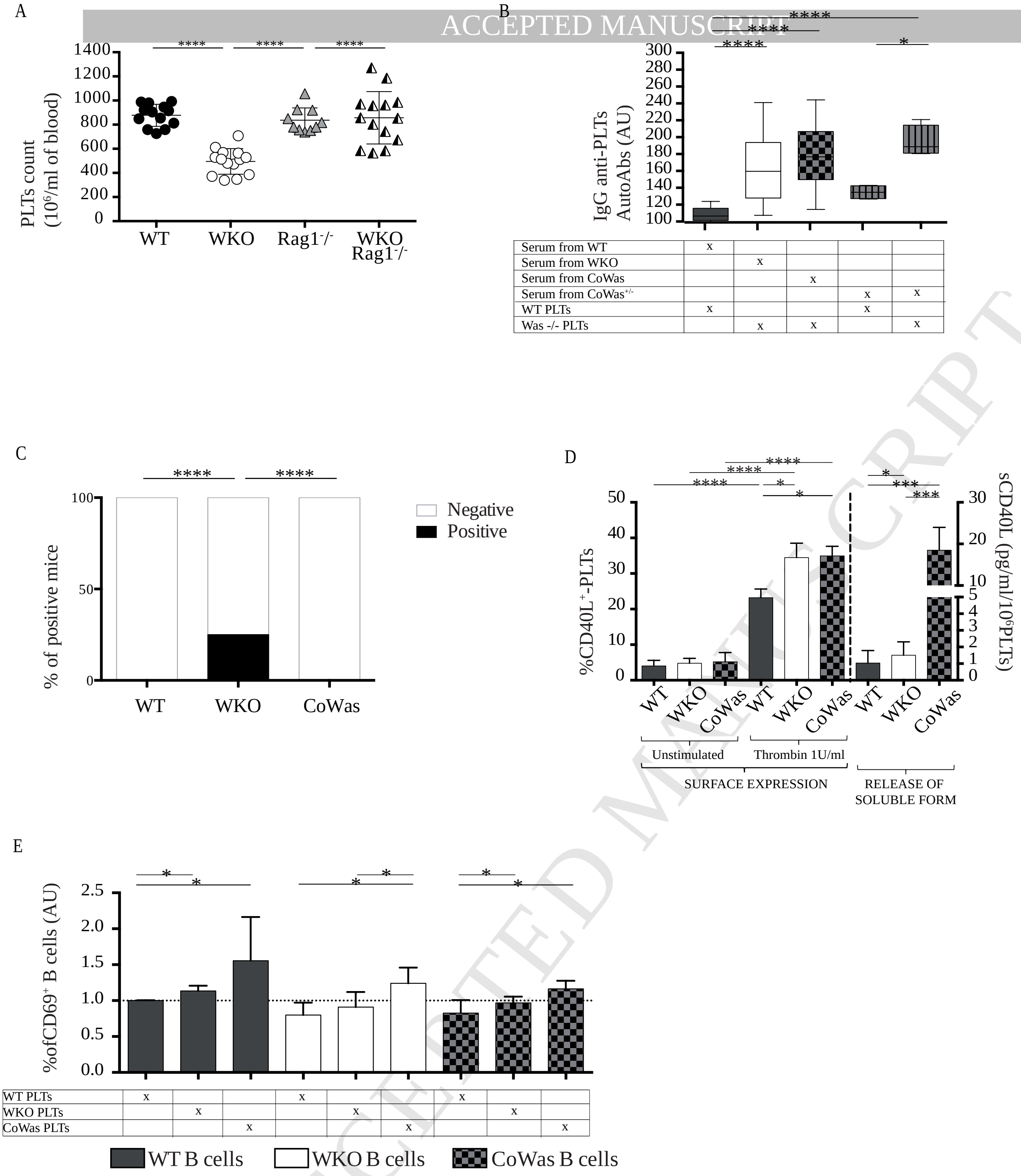


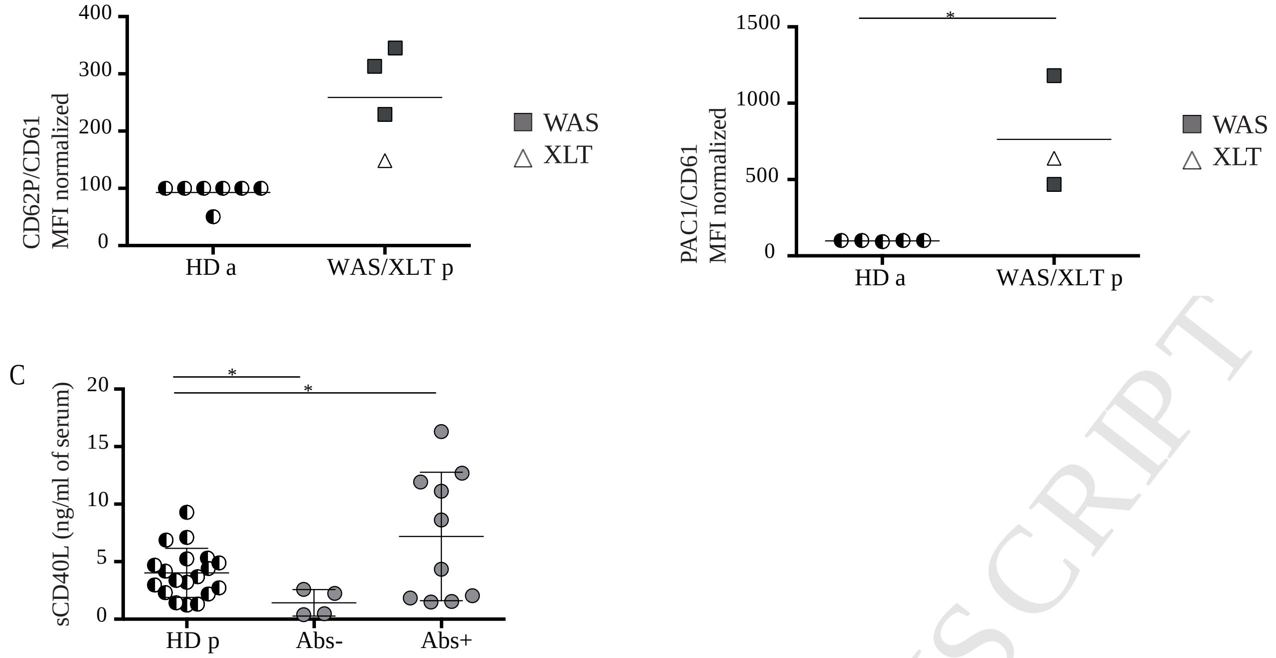
Fig 6: Interaction between platelets and B cells mediated by CD40L



Serum from WT	x				
Serum from WKO		x			
Serum from CoWas			x		
Serum from CoWas$^{+/-}$				x	x
WT PLTs	x			x	
Was -/- PLTs		x	x		x

WT PLTs	x			x			x		
WKO PLTs		x			x			x	
CoWas PLTs			x			x			x

Fig 7: Activation profile of Human PLTs



Supplementary Materials:

Supplementary Materials and Methods

Mice genotyping

Mice were genotyped by PCR on genomic DNA. To amplify *Was* floxed gene, we used SDL1-Forward GCACCTGGAGCCTTAGATTCAACCC and SDL1-Reverse CAGCCTTGCTCTAGTCGGACACTG primers. To evaluate Pf4-Cre expression, genomic DNA was amplified according to the Jackson Laboratories Inc. protocol using the following primers: PF4-Forward CCCATACAGCACACCTTTTG and PF4-Reverse TGCACAGTCAGCAGGTT. Mice have been analysed at 8-12 weeks of age, unless otherwise stated, and have been age-matched in all experiments.

Ploidy distribution

Total bone marrow cells were collected in Mixing Medium (PBS 5% FBS and Tyrode's Buffer pH 6.8 in 1:1 ratio) and counted. Five millions of cells were resuspended in 1 ml of Mixing Medium and incubated with Hoechst 33342 (Life Technologies) at the final concentration of 10 μg/ml at 37 °C for 2 hours. After a washing step, cells were labelled with anti-CD61 and anti-CD41 for 30 minutes on ice. Ploidy distribution was analysed with a FACS Canto II.

Evaluation of proplatelets formation by MKs

Lineage negative cells were isolated and resuspended in Iscove's Modified Dulbecco's Medium (IMDM) (Sigma) supplemented with 0.8% Penicillin/Streptomycin (Gibco, Carlsbad, CA), 62 μM α-thioglycerol (Sigma), 1.5% BSA (Cohn Fraction V, Sigma A-4503), 0.05% Sodium hydrogen carbonate (Gibco), 1% Insulin/Transferrin/Selenium supplement (Gibco), and 2%

lyposomes. Cells were cultured with 10ng/ml recombinant murine TPO (PeproTech) for 4 days. Proplatelet formation was evaluated in triplicate wells by immunofluorescence using DAPI and anti-CD41 (M148); ratio of number of MKs with proplatelets and total number of MKs were calculated.

Proteomic analysis

Enzymatic digestion was conducted by adding trypsin in a ratio 1:50 (w/w) o/n and then a further aliquot in a ratio 1:100 (w/w) was added for 4 h. Each peptide mixture was desalted by Pep-Clean C-18 spin columns (Pierce Biotechnology Inc., Rockford, IL, USA), concentrated at 60°C and finally reconstituted in 0.1% formic acid. Globally, 3 biological samples per condition were analyzed in technical replicates (n=2) by LC-MS/MS label-free method. In particular, the chromatographic separation of peptides was performed using the Eksigent nanoLC-Ultra® 2D System (Eksigent, part of SCIEX Dublin, CA, USA) combined with cHiPLC®- nanoflex system (Eksigent) in trap-elute mode. Peptides were eluted in 100 min with an acetonitrile gradient (mobile phase A: 0.1% formic acid in water; mobile phase A: 0.1% formic acid in acetonitrile), ionized by a nanospray ionization source (EASY-Spray^{TM} Source, Thermo Fisher Scientific, San Josè, CA, USA) and analyzed using QExactive mass spectrometer (Thermo Fisher Scientific, San Josè, CA, USA). Full mass spectra were recorded in positive ion mode in a range of 400-1600 m/z, with a resolution of 70000 FWHM (@ m/z 200) and 1 microscan per second. Each full scan was followed by 7 MS/MS events (resolution of 17,500 FWHM) generated in a data dependent manner on the top seven most abundant isotope patterns with charge ≥ 2 (isolation window of 2 m/z from the survey scan, normalized collision energy of 30 and dynamic exclusion of 30 sec). Proteomics Data Processing and Protein-protein interaction network reconstruction are described in the Supplemental Materials.

Proteomics Data Processing

The experimental tandem mass spectra (MS/MS) produced by LC-MS/MS analysis were matched against the *in-silico* tryptic peptide sequences of the *Mus musculus* protein database (50715 entries) retrieved from UNIPROT (*www.uniprot.org*) on April 2016. Data processing was performed by Discoverer 1.4 software, based on SEQUEST algorithm [1]. Matches between spectra were only retained if they had a minimum Xcorr of 2.0 for +1, 2.5 for +2 and 3.5 for +3 charge state, respectively, protein rank was fixed to 1 while peptide confidence to "*high*". In addition, the FDR was set to < 5%.

The spectral count (SpC) values of the proteins identified were normalized using a Total Signal normalization method [2] (see Supplementary text) and compared by a label-free quantification approach as previously reported [3]. Specifically, protein lists were aligned and then processed by means of Linear Discriminant Analysis (LDA) [4]. A matrix *mxn* consisting of 1300 proteins and 18 samples grouped into three categories (WT, n=6; CoWas, n=6; WKO, n=6) was considered. LDA was applied by using a common covariance matrix for all groups, and the Mahalanobis distance [5] from each point to each group's multivariate mean. To select proteins discriminating the analyzed conditions (WT, CoWas and WKO), we considered those with smallest P-value (≤ 0.05) and F ratio ≥ 3.5. The average Spectral Count (aSpC) values of proteins selected by LDA were pairwise compared by DAve and DCI index of MAProMa software [6] (see Supplementary text); in addition, the fold change was estimated by the natural logarithm of the SpC ratio (SpC_1/SpC_2); the fold change of proteins identified exclusively in one of the two compared conditions was set to +100 [3]. Finally, proteins selected by LDA were evaluated by hierarchical clustering [7] using the Euclidean's distance metric and Complete method.

Protein-protein interaction network reconstruction

Proteins selected by LDA were evaluated at functional level and a corresponding *Mus musculus* protein-protein (PPI) interaction network (219 nodes and 2138 edges) was reconstructed by retrieving interaction from STRING db [8]; only interactions experimentally determined or database annotated were considered. To retrieve and visualize interactions, Cytoscape software was used [9], while Cytoscape plugin BINGO 2.44 [10] allowed to evaluate the most represented GO terms (GO Biological Processes, GO Molecular Functions, GO Cellular Component); specifically, *Mus musculus* organism, hypergeometric test, Benjamini & Hochberg FDR correction and a significance level ≤0.05 were applied.

Total signal normalization method

Given two or more sample S_1, S_2...S_i, and T_1, T_2...T_j the respective sum of SpC for all proteins identified, the goal is to obtain

$$\mathbf{T_1 = T_2 \ldots\ldots = T_j}$$

Therefore, normalization of SpC_{ij} was obtained as follows:

$$\mathbf{nSpC_{ij} = SpC_{ij}/T_j}$$

where T_j is the value obtained by summing SpC value of all proteins belonging to the same list.

Label-free quantitation

DAve and DCI evaluation

Based on a direct correlation between SpC and the relative abundance of the identified proteins (*106*) DAve and DCI indices were used to process the average spectral count (aSpC) corresponding to each analysed platelets conditions (WT, CoWas, WKO). The analysed conditions were pairwise compared (WT vs CoWas, WT vs WKO, CoWas vs WKO).

In detail, DAve, which evaluates changes in protein expression, was defined as:

$$(X-Y)/(X+Y)/0.5$$

while DCI, which evaluates the confidence of differential expression, was defined as:

$$(X+Y)*(X-Y)/2$$

where X and Y represent the aSpC of a given protein in two compared samples. In addition, the DAve value of proteins identified exclusively in one of the two compared samples was set to +2.

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Supplemental Figures and Tables Legends

Supplemental Fig 1: Establishment of CoWas colony

(A) The breeding strategy to establish the colony of conditional mice is shown. (B) Agarose gel with PCR products to screen Complete Was$^{fl/fl}$ ♀ or Was$^{fl/y}$ ♂ mice, Heterozygous ♀ mice Was$^{fl/wt}$ or WT mice. (C) Schematic representation of the genomic organization in the segments amplified by PCR. The two primers SLD1 and SLD2 amplify the region encompassing the *loxP* site on the WAS gene (top panel); if the primers amplify a region containing the *loxP* site, the PCR product is 220 bp while in absence of this site (WT mice) the amplified band is 155 bp. Pf4-Fwd and Pf4-Rev primers amplify the region comprising Pf4 promoter and Cre recombinase gene that substitutes the first exon of Pf4 gene (bottom panel). The presence of the Cre gene produces a 450 bp amplicon. (D) MFI of surface gycoproteins (CD41 on the left, CD61 center and CD36 on the right) was analysed by flow cytometry on PRP.

Supplemental Fig 2: Was-/- MKs show no defect in pro-PLTs production

(A) The frequency on live cells of Megakaryocyte–erythroid progenitor (MEP) (left; CD34^{++}CD38^{++}CD41^{++}CD42^{-}CD61^{-} cells), Megakaryoblasts (center; CD34$^{-/+}$CD38$^{-/+}$CD41^{+}CD42^{-}CD61^{+} cells) and Promegakaryocytes (right; CD34^{-}CD38^{+}CD41^{+}CD42$^{-/+}$CD61^{+} cells), are shown. (B) Ploidy distribution of MKs (CD41^{+} CD61^{+} cells) is shown. The data are reported as percentage of MKs with different DNA quantity on the total MK population (n=7). (C) Analysis of pro-PLTs formation from WT or Was$^{-/-}$ MKs is shown (n=12). (D) Representative images for a MK not producing pro-PLTs (left) and pro-PLTs producing MKs (right) are shown. The top panels show DAPI staining; the central panels show the CD41 staining and the bottom panels show the merge between the two. Images showing pro-PLTs producing MKs in WT and WKO mice are also showed. (E) Raw data from the *in vitro* pro-PLT production experiments are reported in the table. For each experiments (1 to 4) 3 WT and 3 WKO mice have been analysed. The table reports the total number of MKs, as well as the total number and the relative percentage of pro-PLTs producing MKs for each animal analysed. These raw data have been plotted in Graph C. (F) The graph reports the number of MKs (CD41$^+$ CD61$^+$ cells) in WT animals treated with PBS or anti-GPIb Ab (0.5 μg/gr of mouse weight) and sacrificed 18 hours after the injection. (G) The graph reports the percentage of RT-PLTs (Thiazole$^+$) on total PLTs population in WT, WKO and CoWas mice treated with anti-GPIb Ab (0.5 μg/gr of mouse weight) during time (n=5). In graph A, each dot represents a mouse. Graphs B and C are the result of 2 (B) and 4 (C) independent experiments.

Graphs A, C and F report Mean ± SD and is analysed with unpaired t-test. Graph B and G report Mean ± SD and the statistical analysis is performed using Ordinary Two-way ANOVA test (****P<0,0001; ***P<0,001; **P<0,005; *P<0,05).

Supplemental Fig 3: PLTs from mutant mice show a different proteomic profile

2-D maps (Log[MW] vs pI) of proteins identified in WT (A), CoWas (B) and WKO (C) conditions. A color/shape code is assigned to each protein according to the corresponding SEQUEST score value. Proteins with score>10 are shown as red/circle, proteins with 2≤score≤10 are shown as blue/square, and proteins with score<2 are shown as yellow/triangle code. (D) Hierarchical clustering obtained by processing the aSpC of proteins selected by linear discriminant analysis (n=221); Euclidean's distance and Complete method were applied. The heat map is related to the normalized aSpC and indicates down (blue) and up-regulated (red) proteins, respectively.

Supplemental Fig 4: Total pathways identified by proteomic analysis

Mus musculus protein-protein interaction network by considering proteins differentially expressed (Supplementary Table 2). The network was reconstructed by retrieving interaction from STRING db and only physical and database annotated interactions were retained. Functional groups (or clusters) were selected by BINGO Cytoscape plugin (P≤0.05). Node colour gradient corresponds to the normalized aSpC (0-100).

Supplemental Table 1: List of proteins identified in PLTs samples

List of proteins identified in PLTs samples (WT, WKO and CoWas; each n=6). For each protein identified are shown the following parameters: Uniprot ID, Reference, Isoelectric point (pI), Molecular Weight (MW), aSpC, average Score (aScore).

Supplemental Table 2. List of proteins classified as differentially expressed

For each protein the following parameters are shown: Uniprot ID, Gene Name, Reference, aSpC (n=6), Normalized aSpC, F ratio and P-value by Linear Discriminant Analysis (LDA), fold change and DAve-DCI index calculeted by MAProMa software. Proteins were selected by LDA (P-value ≤0.05; F ratio ≥3.5). For each pairwise comparison (WT vs WKO; WT vs CoWas; CoWas vs WKO) fold change value >|0.15| and DAve value >|0.2| were considered.

Supplemental Table 3: Clinical characteristic of WAS and XLT patients analysed

The Table reports all the patients analysed in Figure 7 (panel A-C). For each patient, patient ID, age at analysis, presence of auto-antibodies or other clinical characteristics related to autoimmunity have been analysed in Brescia (Ospedali Civili), Milan (Laboraf, San Raffalele Hospital) and Bethesda (National Institute of Health) according to their standard internal procedures and are reported in the table. In particular, anti-PLTs autoantibodies have been tested using agglutination assay in solid phase on plasma samples (Immucor) or a platelet-associated antibody direct assay by flow cytometry (Arup Laboratories). The last column shows the amount of sCD40L in the plasma of each patient assessed by ELISA test and plotted in Figure 7 panel C. Some patients (indicated with * and §) have been already described in literature.

The first four patients (WAS59, WASHE02, WASHE03, XLT71) have been analysed not only for sCD40L level, but also for the expression of activation markers (Figure 7 Panel A and B).

				WT			WKO			CoWas		
Uniprot ID	**Reference**	**pI**	**MW**	**aSpC**	**aScore**	**Frequency**	**aSpC**	**aScore**	**Frequency**	**aSpC**	**aScore**	**Frequency**
A0A075B5J0	Protein Trbv26 OS=Mus musculus GN=Trbv26 PE=4 SV=6 - [A0A075B5J0_MOUSE]	8.3	13	1.8	5.35	4	1.5	4.58	4	1.5	4.35	4
A0A075B5M7	Protein Igkv5-39 OS=Mus musculus GN=Igkv5-39 PE=1 SV=6 - [A0A075B5M7_MOUSE]	6.3	10	0.0	0.00	0	1.0	2.41	1	0.0	0.00	0
A0A075B5N9	Protein Igkv3-7 OS=Mus musculus GN=Igkv3-7 PE=4 SV=6 - [A0A075B5N9_MOUSE]	6.3	11	1.0	3.70	2	2.0	8.79	2	1.0	4.06	1
A0A075B5P3	Protein Ighg2b (Fragment) OS=Mus musculus GN=Ighg2b PE=1 SV=1 - [A0A075B5P3_MOUSE]	7.4	37	0.0	0.00	0	7.3	23.08	6	4.3	13.69	3
A0A075B5P4	Ig gamma-1 chain C region secreted form (Fragment) OS=Mus musculus GN=Ighg1 PE=1 SV=1 - [A0A075B5P4_	7.4	36	4.0	10.86	6	4.3	11.16	6	2.0	4.75	5
A0A075B5P5	Protein Ighg3 (Fragment) OS=Mus musculus GN=Ighg3 PE=4 SV=1 - [A0A075B5P5_MOUSE]	8.3	36	1.3	3.75	4	3.5	10.44	6	2.5	7.35	4
A0A075B5U4	Protein Ighv1-18 OS=Mus musculus GN=Ighv1-18 PE=1 SV=1 - [A0A075B5U4_MOUSE]	8.7	11	0.0	0.00	0	1.0	2.78	2	0.0	0.00	0
A0A075B5V1	Protein Ighv1-31 OS=Mus musculus GN=Ighv1-31 PE=4 SV=1 - [A0A075B5V1_MOUSE]	8.7	11	0.0	0.00	0	1.0	3.30	2	0.0	0.00	0
A0A075B5V8	Protein Ighv1-47 OS=Mus musculus GN=Ighv1-47 PE=4 SV=1 - [A0A075B5V8_MOUSE]	8.4	11	2.5	6.98	2	0.0	0.00	0	0.0	0.00	0
A0A075B5Y4	Protein Ighv1-81 (Fragment) OS=Mus musculus GN=Ighv1-81 PE=4 SV=1 - [A0A075B5Y4_MOUSE]	8.8	13	0.0	0.00	0	1.0	2.72	1	0.0	0.00	0
A0A075B663	Protein Iglv1 (Fragment) OS=Mus musculus GN=Iglv1 PE=4 SV=1 - [A0A075B663_MOUSE]	5.2	12	0.0	0.00	0	1.0	3.55	3	0.0	0.00	0
A0A075B6A3	Protein Igha (Fragment) OS=Mus musculus GN=Igha PE=1 SV=1 - [A0A075B6A3_MOUSE]	5.2	37	2.0	6.09	1	1.8	5.54	4	0.0	0.00	0
A0A087WNQ6	SAM and SH3 domain-containing protein 3 (Fragment) OS=Mus musculus GN=Sly PE=4 SV=1 - [A0A087WNQ6_MO	9.0	13	1.0	2.60	3	1.0	2.51	1	1.0	2.50	3
A0A087WP81	Ubiquitin carboxyl-terminal hydrolase isozyme L5 (Fragment) OS=Mus musculus GN=Uchl5 PE=1 SV=1 - [A0	4.8	26	1.0	3.18	3	1.7	5.21	3	1.0	3.10	4
A0A087WPH7	26S protease regulatory subunit 6A (Fragment) OS=Mus musculus GN=Psmc3 PE=1 SV=5 - [A0A087WPH7_MOUSE	5.0	34	1.0	2.20	1	1.0	2.39	1	1.0	2.45	2
A0A087WQR0	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (Fragment) OS=Mus musculus GN=Ndufs1 PE	9.1	13	1.0	2.70	1	0.0	0.00	0	1.0	2.45	1
A0A087WQX0	Dual serine/threonine and tyrosine protein kinase (Fragment) OS=Mus musculus GN=Dstyk PE=1 SV=5 - [A	5.2	25	2.0	4.34	1	0.0	0.00	0	0.0	0.00	0
A0A087WR38	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial (Fragment) OS=Mus muscu	4.8	10	2.0	5.79	1	1.0	2.83	3	1.3	3.73	3
A0A087WRM4	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Mus musculus GN=Idh1 PE=1 SV=1 - [A0A087WR	5.0	10	1.0	3.16	1	0.0	0.00	0	1.0	3.08	1
A0A087WRY3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Mus musculus GN=Nucks1 PE=1 SV=	5.1	26	0.0	0.00	0	1.0	2.07	2	1.0	2.07	2
A0A087WS07	Solute carrier family 26 member 6 (Fragment) OS=Mus musculus GN=Slc26a6 PE=1 SV=5 - [A0A087WS07_MOUS	9.1	69	1.0	2.46	1	0.0	0.00	0	0.0	0.00	0
A0A087WS31	Aspartyl aminopeptidase (Fragment) OS=Mus musculus GN=Dnpep PE=1 SV=1 - [A0A087WS31_MOUSE]	9.4	25	0.0	0.00	0	1.0	2.83	1	2.0	6.21	2
A0A087WS46	Elongation factor 1-beta OS=Mus musculus GN=Eef1b2 PE=1 SV=1 - [A0A087WS46_MOUSE]	4.6	20	7.5	27.38	6	6.5	21.74	6	6.5	21.66	6
A0A087WSE4	TAR DNA-binding protein 43 (Fragment) OS=Mus musculus GN=Tardbp PE=1 SV=1 - [A0A087WSE4_MOUSE]	5.6	17	0.0	0.00	0	1.0	2.21	1	0.0	0.00	0
A0A087WSG8	Mucin-2 (Fragment) OS=Mus musculus GN=Muc2 PE=1 SV=1 - [A0A087WSG8_MOUSE]	5.9	98	0.0	0.00	0	1.0	3.11	1	0.0	0.00	0
A0A087WSL1	Mortality factor 4-like protein 1 OS=Mus musculus GN=Morf4l1 PE=4 SV=1 - [A0A087WSL1_MOUSE]	10.0	6	0.0	0.00	0	0.0	0.00	0	1.0	2.53	1
A0A087WSN7	MAP kinase-activated protein kinase 2 (Fragment) OS=Mus musculus GN=Mapkapk2 PE=1 SV=1 - [A0A087WSN7	6.3	19	0.0	0.00	0	1.0	3.21	1	0.0	0.00	0
A0A087WSS7	Solute carrier family 26 member 9 OS=Mus musculus GN=Slc26a9 PE=4 SV=1 - [A0A087WSS7_MOUSE]	8.5	52	0.0	0.00	0	0.0	0.00	0	1.0	2.38	1
A0A0A0MQG7	Uroporphyrinogen decarboxylase (Fragment) OS=Mus musculus GN=Urod PE=1 SV=1 - [A0A0A0MQG7_MOUSE]	9.5	13	0.0	0.00	0	1.0	3.12	2	0.0	0.00	0
A0A0A0MQI9	F-actin-capping protein subunit beta (Fragment) OS=Mus musculus GN=Capzb PE=1 SV=5 - [A0A0A0MQI9_MOU	4.7	13	3.8	11.43	4	2.5	6.92	4	2.3	6.63	6
A0A0A0MQM0	Eukaryotic translation initiation factor 5A (Fragment) OS=Mus musculus GN=Eif5a PE=1 SV=1 - [A0A0A0M	5.0	16	3.5	11.91	2	2.5	7.99	2	1.0	2.58	1
A0A0A0MQM3	NADH-cytochrome b5 reductase 3 (Fragment) OS=Mus musculus GN=Cyb5r3 PE=1 SV=5 - [A0A0A0MQM3_MOUSE	9.7	16	0.0	0.00	0	3.7	13.05	3	4.0	14.05	2
A0A0A6YVP8	Complement factor H OS=Mus musculus GN=Cfh PE=1 SV=1 - [A0A0A6YVP8_MOUSE]	8.0	80	1.0	3.85	2	1.0	4.40	2	1.3	5.23	3
A0A0A6YVU7	Filaggrin OS=Mus musculus GN=Flg PE=1 SV=1 - [A0A0A6YVU7_MOUSE]	10.9	27	0.0	0.00	0	0.0	0.00	0	1.0	3.53	2
A0A0A6YW07	Inositol monophosphatase 1 OS=Mus musculus GN=Impa1 PE=1 SV=1 - [A0A0A6YW07_MOUSE]	5.0	24	0.0	0.00	0	0.0	0.00	0	1.0	2.79	1
A0A0A6YWA9	Guanine nucleotide-binding protein G(i) subunit alpha-2 (Fragment) OS=Mus musculus GN=Gnai2 PE=1 SV=	5.9	18	4.0	12.90	3	3.7	11.74	6	3.8	11.79	6
A0A0A6YWD3	Protein lin-9 homolog (Fragment) OS=Mus musculus GN=Lin9 PE=1 SV=1 - [A0A0A6YWD3_MOUSE]	9.0	59	4.5	10.40	2	4.0	9.10	2	2.0	4.60	1
A0A0A6YWJ1	Transforming protein RhoA (Fragment) OS=Mus musculus GN=Rhoa PE=3 SV=1 - [A0A0A6YWJ1_MOUSE]	4.4	7	2.0	5.70	1	0.0	0.00	0	0.0	0.00	0
A0A0A6YWT1	Formin-binding protein 1 (Fragment) OS=Mus musculus GN=Fnbp1 PE=1 SV=1 - [A0A0A6YWT1_MOUSE]	5.8	40	1.0	2.14	1	1.0	2.53	1	0.0	0.00	0
A0A0A6YXC8	Protein enabled homolog OS=Mus musculus GN=Enah PE=1 SV=1 - [A0A0A6YXC8_MOUSE]	8.0	58	1.0	2.62	2	0.0	0.00	0	0.0	0.00	0
A0A0A6YXX2	Semaphorin-3F (Fragment) OS=Mus musculus GN=Sema3f PE=1 SV=1 - [A0A0A6YXX2_MOUSE]	8.8	13	0.0	0.00	0	1.0	3.05	1	0.0	0.00	0
A0A0A6YY34	Glutathione peroxidase OS=Mus musculus GN=Gpx1 PE=1 SV=1 - [A0A0A6YY34_MOUSE]	7.3	16	1.3	2.81	4	2.0	4.98	5	1.5	3.88	4
A0A0A6YY53	Protein Ighg2c (Fragment) OS=Mus musculus GN=Ighg2c PE=1 SV=1 - [A0A0A6YY53_MOUSE]	8.0	36	0.0	0.00	0	0.0	0.00	0	5.0	15.82	2
A0A0G2JDI4	Glutamate--cysteine ligase regulatory subunit (Fragment) OS=Mus musculus GN=Gclm PE=1 SV=1 - [A0A0G2	6.3	11	3.5	12.98	6	2.3	8.44	6	3.2	11.43	6
A0A0G2JDM6	Carboxylic ester hydrolase OS=Mus musculus GN=Ache PE=1 SV=1 - [A0A0G2JDM6_MOUSE]	6.9	59	1.0	3.60	1	0.0	0.00	0	0.0	0.00	0
A0A0G2JDR6	Leucine-rich repeat flightless-interacting protein 2 (Fragment) OS=Mus musculus GN=Lrrfip2 PE=1 SV=3	5.8	20	1.0	2.88	4	1.0	2.80	4	1.2	3.22	5
A0A0G2JDS8	Uracil-DNA glycosylase OS=Mus musculus GN=Ung PE=1 SV=1 - [A0A0G2JDS8_MOUSE]	10.3	15	1.0	2.52	1	1.0	2.72	2	1.0	2.53	1
A0A0G2JDU1	Microtubule-associated protein (Fragment) OS=Mus musculus GN=Map4 PE=1 SV=1 - [A0A0G2JDU1_MOUSE]	5.4	11	0.0	0.00	0	1.0	2.04	1	0.0	0.00	0
A0A0G2JE27	F-actin-capping protein subunit alpha-1 (Fragment) OS=Mus musculus GN=Capza1 PE=1 SV=3 - [A0A0G2JE27	5.1	13	2.0	7.12	2	2.3	6.79	3	3.0	9.24	3
A0A0G2JE32	Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Mus musculus GN=Ube2d3 PE=1 SV=1 - [A0A0G2JE32_MOUS	6.3	15	0.0	0.00	0	1.0	2.05	3	0.0	0.00	0
A0A0G2JE52	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1 - [A0A0G2JE52_MOUSE]	4.8	18	0.0	0.00	0	7.0	17.41	1	0.0	0.00	0
A0A0G2JEH3	MCG1490, isoform CRA_a OS=Mus musculus GN=Tmem243 PE=1 SV=1 - [A0A0G2JEH3_MOUSE]	6.5	5	1.5	4.12	4	3.2	8.67	6	3.8	10.43	6
A0A0G2JEI9	Protein Rsbn1l OS=Mus musculus GN=Rsbn1l PE=1 SV=1 - [A0A0G2JEI9_MOUSE]	9.5	69	1.5	3.44	2	0.0	0.00	0	0.0	0.00	0
A0A0G2JEP8	Rho-related GTP-binding protein RhoC (Fragment) OS=Mus musculus GN=Rhoc PE=1 SV=1 - [A0A0G2JEP8_MOUS	4.6	13	1.8	7.48	4	0.0	0.00	0	1.3	4.98	4
A0A0G2JF52	Actin related protein 2/3 complex, subunit 1A, isoform CRA_b OS=Mus musculus GN=Arpc1a PE=1 SV=1 - [	9.2	29	1.3	4.63	3	1.0	2.73	1	1.5	4.85	2
A0A0G2JF67	cGMP-specific 3',5'-cyclic phosphodiesterase OS=Mus musculus GN=Pde5a PE=1 SV=1 - [A0A0G2JF67_MOUSE]	6.0	94	11.0	32.29	1	0.0	0.00	0	0.0	0.00	0
A0A0G2JFI8	Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=1 SV=1 - [A0A0G2JFI8_MOUSE]	5.5	17	0.0	0.00	0	1.0	2.87	1	0.0	0.00	0
A0A0G2JFK7	Actin-related protein 2/3 complex subunit 3 (Fragment) OS=Mus musculus GN=Arpc3 PE=1 SV=1 - [A0A0G2J	8.2	16	3.0	8.49	3	2.5	6.37	2	3.0	7.28	4
A0A0G2JFL8	Adenylosuccinate lyase (Fragment) OS=Mus musculus GN=Adsl PE=1 SV=1 - [A0A0G2JFL8_MOUSE]	7.1	4	1.0	3.59	1	0.0	0.00	0	0.0	0.00	0
A0A0G2JFT9	cAMP-dependent protein kinase catalytic subunit beta (Fragment) OS=Mus musculus GN=Prkacb PE=1 SV=1	9.2	13	1.3	3.26	4	0.0	0.00	0	0.0	0.00	0
A0A0G2JFW5	Protein Clca3a2 (Fragment) OS=Mus musculus GN=Clca3a2 PE=1 SV=3 - [A0A0G2JFW5_MOUSE]	5.4	28	1.0	2.05	1	0.0	0.00	0	0.0	0.00	0
A0A0G2JG10	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Mus musculus GN=Dhx15 PE=1 SV=1 - [A0A0	6.8	69	1.0	2.24	1	0.0	0.00	0	0.0	0.00	0
A0A0G2JGC1	Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp1cc PE=1 SV=1 - [A0A0G2JGC1_MOUSE]	6.0	31	3.0	9.03	6	2.0	5.33	5	2.2	5.89	6
A0A0G2JGF3	Protein Clca3a2 (Fragment) OS=Mus musculus GN=Clca3a2 PE=4 SV=1 - [A0A0G2JGF3_MOUSE]	7.6	21	0.0	0.00	0	1.0	3.05	2	0.0	0.00	0

A0A0G2JGY0	Dihydropteridine reductase OS=Mus musculus GN=Qdpr PE=1 SV=1 - [A0A0G2JGY0_MOUSE]	8.2	15	0.0	0.00	0	0.0	0.00	0	1.0	2.38	1
A0A0G2JGY4	Malate dehydrogenase (Fragment) OS=Mus musculus GN=Mdh2 PE=1 SV=1 - [A0A0G2JGY4_MOUSE]	9.3	16	0.0	0.00	0	2.0	4.82	1	0.0	0.00	0
A0A0J9YTQ3	DNA polymerase nu OS=Mus musculus GN=Poln PE=3 SV=1 - [A0A0J9YTQ3_MOUSE]	7.6	92	1.2	2.92	5	1.5	3.46	4	1.4	3.35	5
A0A0J9YTR7	Chemokine (C-X-C motif) ligand 4, isoform CRA_a OS=Mus musculus GN=Pf4 PE=1 SV=1 - [A0A0J9YTR7_MOUSE	7.3	8	5.0	11.50	6	3.7	8.43	6	3.8	8.70	6
A0A0J9YTS1	Protein Fryl (Fragment) OS=Mus musculus GN=Fryl PE=1 SV=1 - [A0A0J9YTS1_MOUSE]	4.9	137	0.0	0.00	0	0.0	0.00	0	1.0	3.28	1
A0A0J9YTY0	Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=1 - [A0A0J9YTY0_MOUSE]	7.0	49	0.0	0.00	0	0.0	0.00	0	1.0	2.82	1
A0A0J9YUG0	General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=1 - [A0A0J9YUG0_MOUSE]	9.4	8	1.0	2.78	1	0.0	0.00	0	1.0	2.52	1
A0A0J9YUS5	Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1 - [A0A0J9YUS5	5.2	145	1.0	2.95	1	1.0	2.89	1	0.0	0.00	0
A0A0J9YUT8	Probable RNA-binding protein 19 OS=Mus musculus GN=Rbm19 PE=1 SV=1 - [A0A0J9YUT8_MOUSE]	6.3	97	1.0	2.06	1	0.0	0.00	0	0.0	0.00	0
A0A0J9YVC1	Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Mus musculus GN=Eif4g1 PE=1 SV=1 -	4.9	87	1.0	2.26	1	0.0	0.00	0	0.0	0.00	0
A0A0M3HEQ7	Coatomer subunit gamma OS=Mus musculus GN=Copg2 PE=1 SV=2 - [A0A0M3HEQ7_MOUSE]	5.9	97	0.0	0.00	0	1.0	2.28	1	1.0	2.38	1
A0A0N4SUI8	T-complex protein 1 subunit eta (Fragment) OS=Mus musculus GN=Cct7 PE=1 SV=1 - [A0A0N4SUI8_MOUSE]	6.0	9	0.0	0.00	0	2.0	5.71	1	1.0	2.83	1
A0A0N4SUJ8	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Fragment) OS=Mus musculus	5.6	9	2.0	7.09	2	0.0	0.00	0	0.0	0.00	0
A0A0N4SUT8	Deoxyribose-phosphate aldolase (Fragment) OS=Mus musculus GN=Dera PE=1 SV=1 - [A0A0N4SUT8_MOUSE]	7.5	8	0.0	0.00	0	0.0	0.00	0	1.0	2.46	1
A0A0N4SV00	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1 - [A0A0N4SV00_MOUSE]	7.8	55	0.0	0.00	0	2.0	5.01	1	1.0	2.11	1
A0A0N4SVB8	ADP-ribosylation factor-like protein 8B OS=Mus musculus GN=Arl8b PE=1 SV=1 - [A0A0N4SVB8_MOUSE]	9.0	16	1.3	3.63	4	1.0	2.66	2	0.0	0.00	0
A0A0N4SVL8	Multimerin-1 OS=Mus musculus GN=Mmrn1 PE=1 SV=1 - [A0A0N4SVL8_MOUSE]	7.7	136	18.2	57.73	6	22.0	72.19	6	0.0	0.00	0
A0A0N4SVM0	F-actin-capping protein subunit alpha-2 (Fragment) OS=Mus musculus GN=Capza2 PE=1 SV=1 - [A0A0N4SVM0	5.4	20	0.0	0.00	0	1.0	3.19	1	0.0	0.00	0
A0A0N4SVQ1	Cytochrome c oxidase subunit NDUFA4 OS=Mus musculus GN=Ndufa4 PE=1 SV=1 - [A0A0N4SVQ1_MOUSE]	8.5	6	1.0	2.23	2	0.0	0.00	0	0.0	0.00	0
A0A0N4SVW8	Src kinase-associated phosphoprotein 2 (Fragment) OS=Mus musculus GN=Skap2 PE=1 SV=2 - [A0A0N4SVW8_M	5.2	15	0.0	0.00	0	0.0	0.00	0	1.0	2.16	1
A0A0N4SW56	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 - [A0A0N4SW56	5.6	39	1.0	2.64	3	0.0	0.00	0	1.0	2.57	1
A0A0N4SW80	Cytosolic 5'-nucleotidase 3A (Fragment) OS=Mus musculus GN=Nt5c3 PE=1 SV=2 - [A0A0N4SW80_MOUSE]	8.1	17	1.5	3.22	2	0.0	0.00	0	0.0	0.00	0
A0A0N4SWE9	Uncharacterized protein OS=Mus musculus PE=4 SV=1 - [A0A0N4SWE9_MOUSE]	6.6	18	1.0	4.65	3	1.0	4.57	1	1.0	4.68	5
A0A0R4IZY0	Thimet oligopeptidase OS=Mus musculus GN=Thop1 PE=1 SV=1 - [A0A0R4IZY0_MOUSE]	6.0	78	0.0	0.00	0	1.0	2.22	1	0.0	0.00	0
A0A0R4J083	Long-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=1 SV=1 - [A0A0	8.1	48	1.2	3.58	5	1.0	2.05	1	1.0	2.86	1
A0A0R4J0H3	Retinol-binding protein 3 OS=Mus musculus GN=Rbp3 PE=1 SV=1 - [A0A0R4J0H3_MOUSE]	5.1	134	0.0	0.00	0	0.0	0.00	0	1.0	2.94	1
A0A0R4J0I1	MCG1051009 OS=Mus musculus GN=Serpina3k PE=1 SV=1 - [A0A0R4J0I1_MOUSE]	5.2	47	124.2	452.14	6	82.0	288.32	4	122.8	436.32	6
A0A0R4J0R1	Vesicle-associated membrane protein 8 OS=Mus musculus GN=Vamp8 PE=1 SV=1 - [A0A0R4J0R1_MOUSE]	8.2	11	1.0	2.29	2	0.0	0.00	0	0.0	0.00	0
A0A0R4J0S2	Insulin-like growth factor-binding protein complex acid labile subunit OS=Mus musculus GN=Igfals PE=	6.6	67	1.0	2.95	1	0.0	0.00	0	1.0	2.77	2
A0A0R4J107	Acylamino-acid-releasing enzyme (Fragment) OS=Mus musculus GN=Apeh PE=1 SV=1 - [A0A0R4J107_MOUSE]	5.6	80	1.0	3.10	3	2.2	6.68	6	1.8	5.49	4
A0A0R4J1B4	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=1 - [A0A0R4J1B4_MOUSE]	7.6	115	0.0	0.00	0	0.0	0.00	0	1.5	4.07	2
A0A0R4J1C2	Calpain small subunit 1 OS=Mus musculus GN=Capns1 PE=1 SV=1 - [A0A0R4J1C2_MOUSE]	5.3	23	3.2	10.50	5	3.0	9.76	6	3.0	9.49	4
A0A0R4J1H6	Golgin subfamily A member 3 OS=Mus musculus GN=Golga3 PE=1 SV=1 - [A0A0R4J1H6_MOUSE]	5.4	163	1.0	2.31	2	1.5	3.47	4	1.0	2.05	1
A0A0R4J1N1	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=1 - [A0A0R4J1N1_MOUSE]	6.6	100	0.0	0.00	0	0.0	0.00	0	2.0	6.58	1
A0A0R4J1N3	Apolipoprotein C-III OS=Mus musculus GN=Apoc3 PE=1 SV=1 - [A0A0R4J1N3_MOUSE]	4.8	11	5.0	18.49	6	8.5	32.29	6	6.5	24.08	6
A0A0R4J1S4	SLAM family member 5 OS=Mus musculus GN=Cd84 PE=1 SV=1 - [A0A0R4J1S4_MOUSE]	5.5	16	1.0	2.17	1	0.0	0.00	0	0.0	0.00	0
A0A0R4J257	Protein unc-13 homolog D OS=Mus musculus GN=Unc13d PE=1 SV=1 - [A0A0R4J257_MOUSE]	6.9	95	3.8	12.61	6	2.2	6.36	5	3.8	12.22	4
A0A0U1RNG5	Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=Mus musculus GN=Iqgap1 PE=1 SV=1 - [A0A0U1RN	6.5	21	0.0	0.00	0	0.0	0.00	0	1.0	2.11	1
A0A0U1RNJ1	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=1 - [A0A0U1RNJ1_MOUSE]	6.6	272	0.0	0.00	0	1.0	2.09	1	1.0	2.08	2
A0A0U1RNQ6	Elongation factor Tu, mitochondrial (Fragment) OS=Mus musculus GN=Tufm PE=1 SV=1 - [A0A0U1RNQ6_MOUSE	4.6	13	1.0	3.35	2	0.0	0.00	0	0.0	0.00	0
A0A0U1RNR3	Electron transfer flavoprotein subunit beta (Fragment) OS=Mus musculus GN=Etfb PE=4 SV=1 - [A0A0U1RN	6.6	19	2.0	6.87	1	0.0	0.00	0	0.0	0.00	0
A0A0U1RP06	DNA repair protein-complementing XP-C cells homolog (Fragment) OS=Mus musculus GN=Xpc PE=1 SV=1 - [A	8.8	78	0.0	0.00	0	1.0	2.57	1	0.0	0.00	0
A0A0U1RP59	Interferon-stimulated gene 20 kDa protein OS=Mus musculus GN=Isg20 PE=1 SV=1 - [A0A0U1RP59_MOUSE]	8.2	16	1.0	2.23	1	0.0	0.00	0	0.0	0.00	0
A0A0U1RPA0	Pleckstrin homology domain-containing family A member 7 (Fragment) OS=Mus musculus GN=Plekha7 PE=1 S	9.3	137	0.0	0.00	0	0.0	0.00	0	1.0	2.48	1
A0A0U1RPU7	Flavin reductase (NADPH) OS=Mus musculus GN=Blvrb PE=1 SV=1 - [A0A0U1RPU7_MOUSE]	7.4	13	3.3	12.81	6	8.0	30.60	1	5.8	21.91	4
A0A0U1RPV6	Transient receptor potential cation channel subfamily M member 1 OS=Mus musculus GN=Trpm1 PE=4 SV=1	7.3	171	1.0	2.14	2	0.0	0.00	0	0.0	0.00	0
A0A0U1RQ14	MICOS complex subunit MIC60 (Fragment) OS=Mus musculus GN=Immt PE=1 SV=1 - [A0A0U1RQ14_MOUSE]	7.4	33	0.0	0.00	0	1.0	3.77	1	1.0	4.07	2
A0A0U1RQ34	WD repeat-containing protein 11 (Fragment) OS=Mus musculus GN=Wdr11 PE=1 SV=1 - [A0A0U1RQ34_MOUSE]	8.2	13	0.0	0.00	0	1.0	2.65	1	0.0	0.00	0
A1BN54	Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=1 SV=1 - [A1BN54_MOUSE]	5.5	103	88.2	291.09	6	58.0	190.46	6	69.8	226.57	6
A2A5E1	DnaJ homolog subfamily C member 7 (Fragment) OS=Mus musculus GN=Dnajc7 PE=1 SV=1 - [A2A5E1_MOUSE]	8.9	17	0.0	0.00	0	1.0	2.97	1	1.0	3.16	1
A2A5F5	Ras-related protein Rab-5C (Fragment) OS=Mus musculus GN=Rab5c PE=1 SV=1 - [A2A5F5_MOUSE]	8.0	9	2.7	6.04	3	3.0	6.98	2	2.5	5.43	4
A2A5F6	Ras-related protein Rab-5C (Fragment) OS=Mus musculus GN=Rab5c PE=1 SV=7 - [A2A5F6_MOUSE]	10.3	3	0.0	0.00	0	1.5	3.32	2	0.0	0.00	0
A2A5I3	Peptidase inhibitor R3HDML OS=Mus musculus GN=R3hdml PE=3 SV=1 - [CRSPL_MOUSE]	9.2	28	0.0	0.00	0	1.0	2.03	1	0.0	0.00	0
A2A5K2	Phospholipid transfer protein OS=Mus musculus GN=Pltp PE=1 SV=1 - [A2A5K2_MOUSE]	6.5	49	0.0	0.00	0	1.0	2.67	1	0.0	0.00	0
A2A6A1	G patch domain-containing protein 8 OS=Mus musculus GN=Gpatch8 PE=1 SV=1 - [GPTC8_MOUSE]	7.6	165	1.0	2.07	1	0.0	0.00	0	0.0	0.00	0
A2A6H1	LIM and SH3 domain protein 1 (Fragment) OS=Mus musculus GN=Lasp1 PE=1 SV=1 - [A2A6H1_MOUSE]	8.5	7	1.0	2.42	2	1.3	2.84	4	1.2	2.89	5
A2A6U5	Septin-9 (Fragment) OS=Mus musculus GN=Sept9 PE=1 SV=1 - [A2A6U5_MOUSE]	8.6	28	2.0	5.20	1	0.0	0.00	0	0.0	0.00	0
A2A7A1	Protein Zfp534 OS=Mus musculus GN=Zfp534 PE=4 SV=2 - [A2A7A1_MOUSE]	8.9	78	0.0	0.00	0	1.0	2.97	1	0.0	0.00	0
A2A7Q8	E3 ubiquitin-protein ligase RNF19B (Fragment) OS=Mus musculus GN=Rnf19b PE=4 SV=7 - [A2A7Q8_MOUSE]	8.4	38	1.5	4.08	4	1.3	3.24	3	2.0	4.87	2
A2A815	Protein deglycase DJ-1 (Fragment) OS=Mus musculus GN=Park7 PE=1 SV=7 - [A2A815_MOUSE]	7.2	14	4.3	16.19	4	3.3	12.06	4	4.0	13.62	5
A2A817	Protein deglycase DJ-1 (Fragment) OS=Mus musculus GN=Park7 PE=1 SV=1 - [A2A817_MOUSE]	5.1	9	3.0	10.24	2	2.5	8.66	2	2.0	7.02	1
A2A839	Protein 4.1 OS=Mus musculus GN=Epb41 PE=1 SV=1 - [A2A839_MOUSE]	6.6	72	6.0	18.62	4	10.0	31.61	3	6.8	19.57	4
A2A842	Protein 4.1 OS=Mus musculus GN=Epb41 PE=1 SV=1 - [A2A842_MOUSE]	5.4	86	8.0	26.70	1	11.0	35.33	3	13.5	43.92	2
A2A855	Protein unc-13 homolog D (Fragment) OS=Mus musculus GN=Unc13d PE=1 SV=1 - [A2A855_MOUSE]	5.9	13	0.0	0.00	0	1.0	3.47	1	0.0	0.00	0
A2A860	WW domain binding protein 2, isoform CRA_a OS=Mus musculus GN=Wbp2 PE=1 SV=1 - [A2A860_MOUSE]	6.3	23	1.0	2.33	1	0.0	0.00	0	1.0	2.78	2
A2A8E8	Carnitine O-palmitoyltransferase 2, mitochondrial (Fragment) OS=Mus musculus GN=Cpt2 PE=1 SV=1 - [A2	9.2	30	0.0	0.00	0	1.0	3.43	1	1.5	5.05	2

A2A998	Complement component C8 alpha chain OS=Mus musculus GN=C8a PE=1 SV=1 - [A2A998_MOUSE]	6.1	61	1.6	4.67	5	0.0	0.00	0	2.3	6.11	3
A2A9X5	5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus GN=Nt5c PE=1 SV=1 - [A2A9X5_MOUSE]	5.3	22	1.2	4.27	5	1.5	5.20	4	1.8	5.54	4
A2ACG7	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=	6.2	67	6.5	20.06	6	3.6	11.27	5	4.0	13.67	6
A2AD32	Protein 4.1 (Fragment) OS=Mus musculus GN=Epb41 PE=1 SV=7 - [A2AD32_MOUSE]	5.8	80	5.0	16.85	1	0.0	0.00	0	0.0	0.00	0
A2AD83	FERM domain-containing protein 7 OS=Mus musculus GN=Frmd7 PE=1 SV=1 - [FRMD7_MOUSE]	8.0	80	1.0	2.08	1	0.0	0.00	0	0.0	0.00	0
A2AEX7	Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1 - [A2AEX7_MOUSE]	8.6	24	3.2	7.55	6	2.8	6.78	6	2.5	5.88	6
A2AG41	Stomatin-like protein 2, mitochondrial (Fragment) OS=Mus musculus GN=Stoml2 PE=1 SV=9 - [A2AG41_MOUS	9.3	24	1.0	2.24	1	0.0	0.00	0	0.0	0.00	0
A2AIM4	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1 - [A2AIM4_MOUSE]	4.7	33	9.8	25.86	6	7.4	19.35	5	8.0	20.63	5
A2AIR1	E3 ubiquitin-protein ligase BRE1A (Fragment) OS=Mus musculus GN=Rnf20 PE=1 SV=1 - [A2AIR1_MOUSE]	5.6	13	1.0	2.92	1	0.0	0.00	0	0.0	0.00	0
A2AIS0	Voltage-dependent N-type calcium channel subunit alpha-1B OS=Mus musculus GN=Cacna1b PE=1 SV=1 - [A2	8.5	257	1.0	2.50	1	0.0	0.00	0	0.0	0.00	0
A2AJ30	Protein BC029214 (Fragment) OS=Mus musculus GN=BC029214 PE=1 SV=1 - [A2AJ30_MOUSE]	5.6	17	0.0	0.00	0	1.0	2.02	1	0.0	0.00	0
A2AKP6	Protein Gm12394 OS=Mus musculus GN=Gm12394 PE=4 SV=1 - [A2AKP6_MOUSE]	8.5	109	2.0	4.31	3	0.0	0.00	0	1.0	2.19	1
A2AKV0	ATP synthase subunit gamma, mitochondrial (Fragment) OS=Mus musculus GN=Atp5c1 PE=1 SV=1 - [A2AKV0_M	10.1	11	1.0	2.55	2	0.0	0.00	0	1.0	2.26	1
A2AKV1	ATP synthase subunit gamma, mitochondrial (Fragment) OS=Mus musculus GN=Atp5c1 PE=1 SV=1 - [A2AKV1_M	9.9	17	0.0	0.00	0	1.0	2.14	1	0.0	0.00	0
A2AL20	Catalase OS=Mus musculus GN=Cat PE=1 SV=1 - [A2AL20_MOUSE]	9.1	20	1.7	4.96	3	2.5	8.32	2	2.0	6.37	1
A2ALB1	RNA exonuclease 4 (Fragment) OS=Mus musculus GN=Rexo4 PE=1 SV=1 - [A2ALB1_MOUSE]	9.8	40	1.0	2.50	1	0.0	0.00	0	0.0	0.00	0
A2ALR8	Ubiquitin carboxyl-terminal hydrolase 48 (Fragment) OS=Mus musculus GN=Usp48 PE=1 SV=1 - [A2ALR8_MOU	7.1	73	1.0	2.11	2	0.0	0.00	0	1.0	2.04	1
A2ALT5	Adenosylhomocysteinase (Fragment) OS=Mus musculus GN=Ahcy PE=1 SV=1 - [A2ALT5_MOUSE]	6.5	10	0.0	0.00	0	0.0	0.00	0	1.0	3.03	1
A2AMH8	Choline transporter-like protein 1 OS=Mus musculus GN=Slc44a1 PE=1 SV=1 - [A2AMH8_MOUSE]	9.0	51	1.0	2.69	2	1.0	2.43	1	0.0	0.00	0
A2AMQ5	Phosphatidate cytidylyltransferase OS=Mus musculus GN=Cds2 PE=1 SV=1 - [A2AMQ5_MOUSE]	7.2	49	3.3	10.83	3	2.3	7.87	3	2.0	6.77	2
A2AN84	55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1 - [A2AN84_MOUSE]	9.2	51	0.0	0.00	0	0.0	0.00	0	4.0	9.90	1
A2ANA0	Protein transport protein Sec23B (Fragment) OS=Mus musculus GN=Sec23b PE=1 SV=1 - [A2ANA0_MOUSE]	6.1	31	1.0	2.56	2	1.0	2.17	2	1.0	2.60	2
A2AQ07	Tubulin beta-1 chain OS=Mus musculus GN=Tubb1 PE=1 SV=1 - [TBB1_MOUSE]	5.1	50	108.5	392.85	6	92.2	324.33	6	110.5	383.39	6
A2AQ25	Sickle tail protein OS=Mus musculus GN=Skt PE=1 SV=1 - [SKT_MOUSE]	7.8	213	0.0	0.00	0	0.0	0.00	0	1.0	3.01	1
A2AQ47	Formin-binding protein 1 (Fragment) OS=Mus musculus GN=Fnbp1 PE=1 SV=1 - [A2AQ47_MOUSE]	6.6	19	1.0	2.27	3	1.0	2.53	1	0.0	0.00	0
A2AT02	NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1 - [A2AT02_MOUSE]	5.1	37	1.0	3.73	2	1.0	3.78	1	1.0	3.54	1
A2AT64	Titin (Fragment) OS=Mus musculus GN=Ttn PE=1 SV=1 - [A2AT64_MOUSE]	5.7	62	0.0	0.00	0	0.0	0.00	0	1.0	2.69	1
A2ATR8	Plasma protease C1 inhibitor OS=Mus musculus GN=Serping1 PE=1 SV=1 - [A2ATR8_MOUSE]	6.0	38	0.0	0.00	0	4.0	12.06	1	0.0	0.00	0
A2AUM9	Centrosomal protein of 152 kDa OS=Mus musculus GN=Cep152 PE=1 SV=1 - [CE152_MOUSE]	5.7	196	1.0	3.38	2	1.0	2.98	2	1.0	3.29	2
A2AUY4	Protein Baz2b OS=Mus musculus GN=Baz2b PE=1 SV=1 - [A2AUY4_MOUSE]	6.6	234	1.0	2.28	5	0.0	0.00	0	1.0	2.02	2
A2AVJ7	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=1 SV=1 - [A2AVJ7_MOUSE]	9.2	158	1.0	2.38	3	0.0	0.00	0	0.0	0.00	0
A2AVR1	Tetratricopeptide repeat protein 4 (Fragment) OS=Mus musculus GN=Ttc4 PE=1 SV=1 - [A2AVR1_MOUSE]	5.5	28	1.0	2.53	1	1.5	3.89	2	1.0	2.66	1
A2AWF8	Receptor-type tyrosine-protein phosphatase eta OS=Mus musculus GN=Ptprj PE=1 SV=1 - [A2AWF8_MOUSE]	5.4	129	1.7	4.06	3	1.0	2.16	1	2.0	5.32	2
A2BDW0	Tyrosine-protein kinase OS=Mus musculus GN=Btk PE=1 SV=1 - [A2BDW0_MOUSE]	8.0	56	1.3	4.84	3	1.5	5.44	2	1.3	4.19	4
A2BFF8	Cytoplasmic dynein 1 intermediate chain 2 OS=Mus musculus GN=Dync1i2 PE=1 SV=1 - [A2BFF8_MOUSE]	5.3	68	1.0	2.27	1	1.0	2.04	1	0.0	0.00	0
A2BIN0	Major urinary protein 11 OS=Mus musculus GN=Mup11 PE=4 SV=1 - [A2BIN0_MOUSE]	4.7	11	1.5	4.48	6	0.0	0.00	0	1.2	3.41	5
A2RT91	Ankyrin and armadillo repeat-containing protein OS=Mus musculus GN=Ankar PE=2 SV=1 - [ANKAR_MOUSE]	7.7	165	0.0	0.00	0	1.0	3.23	1	1.5	4.64	2
A3KG36	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Mus musculus GN=G6pdx PE=1 SV=1 - [A3KG36_MOUSE]	6.3	45	1.0	2.90	3	1.0	3.15	2	1.5	4.76	2
A4Q9F1	Protein monoglycylase TTLL8 OS=Mus musculus GN=Ttll8 PE=1 SV=1 - [TTLL8_MOUSE]	9.0	95	1.0	3.05	1	0.0	0.00	0	0.0	0.00	0
A6X8J1	Protein Gm16405 OS=Mus musculus GN=Gm16405 PE=4 SV=1 - [A6X8J1_MOUSE]	4.2	18	1.0	2.68	2	0.0	0.00	0	1.0	2.54	2
A7L9Z8	Calcium-transporting ATPase type 2C member 2 OS=Mus musculus GN=Atp2c2 PE=2 SV=1 - [AT2C2_MOUSE]	6.4	102	2.7	6.93	6	4.0	10.42	6	3.7	9.54	6
A8DUK4	Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1 - [A8DUK4_MOUSE]	7.7	16	195.8	707.91	6	363.0	1270.20	6	364.8	1262.73	6
A8Y5D3	Septin-9 (Fragment) OS=Mus musculus GN=Sept9 PE=1 SV=1 - [A8Y5D3_MOUSE]	10.0	8	1.2	3.43	5	1.0	2.46	2	1.3	3.18	4
B0R029	Synaptosomal-associated protein 23 (Fragment) OS=Mus musculus GN=Snap23 PE=1 SV=7 - [B0R029_MOUSE]	4.5	10	1.3	4.17	3	1.6	4.89	5	1.0	2.48	2
B0R030	Synaptosomal-associated protein (Fragment) OS=Mus musculus GN=Snap23 PE=1 SV=7 - [B0R030_MOUSE]	4.8	18	4.0	12.14	2	0.0	0.00	0	2.5	7.22	4
B0R0E3	Protein SCAI (Fragment) OS=Mus musculus GN=Scai PE=1 SV=7 - [B0R0E3_MOUSE]	4.4	3	0.0	0.00	0	1.0	3.13	1	0.0	0.00	0
B0R1E3	Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=1 - [B0R1E3_MOUSE]	5.0	13	0.0	0.00	0	1.0	2.28	1	0.0	0.00	0
B1AQ75	Keratin, type I cuticular Ha6 OS=Mus musculus GN=Krt36 PE=1 SV=1 - [KRT36_MOUSE]	5.0	53	1.5	3.62	2	1.5	3.52	2	3.0	7.08	1
B1ASE2	ATP synthase subunit d, mitochondrial (Fragment) OS=Mus musculus GN=Atp5h PE=1 SV=1 - [B1ASE2_MOUSE]	5.2	16	1.0	3.43	4	1.7	5.71	3	1.5	4.88	4
B1ATD1	Lymphocyte cytosolic protein 2 OS=Mus musculus GN=Lcp2 PE=1 SV=1 - [B1ATD1_MOUSE]	5.9	59	1.0	2.18	1	1.0	2.44	2	0.0	0.00	0
B1ATQ3	Malate dehydrogenase, cytoplasmic (Fragment) OS=Mus musculus GN=Mdh1 PE=1 SV=7 - [B1ATQ3_MOUSE]	6.7	17	0.0	0.00	0	2.0	6.39	1	0.0	0.00	0
B1ATS4	Calcium-transporting ATPase OS=Mus musculus GN=Atp2a3 PE=1 SV=1 - [B1ATS4_MOUSE]	5.8	108	22.6	71.68	5	14.5	44.54	4	19.8	60.13	5
B1ATS5	Calcium-transporting ATPase OS=Mus musculus GN=Atp2a3 PE=1 SV=1 - [B1ATS5_MOUSE]	6.0	112	21.0	67.04	1	17.0	51.45	2	22.0	70.98	1
B1AU25	Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1 - [B1AU25_MOUSE]	9.1	66	0.0	0.00	0	0.0	0.00	0	1.0	2.12	1
B1AU76	Nuclear autoantigenic sperm protein OS=Mus musculus GN=Nasp PE=1 SV=1 - [B1AU76_MOUSE]	4.4	49	2.0	5.89	6	1.3	3.82	3	1.5	4.24	4
B1AUY1	Protein Arhgap4 (Fragment) OS=Mus musculus GN=Arhgap4 PE=1 SV=1 - [B1AUY1_MOUSE]	5.2	24	0.0	0.00	0	0.0	0.00	0	1.0	2.74	1
B1AWL2	Protein Zfp462 OS=Mus musculus GN=Zfp462 PE=1 SV=1 - [B1AWL2_MOUSE]	7.3	283	1.0	2.75	1	2.5	6.88	2	1.3	3.67	3
B1AXS6	Zinc finger MYM-type protein 3 OS=Mus musculus GN=Zmym3 PE=1 SV=1 - [B1AXS6_MOUSE]	6.0	142	0.0	0.00	0	0.0	0.00	0	1.0	2.25	1
B1AXW5	Peroxiredoxin-1 (Fragment) OS=Mus musculus GN=Prdx1 PE=1 SV=7 - [B1AXW5_MOUSE]	7.3	19	1.6	3.71	5	1.6	3.64	5	2.2	5.29	5
B1AXX9	DnaJ homolog subfamily A member 1 (Fragment) OS=Mus musculus GN=Dnaja1 PE=1 SV=1 - [B1AXX9_MOUSE]	9.2	14	1.0	2.56	1	0.0	0.00	0	0.0	0.00	0
B1AZI6	THO complex subunit 2 OS=Mus musculus GN=Thoc2 PE=1 SV=1 - [THOC2_MOUSE]	8.4	183	0.0	0.00	0	1.0	2.18	1	0.0	0.00	0
B1B1E2	Latent-transforming growth factor beta-binding protein 1 (Fragment) OS=Mus musculus GN=Ltbp1 PE=1 SV	6.4	107	1.0	2.83	1	0.0	0.00	0	1.0	2.91	1
B2KF34	Mitogen-activated protein kinase 14 (Fragment) OS=Mus musculus GN=Mapk14 PE=1 SV=1 - [B2KF34_MOUSE]	8.3	24	0.0	0.00	0	1.0	3.46	1	1.0	3.57	1
B2KF35	Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 PE=1 SV=1 - [B2KF35_MOUSE]	7.9	30	2.0	5.10	4	3.0	7.69	1	0.0	0.00	0
B2KF55	Ubiquitin-conjugating enzyme E2 variant 2 OS=Mus musculus GN=Ube2v2 PE=1 SV=1 - [B2KF55_MOUSE]	10.3	7	2.0	4.89	1	1.0	2.53	1	2.0	5.28	1
B2RUJ2	Erbb2ip protein OS=Mus musculus GN=Erbb2ip PE=1 SV=1 - [B2RUJ2_MOUSE]	5.4	145	2.0	5.48	5	1.0	2.34	2	1.5	3.18	2

B2RUR8	OTU domain-containing protein 7B OS=Mus musculus GN=Otud7b PE=1 SV=1 - [OTU7B_MOUSE]	6.9	92	0.0	0.00	0	1.0	3.11	1	0.0	0.00	0
B2RXM6	Ly6g6f protein OS=Mus musculus GN=Ly6g6f PE=1 SV=1 - [B2RXM6_MOUSE]	8.9	33	2.0	11.23	6	2.0	10.25	6	2.3	11.17	6
B2RXX5	A disintegrin-like and metallopeptidase (Reprolysin type) with thrombospondin type 1 motif, 14 OS=Mu	7.6	134	0.0	0.00	0	0.0	0.00	0	1.0	3.41	1
B2RY71	Protein Wdr63 OS=Mus musculus GN=Wdr63 PE=1 SV=1 - [B2RY71_MOUSE]	5.5	105	0.0	0.00	0	1.0	3.10	1	0.0	0.00	0
B7FAU9	Filamin, alpha OS=Mus musculus GN=Flna PE=1 SV=1 - [B7FAU9_MOUSE]	6.0	280	293.3	1068.70	6	224.7	796.44	6	257.8	907.20	6
B7ZBY6	Ubiquitin-conjugating enzyme E2 variant 1 (Fragment) OS=Mus musculus GN=Ube2v1 PE=4 SV=7 - [B7ZBY6_M	5.2	14	1.4	3.19	5	1.5	3.50	4	1.4	3.28	5
B7ZCL8	55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1 - [B7ZCL8_MOUSE]	7.2	50	2.3	6.02	3	3.7	9.04	6	6.0	15.81	1
B7ZCL9	55 kDa erythrocyte membrane protein (Fragment) OS=Mus musculus GN=Mpp1 PE=1 SV=1 - [B7ZCL9_MOUSE]	8.7	23	1.0	4.16	1	0.0	0.00	0	2.0	4.63	1
B7ZCM0	55 kDa erythrocyte membrane protein (Fragment) OS=Mus musculus GN=Mpp1 PE=1 SV=1 - [B7ZCM0_MOUSE]	9.0	17	1.0	2.08	1	0.0	0.00	0	0.0	0.00	0
B7ZCP4	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1 - [B7ZCP4_MOUSE]	5.8	53	1.0	2.55	1	0.0	0.00	0	0.0	0.00	0
B7ZNJ1	Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=1 - [B7ZNJ1_MOUSE]	6.1	240	24.2	77.00	6	17.3	56.08	6	19.0	60.81	6
B7ZNL3	Tpm1 protein OS=Mus musculus GN=Tpm1 PE=1 SV=1 - [B7ZNL3_MOUSE]	4.7	33	15.0	38.39	4	13.2	33.86	5	14.0	35.02	6
B7ZWC9	4430402I18Rik protein OS=Mus musculus GN=4430402I18Rik PE=1 SV=1 - [B7ZWC9_MOUSE]	9.8	38	1.0	2.16	4	1.0	2.09	2	1.0	2.03	2
B8JJB1	PDZ and LIM domain protein 7 (Fragment) OS=Mus musculus GN=Pdlim7 PE=1 SV=1 - [B8JJB1_MOUSE]	5.1	6	1.0	2.52	1	0.0	0.00	0	0.0	0.00	0
B8JJM3	Complement factor B (Fragment) OS=Mus musculus GN=Cfb PE=4 SV=1 - [B8JJM3_MOUSE]	8.3	26	0.0	0.00	0	1.0	2.56	1	0.0	0.00	0
B9EJX2	Nance-Horan syndrome (Human) OS=Mus musculus GN=Nhs PE=1 SV=1 - [B9EJX2_MOUSE]	6.9	177	1.0	2.19	1	1.0	2.21	1	0.0	0.00	0
B9EKI3	TATA element modulatory factor OS=Mus musculus GN=Tmf1 PE=1 SV=2 - [TMF1_MOUSE]	4.9	122	1.0	2.75	1	0.0	0.00	0	0.0	0.00	0
D3YTR7	Adenylyl cyclase-associated protein OS=Mus musculus GN=Cap2 PE=1 SV=1 - [D3YTR7_MOUSE]	5.6	40	0.0	0.00	0	1.0	2.11	1	0.0	0.00	0
D3YTY9	Kininogen-1 OS=Mus musculus GN=Kng1 PE=1 SV=1 - [D3YTY9_MOUSE]	5.1	53	1.8	5.58	6	2.2	6.21	5	2.3	7.08	4
D3YUM8	Proteasome subunit beta type OS=Mus musculus GN=Gm4950 PE=1 SV=1 - [D3YUM8_MOUSE]	6.9	23	1.0	2.63	1	0.0	0.00	0	0.0	0.00	0
D3YUQ9	Elongation factor 1-delta (Fragment) OS=Mus musculus GN=Eef1d PE=1 SV=7 - [D3YUQ9_MOUSE]	5.5	22	0.0	0.00	0	2.3	11.74	4	2.7	12.86	3
D3YV43	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 - [D3YV43_MOUSE]	9.5	21	0.0	0.00	0	1.0	2.64	2	0.0	0.00	0
D3YV69	Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=1 - [D3YV69_MOUSE]	5.1	20	9.5	23.97	2	0.0	0.00	0	6.5	16.71	2
D3YV76	Septin-2 (Fragment) OS=Mus musculus GN=Sept2 PE=1 SV=1 - [D3YV76_MOUSE]	9.2	9	2.0	6.92	1	0.0	0.00	0	0.0	0.00	0
D3YVI5	Actin-related protein 2/3 complex subunit 1A (Fragment) OS=Mus musculus GN=Arpc1a PE=1 SV=1 - [D3YVI	8.9	16	0.0	0.00	0	1.0	2.78	1	0.0	0.00	0
D3YVN5	Signal peptide, CUB and EGF-like domain-containing protein 2 OS=Mus musculus GN=Scube2 PE=1 SV=1 - [	6.3	89	0.0	0.00	0	1.0	2.97	1	0.0	0.00	0
D3YVN7	Elongation factor Tu OS=Mus musculus GN=Gm9755 PE=3 SV=1 - [D3YVN7_MOUSE]	7.6	50	1.0	2.99	3	1.5	4.28	2	2.0	5.45	2
D3YVP4	Tubulin-specific chaperone cofactor E-like protein (Fragment) OS=Mus musculus GN=Tbcel PE=1 SV=1 - [	7.1	7	1.0	3.15	2	1.0	3.09	2	1.5	4.60	2
D3YVR4	LDLR chaperone MESD (Fragment) OS=Mus musculus GN=Mesdc2 PE=1 SV=1 - [D3YVR4_MOUSE]	5.0	17	0.0	0.00	0	1.0	3.16	1	0.0	0.00	0
D3YVT5	Ubiquitin-associated and SH3 domain-containing protein B (Fragment) OS=Mus musculus GN=Ubash3b PE=1	9.6	13	0.0	0.00	0	2.0	5.86	1	0.0	0.00	0
D3YVX4	Stromal membrane-associated protein 1 OS=Mus musculus GN=Smap1 PE=1 SV=1 - [D3YVX4_MOUSE]	8.1	38	1.0	3.83	1	0.0	0.00	0	0.0	0.00	0
D3YVY3	Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Mus musculus GN=Idh1 PE=1 SV=1 - [D3YVY3_M	8.4	16	0.0	0.00	0	2.0	5.59	1	0.0	0.00	0
D3YW48	Calpain small subunit 1 (Fragment) OS=Mus musculus GN=Capns1 PE=1 SV=1 - [D3YW48_MOUSE]	5.6	25	4.0	13.62	1	0.0	0.00	0	5.5	17.37	2
D3YW95	Integrin alpha-L OS=Mus musculus GN=Itgal PE=1 SV=1 - [D3YW95_MOUSE]	5.7	84	0.0	0.00	0	1.0	2.30	2	0.0	0.00	0
D3YWB6	Peptidyl-prolyl cis-trans isomerase FKBP14 OS=Mus musculus GN=Fkbp14 PE=1 SV=1 - [D3YWB6_MOUSE]	5.1	14	1.0	2.83	1	2.0	6.36	2	1.3	3.80	3
D3YWG9	WD repeat and FYVE domain-containing protein 1 (Fragment) OS=Mus musculus GN=Wdfy1 PE=1 SV=1 - [D3YW	7.4	8	1.0	2.94	2	0.0	0.00	0	0.0	0.00	0
D3YWT0	Signal peptidase complex catalytic subunit SEC11 OS=Mus musculus GN=Sec11a PE=1 SV=1 - [D3YWT0_MOUSE	9.5	20	1.0	2.46	4	1.0	2.23	2	1.0	2.30	2
D3YWU2	NACHT, LRR and PYD domains-containing protein 9B (Fragment) OS=Mus musculus GN=Nlrp9b PE=4 SV=1 - [D	6.9	28	1.0	3.12	1	0.0	0.00	0	0.0	0.00	0
D3YX79	Proteasome subunit alpha type OS=Mus musculus GN=Gm8394 PE=3 SV=1 - [D3YX79_MOUSE]	4.9	26	1.0	2.27	1	1.0	2.34	2	0.0	0.00	0
D3YXF4	14-3-3 protein zeta/delta (Fragment) OS=Mus musculus GN=Ywhaz PE=1 SV=7 - [D3YXF4_MOUSE]	4.6	5	0.0	0.00	0	6.0	21.79	1	0.0	0.00	0
D3YXF5	Oxidation resistance protein 1 OS=Mus musculus GN=C7 PE=1 SV=2 - [D3YXF5_MOUSE]	6.4	93	0.0	0.00	0	0.0	0.00	0	1.0	2.33	1
D3YXG6	Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=1 - [D3YXG6_MOUSE]	8.0	32	2.2	6.78	5	1.7	5.50	6	1.8	5.07	5
D3YXU1	Trifunctional enzyme subunit beta, mitochondrial (Fragment) OS=Mus musculus GN=Hadhb PE=1 SV=1 - [D3	9.5	19	1.0	2.33	3	1.0	2.41	2	0.0	0.00	0
D3YY36	Protein 1300017J02Rik OS=Mus musculus GN=1300017J02Rik PE=1 SV=1 - [D3YY36_MOUSE]	7.9	69	2.0	6.23	6	3.0	9.35	3	2.3	6.84	3
D3YYA5	Ubiquitin carboxyl-terminal hydrolase 5 (Fragment) OS=Mus musculus GN=Usp5 PE=1 SV=1 - [D3YYA5_MOUSE	7.4	23	3.0	7.66	1	1.8	4.33	4	1.0	2.89	1
D3YYK8	Microtubule-associated protein RP/EB family member 2 (Fragment) OS=Mus musculus GN=Mapre2 PE=1 SV=1	6.4	29	0.0	0.00	0	0.0	0.00	0	1.0	3.43	1
D3YYP8	Integrin beta (Fragment) OS=Mus musculus GN=Itgb2 PE=1 SV=1 - [D3YYP8_MOUSE]	9.3	15	1.0	3.31	3	1.0	2.49	3	1.3	3.48	3
D3YYQ4	Carbonic anhydrase 1 (Fragment) OS=Mus musculus GN=Car1 PE=1 SV=1 - [D3YYQ4_MOUSE]	6.5	10	2.0	4.78	3	0.0	0.00	0	2.0	4.63	4
D3YYY8	Protein Arhgef26 OS=Mus musculus GN=Arhgef26 PE=1 SV=1 - [D3YYY8_MOUSE]	8.7	97	0.0	0.00	0	0.0	0.00	0	2.0	6.05	1
D3YZ10	Smoothelin (Fragment) OS=Mus musculus GN=Smtn PE=1 SV=7 - [D3YZ10_MOUSE]	8.2	16	0.0	0.00	0	0.0	0.00	0	1.0	2.55	1
D3YZ29	Glutathione S-transferase Mu 7 (Fragment) OS=Mus musculus GN=Gstm7 PE=1 SV=1 - [D3YZ29_MOUSE]	5.2	14	0.0	0.00	0	1.0	3.05	2	1.0	3.15	1
D3YZ57	Tyrosine-protein kinase OS=Mus musculus GN=Fyn PE=1 SV=1 - [D3YZ57_MOUSE]	6.2	54	0.0	0.00	0	1.0	2.39	2	1.0	2.14	2
D3YZP9	Coiled-coil domain-containing protein 6 OS=Mus musculus GN=Ccdc6 PE=1 SV=1 - [CCDC6_MOUSE]	7.3	53	1.3	3.43	4	1.0	2.60	1	1.0	2.58	2
D3YZS3	Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1 - [D3YZS3_MOUSE]	8.4	14	0.0	0.00	0	2.0	5.77	1	0.0	0.00	0
D3YZT5	Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Mus musculus GN=Vdac2 PE=1 SV=1 -	7.1	22	1.0	2.69	1	1.0	2.70	2	1.0	2.26	1
D3YZV0	Extracellular matrix protein 1 (Fragment) OS=Mus musculus GN=Ecm1 PE=1 SV=1 - [D3YZV0_MOUSE]	6.5	9	0.0	0.00	0	1.0	3.18	1	0.0	0.00	0
D3Z069	Pleckstrin homology-like domain family B member 2 (Fragment) OS=Mus musculus GN=Phldb2 PE=1 SV=1 - [	6.3	127	0.0	0.00	0	1.0	2.38	1	0.0	0.00	0
D3Z074	Protein diaphanous homolog 1 OS=Mus musculus GN=Diaph1 PE=1 SV=2 - [D3Z074_MOUSE]	5.3	136	3.5	9.55	2	1.0	2.82	2	1.5	4.67	2
D3Z099	Dihydropteridine reductase (Fragment) OS=Mus musculus GN=Qdpr PE=1 SV=7 - [D3Z099_MOUSE]	5.3	15	0.0	0.00	0	1.0	2.72	1	1.0	2.46	1
D3Z0B9	Aldehyde dehydrogenase family 16 member A1 OS=Mus musculus GN=Aldh16a1 PE=1 SV=1 - [D3Z0B9_MOUSE]	6.3	79	0.0	0.00	0	1.0	3.45	1	1.0	2.50	1
D3Z0R5	Glucosamine-6-phosphate isomerase 1 (Fragment) OS=Mus musculus GN=Gnpda1 PE=1 SV=1 - [D3Z0R5_MOUSE]	5.7	15	0.0	0.00	0	1.0	2.06	1	0.0	0.00	0
D3Z0X3	Origin recognition complex subunit 5 (Fragment) OS=Mus musculus GN=Orc5 PE=1 SV=1 - [D3Z0X3_MOUSE]	7.1	36	0.0	0.00	0	1.0	3.16	1	0.0	0.00	0
D3Z0Y2	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=1 - [D3Z0Y2_MOUSE]	8.9	22	7.8	24.81	6	6.5	20.75	6	5.5	16.09	4
D3Z1B6	Regulator of G-protein-signaling 10 (Fragment) OS=Mus musculus GN=Rgs10 PE=1 SV=1 - [D3Z1B6_MOUSE]	4.9	10	1.3	4.06	3	0.0	0.00	0	1.5	4.01	2
D3Z1D3	Protein 3425401B19Rik OS=Mus musculus GN=3425401B19Rik PE=1 SV=1 - [D3Z1D3_MOUSE]	6.3	154	2.0	6.88	1	1.0	2.98	1	1.0	2.96	1
D3Z1K4	Zinc finger protein 276 (Fragment) OS=Mus musculus GN=Zfp276 PE=1 SV=1 - [D3Z1K4_MOUSE]	10.1	25	0.0	0.00	0	1.0	2.86	1	0.0	0.00	0

D3Z1T9	Mitochondrial-processing peptidase subunit beta (Fragment) OS=Mus musculus GN=Pmpcb PE=1 SV=1 - [D3Z	8.5	6	1.5	4.01	2	0.0	0.00	0	1.0	2.51	1
D3Z1U9	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1 PE=1 SV=1 -	7.0	42	1.0	2.86	1	0.0	0.00	0	0.0	0.00	0
D3Z223	Bisphosphoglycerate mutase (Fragment) OS=Mus musculus GN=Bpgm PE=1 SV=1 - [D3Z223_MOUSE]	6.9	20	1.0	4.64	1	0.0	0.00	0	1.0	3.94	1
D3Z2H9	Protein Tpm3-rs7 OS=Mus musculus GN=Tpm3-rs7 PE=3 SV=1 - [D3Z2H9_MOUSE]	4.8	29	34.0	91.33	1	24.5	67.48	2	23.0	62.85	1
D3Z2N7	Major vault protein (Fragment) OS=Mus musculus GN=Mvp PE=1 SV=2 - [D3Z2N7_MOUSE]	7.6	15	1.5	3.69	2	0.0	0.00	0	0.0	0.00	0
D3Z2Q2	Syntaxin-binding protein 5 OS=Mus musculus GN=Stxbp5 PE=1 SV=1 - [D3Z2Q2_MOUSE]	7.0	122	1.0	3.37	1	0.0	0.00	0	0.0	0.00	0
D3Z2Y7	Glutathione peroxidase (Fragment) OS=Mus musculus GN=Gpx3 PE=1 SV=1 - [D3Z2Y7_MOUSE]	5.6	22	1.8	4.27	5	1.7	3.64	3	1.0	2.13	3
D3Z368	Calcium/calmodulin-dependent protein kinase type 1 (Fragment) OS=Mus musculus GN=Camk1 PE=1 SV=1 - [	4.9	18	1.0	3.43	1	1.0	2.73	1	0.0	0.00	0
D3Z373	Protein Borcs8 OS=Mus musculus GN=Borcs8 PE=1 SV=1 - [D3Z373_MOUSE]	6.9	13	0.0	0.00	0	1.0	2.71	1	0.0	0.00	0
D3Z3B2	V-type proton ATPase 16 kDa proteolipid subunit (Fragment) OS=Mus musculus GN=Atp6v0c PE=1 SV=1 - [D	6.6	12	0.0	0.00	0	1.0	2.59	1	1.0	3.12	1
D3Z3I9	Heat shock protein 105 kDa (Fragment) OS=Mus musculus GN=Hsph1 PE=1 SV=1 - [D3Z3I9_MOUSE]	6.5	16	1.0	2.07	1	0.0	0.00	0	0.0	0.00	0
D3Z434	Synaptic vesicle membrane protein VAT-1 homolog-like (Fragment) OS=Mus musculus GN=Vat1l PE=1 SV=1 -	4.9	14	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
D3Z4A4	Peroxiredoxin-2 (Fragment) OS=Mus musculus GN=Prdx2 PE=1 SV=7 - [D3Z4A4_MOUSE]	5.5	16	11.2	37.11	6	18.7	62.05	6	15.3	50.36	6
D3Z4E2	Neuritin OS=Mus musculus GN=Nrn1 PE=1 SV=1 - [D3Z4E2_MOUSE]	5.4	17	0.0	0.00	0	1.0	2.09	2	1.5	3.12	2
D3Z4X1	6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=1 SV=1 - [D3Z4X1_MOUSE]	5.5	19	1.0	3.43	2	1.7	5.47	3	1.0	3.49	1
D3Z525	Smoothelin (Fragment) OS=Mus musculus GN=Smtn PE=1 SV=1 - [D3Z525_MOUSE]	5.7	14	1.0	3.02	4	0.0	0.00	0	1.0	2.08	1
D3Z534	Kalirin OS=Mus musculus GN=Kalrn PE=1 SV=1 - [D3Z534_MOUSE]	6.8	76	6.5	21.05	6	3.7	11.47	6	4.3	12.55	6
D3Z5G7	Carboxylic ester hydrolase OS=Mus musculus GN=Ces1b PE=1 SV=1 - [D3Z5G7_MOUSE]	5.2	62	0.0	0.00	0	12.0	36.05	1	0.0	0.00	0
D3Z5I6	IQ motif and SEC7 domain-containing protein 2 OS=Mus musculus GN=Iqsec2 PE=1 SV=1 - [D3Z5I6_MOUSE]	6.9	128	0.0	0.00	0	0.0	0.00	0	1.0	2.38	1
D3Z5M3	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1 - [D3Z5M3_MO	5.4	31	1.0	3.04	2	0.0	0.00	0	1.0	2.57	2
D3Z5Y0	Endothelial cell-selective adhesion molecule (Fragment) OS=Mus musculus GN=Esam PE=1 SV=1 - [D3Z5Y0_	8.5	27	1.0	2.49	2	0.0	0.00	0	0.0	0.00	0
D3Z6E8	Deleted in lung and esophageal cancer protein 1 homolog OS=Mus musculus GN=Dlec1 PE=4 SV=1 - [D3Z6E8	6.1	194	1.0	2.46	1	0.0	0.00	0	1.0	2.19	1
D3Z6F5	ATP synthase subunit alpha OS=Mus musculus GN=Atp5a1 PE=1 SV=1 - [D3Z6F5_MOUSE]	8.2	55	25.0	88.50	1	0.0	0.00	0	0.0	0.00	0
D3Z6I8	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=1 - [D3Z6I8_MOUSE]	4.8	29	0.0	0.00	0	23.0	63.82	1	0.0	0.00	0
D3Z6Q9	Bridging integrator 2 OS=Mus musculus GN=Bin2 PE=1 SV=1 - [BIN2_MOUSE]	5.3	53	21.7	75.01	6	19.3	66.66	3	19.3	64.06	6
D3Z6V7	IQ motif and SEC7 domain-containing protein 2 OS=Mus musculus GN=Iqsec2 PE=1 SV=1 - [D3Z6V7_MOUSE]	7.2	105	0.0	0.00	0	1.0	2.86	1	1.0	2.69	1
D3Z799	alpha-1,2-Mannosidase OS=Mus musculus GN=Man1a PE=1 SV=1 - [D3Z799_MOUSE]	9.4	42	0.0	0.00	0	1.0	3.29	1	0.0	0.00	0
D3Z7E4	cAMP-dependent protein kinase type I-beta regulatory subunit (Fragment) OS=Mus musculus GN=Prkar1b P	6.0	10	1.0	2.06	2	1.0	2.20	1	0.0	0.00	0
D3Z7H6	Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=1 - [D3Z7H6_MOUSE]	7.0	93	0.0	0.00	0	1.0	2.67	1	0.0	0.00	0
D3Z7K0	Ubiquitin thioesterase OTUB1 (Fragment) OS=Mus musculus GN=Otub1 PE=1 SV=1 - [D3Z7K0_MOUSE]	7.3	11	1.0	2.90	2	0.0	0.00	0	0.0	0.00	0
D3Z7N2	Elongation factor 1-delta (Fragment) OS=Mus musculus GN=Eef1d PE=1 SV=1 - [D3Z7N2_MOUSE]	5.9	14	0.0	0.00	0	0.0	0.00	0	1.0	4.23	1
D3Z7T0	Striated muscle-specific serine/threonine-protein kinase (Fragment) OS=Mus musculus GN=Speg PE=1 SV=	10.2	33	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
D6RDD7	Major facilitator superfamily domain-containing protein 2B OS=Mus musculus GN=Mfsd2b PE=1 SV=1 - [D6	8.6	12	1.0	2.44	2	2.0	4.86	1	1.0	2.16	1
D6REF3	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 - [D6REF3_MOUSE]	5.2	15	0.0	0.00	0	2.0	6.56	1	0.0	0.00	0
D6RET6	G patch domain-containing protein 1 OS=Mus musculus GN=Gpatch1 PE=1 SV=1 - [D6RET6_MOUSE]	6.8	98	1.0	2.60	1	0.0	0.00	0	0.0	0.00	0
D6REV1	Putative Polycomb group protein ASXL2 OS=Mus musculus GN=Asxl2 PE=1 SV=2 - [D6REV1_MOUSE]	8.9	147	0.0	0.00	0	1.0	2.13	1	0.0	0.00	0
D6RFD7	Medium-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadm PE=1 SV=1 - [D6	10.1	18	0.0	0.00	0	1.0	2.25	1	1.0	2.68	1
D6RGM3	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus GN=Eml2 PE=1 SV=1 - [D6RGM3_MOUSE]	6.6	47	3.0	9.45	2	2.5	8.08	4	2.3	7.22	4
D6RHS6	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=1 - [D6RHS6_MOUSE]	5.1	15	2.3	6.13	6	1.4	3.77	5	1.6	4.34	5
E0CXB1	Proteasome subunit alpha type-6 OS=Mus musculus GN=Psma6 PE=1 SV=1 - [E0CXB1_MOUSE]	7.9	25	0.0	0.00	0	0.0	0.00	0	1.0	2.38	1
E0CXJ3	Eukaryotic translation initiation factor 2 subunit 2 (Fragment) OS=Mus musculus GN=Eif2s2 PE=1 SV=1	4.6	14	1.0	3.09	1	1.2	4.55	5	1.0	3.56	4
E0CXV7	Cation-independent mannose-6-phosphate receptor (Fragment) OS=Mus musculus GN=Igf2r PE=4 SV=1 - [E0C	8.1	6	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
E0CXW2	Uncharacterized aarF domain-containing protein kinase 5 OS=Mus musculus GN=Adck5 PE=1 SV=1 - [E0CXW2	8.8	64	0.0	0.00	0	1.0	2.79	2	0.0	0.00	0
E0CY53	Beta-arrestin-1 (Fragment) OS=Mus musculus GN=Arrb1 PE=1 SV=7 - [E0CY53_MOUSE]	7.9	15	0.0	0.00	0	2.0	6.49	1	3.0	8.80	2
E0CY57	Protein Nsmce4a (Fragment) OS=Mus musculus GN=Nsmce4a PE=1 SV=1 - [E0CY57_MOUSE]	5.0	30	1.0	3.08	2	0.0	0.00	0	0.0	0.00	0
E0CY82	Programmed cell death protein 10 (Fragment) OS=Mus musculus GN=Pdcd10 PE=1 SV=1 - [E0CY82_MOUSE]	5.0	8	0.0	0.00	0	1.0	2.60	2	0.0	0.00	0
E0CYQ4	Inositol polyphosphate 1-phosphatase (Fragment) OS=Mus musculus GN=Inpp1 PE=1 SV=1 - [E0CYQ4_MOUSE]	6.6	9	1.3	3.07	4	0.0	0.00	0	0.0	0.00	0
E0CYV5	Traf2 and NCK-interacting protein kinase OS=Mus musculus GN=Tnik PE=1 SV=1 - [E0CYV5_MOUSE]	6.2	25	0.0	0.00	0	1.0	2.69	2	1.0	2.49	1
E0CYZ1	Solute carrier family 35 member C2 OS=Mus musculus GN=Slc35c2 PE=4 SV=1 - [E0CYZ1_MOUSE]	8.8	8	1.0	2.90	1	0.0	0.00	0	1.0	3.23	1
E0CZ90	Proteasome activator complex subunit 2 (Fragment) OS=Mus musculus GN=Psme2 PE=1 SV=1 - [E0CZ90_MOUSE	4.9	19	0.0	0.00	0	1.0	2.87	1	1.5	3.89	2
E0CZA1	T-complex protein 1 subunit epsilon (Fragment) OS=Mus musculus GN=Cct5 PE=1 SV=1 - [E0CZA1_MOUSE]	5.0	22	0.0	0.00	0	0.0	0.00	0	2.0	5.90	1
E0CZD4	Beta-centractin (Fragment) OS=Mus musculus GN=Actr1b PE=1 SV=1 - [E0CZD4_MOUSE]	5.3	16	1.0	3.19	1	0.0	0.00	0	0.0	0.00	0
E0CZF8	Traf2 and NCK-interacting protein kinase OS=Mus musculus GN=Tnik PE=1 SV=1 - [E0CZF8_MOUSE]	7.1	144	0.0	0.00	0	1.0	3.18	1	0.0	0.00	0
E2QRQ3	Double-stranded RNA-binding protein Staufen homolog 2 OS=Mus musculus GN=Stau2 PE=1 SV=1 - [E2QRQ3_M	9.7	52	0.0	0.00	0	0.0	0.00	0	1.0	3.16	1
E9PUD2	Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=1 - [E9PUD2_MOUSE]	7.1	79	5.3	16.66	6	3.0	9.17	5	3.5	10.99	6
E9PUM3	Alpha-1,4 glucan phosphorylase OS=Mus musculus GN=Pygm PE=1 SV=1 - [E9PUM3_MOUSE]	8.5	87	3.0	7.62	4	3.0	7.10	1	0.0	0.00	0
E9PUN1	Protein Nrxn2 OS=Mus musculus GN=Nrxn2 PE=1 SV=1 - [E9PUN1_MOUSE]	6.6	37	1.0	2.83	2	0.0	0.00	0	0.0	0.00	0
E9PUU5	Protein Zfp839 OS=Mus musculus GN=Zfp839 PE=4 SV=1 - [E9PUU5_MOUSE]	5.9	99	0.0	0.00	0	0.0	0.00	0	1.0	3.30	1
E9PV24	Fibrinogen alpha chain OS=Mus musculus GN=Fga PE=1 SV=1 - [FIBA_MOUSE]	6.1	87	88.3	314.04	6	78.5	267.28	6	82.5	281.60	6
E9PVD2	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=1 - [E9PVD2_MOUSE]	6.4	105	15.0	47.28	1	0.0	0.00	0	0.0	0.00	0
E9PW14	Nuclear protein MDM1 OS=Mus musculus GN=Mdm1 PE=1 SV=1 - [E9PW14_MOUSE]	9.6	77	1.0	2.98	1	1.0	2.90	2	0.0	0.00	0
E9PWE9	Tyrosine-protein kinase OS=Mus musculus GN=Syk PE=1 SV=1 - [E9PWE9_MOUSE]	7.2	66	4.6	17.86	5	4.8	19.08	6	3.5	13.99	6
E9PWJ5	E3 ubiquitin-protein ligase RNF43 OS=Mus musculus GN=Rnf43 PE=4 SV=1 - [E9PWJ5_MOUSE]	8.4	82	0.0	0.00	0	0.0	0.00	0	1.0	2.07	1
E9PWM3	Protein Armcx4 OS=Mus musculus GN=Armcx4 PE=1 SV=1 - [E9PWM3_MOUSE]	4.9	243	0.0	0.00	0	0.0	0.00	0	1.0	3.26	1
E9PWS2	Pigment epithelium-derived factor OS=Mus musculus GN=Serpinf1 PE=1 SV=1 - [E9PWS2_MOUSE]	5.8	16	1.0	3.23	1	0.0	0.00	0	1.0	2.68	1
E9PWW9	Protein Rsf1 OS=Mus musculus GN=Rsf1 PE=1 SV=2 - [E9PWW9_MOUSE]	5.0	162	1.0	2.19	1	0.0	0.00	0	0.0	0.00	0

E9PYI8	Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=1 - [E9PYI8_MOUSE]	5.7	52	0.0	0.00	0	1.0	2.35	1	0.0	0.00	0
E9PYT3	Atlastin-3 OS=Mus musculus GN=Atl3 PE=1 SV=1 - [E9PYT3_MOUSE]	5.8	60	1.7	5.69	6	1.0	3.16	2	1.3	4.23	3
E9PZ00	Prosaposin OS=Mus musculus GN=Psap PE=1 SV=1 - [E9PZ00_MOUSE]	5.2	61	1.0	2.06	1	1.0	2.12	1	1.0	2.07	2
E9PZF0	Nucleoside diphosphate kinase OS=Mus musculus GN=Gm20390 PE=3 SV=1 - [E9PZF0_MOUSE]	8.7	30	12.8	43.71	6	14.0	47.73	4	12.2	39.62	5
E9Q0X0	Proteasome subunit alpha type (Fragment) OS=Mus musculus GN=Psma4 PE=1 SV=1 - [E9Q0X0_MOUSE]	5.9	16	1.0	2.20	3	1.0	2.21	3	1.7	3.60	3
E9Q133	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1 - [E9Q133_MOUSE]	6.7	56	5.5	14.28	6	7.0	19.41	2	5.7	14.76	3
E9Q175	Unconventional myosin-VI OS=Mus musculus GN=Myo6 PE=1 SV=1 - [E9Q175_MOUSE]	8.5	145	1.5	4.06	2	0.0	0.00	0	1.0	2.07	1
E9Q197	Glyoxalase domain-containing protein 4 OS=Mus musculus GN=Glod4 PE=1 SV=1 - [E9Q197_MOUSE]	5.3	31	0.0	0.00	0	0.0	0.00	0	1.0	2.59	1
E9Q1D5	Transforming growth factor beta-1-induced transcript 1 protein OS=Mus musculus GN=Tgfb1i1 PE=1 SV=1	6.9	46	2.0	5.57	5	2.2	6.09	6	1.7	4.39	6
E9Q1K3	Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=1 - [E9Q1K3_MOUSE]	6.3	73	4.3	11.72	3	1.5	3.56	2	0.0	0.00	0
E9Q1Y3	Apolipoprotein B-100 (Fragment) OS=Mus musculus GN=Apob PE=1 SV=1 - [E9Q1Y3_MOUSE]	6.8	504	3.0	9.12	2	3.0	8.53	3	1.3	3.33	3
E9Q2Y4	T-lymphoma invasion and metastasis-inducing protein 1 OS=Mus musculus GN=Tiam1 PE=1 SV=1 - [E9Q2Y4_M	5.6	87	1.0	2.28	1	0.0	0.00	0	0.0	0.00	0
E9Q309	Protein Cep350 OS=Mus musculus GN=Cep350 PE=1 SV=1 - [E9Q309_MOUSE]	6.4	346	1.0	3.26	1	0.0	0.00	0	0.0	0.00	0
E9Q3T0	Protein Gm10073 OS=Mus musculus GN=Gm10073 PE=1 SV=1 - [E9Q3T0_MOUSE]	4.4	11	2.3	6.14	6	1.3	3.24	3	1.5	3.75	4
E9Q3T3	Kinesin-like protein OS=Mus musculus GN=Kif14 PE=1 SV=1 - [E9Q3T3_MOUSE]	7.6	181	1.0	2.55	1	0.0	0.00	0	0.0	0.00	0
E9Q3T7	Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=1 SV=1 - [E9Q3T7_MOUSE]	7.8	48	2.0	6.18	1	0.0	0.00	0	0.0	0.00	0
E9Q3V6	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=1 - [E9Q3V6_MOUSE]	6.1	37	5.3	17.39	4	2.5	8.07	6	3.8	11.07	5
E9Q3X9	Serine protease hepsin (Fragment) OS=Mus musculus GN=Hpn PE=4 SV=1 - [E9Q3X9_MOUSE]	8.3	9	0.0	0.00	0	1.0	2.64	1	0.0	0.00	0
E9Q401	Ryanodine receptor 2 OS=Mus musculus GN=Ryr2 PE=1 SV=1 - [RYR2_MOUSE]	6.1	564	0.0	0.00	0	1.0	2.60	1	1.0	2.52	1
E9Q453	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1 - [E9Q453_MOUSE]	4.8	28	11.5	28.29	2	11.0	26.53	2	12.0	27.30	1
E9Q4F7	Protein Ankrd11 OS=Mus musculus GN=Ankrd11 PE=1 SV=1 - [E9Q4F7_MOUSE]	7.0	296	1.0	2.15	1	0.0	0.00	0	0.0	0.00	0
E9Q4F9	Homer protein homolog 2 OS=Mus musculus GN=Homer2 PE=1 SV=1 - [E9Q4F9_MOUSE]	5.5	33	1.0	2.87	1	0.0	0.00	0	1.0	3.63	1
E9Q509	Pyruvate kinase OS=Mus musculus GN=Pklr PE=1 SV=1 - [E9Q509_MOUSE]	6.9	59	7.0	15.95	2	6.0	13.13	3	6.0	13.48	3
E9Q555	E3 ubiquitin-protein ligase RNF213 OS=Mus musculus GN=Rnf213 PE=1 SV=2 - [RN213_MOUSE]	6.8	584	1.0	2.55	1	0.0	0.00	0	0.0	0.00	0
E9Q5E0	Myocyte-specific enhancer factor 2D OS=Mus musculus GN=Mef2d PE=1 SV=1 - [E9Q5E0_MOUSE]	8.4	54	1.3	3.40	3	1.0	2.65	2	1.0	2.67	2
E9Q5F6	Polyubiquitin-C (Fragment) OS=Mus musculus GN=Ubc PE=4 SV=1 - [E9Q5F6_MOUSE]	7.4	23	7.7	25.04	6	7.7	25.09	6	7.3	23.78	6
E9Q5K2	Protein Gm17728 OS=Mus musculus GN=Gm17728 PE=4 SV=1 - [E9Q5K2_MOUSE]	7.9	15	1.0	2.52	1	0.0	0.00	0	0.0	0.00	0
E9Q5L2	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=1 - [E9Q5L2_MOUSE]	6.4	103	11.4	36.09	5	11.0	33.79	6	7.0	23.61	5
E9Q5N7	Protein Nrxn2 OS=Mus musculus GN=Nrxn2 PE=1 SV=2 - [E9Q5N7_MOUSE]	6.0	163	1.0	3.25	2	0.0	0.00	0	1.5	4.69	2
E9Q5R7	NACHT, LRR and PYD domains-containing protein 12 OS=Mus musculus GN=Nlrp12 PE=2 SV=1 - [NAL12_MOUSE]	7.1	119	1.0	2.90	1	3.8	10.93	4	2.0	5.89	3
E9Q624	Protein Zfp644 OS=Mus musculus GN=Zfp644 PE=1 SV=1 - [E9Q624_MOUSE]	8.3	145	0.0	0.00	0	0.0	0.00	0	1.0	2.40	1
E9Q698	Coagulation factor XII OS=Mus musculus GN=F12 PE=1 SV=1 - [E9Q698_MOUSE]	4.8	15	1.0	2.81	1	0.0	0.00	0	1.0	2.50	1
E9Q6F4	Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Npepps PE=1 SV=1 - [E9Q6F4_MOUSE]	5.5	76	1.0	2.30	1	0.0	0.00	0	0.0	0.00	0
E9Q6I9	Transmembrane protein 40 OS=Mus musculus GN=Tmem40 PE=1 SV=1 - [E9Q6I9_MOUSE]	6.8	22	1.8	5.39	5	1.8	5.05	4	1.5	4.23	4
E9Q6R3	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=1 - [E9Q6R3_MOUSE]	5.9	19	1.4	4.07	5	1.0	2.87	2	1.5	4.07	2
E9Q741	Chloride transport protein 6 OS=Mus musculus GN=Clcn6 PE=1 SV=1 - [E9Q741_MOUSE]	7.7	81	0.0	0.00	0	2.3	6.04	3	1.0	2.65	1
E9Q7D8	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=1 SV=1 - [E9Q7D8_MOUSE]	8.9	24	0.0	0.00	0	1.0	2.81	2	0.0	0.00	0
E9Q7H6	Threonine--tRNA ligase, mitochondrial OS=Mus musculus GN=Tars2 PE=1 SV=1 - [E9Q7H6_MOUSE]	7.8	73	2.0	5.38	2	1.0	2.73	3	1.0	2.40	1
E9Q7Q3	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=1 - [E9Q7Q3_MOUSE]	4.7	29	27.3	74.63	6	24.4	66.87	5	25.2	68.32	6
E9Q8F9	Protein 6030445D17Rik OS=Mus musculus GN=6030445D17Rik PE=4 SV=1 - [E9Q8F9_MOUSE]	11.9	16	1.0	2.71	1	0.0	0.00	0	1.0	2.68	2
E9Q8K5	Titin OS=Mus musculus GN=Ttn PE=1 SV=1 - [E9Q8K5_MOUSE]	6.4	3714	0.0	0.00	0	2.0	4.89	1	0.0	0.00	0
E9Q8S5	Microtubule-associated serine/threonine-protein kinase 3 OS=Mus musculus GN=Mast3 PE=1 SV=1 - [E9Q8S	8.6	142	0.0	0.00	0	0.0	0.00	0	2.0	4.59	1
E9Q8T7	Protein Dnah1 OS=Mus musculus GN=Dnah1 PE=1 SV=1 - [E9Q8T7_MOUSE]	5.6	487	0.0	0.00	0	1.0	3.15	1	1.5	4.70	2
E9Q9B8	Clusterin (Fragment) OS=Mus musculus GN=Clu PE=1 SV=1 - [E9Q9B8_MOUSE]	5.2	23	0.0	0.00	0	3.5	8.10	2	2.0	5.15	1
E9Q9D8	Protein Ankrd35 OS=Mus musculus GN=Ankrd35 PE=1 SV=1 - [E9Q9D8_MOUSE]	6.1	109	0.0	0.00	0	0.0	0.00	0	1.0	2.20	2
E9Q9F3	Protein Cald1 (Fragment) OS=Mus musculus GN=Cald1 PE=1 SV=1 - [E9Q9F3_MOUSE]	5.2	30	0.0	0.00	0	4.0	11.24	2	0.0	0.00	0
E9QAB2	Metalloproteinase inhibitor 3 (Fragment) OS=Mus musculus GN=Timp3 PE=1 SV=1 - [E9QAB2_MOUSE]	10.4	6	3.2	7.36	5	2.8	6.55	6	3.2	7.45	5
E9QAQ8	Protein Muc5ac OS=Mus musculus GN=Muc5ac PE=1 SV=4 - [E9QAQ8_MOUSE]	5.9	372	0.0	0.00	0	0.0	0.00	0	1.0	2.95	2
E9QKU9	Tetratricopeptide repeat protein 23 OS=Mus musculus GN=Ttc23 PE=1 SV=1 - [E9QKU9_MOUSE]	8.1	50	1.0	2.63	1	0.0	0.00	0	0.0	0.00	0
E9QKX5	Vacuolar protein sorting-associated protein 13B OS=Mus musculus GN=Vps13b PE=1 SV=1 - [E9QKX5_MOUSE]	6.5	444	1.8	4.02	5	1.7	3.69	3	3.0	6.97	3
E9QLA5	Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1 - [E9QLA5_MOUSE]	5.2	138	1.4	3.88	5	2.0	5.37	5	1.8	4.87	5
E9QLQ7	Ras-related protein Rab-7L1 OS=Mus musculus GN=Rab29 PE=1 SV=1 - [E9QLQ7_MOUSE]	7.2	23	1.0	2.43	3	2.0	4.57	1	1.5	3.45	2
E9QMV2	Costars family protein ABRACL OS=Mus musculus GN=Abracl PE=1 SV=1 - [E9QMV2_MOUSE]	5.8	9	1.8	4.20	4	2.0	4.68	2	1.5	3.47	2
E9QN08	Elongation factor 1-delta (Fragment) OS=Mus musculus GN=Eef1d PE=1 SV=1 - [E9QN08_MOUSE]	5.5	27	3.5	15.58	4	4.0	18.83	2	3.3	14.09	3
E9QNL8	Integrin alpha-L OS=Mus musculus GN=Itgal PE=1 SV=1 - [E9QNL8_MOUSE]	5.9	128	1.8	4.09	4	1.0	2.17	1	0.0	0.00	0
E9QPU1	von Willebrand factor OS=Mus musculus GN=Vwf PE=1 SV=2 - [E9QPU1_MOUSE]	5.5	309	35.3	135.69	6	27.7	101.25	6	27.7	106.53	6
E9QPX1	Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1 PE=1 SV=1 - [E9QPX1_MOUSE]	5.7	182	0.0	0.00	0	1.0	2.55	2	1.0	2.43	2
F2Z405	Serine protease inhibitor A3G OS=Mus musculus GN=Serpina3g PE=1 SV=1 - [F2Z405_MOUSE]	6.9	28	0.0	0.00	0	16.0	57.29	1	0.0	0.00	0
F2Z471	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=1 - [F2Z471_MOU	7.4	28	5.0	13.08	1	4.5	12.83	2	3.0	8.64	3
F6Q4H2	Ephrin type-B receptor 2 (Fragment) OS=Mus musculus GN=Ephb2 PE=1 SV=1 - [F6Q4H2_MOUSE]	5.9	31	0.0	0.00	0	1.0	2.08	1	0.0	0.00	0
F6Q609	T-complex protein 1 subunit gamma (Fragment) OS=Mus musculus GN=Cct3 PE=1 SV=7 - [F6Q609_MOUSE]	5.6	34	3.0	8.07	3	2.5	6.67	4	2.0	5.11	4
F6Q8V7	Prohibitin-2 (Fragment) OS=Mus musculus GN=Phb2 PE=1 SV=1 - [F6Q8V7_MOUSE]	9.9	12	1.0	2.08	1	0.0	0.00	0	0.0	0.00	0
F6QC68	Ras-related protein Ral-B (Fragment) OS=Mus musculus GN=Ralb PE=1 SV=2 - [F6QC68_MOUSE]	5.1	17	1.0	2.50	1	0.0	0.00	0	0.0	0.00	0
F6R587	Copine-1 (Fragment) OS=Mus musculus GN=Cpne1 PE=1 SV=1 - [F6R587_MOUSE]	9.1	22	0.0	0.00	0	1.0	2.12	1	0.0	0.00	0
F6RBL8	Intraflagellar transport protein 52 homolog (Fragment) OS=Mus musculus GN=Ift52 PE=1 SV=1 - [F6RBL8_	8.3	26	0.0	0.00	0	1.0	2.15	2	1.0	2.11	1
F6RU08	Zinc finger protein 827 (Fragment) OS=Mus musculus GN=Zfp827 PE=1 SV=1 - [F6RU08_MOUSE]	6.5	25	2.0	6.07	2	1.0	3.07	1	1.0	3.54	1

F6S397	Next to BRCA1 gene 1 protein (Fragment) OS=Mus musculus GN=Nbr1 PE=1 SV=1 - [F6S397_MOUSE]	5.4	79	0.0	0.00	0	1.0	2.62	1	0.0	0.00	0
F6S4G2	Phosphatidate cytidylyltransferase (Fragment) OS=Mus musculus GN=Cds2 PE=1 SV=1 - [F6S4G2_MOUSE]	7.7	22	2.0	6.41	1	0.0	0.00	0	0.0	0.00	0
F6ST32	Carbonic anhydrase 4 (Fragment) OS=Mus musculus GN=Car4 PE=1 SV=1 - [F6ST32_MOUSE]	9.2	19	0.0	0.00	0	1.0	2.78	1	0.0	0.00	0
F6SUU5	Kinesin-like protein (Fragment) OS=Mus musculus GN=Kif2a PE=1 SV=1 - [F6SUU5_MOUSE]	9.3	19	1.0	2.44	6	1.0	2.52	2	1.0	2.28	4
F6SVV1	Protein Gm9493 OS=Mus musculus GN=Gm9493 PE=4 SV=1 - [F6SVV1_MOUSE]	10.0	22	0.0	0.00	0	2.0	5.94	1	0.0	0.00	0
F6THG2	Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Mus musculus GN=Arpc1b PE=1 SV=1 - [F6THG	8.7	11	1.3	3.70	4	1.0	2.66	4	1.0	2.63	4
F6TS96	Transducin-like enhancer protein 3 (Fragment) OS=Mus musculus GN=Tle3 PE=1 SV=1 - [F6TS96_MOUSE]	7.2	75	0.0	0.00	0	0.0	0.00	0	1.0	2.55	1
F6TW36	DNA excision repair protein ERCC-6-like 2 (Fragment) OS=Mus musculus GN=Ercc6l2 PE=4 SV=1 - [F6TW36_	8.7	22	1.0	2.61	3	0.0	0.00	0	1.0	2.62	1
F6U786	Rho guanine nucleotide exchange factor 38 OS=Mus musculus GN=Arhgef38 PE=4 SV=1 - [F6U786_MOUSE]	5.1	21	0.0	0.00	0	1.0	2.62	1	0.0	0.00	0
F6UKN5	Septin-2 (Fragment) OS=Mus musculus GN=Sept2 PE=1 SV=2 - [F6UKN5_MOUSE]	5.3	12	3.0	9.71	1	0.0	0.00	0	0.0	0.00	0
F6USD5	Mesencephalic astrocyte-derived neurotrophic factor (Fragment) OS=Mus musculus GN=Manf PE=1 SV=1 - [	6.5	14	1.0	2.78	1	0.0	0.00	0	1.5	5.77	2
F6UYN4	Kinesin light chain 1 (Fragment) OS=Mus musculus GN=Klc1 PE=1 SV=1 - [F6UYN4_MOUSE]	8.8	20	1.0	2.31	1	0.0	0.00	0	0.0	0.00	0
F6V072	FYN-binding protein (Fragment) OS=Mus musculus GN=Fyb PE=1 SV=1 - [F6V072_MOUSE]	4.7	20	1.0	2.99	1	1.0	3.49	2	1.0	3.40	2
F6V084	Thioredoxin-related transmembrane protein 1 (Fragment) OS=Mus musculus GN=Tmx1 PE=1 SV=1 - [F6V084_M	5.1	14	1.2	3.54	6	1.3	3.49	4	1.7	4.42	6
F6V4G5	Alpha-adducin (Fragment) OS=Mus musculus GN=Add1 PE=1 SV=1 - [F6V4G5_MOUSE]	9.3	15	0.0	0.00	0	1.5	3.92	2	1.5	3.84	2
F6V6T4	Transmembrane emp24 domain-containing protein 2 (Fragment) OS=Mus musculus GN=Tmed2 PE=1 SV=1 - [F6V	9.1	20	2.5	9.20	2	1.5	4.99	2	3.0	10.85	2
F6V9F1	Protein-L-isoaspartate O-methyltransferase (Fragment) OS=Mus musculus GN=Pcmt1 PE=1 SV=1 - [F6V9F1_M	5.7	19	0.0	0.00	0	1.0	2.41	1	0.0	0.00	0
F6VEI7	Mitogen-activated protein kinase 1 (Fragment) OS=Mus musculus GN=Mapk1 PE=1 SV=1 - [F6VEI7_MOUSE]	5.2	16	1.0	2.30	3	0.0	0.00	0	1.0	2.04	1
F6VQ81	Tumor protein D54 (Fragment) OS=Mus musculus GN=Tpd52l2 PE=1 SV=1 - [F6VQ81_MOUSE]	8.2	18	1.0	2.58	2	0.0	0.00	0	0.0	0.00	0
F6VSK8	Integrin alpha-6 (Fragment) OS=Mus musculus GN=Itga6 PE=1 SV=1 - [F6VSK8_MOUSE]	8.6	75	12.0	39.07	1	4.0	12.65	1	9.0	25.07	1
F6VTH5	Leucine zipper transcription factor-like protein 1 (Fragment) OS=Mus musculus GN=Lztfl1 PE=1 SV=1 -	4.8	27	2.3	5.06	3	1.0	2.06	2	2.8	5.85	4
F6VTL9	Neurobeachin-like protein 2 (Fragment) OS=Mus musculus GN=Nbeal2 PE=1 SV=1 - [F6VTL9_MOUSE]	6.8	224	1.6	4.96	5	1.5	4.41	4	1.0	3.51	2
F6W0C2	Serine/threonine-protein kinase MRCK alpha (Fragment) OS=Mus musculus GN=Cdc42bpa PE=1 SV=1 - [F6W0C	7.0	21	0.0	0.00	0	0.0	0.00	0	1.0	2.57	1
F6W4D3	Protein 1300017J02Rik (Fragment) OS=Mus musculus GN=1300017J02Rik PE=1 SV=1 - [F6W4D3_MOUSE]	7.9	27	0.0	0.00	0	1.0	2.50	1	1.0	2.28	1
F6W7D6	Transcription factor EB (Fragment) OS=Mus musculus GN=Tfeb PE=1 SV=1 - [F6W7D6_MOUSE]	5.5	37	1.0	2.63	1	0.0	0.00	0	0.0	0.00	0
F6WXQ4	Syntaxin-binding protein 5 (Fragment) OS=Mus musculus GN=Stxbp5 PE=1 SV=7 - [F6WXQ4_MOUSE]	8.7	29	1.0	2.28	1	0.0	0.00	0	0.0	0.00	0
F6WYQ5	Phospholipid-transporting ATPase OS=Mus musculus GN=Atp8a1 PE=1 SV=2 - [F6WYQ5_MOUSE]	7.3	130	0.0	0.00	0	1.0	2.62	1	1.0	2.67	2
F6X089	Merlin (Fragment) OS=Mus musculus GN=Nf2 PE=1 SV=1 - [F6X089_MOUSE]	5.8	10	5.7	17.97	6	6.2	19.43	5	6.5	19.77	6
F6X8L5	6-phosphogluconolactonase (Fragment) OS=Mus musculus GN=Pgls PE=1 SV=1 - [F6X8L5_MOUSE]	5.7	20	1.0	2.72	1	2.0	5.96	1	0.0	0.00	0
F6XQ00	Complement factor B OS=Mus musculus GN=Cfb PE=4 SV=1 - [F6XQ00_MOUSE]	7.9	79	2.3	5.65	4	0.0	0.00	0	5.0	14.26	2
F6XU64	G patch domain and KOW motifs-containing protein (Fragment) OS=Mus musculus GN=Gpkow PE=1 SV=1 - [F6	9.7	21	0.0	0.00	0	2.5	5.21	2	0.0	0.00	0
F6XWD4	Protein phosphatase 1 regulatory subunit 12C (Fragment) OS=Mus musculus GN=Ppp1r12c PE=1 SV=1 - [F6X	6.0	77	0.0	0.00	0	1.0	3.37	1	1.0	3.63	1
F6XXE6	Protein Agl (Fragment) OS=Mus musculus GN=Agl PE=1 SV=2 - [F6XXE6_MOUSE]	7.5	93	2.0	6.08	1	0.0	0.00	0	0.0	0.00	0
F6YIW9	Leucine-rich repeat serine/threonine-protein kinase 1 (Fragment) OS=Mus musculus GN=Lrrk1 PE=1 SV=1	6.3	58	0.0	0.00	0	1.0	2.96	1	1.0	2.90	3
F6YSS8	Intelectin-1a (Fragment) OS=Mus musculus GN=Itln1 PE=1 SV=7 - [F6YSS8_MOUSE]	6.1	15	0.0	0.00	0	2.0	6.43	2	2.0	5.98	1
F6Z2S4	Unconventional myosin-Va (Fragment) OS=Mus musculus GN=Myo5a PE=1 SV=1 - [F6Z2S4_MOUSE]	5.0	25	1.0	2.49	1	0.0	0.00	0	0.0	0.00	0
F6Z458	Endoplasmic reticulum lectin 1 (Fragment) OS=Mus musculus GN=Erlec1 PE=1 SV=1 - [F6Z458_MOUSE]	7.5	27	1.0	2.31	2	0.0	0.00	0	0.0	0.00	0
F6ZAX1	Polyadenylate-binding protein 1 (Fragment) OS=Mus musculus GN=Pabpc1 PE=1 SV=1 - [F6ZAX1_MOUSE]	6.0	13	0.0	0.00	0	1.0	3.33	1	0.0	0.00	0
F6ZBD9	BCL-6 corepressor-like protein 1 (Fragment) OS=Mus musculus GN=Bcorl1 PE=1 SV=1 - [F6ZBD9_MOUSE]	9.0	80	1.0	2.04	1	0.0	0.00	0	0.0	0.00	0
F6ZFV0	Plasminogen activator inhibitor 2, macrophage (Fragment) OS=Mus musculus GN=Serpinb2 PE=1 SV=1 - [F6	5.1	22	0.0	0.00	0	1.0	2.46	1	0.0	0.00	0
F6ZTG3	Glyoxalase domain-containing protein 4 (Fragment) OS=Mus musculus GN=Glod4 PE=1 SV=1 - [F6ZTG3_MOUSE	5.1	24	1.0	2.74	1	1.0	2.02	1	1.0	2.96	2
F6ZZB1	Neurobeachin-like protein 2 (Fragment) OS=Mus musculus GN=Nbeal2 PE=1 SV=1 - [F6ZZB1_MOUSE]	6.8	120	0.0	0.00	0	0.0	0.00	0	1.0	2.11	1
F7AAE0	Phosphoinositide phospholipase C (Fragment) OS=Mus musculus GN=Plcd3 PE=1 SV=1 - [F7AAE0_MOUSE]	6.0	52	0.0	0.00	0	1.0	2.94	1	1.0	3.10	1
F7B7L8	26S proteasome non-ATPase regulatory subunit 3 (Fragment) OS=Mus musculus GN=Psmd3 PE=1 SV=1 - [F7B7	10.1	25	1.0	3.52	1	1.0	3.39	1	0.0	0.00	0
F7B9R2	Ras-specific guanine nucleotide-releasing factor 2 (Fragment) OS=Mus musculus GN=Rasgrf2 PE=1 SV=1 -	8.5	66	1.0	2.79	1	1.0	3.00	1	1.5	4.62	2
F7BYZ4	Serine/threonine-protein kinase 4 (Fragment) OS=Mus musculus GN=Stk4 PE=1 SV=1 - [F7BYZ4_MOUSE]	4.8	23	0.0	0.00	0	1.0	2.41	1	0.0	0.00	0
F7C0X9	Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma (Fragment) OS=Mus musculus GN=Pip5k1c PE=1 SV	7.5	24	0.0	0.00	0	1.0	2.11	1	1.0	2.14	1
F7C1S6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment) OS=Mus musculus GN=Manf PE=1 SV=1 - [	7.3	6	0.0	0.00	0	1.0	3.26	1	0.0	0.00	0
F7C3I9	Afadin (Fragment) OS=Mus musculus GN=Mllt4 PE=1 SV=1 - [F7C3I9_MOUSE]	5.1	41	0.0	0.00	0	0.0	0.00	0	1.0	2.96	1
F7CAZ6	F-actin-capping protein subunit beta (Fragment) OS=Mus musculus GN=Capzb PE=1 SV=1 - [F7CAZ6_MOUSE]	6.2	23	4.0	11.35	2	0.0	0.00	0	0.0	0.00	0
F7CLL3	Killer cell lectin-like receptor 5 OS=Mus musculus GN=Klra5 PE=4 SV=1 - [F7CLL3_MOUSE]	7.8	21	1.0	2.06	1	0.0	0.00	0	0.0	0.00	0
F7CR78	Titin (Fragment) OS=Mus musculus GN=Ttn PE=1 SV=1 - [F7CR78_MOUSE]	5.5	913	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
F7CSZ6	Protein Agl (Fragment) OS=Mus musculus GN=Agl PE=1 SV=1 - [F7CSZ6_MOUSE]	6.8	22	1.0	2.66	1	0.0	0.00	0	0.0	0.00	0
F7D1P5	Ankyrin-1 (Fragment) OS=Mus musculus GN=Ank1 PE=1 SV=1 - [F7D1P5_MOUSE]	7.4	121	0.0	0.00	0	3.0	10.80	1	3.0	8.21	2
F7D3P8	ATP synthase subunit O, mitochondrial (Fragment) OS=Mus musculus GN=Atp5o PE=1 SV=7 - [F7D3P8_MOUSE]	8.6	20	2.3	8.33	4	1.5	5.31	2	2.0	6.29	2
F7D5X7	snRNA-activating protein complex subunit 4 (Fragment) OS=Mus musculus GN=Snapc4 PE=4 SV=1 - [F7D5X7_	9.6	30	1.0	3.01	4	1.0	2.91	1	0.0	0.00	0
F8WGE3	ATP-binding cassette sub-family A member 8-A OS=Mus musculus GN=Abca8a PE=1 SV=1 - [F8WGE3_MOUSE]	7.4	184	1.0	2.90	1	1.0	2.13	1	1.0	2.48	2
F8WHP8	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=1 - [F8WHP8_MOUSE]	9.9	9	2.2	5.23	6	2.8	6.57	6	2.0	4.69	6
F8WI55	Programmed cell death protein 10 OS=Mus musculus GN=Pdcd10 PE=1 SV=2 - [F8WI55_MOUSE]	9.2	18	1.0	5.29	3	1.0	4.58	1	1.0	4.60	2
F8WID5	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1 - [F8WID5_MOUSE]	4.7	37	17.5	46.33	2	15.0	37.96	1	0.0	0.00	0
F8WJK8	Hsc70-interacting protein OS=Mus musculus GN=St13 PE=1 SV=1 - [F8WJK8_MOUSE]	5.3	41	1.0	2.39	4	1.0	2.30	3	1.0	2.36	1
G3UVV4	Hexokinase OS=Mus musculus GN=Hk1 PE=1 SV=1 - [G3UVV4_MOUSE]	6.7	102	21.7	66.53	6	12.2	36.56	6	14.2	42.60	6
G3UW31	MCG1031293 OS=Mus musculus GN=Vmn1r176 PE=4 SV=2 - [G3UW31_MOUSE]	9.5	34	1.0	3.09	1	2.0	6.81	1	1.0	3.08	1
G3UWL2	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Fragment) OS=Mus	4.7	16	1.0	2.16	1	0.0	0.00	0	1.0	2.40	3
G3UWL5	Protein Adamtsl3 OS=Mus musculus GN=Adamtsl3 PE=1 SV=1 - [G3UWL5_MOUSE]	8.9	83	1.0	2.71	1	1.0	2.62	1	1.5	4.12	2
G3UWM1	Heterogeneous nuclear ribonucleoprotein Q (Fragment) OS=Mus musculus GN=Syncrip PE=1 SV=1 - [G3UWM1_	4.9	22	1.0	2.20	2	0.0	0.00	0	0.0	0.00	0

G3UWN9	Proteasome activator complex subunit 1 (Fragment) OS=Mus musculus GN=Psme1 PE=1 SV=1 - [G3UWN9_MOUSE	5.4	20	1.8	4.29	5	1.0	2.20	3	1.7	3.75	3
G3UWZ0	Bromodomain adjacent to zinc finger domain protein 1A OS=Mus musculus GN=Baz1a PE=1 SV=1 - [G3UWZ0_M	6.5	178	1.0	3.23	1	0.0	0.00	0	0.0	0.00	0
G3UWZ3	Histone-lysine N-methyltransferase 2C (Fragment) OS=Mus musculus GN=Kmt2c PE=1 SV=1 - [G3UWZ3_MOUSE]	8.6	169	2.0	4.34	1	2.7	5.94	3	1.0	2.23	3
G3UX26	Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Mus musculus GN=Vdac2 PE=1 SV=1 -	7.6	30	3.4	9.71	5	3.0	8.51	2	3.0	8.45	5
G3UX57	Calmodulin (Fragment) OS=Mus musculus GN=Calm3 PE=1 SV=1 - [G3UX57_MOUSE]	4.0	4	1.5	4.40	2	0.0	0.00	0	3.0	9.16	1
G3UX67	26S proteasome non-ATPase regulatory subunit 11 (Fragment) OS=Mus musculus GN=Psmd11 PE=1 SV=1 - [G3	7.3	8	0.0	0.00	0	0.0	0.00	0	1.0	2.08	2
G3UXY0	Proteasome activator complex subunit 1 OS=Mus musculus GN=Psme1 PE=1 SV=1 - [G3UXY0_MOUSE]	6.2	26	5.0	14.53	1	2.7	7.26	3	3.5	11.57	2
G3UY11	Ankyrin-1 OS=Mus musculus GN=Ank1 PE=1 SV=1 - [G3UY11_MOUSE]	7.7	114	1.0	4.23	1	1.0	4.49	1	2.5	11.38	2
G3UY29	MCG22989, isoform CRA_a OS=Mus musculus GN=Rab11b PE=3 SV=1 - [G3UY29_MOUSE]	7.0	17	5.2	12.56	6	4.3	10.55	6	4.2	10.13	6
G3UY63	FK506-binding protein-like (Fragment) OS=Mus musculus GN=Fkbpl PE=4 SV=1 - [G3UY63_MOUSE]	4.8	2	0.0	0.00	0	1.0	2.63	1	0.0	0.00	0
G3UYR4	Serpin B10 OS=Mus musculus GN=Serpinb10 PE=1 SV=1 - [G3UYR4_MOUSE]	6.3	37	6.2	18.78	6	11.0	33.80	6	0.0	0.00	0
G3UYV7	40S ribosomal protein S28 (Fragment) OS=Mus musculus GN=Rps28 PE=1 SV=1 - [G3UYV7_MOUSE]	10.0	6	1.0	2.50	1	1.0	2.45	4	0.0	0.00	0
G3UYY2	Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=1 - [G3UYY2_MOUSE]	5.3	46	0.0	0.00	0	0.0	0.00	0	1.0	4.17	2
G3UZ22	Valine--tRNA ligase (Fragment) OS=Mus musculus GN=Vars PE=1 SV=7 - [G3UZ22_MOUSE]	8.3	24	1.0	2.55	2	0.0	0.00	0	1.0	2.68	1
G3UZI7	Rho GTPase activating protein 6, isoform CRA_b OS=Mus musculus GN=Arhgap6 PE=1 SV=1 - [G3UZI7_MOUSE]	6.7	54	1.0	2.58	1	0.0	0.00	0	0.0	0.00	0
G3UZJ4	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=1 - [G3UZJ4_MOUSE]	9.2	17	6.0	19.29	4	3.5	10.73	4	5.0	15.21	4
G3UZL5	Disks large homolog 4 (Fragment) OS=Mus musculus GN=Dlg4 PE=1 SV=1 - [G3UZL5_MOUSE]	6.5	24	1.0	2.79	3	1.0	3.00	1	1.0	2.75	2
G3UZM8	Apolipoprotein E (Fragment) OS=Mus musculus GN=Apoe PE=1 SV=1 - [G3UZM8_MOUSE]	5.6	17	0.0	0.00	0	2.0	6.18	1	3.7	12.44	3
G3UZZ2	Tapasin (Fragment) OS=Mus musculus GN=Tapbp PE=1 SV=1 - [G3UZZ2_MOUSE]	8.3	13	1.0	2.77	1	0.0	0.00	0	1.0	2.09	2
G3UZZ3	Dynamin-2 (Fragment) OS=Mus musculus GN=Dnm2 PE=1 SV=1 - [G3UZZ3_MOUSE]	8.2	92	2.2	5.08	6	1.4	3.53	5	1.4	3.55	5
G3V004	Calumenin OS=Mus musculus GN=Calu PE=1 SV=1 - [G3V004_MOUSE]	4.5	19	1.5	4.94	2	1.0	2.82	1	0.0	0.00	0
G3X8R4	General transcription factor II H, polypeptide 1 OS=Mus musculus GN=Gtf2h1 PE=1 SV=1 - [G3X8R4_MOUSE	8.8	62	0.0	0.00	0	1.0	3.18	2	0.0	0.00	0
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a OS=Mus musculus GN=Serpi	5.8	47	13.0	45.71	1	15.5	55.92	2	0.0	0.00	0
G3X8V3	Phosphatidylethanolamine-binding protein 4 OS=Mus musculus GN=Pebp4 PE=1 SV=1 - [G3X8V3_MOUSE]	5.5	27	0.0	0.00	0	1.0	2.42	1	0.0	0.00	0
G3X912	SprT-like domain-containing protein Spartan OS=Mus musculus GN=Sprtn PE=2 SV=1 - [SPRTN_MOUSE]	8.9	55	0.0	0.00	0	1.0	2.59	2	1.5	4.14	2
G3X940	Histone acetyltransferase OS=Mus musculus GN=Kat6a PE=1 SV=1 - [G3X940_MOUSE]	5.6	225	2.0	5.23	1	1.4	3.72	5	0.0	0.00	0
G3X9L6	MCG55033 OS=Mus musculus GN=Gm10250 PE=4 SV=1 - [G3X9L6_MOUSE]	5.4	19	3.5	11.42	2	0.0	0.00	0	0.0	0.00	0
G3X9Q3	Histocompatibility (Minor) HA-1, isoform CRA_a OS=Mus musculus GN=Hmha1 PE=1 SV=1 - [G3X9Q3_MOUSE]	5.9	123	1.8	5.54	4	1.5	4.63	2	1.3	4.03	3
G3X9T8	Ceruloplasmin OS=Mus musculus GN=Cp PE=1 SV=1 - [G3X9T8_MOUSE]	5.8	121	13.0	43.37	6	9.7	33.84	6	11.8	38.79	6
G3X9U9	Fission 1 (Mitochondrial outer membrane) homolog (Yeast), isoform CRA_c OS=Mus musculus GN=Fis1 PE=1	9.2	16	1.5	3.35	4	1.0	2.11	2	1.3	2.71	4
G3X9V0	MCG22048, isoform CRA_a OS=Mus musculus GN=Psme2 PE=1 SV=1 - [G3X9V0_MOUSE]	5.2	26	1.8	4.98	4	0.0	0.00	0	3.0	8.42	1
G3XA54	E3 ubiquitin-protein ligase RNF14 OS=Mus musculus GN=Rnf14 PE=1 SV=1 - [G3XA54_MOUSE]	4.8	41	0.0	0.00	0	1.0	2.27	1	0.0	0.00	0
G3XA59	MCG51019, isoform CRA_b OS=Mus musculus GN=Lrrc32 PE=1 SV=1 - [G3XA59_MOUSE]	6.0	72	1.3	3.67	3	1.0	2.66	3	1.0	2.87	1
G5E839	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=1 - [G5E839_MOUSE]	8.0	55	8.2	27.03	6	5.7	18.43	6	6.0	18.84	6
G5E850	Cytochrome b-5, isoform CRA_a OS=Mus musculus GN=Cyb5a PE=1 SV=1 - [G5E850_MOUSE]	5.3	11	3.3	11.63	6	2.7	9.14	6	3.3	11.71	6
G5E8B4	MCG147827 OS=Mus musculus GN=Scgb2b2 PE=1 SV=1 - [G5E8B4_MOUSE]	6.5	13	0.0	0.00	0	0.0	0.00	0	1.0	2.81	1
G5E8J2	Ankyrin 1, erythroid OS=Mus musculus GN=Ank1 PE=1 SV=1 - [G5E8J2_MOUSE]	6.7	202	0.0	0.00	0	8.5	25.41	4	7.0	25.51	1
G5E8P4	Protein cordon-bleu OS=Mus musculus GN=Cobl PE=1 SV=1 - [G5E8P4_MOUSE]	8.2	141	1.0	2.25	4	1.3	2.90	3	1.0	2.10	1
G5E8R1	Tropomyosin 1, alpha, isoform CRA_j OS=Mus musculus GN=Tpm1 PE=1 SV=1 - [G5E8R1_MOUSE]	4.8	29	17.0	41.46	4	14.0	33.75	2	14.5	35.46	2
H3BJA7	Protein Uba7 OS=Mus musculus GN=Uba7 PE=1 SV=1 - [H3BJA7_MOUSE]	5.1	45	1.0	2.65	1	0.0	0.00	0	0.0	0.00	0
H3BJC6	S-formylglutathione hydrolase (Fragment) OS=Mus musculus GN=Esd PE=1 SV=1 - [H3BJC6_MOUSE]	5.5	15	5.0	20.31	1	0.0	0.00	0	0.0	0.00	0
H3BJD4	Disks large-associated protein 4 (Fragment) OS=Mus musculus GN=Dlgap4 PE=1 SV=7 - [H3BJD4_MOUSE]	5.6	13	0.0	0.00	0	1.0	2.04	1	1.0	2.11	1
H3BJP2	S-formylglutathione hydrolase (Fragment) OS=Mus musculus GN=Esd PE=1 SV=1 - [H3BJP2_MOUSE]	6.9	27	4.4	17.14	5	4.8	18.31	4	3.8	14.08	6
H3BJZ9	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=1 SV=1 - [H3BJZ9_MOUSE]	8.5	35	0.0	0.00	0	0.0	0.00	0	2.0	5.27	1
H3BK43	S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 - [H3BK43_MOUSE]	6.7	28	0.0	0.00	0	3.0	9.06	1	0.0	0.00	0
H3BKA1	3-ketoacyl-CoA thiolase A, peroxisomal (Fragment) OS=Mus musculus GN=Acaa1a PE=1 SV=1 - [H3BKA1_MOUS	8.5	21	0.0	0.00	0	1.0	3.33	1	1.0	3.54	2
H3BKA7	Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=1 - [H3BKA7_MOUSE]	6.2	21	1.0	3.14	1	1.0	2.85	1	1.0	2.68	1
H3BKL5	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=1 SV=1 - [H3BKL5_MOUSE]	8.5	38	4.2	12.05	6	1.7	3.91	3	2.0	5.76	3
H3BKL8	Dual-specificity protein phosphatase 3 OS=Mus musculus GN=Dusp3 PE=1 SV=1 - [H3BKL8_MOUSE]	4.8	16	2.8	9.01	6	3.3	9.85	4	2.8	8.71	5
H3BKM0	AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1 SV=1 - [H3BKM0_MOUSE]	5.3	101	3.5	12.13	2	1.5	4.25	4	1.3	3.73	4
H3BKN4	Complement component C9 (Fragment) OS=Mus musculus GN=C9 PE=1 SV=1 - [H3BKN4_MOUSE]	9.5	11	2.3	5.61	4	0.0	0.00	0	2.0	4.57	2
H3BKW8	OTU domain-containing protein 7A (Fragment) OS=Mus musculus GN=Otud7a PE=1 SV=7 - [H3BKW8_MOUSE]	6.7	76	0.0	0.00	0	1.0	2.16	1	0.0	0.00	0
H3BL49	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=1 - [H3BL49_MOUSE]	5.5	53	8.0	20.87	1	5.7	14.76	3	7.5	18.19	2
H3BL99	S-formylglutathione hydrolase (Fragment) OS=Mus musculus GN=Esd PE=1 SV=1 - [H3BL99_MOUSE]	5.4	12	0.0	0.00	0	3.0	14.38	1	0.0	0.00	0
H3BLF7	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Fragment) OS=Mus musculus GN=Gnb1	9.6	12	1.8	4.66	6	1.5	3.77	6	1.5	3.71	6
H3BLI9	TSC22 domain family protein 1 OS=Mus musculus GN=Tsc22d1 PE=1 SV=1 - [H3BLI9_MOUSE]	4.8	9	1.0	2.73	2	1.0	2.08	1	1.0	2.29	2
H3BLR8	Diphosphoinositol polyphosphate phosphohydrolase 1 OS=Mus musculus GN=Nudt3 PE=1 SV=1 - [H3BLR8_MOUS	4.9	14	0.0	0.00	0	1.0	2.22	1	0.0	0.00	0
H6TMF5	cAMP-dependent protein kinase catalytic subunit beta (Fragment) OS=Mus musculus GN=Prkacb PE=1 SV=1	7.6	23	0.0	0.00	0	0.0	0.00	0	1.0	3.41	1
H7BWZ1	Ubiquitin-fold modifier 1 OS=Mus musculus GN=Ufm1 PE=1 SV=1 - [H7BWZ1_MOUSE]	9.2	6	0.0	0.00	0	0.0	0.00	0	1.0	2.07	1
H7BWZ3	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=1 - [H7BWZ3_MOUSE]	8.6	20	5.7	15.49	3	3.8	9.68	4	5.0	14.08	2
H7BX99	Prothrombin OS=Mus musculus GN=F2 PE=1 SV=1 - [H7BX99_MOUSE]	6.4	70	1.7	3.66	3	1.3	2.85	4	2.3	5.21	3
H7BXC3	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=1 - [H7BXC3_MOUSE]	5.6	18	9.8	34.05	6	8.3	28.23	6	8.5	28.03	6
H9KUZ2	Sialoadhesin OS=Mus musculus GN=Siglec1 PE=1 SV=1 - [H9KUZ2_MOUSE]	7.7	38	0.0	0.00	0	1.0	2.05	2	0.0	0.00	0
J3JRU4	Alpha-1-acid glycoprotein OS=Mus musculus GN=Orm3 PE=1 SV=1 - [J3JRU4_MOUSE]	5.2	24	0.0	0.00	0	1.0	2.57	1	0.0	0.00	0
J3QK03	Protein Ighv6-5 OS=Mus musculus GN=Ighv6-5 PE=4 SV=1 - [J3QK03_MOUSE]	5.1	11	0.0	0.00	0	2.3	7.24	3	1.0	2.22	2
J3QK52	Nucleolar complex protein 2 homolog OS=Mus musculus GN=Noc2l PE=1 SV=1 - [J3QK52_MOUSE]	5.8	86	1.0	2.16	1	0.0	0.00	0	1.0	2.10	1

J3QM38	Protein Gm4944 OS=Mus musculus GN=Gm4944 PE=1 SV=1 - [J3QM38_MOUSE]	8.8	77	1.0	2.71	1	0.0	0.00	0	1.0	2.47	1
J3QMG7	Protein Adgra2 OS=Mus musculus GN=Adgra2 PE=1 SV=1 - [J3QMG7_MOUSE]	8.4	120	0.0	0.00	0	0.0	0.00	0	1.0	3.10	1
J3QP41	Protein CREG1 OS=Mus musculus GN=Creg1 PE=1 SV=1 - [J3QP41_MOUSE]	6.8	16	1.0	2.80	1	0.0	0.00	0	0.0	0.00	0
J3QPS8	Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=1 - [J3QPS8_MOUSE]	4.4	8	0.0	0.00	0	0.0	0.00	0	1.0	2.53	1
J3QQ30	Phosphatidylinositol transfer protein alpha isoform OS=Mus musculus GN=Pitpna PE=1 SV=1 - [J3QQ30_MO	6.4	32	1.0	2.18	1	0.0	0.00	0	0.0	0.00	0
K3W4L8	Doublecortin domain-containing protein 2C OS=Mus musculus GN=Dcdc2c PE=4 SV=1 - [K3W4L8_MOUSE]	9.4	39	0.0	0.00	0	1.0	2.29	1	0.0	0.00	0
K3W4Q8	Basigin OS=Mus musculus GN=Bsg PE=1 SV=1 - [K3W4Q8_MOUSE]	5.4	24	1.0	2.69	1	1.7	4.60	3	0.0	0.00	0
K4DI63	Cellular repressor of E1A-stimulated genes 1, isoform CRA_a OS=Mus musculus GN=Creg1 PE=1 SV=1 - [K4	8.0	11	1.0	2.59	2	1.0	2.26	3	2.0	5.05	1
L7N1Z7	Protein Vmn2r2 OS=Mus musculus GN=Vmn2r2 PE=4 SV=1 - [L7N1Z7_MOUSE]	6.6	92	0.0	0.00	0	1.0	2.61	1	0.0	0.00	0
L7N201	Protein Zfp934 OS=Mus musculus GN=Zfp934 PE=4 SV=1 - [L7N201_MOUSE]	9.1	39	0.0	0.00	0	0.0	0.00	0	1.0	3.02	1
L7N2D2	Protein Gm3278 OS=Mus musculus GN=Gm3278 PE=4 SV=1 - [L7N2D2_MOUSE]	6.7	26	1.0	2.91	1	1.0	2.51	1	0.0	0.00	0
M0QWA7	Integrin beta OS=Mus musculus GN=Itgb2 PE=1 SV=1 - [M0QWA7_MOUSE]	7.0	53	1.5	3.97	2	0.0	0.00	0	0.0	0.00	0
M0QWI3	Metal-response element-binding transcription factor 2 (Fragment) OS=Mus musculus GN=Mtf2 PE=1 SV=1 -	7.0	15	1.0	3.38	4	1.6	5.39	5	1.0	3.07	3
M0QWX7	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment) OS=Mus musculus GN=Cox4i1 PE=1 SV	9.0	11	1.0	2.15	1	0.0	0.00	0	0.0	0.00	0
O08529	Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=1 SV=4 - [CAN2_MOUSE]	5.0	80	7.0	26.28	6	5.5	21.85	6	5.7	21.68	6
O08538	Angiopoietin-1 OS=Mus musculus GN=Angpt1 PE=1 SV=2 - [ANGP1_MOUSE]	6.8	57	1.5	3.46	4	1.3	3.05	3	1.8	4.17	4
O08553	Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2 - [DPYL2_MOUSE]	6.4	62	0.0	0.00	0	1.0	2.23	1	1.5	3.96	2
O08709	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3 - [PRDX6_MOUSE]	6.0	25	0.0	0.00	0	0.0	0.00	0	12.0	36.95	2
O08746	Matrilin-2 OS=Mus musculus GN=Matn2 PE=2 SV=2 - [MATN2_MOUSE]	6.6	107	0.0	0.00	0	0.0	0.00	0	1.0	2.78	2
O08749	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2 - [DLDH_MOUSE]	7.9	54	1.0	2.50	1	0.0	0.00	0	0.0	0.00	0
O08756	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4 - [HCD2_MOUSE]	8.4	27	1.5	4.20	2	1.3	3.50	3	1.5	3.61	2
O08795	Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1 - [GLU2B_MOUSE]	4.5	59	1.0	2.23	5	1.5	3.21	2	1.0	2.30	2
O08997	Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=1 SV=1 - [ATOX1_MOUSE]	6.5	7	1.8	4.62	4	2.0	5.14	4	2.0	4.85	4
O09044	Synaptosomal-associated protein 23 OS=Mus musculus GN=Snap23 PE=1 SV=1 - [SNP23_MOUSE]	5.0	23	5.0	16.08	1	0.0	0.00	0	0.0	0.00	0
O09061	Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1 - [PSB1_MOUSE]	7.8	26	1.5	3.63	4	1.0	2.23	4	2.0	5.19	2
O09117	Synaptophysin-like protein 1 OS=Mus musculus GN=Sypl1 PE=1 SV=2 - [SYPL1_MOUSE]	8.8	29	1.7	4.65	3	2.0	5.69	3	1.8	4.97	5
O09131	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2 - [GSTO1_MOUSE]	7.4	27	1.0	2.59	3	0.0	0.00	0	0.0	0.00	0
O09174	Alpha-methylacyl-CoA racemase OS=Mus musculus GN=Amacr PE=1 SV=4 - [AMACR_MOUSE]	7.4	42	1.0	2.61	1	0.0	0.00	0	0.0	0.00	0
O35129	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1 - [PHB2_MOUSE]	9.8	33	1.0	3.17	1	1.0	2.97	3	0.0	0.00	0
O35242	Protein FAN OS=Mus musculus GN=Nsmaf PE=1 SV=2 - [FAN_MOUSE]	5.9	104	1.0	3.19	1	0.0	0.00	0	1.0	2.65	1
O35295	Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3 - [PURB_MOUSE]	5.4	34	1.0	3.41	1	0.0	0.00	0	0.0	0.00	0
O35350	Calpain-1 catalytic subunit OS=Mus musculus GN=Capn1 PE=1 SV=1 - [CAN1_MOUSE]	5.9	82	0.0	0.00	0	0.0	0.00	0	1.0	2.54	1
O35492	Dual specificity protein kinase CLK3 OS=Mus musculus GN=Clk3 PE=1 SV=2 - [CLK3_MOUSE]	9.9	74	0.0	0.00	0	1.0	2.06	1	0.0	0.00	0
O35593	26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psmd14 PE=1 SV=2 - [PSDE_MOUSE]	6.5	35	1.0	2.38	2	0.0	0.00	0	0.0	0.00	0
O35601	FYN-binding protein OS=Mus musculus GN=Fyb PE=1 SV=2 - [FYB_MOUSE]	7.0	90	2.3	7.31	3	3.0	8.67	2	0.0	0.00	0
O35658	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Mus musculus GN=C1qbp PE=1 S	4.9	31	1.0	3.50	1	1.0	3.03	1	0.0	0.00	0
O35685	Nuclear migration protein nudC OS=Mus musculus GN=Nudc PE=1 SV=1 - [NUDC_MOUSE]	5.3	38	0.0	0.00	0	1.0	2.07	1	0.0	0.00	0
O35841	Apoptosis inhibitor 5 OS=Mus musculus GN=Api5 PE=1 SV=2 - [API5_MOUSE]	5.9	57	1.0	2.65	1	0.0	0.00	0	0.0	0.00	0
O35930	Platelet glycoprotein Ib alpha chain OS=Mus musculus GN=Gp1ba PE=1 SV=2 - [GP1BA_MOUSE]	5.9	80	32.5	114.45	6	22.5	75.05	6	28.2	91.67	6
O35945	Aldehyde dehydrogenase, cytosolic 1 OS=Mus musculus GN=Aldh1a7 PE=1 SV=1 - [AL1A7_MOUSE]	7.7	55	0.0	0.00	0	1.0	2.47	1	0.0	0.00	0
O54724	Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1 - [PTRF_MOUSE]	5.5	44	1.0	3.81	2	2.0	6.49	3	1.3	3.81	3
O54734	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddo	5.8	49	1.0	2.13	3	0.0	0.00	0	1.0	2.40	1
O54834	Rho GTPase-activating protein 6 OS=Mus musculus GN=Arhgap6 PE=1 SV=3 - [RHG06_MOUSE]	8.3	109	2.0	4.29	1	1.0	2.09	2	0.0	0.00	0
O54890	Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=1 SV=2 - [ITB3_MOUSE]	5.2	87	23.7	67.59	6	16.7	47.00	6	18.0	51.31	6
O54962	Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1 - [BAF_MOUSE]	6.1	10	1.0	3.56	2	1.2	4.16	5	1.0	3.29	4
O55023	Inositol monophosphatase 1 OS=Mus musculus GN=Impa1 PE=1 SV=1 - [IMPA1_MOUSE]	5.2	30	0.0	0.00	0	1.0	2.11	1	0.0	0.00	0
O55029	Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=1 SV=2 - [COPB2_MOUSE]	5.3	102	1.0	2.44	3	1.0	2.56	1	1.0	2.32	2
O55042	Alpha-synuclein OS=Mus musculus GN=Snca PE=1 SV=2 - [SYUA_MOUSE]	4.8	14	2.3	7.98	4	5.5	20.16	6	0.0	0.00	0
O55131	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1 - [SEPT7_MOUSE]	8.6	51	2.6	8.19	5	2.3	7.07	4	2.2	6.57	5
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2 - [AT2A2_MOU	5.3	115	6.8	18.33	6	3.2	7.85	6	4.2	10.04	6
O55222	Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2 - [ILK_MOUSE]	8.1	51	28.0	78.68	6	22.3	62.87	6	25.0	68.66	6
O55234	Proteasome subunit beta type-5 OS=Mus musculus GN=Psmb5 PE=1 SV=3 - [PSB5_MOUSE]	7.0	29	0.0	0.00	0	1.0	2.09	1	0.0	0.00	0
O70194	Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2 - [EIF3D_MOU	6.0	64	1.0	2.71	2	0.0	0.00	0	0.0	0.00	0
O70362	Phosphatidylinositol-glycan-specific phospholipase D OS=Mus musculus GN=Gpld1 PE=1 SV=1 - [PHLD_MOUS	7.1	93	1.5	4.94	2	2.0	6.38	3	2.5	7.58	2
O70400	PDZ and LIM domain protein 1 OS=Mus musculus GN=Pdlim1 PE=1 SV=4 - [PDLI1_MOUSE]	6.8	36	4.8	13.27	6	5.2	14.17	5	5.0	13.90	6
O70439	Syntaxin-7 OS=Mus musculus GN=Stx7 PE=1 SV=3 - [STX7_MOUSE]	5.8	30	1.0	2.69	1	1.0	2.53	1	1.0	2.33	2
O70443	Guanine nucleotide-binding protein G(z) subunit alpha OS=Mus musculus GN=Gnaz PE=1 SV=4 - [GNAZ_MOUS	7.6	41	5.3	14.71	6	2.7	6.87	6	2.7	6.48	6
O70469	Docking protein 2 OS=Mus musculus GN=Dok2 PE=1 SV=1 - [DOK2_MOUSE]	6.2	45	1.2	2.91	5	1.0	2.21	2	1.0	2.19	5
O70503	Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus GN=Hsd17b12 PE=1 SV=1 - [DHB12_MOUSE]	9.5	35	0.0	0.00	0	0.0	0.00	0	1.0	2.54	1
O70576	Cohesin subunit SA-3 OS=Mus musculus GN=Stag3 PE=1 SV=2 - [STAG3_MOUSE]	6.3	141	1.5	3.12	2	0.0	0.00	0	0.0	0.00	0
O88307	Sortilin-related receptor OS=Mus musculus GN=Sorl1 PE=1 SV=3 - [SORL_MOUSE]	5.5	247	1.0	2.86	1	1.0	2.99	2	1.0	3.02	1
O88342	WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3 - [WDR1_MOUSE]	6.6	66	20.0	89.49	6	14.3	60.79	6	15.8	65.40	6
O88502	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A OS=Mus musculus G	5.8	93	1.0	3.00	1	0.0	0.00	0	0.0	0.00	0
O88668	Protein CREG1 OS=Mus musculus GN=Creg1 PE=1 SV=1 - [CREG1_MOUSE]	6.4	24	0.0	0.00	0	0.0	0.00	0	2.0	5.47	1
O88700	Bloom syndrome protein homolog OS=Mus musculus GN=Blm PE=1 SV=1 - [BLM_MOUSE]	7.3	158	0.0	0.00	0	1.0	2.77	1	0.0	0.00	0
O88703	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 OS=Mus musculus GN=Hc	8.7	95	0.0	0.00	0	1.0	2.59	2	0.0	0.00	0

O88735	Ensconsin OS=Mus musculus GN=Map7 PE=1 SV=1 - [MAP7_MOUSE]	9.4	82	0.0	0.00	0	1.0	2.24	1	1.0	2.20	1
O88737	Protein bassoon OS=Mus musculus GN=Bsn PE=1 SV=4 - [BSN_MOUSE]	7.7	419	0.0	0.00	0	1.0	2.68	1	1.0	2.56	1
O88746	Target of Myb protein 1 OS=Mus musculus GN=Tom1 PE=1 SV=1 - [TOM1_MOUSE]	4.9	54	1.0	3.13	2	1.0	2.17	1	0.0	0.00	0
O88783	Coagulation factor V OS=Mus musculus GN=F5 PE=1 SV=1 - [FA5_MOUSE]	6.0	247	11.0	31.88	6	11.0	30.90	6	3.0	8.00	6
O88792	Junctional adhesion molecule A OS=Mus musculus GN=F11r PE=1 SV=2 - [JAM1_MOUSE]	6.8	32	1.0	3.02	1	1.0	2.81	2	1.0	3.06	1
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2 - [IDHC_MOUSE]	7.2	47	1.0	2.45	2	1.0	2.24	1	1.0	2.25	3
O88866	Hormonally up-regulated neu tumor-associated kinase OS=Mus musculus GN=Hunk PE=2 SV=1 - [HUNK_MOUSE]	9.1	80	1.0	2.81	1	1.0	2.71	3	1.0	2.68	2
O88947	Coagulation factor X OS=Mus musculus GN=F10 PE=1 SV=1 - [FA10_MOUSE]	5.7	54	1.6	3.89	5	1.3	3.07	6	1.3	3.11	6
O89020	Afamin OS=Mus musculus GN=Afm PE=1 SV=2 - [AFAM_MOUSE]	5.8	69	1.0	2.95	2	2.5	6.20	2	1.0	3.12	1
O89032	SH3 and PX domain-containing protein 2A OS=Mus musculus GN=Sh3pxd2a PE=1 SV=2 - [SPD2A_MOUSE]	8.7	124	0.0	0.00	0	1.0	2.78	1	0.0	0.00	0
O89053	Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5 - [COR1A_MOUSE]	6.5	51	21.0	91.60	6	13.5	55.85	6	16.3	71.85	6
O89100	GRB2-related adaptor protein 2 OS=Mus musculus GN=Grap2 PE=1 SV=1 - [GRAP2_MOUSE]	6.6	37	1.0	2.98	1	0.0	0.00	0	0.0	0.00	0
P00405	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1 - [COX2_MOUSE]	4.7	26	3.7	13.69	6	3.4	11.63	5	3.3	11.55	6
P00920	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4 - [CAH2_MOUSE]	7.0	29	13.5	46.50	6	27.2	104.51	6	23.0	83.29	6
P01027	Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3 - [CO3_MOUSE]	6.7	186	48.5	159.66	6	55.7	180.44	6	47.0	147.95	6
P01029	Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3 - [CO4B_MOUSE]	7.5	193	4.0	12.15	6	2.0	5.87	6	2.8	8.53	6
P01592	Immunoglobulin J chain OS=Mus musculus GN=Jchain PE=1 SV=4 - [IGJ_MOUSE]	4.9	18	0.0	0.00	0	1.3	3.91	4	0.0	0.00	0
P01631	Ig kappa chain V-II region 26-10 OS=Mus musculus PE=1 SV=1 - [KV2A7_MOUSE]	8.9	12	0.0	0.00	0	1.0	2.78	4	0.0	0.00	0
P01642	Ig kappa chain V-V region L7 (Fragment) OS=Mus musculus GN=Gm10881 PE=1 SV=1 - [KV5A9_MOUSE]	5.9	13	0.0	0.00	0	2.0	4.98	2	0.0	0.00	0
P01796	Ig heavy chain V-III region A4 OS=Mus musculus PE=1 SV=1 - [HVM27_MOUSE]	7.3	13	0.0	0.00	0	4.0	12.64	1	0.0	0.00	0
P01837	Ig kappa chain C region OS=Mus musculus PE=1 SV=1 - [IGKC_MOUSE]	5.4	12	5.7	15.22	6	8.5	23.09	6	3.8	10.12	4
P01843	Ig lambda-1 chain C region OS=Mus musculus PE=1 SV=1 - [LAC1_MOUSE]	6.3	12	0.0	0.00	0	3.5	10.61	6	1.0	2.29	1
P01863	Ig gamma-2A chain C region, A allele OS=Mus musculus GN=Ighg PE=1 SV=1 - [GCAA_MOUSE]	7.4	36	1.8	6.04	6	0.0	0.00	0	1.0	3.01	2
P01872	Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2 - [IGHM_MOUSE]	7.0	50	6.0	18.52	6	15.7	53.91	6	5.8	19.29	6
P01898	H-2 class I histocompatibility antigen, Q10 alpha chain OS=Mus musculus GN=H2-Q10 PE=1 SV=3 - [HA10_	5.2	37	6.8	20.35	6	5.2	14.85	6	7.2	20.75	6
P01899	H-2 class I histocompatibility antigen, D-B alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=2 - [HA11_M	6.7	41	0.0	0.00	0	0.0	0.00	0	7.0	19.59	1
P02104	Hemoglobin subunit epsilon-Y2 OS=Mus musculus GN=Hbb-y PE=1 SV=2 - [HBE_MOUSE]	8.2	16	0.0	0.00	0	56.3	135.40	3	29.7	71.24	3
P03921	NADH-ubiquinone oxidoreductase chain 5 OS=Mus musculus GN=Mtnd5 PE=1 SV=3 - [NU5M_MOUSE]	9.0	68	1.0	3.27	1	0.0	0.00	0	1.0	2.55	1
P03953	Complement factor D OS=Mus musculus GN=Cfd PE=1 SV=1 - [CFAD_MOUSE]	6.7	28	0.0	0.00	0	1.0	3.03	1	0.0	0.00	0
P03995	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4 - [GFAP_MOUSE]	5.3	50	1.7	3.49	3	2.5	5.16	2	1.0	2.10	4
P04186	Complement factor B OS=Mus musculus GN=Cfb PE=1 SV=2 - [CFAB_MOUSE]	7.4	85	8.0	24.54	2	4.3	12.98	3	4.5	13.48	2
P04202	Transforming growth factor beta-1 OS=Mus musculus GN=Tgfb1 PE=1 SV=1 - [TGFB1_MOUSE]	8.6	44	4.5	14.31	6	4.0	12.26	6	4.5	13.41	6
P04919	Band 3 anion transport protein OS=Mus musculus GN=Slc4a1 PE=1 SV=1 - [B3AT_MOUSE]	5.5	103	3.5	12.74	6	13.7	43.47	6	11.5	35.28	6
P05064	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2 - [ALDOA_MOUSE]	8.1	39	20.8	74.30	6	18.5	67.41	6	17.2	61.22	6
P05132	cAMP-dependent protein kinase catalytic subunit alpha OS=Mus musculus GN=Prkaca PE=1 SV=3 - [KAPCA_M	8.8	41	1.0	3.31	1	1.0	2.96	1	0.0	0.00	0
P05202	Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1 - [AATM_MOUSE]	9.0	47	1.7	4.96	3	1.5	4.63	2	1.5	4.25	2
P06151	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3 - [LDHA_MOUSE]	7.7	36	33.0	116.90	6	30.0	104.54	6	31.0	109.34	6
P06683	Complement component C9 OS=Mus musculus GN=C9 PE=1 SV=2 - [CO9_MOUSE]	5.8	62	4.0	9.55	2	0.0	0.00	0	3.7	8.54	3
P06684	Complement C5 OS=Mus musculus GN=C5 PE=1 SV=2 - [CO5_MOUSE]	6.8	189	2.0	5.71	5	0.0	0.00	0	2.7	7.36	3
P06728	Apolipoprotein A-IV OS=Mus musculus GN=Apoa4 PE=1 SV=3 - [APOA4_MOUSE]	5.5	45	25.8	79.23	6	25.3	78.63	6	23.8	71.10	6
P06745	Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4 - [G6PI_MOUSE]	8.1	63	4.7	12.93	6	4.0	11.26	6	4.3	12.15	6
P07309	Transthyretin OS=Mus musculus GN=Ttr PE=1 SV=1 - [TTHY_MOUSE]	6.2	16	18.7	75.04	6	16.3	60.41	6	15.0	55.14	6
P07724	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 - [ALBU_MOUSE]	6.1	69	165.8	541.46	6	196.7	635.76	6	144.2	466.50	6
P07758	Alpha-1-antitrypsin 1-1 OS=Mus musculus GN=Serpina1a PE=1 SV=4 - [A1AT1_MOUSE]	5.7	46	102.0	449.02	1	64.5	268.06	2	60.5	264.00	2
P07759	Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2 - [SPA3K_MOUSE]	5.2	47	0.0	0.00	0	111.7	395.47	6	0.0	0.00	0
P07901	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4 - [HS90A_MOUSE]	5.0	85	27.0	86.28	6	19.5	60.38	6	21.2	65.93	6
P08003	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3 - [PDIA4_MOUSE]	5.3	72	4.2	10.14	6	1.8	3.91	4	2.8	7.37	6
P08032	Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Spta1 PE=1 SV=3 - [SPTA1_MOUSE]	5.0	280	1.8	5.53	4	11.2	34.77	6	6.8	22.51	6
P08113	Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2 - [ENPL_MOUSE]	4.8	92	25.5	87.76	6	25.5	85.78	6	25.0	80.54	6
P08121	Collagen alpha-1(III) chain OS=Mus musculus GN=Col3a1 PE=1 SV=4 - [CO3A1_MOUSE]	6.5	139	1.0	2.81	1	1.0	2.53	1	0.0	0.00	0
P08226	Apolipoprotein E OS=Mus musculus GN=Apoe PE=1 SV=2 - [APOE_MOUSE]	5.7	36	7.3	23.07	6	5.8	18.16	5	9.3	28.16	3
P08228	Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2 - [SODC_MOUSE]	6.5	16	6.3	17.23	6	5.3	14.44	6	5.5	14.36	6
P08249	Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3 - [MDHM_MOUSE]	8.7	36	10.5	35.41	6	6.8	21.17	5	9.0	26.94	6
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5 - [GNAI2_	5.5	40	5.7	16.29	3	0.0	0.00	0	0.0	0.00	0
P08905	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2 - [LYZ2_MOUSE]	8.8	17	1.0	3.33	2	1.0	3.37	3	0.0	0.00	0
P09055	Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1 - [ITB1_MOUSE]	5.9	88	9.7	28.26	6	10.0	28.08	6	7.5	20.32	6
P09103	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2 - [PDIA1_MOUSE]	4.9	57	14.5	51.54	6	12.8	43.80	6	14.7	49.70	6
P09411	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4 - [PGK1_MOUSE]	7.9	45	12.3	42.28	6	11.5	40.09	6	9.7	33.20	6
P09813	Apolipoprotein A-II OS=Mus musculus GN=Apoa2 PE=1 SV=2 - [APOA2_MOUSE]	7.2	11	6.2	18.74	6	3.3	10.10	3	4.5	12.67	6
P0C191	Platelet glycoprotein VI OS=Mus musculus GN=Gp6 PE=1 SV=2 - [GPVI_MOUSE]	8.6	35	1.7	4.76	6	2.0	5.36	1	1.7	4.31	3
P0C605	cGMP-dependent protein kinase 1 OS=Mus musculus GN=Prkg1 PE=1 SV=1 - [KGP1_MOUSE]	6.0	76	0.0	0.00	0	0.0	0.00	0	1.0	2.43	1
P0C871	Cytosolic phospholipase A2 beta OS=Mus musculus GN=Pla2g4b PE=2 SV=1 - [PA24B_MOUSE]	6.5	88	3.5	10.84	2	2.0	6.21	1	0.0	0.00	0
P10107	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2 - [ANXA1_MOUSE]	7.4	39	1.0	2.05	1	1.0	3.22	2	0.0	0.00	0
P10126	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 - [EF1A1_MOUSE]	9.0	50	13.7	46.57	6	7.7	26.74	6	12.0	41.11	6
P10518	Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=Alad PE=1 SV=1 - [HEM2_MOUSE]	6.8	36	0.0	0.00	0	1.0	3.00	2	0.0	0.00	0
P10639	Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 - [THIO_MOUSE]	4.9	12	1.4	3.37	5	2.2	5.35	6	2.3	5.94	6

P10853	Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1 SV=2 - [H2B1F_MOUSE]	10.3	14	1.0	2.27	1	0.0	0.00	0	1.0	2.31	1
P11438	Lysosome-associated membrane glycoprotein 1 OS=Mus musculus GN=Lamp1 PE=1 SV=2 - [LAMP1_MOUSE]	8.4	44	1.0	2.73	2	1.0	2.86	2	2.0	5.60	2
P11499	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 - [HS90B_MOUSE]	5.0	83	27.2	84.40	6	23.8	73.45	6	22.2	66.90	6
P11679	Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4 - [K2C8_MOUSE]	5.8	55	0.0	0.00	0	1.0	2.21	1	1.0	2.14	1
P11859	Angiotensinogen OS=Mus musculus GN=Agt PE=1 SV=1 - [ANGT_MOUSE]	5.4	52	2.3	6.96	3	2.0	6.63	1	1.0	2.99	3
P11983	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3 - [TCPA_MOUSE]	6.2	60	3.2	9.63	6	3.2	9.33	5	2.7	7.50	6
P12382	ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkl PE=1 SV=4 - [PFKAL_MOUSE]	7.2	85	1.8	4.74	4	1.6	4.66	5	1.5	4.36	4
P12388	Plasminogen activator inhibitor 2, macrophage OS=Mus musculus GN=Serpinb2 PE=1 SV=1 - [PAI2_MOUSE]	5.1	46	3.0	8.04	4	1.7	4.41	3	2.2	5.54	6
P12399	Protein CTLA-2-alpha OS=Mus musculus GN=Ctla2a PE=2 SV=2 - [CTL2A_MOUSE]	5.3	16	2.0	6.43	6	1.8	5.29	5	1.2	3.21	5
P13020	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3 - [GELS_MOUSE]	6.2	86	33.0	135.61	6	29.3	124.44	6	30.2	122.57	6
P13541	Myosin-3 OS=Mus musculus GN=Myh3 PE=2 SV=2 - [MYH3_MOUSE]	5.8	224	0.0	0.00	0	0.0	0.00	0	1.0	2.64	2
P13542	Myosin-8 OS=Mus musculus GN=Myh8 PE=2 SV=2 - [MYH8_MOUSE]	5.8	223	7.3	20.95	6	4.7	13.35	3	9.5	26.35	4
P13597	Intercellular adhesion molecule 1 OS=Mus musculus GN=Icam1 PE=1 SV=1 - [ICAM1_MOUSE]	6.1	59	1.0	3.22	1	0.0	0.00	0	0.0	0.00	0
P13609	Serglycin OS=Mus musculus GN=Srgn PE=1 SV=1 - [SRGN_MOUSE]	4.4	17	1.8	7.83	6	1.0	3.64	4	2.2	8.51	5
P13634	Carbonic anhydrase 1 OS=Mus musculus GN=Ca1 PE=1 SV=4 - [CAH1_MOUSE]	7.0	28	4.0	10.43	1	4.3	13.63	6	9.5	32.20	2
P14152	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3 - [MDHC_MOUSE]	6.6	36	5.2	15.86	6	5.0	14.88	5	5.3	15.60	6
P14206	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4 - [RSSA_MOUSE]	4.9	33	1.0	3.08	3	1.0	3.02	3	1.0	2.09	1
P14211	Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1 - [CALR_MOUSE]	4.5	48	31.3	115.33	6	21.7	79.76	6	24.5	89.87	6
P14428	H-2 class I histocompatibility antigen, K-Q alpha chain (Fragment) OS=Mus musculus GN=H2-K1 PE=1 SV=	6.4	37	3.0	7.48	1	3.0	7.50	1	0.0	0.00	0
P14685	26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=1 SV=3 - [PSMD3_MOUSE]	8.4	61	2.0	6.42	1	0.0	0.00	0	0.0	0.00	0
P15066	Transcription factor jun-D OS=Mus musculus GN=Jund PE=1 SV=1 - [JUND_MOUSE]	7.4	35	2.0	5.33	5	1.5	3.99	4	1.3	3.56	3
P15327	Bisphosphoglycerate mutase OS=Mus musculus GN=Bpgm PE=1 SV=2 - [PMGE_MOUSE]	7.1	30	1.0	3.40	2	2.7	10.19	6	3.0	10.97	4
P15508	Spectrin beta chain, erythrocytic OS=Mus musculus GN=Sptb PE=1 SV=4 - [SPTB1_MOUSE]	5.3	245	4.5	12.11	6	20.2	58.50	6	11.7	32.46	6
P15532	Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1 - [NDKA_MOUSE]	7.4	17	12.8	42.84	5	14.7	48.05	3	12.4	39.45	5
P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Mus musculus GN=Cnp PE=1 SV=3 - [CN37_MOUSE]	9.0	47	1.7	4.51	6	1.5	3.85	4	1.8	4.68	5
P16546	Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=4 - [SPTN1_MOUSE]	5.3	284	55.3	194.14	6	35.2	116.44	6	43.8	144.87	6
P16858	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 - [G3P_MOUSE]	8.3	36	50.0	213.01	2	42.5	175.47	2	51.0	212.89	2
P17182	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3 - [ENOA_MOUSE]	6.8	47	32.8	108.49	6	26.0	84.43	6	30.5	97.77	6
P17427	AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2 - [AP2A2_MOUSE]	6.9	104	1.8	5.28	4	1.0	2.87	2	1.0	3.30	2
P17563	Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 - [SBP1_MOUSE]	6.3	52	0.0	0.00	0	1.0	2.70	1	0.0	0.00	0
P17742	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 - [PPIA_MOUSE]	7.9	18	6.7	17.64	6	6.3	16.79	6	6.7	17.63	6
P18760	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3 - [COF1_MOUSE]	8.1	19	23.3	84.21	6	20.2	71.19	6	19.8	69.91	6
P19157	Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 - [GSTP1_MOUSE]	7.9	24	1.6	5.65	5	1.6	5.58	5	1.8	5.60	5
P19536	Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus musculus GN=Cox5b PE=1 SV=1 - [COX5B_MOUSE]	8.4	14	1.0	2.16	1	1.0	2.23	1	0.0	0.00	0
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Mus musculus GN=Cox4i1 PE=1 SV=2 - [COX41	9.2	20	0.0	0.00	0	0.0	0.00	0	1.0	2.92	1
P20029	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3 - [GRP78_MOUSE]	5.2	72	57.3	185.88	6	52.2	162.10	6	54.3	169.11	6
P20065	Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1 - [TYB4_MOUSE]	5.1	6	1.7	4.71	6	1.0	2.80	1	1.2	3.31	5
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1 - [PRDX3_	7.6	28	2.2	5.75	5	1.8	4.07	4	2.0	4.36	2
P20444	Protein kinase C alpha type OS=Mus musculus GN=Prkca PE=1 SV=3 - [KPCA_MOUSE]	7.1	77	2.0	5.40	1	3.0	7.75	1	0.0	0.00	0
P20918	Plasminogen OS=Mus musculus GN=Plg PE=1 SV=3 - [PLMN_MOUSE]	6.6	91	1.0	2.34	1	1.8	4.28	4	2.0	4.77	2
P21279	Guanine nucleotide-binding protein G(q) subunit alpha OS=Mus musculus GN=Gnaq PE=1 SV=4 - [GNAQ_MOUS	5.7	42	4.7	14.96	6	2.3	6.56	6	2.7	7.23	6
P21614	Vitamin D-binding protein OS=Mus musculus GN=Gc PE=1 SV=2 - [VTDB_MOUSE]	5.5	54	24.8	97.62	6	16.0	58.36	6	19.3	71.29	6
P22437	Prostaglandin G/H synthase 1 OS=Mus musculus GN=Ptgs1 PE=1 SV=1 - [PGH1_MOUSE]	6.8	69	1.5	4.24	4	1.0	2.73	3	1.0	2.40	1
P22599	Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2 - [A1AT2_MOUSE]	5.5	46	86.2	389.85	6	55.3	237.78	6	62.7	279.50	6
P22892	AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=3 - [AP1G1_MOUSE]	6.8	91	3.0	7.90	1	0.0	0.00	0	1.0	2.55	1
P23492	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2 - [PNPH_MOUSE]	6.2	32	2.3	8.54	6	7.2	23.81	6	4.8	16.67	6
P23506	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Mus musculus GN=Pcmt1 PE=1 SV=3 - [PIMT_M	7.6	25	1.2	5.15	5	1.0	4.05	3	1.3	4.55	3
P23780	Beta-galactosidase OS=Mus musculus GN=Glb1 PE=1 SV=1 - [BGAL_MOUSE]	7.5	73	1.0	2.19	1	0.0	0.00	0	0.0	0.00	0
P23953	Carboxylesterase 1C OS=Mus musculus GN=Ces1c PE=1 SV=4 - [EST1C_MOUSE]	5.1	61	27.0	85.60	6	32.2	103.04	6	21.0	65.66	6
P24270	Catalase OS=Mus musculus GN=Cat PE=1 SV=4 - [CATA_MOUSE]	7.9	60	2.5	7.13	2	5.5	16.21	4	6.2	17.83	5
P24369	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=1 SV=2 - [PPIB_MOUSE]	9.6	24	9.7	28.12	6	7.7	21.69	6	8.2	23.81	6
P24527	Leukotriene A-4 hydrolase OS=Mus musculus GN=Lta4h PE=1 SV=4 - [LKHA4_MOUSE]	6.4	69	1.0	2.87	1	1.0	2.62	1	2.0	5.62	2
P24549	Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 - [AL1A1_MOUSE]	7.8	54	0.0	0.00	0	0.0	0.00	0	2.0	5.79	3
P24668	Cation-dependent mannose-6-phosphate receptor OS=Mus musculus GN=M6pr PE=1 SV=1 - [MPRD_MOUSE]	5.4	31	1.0	3.19	4	1.0	3.21	3	1.0	3.29	2
P25911	Tyrosine-protein kinase Lyn OS=Mus musculus GN=Lyn PE=1 SV=4 - [LYN_MOUSE]	7.2	59	3.8	11.93	6	2.6	7.39	5	2.8	7.87	6
P26039	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2 - [TLN1_MOUSE]	6.2	270	454.0	1841.65	6	355.2	1403.38	6	405.7	1593.27	6
P26041	Moesin OS=Mus musculus GN=Msn PE=1 SV=3 - [MOES_MOUSE]	6.6	68	3.0	8.27	5	0.0	0.00	0	1.5	3.86	2
P26231	Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1 - [CTNA1_MOUSE]	6.2	100	1.5	5.46	2	1.0	3.07	2	2.0	6.35	1
P26262	Plasma kallikrein OS=Mus musculus GN=Klkb1 PE=1 SV=2 - [KLKB1_MOUSE]	8.0	71	0.0	0.00	0	0.0	0.00	0	1.0	2.20	2
P26443	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1 - [DHE3_MOUSE]	8.0	61	1.0	2.39	1	0.0	0.00	0	0.0	0.00	0
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=1 SV=2 - [FKB1A_MOUSE]	8.2	12	1.3	4.31	3	1.3	3.97	4	1.3	4.26	3
P27612	Phospholipase A-2-activating protein OS=Mus musculus GN=Plaa PE=1 SV=4 - [PLAP_MOUSE]	6.1	87	0.0	0.00	0	0.0	0.00	0	1.0	3.05	2
P27773	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2 - [PDIA3_MOUSE]	6.2	57	24.2	73.52	6	19.2	58.43	6	24.0	72.75	6
P28271	Cytoplasmic aconitate hydratase OS=Mus musculus GN=Aco1 PE=1 SV=3 - [ACOC_MOUSE]	7.5	98	0.0	0.00	0	0.0	0.00	0	2.0	5.00	1
P28656	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap1l1 PE=1 SV=2 - [NP1L1_MOUSE]	4.5	45	2.8	9.04	5	3.2	9.53	6	2.3	6.45	6
P28660	Nck-associated protein 1 OS=Mus musculus GN=Nckap1 PE=1 SV=2 - [NCKP1_MOUSE]	6.6	129	1.0	2.61	2	1.0	2.30	2	1.0	2.65	2

P28665	Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3 - [MUG1_MOUSE]	6.4	165	61.5	205.90	6	47.5	153.04	6	52.7	170.17	6
P29351	Tyrosine-protein phosphatase non-receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2 - [PTN6_MOUSE]	7.8	68	1.0	2.83	2	0.0	0.00	0	0.0	0.00	0
P29391	Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2 - [FRIL1_MOUSE]	6.0	21	3.7	12.11	6	1.8	5.86	5	5.3	16.44	6
P29477	Nitric oxide synthase, inducible OS=Mus musculus GN=Nos2 PE=1 SV=1 - [NOS2_MOUSE]	7.7	130	1.3	4.44	3	0.0	0.00	0	1.0	3.37	1
P29595	NEDD8 OS=Mus musculus GN=Nedd8 PE=1 SV=2 - [NEDD8_MOUSE]	7.3	9	0.0	0.00	0	1.0	2.39	1	0.0	0.00	0
P29699	Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 - [FETUA_MOUSE]	6.5	37	4.7	26.09	6	4.8	24.60	6	3.2	16.07	6
P29788	Vitronectin OS=Mus musculus GN=Vtn PE=1 SV=2 - [VTNC_MOUSE]	5.9	55	7.0	23.26	6	5.6	16.85	5	5.7	17.95	6
P30412	Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1 - [PPIC_MOUSE]	7.5	23	1.0	2.47	2	1.0	2.37	3	1.0	2.30	2
P31324	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkar2b PE=1 SV=3 -	5.0	46	20.8	68.95	6	15.0	48.16	6	14.5	45.67	6
P31532	Serum amyloid A-4 protein OS=Mus musculus GN=Saa4 PE=1 SV=2 - [SAA4_MOUSE]	9.3	15	1.0	2.64	2	1.0	2.32	1	2.0	5.25	2
P32037	Solute carrier family 2, facilitated glucose transporter member 3 OS=Mus musculus GN=Slc2a3 PE=1 SV=	5.0	53	10.7	35.18	6	6.7	21.23	6	7.5	24.88	6
P32261	Antithrombin-III OS=Mus musculus GN=Serpinc1 PE=1 SV=1 - [ANT3_MOUSE]	6.5	52	9.8	30.98	6	8.3	25.40	6	8.5	25.79	6
P32921	Tryptophan--tRNA ligase, cytoplasmic OS=Mus musculus GN=Wars PE=1 SV=2 - [SYWC_MOUSE]	6.9	54	1.5	4.29	2	0.0	0.00	0	0.0	0.00	0
P34022	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2 - [RANG_MOUSE]	5.2	24	1.0	2.39	5	1.5	3.95	4	1.3	3.21	6
P35235	Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2 - [PTN11_MOUSE	7.3	68	6.7	23.23	6	5.5	17.65	6	5.5	18.05	6
P35278	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2 - [RAB5C_MOUSE]	8.4	23	4.3	11.60	3	4.5	11.58	2	5.0	12.72	2
P35279	Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4 - [RAB6A_MOUSE]	5.5	24	8.3	21.51	4	8.2	21.05	6	9.0	22.93	4
P35282	Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4 - [RAB21_MOUSE]	7.9	24	1.5	4.47	4	1.0	3.18	2	1.0	3.04	1
P35294	Ras-related protein Rab-19 OS=Mus musculus GN=Rab19 PE=1 SV=3 - [RAB19_MOUSE]	6.4	24	1.0	2.60	1	0.0	0.00	0	0.0	0.00	0
P35329	B-cell receptor CD22 OS=Mus musculus GN=Cd22 PE=1 SV=1 - [CD22_MOUSE]	7.9	97	2.0	4.22	4	1.0	2.14	3	1.0	2.14	1
P35441	Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1 - [TSP1_MOUSE]	5.0	130	126.5	414.92	2	108.0	336.77	6	110.4	345.51	5
P35564	Calnexin OS=Mus musculus GN=Canx PE=1 SV=1 - [CALX_MOUSE]	4.6	67	14.3	51.67	6	8.2	29.63	6	10.3	36.41	6
P35585	AP-1 complex subunit mu-1 OS=Mus musculus GN=Ap1m1 PE=1 SV=3 - [AP1M1_MOUSE]	7.3	49	1.3	3.15	3	0.0	0.00	0	0.0	0.00	0
P35821	Tyrosine-protein phosphatase non-receptor type 1 OS=Mus musculus GN=Ptpn1 PE=1 SV=2 - [PTN1_MOUSE]	6.2	50	1.0	2.37	1	1.0	2.60	3	0.0	0.00	0
P35831	Tyrosine-protein phosphatase non-receptor type 12 OS=Mus musculus GN=Ptpn12 PE=1 SV=3 - [PTN12_MOUSE	6.0	86	1.3	3.06	4	0.0	0.00	0	1.0	2.50	4
P35991	Tyrosine-protein kinase BTK OS=Mus musculus GN=Btk PE=1 SV=4 - [BTK_MOUSE]	7.9	76	0.0	0.00	0	1.0	2.47	1	0.0	0.00	0
P36423	Thromboxane-A synthase OS=Mus musculus GN=Tbxas1 PE=1 SV=2 - [THAS_MOUSE]	7.2	60	12.2	38.48	6	7.2	21.13	6	11.8	36.60	6
P36536	GTP-binding protein SAR1a OS=Mus musculus GN=Sar1a PE=1 SV=1 - [SAR1A_MOUSE]	6.9	22	1.0	2.59	2	0.0	0.00	0	0.0	0.00	0
P36993	Protein phosphatase 1B OS=Mus musculus GN=Ppm1b PE=1 SV=1 - [PPM1B_MOUSE]	5.2	43	2.0	5.25	1	0.0	0.00	0	1.0	2.68	2
P38647	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=3 - [GRP75_MOUSE]	6.1	73	1.3	3.24	6	2.0	4.76	1	0.0	0.00	0
P39655	Arachidonate 12-lipoxygenase, 12S-type OS=Mus musculus GN=Alox12 PE=1 SV=4 - [LOX12_MOUSE]	6.2	75	44.8	160.63	6	34.2	118.37	6	37.7	130.08	6
P40124	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4 - [CAP1_MOUSE]	7.5	52	51.5	197.69	6	40.8	150.58	6	43.0	163.17	6
P40142	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1 - [TKT_MOUSE]	7.5	68	3.8	14.01	6	2.3	7.36	4	2.2	7.52	6
P40240	CD9 antigen OS=Mus musculus GN=Cd9 PE=1 SV=2 - [CD9_MOUSE]	7.2	25	0.0	0.00	0	1.0	2.57	2	1.0	2.59	1
P41241	Tyrosine-protein kinase CSK OS=Mus musculus GN=Csk PE=1 SV=2 - [CSK_MOUSE]	7.1	51	2.5	6.28	6	1.0	2.58	3	1.7	3.75	3
P41317	Mannose-binding protein C OS=Mus musculus GN=Mbl2 PE=1 SV=2 - [MBL2_MOUSE]	5.1	26	1.5	4.82	4	2.6	8.50	5	1.7	5.61	3
P42125	Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus GN=Eci1 PE=1 SV=2 - [ECI1_MOUSE]	9.0	32	1.5	3.65	2	1.0	3.09	1	1.0	2.82	2
P42703	Leukemia inhibitory factor receptor OS=Mus musculus GN=Lifr PE=1 SV=1 - [LIFR_MOUSE]	6.0	122	1.0	2.17	2	0.0	0.00	0	0.0	0.00	0
P42932	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3 - [TCPQ_MOUSE]	5.6	60	8.8	22.85	5	6.7	16.73	3	7.0	17.62	4
P43024	Cytochrome c oxidase subunit 6A1, mitochondrial OS=Mus musculus GN=Cox6a1 PE=1 SV=2 - [CX6A1_MOUSE]	10.0	12	1.0	3.48	1	0.0	0.00	0	0.0	0.00	0
P45376	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3 - [ALDR_MOUSE]	7.2	36	2.0	5.23	6	1.2	2.68	5	1.7	3.97	6
P45878	Peptidyl-prolyl cis-trans isomerase FKBP2 OS=Mus musculus GN=Fkbp2 PE=1 SV=1 - [FKBP2_MOUSE]	8.9	15	1.0	2.09	1	0.0	0.00	0	1.0	2.10	1
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadm PE=1 SV=1 - [AC	8.4	46	3.0	9.81	6	1.8	4.63	5	2.4	6.44	5
P46460	Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2 - [NSF_MOUSE]	6.9	83	0.0	0.00	0	0.0	0.00	0	1.0	2.64	1
P46935	E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3 - [NEDD4_MOUSE]	5.3	103	1.0	2.14	1	0.0	0.00	0	0.0	0.00	0
P47738	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 - [ALDH2_MOUSE]	7.6	57	41.3	135.94	6	26.0	84.34	6	32.8	103.05	6
P47753	F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4 - [CAZA1_MOUSE]	5.6	33	5.3	15.59	3	3.0	6.98	2	0.0	0.00	0
P47754	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3 - [CAZA2_MOUSE]	5.8	33	6.2	19.46	6	3.8	10.73	5	4.2	11.64	6
P47811	Mitogen-activated protein kinase 14 OS=Mus musculus GN=Mapk14 PE=1 SV=3 - [MK14_MOUSE]	5.9	41	5.0	14.65	1	6.0	18.01	1	0.0	0.00	0
P47941	Crk-like protein OS=Mus musculus GN=Crkl PE=1 SV=2 - [CRKL_MOUSE]	6.7	34	1.0	3.36	2	0.0	0.00	0	1.0	2.65	1
P48036	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1 - [ANXA5_MOUSE]	5.0	36	10.2	28.74	6	4.6	11.73	5	7.7	19.25	6
P48428	Tubulin-specific chaperone A OS=Mus musculus GN=Tbca PE=1 SV=3 - [TBCA_MOUSE]	5.3	13	1.0	2.77	1	0.0	0.00	0	0.0	0.00	0
P48758	Carbonyl reductase [NADPH] 1 OS=Mus musculus GN=Cbr1 PE=1 SV=3 - [CBR1_MOUSE]	8.3	31	0.0	0.00	0	1.0	2.59	1	0.0	0.00	0
P48962	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4 - [ADT1_MOUSE]	9.7	33	5.8	14.42	4	5.5	14.10	2	4.0	11.09	1
P49138	MAP kinase-activated protein kinase 2 OS=Mus musculus GN=Mapkapk2 PE=1 SV=2 - [MAPK2_MOUSE]	8.6	44	0.0	0.00	0	1.0	3.17	1	0.0	0.00	0
P49442	Inositol polyphosphate 1-phosphatase OS=Mus musculus GN=Inpp1 PE=1 SV=2 - [INPP_MOUSE]	5.0	43	1.0	3.36	1	0.0	0.00	0	0.0	0.00	0
P49722	Proteasome subunit alpha type-2 OS=Mus musculus GN=Psma2 PE=1 SV=3 - [PSA2_MOUSE]	7.4	26	1.7	5.53	3	1.0	2.99	2	1.0	3.56	1
P50247	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3 - [SAHH_MOUSE]	6.5	48	1.0	2.63	3	1.3	3.62	3	1.0	3.03	1
P50396	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3 - [GDIA_MOUSE]	5.1	50	12.0	42.93	6	8.2	28.46	6	9.5	33.32	6
P50516	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2 - [VATA_MOUSE]	5.6	68	3.0	8.68	5	2.3	6.55	3	2.0	5.63	5
P50518	V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2 - [VATE1_MOUSE]	8.4	26	0.0	0.00	0	1.0	2.36	1	0.0	0.00	0
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadvl PE=1 SV=3 -	8.7	71	0.0	0.00	0	0.0	0.00	0	1.0	3.00	1
P50580	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3 - [PA2G4_MOUSE]	6.9	44	1.5	3.95	6	1.5	3.78	6	1.5	3.52	4
P50637	Translocator protein OS=Mus musculus GN=Tspo PE=1 SV=1 - [TSPO_MOUSE]	9.5	19	1.5	5.47	2	1.5	5.10	2	1.0	3.38	3
P51150	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2 - [RAB7A_MOUSE]	6.7	23	5.2	15.19	6	3.7	10.26	6	3.8	10.92	6
P51881	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3 - [ADT2_MOUSE]	9.7	33	8.3	21.77	6	8.0	21.25	6	7.3	19.19	6

P52430	Serum paraoxonase/arylesterase 1 OS=Mus musculus GN=Pon1 PE=1 SV=2 - [PON1_MOUSE]	5.2	40	1.8	5.78	5	2.3	7.62	6	2.3	7.43	3
P52480	Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4 - [KPYM_MOUSE]	7.5	58	63.3	222.51	6	52.8	180.08	6	54.2	184.54	6
P52760	Ribonuclease UK114 OS=Mus musculus GN=Hrsp12 PE=1 SV=3 - [UK114_MOUSE]	8.7	14	2.7	7.21	6	2.0	5.34	5	2.2	6.53	5
P53994	Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1 - [RAB2A_MOUSE]	6.5	24	2.0	5.64	1	2.3	6.43	3	2.0	4.87	1
P54071	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3 - [IDHP_MOUSE]	8.7	51	2.0	5.38	5	1.0	2.97	5	1.5	4.28	2
P54116	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3 - [STOM_MOUSE]	6.9	31	6.0	16.19	6	11.8	35.77	6	7.6	21.01	5
P54775	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2 - [PRS6B_MOUSE]	5.2	47	1.0	2.58	1	0.0	0.00	0	0.0	0.00	0
P56400	Platelet glycoprotein Ib beta chain OS=Mus musculus GN=Gp1bb PE=1 SV=1 - [GP1BB_MOUSE]	10.4	22	2.8	8.67	5	3.3	10.91	6	3.6	11.19	5
P56480	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2 - [ATPB_MOUSE]	5.3	56	40.3	131.92	6	32.8	106.48	6	34.7	110.04	6
P57776	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3 - [EF1D_MOUSE]	5.0	31	5.0	19.14	2	0.0	0.00	0	0.0	0.00	0
P57780	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1 - [ACTN4_MOUSE]	5.4	105	65.7	212.25	6	42.5	134.02	6	51.3	161.00	6
P57787	Monocarboxylate transporter 4 OS=Mus musculus GN=Slc16a3 PE=1 SV=1 - [MOT4_MOUSE]	8.0	50	1.0	2.59	1	0.0	0.00	0	0.0	0.00	0
P58389	Serine/threonine-protein phosphatase 2A activator OS=Mus musculus GN=Ppp2r4 PE=1 SV=1 - [PTPA_MOUSE]	6.4	37	1.2	3.08	5	1.6	3.95	5	1.3	3.28	6
P58459	A disintegrin and metalloproteinase with thrombospondin motifs 10 OS=Mus musculus GN=Adamts10 PE=2 S	8.0	121	1.0	2.74	3	1.0	2.72	3	1.3	3.47	3
P59055	Cysteine/serine-rich nuclear protein 3 OS=Mus musculus GN=Csrnp3 PE=1 SV=2 - [CSRN3_MOUSE]	4.7	66	1.0	3.04	1	0.0	0.00	0	0.0	0.00	0
P59999	Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3 - [ARPC4_MOUSE]	8.4	20	3.3	8.82	6	4.2	10.88	6	3.5	9.13	6
P60335	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 - [PCBP1_MOUSE]	7.1	37	1.2	3.03	5	0.0	0.00	0	1.0	2.36	1
P60710	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 - [ACTB_MOUSE]	5.5	42	183.5	702.21	6	156.5	607.85	6	162.2	618.18	6
P60766	Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2 - [CDC42_MOUSE]	6.6	21	7.5	22.85	6	5.0	14.84	5	5.5	15.80	6
P60843	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1 - [IF4A1_MOUSE]	5.5	46	6.8	19.41	4	6.7	18.44	6	6.3	18.01	3
P61027	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1 - [RAB10_MOUSE]	8.4	23	10.2	25.12	6	9.2	22.85	5	8.8	22.03	6
P61028	Ras-related protein Rab-8B OS=Mus musculus GN=Rab8b PE=1 SV=1 - [RAB8B_MOUSE]	9.1	24	7.7	19.94	6	7.0	18.04	4	7.0	18.17	6
P61089	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1 - [UBE2N_MOUSE]	6.6	17	2.2	6.98	6	1.5	4.91	2	1.4	4.41	5
P61161	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1 - [ARP2_MOUSE]	6.7	45	7.0	22.38	6	6.2	19.56	6	6.2	18.57	6
P61164	Alpha-centractin OS=Mus musculus GN=Actr1a PE=1 SV=1 - [ACTZ_MOUSE]	6.6	43	2.8	8.89	5	1.3	3.98	4	2.5	8.08	2
P61205	ADP-ribosylation factor 3 OS=Mus musculus GN=Arf3 PE=2 SV=2 - [ARF3_MOUSE]	7.4	21	10.0	31.30	4	8.7	25.51	6	9.3	27.51	6
P61211	ADP-ribosylation factor-like protein 1 OS=Mus musculus GN=Arl1 PE=1 SV=1 - [ARL1_MOUSE]	5.7	20	1.0	2.27	1	0.0	0.00	0	0.0	0.00	0
P61222	ATP-binding cassette sub-family E member 1 OS=Mus musculus GN=Abce1 PE=1 SV=1 - [ABCE1_MOUSE]	8.3	67	1.0	4.06	1	0.0	0.00	0	0.0	0.00	0
P61226	Ras-related protein Rap-2b OS=Mus musculus GN=Rap2b PE=1 SV=1 - [RAP2B_MOUSE]	4.8	20	1.5	4.04	4	1.0	2.28	2	2.0	4.94	3
P61294	Ras-related protein Rab-6B OS=Mus musculus GN=Rab6b PE=1 SV=1 - [RAB6B_MOUSE]	5.5	23	5.5	14.21	2	0.0	0.00	0	4.5	11.69	2
P61750	ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2 - [ARF4_MOUSE]	7.1	20	0.0	0.00	0	0.0	0.00	0	8.0	25.64	1
P61967	AP-1 complex subunit sigma-1A OS=Mus musculus GN=Ap1s1 PE=1 SV=1 - [AP1S1_MOUSE]	5.7	19	1.0	3.80	2	0.0	0.00	0	0.0	0.00	0
P61982	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2 - [1433G_MOUSE]	4.9	28	16.8	50.79	6	11.8	35.04	5	14.3	42.71	6
P62071	Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1 - [RRAS2_MOUSE]	6.0	23	0.0	0.00	0	1.0	2.21	1	0.0	0.00	0
P62192	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1 - [PRS4_MOUSE]	6.2	49	1.0	2.88	1	0.0	0.00	0	0.0	0.00	0
P62204	Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2 - [CALM_MOUSE]	4.2	17	10.8	39.93	4	7.0	25.80	6	8.8	32.09	5
P62259	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 - [1433E_MOUSE]	4.7	29	19.5	60.60	6	14.8	45.32	5	16.2	49.35	6
P62264	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=1 SV=3 - [RS14_MOUSE]	10.1	16	0.0	0.00	0	2.0	4.64	1	0.0	0.00	0
P62331	ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2 - [ARF6_MOUSE]	9.0	20	1.5	3.48	6	1.8	4.00	5	1.5	3.40	6
P62334	26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 - [PRS10_MOUSE]	7.5	44	1.0	2.89	1	1.0	2.38	1	1.5	3.67	2
P62746	Rho-related GTP-binding protein RhoB OS=Mus musculus GN=Rhob PE=1 SV=1 - [RHOB_MOUSE]	5.2	22	3.0	11.31	1	0.0	0.00	0	0.0	0.00	0
P62774	Myotrophin OS=Mus musculus GN=Mtpn PE=1 SV=2 - [MTPN_MOUSE]	5.5	13	2.5	8.16	6	2.2	6.86	6	2.7	8.44	6
P62806	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2 - [H4_MOUSE]	11.4	11	1.0	2.45	1	0.0	0.00	0	1.0	2.32	1
P62827	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3 - [RAN_MOUSE]	7.5	24	1.8	5.09	5	1.2	3.08	5	1.6	4.61	5
P62830	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1 - [RL23_MOUSE]	10.5	15	1.0	2.68	2	0.0	0.00	0	0.0	0.00	0
P62835	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1 - [RAP1A_MOUSE]	6.7	21	33.5	96.18	6	25.5	73.08	2	27.3	76.05	4
P63001	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1 - [RAC1_MOUSE]	8.5	21	2.2	5.97	6	2.2	5.87	6	2.2	5.76	6
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Mus musculus GN=Pafah1b1 PE=1 SV=2 -	7.4	47	1.8	4.67	5	1.0	2.51	5	1.3	3.01	4
P63017	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1 - [HSP7C_MOUSE]	5.5	71	55.7	180.01	6	46.5	145.92	6	50.7	159.74	6
P63024	Vesicle-associated membrane protein 3 OS=Mus musculus GN=Vamp3 PE=1 SV=1 - [VAMP3_MOUSE]	8.5	11	1.0	3.35	5	1.3	4.02	4	1.5	4.17	2
P63028	Translationally-controlled tumor protein OS=Mus musculus GN=Tpt1 PE=1 SV=1 - [TCTP_MOUSE]	4.9	19	3.2	11.47	6	3.5	11.74	6	3.0	9.65	6
P63038	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 - [CH60_MOUSE]	6.2	61	15.0	46.92	6	10.0	31.24	6	8.2	24.66	6
P63085	Mitogen-activated protein kinase 1 OS=Mus musculus GN=Mapk1 PE=1 SV=3 - [MK01_MOUSE]	7.0	41	0.0	0.00	0	2.0	6.22	1	0.0	0.00	0
P63101	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1 - [1433Z_MOUSE]	4.8	28	49.5	178.48	6	36.7	129.81	6	42.2	147.42	6
P68033	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1 - [ACTC_MOUSE]	5.4	42	94.2	305.10	6	76.5	246.15	6	81.8	261.77	6
P68037	Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1 - [UB2L3_MOUSE]	8.5	18	6.2	21.75	6	5.0	17.39	5	4.5	15.50	6
P68254	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1 - [1433T_MOUSE]	4.8	28	13.2	35.90	6	8.3	22.92	4	8.4	22.20	5
P68368	Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 - [TBA4A_MOUSE]	5.1	50	83.3	291.56	6	65.0	221.37	6	75.3	255.91	6
P68369	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 - [TBA1A_MOUSE]	5.1	50	76.5	274.66	6	65.0	226.68	5	67.2	235.21	6
P68372	Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1 - [TBB4B_MOUSE]	4.9	50	70.2	258.17	6	67.7	241.19	6	66.6	232.50	5
P68373	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 - [TBA1C_MOUSE]	5.1	50	0.0	0.00	0	48.0	164.61	1	0.0	0.00	0
P68510	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2 - [1433F_MOUSE]	4.9	28	23.3	71.44	6	15.0	46.83	6	17.3	51.83	6
P70168	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2 - [IMB1_MOUSE]	4.8	97	5.8	18.86	6	4.2	14.04	5	4.3	13.33	6
P70188	Kinesin-associated protein 3 OS=Mus musculus GN=Kifap3 PE=1 SV=1 - [KIFA3_MOUSE]	5.1	91	0.0	0.00	0	1.0	3.02	1	0.0	0.00	0
P70302	Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=2 - [STIM1_MOUSE]	6.5	78	8.0	22.12	6	4.2	11.30	6	5.0	13.25	6
P70305	Phosphatidylinositol 3-kinase regulatory subunit alpha (Fragment) OS=Mus musculus GN=Pik3r1 PE=1 SV=	7.6	13	1.0	2.74	1	0.0	0.00	0	0.0	0.00	0

P70315	Wiskott-Aldrich syndrome protein homolog OS=Mus musculus GN=Was PE=1 SV=1 - [WASP_MOUSE]	6.7	54	1.0	3.10	1	0.0	0.00	0	0.0	0.00	0
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3 - [NHRF1_MOUSE	5.9	39	1.0	2.88	1	1.0	2.73	1	0.0	0.00	0
P70452	Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1 - [STX4_MOUSE]	6.1	34	1.0	3.20	1	1.0	2.63	1	1.0	3.14	1
P70460	Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4 - [VASP_MOUSE]	8.5	40	2.3	6.76	3	2.8	8.37	4	2.3	7.01	3
P70677	Caspase-3 OS=Mus musculus GN=Casp3 PE=1 SV=1 - [CASP3_MOUSE]	6.9	31	1.5	3.72	6	1.5	3.50	6	1.8	4.29	4
P80314	T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4 - [TCPB_MOUSE]	6.4	57	8.5	29.66	6	7.7	26.80	6	8.3	28.07	6
P80316	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1 - [TCPE_MOUSE]	6.0	60	4.3	13.48	6	2.3	6.57	6	3.8	11.83	5
P80317	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3 - [TCPZ_MOUSE]	7.1	58	4.2	15.72	5	4.2	14.56	5	3.7	12.17	6
P83626	Tumor necrosis factor receptor superfamily member 26 OS=Mus musculus GN=Tnfrsf26 PE=2 SV=1 - [TNR26_	7.1	23	0.0	0.00	0	1.0	3.71	1	0.0	0.00	0
P83887	Tubulin gamma-1 chain OS=Mus musculus GN=Tubg1 PE=1 SV=1 - [TBG1_MOUSE]	6.0	51	0.0	0.00	0	1.0	3.02	1	0.0	0.00	0
P84084	ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2 - [ARF5_MOUSE]	6.8	21	8.5	27.84	2	7.0	20.91	2	9.5	29.92	2
P97290	Plasma protease C1 inhibitor OS=Mus musculus GN=Serping1 PE=1 SV=3 - [IC1_MOUSE]	6.3	56	5.7	24.86	6	5.2	22.31	5	5.0	20.97	6
P97315	Cysteine and glycine-rich protein 1 OS=Mus musculus GN=Csrp1 PE=1 SV=3 - [CSRP1_MOUSE]	8.6	21	5.7	13.98	6	2.5	5.74	6	4.5	11.34	6
P97450	ATP synthase-coupling factor 6, mitochondrial OS=Mus musculus GN=Atp5j PE=1 SV=1 - [ATP5J_MOUSE]	9.4	12	0.0	0.00	0	1.0	2.28	2	0.0	0.00	0
P97807	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3 - [FUMH_MOUSE]	9.0	54	3.5	9.87	6	1.6	4.09	5	3.0	7.68	4
P97855	Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1 - [G3BP1_MOUSE]	5.6	52	1.0	2.28	1	0.0	0.00	0	0.0	0.00	0
P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Mus musculus GN=Fmo5 PE=1 SV=4 - [FMO5_MOUSE]	8.7	60	9.5	29.55	6	8.5	25.80	6	9.3	27.64	6
P99024	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1 - [TBB5_MOUSE]	4.9	50	60.0	212.67	6	59.7	205.85	6	61.0	207.81	6
P99026	Proteasome subunit beta type-4 OS=Mus musculus GN=Psmb4 PE=1 SV=1 - [PSB4_MOUSE]	5.6	29	0.0	0.00	0	1.7	4.79	3	1.3	3.52	3
P99027	60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3 - [RLA2_MOUSE]	4.5	12	1.4	4.33	5	1.0	3.23	4	1.0	2.97	6
P99029	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2 - [PRDX5_MOUSE]	8.9	22	9.5	30.45	2	4.5	15.05	2	4.0	13.33	2
Q00612	Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3 - [G6PD1_MOUSE]	6.5	59	2.0	6.17	1	1.0	2.95	1	0.0	0.00	0
Q00623	Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=2 - [APOA1_MOUSE]	5.7	31	42.0	124.04	6	41.0	132.95	6	47.0	160.27	6
Q00724	Retinol-binding protein 4 OS=Mus musculus GN=Rbp4 PE=1 SV=2 - [RET4_MOUSE]	6.0	23	1.0	2.19	1	1.0	2.21	1	1.0	2.19	2
Q00896	Alpha-1-antitrypsin 1-3 OS=Mus musculus GN=Serpina1c PE=1 SV=2 - [A1AT3_MOUSE]	5.4	46	81.4	359.62	5	36.5	152.47	4	66.5	285.25	4
Q00897	Alpha-1-antitrypsin 1-4 OS=Mus musculus GN=Serpina1d PE=1 SV=1 - [A1AT4_MOUSE]	5.4	46	73.0	317.37	6	49.7	214.11	6	59.2	249.46	6
Q00898	Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e PE=1 SV=1 - [A1AT5_MOUSE]	5.7	46	88.5	399.81	6	32.5	149.74	4	65.2	292.75	6
Q01102	P-selectin OS=Mus musculus GN=Selp PE=1 SV=1 - [LYAM3_MOUSE]	6.0	83	1.3	3.31	3	1.3	3.14	4	1.0	2.35	3
Q01730	Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=1 SV=3 - [RSU1_MOUSE]	8.9	32	31.0	105.94	6	20.5	69.84	6	24.5	83.06	6
Q01853	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4 - [TERA_MOUSE]	5.3	89	31.0	99.00	6	24.0	74.81	6	26.7	83.14	6
Q02013	Aquaporin-1 OS=Mus musculus GN=Aqp1 PE=1 SV=3 - [AQP1_MOUSE]	7.4	29	1.0	4.99	2	2.0	10.12	1	1.0	4.91	2
Q02053	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1 - [UBA1_MOUSE]	5.7	118	18.7	59.74	6	14.8	45.87	6	15.3	47.34	6
Q03265	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 - [ATPA_MOUSE]	9.2	60	23.0	81.58	5	16.3	56.76	6	19.2	66.39	6
Q03719	Potassium voltage-gated channel subfamily D member 1 OS=Mus musculus GN=Kcnd1 PE=1 SV=1 - [KCND1_MOU	8.2	72	1.0	2.59	1	0.0	0.00	0	0.0	0.00	0
Q03734	Serine protease inhibitor A3M OS=Mus musculus GN=Serpina3m PE=1 SV=2 - [SPA3M_MOUSE]	6.1	47	45.0	147.49	1	25.0	80.78	1	0.0	0.00	0
Q04447	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1 - [KCRB_MOUSE]	5.7	43	2.8	8.13	5	2.8	8.10	6	2.8	8.18	6
Q04750	DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2 - [TOP1_MOUSE]	9.3	91	0.0	0.00	0	1.0	2.04	1	0.0	0.00	0
Q05020	Apolipoprotein C-II OS=Mus musculus GN=Apoc2 PE=2 SV=1 - [APOC2_MOUSE]	4.8	11	1.7	4.60	3	1.3	3.10	3	1.0	2.33	2
Q06138	Calcium-binding protein 39 OS=Mus musculus GN=Cab39 PE=1 SV=2 - [CAB39_MOUSE]	6.9	40	2.0	4.30	2	0.0	0.00	0	0.0	0.00	0
Q06770	Corticosteroid-binding globulin OS=Mus musculus GN=Serpina6 PE=1 SV=1 - [CBG_MOUSE]	5.2	45	1.2	3.26	5	6.0	18.16	6	2.3	7.61	3
Q06890	Clusterin OS=Mus musculus GN=Clu PE=1 SV=1 - [CLUS_MOUSE]	5.7	52	6.8	19.66	6	3.3	8.46	4	4.4	11.96	5
Q07076	Annexin A7 OS=Mus musculus GN=Anxa7 PE=1 SV=2 - [ANXA7_MOUSE]	6.2	50	0.0	0.00	0	1.0	2.71	1	0.0	0.00	0
Q07235	Glia-derived nexin OS=Mus musculus GN=Serpine2 PE=1 SV=2 - [GDN_MOUSE]	9.8	44	22.2	72.89	6	18.3	56.58	6	19.3	59.34	6
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acads PE=1 SV=2 - [ACA	8.5	45	0.0	0.00	0	1.0	2.12	1	1.0	2.20	2
Q07456	Protein AMBP OS=Mus musculus GN=Ambp PE=1 SV=2 - [AMBP_MOUSE]	6.3	39	0.0	0.00	0	1.0	2.10	1	0.0	0.00	0
Q07797	Galectin-3-binding protein OS=Mus musculus GN=Lgals3bp PE=1 SV=1 - [LG3BP_MOUSE]	5.1	64	5.3	20.89	6	3.3	12.87	6	4.8	18.39	6
Q08093	Calponin-2 OS=Mus musculus GN=Cnn2 PE=1 SV=1 - [CNN2_MOUSE]	7.6	33	14.2	45.56	6	11.7	36.07	6	12.3	39.27	6
Q0VBD0	Integrin beta OS=Mus musculus GN=Itgb8 PE=1 SV=1 - [Q0VBD0_MOUSE]	7.1	84	3.0	9.16	1	1.0	3.30	1	1.0	3.11	1
Q148B1	Cytochrome P450, family 2, subfamily c, polypeptide 65 OS=Mus musculus GN=Cyp2c65 PE=1 SV=1 - [Q148B	7.7	56	1.5	3.15	4	1.0	2.08	1	0.0	0.00	0
Q14B01	Protein Rnf113a2 OS=Mus musculus GN=Rnf113a2 PE=1 SV=1 - [Q14B01_MOUSE]	6.5	38	0.0	0.00	0	0.0	0.00	0	2.0	4.19	1
Q1MX41	Protein kinase C OS=Mus musculus GN=Prkcd PE=1 SV=1 - [Q1MX41_MOUSE]	8.0	63	1.0	2.64	1	0.0	0.00	0	0.0	0.00	0
Q1WG82	GATA-type zinc finger protein 1 OS=Mus musculus GN=Zglp1 PE=2 SV=1 - [ZGLP1_MOUSE]	9.1	29	1.0	3.22	1	1.0	2.48	1	1.0	2.86	1
Q1WNP4	Cardiac myosin heavy chain alpha (Fragment) OS=Mus musculus GN=Myh6 PE=1 SV=1 - [Q1WNP4_MOUSE]	5.0	11	0.0	0.00	0	0.0	0.00	0	1.0	2.16	1
Q2PZL6	Protocadherin Fat 4 OS=Mus musculus GN=Fat4 PE=1 SV=2 - [FAT4_MOUSE]	4.9	540	0.0	0.00	0	1.0	2.31	1	0.0	0.00	0
Q2TA57	Aspartate beta-hydroxylase domain-containing protein 1 OS=Mus musculus GN=Asphd1 PE=2 SV=2 - [ASPH1_	8.3	38	1.0	2.61	1	0.0	0.00	0	0.0	0.00	0
Q3LAC4	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Mus musculus GN=Prex2	7.3	182	1.0	2.07	2	1.0	2.19	2	1.0	2.21	2
Q3TC93	HCLS1-binding protein 3 OS=Mus musculus GN=Hs1bp3 PE=1 SV=2 - [H1BP3_MOUSE]	5.0	44	1.0	3.12	1	0.0	0.00	0	0.0	0.00	0
Q3TCJ1	BRISC complex subunit Abro1 OS=Mus musculus GN=Fam175b PE=1 SV=1 - [F175B_MOUSE]	6.2	47	10.5	28.42	6	9.5	25.54	6	9.7	25.85	6
Q3TEG7	Ras-related protein Rab-2B OS=Mus musculus GN=Rab2b PE=1 SV=1 - [Q3TEG7_MOUSE]	6.5	21	1.0	2.77	1	0.0	0.00	0	2.0	5.55	1
Q3TEK6	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide OS=Mus musculus GN=Dap	7.8	28	3.8	13.02	6	3.5	12.13	6	3.2	10.35	6
Q3TG90	Microtubule-associated protein RP/EB family member 2 OS=Mus musculus GN=Mapre2 PE=1 SV=1 - [Q3TG90_M	7.9	20	1.0	2.37	3	0.0	0.00	0	0.0	0.00	0
Q3TIR6	Prefoldin subunit 3 OS=Mus musculus GN=Vbp1 PE=1 SV=1 - [Q3TIR6_MOUSE]	8.8	15	1.0	3.74	1	0.0	0.00	0	0.0	0.00	0
Q3TIV5	Zinc finger CCCH domain-containing protein 15 OS=Mus musculus GN=Zc3h15 PE=1 SV=2 - [ZC3HF_MOUSE]	5.3	48	1.0	2.34	1	1.0	2.11	1	0.0	0.00	0
Q3TJ56	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1 - [Q3TJ56_MOUS	9.2	68	0.0	0.00	0	1.5	3.65	2	0.0	0.00	0
Q3TJD7	PDZ and LIM domain protein 7 OS=Mus musculus GN=Pdlim7 PE=1 SV=1 - [PDLI7_MOUSE]	8.5	50	2.4	5.83	5	2.2	5.63	6	2.2	5.21	6
Q3TL44	NLR family member X1 OS=Mus musculus GN=Nlrx1 PE=1 SV=1 - [NLRX1_MOUSE]	7.4	108	2.3	7.11	6	1.0	2.70	1	1.0	2.64	4

Q3TML0	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=1 - [Q3TML0_MOUSE]	5.2	49	20.0	66.01	1	0.0	0.00	0	0.0	0.00	0
Q3TRH2	26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psmd12 PE=1 SV=1 - [Q3TRH2_MOUSE	7.3	48	1.0	2.45	5	1.0	2.45	3	1.5	3.68	4
Q3TWV4	AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1 - [Q3TWV4_MOUSE]	9.5	49	1.0	3.83	1	0.0	0.00	0	0.0	0.00	0
Q3TYR7	Endophilin B1 testis variant OS=Mus musculus GN=Sh3glb1 PE=1 SV=1 - [Q3TYR7_MOUSE]	6.3	40	1.0	3.56	1	1.0	2.44	1	1.0	2.46	2
Q3U0I3	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1 - [Q3U0I3_MOUSE]	7.3	58	0.0	0.00	0	6.0	14.18	1	0.0	0.00	0
Q3U108	AT-rich interactive domain-containing protein 5A OS=Mus musculus GN=Arid5a PE=1 SV=1 - [ARI5A_MOUSE]	9.0	64	1.0	2.65	1	0.0	0.00	0	0.0	0.00	0
Q3U1F9	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1 OS=Mus musculus GN=Pag1 PE=	4.8	47	1.5	4.66	2	2.0	6.83	1	3.0	9.72	2
Q3U2G2	Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1 - [Q3U2G2_MOUSE]	5.2	94	4.8	13.18	4	5.0	13.65	4	4.0	10.82	4
Q3U4W8	Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus GN=Usp5 PE=1 SV=1 - [Q3U4W8_MOUSE]	5.1	93	2.6	7.97	5	3.0	8.87	2	2.6	7.73	5
Q3U5V8	MCG49559 OS=Mus musculus GN=Stx11 PE=1 SV=1 - [Q3U5V8_MOUSE]	7.1	33	4.7	13.67	6	3.2	9.27	6	2.2	6.42	6
Q3U7R1	Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 SV=2 - [ESYT1_MOUSE]	5.9	121	1.2	2.72	5	1.0	2.44	1	1.0	2.36	2
Q3UCQ1	Forkhead box protein K2 OS=Mus musculus GN=Foxk2 PE=1 SV=3 - [FOXK2_MOUSE]	9.5	68	0.0	0.00	0	1.7	4.33	3	0.0	0.00	0
Q3UEG7	Inter-alpha-trypsin inhibitor heavy chain H2 (Fragment) OS=Mus musculus GN=Itih2 PE=1 SV=1 - [Q3UEG7	6.2	51	2.2	6.99	6	1.8	5.60	4	1.8	5.71	5
Q3UFB2	Box C/D snoRNA protein 1 OS=Mus musculus GN=Znhit6 PE=1 SV=2 - [BCD1_MOUSE]	5.6	52	0.0	0.00	0	0.0	0.00	0	1.0	2.07	1
Q3UGF1	WD repeat-containing protein 19 OS=Mus musculus GN=Wdr19 PE=1 SV=1 - [WDR19_MOUSE]	6.6	151	1.0	2.65	1	0.0	0.00	0	0.0	0.00	0
Q3UJQ9	Succinyl-CoA:3-ketoacid-coenzyme A transferase OS=Mus musculus GN=Oxct1 PE=1 SV=1 - [Q3UJQ9_MOUSE]	8.9	52	1.0	3.71	1	0.0	0.00	0	0.0	0.00	0
Q3ULK5	Protein Gm6086 OS=Mus musculus GN=Gm6086 PE=2 SV=1 - [Q3ULK5_MOUSE]	8.6	47	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
Q3ULP7	Protein Ctsll3 OS=Mus musculus GN=Ctsll3 PE=2 SV=1 - [Q3ULP7_MOUSE]	6.4	37	0.0	0.00	0	0.0	0.00	0	1.0	3.04	2
Q3UM45	Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2 - [PP1R7_MOUSE]	4.9	41	1.0	2.73	5	1.0	3.24	3	1.0	2.10	1
Q3UND0	Src kinase-associated phosphoprotein 2 OS=Mus musculus GN=Skap2 PE=1 SV=2 - [SKAP2_MOUSE]	4.7	41	2.7	7.10	6	1.5	5.54	2	1.3	4.96	3
Q3UPY5	Beta-galactosidase-1-like protein 2 OS=Mus musculus GN=Glb1l2 PE=1 SV=1 - [GLBL2_MOUSE]	7.9	72	1.0	2.79	1	0.0	0.00	0	1.0	2.50	1
Q3UR44	Protein MRVI1 (Fragment) OS=Mus musculus GN=Mrvi1 PE=1 SV=1 - [Q3UR44_MOUSE]	5.7	78	1.0	3.20	2	2.0	5.60	5	2.0	6.47	3
Q3UV74	Integrin beta-2-like protein OS=Mus musculus GN=Itgb2l PE=1 SV=1 - [ITB2L_MOUSE]	7.1	81	0.0	0.00	0	1.0	2.95	1	0.0	0.00	0
Q3UV95	Erythrocyte membrane protein band 4.2 OS=Mus musculus GN=Epb42 PE=1 SV=1 - [Q3UV95_MOUSE]	7.8	75	0.0	0.00	0	3.0	7.82	2	0.0	0.00	0
Q3UX10	Tubulin alpha chain-like 3 OS=Mus musculus GN=Tubal3 PE=2 SV=2 - [TBAL3_MOUSE]	5.6	50	2.8	10.35	6	1.7	5.85	6	2.6	9.12	5
Q3UXZ9	Lysine-specific demethylase 5A OS=Mus musculus GN=Kdm5a PE=1 SV=2 - [KDM5A_MOUSE]	6.4	192	0.0	0.00	0	0.0	0.00	0	1.0	2.09	1
Q3UYK3	TBC1 domain family member 9 OS=Mus musculus GN=Tbc1d9 PE=2 SV=2 - [TBCD9_MOUSE]	5.3	143	1.0	2.10	1	0.0	0.00	0	0.0	0.00	0
Q3UZ39	Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfip1 PE=1 SV=2 - [LRRF1_M	4.8	79	0.0	0.00	0	1.0	2.76	1	1.0	3.40	1
Q3V036	Coiled-coil domain-containing protein 27 OS=Mus musculus GN=Ccdc27 PE=2 SV=1 - [CCD27_MOUSE]	5.4	74	1.5	3.99	2	0.0	0.00	0	1.0	2.63	1
Q3V0K9	Plastin-1 OS=Mus musculus GN=Pls1 PE=1 SV=1 - [PLSI_MOUSE]	5.4	70	16.7	52.48	6	11.4	36.77	5	11.8	38.48	6
Q3V0P3	Protein Gm1527 OS=Mus musculus GN=Gm1527 PE=2 SV=1 - [Q3V0P3_MOUSE]	8.6	74	1.0	3.21	3	1.0	3.56	1	1.0	3.41	3
Q3V2Y9	Dual-specificity protein phosphatase 3 OS=Mus musculus GN=Dusp3 PE=1 SV=1 - [Q3V2Y9_MOUSE]	8.5	13	0.0	0.00	0	1.0	3.47	2	0.0	0.00	0
Q3V3K3	Serine/threonine-protein kinase TAO3 OS=Mus musculus GN=Taok3 PE=1 SV=1 - [Q3V3K3_MOUSE]	9.2	53	0.0	0.00	0	1.0	2.46	2	1.0	3.40	1
Q3V3M1	Nuclear factor erythroid 2-related factor 1 OS=Mus musculus GN=Nfe2l1 PE=1 SV=1 - [Q3V3M1_MOUSE]	5.1	50	0.0	0.00	0	0.0	0.00	0	1.0	2.63	1
Q499X9	Methionine--tRNA ligase, mitochondrial OS=Mus musculus GN=Mars2 PE=1 SV=2 - [SYMM_MOUSE]	8.1	66	0.0	0.00	0	1.0	2.07	1	0.0	0.00	0
Q4G0F8	Ubinuclein-1 OS=Mus musculus GN=Ubn1 PE=2 SV=1 - [UBN1_MOUSE]	9.3	122	1.0	2.33	1	0.0	0.00	0	0.0	0.00	0
Q4LDG0	Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=1 SV=2 - [S27A5_MOUSE]	8.4	76	1.0	2.14	1	0.0	0.00	0	0.0	0.00	0
Q4VA93	Protein kinase C OS=Mus musculus GN=Prkca PE=1 SV=1 - [Q4VA93_MOUSE]	7.0	77	4.6	13.00	5	3.6	9.38	5	4.7	12.86	6
Q4W8U9	Scg2 protein OS=Mus musculus GN=Scg2 PE=1 SV=1 - [Q4W8U9_MOUSE]	4.7	66	1.0	2.64	2	0.0	0.00	0	1.0	2.53	1
Q562D6	tRNA (adenine(37)-N6)-methyltransferase OS=Mus musculus GN=Trmo PE=2 SV=2 - [TRMO_MOUSE]	6.7	48	0.0	0.00	0	1.0	2.24	1	0.0	0.00	0
Q5BKQ4	Inactive pancreatic lipase-related protein 1 OS=Mus musculus GN=Pnliprp1 PE=1 SV=2 - [LIPR1_MOUSE]	6.3	53	1.0	2.91	1	0.0	0.00	0	0.0	0.00	0
Q5DTT1	Protein KIAA2022 OS=Mus musculus GN=Kiaa2022 PE=2 SV=3 - [K2022_MOUSE]	6.0	167	1.0	2.53	1	1.0	2.59	1	0.0	0.00	0
Q5DU02	Ubiquitin carboxyl-terminal hydrolase 22 OS=Mus musculus GN=Usp22 PE=2 SV=2 - [UBP22_MOUSE]	8.0	60	1.0	2.26	1	0.0	0.00	0	0.0	0.00	0
Q5F226	Protocadherin Fat 2 OS=Mus musculus GN=Fat2 PE=1 SV=1 - [FAT2_MOUSE]	5.1	480	0.0	0.00	0	1.0	2.66	1	0.0	0.00	0
Q5F2D9	Arrestin, beta 2 OS=Mus musculus GN=Arrb2 PE=1 SV=1 - [Q5F2D9_MOUSE]	7.8	46	0.0	0.00	0	0.0	0.00	0	1.0	3.79	2
Q5FWK3	Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1 - [RHG01_MOUSE]	6.4	50	3.7	9.93	6	2.0	4.90	3	1.5	3.56	4
Q5GAM9	Putative inactive ribonuclease 11 OS=Mus musculus GN=Rnase11 PE=2 SV=1 - [RNS11_MOUSE]	9.4	21	1.0	2.97	1	0.0	0.00	0	0.0	0.00	0
Q5H8B9	FRAS1-related extracellular matrix protein 3 OS=Mus musculus GN=Frem3 PE=2 SV=2 - [FREM3_MOUSE]	5.2	235	0.0	0.00	0	1.0	2.57	1	0.0	0.00	0
Q5NC80	Nucleoside diphosphate kinase (Fragment) OS=Mus musculus GN=Nme1 PE=1 SV=1 - [Q5NC80_MOUSE]	9.1	14	0.0	0.00	0	6.0	19.47	1	0.0	0.00	0
Q5PR69	Uncharacterized protein KIAA1211 OS=Mus musculus GN=Kiaa1211 PE=1 SV=3 - [K1211_MOUSE]	5.4	132	1.5	4.89	2	0.0	0.00	0	0.0	0.00	0
Q5PR73	GTP-binding protein Di-Ras2 OS=Mus musculus GN=Diras2 PE=1 SV=1 - [DIRA2_MOUSE]	8.8	22	0.0	0.00	0	0.0	0.00	0	1.0	2.25	2
Q5RI75	Ras and EF-hand domain-containing protein homolog OS=Mus musculus GN=Rasef PE=1 SV=1 - [RASEF_MOUSE]	5.4	71	0.0	0.00	0	1.0	2.55	1	1.0	2.45	1
Q5RKN9	Capping protein (Actin filament) muscle Z-line, alpha 1 OS=Mus musculus GN=Capza1 PE=1 SV=1 - [Q5RKN	5.6	33	7.0	21.93	1	4.0	10.58	1	4.7	13.37	3
Q5S003	Sperm-associated antigen 17 OS=Mus musculus GN=Spag17 PE=1 SV=2 - [SPG17_MOUSE]	6.2	263	1.0	2.79	1	1.0	2.60	1	1.5	4.62	2
Q5SP75	CDK5 regulatory subunit-associated protein 2 (Fragment) OS=Mus musculus GN=Cdk5rap2 PE=1 SV=2 - [Q5S	5.4	44	2.0	5.97	1	0.0	0.00	0	1.0	2.73	2
Q5SPX1	Coiled-coil domain-containing protein 157 OS=Mus musculus GN=Ccdc157 PE=1 SV=1 - [CC157_MOUSE]	7.1	80	2.0	4.39	2	1.0	2.06	1	1.0	2.09	1
Q5SQG5	Prohibitin (Fragment) OS=Mus musculus GN=Phb PE=1 SV=1 - [Q5SQG5_MOUSE]	6.4	23	1.5	3.54	2	1.0	2.14	3	0.0	0.00	0
Q5SSE9	ATP-binding cassette sub-family A member 13 OS=Mus musculus GN=Abca13 PE=2 SV=1 - [ABCAD_MOUSE]	6.5	569	1.0	3.41	1	0.0	0.00	0	0.0	0.00	0
Q5SUH7	Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=1 - [Q5SUH7_MOUSE]	6.4	68	1.0	2.61	1	1.0	2.45	2	1.0	2.32	3
Q5SVG5	AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=1 - [Q5SVG5_MOUSE]	5.2	101	3.4	11.69	5	1.0	4.70	3	2.5	6.91	2
Q5SW88	Protein Rab1a OS=Mus musculus GN=Rab1a PE=1 SV=1 - [Q5SW88_MOUSE]	6.2	22	12.0	34.40	6	10.4	28.43	5	9.7	27.07	6
Q5SX49	Profilin OS=Mus musculus GN=Pfn1 PE=1 SV=1 - [Q5SX49_MOUSE]	4.9	12	80.3	248.98	6	64.3	197.64	6	71.3	217.40	6
Q5XJY5	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=1 SV=2 - [COPD_MOUSE]	6.2	57	1.0	2.71	2	1.0	3.13	1	1.0	2.39	3
Q60597	2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3 - [ODO1_MOUSE]	6.8	116	3.0	10.21	4	0.0	0.00	0	3.0	9.59	5
Q60605	Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3 - [MYL6_MOUSE]	4.7	17	23.3	79.61	6	18.8	62.29	6	22.3	74.36	6
Q60682	Killer cell lectin-like receptor 8 OS=Mus musculus GN=Klra8 PE=1 SV=1 - [KLRA8_MOUSE]	8.8	31	1.0	2.60	2	1.0	2.53	1	1.0	2.65	2

Q60779	Growth arrest-specific protein 8 OS=Mus musculus GN=Gas8 PE=1 SV=2 - [GAS8_MOUSE]	7.9	56	2.0	4.21	1	0.0	0.00	0	0.0	0.00	0
Q60787	Lymphocyte cytosolic protein 2 OS=Mus musculus GN=Lcp2 PE=1 SV=2 - [LCP2_MOUSE]	6.2	60	2.4	6.49	5	2.3	6.13	3	2.0	5.13	3
Q60790	Ras GTPase-activating protein 3 OS=Mus musculus GN=Rasa3 PE=1 SV=2 - [RASA3_MOUSE]	7.3	96	5.5	17.33	6	4.0	10.96	6	5.0	15.81	5
Q60864	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1 - [STIP1_MOUSE]	6.8	63	4.0	11.73	6	4.3	12.20	6	3.5	9.52	6
Q60931	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1 - [VDAC3_MOUS	8.8	31	1.5	3.99	2	1.3	3.05	3	2.0	4.29	1
Q60932	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3 - [VDAC1_MOUS	8.4	32	6.0	18.63	5	4.8	12.96	4	6.3	18.65	3
Q60943	Interleukin-17 receptor A OS=Mus musculus GN=Il17ra PE=1 SV=1 - [I17RA_MOUSE]	5.1	98	0.0	0.00	0	1.0	3.16	1	0.0	0.00	0
Q60994	Adiponectin OS=Mus musculus GN=Adipoq PE=1 SV=2 - [ADIPO_MOUSE]	5.6	27	0.0	0.00	0	1.0	2.61	2	0.0	0.00	0
Q61035	Histidine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Hars PE=1 SV=2 - [SYHC_MOUSE]	6.0	57	1.0	2.29	2	1.0	2.51	1	1.0	2.12	3
Q61081	Hsp90 co-chaperone Cdc37 OS=Mus musculus GN=Cdc37 PE=1 SV=1 - [CDC37_MOUSE]	5.3	45	1.0	2.44	1	0.0	0.00	0	1.0	2.25	1
Q61129	Complement factor I OS=Mus musculus GN=Cfi PE=1 SV=3 - [CFAI_MOUSE]	7.5	67	1.3	4.25	3	1.0	2.99	1	1.0	3.10	1
Q61136	Serine/threonine-protein kinase PRP4 homolog OS=Mus musculus GN=Prpf4b PE=1 SV=3 - [PRP4B_MOUSE]	10.2	117	0.0	0.00	0	1.0	3.02	1	0.0	0.00	0
Q61143	Short transient receptor potential channel 6 OS=Mus musculus GN=Trpc6 PE=1 SV=3 - [TRPC6_MOUSE]	7.0	107	1.0	2.31	1	0.0	0.00	0	0.0	0.00	0
Q61166	Microtubule-associated protein RP/EB family member 1 OS=Mus musculus GN=Mapre1 PE=1 SV=3 - [MARE1_MO	5.2	30	1.7	4.21	6	2.0	5.40	3	1.8	4.39	4
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta OS=Mus musculus GN=Pafah1b2 PE=1 SV=2 - [	5.9	26	2.0	4.85	2	1.3	2.67	4	2.5	5.37	2
Q61247	Alpha-2-antiplasmin OS=Mus musculus GN=Serpinf2 PE=1 SV=1 - [A2AP_MOUSE]	6.3	55	8.0	23.98	6	8.5	25.78	4	5.3	15.87	6
Q61316	Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1 - [HSP74_MOUSE]	5.2	94	5.0	13.86	2	2.0	5.32	2	5.0	13.68	2
Q61335	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=4 - [BAP31_MOUSE]	8.7	28	4.8	17.65	6	4.3	15.10	6	4.3	14.44	6
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mus musculus GN=Hadh PE=1 SV=2 - [HCDH_MOUSE	8.6	34	0.0	0.00	0	0.0	0.00	0	1.0	2.09	1
Q61527	Receptor tyrosine-protein kinase erbB-4 OS=Mus musculus GN=Erbb4 PE=1 SV=5 - [ERBB4_MOUSE]	6.4	147	1.0	2.94	2	0.0	0.00	0	1.0	2.99	1
Q61598	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1 - [GDIB_MOUSE]	6.3	51	13.2	49.08	6	8.7	29.41	6	11.0	36.03	6
Q61599	Rho GDP-dissociation inhibitor 2 OS=Mus musculus GN=Arhgdib PE=1 SV=3 - [GDIR2_MOUSE]	5.1	23	16.8	59.31	6	13.7	46.74	6	15.3	51.79	6
Q61635	GTP-binding protein OS=Mus musculus GN=Ifi47 PE=1 SV=1 - [Q61635_MOUSE]	6.7	47	14.3	38.89	6	9.3	23.16	6	9.8	24.22	6
Q61646	Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1 - [HPT_MOUSE]	6.3	39	4.5	14.58	4	0.0	0.00	0	0.0	0.00	0
Q61702	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Mus musculus GN=Itih1 PE=1 SV=2 - [ITIH1_MOUSE]	7.0	101	2.5	8.72	6	3.0	11.34	4	3.0	11.77	3
Q61703	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Mus musculus GN=Itih2 PE=1 SV=1 - [ITIH2_MOUSE]	7.3	106	0.0	0.00	0	5.5	16.96	2	3.0	8.72	1
Q61735	Leukocyte surface antigen CD47 OS=Mus musculus GN=Cd47 PE=1 SV=2 - [CD47_MOUSE]	8.6	33	3.3	9.65	6	1.8	5.55	5	2.2	6.12	6
Q61739	Integrin alpha-6 OS=Mus musculus GN=Itga6 PE=1 SV=3 - [ITA6_MOUSE]	7.0	122	11.4	35.12	5	8.4	27.11	5	10.6	29.37	5
Q61838	Pregnancy zone protein OS=Mus musculus GN=Pzp PE=1 SV=3 - [PZP_MOUSE]	6.7	166	95.3	335.81	6	84.2	287.54	6	84.0	288.20	6
Q61990	Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1 - [PCBP2_MOUSE]	6.8	38	1.0	2.42	2	0.0	0.00	0	0.0	0.00	0
Q62029	Polyadenylate-binding protein OS=Mus musculus GN=Pabpc2 PE=1 SV=1 - [Q62029_MOUSE]	8.8	69	1.0	2.14	1	0.0	0.00	0	0.0	0.00	0
Q62095	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2 - [DDX3Y_MOUSE]	7.5	73	1.0	2.17	2	0.0	0.00	0	1.0	2.17	1
Q62168	Keratin, type I cuticular Ha2 OS=Mus musculus GN=Krt32 PE=1 SV=2 - [K1H2_MOUSE]	4.8	46	1.5	4.54	2	0.0	0.00	0	1.0	3.42	1
Q62186	Translocon-associated protein subunit delta OS=Mus musculus GN=Ssr4 PE=1 SV=1 - [SSRD_MOUSE]	5.8	19	1.7	4.26	3	1.0	2.45	1	1.0	2.25	3
Q62261	Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2 - [SPTB2_MOUSE]	5.6	274	30.7	99.79	6	18.7	58.87	6	25.2	76.44	6
Q62277	Synaptophysin OS=Mus musculus GN=Syp PE=1 SV=2 - [SYPH_MOUSE]	4.9	34	2.0	5.15	2	1.0	2.52	1	1.0	2.77	2
Q62348	Translin OS=Mus musculus GN=Tsn PE=1 SV=1 - [TSN_MOUSE]	6.4	26	0.0	0.00	0	1.0	2.10	1	0.0	0.00	0
Q62418	Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2 - [DBNL_MOUSE]	4.9	49	1.0	2.85	1	0.0	0.00	0	0.0	0.00	0
Q62422	Osteoclast-stimulating factor 1 OS=Mus musculus GN=Ostf1 PE=1 SV=2 - [OSTF1_MOUSE]	5.7	24	1.3	2.96	4	1.0	2.49	1	1.5	3.63	2
Q62426	Cystatin-B OS=Mus musculus GN=Cstb PE=1 SV=1 - [CYTB_MOUSE]	7.4	11	1.0	3.62	1	0.0	0.00	0	0.0	0.00	0
Q62433	Protein NDRG1 OS=Mus musculus GN=Ndrg1 PE=1 SV=1 - [NDRG1_MOUSE]	6.1	43	2.2	6.56	5	1.5	4.15	4	2.0	5.58	3
Q62469	Integrin alpha-2 OS=Mus musculus GN=Itga2 PE=1 SV=2 - [ITA2_MOUSE]	5.2	129	5.7	19.05	6	3.7	11.40	6	3.8	12.37	6
Q63918	Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3 - [SDPR_MOUSE]	5.2	47	11.2	40.21	6	10.3	36.87	6	13.3	47.64	6
Q64310	Surfeit locus protein 4 OS=Mus musculus GN=Surf4 PE=1 SV=1 - [SURF4_MOUSE]	7.8	30	0.0	0.00	0	0.0	0.00	0	1.0	2.17	2
Q64324	Syntaxin-binding protein 2 OS=Mus musculus GN=Stxbp2 PE=1 SV=1 - [STXB2_MOUSE]	6.7	66	5.5	18.05	6	3.0	9.22	5	2.5	7.11	6
Q64339	Ubiquitin-like protein ISG15 OS=Mus musculus GN=Isg15 PE=1 SV=4 - [ISG15_MOUSE]	7.9	18	1.0	2.84	1	2.0	6.88	5	1.0	3.41	4
Q64433	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2 - [CH10_MOUSE]	8.4	11	2.3	7.40	6	1.0	3.06	2	1.0	2.82	1
Q64442	Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 - [DHSO_MOUSE]	7.0	38	11.2	37.60	6	2.0	6.04	5	11.5	38.68	6
Q64521	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2 - [GPDM_MOUSE]	6.6	81	5.3	14.53	6	1.7	3.84	6	2.7	6.92	6
Q64726	Zinc-alpha-2-glycoprotein OS=Mus musculus GN=Azgp1 PE=1 SV=2 - [ZA2G_MOUSE]	6.2	35	1.0	2.26	1	1.0	2.50	2	0.0	0.00	0
Q64727	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4 - [VINC_MOUSE]	6.0	117	161.2	605.81	6	132.8	492.93	6	148.7	547.89	6
Q65CL1	Catenin alpha-3 OS=Mus musculus GN=Ctnna3 PE=1 SV=2 - [CTNA3_MOUSE]	6.5	100	2.0	4.74	6	4.7	11.41	6	3.8	9.21	6
Q66X01	NACHT, LRR and PYD domains-containing protein 9C OS=Mus musculus GN=Nlrp9c PE=2 SV=1 - [NAL9C_MOUSE	7.6	116	0.0	0.00	0	0.0	0.00	0	1.0	3.13	1
Q68FD5	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3 - [CLH1_MOUSE]	5.7	191	16.3	52.77	6	11.3	38.03	6	11.2	37.38	6
Q6DR99	Neuregulin 1 OS=Mus musculus GN=Nrg1 PE=1 SV=1 - [Q6DR99_MOUSE]	6.6	76	0.0	0.00	0	0.0	0.00	0	1.0	2.96	1
Q6IFZ9	Keratin, type II cytoskeletal 74 OS=Mus musculus GN=Krt74 PE=3 SV=1 - [K2C74_MOUSE]	5.7	55	1.5	3.98	2	0.0	0.00	0	2.0	4.43	1
Q6IRU2	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=1 SV=3 - [TPM4_MOUSE]	4.7	28	35.3	122.94	6	27.3	96.86	6	28.7	99.69	6
Q6NV99	Protein Haus6 OS=Mus musculus GN=Haus6 PE=1 SV=1 - [Q6NV99_MOUSE]	6.7	106	0.0	0.00	0	0.0	0.00	0	1.0	2.48	1
Q6NXH9	Keratin, type II cytoskeletal 73 OS=Mus musculus GN=Krt73 PE=1 SV=1 - [K2C73_MOUSE]	8.1	59	0.0	0.00	0	0.0	0.00	0	1.0	2.57	1
Q6NZD2	Sorting nexin 1 OS=Mus musculus GN=Snx1 PE=1 SV=1 - [Q6NZD2_MOUSE]	5.3	59	0.0	0.00	0	1.0	2.46	1	0.0	0.00	0
Q6NZH9	Protein Rasgrp3 OS=Mus musculus GN=Rasgrp3 PE=1 SV=1 - [Q6NZH9_MOUSE]	6.7	78	1.8	6.93	5	1.3	4.89	3	2.0	7.83	2
Q6NZQ4	PAX-interacting protein 1 OS=Mus musculus GN=Paxip1 PE=1 SV=1 - [PAXI1_MOUSE]	7.2	119	1.0	2.56	1	0.0	0.00	0	0.0	0.00	0
Q6P1B1	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=1 SV=1 - [XPP1_MOUSE]	5.5	70	1.7	4.00	6	1.0	2.15	1	3.0	7.31	2
Q6P1D7	Structure-specific endonuclease subunit SLX4 OS=Mus musculus GN=Slx4 PE=1 SV=1 - [SLX4_MOUSE]	5.5	172	1.4	3.30	5	1.5	3.45	2	1.5	3.47	4
Q6P9Q4	FH1/FH2 domain-containing protein 1 OS=Mus musculus GN=Fhod1 PE=1 SV=3 - [FHOD1_MOUSE]	6.3	130	4.5	14.76	6	2.8	8.33	5	3.2	9.25	6
Q6P9Q6	FK506-binding protein 15 OS=Mus musculus GN=Fkbp15 PE=1 SV=2 - [FKB15_MOUSE]	5.1	133	0.0	0.00	0	0.0	0.00	0	1.0	2.41	1

Q6P9S7	Polypeptide N-acetylgalactosaminyltransferase 10 OS=Mus musculus GN=Galnt10 PE=2 SV=1 - [GLT10_MOUSE	8.4	69	0.0	0.00	0	1.0	2.54	1	0.0	0.00	0
Q6PAC4	Uncharacterized protein C2orf71 homolog OS=Mus musculus PE=2 SV=1 - [CB071_MOUSE]	8.1	139	1.0	2.13	1	0.0	0.00	0	0.0	0.00	0
Q6PB93	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Mus musculus GN=Galnt2 PE=1 SV=1 - [GALT2_MOUSE]	8.5	64	1.0	2.15	2	0.0	0.00	0	1.0	2.22	1
Q6PBC0	Cds2 protein OS=Mus musculus GN=Cds2 PE=1 SV=1 - [Q6PBC0_MOUSE]	4.9	15	2.0	7.59	2	2.0	7.24	2	1.7	5.81	3
Q6PCS8	Protein Zbtb40 OS=Mus musculus GN=Zbtb40 PE=1 SV=1 - [Q6PCS8_MOUSE]	6.2	138	0.0	0.00	0	1.0	2.18	1	0.0	0.00	0
Q6PDI6	Protein FAM63B OS=Mus musculus GN=Fam63b PE=1 SV=1 - [FA63B_MOUSE]	4.6	66	0.0	0.00	0	1.3	3.45	3	0.0	0.00	0
Q6PDN3	Myosin light chain kinase, smooth muscle OS=Mus musculus GN=Mylk PE=1 SV=3 - [MYLK_MOUSE]	6.3	213	1.4	3.50	5	1.0	2.43	2	2.0	4.83	2
Q6PFV6	Epha5 protein OS=Mus musculus GN=Epha5 PE=1 SV=1 - [Q6PFV6_MOUSE]	6.4	91	0.0	0.00	0	0.0	0.00	0	1.0	2.54	1
Q6PG04	Coiled-coil domain-containing protein 82 OS=Mus musculus GN=Ccdc82 PE=2 SV=1 - [CCD82_MOUSE]	5.4	61	1.0	2.66	1	1.0	2.75	2	1.0	2.38	1
Q6PZD9	CCAAT/enhancer-binding protein epsilon OS=Mus musculus GN=Cebpe PE=1 SV=1 - [CEBPE_MOUSE]	9.0	31	2.0	5.84	2	1.5	4.52	4	1.3	3.61	4
Q6PZE0	Mucin-19 OS=Mus musculus GN=Muc19 PE=2 SV=2 - [MUC19_MOUSE]	5.5	693	1.0	2.25	1	0.0	0.00	0	0.0	0.00	0
Q6Y685	Transforming acidic coiled-coil-containing protein 1 OS=Mus musculus GN=Tacc1 PE=1 SV=1 - [TACC1_MOU	5.0	84	0.0	0.00	0	1.0	2.89	1	0.0	0.00	0
Q6YJU1	Fetuin-B OS=Mus musculus GN=Fetub PE=1 SV=1 - [Q6YJU1_MOUSE]	6.5	34	1.3	4.76	6	3.8	12.90	5	2.3	7.67	4
Q6ZPJ3	(E3-independent) E2 ubiquitin-conjugating enzyme UBE2O OS=Mus musculus GN=Ube2o PE=1 SV=3 - [UBE2O_M	5.1	141	4.5	12.44	6	4.5	12.82	6	5.8	15.91	5
Q6ZQ04	FERM domain-containing protein 4B (Fragment) OS=Mus musculus GN=Frmd4b PE=1 SV=1 - [Q6ZQ04_MOUSE]	8.5	112	1.0	2.56	1	0.0	0.00	0	1.0	2.58	1
Q6ZQ06	Centrosomal protein of 162 kDa OS=Mus musculus GN=Cep162 PE=1 SV=2 - [CE162_MOUSE]	5.5	161	1.0	2.47	2	0.0	0.00	0	0.0	0.00	0
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=1 SV=2 - [CAND1_MOUSE]	5.8	136	3.4	9.66	5	2.3	6.25	3	2.3	6.40	4
Q6ZQI3	Malectin OS=Mus musculus GN=Mlec PE=1 SV=2 - [MLEC_MOUSE]	6.0	32	5.3	15.85	6	3.8	12.33	6	4.2	12.80	6
Q6ZWQ9	MCG5400 OS=Mus musculus GN=Myl12a PE=1 SV=1 - [Q6ZWQ9_MOUSE]	4.8	20	19.5	69.48	6	15.7	57.82	6	17.0	59.32	6
Q6ZWR6	Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2 - [SYNE1_MOUSE]	5.6	1009	1.0	2.48	1	1.0	2.19	1	0.0	0.00	0
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3 - [IF2A_MOU	5.1	36	1.0	2.28	2	1.0	3.01	1	1.0	2.34	1
Q71LX4	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3 - [TLN2_MOUSE]	5.8	253	24.3	70.13	6	21.5	61.08	6	24.5	69.89	6
Q76LS9	Protein FAM63A OS=Mus musculus GN=Fam63a PE=1 SV=1 - [FA63A_MOUSE]	4.7	51	1.7	5.98	6	1.7	6.53	6	1.8	6.67	6
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN	5.1	65	4.2	12.84	5	2.2	6.99	6	1.3	4.77	3
Q78PY7	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1 - [SND1_MOUSE]	7.4	102	5.3	15.23	6	6.3	16.51	4	5.2	13.30	6
Q78Y63	Phosducin-like protein 2 OS=Mus musculus GN=Pdcl2 PE=1 SV=1 - [PDCL2_MOUSE]	4.9	28	0.0	0.00	0	1.0	2.05	1	0.0	0.00	0
Q78ZA7	Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap1l4 PE=1 SV=1 - [NP1L4_MOUSE]	4.7	43	1.8	5.05	5	2.0	4.84	2	1.7	4.15	3
Q7TMM9	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1 - [TBB2A_MOUSE]	4.9	50	61.0	223.18	6	58.8	206.46	6	61.2	212.03	6
Q7TMR0	Lysosomal Pro-X carboxypeptidase OS=Mus musculus GN=Prcp PE=1 SV=2 - [PCP_MOUSE]	6.8	55	1.8	6.30	5	1.0	2.97	2	2.0	7.00	2
Q7TNG5	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus GN=Eml2 PE=1 SV=1 - [EMAL2_MOUSE]	6.3	71	3.8	11.30	4	2.5	7.56	2	3.0	9.19	2
Q7TNQ1	Coatomer protein complex, subunit gamma OS=Mus musculus GN=Copg1 PE=1 SV=1 - [Q7TNQ1_MOUSE]	7.9	13	0.0	0.00	0	1.0	2.59	1	0.0	0.00	0
Q7TPM0	Cbx1 protein OS=Mus musculus GN=Cbx1 PE=1 SV=1 - [Q7TPM0_MOUSE]	5.0	16	0.0	0.00	0	1.0	3.04	1	0.0	0.00	0
Q7TPQ3	E3 ubiquitin-protein ligase SHPRH OS=Mus musculus GN=Shprh PE=1 SV=1 - [SHPRH_MOUSE]	7.5	191	0.0	0.00	0	1.0	2.87	1	0.0	0.00	0
Q7TQE2	Zyx protein OS=Mus musculus GN=Zyx PE=1 SV=1 - [Q7TQE2_MOUSE]	6.6	57	12.7	46.68	6	10.2	37.86	6	12.7	44.81	6
Q7TQI8	Testis-specific Y-encoded-like protein 2 OS=Mus musculus GN=Tspyl2 PE=1 SV=1 - [TSYL2_MOUSE]	4.8	78	0.0	0.00	0	1.0	2.06	1	0.0	0.00	0
Q7TS74	Cytoskeleton-associated protein 2-like OS=Mus musculus GN=Ckap2l PE=1 SV=1 - [CKP2L_MOUSE]	9.7	83	5.7	12.74	6	4.8	10.66	6	4.7	10.24	6
Q7TSC3	Serine/threonine-protein kinase Nek5 OS=Mus musculus GN=Nek5 PE=2 SV=1 - [NEK5_MOUSE]	5.5	72	2.0	4.38	5	1.8	3.89	4	1.8	3.82	4
Q7TSG6	Radixin OS=Mus musculus GN=Rdx PE=1 SV=1 - [Q7TSG6_MOUSE]	8.5	46	0.0	0.00	0	1.0	2.39	1	1.0	2.15	2
Q7TSV4	Phosphoglucomutase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1 - [PGM2_MOUSE]	6.1	69	2.5	8.47	6	1.8	5.29	4	1.8	5.67	5
Q80ST9	Lebercilin OS=Mus musculus GN=Lca5 PE=1 SV=1 - [LCA5_MOUSE]	8.2	80	1.0	3.10	1	0.0	0.00	0	0.0	0.00	0
Q80U44	Zinc finger FYVE domain-containing protein 16 OS=Mus musculus GN=Zfyve16 PE=1 SV=2 - [ZFY16_MOUSE]	4.8	167	0.0	0.00	0	0.0	0.00	0	1.0	2.11	1
Q80UG2	Plexin-A4 OS=Mus musculus GN=Plxna4 PE=1 SV=3 - [PLXA4_MOUSE]	6.8	212	1.0	2.55	1	1.0	2.77	2	1.0	2.57	1
Q80UJ7	Rab3 GTPase-activating protein catalytic subunit OS=Mus musculus GN=Rab3gap1 PE=1 SV=4 - [RB3GP_MOUS	5.7	110	0.0	0.00	0	1.0	3.34	1	0.0	0.00	0
Q80VM8	PNMA-like protein 1 OS=Mus musculus GN=Pnmal1 PE=2 SV=1 - [PNML1_MOUSE]	9.5	48	1.0	2.15	1	0.0	0.00	0	0.0	0.00	0
Q80XU2	Tyrosine-protein kinase OS=Mus musculus GN=Src PE=1 SV=1 - [Q80XU2_MOUSE]	7.4	60	3.7	10.80	6	2.0	5.35	1	0.0	0.00	0
Q80YP4	Guanylate cyclase soluble subunit beta-1 OS=Mus musculus GN=Gucy1b3 PE=1 SV=1 - [Q80YP4_MOUSE]	5.5	69	1.4	3.31	5	1.0	2.20	2	1.0	2.17	3
Q80YQ1	Thrombospondin 1 OS=Mus musculus GN=Thbs1 PE=1 SV=1 - [Q80YQ1_MOUSE]	4.9	130	131.0	418.70	4	0.0	0.00	0	125.0	368.48	1
Q80YR6	DNA endonuclease RBBP8 OS=Mus musculus GN=Rbbp8 PE=1 SV=1 - [COM1_MOUSE]	6.7	101	1.0	2.29	4	1.0	2.54	2	1.0	2.40	2
Q80Z71	Tenascin-N OS=Mus musculus GN=Tnn PE=1 SV=2 - [TENN_MOUSE]	5.4	173	1.0	2.41	1	0.0	0.00	0	0.0	0.00	0
Q80ZJ2	Impa1 protein OS=Mus musculus GN=Impa1 PE=1 SV=1 - [Q80ZJ2_MOUSE]	4.8	30	1.0	2.10	1	0.0	0.00	0	0.0	0.00	0
Q80ZJ6	Protein zer-1 homolog OS=Mus musculus GN=Zer1 PE=1 SV=1 - [ZER1_MOUSE]	5.9	89	0.0	0.00	0	0.0	0.00	0	1.0	2.11	1
Q810Y8	PRAMEl7 OS=Mus musculus GN=Pramel7 PE=2 SV=1 - [Q810Y8_MOUSE]	7.2	56	1.6	3.37	5	1.0	2.11	2	1.0	2.15	2
Q811C2	Cysteine protease ATG4C OS=Mus musculus GN=Atg4c PE=1 SV=2 - [ATG4C_MOUSE]	6.4	52	1.7	4.36	3	2.5	6.60	2	2.0	5.23	1
Q811U4	Mitofusin-1 OS=Mus musculus GN=Mfn1 PE=1 SV=3 - [MFN1_MOUSE]	6.5	84	1.0	2.19	2	0.0	0.00	0	1.0	2.11	1
Q8BGD6	Sodium-coupled neutral amino acid transporter 9 OS=Mus musculus GN=Slc38a9 PE=1 SV=1 - [S38A9_MOUSE]	7.5	63	1.8	3.99	5	1.5	3.13	2	1.0	2.07	1
Q8BGG7	Ubiquitin-associated and SH3 domain-containing protein B OS=Mus musculus GN=Ubash3b PE=1 SV=1 - [UBS	6.8	71	7.3	23.77	6	5.6	16.76	5	5.7	16.31	6
Q8BGI7	Leucine-rich repeat-containing protein 39 OS=Mus musculus GN=Lrrc39 PE=1 SV=1 - [LRC39_MOUSE]	6.1	39	0.0	0.00	0	1.0	2.94	1	0.0	0.00	0
Q8BGT7	Survival of motor neuron-related-splicing factor 30 OS=Mus musculus GN=Smndc1 PE=1 SV=1 - [SPF30_MOU	7.2	27	2.0	4.54	2	0.0	0.00	0	1.0	2.25	1
Q8BGZ7	Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt75 PE=1 SV=1 - [K2C75_MOUSE]	8.3	60	0.0	0.00	0	0.0	0.00	0	1.0	2.49	1
Q8BH04	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=1 SV=1 - [PCKGM_MO	7.3	70	1.0	2.63	5	1.0	2.42	1	1.0	2.62	5
Q8BH35	Complement component C8 beta chain OS=Mus musculus GN=C8b PE=1 SV=1 - [CO8B_MOUSE]	7.8	66	1.8	5.59	5	0.0	0.00	0	2.0	4.61	2
Q8BH61	Coagulation factor XIII A chain OS=Mus musculus GN=F13a1 PE=1 SV=3 - [F13A_MOUSE]	5.9	83	5.0	13.43	6	2.8	7.32	4	4.0	10.67	6
Q8BH78	Reticulon OS=Mus musculus GN=Rtn4 PE=1 SV=1 - [Q8BH78_MOUSE]	4.8	38	6.2	20.43	6	6.7	21.12	6	7.0	21.17	6
Q8BHN3	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1 - [GANAB_MOUSE]	6.1	107	2.0	6.78	5	1.0	3.13	5	1.5	5.39	4
Q8BI71	Exocyst complex component 3-like protein OS=Mus musculus GN=Exoc3l1 PE=1 SV=1 - [EX3L1_MOUSE]	5.9	81	1.3	3.29	4	1.0	2.62	2	1.0	2.53	4
Q8BIW1	Protein prune homolog OS=Mus musculus GN=Prune PE=1 SV=1 - [PRUNE_MOUSE]	5.1	50	1.0	2.11	2	1.0	2.58	2	1.0	2.37	4

Q8BJ34	Meiosis arrest female protein 1 OS=Mus musculus GN=Marf1 PE=1 SV=3 - [MARF1_MOUSE]	8.2	192	1.0	2.26	1	0.0	0.00	0	0.0	0.00	0
Q8BKC5	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3 - [IPO5_MOUSE]	4.9	124	1.3	3.52	3	0.0	0.00	0	0.0	0.00	0
Q8BMD8	Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Mus musculus GN=Slc25a24 PE=1 SV=1 - [SCMC1	7.4	53	1.8	4.73	6	1.5	3.59	2	1.0	2.04	1
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochond	8.6	68	1.5	3.95	4	0.0	0.00	0	1.0	2.28	2
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Lars PE=1 SV=2 - [SYLC_MOUSE]	7.0	134	1.0	3.03	2	1.0	2.84	1	1.0	2.62	1
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 - [ECHA_MOUSE]	9.1	83	3.5	12.35	6	2.0	5.68	5	4.3	13.92	3
Q8BND5	Sulfhydryl oxidase 1 OS=Mus musculus GN=Qsox1 PE=1 SV=1 - [QSOX1_MOUSE]	7.2	83	2.3	7.40	4	2.6	8.27	5	2.0	5.90	6
Q8BPI2	Transmembrane emp24 domain-containing protein 2 (Fragment) OS=Mus musculus GN=Tmed2 PE=1 SV=1 - [Q8B	5.5	13	1.0	2.72	3	1.0	2.31	2	0.0	0.00	0
Q8BPM0	Disheveled-associated activator of morphogenesis 1 OS=Mus musculus GN=Daam1 PE=1 SV=4 - [DAAM1_MOUSE	7.5	123	2.5	7.31	4	0.0	0.00	0	2.0	6.10	1
Q8BPW9	Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=1 SV=1 - [Q8BPW9_MOUSE]	7.4	52	2.0	6.43	5	1.8	4.72	4	1.0	2.44	3
Q8BQX0	RAB37, member of RAS oncogene family, isoform CRA_a OS=Mus musculus GN=Rab37 PE=1 SV=1 - [Q8BQX0_MO	6.7	24	0.0	0.00	0	4.0	10.26	1	0.0	0.00	0
Q8BRG6	Kelch-like protein 24 OS=Mus musculus GN=Klhl24 PE=2 SV=2 - [KLH24_MOUSE]	6.4	68	1.0	2.95	1	0.0	0.00	0	0.0	0.00	0
Q8BRK9	Alpha-mannosidase 2x OS=Mus musculus GN=Man2a2 PE=1 SV=2 - [MA2A2_MOUSE]	6.9	131	3.0	8.92	1	2.0	5.78	1	1.0	3.20	1
Q8BT23	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=2 SV=1 - [Q8BT23_MOUSE]	4.7	11	1.0	2.08	1	1.0	3.04	1	0.0	0.00	0
Q8BTU6	Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=1 SV=1 - [Q8BTU6_MOUSE]	5.6	41	5.5	15.33	2	0.0	0.00	0	4.0	10.44	3
Q8BTW8	CDK5 regulatory subunit-associated protein 1 OS=Mus musculus GN=Cdk5rap1 PE=2 SV=2 - [CK5P1_MOUSE]	8.6	66	1.5	4.06	4	1.0	2.80	1	1.0	2.70	3
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Iars PE=1 SV=2 - [SYIC_MOUSE]	6.6	144	1.3	3.80	4	1.0	3.45	3	1.3	4.44	3
Q8BV79	TPR and ankyrin repeat-containing protein 1 OS=Mus musculus GN=Trank1 PE=2 SV=3 - [TRNK1_MOUSE]	7.8	343	1.8	3.90	4	0.0	0.00	0	1.0	2.12	3
Q8BWG8	Beta-arrestin-1 OS=Mus musculus GN=Arrb1 PE=1 SV=1 - [ARRB1_MOUSE]	6.3	47	4.2	13.92	6	3.8	11.46	5	4.3	12.28	4
Q8BWY3	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Etf1 PE=1 SV=4 - [ERF1_MOUSE]	5.7	49	0.0	0.00	0	0.0	0.00	0	1.0	2.23	2
Q8BWZ3	N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Mus musculus GN=Naa25 PE=1 SV=1 - [NAA25_MOU	6.5	112	0.0	0.00	0	0.0	0.00	0	1.0	3.16	1
Q8BX23	Protein Zfp874a OS=Mus musculus GN=Zfp874a PE=2 SV=1 - [Q8BX23_MOUSE]	7.6	52	0.0	0.00	0	1.5	4.63	2	0.0	0.00	0
Q8BXF8	Actin-related protein T3 OS=Mus musculus GN=Actrt3 PE=1 SV=1 - [ACTT3_MOUSE]	5.7	40	2.2	5.89	5	1.6	4.25	5	1.5	4.02	6
Q8BYY9	Serine protease inhibitor A3B OS=Mus musculus GN=Serpina3b PE=2 SV=1 - [SPA3B_MOUSE]	7.2	47	1.0	2.48	1	0.0	0.00	0	0.0	0.00	0
Q8C0C4	Serine-rich coiled-coil domain-containing protein 1 OS=Mus musculus GN=Ccser1 PE=2 SV=2 - [CCSE1_MOU	8.1	98	5.0	13.31	5	4.0	11.18	4	6.5	16.98	4
Q8C0Q9	Rap guanine nucleotide exchange factor 5 OS=Mus musculus GN=Rapgef5 PE=2 SV=2 - [RPGF5_MOUSE]	6.2	94	1.0	3.10	1	0.0	0.00	0	0.0	0.00	0
Q8C159	Tetratricopeptide repeat protein 22 OS=Mus musculus GN=Ttc22 PE=2 SV=1 - [TTC22_MOUSE]	5.1	63	0.0	0.00	0	0.0	0.00	0	1.0	2.96	1
Q8C4Y3	Negative elongation factor B OS=Mus musculus GN=Nelfb PE=1 SV=2 - [NELFB_MOUSE]	6.0	66	0.0	0.00	0	0.0	0.00	0	1.0	2.95	1
Q8C522	Endonuclease domain-containing 1 protein OS=Mus musculus GN=Endod1 PE=1 SV=2 - [ENDD1_MOUSE]	6.2	55	1.5	4.78	6	1.5	4.68	4	1.3	4.03	6
Q8C605	ATP-dependent 6-phosphofructokinase OS=Mus musculus GN=Pfkp PE=1 SV=1 - [Q8C605_MOUSE]	6.9	85	2.0	5.30	2	0.0	0.00	0	0.0	0.00	0
Q8C7J6	Potassium channel tetramerisation domain containing 12b OS=Mus musculus GN=Kctd12b PE=1 SV=1 - [Q8C7	5.9	33	1.0	2.51	1	0.0	0.00	0	0.0	0.00	0
Q8C872	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1 - [Q8C872_MOUSE]	6.5	57	0.0	0.00	0	1.0	3.46	2	0.0	0.00	0
Q8C8Q4	Voltage-dependent L-type calcium channel subunit alpha-1F (Fragment) OS=Mus musculus GN=Cacna1f PE=2	7.4	94	1.0	2.84	1	0.0	0.00	0	0.0	0.00	0
Q8C9V1	Carabin OS=Mus musculus GN=Tbc1d10c PE=1 SV=1 - [TB10C_MOUSE]	8.9	50	1.0	2.69	1	0.0	0.00	0	0.0	0.00	0
Q8C9W3	A disintegrin and metalloproteinase with thrombospondin motifs 2 OS=Mus musculus GN=Adamts2 PE=1 SV=	7.2	135	1.3	3.44	3	1.0	2.52	1	0.0	0.00	0
Q8CAA7	Glucose 1,6-bisphosphate synthase OS=Mus musculus GN=Pgm2l1 PE=1 SV=1 - [PGM2L_MOUSE]	6.5	70	1.0	2.57	1	0.0	0.00	0	0.0	0.00	0
Q8CAG6	Pleckstrin OS=Mus musculus GN=Plek PE=1 SV=1 - [Q8CAG6_MOUSE]	7.4	37	35.2	166.43	6	28.5	128.67	6	29.7	135.30	6
Q8CB59	Protein FAM161B OS=Mus musculus GN=Fam161b PE=1 SV=1 - [F161B_MOUSE]	9.5	67	1.0	2.65	3	1.0	2.69	1	1.0	2.46	1
Q8CB62	Centrobin OS=Mus musculus GN=Cntrob PE=2 SV=2 - [CNTRB_MOUSE]	5.6	99	0.0	0.00	0	0.0	0.00	0	1.0	2.63	2
Q8CBD1	Nuclear receptor-interacting protein 1 OS=Mus musculus GN=Nrip1 PE=1 SV=1 - [NRIP1_MOUSE]	8.0	126	1.0	2.63	1	0.0	0.00	0	0.0	0.00	0
Q8CBG6	6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=1 SV=1 - [Q8CBG6_MOUSE]	6.2	23	2.3	8.05	3	3.0	8.74	1	3.0	9.96	3
Q8CBP6	NK-tumor recognition protein (Fragment) OS=Mus musculus GN=Nktr PE=1 SV=1 - [Q8CBP6_MOUSE]	10.2	109	0.0	0.00	0	1.0	2.63	1	0.0	0.00	0
Q8CCT4	Transcription elongation factor A protein-like 5 OS=Mus musculus GN=Tceal5 PE=1 SV=1 - [TCAL5_MOUSE]	6.2	22	0.0	0.00	0	1.0	2.92	1	0.0	0.00	0
Q8CDG4	Serine/threonine-protein kinase 4 OS=Mus musculus GN=Stk4 PE=1 SV=1 - [Q8CDG4_MOUSE]	9.4	15	0.0	0.00	0	0.0	0.00	0	1.0	2.27	1
Q8CDI6	Coiled-coil domain-containing protein 158 OS=Mus musculus GN=Ccdc158 PE=2 SV=1 - [CD158_MOUSE]	6.4	127	1.5	4.15	2	0.0	0.00	0	1.0	2.75	1
Q8CDN6	Thioredoxin-like protein 1 OS=Mus musculus GN=Txnl1 PE=1 SV=3 - [TXNL1_MOUSE]	5.0	32	1.0	2.67	2	1.0	2.67	4	1.2	3.05	6
Q8CFQ9	Fusion, derived from t(1216) malignant liposarcoma (Human) OS=Mus musculus GN=Fus PE=1 SV=1 - [Q8CFQ	9.4	53	1.0	3.13	1	0.0	0.00	0	0.0	0.00	0
Q8CG03	cGMP-specific 3',5'-cyclic phosphodiesterase OS=Mus musculus GN=Pde5a PE=1 SV=2 - [PDE5A_MOUSE]	6.0	98	12.2	35.88	5	10.8	30.96	6	11.2	30.72	6
Q8CG14	Complement C1s-A subcomponent OS=Mus musculus GN=C1sa PE=2 SV=2 - [CS1A_MOUSE]	5.1	77	1.0	2.56	2	1.0	2.82	1	1.0	2.52	1
Q8CG19	Latent-transforming growth factor beta-binding protein 1 OS=Mus musculus GN=Ltbp1 PE=1 SV=2 - [LTBP1	6.0	187	2.0	7.02	3	1.5	4.61	2	1.5	4.35	2
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4 - [SYEP_MOUSE]	7.7	170	1.5	4.22	6	1.0	2.50	2	1.4	3.96	5
Q8CGS6	DNA polymerase theta OS=Mus musculus GN=Polq PE=1 SV=2 - [DPOLQ_MOUSE]	7.3	281	1.0	2.61	1	0.0	0.00	0	0.0	0.00	0
Q8CHC8	ADNP homeobox protein 2 OS=Mus musculus GN=Adnp2 PE=2 SV=2 - [ADNP2_MOUSE]	9.0	127	1.0	2.64	1	0.0	0.00	0	0.0	0.00	0
Q8CHG3	GRIP and coiled-coil domain-containing protein 2 OS=Mus musculus GN=Gcc2 PE=1 SV=2 - [GCC2_MOUSE]	5.1	194	0.0	0.00	0	1.0	2.20	1	0.0	0.00	0
Q8CHK3	Lysophospholipid acyltransferase 7 OS=Mus musculus GN=Mboat7 PE=1 SV=1 - [MBOA7_MOUSE]	8.7	53	2.0	6.91	1	0.0	0.00	0	0.0	0.00	0
Q8CI43	Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=1 SV=1 - [MYL6B_MOUSE]	5.5	23	0.0	0.00	0	4.0	11.15	2	0.0	0.00	0
Q8CI47	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 OS=Mus musculus GN=Acap1 PE=	8.0	60	1.0	2.85	1	0.0	0.00	0	0.0	0.00	0
Q8CI94	Glycogen phosphorylase, brain form OS=Mus musculus GN=Pygb PE=1 SV=3 - [PYGB_MOUSE]	6.7	97	9.8	30.69	6	9.8	29.52	6	8.3	24.67	6
Q8CIE6	Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=2 - [COPA_MOUSE]	7.6	138	1.3	3.75	3	1.0	2.27	1	1.0	2.42	1
Q8CIH5	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 OS=Mus musculus GN=Plcg2 PE=1 SV=1	6.8	147	2.3	7.61	6	2.0	6.35	4	1.6	4.72	5
Q8CJ40	Rootletin OS=Mus musculus GN=Crocc PE=1 SV=2 - [CROCC_MOUSE]	5.6	227	3.7	8.19	6	2.8	6.12	5	3.2	6.94	6
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1 - [EIF3B_MOU	5.0	91	0.0	0.00	0	1.0	2.65	1	0.0	0.00	0
Q8JZR2	Adapter molecule crk OS=Mus musculus GN=Crk PE=1 SV=1 - [Q8JZR2_MOUSE]	5.5	23	2.0	5.66	4	1.5	3.39	2	1.0	2.57	3
Q8K0E8	Fibrinogen beta chain OS=Mus musculus GN=Fgb PE=1 SV=1 - [FIBB_MOUSE]	7.1	55	105.7	371.28	6	87.0	306.07	6	98.3	339.62	6
Q8K0Q5	Rho GTPase-activating protein 18 OS=Mus musculus GN=Arhgap18 PE=1 SV=1 - [RHG18_MOUSE]	6.7	75	2.7	7.32	6	1.7	3.81	3	1.3	3.33	6
Q8K0T2	Cytoplasmic dynein 2 light intermediate chain 1 OS=Mus musculus GN=Dync2li1 PE=1 SV=1 - [DC2L1_MOUSE	8.1	39	1.0	2.80	1	0.0	0.00	0	0.0	0.00	0

Q8K124	Pleckstrin homology domain-containing family O member 2 OS=Mus musculus GN=Plekho2 PE=1 SV=1 - [PKHO	5.5	54	1.3	4.76	4	1.7	6.87	3	1.0	4.40	4
Q8K1B8	Fermitin family homolog 3 OS=Mus musculus GN=Fermt3 PE=1 SV=1 - [URP2_MOUSE]	7.0	76	77.8	261.51	6	64.2	214.53	6	74.5	244.24	6
Q8K1I7	WAS/WASL-interacting protein family member 1 OS=Mus musculus GN=Wipf1 PE=1 SV=1 - [WIPF1_MOUSE]	11.4	50	2.0	5.88	2	0.0	0.00	0	0.0	0.00	0
Q8K1K2	26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1 - [Q8K1K2_MOUSE]	6.0	39	1.0	3.68	2	1.0	2.24	2	1.0	2.71	1
Q8K1R7	Serine/threonine-protein kinase Nek9 OS=Mus musculus GN=Nek9 PE=1 SV=2 - [NEK9_MOUSE]	5.6	107	0.0	0.00	0	0.0	0.00	0	1.0	2.07	1
Q8K1S4	Netrin receptor UNC5A OS=Mus musculus GN=Unc5a PE=1 SV=1 - [UNC5A_MOUSE]	6.9	99	1.3	2.85	3	1.0	2.11	2	1.0	2.09	2
Q8K1X4	NCK associated protein 1 like OS=Mus musculus GN=Nckap1l PE=1 SV=1 - [Q8K1X4_MOUSE]	6.6	129	0.0	0.00	0	1.0	2.10	2	1.0	2.12	1
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=	7.4	73	1.5	4.04	2	1.0	3.01	2	1.0	2.66	2
Q8K2D2	Osbpl1a protein OS=Mus musculus GN=Osbpl1a PE=1 SV=1 - [Q8K2D2_MOUSE]	8.6	38	1.0	2.75	1	1.5	4.24	2	1.5	4.22	4
Q8K2H2	OTU domain-containing protein 6B OS=Mus musculus GN=Otud6b PE=1 SV=1 - [OTU6B_MOUSE]	5.5	34	0.0	0.00	0	0.0	0.00	0	1.0	3.24	1
Q8K389	CDK5 regulatory subunit-associated protein 2 OS=Mus musculus GN=Cdk5rap2 PE=1 SV=3 - [CK5P2_MOUSE]	5.3	206	0.0	0.00	0	1.0	2.92	1	0.0	0.00	0
Q8K424	Transient receptor potential cation channel subfamily V member 3 OS=Mus musculus GN=Trpv3 PE=1 SV=2	6.3	91	1.5	4.89	2	1.3	4.24	3	1.0	3.03	1
Q8K4F0	CD226 antigen OS=Mus musculus GN=Cd226 PE=2 SV=1 - [CD226_MOUSE]	9.0	38	1.0	4.24	1	0.0	0.00	0	1.0	4.53	1
Q8K4P8	E3 ubiquitin-protein ligase HECW1 OS=Mus musculus GN=Hecw1 PE=1 SV=3 - [HECW1_MOUSE]	5.4	179	2.0	6.87	2	1.0	3.03	3	2.5	8.07	2
Q8K558	Trem-like transcript 1 protein OS=Mus musculus GN=Treml1 PE=1 SV=2 - [TRML1_MOUSE]	5.2	34	15.2	41.28	6	12.7	34.25	6	12.3	32.65	6
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 - [THIL_MOUSE]	8.5	45	5.3	16.03	6	3.2	8.34	6	4.2	10.76	6
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1 - [EIF3L_MOU	6.4	67	1.3	3.47	4	1.0	2.33	1	0.0	0.00	0
Q8QZY6	Tetraspanin-14 OS=Mus musculus GN=Tspan14 PE=1 SV=1 - [TSN14_MOUSE]	6.5	31	1.5	3.66	4	1.0	2.31	2	1.0	2.40	1
Q8R0P8	Protein ABHD8 OS=Mus musculus GN=Abhd8 PE=2 SV=1 - [ABHD8_MOUSE]	6.6	48	3.2	8.57	5	2.5	6.71	4	1.8	4.44	4
Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 - [AL1L1_MOUS	5.9	99	0.0	0.00	0	0.0	0.00	0	1.0	2.23	2
Q8R121	Protein Z-dependent protease inhibitor OS=Mus musculus GN=Serpina10 PE=1 SV=1 - [ZPI_MOUSE]	5.7	52	1.0	2.82	1	0.0	0.00	0	0.0	0.00	0
Q8R164	Valacyclovir hydrolase OS=Mus musculus GN=Bphl PE=1 SV=1 - [BPHL_MOUSE]	8.9	33	1.0	2.93	1	0.0	0.00	0	0.0	0.00	0
Q8R1I1	Cytochrome b-c1 complex subunit 9 OS=Mus musculus GN=Uqcr10 PE=1 SV=1 - [QCR9_MOUSE]	9.2	7	1.0	2.61	1	0.0	0.00	0	0.0	0.00	0
Q8R2E9	ERO1-like protein beta OS=Mus musculus GN=Ero1b PE=1 SV=1 - [ERO1B_MOUSE]	8.1	53	1.0	2.35	1	0.0	0.00	0	0.0	0.00	0
Q8R314	Solute carrier family 35 member F5 OS=Mus musculus GN=Slc35f5 PE=2 SV=1 - [S35F5_MOUSE]	8.9	59	0.0	0.00	0	1.0	2.55	1	0.0	0.00	0
Q8R3L0	Membrane magnesium transporter 2 OS=Mus musculus GN=Mmgt2 PE=2 SV=1 - [MMGT2_MOUSE]	9.2	14	1.0	2.52	1	0.0	0.00	0	0.0	0.00	0
Q8R4B8	NACHT, LRR and PYD domains-containing protein 3 OS=Mus musculus GN=Nlrp3 PE=1 SV=1 - [NLRP3_MOUSE]	6.9	118	1.0	3.03	1	1.7	5.53	3	0.0	0.00	0
Q8R4U0	Stabilin-2 OS=Mus musculus GN=Stab2 PE=1 SV=1 - [STAB2_MOUSE]	6.9	277	1.0	2.61	1	0.0	0.00	0	0.0	0.00	0
Q8R4U7	Leucine zipper protein 1 OS=Mus musculus GN=Luzp1 PE=1 SV=2 - [LUZP1_MOUSE]	8.0	119	1.0	2.58	3	1.0	2.65	3	1.0	2.70	1
Q8R5G7	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 OS=Mus musculus GN=Arap3	6.8	170	1.0	2.05	1	0.0	0.00	0	0.0	0.00	0
Q8R5M0	PDZ domain-containing protein GIPC3 OS=Mus musculus GN=Gipc3 PE=1 SV=1 - [GIPC3_MOUSE]	5.7	32	1.5	4.48	2	0.0	0.00	0	0.0	0.00	0
Q8VBW5	HMG box transcription factor BBX OS=Mus musculus GN=Bbx PE=1 SV=2 - [BBX_MOUSE]	8.6	101	0.0	0.00	0	1.0	2.20	2	1.0	2.26	1
Q8VCM7	Fibrinogen gamma chain OS=Mus musculus GN=Fgg PE=1 SV=1 - [FIBG_MOUSE]	5.9	49	46.0	170.02	6	41.0	150.40	6	44.7	159.93	6
Q8VCQ8	Caldesmon 1 OS=Mus musculus GN=Cald1 PE=1 SV=1 - [Q8VCQ8_MOUSE]	7.4	60	10.0	26.62	6	5.8	15.41	4	6.7	18.30	6
Q8VD65	Phosphoinositide 3-kinase regulatory subunit 4 OS=Mus musculus GN=Pik3r4 PE=1 SV=3 - [PI3R4_MOUSE]	7.1	153	1.0	2.29	3	1.3	3.13	3	1.0	2.19	2
Q8VDD5	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4 - [MYH9_MOUSE]	5.7	226	357.2	1340.72	6	272.3	1013.38	6	329.3	1217.81	6
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1 - [AT1A1_MO	5.5	113	1.0	2.80	1	0.0	0.00	0	1.0	2.63	1
Q8VE70	Programmed cell death protein 10 OS=Mus musculus GN=Pdcd10 PE=1 SV=1 - [PDC10_MOUSE]	8.2	25	2.5	9.74	2	2.0	7.64	1	3.0	10.43	1
Q8VED5	Keratin, type II cytoskeletal 79 OS=Mus musculus GN=Krt79 PE=1 SV=2 - [K2C79_MOUSE]	7.7	58	1.5	4.71	2	0.0	0.00	0	0.0	0.00	0
Q8VED8	Mitochondrial fission regulator 2 OS=Mus musculus GN=Mtfr2 PE=1 SV=2 - [MTFR2_MOUSE]	6.5	41	1.5	3.91	2	0.0	0.00	0	1.0	2.53	1
Q8VED9	Galectin-related protein OS=Mus musculus GN=Lgalsl PE=1 SV=1 - [LEGL_MOUSE]	5.4	19	4.7	13.48	6	2.3	6.54	6	3.3	9.12	6
Q8VEM8	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1 - [MPCP_MOUSE]	9.3	40	4.5	12.57	6	2.0	6.30	4	2.6	7.15	5
Q8VEY6	MCG141924 OS=Mus musculus GN=Olfr1330 PE=2 SV=1 - [Q8VEY6_MOUSE]	8.0	36	0.0	0.00	0	1.0	3.37	1	1.0	3.60	2
Q8VFG4	Olfactory receptor OS=Mus musculus GN=Olfr1370 PE=2 SV=1 - [Q8VFG4_MOUSE]	8.9	35	0.0	0.00	0	1.0	2.92	1	0.0	0.00	0
Q8VHK1	Caskin-2 OS=Mus musculus GN=Caskin2 PE=1 SV=3 - [CSKI2_MOUSE]	7.4	127	0.0	0.00	0	1.0	3.20	1	0.0	0.00	0
Q8VHL0	Urea transporter 1 OS=Mus musculus GN=Slc14a1 PE=1 SV=2 - [UT1_MOUSE]	7.9	42	1.0	2.35	4	1.0	2.58	1	0.0	0.00	0
Q8VIM5	Myocardin OS=Mus musculus GN=Myocd PE=1 SV=2 - [MYCD_MOUSE]	6.3	101	2.3	6.13	6	2.0	5.30	6	3.4	8.70	5
Q91V12	Cytosolic acyl coenzyme A thioester hydrolase OS=Mus musculus GN=Acot7 PE=1 SV=2 - [BACH_MOUSE]	8.7	43	1.4	3.62	5	1.0	2.77	3	1.3	3.16	6
Q91V41	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3 - [RAB14_MOUSE]	6.2	24	8.7	26.05	6	7.0	20.44	5	6.8	19.10	6
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Mus musculus GN=Idh3b PE=1 SV=1 - [Q91VA7_M	8.6	42	1.0	2.83	1	1.0	2.60	1	0.0	0.00	0
Q91VB8	Alpha globin 1 OS=Mus musculus GN=Hba-a1 PE=1 SV=1 - [Q91VB8_MOUSE]	8.2	15	211.7	830.55	6	445.7	1727.06	6	409.8	1559.33	6
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2 - [	5.7	80	2.0	5.65	3	0.0	0.00	0	0.0	0.00	0
Q91VI7	Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 - [RINI_MOUSE]	4.8	50	1.0	3.56	1	1.0	3.60	1	1.0	3.47	1
Q91VL6	Protein Zfp825 OS=Mus musculus GN=Zfp825 PE=1 SV=1 - [Q91VL6_MOUSE]	7.7	32	1.0	2.59	1	0.0	0.00	0	1.0	2.79	1
Q91VN4	MICOS complex subunit Mic25 OS=Mus musculus GN=Chchd6 PE=1 SV=2 - [MIC25_MOUSE]	8.4	30	0.0	0.00	0	0.0	0.00	0	1.0	2.14	2
Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Mus musculus GN=Sh3bgrl3 PE=1 SV=1 - [SH3L3_	5.1	10	3.3	12.38	6	2.7	9.99	6	2.8	10.11	6
Q91VW5	Golgin subfamily A member 4 OS=Mus musculus GN=Golga4 PE=1 SV=2 - [GOGA4_MOUSE]	5.4	257	1.0	2.69	2	0.0	0.00	0	0.0	0.00	0
Q91WE6	Threonylcarbamoyladenosine tRNA methylthiotransferase OS=Mus musculus GN=Cdkal1 PE=2 SV=1 - [CDKAL_M	7.6	65	0.0	0.00	0	1.0	2.59	1	0.0	0.00	0
Q91WZ8	Dysbindin OS=Mus musculus GN=Dtnbp1 PE=1 SV=1 - [DTBP1_MOUSE]	4.7	40	1.0	2.72	2	0.0	0.00	0	0.0	0.00	0
Q91X72	Hemopexin OS=Mus musculus GN=Hpx PE=1 SV=2 - [HEMO_MOUSE]	7.8	51	36.7	102.15	6	23.3	63.41	6	28.3	76.74	6
Q91XF0	Pyridoxine-5'-phosphate oxidase OS=Mus musculus GN=Pnpo PE=1 SV=1 - [PNPO_MOUSE]	8.2	30	0.0	0.00	0	1.0	2.99	1	0.0	0.00	0
Q91XL1	Leucine-rich HEV glycoprotein OS=Mus musculus GN=Lrg1 PE=1 SV=1 - [Q91XL1_MOUSE]	6.6	37	2.2	7.02	6	1.8	5.46	4	2.2	6.69	6
Q91XY3	MCG133388, isoform CRA_w OS=Mus musculus GN=Pcdhga5 PE=2 SV=1 - [Q91XY3_MOUSE]	5.0	101	0.0	0.00	0	0.0	0.00	0	1.0	2.51	1
Q91XY9	Protein Pcdhga10 OS=Mus musculus GN=Pcdhga10 PE=2 SV=1 - [Q91XY9_MOUSE]	4.9	101	1.0	3.21	1	0.0	0.00	0	0.0	0.00	0
Q91Y47	Coagulation factor XI OS=Mus musculus GN=F11 PE=2 SV=2 - [FA11_MOUSE]	8.3	70	0.0	0.00	0	0.0	0.00	0	1.0	2.57	1
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=	6.5	68	3.5	11.16	4	2.3	7.11	6	3.5	10.44	6

Q91YR1	Twinfilin-1 OS=Mus musculus GN=Twf1 PE=1 SV=2 - [TWF1_MOUSE]	6.7	40	1.3	4.05	4	1.0	2.70	2	1.0	3.12	1
Q91ZE0	Trimethyllysine dioxygenase, mitochondrial OS=Mus musculus GN=Tmlhe PE=1 SV=2 - [TMLH_MOUSE]	8.3	50	0.0	0.00	0	1.0	2.97	1	0.0	0.00	0
Q91ZI0	Cadherin EGF LAG seven-pass G-type receptor 3 OS=Mus musculus GN=Celsr3 PE=2 SV=2 - [CELR3_MOUSE]	6.6	358	0.0	0.00	0	1.0	3.04	1	0.0	0.00	0
Q920G5	Olfactory receptor OS=Mus musculus GN=Olfr713 PE=3 SV=1 - [Q920G5_MOUSE]	8.8	36	0.0	0.00	0	1.0	2.66	1	1.0	2.68	1
Q921I1	Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1 - [TRFE_MOUSE]	7.2	77	42.3	128.50	6	47.0	141.92	6	36.3	110.08	6
Q921J2	GTP-binding protein Rheb OS=Mus musculus GN=Rheb PE=1 SV=1 - [RHEB_MOUSE]	5.9	20	1.0	3.06	1	0.0	0.00	0	0.0	0.00	0
Q921L3	Transmembrane and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Tmco1 PE=1 SV=1 - [TMCO	9.7	21	1.0	2.58	2	1.0	2.67	1	0.0	0.00	0
Q921L6	Cortactin, isoform CRA_a OS=Mus musculus GN=Cttn PE=1 SV=1 - [Q921L6_MOUSE]	5.3	57	2.0	5.19	1	1.3	3.44	4	1.0	2.55	3
Q922B2	Aspartate--tRNA ligase, cytoplasmic OS=Mus musculus GN=Dars PE=1 SV=2 - [SYDC_MOUSE]	6.5	57	2.2	8.53	5	1.7	6.33	6	3.0	10.85	5
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4 - [C1TC_MOUSE]	7.1	101	0.0	0.00	0	1.8	4.34	4	1.0	2.29	3
Q922G7	Tektin-2 OS=Mus musculus GN=Tekt2 PE=1 SV=1 - [TEKT2_MOUSE]	6.3	50	0.0	0.00	0	1.0	2.61	1	0.0	0.00	0
Q922Q8	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=1 SV=1 - [LRC59_MOUSE]	9.5	35	1.5	3.68	4	2.5	5.77	2	1.7	3.88	3
Q922R8	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3 - [PDIA6_MOUSE]	5.1	48	20.2	67.74	5	14.0	45.64	6	16.2	52.17	6
Q922U2	Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1 - [K2C5_MOUSE]	7.8	62	1.0	2.98	1	0.0	0.00	0	0.0	0.00	0
Q923D1	Protein Zfp61 OS=Mus musculus GN=Zfp61 PE=2 SV=1 - [Q923D1_MOUSE]	9.1	62	0.0	0.00	0	1.0	3.53	1	0.0	0.00	0
Q923D2	Flavin reductase (NADPH) OS=Mus musculus GN=Blvrb PE=1 SV=3 - [BLVRB_MOUSE]	7.0	22	0.0	0.00	0	11.6	49.93	5	13.0	56.18	2
Q923Q2	StAR-related lipid transfer protein 13 OS=Mus musculus GN=Stard13 PE=1 SV=5 - [STA13_MOUSE]	7.5	125	1.3	2.69	4	1.0	2.14	3	1.3	2.84	3
Q924Z4	Ceramide synthase 2 OS=Mus musculus GN=Cers2 PE=1 SV=1 - [CERS2_MOUSE]	8.7	45	1.0	2.67	1	1.0	2.71	2	1.0	2.94	2
Q925I8	OL-protocadherin isoform OS=Mus musculus GN=Pcdh10 PE=1 SV=1 - [Q925I8_MOUSE]	4.9	113	1.0	2.55	1	1.0	2.54	1	0.0	0.00	0
Q93092	Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2 - [TALDO_MOUSE]	7.0	37	0.0	0.00	0	0.0	0.00	0	1.0	2.51	1
Q99246	Voltage-dependent L-type calcium channel subunit alpha-1D OS=Mus musculus GN=Cacna1d PE=1 SV=3 - [CA	6.8	247	1.0	2.08	1	0.0	0.00	0	0.0	0.00	0
Q99J56	Derlin-1 OS=Mus musculus GN=Derl1 PE=1 SV=1 - [DERL1_MOUSE]	9.5	29	1.6	3.94	5	1.5	3.58	4	1.0	2.26	4
Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase) OS=Mus musculus GN=Nans PE=1 SV=1 - [Q99J77_	7.1	40	1.2	4.25	5	1.0	3.57	2	1.0	3.46	5
Q99JI6	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=1 SV=2 - [RAP1B_MOUSE]	5.8	21	41.5	123.24	6	30.5	89.21	6	33.7	98.11	6
Q99JR1	Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3 - [SFXN1_MOUSE]	9.2	36	1.7	4.92	3	1.0	2.91	1	1.2	3.48	5
Q99JW4	LIM and senescent cell antigen-like-containing domain protein 1 OS=Mus musculus GN=Lims1 PE=1 SV=3 -	8.0	37	3.3	9.07	6	3.5	9.40	6	3.5	9.42	6
Q99JY9	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3 - [ARP3_MOUSE]	5.9	47	12.5	42.57	6	13.5	44.58	6	14.3	47.08	6
Q99JZ4	GTP-binding protein SAR1a OS=Mus musculus GN=Sar1a PE=1 SV=1 - [Q99JZ4_MOUSE]	6.7	22	1.0	2.37	1	0.0	0.00	0	1.0	2.04	1
Q99K23	Ufm1-specific protease 2 OS=Mus musculus GN=Ufsp2 PE=1 SV=1 - [UFSP2_MOUSE]	6.8	52	2.7	5.69	6	3.0	6.41	5	2.5	5.26	6
Q99K41	EMILIN-1 OS=Mus musculus GN=Emilin1 PE=1 SV=1 - [EMIL1_MOUSE]	5.3	108	6.8	26.25	6	5.5	18.96	6	6.2	22.35	6
Q99K70	Ras-related GTP-binding protein C OS=Mus musculus GN=Rragc PE=1 SV=1 - [RRAGC_MOUSE]	5.1	44	1.0	2.93	1	0.0	0.00	0	1.0	2.69	1
Q99KF1	Transmembrane emp24 domain-containing protein 9 OS=Mus musculus GN=Tmed9 PE=1 SV=2 - [TMED9_MOUSE]	8.4	27	0.0	0.00	0	1.0	2.68	1	1.3	3.13	4
Q99KI0	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1 - [ACON_MOUSE]	7.9	85	1.4	3.70	5	1.0	2.57	3	1.5	4.04	4
Q99KJ8	Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3 - [DCTN2_MOUSE]	5.3	44	1.7	4.39	3	2.0	4.08	1	1.0	2.16	2
Q99KK7	Dipeptidyl peptidase 3 OS=Mus musculus GN=Dpp3 PE=1 SV=2 - [DPP3_MOUSE]	5.4	83	1.5	4.35	2	1.0	2.99	2	1.0	2.21	1
Q99KR7	Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Mus musculus GN=Ppif PE=1 SV=1 - [PPIF_MOUSE	9.2	22	1.0	2.55	1	2.0	4.43	1	1.0	2.26	1
Q99KV1	DnaJ homolog subfamily B member 11 OS=Mus musculus GN=Dnajb11 PE=1 SV=1 - [DJB11_MOUSE]	6.3	41	1.2	3.10	5	1.0	2.32	2	1.7	4.34	6
Q99LB4	Capping protein (Actin filament), gelsolin-like OS=Mus musculus GN=Capg PE=1 SV=1 - [Q99LB4_MOUSE]	6.9	39	0.0	0.00	0	0.0	0.00	0	1.0	2.28	1
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Mus musculus GN=Nduf	7.8	41	2.0	4.25	1	0.0	0.00	0	0.0	0.00	0
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2 - [ETF	8.4	35	1.3	3.51	4	2.0	4.74	1	1.0	2.30	1
Q99MN1	Lysine--tRNA ligase OS=Mus musculus GN=Kars PE=1 SV=1 - [SYK_MOUSE]	5.9	68	1.0	2.04	1	0.0	0.00	0	1.0	3.43	2
Q99N15	17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus mus	8.8	27	2.7	8.17	3	1.0	2.99	1	2.5	7.15	2
Q99NA9	Polycomb group RING finger protein 6 OS=Mus musculus GN=Pcgf6 PE=1 SV=1 - [PCGF6_MOUSE]	5.2	40	1.0	2.95	1	0.0	0.00	0	0.0	0.00	0
Q99P58	Ras-related protein Rab-27B OS=Mus musculus GN=Rab27b PE=1 SV=3 - [RB27B_MOUSE]	5.5	25	6.3	14.87	6	4.8	12.55	6	4.8	11.16	6
Q99PG4	Regulator of G-protein signaling 18 OS=Mus musculus GN=Rgs18 PE=1 SV=1 - [RGS18_MOUSE]	8.5	28	1.5	4.85	6	1.5	5.04	6	1.2	3.42	6
Q99PT1	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3 - [GDIR1_MOUSE]	5.2	23	15.3	53.04	6	13.7	45.73	6	14.8	49.01	6
Q9CPQ8	ATP synthase subunit g, mitochondrial OS=Mus musculus GN=Atp5l PE=1 SV=1 - [ATP5L_MOUSE]	9.7	11	1.8	4.33	5	1.0	2.22	2	1.0	2.28	2
Q9CPU0	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3 - [LGUL_MOUSE]	5.5	21	1.0	2.44	1	1.0	2.56	2	1.0	2.46	2
Q9CPW4	Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=1 SV=3 - [ARPC5_MOUSE]	5.7	16	2.2	7.76	6	2.3	8.01	6	2.0	7.03	6
Q9CQ19	Myosin regulatory light polypeptide 9 OS=Mus musculus GN=Myl9 PE=1 SV=3 - [MYL9_MOUSE]	4.9	20	27.0	96.26	6	22.0	79.85	6	24.3	84.88	6
Q9CQ76	Nephrocan OS=Mus musculus GN=Nepn PE=1 SV=1 - [NEPN_MOUSE]	8.2	58	0.0	0.00	0	1.0	2.89	1	0.0	0.00	0
Q9CQE5	Regulator of G-protein signaling 10 OS=Mus musculus GN=Rgs10 PE=1 SV=1 - [RGS10_MOUSE]	6.8	21	3.0	8.38	3	1.5	3.36	2	2.0	4.69	3
Q9CQI6	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3 - [COTL1_MOUSE]	5.4	16	5.3	12.45	6	3.0	7.02	5	4.8	10.66	4
Q9CQQ7	ATP synthase F(0) complex subunit B1, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1 - [AT5F1_MOU	9.1	29	1.0	2.99	1	0.0	0.00	0	0.0	0.00	0
Q9CQV8	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3 - [1433B_MOUSE]	4.8	28	14.8	41.91	6	10.2	28.67	5	11.2	30.03	6
Q9CQW9	Interferon-induced transmembrane protein 3 OS=Mus musculus GN=Ifitm3 PE=1 SV=1 - [IFM3_MOUSE]	7.4	15	1.0	2.60	1	0.0	0.00	0	0.0	0.00	0
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1 - [UCRI_M	8.7	29	1.5	4.28	2	0.0	0.00	0	1.0	2.54	2
Q9CU65	Zinc finger MYM-type protein 2 OS=Mus musculus GN=Zmym2 PE=1 SV=3 - [ZMYM2_MOUSE]	6.4	155	0.0	0.00	0	1.0	2.67	1	0.0	0.00	0
Q9CVB6	Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3 - [ARPC2_MOUSE]	7.4	34	6.0	20.25	1	0.0	0.00	0	0.0	0.00	0
Q9CWD0	Gametocyte-specific factor 1-like OS=Mus musculus GN=Gtsf1l PE=1 SV=1 - [GTSFL_MOUSE]	7.9	17	1.0	2.55	1	0.0	0.00	0	0.0	0.00	0
Q9CWJ9	Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2 - [PUR9_MOUSE]	6.8	64	5.5	18.33	6	5.7	18.84	6	4.7	14.28	6
Q9CY50	Translocon-associated protein subunit alpha OS=Mus musculus GN=Ssr1 PE=1 SV=1 - [SSRA_MOUSE]	4.4	32	1.0	2.76	2	1.0	2.17	1	1.0	2.41	3
Q9CY64	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=1 SV=1 - [BIEA_MOUSE]	7.0	34	2.0	5.87	6	1.8	5.02	6	2.2	5.93	6
Q9CYN2	Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1 - [SPCS2_MOUSE]	8.6	25	1.0	3.72	1	0.0	0.00	0	0.0	0.00	0
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2 - [QCR1_MOUSE]	6.2	53	1.0	2.16	2	0.0	0.00	0	0.0	0.00	0
Q9CZ44	NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1 - [NSF1C_MOUSE]	5.1	41	1.0	2.76	1	1.5	4.75	4	1.8	5.41	5

Q9CZD3	Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1 - [SYG_MOUSE]	6.7	82	1.8	5.37	5	0.0	0.00	0	1.0	2.61	3
Q9CZT4	DNA-directed RNA polymerase III subunit RPC5 OS=Mus musculus GN=Polr3e PE=1 SV=2 - [RPC5_MOUSE]	6.3	80	1.3	3.65	3	0.0	0.00	0	0.0	0.00	0
Q9CZU6	Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1 - [CISY_MOUSE]	8.6	52	3.8	15.15	6	2.6	9.74	5	2.7	9.64	6
Q9D020	Cytosolic 5'-nucleotidase 3A OS=Mus musculus GN=Nt5c3a PE=1 SV=4 - [5NT3A_MOUSE]	6.7	37	1.3	3.28	4	1.0	2.93	1	1.3	2.98	3
Q9D034	Guanine nucleotide-binding protein subunit alpha-13 OS=Mus musculus GN=Gna13 PE=1 SV=1 - [Q9D034_MOU	9.3	20	0.0	0.00	0	1.0	2.20	1	0.0	0.00	0
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1 -	6.9	39	0.0	0.00	0	0.0	0.00	0	1.0	2.01	1
Q9D154	Leukocyte elastase inhibitor A OS=Mus musculus GN=Serpinb1a PE=1 SV=1 - [ILEUA_MOUSE]	6.2	43	24.8	75.92	6	19.7	61.48	6	20.5	62.78	6
Q9D168	Integrator complex subunit 12 OS=Mus musculus GN=Ints12 PE=1 SV=1 - [INT12_MOUSE]	9.7	49	0.0	0.00	0	1.0	3.13	1	1.0	3.00	1
Q9D1A2	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1 - [CNDP2_MOUSE]	5.7	53	6.5	17.61	6	2.7	7.25	3	2.7	7.09	6
Q9D1D4	Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=1 SV=1 - [TMEDA_MOUS	6.7	25	1.0	2.99	1	1.0	3.27	2	1.5	4.43	2
Q9D1G1	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1 - [RAB1B_MOUSE]	5.7	22	10.2	28.34	6	10.0	26.32	4	8.5	23.22	6
Q9D1Q6	Endoplasmic reticulum resident protein 44 OS=Mus musculus GN=Erp44 PE=1 SV=1 - [ERP44_MOUSE]	5.3	47	0.0	0.00	0	1.0	2.98	5	1.0	3.23	2
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, m	9.0	49	0.0	0.00	0	0.0	0.00	0	1.0	2.78	1
Q9D2Z1	Protein Ceacam20 OS=Mus musculus GN=Ceacam20 PE=2 SV=1 - [Q9D2Z1_MOUSE]	7.2	63	0.0	0.00	0	0.0	0.00	0	1.0	2.76	1
Q9D358	Low molecular weight phosphotyrosine protein phosphatase OS=Mus musculus GN=Acp1 PE=1 SV=3 - [PPAC_M	6.7	18	0.0	0.00	0	1.0	2.26	1	0.0	0.00	0
Q9D3D9	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1 - [ATPD_MOUSE]	5.1	18	1.0	2.32	1	0.0	0.00	0	0.0	0.00	0
Q9D3J3	BCL2-like 12 (Proline rich), isoform CRA_b OS=Mus musculus GN=Bcl2l12 PE=1 SV=1 - [Q9D3J3_MOUSE]	6.4	27	0.0	0.00	0	1.0	2.11	1	0.0	0.00	0
Q9D524	Probable low affinity copper uptake protein 2 OS=Mus musculus GN=Slc31a2 PE=1 SV=1 - [Q9D524_MOUSE]	8.2	16	0.0	0.00	0	1.0	2.48	1	0.0	0.00	0
Q9D5T2	MCG15536 OS=Mus musculus GN=4921524L21Rik PE=2 SV=1 - [Q9D5T2_MOUSE]	7.0	50	0.0	0.00	0	1.0	2.06	1	0.0	0.00	0
Q9D6E4	Tetratricopeptide repeat protein 9B OS=Mus musculus GN=Ttc9b PE=1 SV=1 - [TTC9B_MOUSE]	9.5	26	2.0	5.40	4	1.0	2.69	2	1.3	3.58	3
Q9D6F9	Tubulin beta-4A chain OS=Mus musculus GN=Tubb4a PE=1 SV=3 - [TBB4A_MOUSE]	4.9	50	0.0	0.00	0	0.0	0.00	0	66.0	227.94	1
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Mus musculus GN=Ndufv2 PE=1 SV=2 -	7.4	27	1.0	2.25	5	0.0	0.00	0	0.0	0.00	0
Q9D6K8	FUN14 domain-containing protein 2 OS=Mus musculus GN=Fundc2 PE=1 SV=1 - [FUND2_MOUSE]	9.7	17	1.0	2.52	3	1.0	2.20	2	0.0	0.00	0
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1 - [ID	6.7	40	0.0	0.00	0	1.0	2.41	1	0.0	0.00	0
Q9D819	Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 - [IPYR_MOUSE]	5.6	33	1.0	2.17	1	1.0	2.52	1	0.0	0.00	0
Q9D832	DnaJ homolog subfamily B member 4 OS=Mus musculus GN=Dnajb4 PE=1 SV=1 - [DNJB4_MOUSE]	8.6	38	2.2	5.79	6	1.8	4.64	4	1.4	3.29	5
Q9D8N0	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 - [EF1G_MOUSE]	6.7	50	3.8	11.86	6	2.3	7.06	6	2.5	7.77	6
Q9D9C6	Coiled-coil domain-containing protein 182 OS=Mus musculus GN=Ccdc182 PE=2 SV=1 - [CC182_MOUSE]	8.0	17	1.0	2.19	2	1.0	2.12	2	0.0	0.00	0
Q9D9E9	Protein 1700086D15Rik OS=Mus musculus GN=1700086D15Rik PE=2 SV=1 - [Q9D9E9_MOUSE]	7.4	17	1.0	2.06	1	0.0	0.00	0	0.0	0.00	0
Q9D9G4	1700080O16Rik protein OS=Mus musculus GN=1700080O16Rik PE=2 SV=1 - [Q9D9G4_MOUSE]	6.0	32	1.0	2.07	1	0.0	0.00	0	0.0	0.00	0
Q9DAC2	Complement component 8, gamma subunit, isoform CRA_b OS=Mus musculus GN=C8g PE=1 SV=1 - [Q9DAC2_MO	8.3	19	1.5	5.24	4	0.0	0.00	0	1.0	3.64	3
Q9DAK4	Fatty acid-binding protein 12 OS=Mus musculus GN=Fabp12 PE=2 SV=1 - [FBP12_MOUSE]	8.1	15	0.0	0.00	0	0.0	0.00	0	1.0	2.36	1
Q9DAM2	EF-hand calcium-binding domain-containing protein 9 OS=Mus musculus GN=Efcab9 PE=2 SV=2 - [EFCB9_MOU	8.6	26	1.0	3.11	1	0.0	0.00	0	0.0	0.00	0
Q9DB05	Alpha-soluble NSF attachment protein OS=Mus musculus GN=Napa PE=1 SV=1 - [SNAA_MOUSE]	5.5	33	1.0	2.61	1	1.0	2.20	2	1.0	2.40	2
Q9DB16	Calcium-binding protein 39-like OS=Mus musculus GN=Cab39l PE=1 SV=3 - [CB39L_MOUSE]	8.3	39	1.0	2.12	1	0.0	0.00	0	0.0	0.00	0
Q9DB20	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1 - [ATPO_MOUSE]	10.0	23	4.0	12.58	2	3.0	8.92	2	4.0	13.05	2
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1 - [QCR2_MOUSE]	9.2	48	1.2	3.18	5	0.0	0.00	0	1.0	2.46	3
Q9DBB9	Carboxypeptidase N subunit 2 OS=Mus musculus GN=Cpn2 PE=1 SV=2 - [CPN2_MOUSE]	5.9	60	1.7	3.99	3	2.0	5.82	2	1.3	2.94	4
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3 -	5.4	43	1.0	2.63	2	0.0	0.00	0	3.0	8.27	1
Q9DBJ1	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3 - [PGAM1_MOUSE]	7.2	29	6.0	20.75	6	4.8	16.36	6	5.8	18.58	6
Q9DBK7	MCG18845, isoform CRA_d OS=Mus musculus GN=Uba7 PE=1 SV=1 - [Q9DBK7_MOUSE]	6.0	109	2.4	6.43	5	1.0	2.41	2	2.4	7.38	5
Q9DBP5	UMP-CMP kinase OS=Mus musculus GN=Cmpk1 PE=1 SV=1 - [KCY_MOUSE]	5.8	22	2.7	8.32	6	1.5	4.40	4	2.7	7.32	3
Q9DBR7	Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2 - [MYPT1_MOUSE]	5.5	115	1.0	2.67	2	0.0	0.00	0	0.0	0.00	0
Q9DBX5	Phospholipase A2 OS=Mus musculus GN=Pla2g4a PE=1 SV=1 - [Q9DBX5_MOUSE]	5.4	84	1.0	3.44	1	0.0	0.00	0	0.0	0.00	0
Q9DC50	Peroxisomal carnitine O-octanoyltransferase OS=Mus musculus GN=Crot PE=1 SV=1 - [OCTC_MOUSE]	6.7	70	0.0	0.00	0	0.0	0.00	0	1.0	2.06	1
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=1 SV=3 - [6PGD_MOUSE]	7.2	53	3.5	10.46	6	2.4	6.90	5	3.0	8.49	6
Q9DCE9	Protein Igtp OS=Mus musculus GN=Igtp PE=1 SV=1 - [Q9DCE9_MOUSE]	7.8	48	9.2	31.84	6	6.8	23.42	6	7.8	25.99	6
Q9DCF9	Translocon-associated protein subunit gamma OS=Mus musculus GN=Ssr3 PE=1 SV=1 - [SSRG_MOUSE]	9.6	21	1.0	3.09	3	1.0	2.52	1	1.0	3.16	2
Q9DCN2	NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3 - [NB5R3_MOUSE]	8.4	34	5.8	20.96	6	4.3	16.13	3	5.5	18.29	4
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1	7.2	30	1.0	2.77	2	0.0	0.00	0	0.0	0.00	0
Q9DCW4	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 - [ETFB_MOUSE]	8.1	28	2.0	7.34	1	2.0	7.01	2	0.0	0.00	0
Q9DCZ1	GMP reductase 1 OS=Mus musculus GN=Gmpr PE=1 SV=1 - [GMPR1_MOUSE]	7.1	37	3.7	10.47	6	3.0	7.94	5	3.2	8.66	6
Q9EP69	Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=1 SV=1 - [SAC1_MOUSE]	7.3	67	1.2	2.75	5	0.0	0.00	0	1.0	2.09	1
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD OS=Mus musculus GN=Pycard PE=1 SV=1 - [ASC	5.4	21	1.7	4.61	3	1.0	2.66	2	1.0	2.35	2
Q9EPX2	Papilin OS=Mus musculus GN=Papln PE=2 SV=2 - [PPN_MOUSE]	7.8	139	1.0	3.28	1	0.0	0.00	0	1.0	3.29	1
Q9EQC0	Carbohydrate sulfotransferase 1 OS=Mus musculus GN=Chst1 PE=2 SV=1 - [CHST1_MOUSE]	8.8	47	1.0	2.33	1	1.0	2.23	1	0.0	0.00	0
Q9EQH3	Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1 - [VPS35_MOUSE]	5.4	92	1.0	2.86	2	0.0	0.00	0	0.0	0.00	0
Q9EQI5	Chemokine (C-X-C motif) ligand 7, isoform CRA_b OS=Mus musculus GN=Ppbp PE=1 SV=1 - [Q9EQI5_MOUSE]	8.7	12	11.5	33.56	6	9.2	25.92	6	10.7	30.57	6
Q9EQK5	Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4 - [MVP_MOUSE]	5.6	96	1.0	3.52	1	0.0	0.00	0	0.0	0.00	0
Q9EQP2	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1 - [EHD4_MOUSE]	6.8	61	26.0	74.97	6	21.0	60.19	6	24.3	67.26	6
Q9ER00	Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1 - [STX12_MOUSE]	5.4	31	1.0	2.05	1	0.0	0.00	0	0.0	0.00	0
Q9ER72	Cysteine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2 - [SYCC_MOUSE]	6.8	95	0.0	0.00	0	2.0	5.25	1	0.0	0.00	0
Q9ERB0	Synaptosomal-associated protein 29 OS=Mus musculus GN=Snap29 PE=1 SV=1 - [SNP29_MOUSE]	5.4	30	1.0	2.37	1	0.0	0.00	0	0.0	0.00	0
Q9ERI2	Ras-related protein Rab-27A OS=Mus musculus GN=Rab27a PE=1 SV=1 - [RB27A_MOUSE]	5.4	25	1.5	4.01	2	1.0	2.69	2	1.0	2.84	1
Q9ERL9	Guanylate cyclase soluble subunit alpha-3 OS=Mus musculus GN=Gucy1a3 PE=1 SV=2 - [GCYA3_MOUSE]	7.2	78	0.0	0.00	0	0.0	0.00	0	1.0	2.30	2
Q9ES46	Beta-parvin OS=Mus musculus GN=Parvb PE=1 SV=1 - [PARVB_MOUSE]	6.3	42	32.7	114.44	6	25.3	87.53	6	27.3	91.81	6

Q9ES52	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2 - [SHIP	7.8	133	1.0	2.98	1	1.0	2.05	1	1.0	2.73	2
Q9ES97	Reticulon-3 OS=Mus musculus GN=Rtn3 PE=1 SV=2 - [RTN3_MOUSE]	4.9	104	1.3	3.44	3	0.0	0.00	0	0.0	0.00	0
Q9ESB3	Histidine-rich glycoprotein OS=Mus musculus GN=Hrg PE=1 SV=2 - [HRG_MOUSE]	7.7	59	3.2	10.42	6	2.3	7.18	6	2.2	6.76	6
Q9ESP1	Stromal cell-derived factor 2-like protein 1 OS=Mus musculus GN=Sdf2l1 PE=1 SV=2 - [SDF2L_MOUSE]	7.4	24	0.0	0.00	0	1.0	2.67	1	0.0	0.00	0
Q9ET77	Junctophilin-3 OS=Mus musculus GN=Jph3 PE=1 SV=1 - [JPH3_MOUSE]	9.2	81	1.0	3.15	1	1.0	3.13	1	1.0	3.07	3
Q9JHJ0	Tropomodulin-3 OS=Mus musculus GN=Tmod3 PE=1 SV=1 - [TMOD3_MOUSE]	5.1	39	4.3	12.18	6	1.5	4.32	6	3.7	10.83	6
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2 - [DYHC1_MOUSE]	6.4	532	9.2	27.01	6	3.7	11.11	6	4.3	12.91	6
Q9JHU9	Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 PE=1 SV=1 - [INO1_MOUSE]	6.4	61	0.0	0.00	0	0.0	0.00	0	1.0	2.38	1
Q9JI11	Serine/threonine-protein kinase 4 OS=Mus musculus GN=Stk4 PE=1 SV=1 - [STK4_MOUSE]	5.2	56	2.8	8.54	6	1.0	2.48	2	1.8	4.85	4
Q9JI78	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Mus musculus GN=Ngly1 PE=1 SV=2 - [NG	6.9	74	1.0	2.59	1	1.0	2.58	1	1.0	2.64	1
Q9JIF7	Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1 - [COPB_MOUSE]	6.0	107	1.6	3.88	5	1.6	3.81	5	1.0	2.45	3
Q9JII6	Alcohol dehydrogenase [NADP(+)] OS=Mus musculus GN=Akr1a1 PE=1 SV=3 - [AK1A1_MOUSE]	7.4	37	1.3	4.30	4	1.0	3.33	2	1.3	3.54	4
Q9JJ28	Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1 SV=1 - [FLII_MOUSE]	6.1	145	1.5	3.24	2	0.0	0.00	0	1.0	2.21	1
Q9JJN5	Carboxypeptidase N catalytic chain OS=Mus musculus GN=Cpn1 PE=1 SV=1 - [CBPN_MOUSE]	8.3	52	1.0	2.61	2	1.0	3.52	2	1.5	4.92	2
Q9JJZ2	Tubulin alpha-8 chain OS=Mus musculus GN=Tuba8 PE=1 SV=1 - [TBA8_MOUSE]	5.1	50	62.8	216.22	6	44.3	149.35	6	51.8	173.96	6
Q9JK30	Origin recognition complex subunit 3 OS=Mus musculus GN=Orc3 PE=1 SV=1 - [ORC3_MOUSE]	7.4	82	4.2	12.48	6	4.2	11.88	6	3.5	10.52	6
Q9JK42	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 2, mitochondrial OS=Mus musculus GN=Pd	6.6	46	0.0	0.00	0	1.5	3.97	2	1.0	2.53	1
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Mus musculus GN=Uchl3 PE=1 SV=2 - [UCHL3_MOUSE]	5.0	26	1.0	3.18	1	0.0	0.00	0	0.0	0.00	0
Q9JKF1	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=2 - [IQGA1_MOUSE]	6.5	189	2.0	4.67	1	0.0	0.00	0	0.0	0.00	0
Q9JKK7	Tropomodulin-2 OS=Mus musculus GN=Tmod2 PE=1 SV=2 - [TMOD2_MOUSE]	5.4	39	1.0	2.19	1	1.0	2.31	2	1.0	2.39	3
Q9JKR6	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1 - [HYOU1_MOUSE]	5.2	111	5.3	15.08	6	2.8	7.47	5	4.2	12.15	6
Q9JL99	C-type lectin domain family 1 member B OS=Mus musculus GN=Clec1b PE=1 SV=1 - [CLC1B_MOUSE]	8.7	26	3.3	10.14	6	2.5	7.44	6	2.3	7.02	6
Q9JLJ2	4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_MOUSE]	7.0	53	1.0	3.13	2	1.0	2.90	4	1.0	2.83	3
Q9JME5	AP-3 complex subunit beta-2 OS=Mus musculus GN=Ap3b2 PE=1 SV=2 - [AP3B2_MOUSE]	5.6	119	1.0	2.78	1	0.0	0.00	0	0.0	0.00	0
Q9QUG9	RAS guanyl-releasing protein 2 OS=Mus musculus GN=Rasgrp2 PE=1 SV=2 - [GRP2_MOUSE]	7.7	69	8.3	28.25	6	3.7	12.62	6	5.0	16.34	6
Q9QUM0	Integrin alpha-IIb OS=Mus musculus GN=Itga2b PE=1 SV=2 - [ITA2B_MOUSE]	5.8	113	72.7	259.48	6	55.7	195.11	6	58.3	202.45	6
Q9QUM4	Signaling lymphocytic activation molecule OS=Mus musculus GN=Slamf1 PE=1 SV=1 - [SLAF1_MOUSE]	7.0	38	1.3	4.27	6	1.3	3.89	6	1.6	4.70	5
Q9QX15	Calcium-sensitive chloride conductance protein-1 OS=Mus musculus GN=Clca3a1 PE=1 SV=1 - [Q9QX15_MOUS	6.9	100	1.0	2.34	2	2.0	4.52	2	2.5	5.92	2
Q9QXY6	EH domain-containing protein 3 OS=Mus musculus GN=Ehd3 PE=1 SV=2 - [EHD3_MOUSE]	6.5	61	13.5	40.07	6	8.8	25.83	6	11.5	33.36	6
Q9QY96	Extracellular calcium-sensing receptor OS=Mus musculus GN=Casr PE=1 SV=2 - [CASR_MOUSE]	6.1	121	0.0	0.00	0	0.0	0.00	0	1.0	2.25	1
Q9QYB1	Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3 - [CLIC4_MOUSE]	5.6	29	3.0	8.22	6	2.0	4.75	4	1.6	3.58	5
Q9QYB5	Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=2 - [ADDG_MOUSE]	5.9	79	2.0	5.30	4	1.0	2.14	3	1.6	4.01	5
Q9QYC0	Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2 - [ADDA_MOUSE]	5.9	81	4.7	11.94	3	4.0	9.71	1	3.0	7.30	4
Q9QYE3	B-cell lymphoma/leukemia 11A OS=Mus musculus GN=Bcl11a PE=1 SV=1 - [BC11A_MOUSE]	6.3	84	2.8	7.86	4	1.5	4.67	2	2.2	6.59	5
Q9QZC7	Pleckstrin homology domain-containing family B member 2 OS=Mus musculus GN=Plekhb2 PE=1 SV=1 - [PKHB	5.6	25	0.0	0.00	0	0.0	0.00	0	1.0	2.51	3
Q9QZU3	Platelet glycoprotein V (Fragment) OS=Mus musculus GN=Gp5 PE=1 SV=1 - [Q9QZU3_MOUSE]	8.8	63	20.2	71.02	6	10.8	37.82	6	15.8	54.54	6
Q9QZU9	Ubiquitin/ISG15-conjugating enzyme E2 L6 OS=Mus musculus GN=Ube2l6 PE=1 SV=3 - [UB2L6_MOUSE]	8.1	18	1.0	3.15	1	1.0	3.58	2	1.0	2.89	3
Q9R0N0	Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2 - [GALK1_MOUSE]	5.3	42	1.5	3.51	4	1.0	2.98	2	1.0	3.23	4
Q9R0P5	Destrin OS=Mus musculus GN=Dstn PE=1 SV=3 - [DEST_MOUSE]	8.0	19	6.5	21.91	6	5.5	18.77	6	5.0	17.06	6
Q9R0Q1	Synaptotagmin-like protein 4 OS=Mus musculus GN=Sytl4 PE=1 SV=1 - [SYTL4_MOUSE]	8.8	76	2.5	7.47	6	2.6	7.96	5	2.4	7.82	5
Q9R0Q7	Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1 - [TEBP_MOUSE]	4.6	19	1.0	2.53	3	0.0	0.00	0	1.5	3.55	2
Q9R111	Guanine deaminase OS=Mus musculus GN=Gda PE=1 SV=1 - [GUAD_MOUSE]	5.5	51	0.0	0.00	0	2.0	4.18	1	1.0	2.10	1
Q9R1P4	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1 PE=1 SV=1 - [PSA1_MOUSE]	6.5	30	1.0	2.30	1	1.2	2.88	5	1.3	2.97	4
Q9R1Q8	Transgelin-3 OS=Mus musculus GN=Tagln3 PE=1 SV=1 - [TAGL3_MOUSE]	7.3	22	2.0	5.32	2	0.0	0.00	0	0.0	0.00	0
Q9R269	Periplakin OS=Mus musculus GN=Ppl PE=1 SV=1 - [PEPL_MOUSE]	5.5	204	1.0	2.82	1	0.0	0.00	0	1.0	2.34	1
Q9WTK8	Meiotic recombination protein SPO11 OS=Mus musculus GN=Spo11 PE=2 SV=2 - [SPO11_MOUSE]	8.6	45	0.0	0.00	0	0.0	0.00	0	1.0	2.13	2
Q9WTU6	Mitogen-activated protein kinase 9 OS=Mus musculus GN=Mapk9 PE=1 SV=2 - [MK09_MOUSE]	6.0	48	1.0	2.09	2	1.0	2.14	1	0.0	0.00	0
Q9WTX5	S-phase kinase-associated protein 1 OS=Mus musculus GN=Skp1 PE=1 SV=3 - [SKP1_MOUSE]	4.5	19	1.0	2.57	2	1.0	2.80	2	1.0	2.86	2
Q9WU78	Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=3 - [PDC6I_MOUSE]	6.5	96	1.8	5.15	6	1.6	4.88	5	2.3	6.47	6
Q9WUH7	Semaphorin-4G OS=Mus musculus GN=Sema4g PE=1 SV=1 - [SEM4G_MOUSE]	7.9	92	0.0	0.00	0	0.0	0.00	0	1.0	2.33	1
Q9WUM3	Coronin-1B OS=Mus musculus GN=Coro1b PE=1 SV=1 - [COR1B_MOUSE]	5.8	54	1.7	4.36	3	1.0	2.27	3	1.0	2.21	3
Q9WUM4	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2 - [COR1C_MOUSE]	7.1	53	3.6	16.50	5	3.0	14.33	5	2.0	9.47	6
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV	9.4	36	1.0	2.85	2	0.0	0.00	0	0.0	0.00	0
Q9WV08	Apelin receptor OS=Mus musculus GN=Aplnr PE=2 SV=1 - [APJ_MOUSE]	7.5	42	0.0	0.00	0	0.0	0.00	0	1.5	3.84	2
Q9WVA4	Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4 - [TAGL2_MOUSE]	8.2	22	31.0	96.79	6	20.2	63.06	6	22.0	69.60	6
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2 OS=Mus musculus GN=Pacsin2 PE=1 SV	5.2	56	1.7	4.23	6	1.5	3.62	4	1.6	3.84	5
Q9WVF5	Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1 - [Q9WVF5_MOUSE]	7.0	73	2.2	6.50	5	1.5	3.44	2	1.8	4.59	5
Q9WVK4	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1 - [EHD1_MOUSE]	6.8	61	7.8	23.53	6	5.4	17.56	5	5.0	15.18	6
Q9Z0F8	Disintegrin and metalloproteinase domain-containing protein 17 OS=Mus musculus GN=Adam17 PE=1 SV=3 -	5.9	93	0.0	0.00	0	1.0	3.40	1	0.0	0.00	0
Q9Z0G0	PDZ domain-containing protein GIPC1 OS=Mus musculus GN=Gipc1 PE=1 SV=1 - [GIPC1_MOUSE]	5.9	36	1.5	4.25	2	1.0	2.65	1	1.0	2.31	1
Q9Z0G9	Claudin-3 OS=Mus musculus GN=Cldn3 PE=1 SV=1 - [CLD3_MOUSE]	7.8	23	0.0	0.00	0	1.0	3.18	1	0.0	0.00	0
Q9Z0J1	Reversion-inducing cysteine-rich protein with Kazal motifs OS=Mus musculus GN=Reck PE=1 SV=2 - [RECK	6.7	106	1.0	3.41	1	0.0	0.00	0	0.0	0.00	0
Q9Z0P5	Twinfilin-2 OS=Mus musculus GN=Twf2 PE=1 SV=1 - [TWF2_MOUSE]	6.8	39	1.7	5.95	6	1.4	4.96	5	1.3	4.85	6
Q9Z0U1	Tight junction protein ZO-2 OS=Mus musculus GN=Tjp2 PE=1 SV=2 - [ZO2_MOUSE]	6.8	131	2.5	6.08	2	1.0	2.52	1	0.0	0.00	0
Q9Z1F6	Leukocyte cell-derived chemotaxin 1 OS=Mus musculus GN=Lect1 PE=1 SV=2 - [LECT1_MOUSE]	6.3	37	1.0	2.14	1	1.0	2.23	1	0.0	0.00	0
Q9Z1F9	SUMO-activating enzyme subunit 2 OS=Mus musculus GN=Uba2 PE=1 SV=1 - [SAE2_MOUSE]	5.2	71	0.0	0.00	0	0.0	0.00	0	1.0	2.81	1

Q9Z1Q5	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3 - [CLIC1_MOUSE]	5.2	27	5.5	17.97	6	5.0	15.55	6	5.0	15.84	6
Q9Z1R9	MCG124046 OS=Mus musculus GN=Prss1 PE=1 SV=1 - [Q9Z1R9_MOUSE]	4.9	26	6.2	18.04	6	6.8	21.16	6	6.8	20.53	6
Q9Z1Z0	General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=2 - [USO1_MOUSE]	4.9	107	2.3	7.45	3	1.0	2.54	2	2.0	7.09	1
Q9Z2E1	Methyl-CpG-binding domain protein 2 OS=Mus musculus GN=Mbd2 PE=2 SV=2 - [MBD2_MOUSE]	10.0	43	1.0	2.33	1	1.0	2.15	1	1.0	2.11	1
Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2 -	7.0	50	2.0	10.13	1	0.0	0.00	0	0.0	0.00	0
Q9Z2U0	Proteasome subunit alpha type-7 OS=Mus musculus GN=Psma7 PE=1 SV=1 - [PSA7_MOUSE]	8.5	28	1.2	3.18	6	1.3	3.41	4	1.0	2.79	4
Q9Z2U2	Zinc finger protein 292 OS=Mus musculus GN=Zfp292 PE=1 SV=2 - [ZN292_MOUSE]	7.5	301	1.0	2.12	1	1.0	2.12	1	1.0	2.13	1
S4R171	Bridging integrator 2 (Fragment) OS=Mus musculus GN=Bin2 PE=1 SV=1 - [S4R171_MOUSE]	7.0	23	0.0	0.00	0	15.3	54.08	3	0.0	0.00	0
S4R173	Protein 1700018B08Rik (Fragment) OS=Mus musculus GN=1700018B08Rik PE=4 SV=1 - [S4R173_MOUSE]	10.0	22	2.0	6.12	1	0.0	0.00	0	0.0	0.00	0
S4R1E5	Glutathione peroxidase OS=Mus musculus GN=Gpx4 PE=1 SV=1 - [S4R1E5_MOUSE]	7.9	18	1.8	4.92	6	1.2	3.17	5	1.5	3.81	6
S4R1L5	Baculoviral IAP repeat-containing protein 6 OS=Mus musculus GN=Birc6 PE=1 SV=1 - [S4R1L5_MOUSE]	6.0	529	1.0	2.64	1	1.0	2.80	2	1.0	2.52	1
S4R1Q4	AP-1 complex subunit mu-1 (Fragment) OS=Mus musculus GN=Ap1m1 PE=1 SV=1 - [S4R1Q4_MOUSE]	4.7	13	1.0	3.11	1	0.0	0.00	0	0.0	0.00	0
S4R1S6	Rho guanine nucleotide exchange factor 40 OS=Mus musculus GN=Arhgef40 PE=1 SV=1 - [S4R1S6_MOUSE]	5.5	53	3.3	7.91	4	3.0	7.46	4	3.0	7.68	4
S4R1V0	PDZ and LIM domain protein 1 (Fragment) OS=Mus musculus GN=Pdlim1 PE=1 SV=1 - [S4R1V0_MOUSE]	6.4	21	0.0	0.00	0	1.0	3.52	1	0.0	0.00	0
S4R232	Ras-related protein Rab-4B OS=Mus musculus GN=Rab4b PE=1 SV=1 - [S4R232_MOUSE]	9.2	11	4.3	11.35	3	4.0	10.30	2	5.0	12.98	3
S4R257	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Mus musculus GN=Gapdh PE=1 SV=1 - [S4R257_MO	8.4	30	34.8	143.83	4	26.3	106.92	4	34.5	132.49	4
S4R2M6	MCG116386, isoform CRA_c OS=Mus musculus GN=Rbm3 PE=1 SV=1 - [S4R2M6_MOUSE]	4.8	10	1.0	3.18	1	0.0	0.00	0	0.0	0.00	0
S4W6L8	Ankyrin repeat and SOCS box protein 1 (Fragment) OS=Mus musculus GN=Asb1 PE=1 SV=1 - [S4W6L8_MOUSE]	7.7	24	0.0	0.00	0	1.0	2.55	1	2.0	5.13	1
V9GX06	Protein Gm11214 (Fragment) OS=Mus musculus GN=Gm11214 PE=1 SV=1 - [V9GX06_MOUSE]	7.4	20	0.0	0.00	0	0.0	0.00	0	8.0	21.21	2
V9GX87	Double-stranded RNA-binding protein Staufen homolog 1 OS=Mus musculus GN=Stau1 PE=1 SV=1 - [V9GX87_M	9.9	49	0.0	0.00	0	0.0	0.00	0	1.0	2.90	1
V9GXB9	Protein Rhox2c OS=Mus musculus GN=Rhox2c PE=4 SV=1 - [V9GXB9_MOUSE]	4.8	20	1.0	3.02	1	0.0	0.00	0	0.0	0.00	0
V9GXM6	Copine-1 (Fragment) OS=Mus musculus GN=Cpne1 PE=1 SV=1 - [V9GXM6_MOUSE]	7.0	22	0.0	0.00	0	0.0	0.00	0	1.0	3.01	1
V9GXV0	Protein Idh3b (Fragment) OS=Mus musculus GN=Idh3b PE=1 SV=1 - [V9GXV0_MOUSE]	10.4	9	1.0	2.70	1	0.0	0.00	0	1.0	2.07	1
Z4YJV4	2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=1 - [Z4YJV4_MOUSE]	7.0	116	3.0	9.59	1	2.0	6.28	2	0.0	0.00	0
Z4YKV1	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Mus musculus GN=Gnas PE=1 SV	6.5	44	1.3	2.91	3	0.0	0.00	0	0.0	0.00	0
Z4YL78	Cytoskeleton-associated protein 5 OS=Mus musculus GN=Ckap5 PE=1 SV=1 - [Z4YL78_MOUSE]	8.1	219	1.0	2.73	1	1.0	2.41	2	1.0	2.39	2
Z4YN97	Adenylate kinase isoenzyme 1 (Fragment) OS=Mus musculus GN=Ak1 PE=1 SV=1 - [Z4YN97_MOUSE]	8.7	10	1.0	2.36	1	1.0	2.33	1	0.0	0.00	0

			aSpC			Normalized aSpC			LDA		Fold change ($\ln(SpC_1/SpC_2)$)			MAProMa DAVE	MAProMa DCI	MAProMa DAVE	MAProMa DCI	MAProMa DAVE	MAProMa DCI
Uniprot ID	**Gene Name**	**Reference**	**WT**	**WKO**	**CoWas**	**WT**	**WKO**	**CoWas**	**F ratio**	**Prob>F**	**WT vs WKO**	**WT vs CoWas**	**CoWas vs WKO**	**WT vs WKO**	**WT vs WKO**	**WT vs CoWas**	**WT vs CoWas**	**CoWas vs WKO**	**CoWas vs WKO**
P63101	YWHAZ	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1 - [1433Z_MOUSE]	49.7	36.9	42.7	100.0	74.3	86.0	7.5	5.58E-03	0.30	0.15	0.15	0.30	553.78				
P68254	YWHAQ	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1 - [1433T_MOUSE]	12.9	5.3	7.2	100.0	41.1	56.1	5.4	1.70E-02	0.89	0.58	0.31	0.84	69.01	0.56	56.91	0.31	12.11
P68510	YWHAH	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2 - [1433F_MOUSE]	23.4	14.5	17.4	100.0	62.1	74.7	14.0	3.69E-04	0.48	0.29	0.18	0.47	167.34	0.29	120.42		
P61982	YWHAG	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2 - [1433G_MOUSE]	16.7	9.1	14.3	100.0	54.3	85.5	7.3	6.09E-03	0.61	0.16	0.45	0.59	98.27			0.45	60.69
P62259	YWHAE	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 - [1433E_MOUSE]	19.4	12.2	16.4	100.0	63.2	84.5	5.9	1.32E-02	0.46	0.17	0.29	0.45	112.77			0.29	58.98
Q9CQV8	YWHAB	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3 - [1433B_MOUSE]	14.7	7.8	11.2	100.0	53.4	76.6	6.2	1.08E-02	0.63	0.27	0.36	0.61	76.82	0.27	44.48	0.36	32.34
Q6P1B1	XPNPEP1	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=1 SV=1 - [XPP1_MOUSE]	1.6	0.2	0.8	100.0	10.7	51.3	3.9	4.42E-02	2.23	0.67	1.57	1.61	1.24	0.64	0.93	1.31	0.32
Q01853	VCP	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4 - [TERA_MOUSE]	30.8	23.8	26.6	100.0	77.2	86.3	5.7	1.42E-02	0.26	0.15		0.26	191.48				
Q64727	VCL	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4 - [VINC_MOUSE]	161.7	131.5	150.4	100.0	81.3	93.0	13.2	4.97E-04	0.21			0.21	4427.02				
Q9DB77	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1 - [QCR2_MOUS	1.1	0.0	0.5	100.0	0.0	47.9	6.3	1.01E-02	100.00	0.74	100.00	2.00	0.55	0.71	0.43	2.00	0.13
P61089	UBE2N	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1 - [UBE2N_MOUSE]	2.2	0.5	1.2	100.0	22.1	54.0	7.1	6.61E-03	1.51	0.62	0.89	1.28	2.23	0.60	1.66	0.84	0.57
A0A0G2JE32	UBE2D3	Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Mus musculus GN=Ube2d3 PE=1 SV=1 - [A0A0G2JE32_M	0.0	0.4	0.0	0.0	100.0	0.0	4.9	2.33E-02	-100.00		-100.00	-2.00	-0.10			-2.00	-0.10
Q9DBK7	UBA7	MCG18845, isoform CRA_d OS=Mus musculus GN=Uba7 PE=1 SV=1 - [Q9DBK7_MOUSE]	2.2	0.3	1.9	100.0	14.2	87.3	6.7	8.55E-03	1.95		1.82	1.50	2.36			1.44	1.79
Q8CDN6	TXNL1	Thioredoxin-like protein 1 OS=Mus musculus GN=Txnl1 PE=1 SV=3 - [TXNL1_MOUSE]	0.4	0.7	1.2	30.5	54.8	100.0	3.7	4.88E-02	-0.59	-1.19	0.60	-0.57	-0.15	-1.07	-0.67	0.58	0.51
P10639	TXN	Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 - [THIO_MOUSE]	1.1	2.3	2.4	46.2	95.5	100.0	4.9	2.37E-02	-0.73	-0.77		-0.70	-2.04	-0.74	-2.30		
A2AQ07	TUBB1	Tubulin beta-1 chain OS=Mus musculus GN=Tubb1 PE=1 SV=1 - [TBB1_MOUSE]	109.3	91.2	111.8	97.7	81.6	100.0	7.2	6.50E-03	0.18		0.20					0.20	2089.55
Q9JJZ2	TUBA8	Tubulin alpha-8 chain OS=Mus musculus GN=Tuba8 PE=1 SV=1 - [TBA8_MOUSE]	62.8	43.8	52.7	100.0	69.8	83.9	24.6	1.85E-05	0.36	0.18	0.18	0.36	1010.79				
P68368	TUBA4A	Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 - [TBA4A_MOUSE]	83.3	64.7	76.7	100.0	77.7	92.0	14.2	3.50E-04	0.25		0.17	0.25	1374.89				
P68369	TUBA1A	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 - [TBA1A_MOUSE]	76.7	51.3	68.6	100.0	66.8	89.4	4.0	3.95E-02	0.40		0.29	0.40	1630.33			0.29	1038.85
Q8BV79	TRANK1	TPR and ankyrin repeat-containing protein 1 OS=Mus musculus GN=Trank1 PE=2 SV=3 - [TRNK1_MOUSE]	1.3	0.0	0.6	100.0	0.0	44.6	4.7	2.55E-02	100.00	0.81	100.00	2.00	0.82	0.77	0.65	2.00	0.16
Q6IRU2	TPM4	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=1 SV=3 - [TPM4_MOUSE]	35.0	27.6	28.4	100.0	78.8	81.3	6.1	1.13E-02	0.24	0.21		0.24	231.88	0.21	207.67		
P20065	TMSB4X	Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1 - [TYB4_MOUSE]	1.7	0.1	1.0	100.0	8.0	59.3	11.2	1.08E-03	2.52	0.52	2.00	1.70	1.45	0.51	0.94	1.52	0.50
Q9JHJ0	TMOD3	Tropomodulin-3 OS=Mus musculus GN=Tmod3 PE=1 SV=1 - [TMOD3_MOUSE]	4.5	1.5	3.4	100.0	34.3	75.4	5.2	1.93E-02	1.07	0.28	0.79	0.98	8.75	0.28	4.28	0.75	4.47
A0A0G2JEH3	TMEM243	MCG1490, isoform CRA_a OS=Mus musculus GN=Tmem243 PE=1 SV=1 - [A0A0G2JEH3_MOUSE]	1.0	3.2	3.8	26.4	82.4	100.0	7.2	6.44E-03	-1.14	-1.33	0.19	-1.03	-4.49	-1.16	-6.86		
Q99KF1	TMED9	Transmembrane emp24 domain-containing protein 9 OS=Mus musculus GN=Tmed9 PE=1 SV=2 - [TMED9_MO	0.0	0.1	0.8	0.0	17.0	100.0	5.9	1.29E-02	-100.00	-100.00	1.77	-2.00	-0.01	-2.00	-0.31	1.42	0.31
P26039	TLN1	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2 - [TLN1_MOUSE]	453.8	351.9	408.9	100.0	77.6	90.1	12.2	7.20E-04	0.25		0.15	0.25	41027.49				
P36423	TBXAS1	Thromboxane-A synthase OS=Mus musculus GN=Tbxas1 PE=1 SV=2 - [THAS_MOUSE]	11.9	7.1	11.5	100.0	59.1	96.2	8.0	4.36E-03	0.53		0.49	0.51	46.38			0.48	41.13
Q9WVA4	TAGLN2	Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4 - [TAGL2_MOUSE]	30.8	19.4	21.8	100.0	63.1	70.8	20.9	4.63E-05	0.46	0.35		0.45	285.09	0.34	236.17		
Q64324	STXBP2	Syntaxin-binding protein 2 OS=Mus musculus GN=Stxbp2 PE=1 SV=1 - [STXB2_MOUSE]	5.4	2.3	2.4	100.0	41.5	44.8	9.5	2.17E-03	0.88	0.80		0.83	12.17	0.76	11.75		
Q3U5V8	STX11	MCG49559 OS=Mus musculus GN=Stx11 PE=1 SV=1 - [Q3U5V8_MOUSE]	4.7	3.1	2.0	100.0	66.1	43.4	9.5	2.15E-03	0.41	0.83	-0.42	0.41	6.12	0.79	8.83	-0.42	-2.71
P54116	STOM	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3 - [STOM_MOUSE]	5.9	11.9	6.3	49.6	100.0	52.5	5.6	1.54E-02	-0.70		-0.64	-0.67	-53.77			-0.62	-51.65
Q9JI11	STK4	Serine/threonine-protein kinase 4 OS=Mus musculus GN=Stk4 PE=1 SV=1 - [STK4_MOUSE]	2.9	0.5	1.3	100.0	17.1	47.2	7.5	5.41E-03	1.76	0.75	1.01	1.41	3.94	0.72	3.16	0.93	0.79
P70302	STIM1	Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=2 - [STIM1_MOUSE]	8.1	3.9	5.0	100.0	48.7	62.0	15.5	2.23E-04	0.72	0.48	0.24	0.69	24.81	0.47	20.03	0.24	4.78
Q80XU2	SRC	Tyrosine-protein kinase OS=Mus musculus GN=Src PE=1 SV=1 - [Q80XU2_MOUSE]	3.7	0.3	0.0	100.0	7.4	0.0	60.3	6.72E-08	2.60	100.00	-100.00	1.72	6.64	2.00	6.67	-2.00	-0.04
P15508	SPNB1	Spectrin beta chain, erythrocytic OS=Mus musculus GN=Sptb PE=1 SV=4 - [SPTB1_MOUSE]	4.6	21.6	11.5	21.4	100.0	53.3	9.0	2.66E-03	-1.54	-0.91	-0.63	-1.29	-221.61	-0.85	-55.23	-0.61	-166.38
P16546	SPTAN1	Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=4 - [SPTN1_MOUSE]	55.2	34.4	43.6	100.0	62.3	79.0	28.2	8.24E-06	0.47	0.24	0.24	0.46	932.18	0.24	574.16	0.24	358.01
P08032	SPTA1	Spectrin alpha chain, erythrocytic 1 OS=Mus musculus GN=Spta1 PE=1 SV=3 - [SPTA1_MOUSE]	1.2	12.0	6.3	10.4	100.0	52.4	7.3	5.96E-03	-2.27	-1.62	-0.65	-1.62	-71.55	-1.34	-19.05	-0.63	-52.50
Q64442	SORD	Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 - [DHSO_MOUSE]	11.3	1.7	11.7	97.1	14.5	100.0	58.1	8.60E-08	1.90		1.93	1.48	62.72			1.49	66.59
O55042	SNCA	Alpha-synuclein OS=Mus musculus GN=Snca PE=1 SV=2 - [SYUA_MOUSE]	1.6	5.8	0.0	28.1	100.0	0.0	23.3	2.52E-05	-1.27	100.00	-100.00	-1.12	-15.25	2.00	1.30	-2.00	-16.55
F7D5X7	SNAPC4	snRNA-activating protein complex subunit 4 (Fragment) OS=Mus musculus GN=Snapc4 PE=4 SV=1 - [F7D5X7_	0.7	0.1	0.0	100.0	19.5	0.0	6.0	1.25E-02	1.63	100.00	-100.00	1.35	0.23	2.00	0.24	-2.00	-0.01
P04919	SLC4A1	Band 3 anion transport protein OS=Mus musculus GN=Slc4a1 PE=1 SV=1 - [B3AT_MOUSE]	3.4	14.1	10.8	24.3	100.0	76.7	11.4	9.87E-04	-1.42	-1.15	-0.26	-1.22	-93.32	-1.04	-52.54	-0.26	-40.78
Q8BGD6	SLC38A9	Sodium-coupled neutral amino acid transporter 9 OS=Mus musculus GN=Slc38a9 PE=1 SV=1 - [S38A9_MOUSE	1.6	0.5	0.1	100.0	28.5	8.6	5.4	1.75E-02	1.25	2.45	-1.20	1.11	1.16	1.68	1.25	-1.07	-0.09
P32037	SLC2A3	Solute carrier family 2, facilitated glucose transporter member 3 OS=Mus musculus GN=Slc2a3 PE=1 SV=	10.9	6.9	7.6	100.0	63.1	70.0	4.7	2.55E-02	0.46	0.36		0.45	35.50	0.35	30.04		
Q8VEM8	SLC25A3	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1 - [MPCP_MOUSE]	4.5	1.2	2.3	100.0	26.9	52.2	11.6	9.07E-04	1.31	0.65	0.66	1.15	9.29	0.63	7.29	0.64	2.00
Q8BMD8	SLC25A24	Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Mus musculus GN=Slc25a24 PE=1 SV=1 - [SCMC1	1.8	0.4	0.2	100.0	23.1	11.3	10.3	1.52E-03	1.46	2.18	-0.71	1.25	1.47	1.59	1.54	-0.68	-0.06
Q8VHL0	SLC14A1	Urea transporter 1 OS=Mus musculus GN=Slc14a1 PE=1 SV=2 - [UT1_MOUSE]	0.7	0.1	0.0	100.0	19.5	0.0	6.0	1.24E-02	1.63	100.00	-100.00	1.35	0.23	2.00	0.24	-2.00	-0.01
Q3UND0	SKAP2	Src kinase-associated phosphoprotein 2 OS=Mus musculus GN=Skap2 PE=1 SV=2 - [SKAP2_MOUSE]	2.6	0.5	0.8	100.0	20.2	29.3	9.0	2.67E-03	1.60	1.23	0.37	1.33	3.36	1.09	3.20	0.37	0.16
Q9D154	SERPINB1A	Leukocyte elastase inhibitor A OS=Mus musculus GN=Serpinb1a PE=1 SV=1 - [ILEUA_MOUSE]	24.6	19.6	20.6	100.0	79.8	84.0	8.7	3.05E-03	0.23	0.17		0.23	109.73				
G3UYR4	SERPINB10	Serpin B10 OS=Mus musculus GN=Serpinb10 PE=1 SV=1 - [G3UYR4_MOUSE]	6.1	10.8	0.0	56.6	100.0	0.0	74.1	1.67E-08	-0.57	100.00	-100.00	-0.55	-39.52	2.00	18.61	-2.00	-58.12
Q06770	SERPINA6	Corticosteroid-binding globulin OS=Mus musculus GN=Serpina6 PE=1 SV=1 - [CBG_MOUSE]	1.1	6.5	1.2	16.1	100.0	18.9	6.5	9.02E-03	-1.83		-1.67	-1.45	-20.78			-1.36	-20.57
P07759	SERPINA3K	Serine protease inhibitor A3K OS=Mus musculus GN=Serpina3k PE=1 SV=2 - [SPA3K_MOUSE]	125.1	164.4	126.4	76.1	100.0	76.9	4.0	4.03E-02	-0.27		-0.26	-0.27	-5685.24			-0.26	-5514.22
Q00898	SERPINA1E	Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e PE=1 SV=1 - [A1AT5_MOUSE]	89.3	19.3	66.6	100.0	21.6	74.6	23.0	2.67E-05	1.53	0.29	1.24	1.29	3804.01	0.29	1770.97	1.10	2033.05
P22599	SERPINA1B	Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2 - [A1AT2_MOUSE]	86.1	54.1	63.8	100.0	62.9	74.0	5.0	2.21E-02	0.46	0.30	0.16	0.46	2242.88	0.30	1675.49		
A8Y5D3	SEPT9	Septin-9 (Fragment) OS=Mus musculus GN=Sept9 PE=1 SV=1 - [A8Y5D3_MOUSE]	1.3	0.4	0.8	100.0	26.2	59.5	4.4	3.13E-02	1.34	0.52	0.82	1.17	0.84	0.51	0.58	0.78	0.26
Q9EP69	SACM1L	Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=1 SV=1 - [SAC1_MOUSE]	1.0	0.0	0.1	100.0	0.0	13.8	12.1	7.54E-04	100.00	1.98	100.00	2.00	0.48	1.51	0.47	2.00	0.01
Q9ES97	RTN3	Reticulon-3 OS=Mus musculus GN=Rtn3 PE=1 SV=2 - [RTN3_MOUSE]	0.6	0.0	0.0	100.0	0.0	0.0	4.5	2.91E-02	100.00	100.00		2.00	0.21	2.00	0.21		
Q01730	RSU1	Ras suppressor protein 1 OS=Mus musculus GN=Rsu1 PE=1 SV=3 - [RSU1_MOUSE]	30.9	19.9	24.2	100.0	64.3	78.2	21.8	3.61E-05	0.44	0.25	0.20	0.43	280.86	0.24	186.08		
A2AVJ7	RRBP1	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=1 SV=1 - [A2AVJ7_MOUSE]	0.5	0.0	0.0	100.0	0.0	0.0	4.9	2.36E-02	100.00	100.00		2.00	0.13	2.00	0.13		
G3UYV7	RPS28	40S ribosomal protein S28 (Fragment) OS=Mus musculus GN=Rps28 PE=1 SV=1 - [G3UYV7_MOUSE]	0.1	0.7	0.0	19.7	100.0	0.0	5.6	1.56E-02	-1.62	100.00	-100.00	-1.34	-0.25	2.00	0.01	-2.00	-0.26
A2ACG7	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=	6.4	2.7	3.9	100.0	41.9	61.3	9.5	2.21E-03	0.87	0.49	0.38	0.82	16.85	0.48	12.74	0.38	4.11
A0A0G2JEP8	RHOC	Rho-related GTP-binding protein RhoC (Fragment) OS=Mus musculus GN=Rhoc PE=1 SV=1 - [A0A0G2JEP8_M	1.2	0.0	0.9	100.0	0.0	75.2	4.1	3.90E-02	100.00	0.28	100.00	2.00	0.71	0.28	0.31	2.00	0.40
Q9QUG9	RASGRP2	RAS guanyl-releasing protein 2 OS=Mus musculus GN=Rasgrp2 PE=1 SV=2 - [GRP2_MOUSE]	8.1	3.5	4.7	100.0	42.5	58.3	7.6	5.29E-03	0.86	0.54	0.32	0.81	26.99	0.53	21.76	0.31	5.23
Q99JI6	RAP1B	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=1 SV=2 - [RAP1B_MOUSE]	41.6	30.0	34.6	100.0	72.2	83.3	8.2	3.88E-03	0.33	0.18		0.32	413.36				
P62835	RAP1A	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1 - [RAP1A_MOUSE]	33.5	9.4	18.7	100.0	27.9	55.8	7.7	5.10E-03	1.28	0.58	0.69	1.13	516.98	0.57	386.39	0.66	130.59
E9PUM3	PYGM	Alpha-1,4 glucan phosphorylase OS=Mus musculus GN=Pygm PE=1 SV=1 - [E9PUM3_MOUSE]	1.9	0.5	0.0	100.0	28.2	0.0	4.3	3.24E-02	1.27	100.00	-100.00	1.12	1.72	2.00	1.87	-2.00	-0.15
P35831	PTPN12	Tyrosine-protein phosphatase non-receptor type 12 OS=Mus musculus GN=Ptpn12 PE=1 SV=3 - [PTN12_MOUS	0.9	0.0	0.7	100.0	0.0	77.6	4.2	3.59E-02	100.00	0.25	100.00	2.00	0.41	0.25	0.16	2.00	0.25
P31324	PRKAR2B	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkar2b PE=1 SV=3 -	20.8	14.4	14.1	100.0	69.3	67.6	7.9	4.51E-03	0.37	0.39		0.36	112.27	0.39	117.47		
A0A0G2JFT9	PRKACB	cAMP-dependent protein kinase catalytic subunit beta (Fragment) OS=Mus musculus GN=Prkacb PE=1 SV=1	0.8	0.0	0.1	100.0	0.0	17.1	5.7	1.47E-02	100.00	1.77	100.00	2.00	0.31	1.42	0.30	2.00	0.01
P99029	PRDX5	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2 - [PRDX5_MOUSE]	7.1	3.7	4.8	100.0	52.8	68.3	8.3	3.77E-03	0.64	0.38	0.26	0.62	18.07	0.38	13.35	0.26	4.72
D3Z4A4	PRDX2	Peroxiredoxin-2 (Fragment) OS=Mus musculus GN=Prdx2 PE=1 SV=7 - [D3Z4A4_MOUSE]	11.3	19.5	15.1	57.9	100.0	77.5	8.6	3.25E-03	-0.55	-0.29	-0.26	-0.53	-126.56	-0.29	-50.41	-0.25	-76.15
Q7TMR0	PRCP	Lysosomal Pro-X carboxypeptidase OS=Mus musculus GN=Prcp PE=1 SV=2 - [PCP_MOUSE]	1.4	0.3	0.5	100.0	18.9	37.7	3.9	4.38E-02	1.67	0.98	0.69	1.36	1.00	0.90	0.89	0.66	0.11
Q810Y8	PRAMEL7	PRAMEl7 OS=Mus musculus GN=Pramel7 PE=2 SV=1 - [Q810Y8_MOUSE]	1.3	0.4	0.3	100.0	26.9	23.8	4.6	2.72E-02	1.31	1.44		1.15	0.82	1.23	0.83		
Q76MZ3	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN	3.7	2.2	1.2	100.0	59.1	31.3	7.9	4.61E-03	0.53	1.16	-0.63	0.51	4.46	1.05	6.18	-0.61	-1.72
A0A0G2JGC1	PPP1CC	Serine/threonine-protein phosphatase OS=Mus musculus GN=Ppp1cc PE=1 SV=1 - [A0A0G2JGC1_MOUSE]	3.0	1.6	2.2	100.0	53.6	74.6	3.9	4.20E-02	0.62	0.29	0.33	0.60	3.19	0.29	1.99	0.33	1.20
Q9CZT4	POLR3E	DNA-directed RNA polymerase III subunit RPC5 OS=Mus musculus GN=Polr3e PE=1 SV=2 - [RPC5_MOUSE]	0.7	0.0	0.0	100.0	0.0	0.0	3.8	4.70E-02	100.00	100.00		2.00	0.24	2.00	0.24		
P23492	PNP	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2 - [PNPH_MOUSE]	2.4	7.3	4.9	33.1	100.0	67.4	23.1	2.62E-05	-1.11	-0.71	-0.40	-1.01	-23.49	-0.68	-9.08	-0.39	-14.40
Q3V0K9	PLS1	Plastin-1 OS=Mus musculus GN=Pls1 PE=1 SV=1 - [PLSI_MOUSE]	16.3	8.9	11.5	100.0	54.3	70.6	4.8	2.51E-02	0.61	0.35	0.26	0.59	93.89	0.34	66.80	0.26	27.10

Q9QZC7	PLEKHB2	Pleckstrin homology domain-containing family B member 2 OS=Mus musculus GN=Plekhb2 PE=1 SV=1 - [PKHE	0.0	0.0	0.5	0.0	0.0	100.0	4.8	2.40E-02		-100.00	100.00			-2.00	-0.13	2.00	0.13
Q8CAG6	PLEK	Pleckstrin OS=Mus musculus GN=Plek PE=1 SV=1 - [Q8CAG6_MOUSE]	35.0	27.5	29.8	100.0	78.7	85.1	5.2	1.90E-02	0.24	0.16		0.24	233.72				
P52480	PKM	Pyruvate kinase PKM OS=Mus musculus GN=Pkm PE=1 SV=4 - [KPYM_MOUSE]	63.2	52.4	55.1	100.0	83.0	87.3	4.5	2.91E-02	0.19								
Q7TSV4	PGM2	Phosphoglucomutase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1 - [PGM2_MOUSE]	2.5	1.1	1.4	100.0	44.1	56.7	4.0	4.00E-02	0.82	0.57	0.25	0.78	2.52	0.55	2.12	0.25	0.40
Q9DCD0	PGD	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=1 SV=3 - [6PGD_MOUSE	3.6	1.9	3.1	100.0	53.6	86.6	6.8	7.86E-03	0.62		0.48	0.60	4.50			0.47	2.92
A0A0J9YTR7	PF4	Chemokine (C-X-C motif) ligand 4, isoform CRA_a OS=Mus musculus GN=Pf4 PE=1 SV=1 - [A0A0J9YTR7_MO	4.9	3.6	3.9	100.0	73.2	78.2	5.7	1.46E-02	0.31	0.25		0.31	5.67	0.25	4.76		
D6RHS6	PEBP1	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=1 - [D6RHS6_MOUSE]	2.4	1.1	1.4	100.0	47.5	58.1	4.6	2.78E-02	0.74	0.54	0.20	0.71	2.14	0.53	1.83	0.20	0.31
Q922R8	PDIA6	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3 - [PDIA6_MOUSE]	20.4	13.7	16.5	100.0	67.3	80.8	4.8	2.48E-02	0.40	0.21	0.18	0.39	113.96	0.21	72.25		
P08003	PDIA4	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3 - [PDIA4_MOUSE]	4.3	1.1	2.9	100.0	26.6	68.7	5.2	1.90E-02	1.33	0.38	0.95	1.16	8.51	0.37	4.83	0.88	3.68
Q8BH04	PCK2	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=1 SV=1 - [PCKGM_	0.8	0.1	0.8	100.0	16.5	100.0	6.0	1.20E-02	1.80		1.80	1.43	0.33	0.00	0.00	1.43	0.33
P60335	PCBP1	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 - [PCBP1_MOUSE]	1.0	0.0	0.2	100.0	0.0	18.7	7.4	5.90E-03	100.00	1.68	100.00	2.00	0.51	1.37	0.49	2.00	0.02
Q9ES46	PARVB	Beta-parvin OS=Mus musculus GN=Parvb PE=1 SV=1 - [PARVB_MOUSE]	32.7	24.8	28.0	100.0	75.8	85.7	5.8	1.37E-02	0.28	0.15		0.28	227.43				
Q3TL44	NLRX1	NLR family member X1 OS=Mus musculus GN=Nlrx1 PE=1 SV=1 - [NLRX1_MOUSE]	2.3	0.2	0.7	100.0	7.4	30.4	22.7	2.89E-05	2.61	1.19	1.42	1.73	2.66	1.07	2.43	1.22	0.23
E9Q5R7	NLRP12	NACHT, LRR and PYD domains-containing protein 12 OS=Mus musculus GN=Nlrp12 PE=2 SV=1 - [NAL12_MO	0.1	2.6	0.9	5.5	100.0	33.8	4.2	3.52E-02	-2.89	-1.81	-1.09	-1.79	-3.27	-1.44	-0.36	-0.99	-2.90
Q9D6J6	NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Mus musculus GN=Ndufv2 PE=1 SV=2 -	0.8	0.0	0.0	100.0	0.0	0.0	23.0	2.68E-05	100.00	100.00		2.00	0.35	2.00	0.35		
Q91VD9	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2 - [	1.3	0.0	0.2	100.0	0.0	14.5	6.3	1.06E-02	100.00	1.93	100.00	2.00	0.82	1.49	0.80	2.00	0.02
Q60605	MYL6	Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3 - [MYL6_MOUSE]	23.2	18.4	22.0	100.0	79.2	95.1	5.2	1.97E-02	0.23		0.18	0.23	99.93				
Q8VDD5	MYH9	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4 - [MYH9_MOUSE]	358.2	272.2	332.7	100.0	76.0	92.9	26.8	1.11E-05	0.27		0.20	0.27	27128.52			0.20	18318.74
Q9EQK5	MVP	Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4 - [MVP_MOUSE]	0.7	0.0	0.0	100.0	0.0	0.0	3.9	4.32E-02	100.00	100.00		2.00	0.27	2.00	0.27		
A2BIN0	MUP11	Major urinary protein 11 OS=Mus musculus GN=Mup11 PE=4 SV=1 - [A2BIN0_MOUSE]	1.5	0.0	1.0	100.0	0.0	69.3	10.0	1.76E-03	100.00	0.37	100.00	2.00	1.10	0.36	0.57	2.00	0.53
Q922D8	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4 - [C1TC_MOUSE]	0.0	1.3	0.5	0.0	100.0	40.6	4.2	3.66E-02	-100.00	-100.00	-0.90	-2.00	-0.83	-2.00	-0.14	-0.84	-0.69
P26041	MSN	Moesin OS=Mus musculus GN=Msn PE=1 SV=3 - [MOES_MOUSE]	2.4	0.0	0.4	100.0	0.0	17.1	9.5	2.16E-03	100.00	1.77	100.00	2.00	2.85	1.42	2.76	2.00	0.08
A0A0N4SVL8	MMRN1	Multimerin-1 OS=Mus musculus GN=Mmrn1 PE=1 SV=1 - [A0A0N4SVL8_MOUSE]	18.5	21.8	0.0	85.1	100.0	0.0	24.6	1.85E-05	-0.16	100.00	-100.00			2.00	171.65	-2.00	-237.26
P08249	MDH2	Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3 - [MDHM_MOUSE]	10.5	6.1	9.2	100.0	57.7	87.6	6.1	1.13E-02	0.55		0.42	0.54	37.09			0.41	24.20
Q8VED9	LGALSL	Galectin-related protein OS=Mus musculus GN=Lgalsl PE=1 SV=1 - [LEGL_MOUSE]	4.8	2.3	3.5	100.0	48.7	72.9	7.2	6.51E-03	0.72	0.32	0.40	0.69	8.69	0.31	5.34	0.40	3.36
F6SUU5	KIF2A	Kinesin-like protein (Fragment) OS=Mus musculus GN=Kif2a PE=1 SV=1 - [F6SUU5_MOUSE]	1.0	0.3	0.7	100.0	26.8	69.3	5.0	2.22E-02	1.32	0.37	0.95	1.16	0.48	0.36	0.27	0.89	0.21
G3X940	KAT6A	Histone acetyltransferase OS=Mus musculus GN=Kat6a PE=1 SV=1 - [G3X940_MOUSE]	0.3	1.2	0.0	24.0	100.0	0.0	6.7	8.23E-03	-1.43	100.00	-100.00	-1.22	-0.65	2.00	0.04	-2.00	-0.69
D3Z534	KALRN	Kalirin OS=Mus musculus GN=Kalrn PE=1 SV=1 - [D3Z534_MOUSE]	6.4	3.6	4.2	100.0	55.4	65.9	10.5	1.39E-03	0.59	0.42	0.17	0.57	14.30	0.41	11.68		
P01592	JCHAIN	Immunoglobulin J chain OS=Mus musculus GN=Jchain PE=1 SV=4 - [IGJ_MOUSE]	0.0	0.9	0.0	0.0	100.0	0.0	7.1	6.80E-03	-100.00		-100.00	-2.00	-0.40	0.00	0.00	-2.00	-0.40
E9Q5L2	ITIH4	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4 PE=1 SV=1 - [E9Q5L2_MOUSE]	12.0	10.8	6.1	100.0	89.5	51.0	4.0	4.19E-02		0.67	-0.56			0.65	53.38	-0.55	-39.08
O54890	ITGB3	Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=1 SV=2 - [ITB3_MOUSE]	23.8	17.0	18.2	100.0	71.2	76.2	10.2	1.60E-03	0.34	0.27		0.34	139.96	0.27	118.98		
P09055	ITGB1	Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1 - [ITB1_MOUSE]	9.5	10.1	7.6	93.8	100.0	75.5	4.3	3.42E-02		0.22	-0.28	-0.06	-6.15	0.22	15.71	-0.28	-21.86
E9QNL8	ITGAL	Integrin alpha-L OS=Mus musculus GN=Itgal PE=1 SV=1 - [E9QNL8_MOUSE]	1.2	0.5	0.0	100.0	43.6	0.0	4.0	4.09E-02	0.83	100.00	-100.00	0.79	0.55	2.00	0.68	-2.00	-0.13
Q9QUM0	ITGA2B	Integrin alpha-IIb OS=Mus musculus GN=Itga2b PE=1 SV=2 - [ITA2B_MOUSE]	72.4	55.1	58.3	100.0	76.1	80.5	19.4	6.87E-05	0.27	0.22		0.27	1101.77	0.22	922.99		
Q64339	ISG15	Ubiquitin-like protein ISG15 OS=Mus musculus GN=Isg15 PE=1 SV=4 - [ISG15_MOUSE]	0.2	1.6	0.6	11.8	100.0	40.3	8.1	4.12E-03	-2.14	-1.23	-0.91	-1.58	-1.26	-1.10	-0.19	-0.85	-1.07
Q8BKC5	IPO5	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3 - [IPO5_MOUSE]	0.7	0.0	0.0	100.0	0.0	0.0	3.8	4.70E-02	100.00	100.00		2.00	0.24	2.00	0.24		
P49442	INPP1	Inositol polyphosphate 1-phosphatase OS=Mus musculus GN=Inpp1 PE=1 SV=2 - [INPP_MOUSE]	1.1	0.0	0.0	100.0	0.0	0.0	13.0	5.35E-04	100.00	100.00		2.00	0.56	2.00	0.56		
O55222	ILK	Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2 - [ILK_MOUSE]	28.2	22.7	25.2	100.0	80.7	89.6	5.4	1.76E-02	0.21			0.21	138.49				
A0A075B663	IGLV1	Protein Iglv1 (Fragment) OS=Mus musculus GN=Iglv1 PE=4 SV=1 - [A0A075B663_MOUSE]	0.0	0.6	0.0	0.0	100.0	0.0	4.5	2.87E-02	-100.00		-100.00	-2.00	-0.15			-2.00	-0.15
P01843	IGLC1	Ig lambda-1 chain C region OS=Mus musculus PE=1 SV=1 - [LAC1_MOUSE]	0.0	3.8	0.2	0.0	100.0	4.8	24.5	1.90E-05	-100.00	-100.00	-3.03	-2.00	-7.07	-2.00	-0.02	-1.82	-7.05
P01837	IGKC	Ig kappa chain C region OS=Mus musculus PE=1 SV=1 - [IGKC_MOUSE]	5.7	10.1	2.4	56.7	100.0	24.0	5.5	1.66E-02	-0.57	0.86	-1.43	-0.55	-34.35	0.81	13.37	-1.23	-47.73
P01872	IGHM	Ig mu chain C region OS=Mus musculus GN=Ighm PE=1 SV=2 - [IGHM_MOUSE]	6.1	16.5	5.9	36.8	100.0	35.7	10.6	1.35E-03	-1.00		-1.03	-0.92	-118.15			-0.95	-119.26
A0A075B5P5	IGHG3	Protein Ighg3 (Fragment) OS=Mus musculus GN=Ighg3 PE=4 SV=1 - [A0A075B5P5_MOUSE]	0.8	3.6	1.5	21.9	100.0	42.9	5.2	1.95E-02	-1.52	-0.67	-0.85	-1.28	-6.16	-0.65	-0.88	-0.80	-5.28
A0A075B5P3	IGHG2B	Protein Ighg2b (Fragment) OS=Mus musculus GN=Ighg2b PE=1 SV=1 - [A0A075B5P3_MOUSE]	0.0	7.3	1.9	0.0	100.0	26.7	16.6	1.60E-04	-100.00	-100.00	-1.32	-2.00	-26.47	-2.00	-1.89	-1.16	-24.59
P01863	IGHG	Ig gamma-2A chain C region, A allele OS=Mus musculus GN=Ighg PE=1 SV=1 - [GCAA_MOUSE]	1.8	0.0	0.4	100.0	0.0	20.7	23.4	2.47E-05	100.00	1.57	100.00	2.00	1.63	1.31	1.56	2.00	0.07
A0A075B6A3	IGHA	Protein Igha (Fragment) OS=Mus musculus GN=Igha PE=1 SV=1 - [A0A075B6A3_MOUSE]	0.3	1.1	0.0	26.3	100.0	0.0	4.1	3.85E-02	-1.34	100.00	-100.00	-1.17	-0.55	2.00	0.04	-2.00	-0.60
Q61635	IFI47	GTP-binding protein OS=Mus musculus GN=Ifi47 PE=1 SV=1 - [Q61635_MOUSE]	14.2	9.1	9.6	100.0	64.1	67.5	7.3	6.03E-03	0.44	0.39		0.44	59.68	0.39	55.18		
Q9JKR6	HYOU1	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1 - [HYOU1_MOUSE]	5.4	2.1	4.1	100.0	39.9	75.3	7.5	5.53E-03	0.92	0.28	0.64	0.86	12.21	0.28	6.28	0.62	5.93
Q64433	HSPE1	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2 - [CH10_MOUSE]	2.3	0.3	0.2	100.0	11.7	7.9	62.8	5.12E-08	2.14	2.54	-0.40	1.58	2.64	1.71	2.66	-0.40	-0.02
P63038	HSPD1	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 - [CH60_MOUSE]	14.8	9.6	7.9	100.0	64.4	53.6	14.1	3.54E-04	0.44	0.62	-0.18	0.43	64.45	0.60	78.52		
P38647	HSPA9	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=3 - [GRP75_MOUSE]	1.3	0.5	0.0	100.0	36.4	0.0	4.5	2.99E-02	1.01	100.00	-100.00	0.93	0.74	2.00	0.85	-2.00	-0.11
P63017	HSPA8	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1 - [HSP7C_MOUSE]	55.8	46.2	50.7	100.0	82.8	90.9	6.0	1.20E-02	0.19								
P07901	HSP90AA1	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4 - [HS90A_MOUSE]	27.2	20.2	21.8	100.0	74.3	79.9	4.0	4.10E-02	0.30	0.22		0.30	166.39	0.22	133.98		
Q61646	HP	Haptoglobin OS=Mus musculus GN=Hp PE=1 SV=1 - [HPT_MOUSE]	3.3	0.0	0.0	100.0	0.0	0.0	6.2	1.09E-02	100.00	100.00		2.00	5.32	2.00	5.32		
G3UVV4	HK1	Hexokinase OS=Mus musculus GN=Hk1 PE=1 SV=1 - [G3UVV4_MOUSE]	22.1	12.2	14.7	100.0	55.2	66.8	10.2	1.60E-03	0.59	0.40	0.19	0.58	169.27	0.40	134.72		
A8DUK4	HBBT1	Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1 - [A8DUK4_MOUSE]	196.7	366.8	347.8	53.6	100.0	94.8	10.2	1.59E-03	-0.62	-0.57		-0.60	-47928.57	-0.55	-41127.77		
Q91VB8	HBA-A2	Alpha globin 1 OS=Mus musculus GN=Hba-a1 PE=1 SV=1 - [Q91VB8_MOUSE]	213.0	456.0	390.6	46.7	100.0	85.7	11.9	8.15E-04	-0.76	-0.61	-0.15	-0.73	-81303.57	-0.59	-53605.42		
O09131	GSTO1	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2 - [GSTO1_MOUSE]	0.5	0.0	0.0	100.0	0.0	0.0	5.0	2.17E-02	100.00	100.00		2.00	0.15	2.00	0.15		
Q64521	GPD2	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2 - [GPDM_MOUS	5.3	1.6	2.8	100.0	29.6	51.9	13.1	5.13E-04	1.22	0.66	0.56	1.09	13.05	0.63	10.44	0.55	2.60
P0C191	GP6	Platelet glycoprotein VI OS=Mus musculus GN=Gp6 PE=1 SV=2 - [GPVI_MOUSE]	1.6	0.3	0.7	100.0	17.1	46.7	4.7	2.63E-02	1.76	0.76	1.00	1.42	1.22	0.73	0.98	0.93	0.24
Q9QZU3	GP5	Platelet glycoprotein V (Fragment) OS=Mus musculus GN=Gp5 PE=1 SV=1 - [Q9QZU3_MOUSE]	19.5	9.9	15.5	100.0	50.8	79.3	4.4	3.16E-02	0.68	0.23	0.45	0.65	140.88	0.23	70.31	0.44	70.56
O35930	GP1BA	Platelet glycoprotein Ib alpha chain OS=Mus musculus GN=Gp1ba PE=1 SV=2 - [GP1BA_MOUSE]	32.6	21.5	28.5	100.0	66.0	87.4	8.2	4.02E-03	0.42		0.28	0.41	299.21			0.28	173.68
O70443	GNAZ	Guanine nucleotide-binding protein G(z) subunit alpha OS=Mus musculus GN=Gnaz PE=1 SV=4 - [GNAZ_MOU	5.4	2.7	2.8	100.0	49.5	52.5	8.7	3.16E-03	0.70	0.64		0.68	10.88	0.62	10.44		
Z4YKV1	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Mus musculus GN=Gnas PE=1 SV	0.7	0.0	0.0	100.0	0.0	0.0	4.0	3.97E-02	100.00	100.00		2.00	0.27	2.00	0.27		
P21279	GNAQ	Guanine nucleotide-binding protein G(q) subunit alpha OS=Mus musculus GN=Gnaq PE=1 SV=4 - [GNAQ_MOU	4.8	2.3	2.8	100.0	47.7	58.6	5.2	1.90E-02	0.74	0.53	0.21	0.71	8.87	0.52	7.53	0.21	1.34
E9Q3T0	GM10073	Protein Gm10073 OS=Mus musculus GN=Gm10073 PE=1 SV=1 - [E9Q3T0_MOUSE]	2.3	0.7	0.9	100.0	28.3	40.0	7.8	4.81E-03	1.26	0.92	0.35	1.12	2.48	0.86	2.27	0.34	0.22
Q9CZD3	GARS	Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1 - [SYG_MOUSE]	1.5	0.0	0.5	100.0	0.0	31.7	8.1	4.21E-03	100.00	1.15	100.00	2.00	1.11	1.04	0.99	2.00	0.11
P16858	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 - [G3P_MOUSE]	39.6	30.8	39.9	99.3	77.3	100.0	8.7	3.08E-03	0.25		0.26	0.25	307.86			0.26	319.38
P29391	FTL1	Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2 - [FRIL1_MOUSE]	3.7	1.5	5.4	69.2	27.3	100.0	13.8	3.95E-04	0.93	-0.37	1.30	0.87	5.86	-0.36	-7.57	1.14	13.43
A2AQ47	FNBP1	Formin-binding protein 1 (Fragment) OS=Mus musculus GN=Fnbp1 PE=1 SV=1 - [A2AQ47_MOUSE]	0.7	0.3	0.0	100.0	44.2	0.0	4.1	3.76E-02	0.82	100.00	-100.00	0.77	0.19	2.00	0.24	-2.00	-0.05
B7FAU9	FLNA	Filamin, alpha OS=Mus musculus GN=Flna PE=1 SV=1 - [B7FAU9_MOUSE]	293.2	225.1	259.3	100.0	76.8	88.4	22.3	3.23E-05	0.26			0.26	17662.76				
Q8K0E8	FGB	Fibrinogen beta chain OS=Mus musculus GN=Fgb PE=1 SV=1 - [FIBB_MOUSE]	105.7	86.5	98.5	100.0	81.8	93.2	10.7	1.31E-03	0.20			0.20	1845.14				
Q8K1B8	FERMT3	Fermitin family homolog 3 OS=Mus musculus GN=Fermt3 PE=1 SV=1 - [URP2_MOUSE]	77.5	64.1	74.5	100.0	82.8	96.2	7.7	4.97E-03	0.19		0.15						
Q6PDI6	FAM63B	Protein FAM63B OS=Mus musculus GN=Fam63b PE=1 SV=1 - [FA63B_MOUSE]	0.0	0.8	0.0	0.0	100.0	0.0	4.4	3.14E-02	-100.00		-100.00	-2.00	-0.29			-2.00	-0.29
O88783	F5	Coagulation factor V OS=Mus musculus GN=F5 PE=1 SV=1 - [FA5_MOUSE]	11.0	10.8	3.1	100.0	98.3	27.9	23.6	2.31E-05		1.28	-1.26			1.13	55.44	-1.12	-53.46
Q8BH61	F13A1	Coagulation factor XIII A chain OS=Mus musculus GN=F13a1 PE=1 SV=3 - [F13A_MOUSE]	4.8	1.8	3.8	100.0	36.7	79.5	6.5	9.39E-03	1.00	0.23	0.77	0.93	10.12	0.23	4.31	0.74	5.81
Q3U7R1	ESYT1	Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 SV=2 - [ESYT1_MOUSE]	1.0	0.1	0.3	100.0	14.0	32.4	5.2	1.88E-02	1.97	1.13	0.84	1.51	0.47	1.02	0.43	0.79	0.04
Q9D1Q6	ERP44	Endoplasmic reticulum resident protein 44 OS=Mus musculus GN=Erp44 PE=1 SV=1 - [ERP44_MOUSE]	0.0	0.9	0.3	0.0	100.0	30.2	9.4	2.30E-03	-100.00	-100.00	-1.20	-2.00	-0.41	-2.00	-0.04	-1.07	-0.37
Q8CGC7	EPRS	Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4 - [SYEP_MOUSE]	1.6	0.3	1.2	100.0	22.2	75.3	3.7	4.97E-02	1.51	0.28	1.22	1.27	1.16	0.28	0.53	1.09	0.63

A2A839	EPB41	Protein 4.1 OS=Mus musculus GN=Epb41 PE=1 SV=1 - [A2A839_MOUSE]	6.2	11.0	8.8	56.7	100.0	79.7	5.2	1.96E-02	-0.57	-0.34	-0.23	-0.55	-40.92	-0.34	-18.93	-0.23	-21.99
P17182	ENO1	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3 - [ENOA_MOUSE]	33.1	26.2	31.1	100.0	79.0	94.0	4.4	3.16E-02	0.24		0.17	0.23	206.52				
Q8QZY1	EIF3L	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1 - [EIF3L_MOU	0.9	0.1	0.0	100.0	15.6	0.0	5.1	2.03E-02	1.86	100.00	-100.00	1.46	0.37	2.00	0.38	-2.00	-0.01
E0CXJ3	EIF2S2	Eukaryotic translation initiation factor 2 subunit 2 (Fragment) OS=Mus musculus GN=Eif2s2 PE=1 SV=1	0.2	1.0	0.6	18.0	100.0	64.1	3.9	4.33E-02	-1.72	-1.27	-0.45	-1.39	-0.49	-1.12	-0.19	-0.44	-0.30
Q9EQP2	EHD4	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1 - [EHD4_MOUSE]	26.2	21.4	24.7	100.0	82.0	94.4	4.6	2.84E-02	0.20			0.20	112.29				
Q9QXY6	EHD3	EH domain-containing protein 3 OS=Mus musculus GN=Ehd3 PE=1 SV=2 - [EHD3_MOUSE]	13.5	8.7	11.6	100.0	64.3	85.9	6.1	1.17E-02	0.44	0.15	0.29	0.43	53.21			0.29	29.38
Q9WVK4	EHD1	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1 - [EHD1_MOUSE]	7.6	4.4	4.8	100.0	57.0	63.1	4.0	3.97E-02	0.56	0.46		0.55	19.70	0.45	17.56		
Q9D8N0	EEF1G	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 - [EF1G_MOUSE]	3.8	2.2	2.6	100.0	58.5	66.8	6.1	1.14E-02	0.54	0.40		0.52	4.84	0.40	4.08		
P10126	EEF1A1	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 - [EF1A1_MOUSE]	13.6	8.2	11.8	100.0	60.1	86.8	8.7	3.07E-03	0.51		0.37	0.50	58.97			0.36	36.22
Q9JHU4	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2 - [DYHC1_MOUSE]	9.0	3.5	4.4	100.0	38.5	48.9	21.2	4.24E-05	0.95	0.71	0.24	0.89	34.81	0.69	31.09	0.24	3.72
E9PUD2	DNM1L	Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=1 - [E9PUD2_MOUSE]	5.3	2.4	3.5	100.0	46.2	66.1	4.9	2.25E-02	0.77	0.41	0.36	0.74	10.90	0.41	7.80	0.35	3.09
Q99KV1	DNAJB11	DnaJ homolog subfamily B member 11 OS=Mus musculus GN=Dnajb11 PE=1 SV=1 - [DJB11_MOUSE]	1.0	0.3	1.7	58.6	19.0	100.0	7.7	4.89E-03	1.13	-0.53	1.66	1.02	0.43	-0.52	-0.91	1.36	1.34
Q8BMF4	DLAT	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochond	1.0	0.0	0.3	100.0	0.0	32.9	4.3	3.28E-02	100.00	1.11	100.00	2.00	0.47	1.01	0.42	2.00	0.05
Q8BPM0	DAAM1	Disheveled-associated activator of morphogenesis 1 OS=Mus musculus GN=Daam1 PE=1 SV=4 - [DAAM1_MO	1.6	0.0	0.3	100.0	0.0	16.5	4.5	3.01E-02	100.00	1.80	100.00	2.00	1.33	1.43	1.29	2.00	0.04
Q148B1	CYP2C65	Cytochrome P450, family 2, subfamily c, polypeptide 65 OS=Mus musculus GN=Cyp2c65 PE=1 SV=1 - [Q148B	1.0	0.1	0.0	100.0	13.4	0.0	5.1	2.08E-02	2.01	100.00	-100.00	1.53	0.50	2.00	0.51	-2.00	-0.01
G5E850	CYB5A	Cytochrome b-5, isoform CRA_a OS=Mus musculus GN=Cyb5a PE=1 SV=1 - [G5E850_MOUSE]	3.4	2.7	3.3	100.0	80.1	99.5	5.0	2.18E-02	0.22		0.22	0.22	2.03			0.22	1.96
Q65CL1	CTNNA3	Catenin alpha-3 OS=Mus musculus GN=Ctnna3 PE=1 SV=2 - [CTNA3_MOUSE]	2.0	4.7	3.9	42.3	100.0	82.4	11.1	1.08E-03	-0.86	-0.67	-0.19	-0.81	-9.03	-0.64	-5.51		
P97315	CSRP1	Cysteine and glycine-rich protein 1 OS=Mus musculus GN=Csrp1 PE=1 SV=3 - [CSRP1_MOUSE]	5.7	2.6	4.6	100.0	45.8	80.4	23.3	2.48E-05	0.78	0.22	0.56	0.74	12.73	0.22	5.69	0.55	7.04
P41241	CSK	Tyrosine-protein kinase CSK OS=Mus musculus GN=Csk PE=1 SV=2 - [CSK_MOUSE]	2.5	0.5	0.7	100.0	19.0	28.7	12.2	7.14E-04	1.66	1.25	0.42	1.36	3.11	1.11	2.96	0.41	0.15
Q8CJ40	CROCC	Rootletin OS=Mus musculus GN=Crocc PE=1 SV=2 - [CROCC_MOUSE]	3.7	2.2	3.2	100.0	59.0	87.1	6.1	1.15E-02	0.53		0.39	0.52	4.43			0.38	2.79
O89053	CORO1A	Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5 - [COR1A_MOUSE]	20.7	12.9	16.6	100.0	62.3	80.0	6.8	7.80E-03	0.47	0.22	0.25	0.47	131.48	0.22	77.24	0.25	54.24
Q9D1A2	CNDP2	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1 - [CNDP2_MOUSE]	6.6	1.2	2.7	100.0	17.4	40.7	12.9	5.42E-04	1.75	0.90	0.85	1.41	21.41	0.84	18.42	0.80	2.99
Q9DBP5	CMPK1	UMP-CMP kinase OS=Mus musculus GN=Cmpk1 PE=1 SV=1 - [KCY_MOUSE]	2.6	0.9	1.1	100.0	35.8	43.6	4.8	2.44E-02	1.03	0.83	0.20	0.95	2.94	0.79	2.74	0.20	0.21
Q68FD5	CLTC	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3 - [CLH1_MOUSE]	16.0	11.2	10.9	100.0	69.9	68.0	9.2	2.44E-03	0.36	0.39		0.35	65.67	0.38	69.04		
Q9QYB1	CLIC4	Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3 - [CLIC4_MOUSE]	3.0	1.2	1.5	100.0	41.5	48.7	5.3	1.84E-02	0.88	0.72	0.16	0.83	3.74	0.69	3.45		
Q61735	CD47	Leukocyte surface antigen CD47 OS=Mus musculus GN=Cd47 PE=1 SV=2 - [CD47_MOUSE]	3.3	1.4	2.4	100.0	42.8	70.6	5.1	2.02E-02	0.85	0.35	0.50	0.80	4.54	0.34	2.79	0.49	1.75
P80316	CCT5	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1 - [TCPE_MOUSE]	4.3	2.3	3.3	100.0	53.6	76.9	5.2	1.87E-02	0.62	0.26	0.36	0.60	6.69	0.26	3.84	0.36	2.85
G5E839	CCT4	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=1 - [G5E839_MOUSE]	8.3	5.6	5.9	100.0	68.1	71.7	6.0	1.21E-02	0.38	0.33		0.38	18.28	0.33	16.55		
P24270	CAT	Catalase OS=Mus musculus GN=Cat PE=1 SV=4 - [CATA_MOUSE]	1.8	4.8	5.3	33.4	89.3	100.0	5.1	2.05E-02	-0.98	-1.10		-0.91	-9.78	-1.00	-12.68		
P47754	CAPZA2	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3 - [CAZA2_MOUSE]	6.1	3.2	4.1	100.0	53.3	67.5	7.2	6.29E-03	0.63	0.39	0.24	0.61	13.17	0.39	10.02	0.23	3.15
P40124	CAP1	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4 - [CAP1_MOUSE]	51.4	39.4	43.4	100.0	76.6	84.3	4.8	2.44E-02	0.27	0.17		0.27	547.55				
P35564	CANX	Calnexin OS=Mus musculus GN=Canx PE=1 SV=1 - [CALX_MOUSE]	14.5	8.2	10.7	100.0	56.9	74.2	12.7	5.83E-04	0.56	0.30	0.26	0.55	70.72	0.30	47.08	0.26	23.65
Q8VCQ8	CALD1	Caldesmon 1 OS=Mus musculus GN=Cald1 PE=1 SV=1 - [Q8VCQ8_MOUSE]	10.1	5.4	7.0	100.0	52.7	69.0	8.4	3.65E-03	0.64	0.37	0.27	0.62	37.17	0.37	26.94	0.27	10.22
P00920	CA2	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4 - [CAH2_MOUSE]	13.4	27.5	22.0	49.0	100.0	80.2	14.1	3.63E-04	-0.71	-0.49	-0.22	-0.69	-286.80	-0.48	-152.51	-0.22	-134.29
P06683	C9	Complement component C9 OS=Mus musculus GN=C9 PE=1 SV=2 - [CO9_MOUSE]	2.8	0.0	2.6	100.0	0.0	91.4	7.6	5.29E-03	100.00		100.00	2.00	3.95			2.00	3.30
Q9DAC2	C8G	Complement component 8, gamma subunit, isoform CRA_b OS=Mus musculus GN=C8g PE=1 SV=1 - [Q9DAC2	1.0	0.0	0.5	100.0	0.0	51.8	3.9	4.37E-02	100.00	0.66	100.00	2.00	0.47	0.63	0.34	2.00	0.13
P15327	BPGM	Bisphosphoglycerate mutase OS=Mus musculus GN=Bpgm PE=1 SV=2 - [PMGE_MOUSE]	0.5	2.8	2.2	16.8	100.0	78.2	6.5	9.17E-03	-1.78	-1.54	-0.25	-1.42	-3.72	-1.29	-2.23	-0.24	-1.49
Q923D2	BLVRB	Flavin reductase (NADPH) OS=Mus musculus GN=Blvrb PE=1 SV=3 - [BLVRB_MOUSE]	3.4	11.3	7.9	30.1	100.0	69.4	15.2	2.43E-04	-1.20	-0.83	-0.37	-1.07	-58.23	-0.79	-25.00	-0.36	-33.22
D3Z6Q9	BIN2	Bridging integrator 2 OS=Mus musculus GN=Bin2 PE=1 SV=1 - [BIN2_MOUSE]	21.9	17.5	19.5	100.0	79.9	89.3	5.8	1.37E-02	0.22			0.22	86.30				
A2AUY4	BAZ2B	Protein Baz2b OS=Mus musculus GN=Baz2b PE=1 SV=1 - [A2AUY4_MOUSE]	0.9	0.0	0.4	100.0	0.0	44.6	6.2	1.10E-02	100.00	0.81	100.00	2.00	0.38	0.77	0.30	2.00	0.08
P56480	ATP5B	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2 - [ATPB_MOUSE]	40.1	31.8	34.1	100.0	79.3	84.9	4.3	3.29E-02	0.23	0.16		0.23	298.78				
Q03265	ATP5A1	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 - [ATPA_MOUSE]	23.3	16.3	19.4	100.0	69.8	83.1	18.2	9.65E-05	0.36	0.19	0.17	0.36	139.44				
B1ATS5	ATP2A3	Calcium-transporting ATPase OS=Mus musculus GN=Atp2a3 PE=1 SV=1 - [B1ATS5_MOUSE]	22.9	15.7	20.8	100.0	68.5	91.1	4.2	3.65E-02	0.38		0.28	0.37	138.89			0.28	94.18
O55143	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2 - [AT2A2_M	6.9	3.1	4.5	100.0	45.0	66.1	6.5	9.29E-03	0.80	0.41	0.38	0.76	18.72	0.41	13.22	0.38	5.49
E9PYT3	ATL3	Atlastin-3 OS=Mus musculus GN=Atl3 PE=1 SV=1 - [E9PYT3_MOUSE]	1.6	0.3	0.6	100.0	20.0	37.6	5.0	2.21E-02	1.61	0.98	0.63	1.33	1.21	0.91	1.08	0.61	0.13
A0A0N4SVB8	ARL8B	ADP-ribosylation factor-like protein 8B OS=Mus musculus GN=Arl8b PE=1 SV=1 - [A0A0N4SVB8_MOUSE]	0.8	0.3	0.0	100.0	34.5	0.0	4.6	2.78E-02	1.07	100.00	-100.00	0.97	0.27	2.00	0.31	-2.00	-0.04
Q8K0Q5	ARHGAP18	Rho GTPase-activating protein 18 OS=Mus musculus GN=Arhgap18 PE=1 SV=1 - [RHG18_MOUSE]	2.6	0.8	1.4	100.0	31.2	51.0	9.5	2.16E-03	1.17	0.67	0.49	1.05	3.16	0.65	2.59	0.48	0.57
Q5FWK3	ARHGAP1	Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1 - [RHG01_MOUSE]	3.8	1.1	1.0	100.0	27.5	25.1	5.3	1.85E-02	1.29	1.38		1.14	6.76	1.20	6.85		
A0A0R4J107	APEH	Acylamino-acid-releasing enzyme (Fragment) OS=Mus musculus GN=Apeh PE=1 SV=1 - [A0A0R4J107_MOUSI	0.5	2.2	1.1	21.7	100.0	48.7	5.2	1.96E-02	-1.53	-0.81	-0.72	-1.29	-2.28	-0.77	-0.46	-0.69	-1.82
P35585	AP1M1	AP-1 complex subunit mu-1 OS=Mus musculus GN=Ap1m1 PE=1 SV=3 - [AP1M1_MOUSE]	0.8	0.0	0.0	100.0	0.0	0.0	8.2	3.97E-03	100.00	100.00		2.00	0.31	2.00	0.31		
Q5SVG5	AP1B1	AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=1 - [Q5SVG5_MOUSE]	2.8	0.4	0.9	100.0	16.1	33.4	5.9	1.26E-02	1.83	1.10	0.73	1.45	3.77	1.00	3.44	0.70	0.33
P48036	ANXA5	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1 - [ANXA5_MOUSE]	9.9	3.6	7.4	100.0	36.7	75.0	6.4	9.77E-03	1.00	0.29	0.72	0.93	42.65	0.29	21.54	0.69	21.11
G5E8J2	ANK1	Ankyrin 1, erythroid OS=Mus musculus GN=Ank1 PE=1 SV=1 - [G5E8J2_MOUSE]	0.1	6.8	2.8	2.1	100.0	42.1	6.1	1.17E-02	-3.85	-2.99	-0.87	-1.92	-22.88	-1.81	-4.04	-0.82	-18.84
P39655	ALOX12	Arachidonate 12-lipoxygenase, 12S-type OS=Mus musculus GN=Alox12 PE=1 SV=4 - [LOX12_MOUSE]	44.6	33.8	38.0	100.0	75.9	85.2	11.2	1.07E-03	0.28	0.16		0.27	420.28				
P05064	ALDOA	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2 - [ALDOA_MOUSE]	20.7	18.4	17.0	100.0	88.9	82.0	4.9	2.30E-02		0.20				0.20	70.36		
P47738	ALDH2	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 - [ALDH2_MOUSE]	41.4	25.9	33.1	100.0	62.5	79.9	64.9	4.11E-08	0.47	0.22	0.24	0.46	522.92	0.22	310.60	0.24	212.32
P24549	ALDH1A1	Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 - [AL1A1_MOUSE]	0.0	0.0	0.9	0.0	0.0	100.0	4.3	3.36E-02		-100.00	100.00			-2.00	-0.38	2.00	0.38
P45376	AKR1B1	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3 - [ALDR_MOUSE]	2.0	1.0	1.7	100.0	48.3	86.0	3.7	4.97E-02	0.73	0.15	0.58	0.70	1.56			0.56	1.03
Q9QYC0	ADD1	Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2 - [ADDA_MOUSE]	4.6	1.8	2.6	100.0	40.2	56.8	5.6	1.50E-02	0.91	0.57	0.35	0.85	8.77	0.55	7.09	0.34	1.68
P57780	ACTN4	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1 - [ACTN4_MOUSE]	65.9	41.4	51.8	100.0	62.8	78.7	23.8	2.22E-05	0.47	0.24	0.23	0.46	1314.78	0.24	826.61	0.22	488.16
A1BN54	ACTN1	Alpha actinin 1a OS=Mus musculus GN=Actn1 PE=1 SV=1 - [A1BN54_MOUSE]	88.7	56.8	71.4	100.0	64.0	80.5	13.6	4.33E-04	0.45	0.22	0.23	0.44	2321.03	0.22	1383.52	0.23	937.51
P68033	ACTC1	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1 - [ACTC_MOUSE]	94.9	77.0	83.1	100.0	81.2	87.6	7.8	4.83E-03	0.21			0.21	1534.88				
P60710	ACTB	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 - [ACTB_MOUSE]	183.9	156.0	163.0	100.0	84.8	88.6	5.9	1.26E-02	0.16			0.16	4735.56				
A0A0R4J083	ACADL	Long-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=1 SV=1 - [A0A0	1.0	0.2	0.2	100.0	18.0	18.3	4.7	2.64E-02	1.72	1.70		1.39	0.50	1.38	0.49		
H3BKL5	ACAA1A	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=1 SV=1 - [H3BKL5_MOUSE]	4.2	1.0	1.7	100.0	24.1	39.6	14.3	3.30E-04	1.42	0.93	0.50	1.22	8.30	0.86	7.43	0.49	0.87

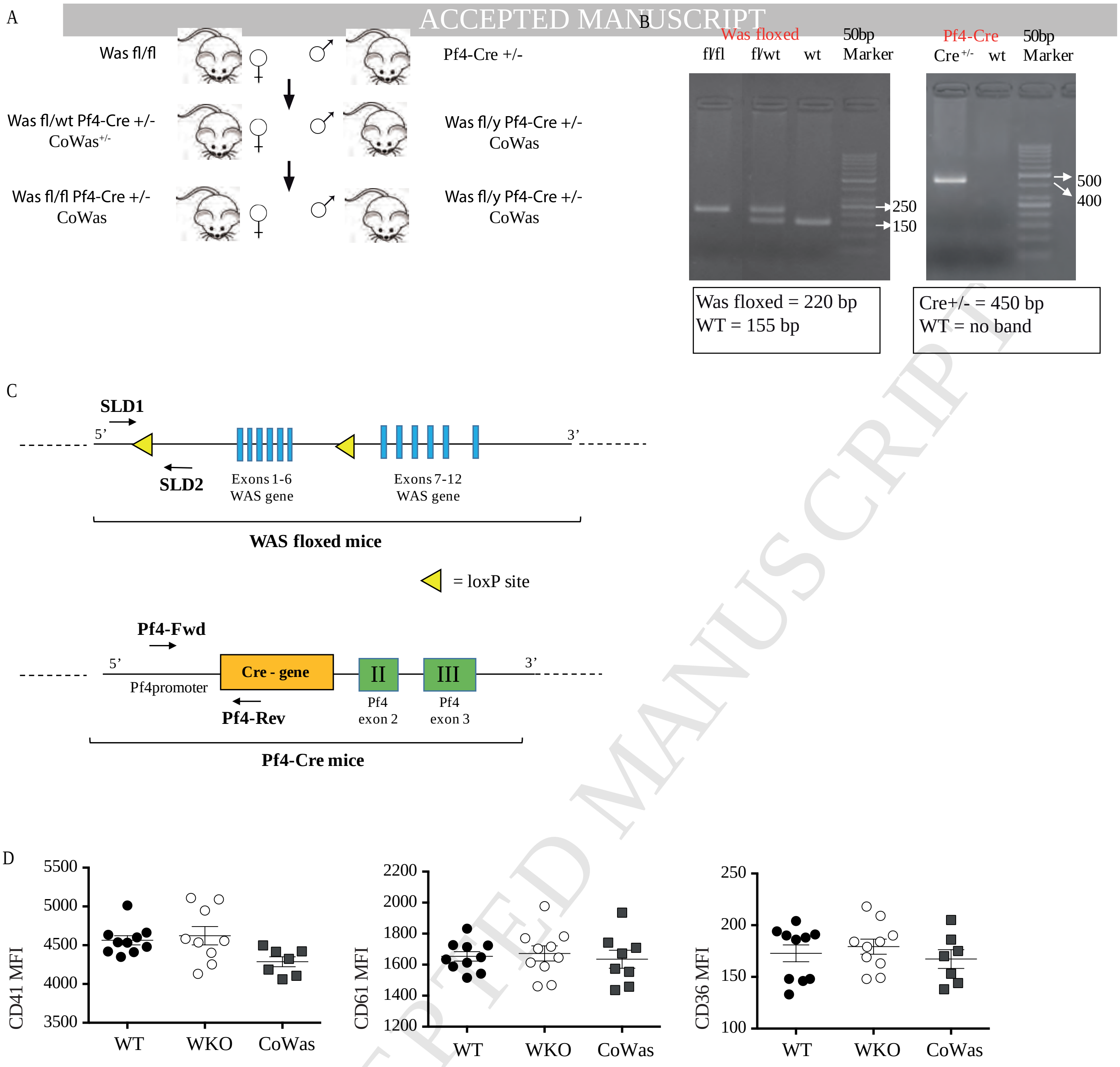
Supplemental Table 3: Clinical characteristic of WAS and XLT patients analysed

Patient ID	Age at analysis	Auto-antibodies or clinical characteristics	sCD40L (ng/ml)
WAS59	3y	PLT, Coombs	11,12
WAS2P	14y	cANCA	2,03
WAS3P	3y	PLT	1,84
XLT71	1y	ND	2,81
WAS13[§]	27y	-	0,48
WAS14[§]	2y	Colitis, Vasculitis	4,33
WAS1[§]	20y	-	0,39
WAS1N	13y	PR3, Arthritis, IgA Nephropathy	1,49
XLT40*	18y	-	2,23
XLT33*	8y	ANA, ANCA, ASMA	16,31
XLT37*	16y	ANA	1,53
WAS35*	8m	Coombs, ANCA	12,69
WAS3*	4m	ND	1,6
WAS25*	2y	PLT, TPO	8,62
WAS17*	4y	-	2,58
WAS9*	2y	ANA	11,92

ANA, anti-nuclear antibodies; ANCA, anti-neutrophil cytoplasmic antibodies; PLT, anti-PLT antibodies; TPO, anti- thyroid peroxidase antibodies; PR3, proteinase 3; ND, not done

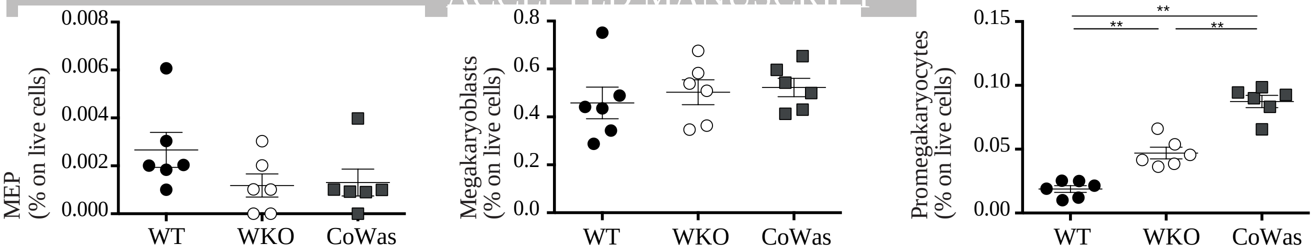
*Pt ID described in Crestani et al., *JACI*, 2015
[§] Pt ID described in Marangoni et al., *JEM*, 2007

Supplemental Fig 1: Establishment of CoWas colony



Supplemental Fig 2: Was-/- MKs show no defect in pro-PLT production

A



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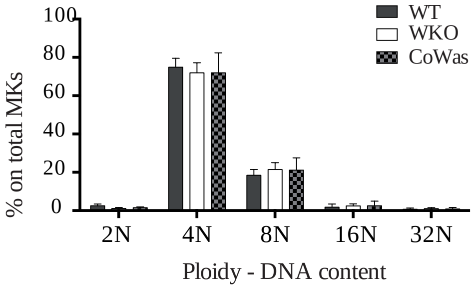
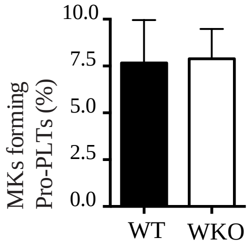
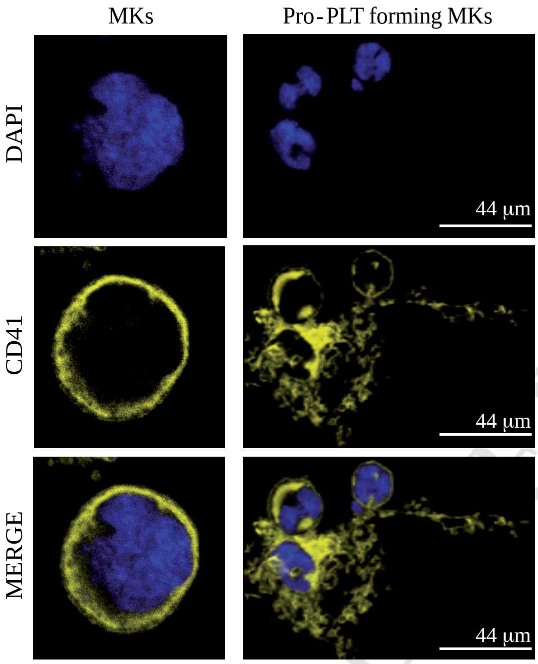


C



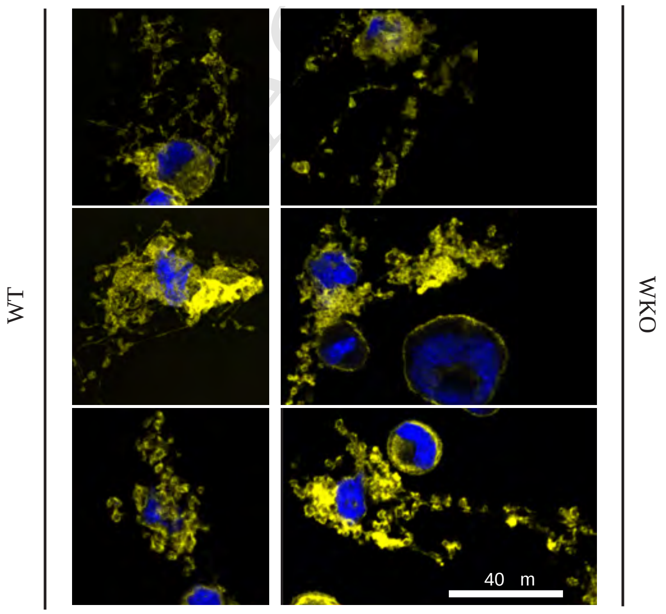
D

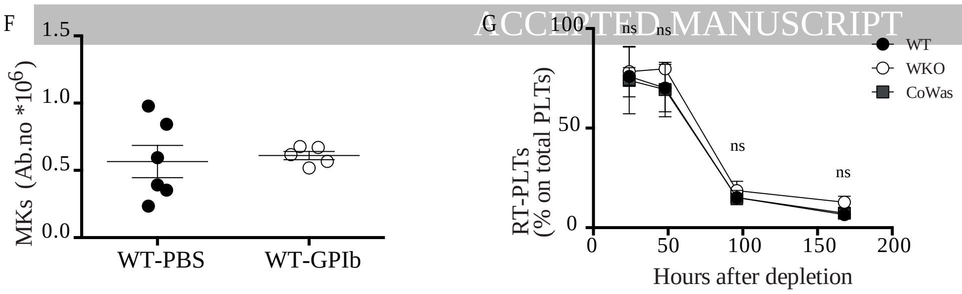


E

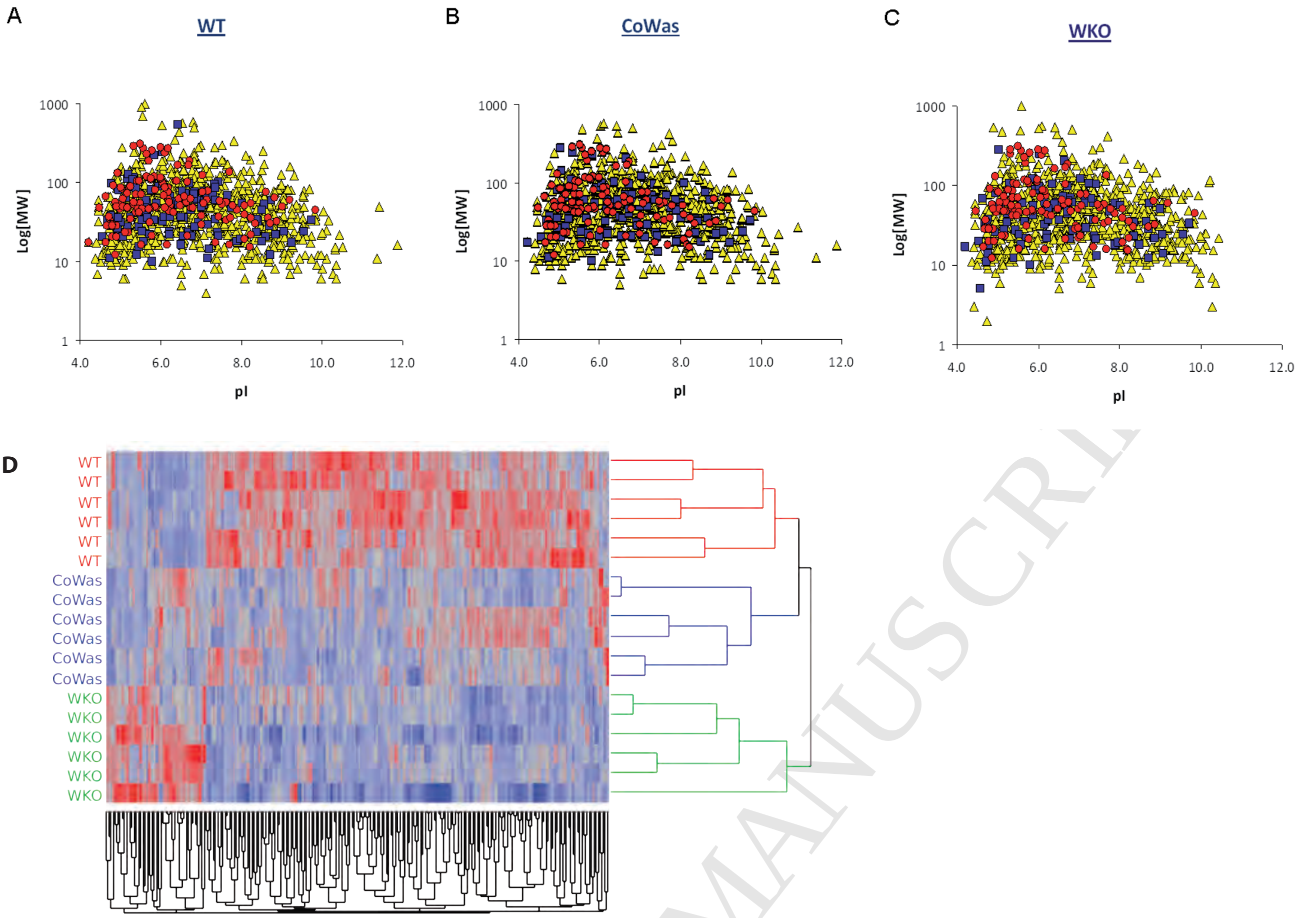
		MKs counted (Total no.)	Pro-PLT forming MKs (Ab.no.)	Pro-PLT forming MKs (% of Total)
Exp 1	**WT1**	287	26	9,1
	WT2	287	15	5,2
	WT3	242	20	8,3
	WKO1	343	44	12,8
	WKO2	354	36	10,2
	WKO3	388	28	7,2
Exp 2	**WT1**	302	46	15,2
	WT2	315	44	14,0
	WT3	302	34	11,3
	WKO1	299	33	11,0
	WKO2	311	34	10,9
	WKO3	459	13	2,8 *
Exp 3	**WT1**	358	11	3,1
	WT2	300	20	6,7 *
	WT3	369	48	13,0
	WKO1	300	19	6,3
	WKO2	318	23	7,2
	WKO3	326	17	5,2
Exp 4	**WT1**	311	14	4,5
	WT2	365	6	1,6
	WT3	541	4	0,7
	WKO1	311	19	6,1
	WKO2	407	13	3,2
	WKO3	321	11	3,4

Pro-PLT forming MKs




F
1.5
1.0
0.5
0.0
MKs (Ab.no *10^6)
WT-PBS
WT-GPIb
G
100
50
0
RT-PLTs
(% on total PLTs)
ns
ns
ns
ns
0
50
100
150
200
Hours after depletion
WT
WKO
CoWas

Supplemental Fig 3: PLTs from mutant mice show a different proteomic profile



Supplemental Fig 4: Total pathways identified by proteomic analysis