

Reduction of *Fmr1* mRNA Levels Rescues Pathological Features in Cortical Neurons in a Model of FXTAS

Malgorzata Drozd,^{1,4} Sébastien Delhaye,^{1,4} Thomas Maurin,^{1,4} Sara Castagnola,¹ Mauro Grossi,¹ Frédéric Brau,¹ Marielle Jarjat,¹ Rob Willemsen,² Maria Capovilla,¹ Renate K. Hukema,² Enzo Lalli,³ and Barbara Bardoni³

¹Université Côte d'Azur, CNRS, Institute of Molecular and Cellular Pharmacology, 06560 Valbonne Sophia Antipolis, France; ²Department of Clinical Genetics, Erasmus Medical Center, Rotterdam, the Netherlands; ³Université Côte d'Azur, INSERM, CNRS, Institute of Molecular and Cellular Pharmacology, 06560 Valbonne Sophia Antipolis, France

Fragile X-associated tremor ataxia syndrome (FXTAS) is a rare disorder associated to the presence of the fragile X premutation, a 55–200 CGG repeat expansion in the 5' UTR of the *FMRI* gene. Two main neurological phenotypes have been described in carriers of the CGG premutation: (1) neurodevelopmental disorders characterized by anxiety, attention deficit hyperactivity disorder (ADHD), social deficits, or autism spectrum disorder (ASD); and (2) after 50 years old, the FXTAS phenotype. This neurodegenerative disorder is characterized by ataxia and a form of parkinsonism. The molecular pathology of this disorder is characterized by the presence of elevated levels of *Fragile X Mental Retardation 1 (FMRI)* mRNA, presence of a repeat-associated non-AUG (RAN) translated peptide, and *FMRI* mRNA-containing nuclear inclusions. Whereas in the past FXTAS was mainly considered as a late-onset disorder, some phenotypes of patients and altered learning and memory behavior of a mouse model of FXTAS suggested that this disorder involves neurodevelopment. To better understand the physiopathological role of the increased levels of *Fmr1* mRNA during neuronal differentiation, we used a small interfering RNA (siRNA) approach to reduce the abundance of this mRNA in cultured cortical neurons from the FXTAS mouse model. Morphological alterations of neurons were rescued by this approach. This cellular phenotype is associated to differentially expressed proteins that we identified by mass spectrometry analysis. Interestingly, phenotype rescue is also associated to the rescue of the abundance of 29 proteins that are involved in various pathways, which represent putative targets for early therapeutic approaches.

INTRODUCTION

The *Fragile X Mental Retardation 1 (FMRI)* gene encodes the fragile X mental retardation protein (FMRP), an RNA binding protein whose functional absence causes fragile X syndrome (FXS), the most common form of intellectual disability (ID) and autism spectrum disorder (ASD). The mutation in the *FMRI* gene causing FXS is the presence of a repeated sequence encompassing >200 CGG repeats in its 5' UTR. Hypermethylation of this sequence determines

gene promoter inactivation, causing the silencing of the *FMRI* gene.¹ Although 6–54 CGG repeats in the 5' UTR of *FMRI* is a polymorphism in normal individuals, a repeat sequence of variable length (55–200 CGG repeats) represents the premutation¹ that can cause fragile X tremor ataxia syndrome (FXTAS) in patients over 50 years of age.^{2,3} This is an adult-onset progressive neurodegenerative disorder leading to a variable combination of ataxia, essential tremor, gait imbalance, parkinsonism, peripheral neuropathy, anxiety, and cognitive decline, occurring predominantly in older men carrying the premutation. It is known that people carrying the premutation have a reduced hippocampal volume that correlates with impaired performance in standardized tests of memory.³ At the cellular level, this disorder is characterized by the presence of eosinophilic, ubiquitin-positive nuclear inclusions, which have been observed throughout the brain, with a high percentage being located in the hippocampus of patients, as well as in the animal model of the disease.^{3,4} Inclusions are negative for tau isoforms, alpha-synuclein, or polyglutamine peptides, reflecting a new class of inclusion disorder.³ At the molecular level, FXTAS is characterized by an elevated (2- to 8-fold) level of *FMRI* mRNA, whereas the level of FMRP is normal or slightly reduced in patients, as well in the CGG-KI mouse model.^{2–4} The *FMRI* mRNA is a component of nuclear inclusions³. The product of repeat-associated non-ATG (RAN) translation of the *FMRI* mRNA was also reported to be involved in the generation of inclusions when overexpressed.^{5,6} Although FXTAS is a late-onset disorder, it is also characterized by a set of developmental hallmarks, such as self-reported memory problems, autism-related traits, attention deficit hyperactivity disorder (ADHD), executive functioning, and psychopathology.⁷ Knockin (KI) mouse models have been generated displaying both neurodegenerative and neurodevelopmental

Received 18 July 2019; accepted 8 September 2019;
<https://doi.org/10.1016/j.omtn.2019.09.018>.

⁴These authors contributed equally to this work.

Correspondence: Barbara Bardoni, Université Côte d'Azur, INSERM, CNRS, Institute of Molecular and Cellular Pharmacology, 06560 Valbonne Sophia Antipolis, France.

E-mail: bardoni@ipmc.cnrs.fr



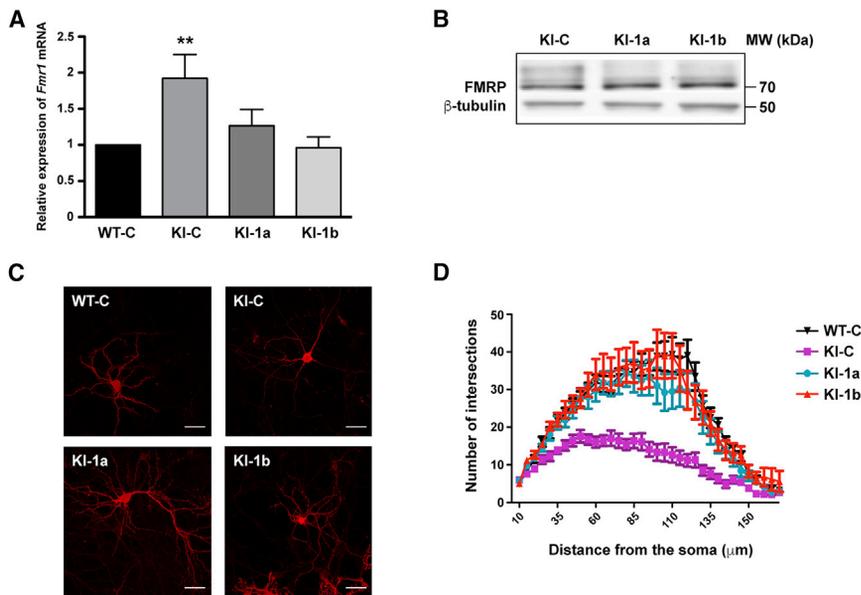


Figure 1. Role of *Fmr1* mRNA Levels in Dendritic Arborization

(A) RNA was prepared from cultured WT and knockin-CGG (KI-CGG) neurons transduced with the control (C) shRNA or two different shRNAs directed against *Fmr1* mRNA (1a and 1b). The level of *Fmr1* mRNA was measured by qRT-PCR using specific primers. Ten different experiments have been carried out for each transduced lentivirus, and a reduction of *Fmr1* levels was observed by using both shRNAs. Results are presented as mean \pm SEM; one-way ANOVA with Tukey's multiple comparisons test, ** $p < 0.01$. (B) Representative western blot analysis of cell cultures of cortical neurons transduced with C, 1a, or 1b shRNAs. FMRP (70 kDa) and β -tubulin (50 kDa) were revealed with specific antibodies. (C) Image of WT and KI-CGG cortical neurons transduced with lentiviruses expressing C, 1a, or 1b shRNAs. Scale bars: 20 μ m. (D) Sholl analysis of WT and KI cultured mouse cortical neurons transduced with C or 1a or 1b shRNAs. Reduced arborization of KI-CGG neurons is rescued by *Fmr1* knockdown. Two-way ANOVA was used to compare KI-C and 1a treatments: genotype F(2; 1,527) = 227.9, $p < 0.0001$;

treatment (34; 1,527) = 34.12, $p < 0.0001$; interaction F(68; 1,527) = 3.067, $p < 0.0001$; two-way ANOVA was used to compare KI-C and 1b treatments: genotype F(2; 1,318) = 293.6, **** $p < 0.0001$; treatment F(34; 1,318) = 36.21, **** $p < 0.0001$; interaction F(68; 1,318) = 3,803, $p < 0.0001$.

phenotypes. It was reported that neuronal abnormalities and behavioral alterations in the animal model are present before the appearance of neuronal inclusions. Indeed, cultured hippocampal neurons obtained from a CGG-KI display shorter dendritic length and reduced dendritic complexity.^{4,8-10} In CGG-KI mice, cortical migration is also affected. Indeed, at embryonic day (E) 17, a 2-fold higher percentage of migrating neurons was detected to be oriented toward the ventricle in wild-type (WT) compared with CGG-KI mice.¹¹ All of these abnormalities were observed in inclusion-free cells, because CGG-KI mice display ubiquitin-positive intranuclear inclusions in neurons and astrocytes of the hippocampus and cerebellar internal cell layer starting at 12 weeks of age.^{4,8,9,11} Here we investigated the impact of normalization of *Fmr1* mRNA levels on the morphology and proteomics of cortical cultured neurons obtained from a FXTAS mouse model (CGG-KI)^{8,9} before the generation of nuclear inclusions. By this analysis we have obtained a deeper insight into the physiopathological role of *Fmr1* mRNA levels in FXTAS and identified putative targetable pathways for early treatments.

RESULTS

Hippocampal neurons were isolated from knockin-CGG (KI-CGG) E15.5 mice harboring the CGG premutated allele. It has been shown that these mice display abnormal cortical neuron migration patterns *in utero*.^{10,11} Furthermore, abnormal dendritic architecture and reduced cellular viability have been observed in hippocampal primary neurons of KI-CGG mice, where increased expression of *Fmr1* is already present even if nuclear inclusions are not detected.¹⁰ Indeed, nuclear inclusions appear first in the hippocampus of these mice at the age of 3 months, whereas the same hallmark appears later in the parietal neocortex.^{8,9} We decided to explore whether cultured cortical neurons obtained from these mice have an abnormal

morphology of dendrites and axons during development before the appearance of nuclear inclusions. We studied the dendritic arborization of wild-type (WT) and KI-CGG cortical neurons by Sholl analysis, as previously described,¹² and observed that KI-CGG neurons have a reduced arborization compared with controls (Figures S1A and S1B). To assess whether *Fmr1* mRNA levels impact the morphology of these cultured neurons, we produced lentiviruses expressing two different shRNAs selectively reducing the expression of *Fmr1* mRNA (sh-1a and sh-1b) and one shRNA control (sh-C),¹³ and we used them to transduce cortical cultured neurons obtained from WT and from KI-CGG mice. The infection was performed at 5 DIV (days *in vitro*), and RNA and proteins were prepared from these cultures at 20 DIV. As expected,^{4,13} *Fmr1* mRNA levels were elevated 2-fold in cultured KI cortical neurons compared with WT. sh-1a reduced *Fmr1* transcript levels by 30%, whereas sh-1b reduced them by 50%, (Figure 1A). FMRP levels are not changed in KI cultured neurons compared with WT,^{10,13} and as previously shown in patients.^{2,3} Similarly, the expression level of FMRP was not affected by *Fmr1* knockdown in KI neurons (Figure 1B), as we already observed by transfecting fibroblasts obtained from FXTAS patients with the same shRNAs.¹³ We then analyzed the arborization of WT and KI cortical neurons transduced with *Fmr1* shRNAs. We confirmed that KI neurons transduced with the lentivirus expressing the control shRNA (KI-C) are less arborized than WT neurons transduced with the same lentivirus (Figures 1C and 1D). However, KI neurons transduced with lentivirus expressing either sh-1a or sh-1b displayed a normal dendritic arborization (Figures 1C and 1D).

In 2 DIV neurons we measured the axon length, and we found that they are significantly shorter in *Fmr1*-KI neurons compared with

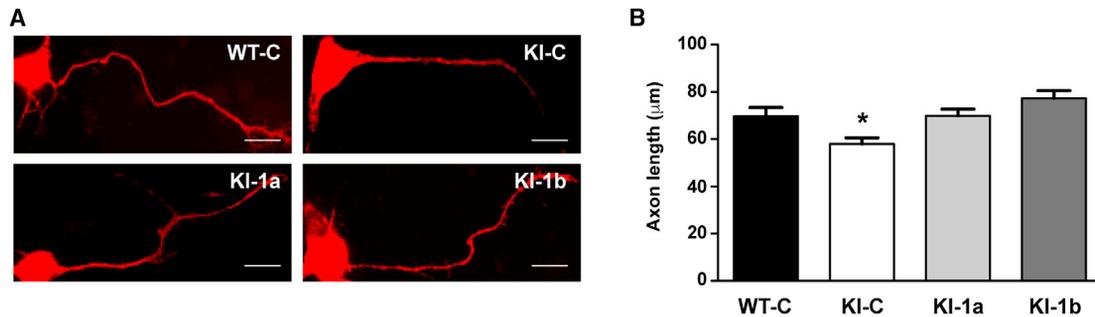


Figure 2. *Fmr1* mRNA Levels Are Associated to Axon Growth

(A) Representative pictures of 2 days *in vitro* cultured WT-C, KI-C, KI-1a, and KI-1b primary cortical neurons. Scale bars: 10 μm. (B) Histogram of axon length of WT and KI cultured neurons transfected with C, 1a, or 1b shRNAs. Results show mean axon length ± SEM of 150 randomly selected cells for each condition from three independent cultures. One-way ANOVA with Tukey's multiple comparisons test, * $p < 0.05$.

WT (Figure S2). We confirmed that KI-C neurons have shorter axons than WT-C, but the length of these axons was normalized in KI-1a and KI-1b neurons (Figures 2A and 2B).

We then focused on dendritic spine abnormalities. The absence of FMRP causes a peculiar morphology of dendritic spines that has been described in FXS patients and in the mouse model, where it is particularly evident in young animals.^{14,15} Conversely, the study of dendritic spines in the brain of FXTAS patients was never reported, and in *Fmr1* KI mice it was studied only in hippocampi and in the visual cortex from adult animals, displaying an increased length of spines.^{4,16} Here we studied the morphology of dendritic spines of 20 DIV cultured cortical neurons. KI-C spines are longer, denser, and larger than controls. All of these hallmarks are rescued in KI-1a and KI-1b neurons (Figures 3A–3D), indicating that the elevated level of *Fmr1* mRNA causes a set of morphological alterations in KI-CGG neurons. However, the percentage of the different types of spines (thin, stubby, and mushroom) is not significantly different in the two genotypes (Figures 3E–3G).

To get deeper insight into the molecular pathology of FXTAS cultured neurons, we performed a proteomic analysis of neurons that have been transduced with control shRNA or with the shRNAs targeting the *Fmr1* mRNA. Protein extracts of three replicates for each condition were analyzed by nano-liquid chromatography-tandem mass spectrometry (nano-LC-MS/MS) after tryptic digestion.¹⁷ A total of 487 proteins were identified (Table S1), among which 251 have a ratio >2 (upregulation) or <0.5 (downregulation) for at least one of the three comparisons (WT-C versus KI-C, WT-C versus KI-1a, and WT-C versus KI-1b) with a p value <0.10. Interestingly, the abundance of 29 differentially expressed proteins is rescued after reduction of *Fmr1* mRNA by using both specific shRNAs (Table 1). Gene Ontology analysis of these proteins reveals a significant enrichment of proteins involved in different biochemical pathways, among which are GTP binding and RNA binding proteins (Figure 4; Table S2).

DISCUSSION

Two main neurological phenotypes have been described in carriers of the CGG premutation: those exhibiting neurodevelopmental disorders characterized by anxiety, ADHD, social deficits, or ASD, and after 50 years old, FXTAS, a neurodegenerative disorder.³ For some time, nuclear inclusions have been considered as the cause of neurodegeneration, whereas more recent studies suggest that nuclear inclusions may represent a mechanism used by neurons to protect themselves from toxic events.^{4,18–20} So far, two other main physiopathological elements are known to underpin the FXTAS phenotype: the elevated abundance of *FMR1* mRNA² and the presence of a RAN polypeptide.^{5,6} We considered that it is crucial to unravel the role of each element in the molecular pathology of FXTAS to understand the progression of the disorder and its role in pathophysiology. Indeed, it is interesting to remind that neuronal abnormal dendritic morphology (e.g., reduced length and number of dendrites that display longer spines) has been observed in FXTAS neurons at a time of development when nuclear inclusions are not detectable.^{3,4,8–11} These findings suggest that some developmental abnormalities may contribute to the late manifestation of neurodegenerative process and/or that the disease appears, with subtle phenotypes, earlier than predicted up to date. So far, no specific treatment is available for FXTAS patients. A therapy based on allopregnanolone was shown to improve cognitive functioning in patients with FXTAS and to partially alleviate some aspects of neurodegeneration,²¹ opening the possibility to search for new targetable pathways in young patients. In this study, we used a murine model of FXTAS to investigate the impact that the reduced level of *Fmr1* mRNA, but not of its encoded protein, has on the morphological and molecular phenotypes of FXTAS cultured neurons. Certainly, by reducing *Fmr1* mRNA levels, we are also supposed to reduce RAN levels, which is possibly involved in the pathophysiology of FXTAS.⁶ However, that peptide was never detected at endogenous levels in neurons so far.^{3,22}

First, we defined phenotypes that were never considered before in cultured cortical neurons obtained from the FXTAS mouse

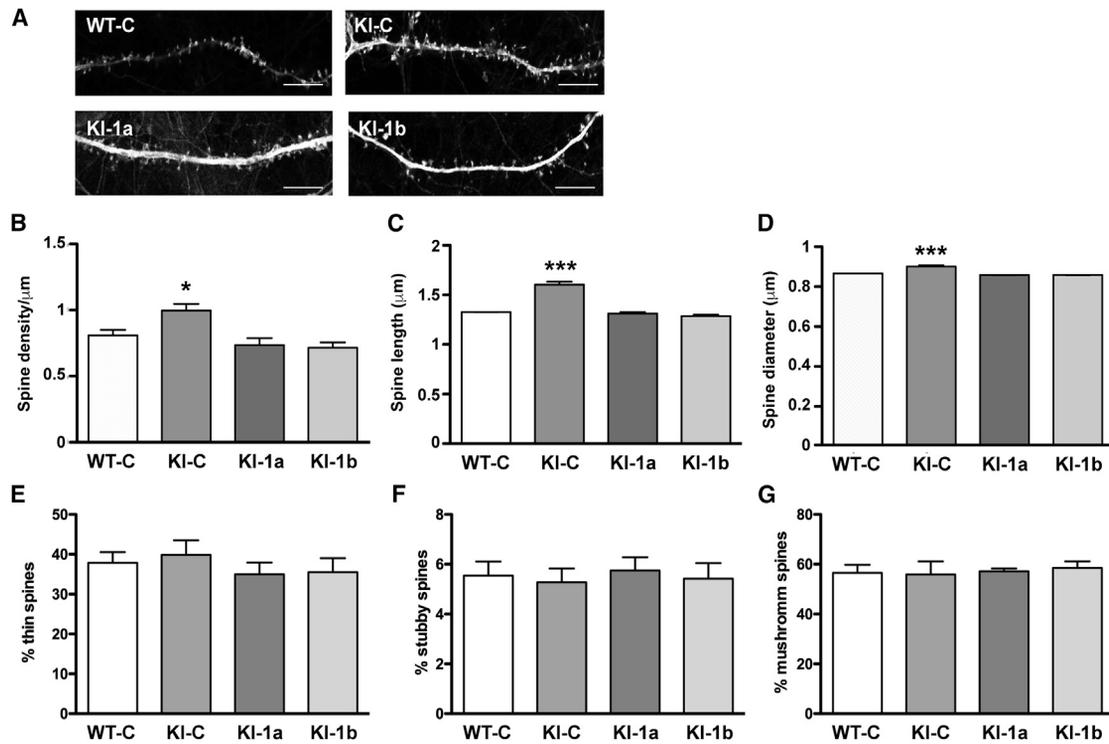


Figure 3. Reduction of *Fmr1* mRNA Levels Normalizes Dendritic Spine Morphology in KI Cortical Neurons

(A) Representative high-resolution confocal images showing dendritic spine morphology were assessed using NeuronStudio software and compared with the measurement obtained from control transduced neurons. Scale bars: 2 μm . All histograms present mean \pm SEM values. Statistical significance was assessed by one-way ANOVA with Tukey's multiple comparisons test. (B–G) Histograms showing the mean \pm SEM values of (B) protrusion frequency in the various cultures, * $p < 0.05$; (C) spine length, *** $p < 0.001$; (D) spine head size, *** $p < 0.001$; (E) percentage of thin spines; (F) percentage of stubby spines; and (G) percentage of mushroom spines.

model: axon length and dendrite morphology. All of these new phenotypes are detected in cells not yet displaying nuclear inclusions, which are known to first appear in hippocampal neurons of 12-week-old KI-CGG mice.⁹ Interestingly, these animals have mild learning and memory deficits,^{4,9} and this behavioral phenotype is consistent with the phenotype that we observed in cultured cortical neurons. Importantly, we confirm that these phenotypes are associated with the levels of *Fmr1* mRNA because they are rescued after the expression of shRNAs specifically targeting this mRNA. We can deduce that an elevated abundance of *Fmr1* mRNA may interfere with normal RNA metabolism. We can predict that the overexpression of *Fmr1* mRNA may also likely interfere with the normal activity of RNA binding proteins or microRNAs (miRNAs) in neuronal soma, and at the synapse by competing for their binding at specific sites or at miRNA response elements (MREs).¹³ All of these considerations suggest that *Fmr1* mRNA metabolism can be regulated by a large number of RNA binding proteins and can be co-regulated with a plethora of other RNAs. For this reason, as the second step of our study, we performed a differential proteomic analysis of neurons expressing control or *Fmr1*-specific shRNAs, and we observed that a set of proteins, whose expression is deregulated in KI-CGG neurons, is normalized after treatment. Consistently, several proteins rescued by *Fmr1*-specific shRNAs are RNA binding proteins (e.g., Tial1,

Hnrnp11, and ROAA). In addition, some proteins whose levels were rescued by the reduction of *Fmr1* mRNA abundance are involved in the regulation of actin cytoskeleton dynamics, which is known to modulate the morphology of neurons and, in particular, of dendritic spines. Defective synaptic actin regulation seems to be involved in different neurodevelopmental and psychiatric disorders.²³ Interestingly, we have shown here that in KI-CGG neurons, dendritic spines are more numerous, and they appear overall longer and with a larger head, but the percentage of the various types of spines is unchanged. These results are consistent with a previous study displaying longer, but not immature, spines in the CGG-KI visual cortex.¹⁶ In addition, our findings suggest that, at least at 20 DIV, the elevated levels of *Fmr1* mRNA do not interfere with the spine maturation process but cause subtle abnormalities of their features, which may have an impact on synaptic transmission. Other rescued proteins belong to the Rab-GTPase family, a sub-class of the RAS superfamily, which spatially and temporally orchestrates specific vesicular trafficking that is critical for synaptic function in neurons in brain developmental disorders,²⁴ as well as in Parkinson's disease.²⁵ Along the same direction, another interesting protein is CLIP2, a cytoplasmic linker factor that is considered as a mediator between organelles and the cytoskeleton.²⁶ Consistent with their role in neurons, mutants of this class of proteins are associated with impaired cognitive

Table 1. Proteins Differentially Expressed in the Different Samples Studied

Name	UniProt Accession Number	WT-C	KI-C	WT-C/ Ki-C	Log (Fold Change)	p Value	KI-1a	WT-C/ Ki-1a	Log (Fold Change)	p Value	KI-1b	WT-C/ KI-1b	Log (Fold Change)	p Value
sp O89023 TPP1_MOUSE	O89023	0.00	0.93	0.00	NA	0.00001	0.00	NA	NA	1.00000	0.00	NA	NA	1.00000
sp P05132 KAPCA_MOUSE	P05132	5.16	10.17	0.51	-0.29	0.00132	5.83	0.89	-0.05	0.81905	4.79	1.08	0.03	0.81905
sp P21126 UBL4A_MOUSE	P21126	0.33	1.53	0.21	-0.67	0.04762	0.66	0.49	-0.31	0.51266	0.38	0.85	-0.07	0.51266
sp P21278 GNA11_MOUSE	P21278	7.43	4.06	1.83	0.26	0.03470	6.49	1.14	0.06	0.69780	7.98	0.93	-0.03	0.69780
sp P24369 PPIB_MOUSE	P24369	8.43	12.31	0.68	-0.16	0.03540	6.73	1.25	0.10	0.68137	9.91	0.85	-0.07	0.68137
sp P30677 GNA14_MOUSE	P30677	2.57	0.93	2.77	0.44	0.04928	2.40	1.07	0.03	0.88974	3.24	0.79	-0.10	0.88974
sp P35283 RAB12_MOUSE	P35283	5.82	3.08	1.89	0.28	0.00979	5.87	0.99	0.00	0.95886	5.51	1.06	0.02	0.95886
sp P52912 TIA1_MOUSE	P52912	0.00	0.93	0.00	NA	0.00001	0.00	NA	NA	1.00000	0.32	0.00	NA	1.00000
sp P56371 RAB4A_MOUSE	P56371	5.81	3.08	1.89	0.28	0.00560	5.87	0.99	0.00	0.94159	5.19	1.12	0.05	0.94159
sp Q80TS3 AGRL3_MOUSE	Q80TS3	0.97	2.16	0.45	-0.35	0.01678	0.37	2.64	0.42	0.17665	0.38	2.53	0.40	0.17665
sp Q8BGH2 SAM50_MOUSE	Q8BGH2	2.28	0.29	7.74	0.89	0.01329	2.07	1.10	0.04	0.79778	2.13	1.07	0.03	0.79778
sp Q8BHC4 DCAKD_MOUSE	Q8BHC4	0.00	0.93	0.00	NA	0.00001	0.31	0.00	NA	0.37390	0.00	NA	NA	0.37390
sp Q8CHT0 AL4A1_MOUSE	Q8CHT0	2.94	0.63	4.64	0.67	0.02926	2.43	1.21	0.08	0.54007	1.95	1.51	0.18	0.54007
sp Q91ZR1 RAB4B_MOUSE	Q91ZR1	5.82	3.68	1.58	0.20	0.02923	5.51	1.05	0.02	0.71442	5.19	1.12	0.05	0.71442
sp Q921F4 HNRL1_MOUSE	Q921F4	0.97	0.00	∞	NA	0.00000	0.98	0.99	0.00	0.98875	0.78	1.24	0.09	0.98875
sp Q922D8 C1TC_MOUSE	Q922D8	1.28	2.78	0.46	-0.34	0.00809	0.92	1.40	0.15	0.72353	1.29	1.00	0.00	0.72353
sp Q99020 ROAA_MOUSE	Q99020	1.63	0.31	5.34	0.73	0.04589	1.69	0.97	-0.02	0.90543	2.19	0.74	-0.13	0.90543
sp Q99PU5 ACBG1_MOUSE	Q99PU5	2.92	1.55	1.88	0.27	0.01399	2.73	1.07	0.03	0.62466	2.61	1.12	0.05	0.62466
sp Q9CPY7 AMPL_MOUSE	Q9CPY7	1.61	3.38	0.48	-0.32	0.00921	2.00	0.81	-0.09	0.53465	1.43	1.13	0.05	0.53465
sp Q9CW03 SMC3_MOUSE	Q9CW03	0.33	1.53	0.21	-0.67	0.04762	0.71	0.46	-0.34	0.64890	0.38	0.85	-0.07	0.64890
sp Q9CYR6 AGM1_MOUSE	Q9CYR6	0.33	1.86	0.18	-0.75	0.01091	0.00	∞	∞	0.37390	0.32	1.04	0.02	0.37390
sp Q9DCN2 NB5R3_MOUSE	Q9DCN2	4.53	6.79	0.67	-0.18	0.00385	4.79	0.95	-0.02	0.62926	4.48	1.01	0.00	0.62926
sp Q9WTX2 PRKRA_MOUSE	Q9WTX2	0.33	1.53	0.21	-0.67	0.04762	0.00	∞	∞	0.37390	0.00	∞	∞	0.37390
sp Q9Z0H8 CLIP2_MOUSE	Q9Z0H8	4.51	8.09	0.56	-0.25	0.04003	4.68	0.96	-0.02	0.88427	5.62	0.80	-0.10	0.88427
tr A0A087WPM2 A0A087WPM2_MOUSE	A0A087WPM2	1.94	2.78	0.70	-0.16	0.00099	1.64	1.18	0.07	0.61624	1.12	1.73	0.24	0.61624
tr A0AUM9 A0AUM9_MOUSE	A0AUM9	0.00	0.93	0.00	NA	0.00001	0.00	NA	NA	1.00000	0.00	NA	NA	1.00000
tr D3YZ68 D3YZ68_MOUSE	D3YZ68	39.80	47.10	0.84	-0.07	0.03447	38.80	1.03	0.01	0.89853	36.50	1.09	0.04	0.89853
tr E9Q7C9 E9Q7C9_MOUSE	E9Q7C9	7.46	9.91	0.75	-0.12	0.03009	5.75	1.30	0.11	0.10120	7.97	0.94	-0.03	0.10120
tr S4R232 S4R232_MOUSE	S4R232	5.50	3.04	1.81	0.26	0.03279	5.50	1.00	0.00	0.99389	5.17	1.06	0.03	0.99389

NA, not applicable.

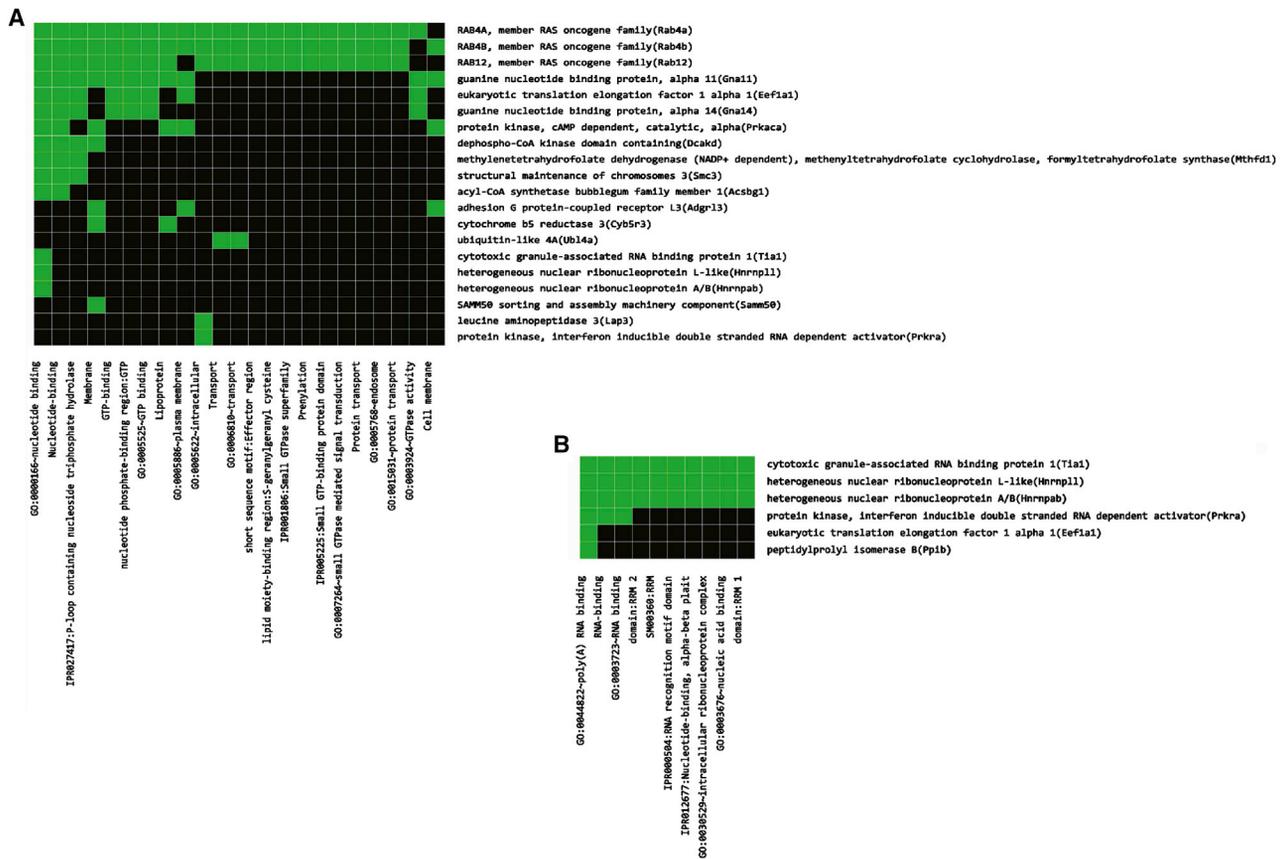


Figure 4. Gene Ontology Classification of Rescued Proteins in KI-CGG Neurons

(A and B) The DAVID Gene Ontology Functional Annotation Clustering tool⁴⁰ was used to show functional classification of rescued proteins in KI-CGG neurons involved in (A) nucleotide-GTP binding and (B) RNA binding.

functions.^{21,24,27} Importantly, we also found mitochondrial proteins (e.g., pyrroline-5-carboxylate dehydrogenase [Aldh4a1/P5CDH] and Samm50) that are deregulated in CGG-KI neurons, confirming the importance of mitochondria in the pathophysiology of FXTAS, as previously reported by independent studies.^{28,29} This result suggests that an altered mitochondrial function is probably involved in early phenotypes of this disorder. Remarkably, the levels of those proteins were normalized by the reduction of *Fmr1* mRNA abundance. Thus, our data show molecular alterations that may contribute to explain the neurodevelopmental phenotypes of the mouse model and patients carrying the CGG premutation, thus providing an indication for future early therapies to treat CGG-premutation carriers. For instance, Aldh4a1/P5CDH is a mitochondrial matrix NAD(+)-dependent dehydrogenase that catalyzes the second step of the proline degradation pathway, converting pyrroline-5-carboxylate to glutamate. Altered function of this enzyme can result in a deregulation of the glutamate signaling, which is at the basis of various forms of brain disorders, as well as of Parkinson’s disease.^{30,31} Thus, Aldh4a1/P5CDH could be a therapeutic target for FXTAS patients during different periods of life and phases of the disorder associated with the CGG premutation. Other targets may be small GTPases by

using, in this case, a strategy based on the modulation of their regulators, as recently proposed.^{32,33} In conclusion, by our approach, we defined altered pathways in FXTAS neurons that are due to the increased levels of *Fmr1* mRNA and impact on neuronal morphology. They represent the molecular pathology underpinning the late FXTAS phenotype. In particular, differentially expressed proteins between WT and CGG-KI neurons are promising pharmacological targetable molecules for early therapeutic intervention for FXTAS. On the other side, future gene therapies could also target the CGG-repeat by excising it, as already shown in an induced pluripotent stem cell (iPSC) line.³⁴

MATERIALS AND METHODS

Animals

The experiments were performed following the Animals in Research: Reporting *In Vivo* Experiments (ARRIVE) guidelines.³⁵ *Fmr1* knockin (KI) and wild-type (WT) mice on a C57BL/6J congenic background were produced as described previously.³⁶ All animals were generated and housed in groups of four in standard laboratory conditions (22°C, 55% ± 10% humidity, and 12-h light/12-h dark diurnal cycles) with food and water provided *ad libitum*. Animal care was

conducted in accordance with the European Community Directive 2010/63/EU. All experiments were approved by the local ethics committee (Comité d’Ethique en Expérimentation Animale CIEPAL-AZUR N. 00788.01).

Lentivirus Generation

Lentivirus particles were produced as previously described.³⁷

Axon Length Measurements

Dissociated neurons were transfected with lentivirus plasmids by using Nucleofector as previously described.¹³ Neurons were cultured for 48 h and then fixed. Axons were labeled with anti-Tuj1 antibody, and the size of individual growing axons (distance from the soma to the tip of the axon) was manually measured using the ImageJ software.¹⁵

Neuronal Culture and Dendritic Spine Morphology Analysis

Primary neurons were prepared from E15.5 pregnant C57BL/6 *Fmr1*^{CGG/ly} and WT mice as previously described.^{12,15} Neurons (5 days *in vitro*) were transduced with lentivirus as previously described.¹² Transduced neurons (20 days *in vitro*) were rinsed twice in PBS at room temperature (RT) after 19 h of transduction and then fixed with 4% paraformaldehyde and Triton-permeabilized. Sequential confocal images (512 × 220 pixels; zoom 3.0; average 4; speed 7) of GFP-expressing neurons were acquired with a 63× oil-immersion lens (NA 1.4) on an inverted Zeiss LSM780 confocal microscope. z series of seven to eight images of randomly selected secondary dendrites were analyzed using the NeuronStudio software, which allows for the automated detection and quantification of dendrite parameters and morphological classification, as previously performed.¹⁵

Protein Extraction and Western Blot Analysis

Immunoblotting was performed as follows: cells or grinded tissues were homogenized in lysis buffer, and debris was removed by centrifugation (20,000 × g, 10 min, 4°C).³⁸ Protein content in the supernatant was measured using the Bradford assay (Bio-Rad), and samples were separated on NuPAGE Bis-Tris 4%–12% gels in MOPS buffer. Separated proteins were transferred to nitrocellulose membranes (Bio-Rad). Membranes were blocked with PBS-Tween (0.05%) and milk (5%), and incubated with primary antibodies overnight.

Antibodies

The monoclonal 1C3 anti-FMRP antibody³⁹ was used at a 1:1,000 dilution, the anti-Tuj1 (BioLegend; TUJ1 1-15-56) antibody was used following the manufacturer’s instructions, and the monoclonal anti-β-tubulin antibody (Sigma) was used at a 1:10,000 dilution.

qRT-PCR

qPCR was performed on a LightCycler 480 (Roche) with MasterMix SYBRGreen (Roche) as previously described.¹³ Primers used to amplify *Fmr1* mRNA were previously reported.³⁷

Protein Identification and Analysis

Proteomic analysis was performed as previously described¹⁷ and resulted in the identification of around 2,000 proteins for each condition. These proteins were then compared to highlight the proteins identified under only one condition or under several conditions (“on/off” effect) and to highlight proteins predominantly identified in one condition relative to another (up if ratio >2, down if ratio <0.5). In order to compile a short list of differentially regulated proteins, a Student’s t test was performed after normalization of the spectral count quantification data. This allowed us to obtain a p value used to make this short list: from the global alignment table of the 2,888 different proteins, we focused on proteins with a p value threshold less than 0.10.

Statistical Analysis

Results are expressed as mean ± SEM. All statistical analyses were based on biological replicates. Appropriate statistical tests used for each experiment are described in the corresponding figure legends. All statistical analyses were carried out using GraphPad Prism version 6.0e.

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.omtn.2019.09.018>.

AUTHOR CONTRIBUTIONS

M.D., S.D., T.M., S.M., M.G., F.B., M.J., and M.C. performed the experiments; R.W. and R.K.H. provided material; T.M., E.L., and B.B. designed the experiments; M.C., E.L., R.K.H., and B.B. wrote the manuscript.

CONFLICTS OF INTEREST

The authors declare no competing interests.

ACKNOWLEDGMENTS

The authors are grateful to S. Zongaro, P. Hammann, L. Khunn, and S. Abekhouk for help. This study was supported by CNRS, INSERM, Association Française contre les Myopathies (AFM), Fondation Recherche Médicale (FRM) grant DEQ20140329490, Fondation Recherche sur le Cerveau (FRC), and Agence Nationale de la Recherche grants ANR-15-CE16-0015 and ANR-11-LABX-0028-01. M.D. and S.C. were recipients of a fellowship from the international PhD LabEx “Signalife” Program. S.D. was a recipient of a MRES fellowship.

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Supplemental Information

Reduction of *Fmr1* mRNA Levels Rescues

Pathological Features in Cortical

Neurons in a Model of FXTAS

Malgorzata Drozd, Sébastien Delhayé, Thomas Maurin, Sara Castagnola, Mauro Grossi, Frédéric Brau, Marielle Jarjat, Rob Willemsen, Maria Capovilla, Renate K. Hukema, Enzo Lalli, and Barbara Bardoni

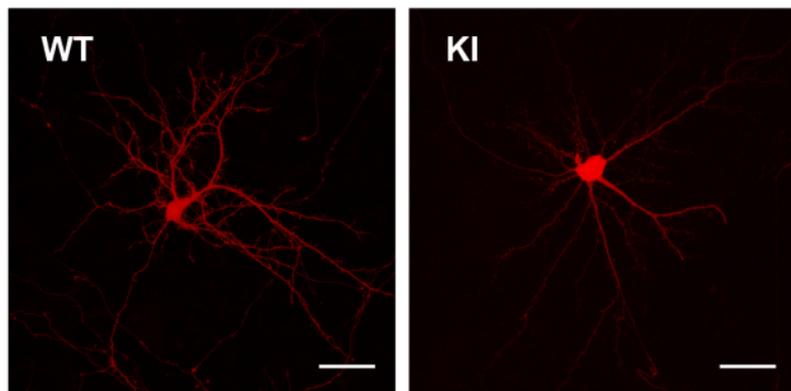
Supplementary Figure legends

Supp. Figure 1. Dendritic arborization of WT and KI mouse cortical neurons. (A) Representative images of cultured cortical WT and KI-CGG neurons. Scale bars: 20 μ m (B) Sholl analysis of cultured WT and KI-CGG mouse cortical neurons. A reduced arborization is observed for CGG-KI. Repeated measures ANOVA with two factors: $f(1,72)=9.943$ $p=0.0024$.

Supp. Figure 2. Axons of 2 DIV cultures of KI-CGG cortical neurons are shorter than WT. (A) Representative pictures of 2 days *in vitro* cultured WT and KI-CGG primary cortical neurons. Scale bars: 10 μ m. (B) Histogram of axon length of WT and KI-CGG. Results show the mean axon length \pm SEM of 150 randomly selected cells for each condition from three independent cultures. Mann-Whitney test *** $p<0.001$.

Fig. S1

A



B

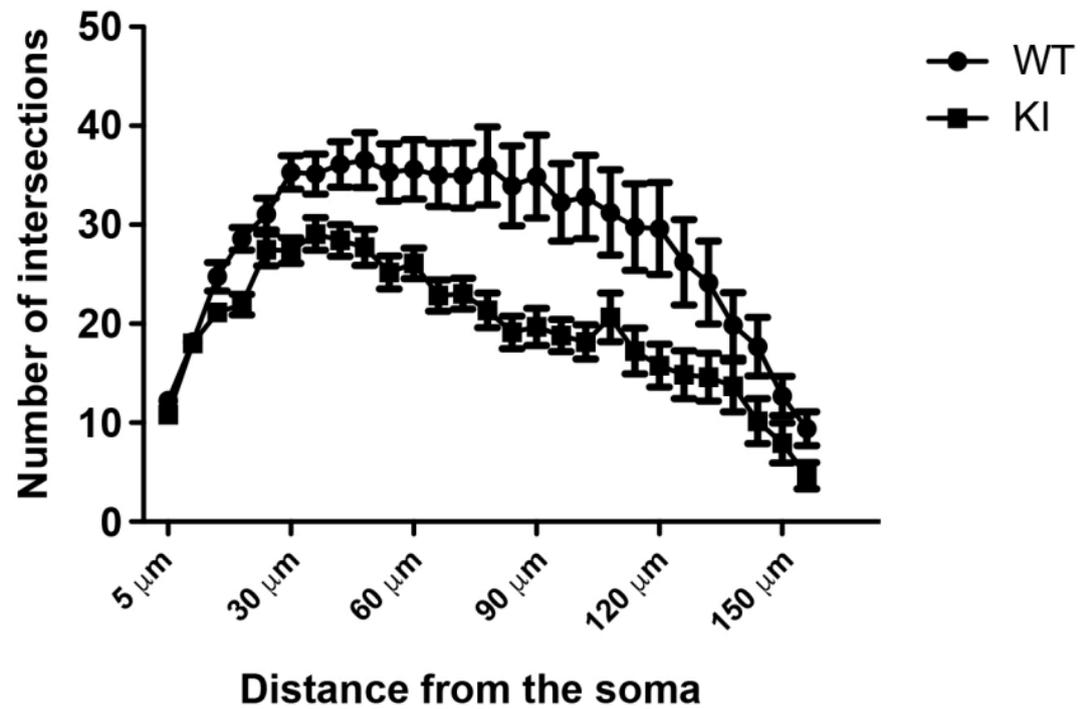
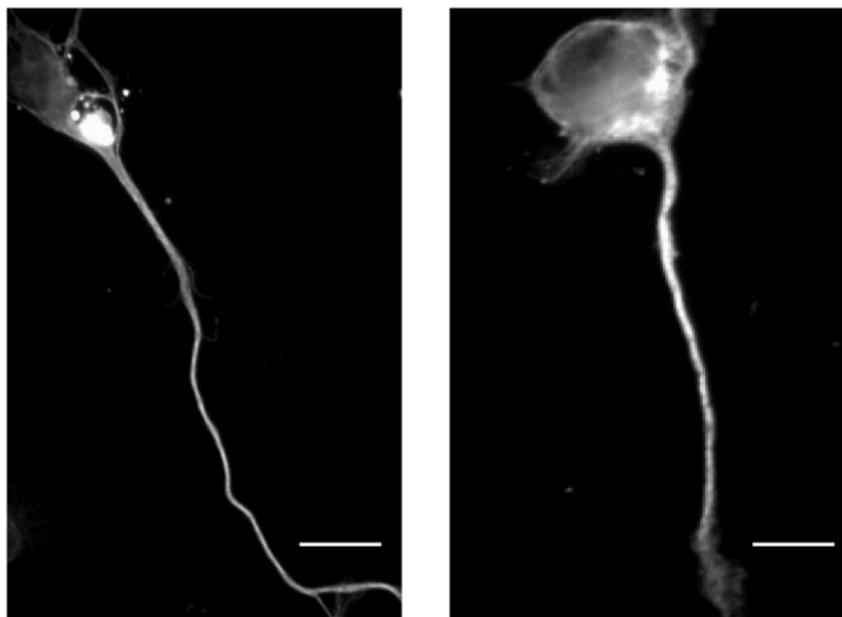


Fig. S2

A



WT

KI

B

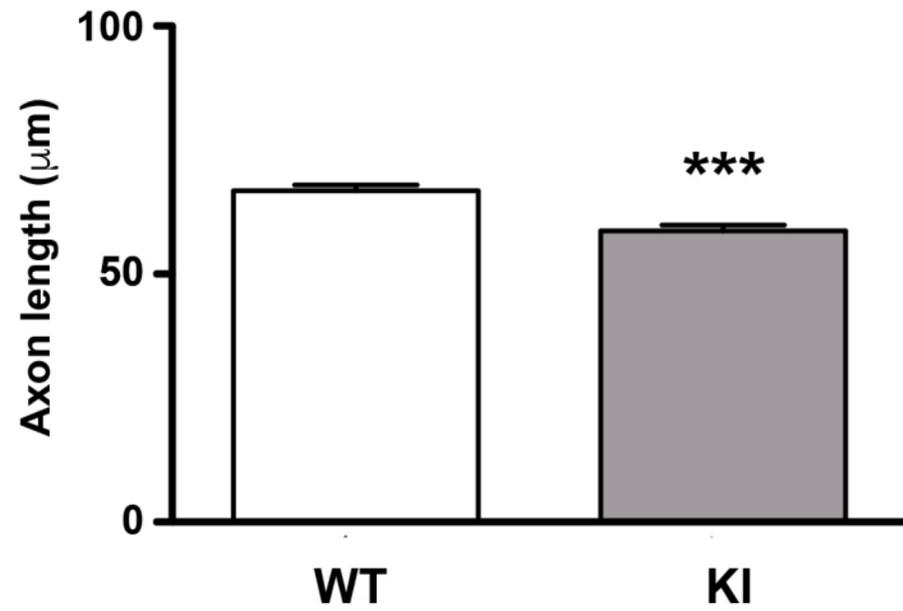


Table S1. Proteins identified in the various samples by nanoLC MS/MS.

LEGEND:		ratio		ratio		STATISTICS:	
# ratio	KI-93 only, and ratio(KIscr/WT)>2	# ratio	KI-93 only, and ratio(KI93/WT)>2	Columns EN, EP and ER		Student t-test between 2 conditions, with 3 replicates for each condition.	
# Spectra	=1 spectrum in KI-scr samples	# Spectra	=1 spectrum in KI-93 samples	p-values returned by the t-test are listed before the corresponding ratios (columns EO, EQ and ES).		Data have been normalized before statistics.	
# Spectra	=2-5 spectra in KI-scr samples	# Spectra	=2-5 spectra in KI-93 samples	p-value <0.05			
# Spectra	=6-10 spectra in KI-scr samples	# Spectra	=6-10 spectra in KI-93 samples	p-value 0.05-0.10			
# Spectra	=11-30 spectra in KI-scr samples	# Spectra	=11-30 spectra in KI-93 samples				
# Spectra	=31 spectra minimum in KI-scr samples	# Spectra	=31 spectra minimum in KI-93 samples				
# ratio	WT only, and ratio(KIscr/WT)<0.5	# ratio	KI-82 only, and ratio(KI82/WT)>2				
# Spectra	=1 spectrum in WT samples	# Spectra	=1 spectrum in KI-82 samples				
# Spectra	=2-5 spectra in WT samples	# Spectra	=2-5 spectra in KI-82 samples				
# Spectra	=6-10 spectra in WT samples	# Spectra	=6-10 spectra in KI-82 samples				
# Spectra	=11-30 spectra in WT samples	# Spectra	=11-30 spectra in KI-82 samples				
# Spectra	=31 spectra minimum in WT samples	# Spectra	=31 spectra minimum in KI-82 samples				
UniProt annotations	It contains "trans", "dentit", "axon", "synap"						

NO FILTER

Total number of proteins:

accession	description	protein_set_score	BASIC Spectral Count (Protein)											
			WT			KI-scr			KI-93			KI-82		
Total Number of Proteins identified in a dedicated samples in the M.musculus taxonomy from UniPr			2047	1979	1803	2053	2224	2069	2182	1854	1893	2039	1817	1718
Concentration (µg/L) obtained after a Bradford assay (performed by the proteomics facility)			2.08	1.31	2.28	1.79	2.26	2.52	1.31	2.33	2.15	1.61	2.08	2.22

Proteins only identified in all 3 KI samples (scr + 93 + 82):

accession	description	protein_set_score	Exp. from 01/02/2017												Exp. 01/02/2017			
			BASIC Spectral Count (Protein)												# Repl.			
			WT			KI-scr			KI-93			KI-82			WT	KI-scr	KI-93	KI-82
sp Q6Z058 LARP1_MOUSE	La-related protein 1 OS=Mus musculus (M	209.47	3	2	1	2	1	1	1	1	1	1	1	1	0	3	1	1
sp A2B40 ARI1_MOUSE	AT-rich interactive domain-containing protein	144.43	3	2	1	2	1	1	1	1	1	1	1	1	0	2	1	1
sp P0DN34 NDU1_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	35.77	2	2	1	2	1	1	1	1	1	1	1	1	0	2	1	1
sp Q0C0W1 YKT6_MOUSE	Synaptobrevin homolog YKT6 OS=Mus mus	442.81	2	1	2	2	1	1	1	1	1	1	1	1	0	3	1	3
sp Q0PCX7 IRGMA_MOUSE	Repulsive guidance molecule A OS=Mus m	102.65	2	1	1	1	1	1	2	1	1	1	1	1	0	3	3	3
sp Q0B25 EIF3K_MOUSE	Eukaryotic translation initiation factor 3 sub	153.19	2	1	1	1	1	3	2	1	1	1	1	1	0	3	2	1
sp Q8VFK0 CC50A_MOUSE	Cell cycle control protein 50A OS=Mus mus	247.64	3	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp P24638 PPAL_MOUSE	Lysosomal acid phosphatase OS=Mus mus	102.66	2	1	1	1	1	1	2	1	1	1	1	1	0	2	2	1
sp Q0R118 HTRA1_MOUSE	Serine protease HTRA1 OS=Mus musculus	498.96	2	1	1	1	1	1	2	1	1	1	1	1	0	2	1	1
sp A2A699 F1712_MOUSE	Protein FAM171A2 OS=Mus musculus (Mo	485.37	4	1	2	2	2	2	2	1	2	2	1	2	0	3	1	3
sp Q8VW6 UL1_MOUSE	NEDD8-activating enzyme E1 regulatory sub	213.87	1	3	2	1	1	1	2	2	1	1	1	1	0	3	2	1
tr EPX228 EPX28_MOUSE	Protein Pctm 10 OS=Mus musculus (Mouse	221.95	1	1	3	1	1	1	1	1	1	1	1	1	0	3	2	1
sp Q85239 AGR3_MOUSE	Adhesion G protein-coupled receptor 33 O	479.09	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q0D50 AP1S2_MOUSE	AP-1 complex subunit sigma2 OS=Mus m	148.57	1	1	1	2	2	2	2	1	1	1	1	1	0	3	2	2
sp P46414 CDN1_MOUSE	Cyclin-dependent kinase inhibitor 1B OS=A	76.23	1	1	1	1	1	1	1	1	1	1	1	1	0	3	3	3
sp Q8CV8 TBCO_MOUSE	Tubulin-specific chaperone E OS=Mus mus	97.68	1	1	1	1	1	1	1	1	1	1	1	1	0	3	2	1
sp Q85C22 ENDO1_MOUSE	Endonuclease domain-containing 1 protein	218.67	1	1	1	1	1	1	1	1	1	1	1	1	0	2	3	1
sp Q03517 RCO2_MOUSE	Secretogranin-2 OS=Mus musculus (Mouse	197.8	1	1	1	5	1	1	1	1	1	1	1	1	0	2	1	1
sp Q0R903 SYT11_MOUSE	Synaptotagmin-11 OS=Mus musculus (Mox	54.01	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	2
sp Q08915 AIP_MOUSE	AH receptor-interacting protein OS=Mus m	118.06	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q8XU9 EIF1B_MOUSE	Eukaryotic translation initiation factor 1b O	72.41	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q80M7 AGF2_MOUSE	AuF-GAP domain and FG repeat-containing	146.32	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q0D82 CJ035_MOUSE	Uncharacterized protein C10orf35 homolog	57.2	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q92281 MACD1_MOUSE	O-acetyl-ADP-ribose deacetylase MACROD	60.96	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q8C0F0 RM1_MOUSE	39S ribosomal protein L11, mitochondrial C	76.19	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q82F39 AGR3_MOUSE	Adhesion G protein-coupled receptor 33 O	479.09	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q3UHX2 HAP2_MOUSE	28 kDa heat- and acid-stable phosphoprote	454.99	1	1	1	2	2	2	2	1	1	1	1	1	0	2	1	1
sp P55096 ABCD3_MOUSE	ATP-binding cassette sub-family D member	548.53	1	1	1	1	2	2	2	1	1	1	1	1	0	1	3	2
sp Q99J36 THUM1_MOUSE	THUMP domain-containing protein 1 OS=N	103.47	1	1	1	1	1	1	1	1	1	1	1	1	0	1	2	1
sp P52760 UK114_MOUSE	Ribonuclease UK114 OS=Mus musculus (H	99.92	1	1	1	1	1	1	2	1	1	1	1	1	0	1	1	1
sp P49070 CAM1_MOUSE	Cadherin-modulator protein 1 OS=Mus mus	213.39	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
sp Q08992 SDC1_MOUSE	Syntenin-1 OS=Mus musculus (Mouse) GN	177.63	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
sp Q05186 RCN1_MOUSE	Reticulocalbin-1 OS=Mus musculus (Mous	124.37	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
sp B9EJ88 OSB1_MOUSE	Oxytetracycline-binding protein-related prote	209.82	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
tr Q8R27 GSRCT_MOUSE	DEAD (Asp-Glu-His-Asp) box polypeptide 1'	187.86	2	2	2	2	1	1	1	1	1	1	1	1	0	2	2	2
sp Q4PDS3 SARM1_MOUSE	Sialic alpha and TIR motif-containing prote	478.44	2	2	2	2	2	2	1	1	1	1	1	1	0	2	1	2
sp P46061 RAGP1_MOUSE	Ran GTPase-activating protein 1 OS=Mus	316.86	2	2	3	3	3	3	1	1	1	1	1	1	0	2	1	1
sp Q08553 NFM_MOUSE	Neurofilament medium polypeptide OS=Mu	294.41	2	2	2	2	1	4	1	1	1	1	1	1	0	2	2	2
sp Q8C189 FERM2_MOUSE	Fermin family homolog 2 OS=Mus musculu	463.85	4	1	1	2	1	1	2	1	1	1	1	1	0	2	3	1
sp Q0D017 RAM10_MOUSE	Armadillo repeat-containing protein 10 OS	300.99	2	1	2	2	1	1	1	1	1	1	1	1	0	2	2	3
sp Q0Z226 MECP2_MOUSE	Methyl-CpG-binding protein 2 OS=Mus mu	297.23	2	1	1	1	1	1	2	1	1	1	1	1	0	1	2	2
sp Q8R0H0 GGA1_MOUSE	ADP-ribosylation factor-binding protein GGA	393.51	2	1	1	1	1	1	1	1	1	1	1	1	0	1	2	2
sp Q0Z230 MTMR7_MOUSE	Myotubularin-related protein 7 OS=Mus mu	145.49	2	2	2	1	1	1	1	1	1	1	1	1	0	1	2	1
sp Q8EPL8 IF07_MOUSE	Intronin-7 OS=Mus musculus (Mouse) GN	688.61	1	2	3	1	1	1	2	1	1	1	1	1	0	2	1	2
sp Q0CYV4 LUTL_MOUSE	Relative RNA-binding protein LUT4e1 O	219.87	2	1	2	2	2	2	1	1	1	1	1	1	0	2	1	1
sp P0C027 NUD10_MOUSE	Diphosphoinositol polyphosphate phospho	323.65	2	1	2	1	1	1	1	1	1	1	1	1	0	2	3	1
sp Q8736 DHB7_MOUSE	3-keto-steroid reductase OS=Mus musculu	126.73	1	2	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q84152 BT3_MOUSE	Transcription factor BT3 OS=Mus musculu	106.7	1	2	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q08110 U51_MOUSE	U5 snRNP small nuclear ribonucleoprotei	466.46	1	1	1	3	1	2	1	1	1	1	1	1	0	2	1	1
sp Q8C570 RAE1L_MOUSE	mRNA export factor OS=Mus musculus (M	138.31	2	1	1	2	2	2	1	1	1	1	1	1	0	2	2	1
sp Q9JM31 EDF1_MOUSE	Endothelial differentiation-related factor 1	152.87	1	1	1	2	1	2	1	1	1	1	1	1	0	2	1	1
tr E9107 E9Q107_MOUSE		32.95	1	1	1	2	1	1	1	1	1	1	1	1	0	2	1	1
sp Q8C4M4 FPD1_MOUSE	Prefoldin subunit 1 OS=Mus musculus (M	195.14	1	1	1	1	2	1	2	1	1	1	1	1	0	2	2	2
sp Q82289 TCM1_MOUSE	Tetrahymena OS=Mus musculus (Mouse) GN	46.52	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	3
sp Q92472 RT02_MOUSE	28S ribosomal protein S2, mitochondrial ON	45.32	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q92572 2ABD_MOUSE	Serine/threonine-protein phosphatase 2A 5	262.12	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q05633 EMM1_MOUSE	Echinoderm microtubule-associated protei	69.59	1	1	1	1	2	1	1	1	1	1	1	1	0	2	2	1
sp Q03551 NFL_MOUSE	Neurofilament light polypeptide OS=Mus m	328.62	1	1	1	1	2	2	1	1	1	1	1	1	0	2	2	2
sp Q0Z257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus (M	351.57	1	1	1	2	1	2	2	1	2	2	1	2	0	2	2	2
sp Q8URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus (Mouse) GN	409.38	1	1	1	1	1	2	3	1	1	1	1	1	0	2	3	3
sp Q8E870 TRIP_C_MOUSE	E3 ubiquitin-protein ligase TRIP12 OS=Mu	57.95	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp Q8BU14 SEC62_MOUSE	Translocation protein SEC62 OS=Mus mus	141.23	1	1	1	1	1	1	1	1	1	1	1	1	0	2	2	1
sp P41202 OSG2_MOUSE	COP9 signalosome complex subunit 2 OS	400.7	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	2
sp P41216 ACSL1_MOUSE	Long-chain-fatty-acyl-CoA ligase 1 OS=M	285.75	1	1	1	1	2	1	1	1	1	1	1	1	0	2	1	1
sp Q035900 LSM2_MOUSE	U6 snRNA-associated Sm-like protein LSM2	95.05	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	3
sp P97823 YPA1_MOUSE	Acylprotein thioesterase 1 OS=Mus muscu	102.05	1	1	1	1	1	1	1	1	1	1	1	1	0	2	1	1
sp Q81686 CX45_MOUSE																		

Accession	Description	Protein Set Score	1	2	3	1	2	3	1	2	3	1	2	3	# Rep.	KI-scr / WT-scr	KI-93 / WT-scr	KI-82 / WT-scr
sp O35972 RM23_MOUSE	39S ribosomal protein L23, mitochondrial	49.71	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp Q8BGR6 ARL15_MOUSE	ADP-ribosylation factor-like protein 15	44.41	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp Q8R466 NUP53_MOUSE	Nucleoporin NUP53	35.48	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp Q8V870 TMX1_MOUSE	Thioredoxin-related transmembrane protein	85.48	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp Q6PH08 NAA3_MOUSE	Nalpa-acetyltransferase 35, Na/C auxiliary	115.24	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp O05512 MARK2_MOUSE	Serine/threonine-protein kinase MARK2	278.66	1	1	1	1	1	1	0	2	1	0	0	0	0.11728	KI-scr only	0.37390	KI-93 only
sp Q8C3F2 F120C_MOUSE	Constitutive coactivator of PPAR-gamma-like	219.45	1	1	1	2	1	1	0	2	1	0	0	0	0.11661	KI-scr only	0.37390	KI-93 only
sp P11531 DMO1_MOUSE	Hypoxanthine phosphoribosyl transferase	52.75	1	1	1	1	1	1	0	2	1	0	0	0	0.11661	KI-scr only	0.00005	KI-93 only
sp Q8V026 IMP3_MOUSE	Inositol monophosphatase 3	81.94	1	1	1	2	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.14329	KI-93 only
sp Q8P906 FKB15_MOUSE	FK506-binding protein 15	63.91	1	1	1	2	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8C166 CPNE1_MOUSE	Copine-1	142.14	1	1	1	2	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q62WV2 Q62WV_MOUSE	Theta 4, X chromosome	48.74	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp P49769 PSM1_MOUSE	Presenilin-1	37.89	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q01G21 G21_MOUSE	Phosphomevalonate kinase	159.96	2	2	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q6Z008 CNOT1_MOUSE	OCR4-NOT transcription complex subunit 1	236.17	2	2	1	2	1	1	0	0	2	1	0	0	0.15432	KI-scr only	0.37390	KI-93 only
sp Q6R216 NDT4_MOUSE	Diphosphoinositidyl polyphosphate phosphatase	148.53	2	2	1	1	1	1	0	0	2	2	0	0	0.37390	KI-scr only	0.11624	KI-93 only
sp Q8EKR1 PPT2_MOUSE	Receptor-type tyrosine-protein phosphatase	135.73	2	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.18328	KI-93 only
sp A9C473 A9C473_MOUSE	Protein A630010A05Rik (Fragment)	31.7	2	2	2	2	2	2	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp P70429 EVL_MOUSE	Ena/VASP-like protein	380.87	2	2	2	2	2	2	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q3UE37 UBE2Z_MOUSE	Ubiquitin-conjugating enzyme E2 Z	163.62	2	2	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11834	KI-93 only
sp P53811 PMP2_MOUSE	Phosphatidylinositol transfer protein beta 1	174.35	2	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp P22315 HEMH_MOUSE	Ferrochelatase, mitochondrial	126.93	2	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q64737 PUR2_MOUSE	Trifunctional purine biosynthetic protein	223.96	1	2	1	1	2	1	0	0	2	2	0	0	0.16239	KI-scr only	0.17504	KI-93 only
sp P26039 TLN1_MOUSE	Talin-1	163.8	1	1	1	1	1	1	0	0	2	2	0	0	0.11626	KI-scr only	0.11834	KI-93 only
sp D44FX7 DAFX7_MOUSE	Protein Dnaaj13	128.46	1	1	1	1	1	1	0	0	2	2	0	0	0.11626	KI-scr only	0.11834	KI-93 only
sp Q3TAS6 EMC10_MOUSE	ER membrane protein complex subunit 10	86.8	1	1	1	1	1	1	0	0	1	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q8K120 COO9_MOUSE	Ubiquitin ubiquitin-protein complex COO9, mb	112.45	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q920A5 RSC_MOUSE	Retinoid-inducible serine carboxypeptidase	78.79	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp P83870 PHF5A_MOUSE	PHD finger-like domain-containing protein 5	189.55	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q7T741 MBE1A_MOUSE	Myo-binding protein 1A	303.45	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp E9Q740 E9Q740_MOUSE	Protein Sp72	466.95	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q9WU28 PF05_MOUSE	Prefoldin subunit 5	156.04	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q9CY27 TECR_MOUSE	Very-long-chain enoyl-CoA reductase	200.24	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q35V16 RPK2_MOUSE	Rap1 GTPase-activating protein 2	43.76	1	1	1	1	1	1	0	0	2	1	0	0	0.11626	KI-scr only	0.37390	KI-93 only
sp Q9K0C4 CPS1A_MOUSE	Lanosterol 14-alpha demethylase	334.38	1	1	1	1	1	1	0	0	2	2	0	0	0.11626	KI-scr only	0.11624	KI-93 only
sp Q9R1V7 ADK3_MOUSE	Disintegrin and metalloproteinase domain-containing protein 3	69.29	1	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9H393 PLXD1_MOUSE	Plexin-D1	64.86	1	1	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11948	KI-93 only
sp P50544 ACADV_MOUSE	Very-long-chain specific acyl-CoA dehydrogenase	276.89	1	1	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11948	KI-93 only
sp Q9R313 EXOC8_MOUSE	Exocyst complex component 8	70.99	1	1	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11834	KI-93 only
sp Q8BNW9 KBTB_MOUSE	Kelch repeat and BTB domain-containing protein 9	65.66	1	1	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11834	KI-93 only
sp Q3TDQ1 STT3B_MOUSE	Dolichyl-diphosphoglycerate-protein	140.56	1	1	1	1	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.11834	KI-93 only
sp Q8VHY0 CSPG4_MOUSE	Chondroitin sulfate proteoglycan 4	65.04	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8D766 ACAD8_MOUSE	Acyl-CoA oxidase 8, mitochondrial	46	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9R1X9 ZFNB2_MOUSE	ANK repeat and zinc finger protein ZFNB2	44.42	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q7T5Y6 CELFA_MOUSE	CUGBP Elav-like family member 4	127.95	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q04690 INF1_MOUSE	Proteasome activator complex subunit 2	205.39	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp P97372 PSM2_MOUSE	Proteasome activator complex subunit 2 C	112.16	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9D067 MCT1_MOUSE	Malignant cell-associated sequence 1	285.27	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q3UHK6 TEN4_MOUSE	Tensin-4	96.83	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8CH72 TR13_MOUSE	E3 ubiquitin-protein ligase TRIM32	50.98	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q35459 ECH1_MOUSE	Delta(3,5)Delta(2,4)dienoyl-CoA isomerase	90.64	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q89863 STX6_MOUSE	Syntaxin-6	76.02	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp D3YW03 D3YW03_MOUSE	Dicyclophosphatase	146.89	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8C0L0 TMX4_MOUSE	Thioredoxin-related transmembrane protein	239.26	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8K3C3 LZIC_MOUSE	Protein LZIC	194.67	2	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q7TN66 IGS21_MOUSE	Immunoglobulin superfamily member 21	184.28	1	2	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9B917 L2L1_MOUSE	Leish2 ligand larva protein	101.38	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9R001 PDXK1_MOUSE	Pyridoxal-dependent decarboxylase domain-containing protein 1	50.61	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp P32233 DRG1_MOUSE	Developmentally-regulated GTP-binding protein 2.4	38.76	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9C062 DECR_MOUSE	2.4-dienoyl-CoA reductase, mitochondrial	106.01	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q6N200 DNJC8_MOUSE	DnaJ homolog subfamily C member 8	138.44	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp D8R354 PLXB2_MOUSE	Plexin-B2	287.35	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9G0S1 SCMC3_MOUSE	Calcium-binding mitochondrial carrier protein	104.92	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9C0M5 TXD17_MOUSE	Thioredoxin domain-containing protein 17	108.04	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q9L533 SERB_MOUSE	Phosphoserine phosphatase	64.08	1	1	1	2	1	1	0	0	1	2	0	0	0.37390	KI-scr only	0.16207	KI-93 only
sp Q9B327 GBZ5_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)	60.71	1	1	1	1	1	1	0	0	1	1	0	0	0.37390	KI-scr only	0.37390	KI-93 only
sp Q8R2Y8 PTH2_MOUSE	Peptidyl-HRNA hydrolase 2, mitochondrial	151.																

sp O9CY0 NJMU_MOUSE	Protein Njmu-R1	OS=Mus musculus (Mouse)	35.19	1	0	1	0	0	0.37390	Ki-scr only
sp O9C23 DJCT0_MOUSE	DnaI homolog subfamily C member 10	OS=	33.44	1	0	1	0	0	0.37390	Ki-scr only
sp O9ZK3 SYNE2_MOUSE	Nesprin-2	OS=Mus musculus (Mouse) GN=	32.42	1	0	1	0	0	0.37390	Ki-scr only
sp P59708 SF3B6_MOUSE	Splicing factor 3B subunit 6	OS=Mus musc.	32.05	1	0	1	0	0	0.37390	Ki-scr only
sp O9DBR4 APBB2_MOUSE	Amyloid beta A4 precursor protein-binding f		31.92	1	0	1	0	0	0.37390	Ki-scr only
sp O3Q4D0 WDR41_MOUSE	WD repeat-containing protein 41	OS=Mus i	31.88	1	0	1	0	0	0.37390	Ki-scr only
sp P78404 TAGL_MOUSE	Transgelin	OS=Mus musculus (Mouse) GN=	31.86	1	0	1	0	0	0.37390	Ki-scr only
sp O9Q0B15 RM12_MOUSE	39S ribosomal protein L12	mitochondrial C	31.15	1	0	1	0	0	0.37390	Ki-scr only
sp O55074 AKA7A_MOUSE	A-kinase anchor protein 7 isoform alpha	OS=	29.95	1	0	1	0	0	0.37390	Ki-scr only
sp O7T3C3 NEK5_MOUSE	Serine/threonine-protein kinase Nek5	OS=M	29.79	1	0	1	0	0	0.37390	Ki-scr only
sp O8R1M4 NUOC3_MOUSE	NuclD domain-containing protein 3	OS=Mus	141.89	1	0	1	0	0	0.37390	Ki-scr only
sp O5S5F2 LCT1_3_MOUSE	Lactoferrin-like protein 3	OS=Mus muscu	186.6	1	0	1	0	0	0.37390	Ki-scr only
sp P60904 DNAC5_MOUSE	DnaI homolog subfamily C member 5	OS=	311.67	1	0	1	0	0	0.37390	Ki-scr only
sp O9J90 RNF14_MOUSE	E3 ubiquitin-protein ligase RNF14	OS=Mu	263.19	1	0	1	0	0	0.37390	Ki-scr only
sp O9D710 TMX2_MOUSE	Thioredoxin-related transmembrane protein		180.02	1	0	1	0	0	0.37390	Ki-scr only
sp O9Z0J0 NFC2_MOUSE	Epididymal secretory protein E1	OS=Mus n	63.99	1	0	1	0	0	0.37390	Ki-scr only
sp O9BR93 F177A_MOUSE	Protein FAM177A1	OS=Mus musculus (M	183.01	1	0	1	0	0	0.37390	Ki-scr only
sp O5S19 CLU_MOUSE	Clustered mitochondria protein homolog	OS=	200.53	1	0	1	0	0	0.37390	Ki-scr only
sp O55135 IF6_MOUSE	Eukaryotic translation initiation factor 6	OS=	96.91	1	0	1	0	0	0.37390	Ki-scr only
sp O9DA02 IFT22_MOUSE	Intraflagellar transport protein 22 homolog		44.56	1	0	1	0	0	0.37390	Ki-scr only

Proteins only identified in 1 KI sample (KI-93):

accession	description	protein_set_score	Exp. from 01/02/2017												Exp. 01/02/2017						
			BASIC Spectral Count (Proline)												Exp. 01/02/2017						
			WT			Ki-scr			KI-93			KI-82			# Repl.	Ki-scr / WT-scr		KI-93 / WT-scr			
1	2	3	1	2	3	1	2	3	1	2	3	WT	Ki-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio		
sp O8K4R4 PITC1_MOUSE	Cytoplasmic phosphatidylinositol transfer pn	303.78				2	2	1						0	0	3	0	0.00715		KI-93 only	
sp O3587 CALU1_MOUSE	Calumenin	434.64				4	4	1						0	0	1	0	0.37390		KI-93 only	
sp O9R4F1 NTNG2_MOUSE	Netrin-G2	92.39				2								0	0	1	0	0.37390		KI-93 only	
sp O9CRD0 OCAD1_MOUSE	OCIA domain-containing protein 1	147.41				2								0	0	1	0	0.37390		KI-93 only	
sp O9D6U8 F162A_MOUSE	Protein FAM162A	107.03				2								0	0	1	0	0.37390		KI-93 only	
sp P5508 AQR1_MOUSE	Aquaporin-4	96.51				1	1	1						0	0	3	0	0.00005		KI-93 only	
sp O1290 CAC1E_MOUSE	Voltage-dependent L-type calcium channel	39.61				1	1	1						0	0	0	0	0.00005		KI-93 only	
sp O8R180 ERO1A_MOUSE	ERO1-like protein alpha	146.71				1	1	1						0	0	3	0	0.00005		KI-93 only	
sp O08842 GFR2_MOUSE	GDNF family receptor alpha-2	64.44				1	1	1						0	0	2	0	0.11948		KI-93 only	
sp O9B8D7 CRT1_MOUSE	CREB-regulated transcription coactivator 1	104.36				1	1	1						0	0	2	0	0.11948		KI-93 only	
sp P5524 AKK_MOUSE	Adenosine kinase	76.21				1								0	0	1	0	0.11834		KI-93 only	
sp O9WVE8 PACN2_MOUSE	Protein kinase C and casein kinase substra	101.97				1		1						0	0	1	0	0.37390		KI-93 only	
sp P62500 T2D1_MOUSE	TSC22 domain family protein 1	73.41				1								0	0	1	0	0.37390		KI-93 only	
sp O35075 DSCR3_MOUSE	Down syndrome critical region protein 3 hon	62.36				1								0	0	1	0	0.37390		KI-93 only	
sp O9CR62 NHAF2_MOUSE	H/ACA ribonucleoprotein complex subunit 2	55.19				1								0	0	1	0	0.37390		KI-93 only	
sp P42275 STAT3_MOUSE	Signal transducer and activator of transcript	107.81				1								0	0	1	0	0.37390		KI-93 only	
sp O9D116 RM14_MOUSE	39S ribosomal protein L14	72.85				1								0	0	1	0	0.37390		KI-93 only	
sp O88986 KBL_MOUSE	2-amino-3-ketobutyrate coenzyme A ligase	71.94				1								0	0	1	0	0.37390		KI-93 only	
sp P70445 HEBP2_MOUSE	Eukaryotic translation initiation factor 4E-bin	70.75				1								0	0	1	0	0.37390		KI-93 only	
sp O9Z313 TGO1_MOUSE	Tango-3 network integral protein	64.23				1								0	0	1	0	0.37390		KI-93 only	
sp O8BV15 STX16_MOUSE	Syntaxin-16	61.94				1								0	0	1	0	0.37390		KI-93 only	
sp O8B84 MA3_MOUSE	Melanoma inhibitory activity protein 3	60.44				1								0	0	1	0	0.37390		KI-93 only	
sp O8M65 NYP2_MOUSE	Neuronal tyrosine-phosphorylated phospho	58.06				1								0	0	1	0	0.37390		KI-93 only	
sp O9R0M0 CELR2_MOUSE	Cadherin EGF_LAG seven-pass G-type rec	52.45				1								0	0	1	0	0.37390		KI-93 only	
sp P50429 ARSB_MOUSE	Arylsulfatase B	48.93				1								0	0	1	0	0.37390		KI-93 only	
sp O7T3C1 PRC2A_MOUSE	Protein PRRC2A	44.92				1								0	0	1	0	0.37390		KI-93 only	
sp O9E006 DHB11_MOUSE	Estradiol 17-beta-dehydrogenase 11	42.2				1								0	0	1	0	0.37390		KI-93 only	
sp O9VE44 IM40_MOUSE	Mitochondrial intermembrane space import	41.37				1								0	0	1	0	0.37390		KI-93 only	
sp O9ER00 SCAM2_MOUSE	Serine/cysteine-aminotransferase membrane prot	39.89				1								0	0	1	0	0.37390		KI-93 only	
sp O9VBD0 QOVBDO_MOUSE	Integrin beta	37.95				1								0	0	1	0	0.37390		KI-93 only	
sp O31125 S39A7_MOUSE	Zinc transporter SLC39A7	37.63				1								0	0	1	0	0.37390		KI-93 only	
sp O9C000 TM261_MOUSE	Transmembrane protein 261	37.04				1								0	0	1	0	0.37390		KI-93 only	
sp O9XV0 PCSK1_MOUSE	ProSAA5	36.66				1								0	0	1	0	0.37390		KI-93 only	
sp O9C0X8 RT8_MOUSE	RS ribosomal protein S36	35.67				1								0	0	1	0	0.37390		KI-93 only	
sp O9Z2U1 PRPF3_MOUSE	U4/U6 small nuclear ribonucleoprotein Prp3	34.28				1								0	0	1	0	0.37390		KI-93 only	
sp O8CCP0 NEMF_MOUSE	Nuclear export mediator factor Nemf	33.26				1								0	0	1	0	0.37390		KI-93 only	
sp O9D1H8 RM53_MOUSE	39S ribosomal protein L53	32.84				1								0	0	1	0	0.37390		KI-93 only	
sp P97467 AMD_MOUSE	Peptidyl-glycine alpha-aminating monooxyg	32.82				1								0	0	1	0	0.37390		KI-93 only	
sp O9WUN2 TBK1_MOUSE	Serine/threonine-protein kinase TBK1	32.72				1								0	0	1	0	0.37390		KI-93 only	
sp O9EPE9 AT131_MOUSE	Manganese-transporting ATPase 13A1	32.42				1								0	0	1	0	0.37390		KI-93 only	
sp O81337 BAD_MOUSE	Bd2-associated agonist of cell death	31.86				1								0	0	1	0	0.37390		KI-93 only	
sp O9B8WM PCE2_MOUSE	Prostaglandin G synthase 2	31.59				1								0	0	1	0	0.37390		KI-93 only	
sp E9K079 E9K079_MOUSE	Protein Dna11	31.44				1								0	0	1	0	0.37390		KI-93 only	
sp O9C7K6 PCYXL_MOUSE	Prenylcysteine oxidase-like	201.14				1								0	0	1	0	0.37390		KI-93 only	
sp O91YH5 ATL3_MOUSE	Atlastin-3	106.88				1								0	0	1	0	0.37390		KI-93 only	
sp O9P2B1 TNP03_MOUSE	Transferrin-3	211.94				1								0	0	1	0	0.37390		KI-93 only	
sp O9VH45 MARK1_MOUSE	Serine/threonine-protein kinase MARK1	247.76				1								0	0	1	0	0.37390		KI-93 only	
sp O9DFW4 NOP58_MOUSE	Nucleolar protein 58	267.84				1								0	0	1	0	0.37390		KI-93 only	
sp O9VED9 LEGL_MOUSE	Galectin-related protein	83.26				1								0	0	1	0	0.37390		KI-93 only	
sp O9C2B0 C60_MOUSE	Succinate dehydrogenase cytochrome b56i	81.93				1								0	0	1	0	0.37390		KI-93 only	
sp O9BLV3 SLA7_MOUSE	Sodium/hydrogen exchanger 7	80.5				1								0	0	1	0	0.37390		KI-93 only	
sp O9WUKZ T18_MOUSE	Zinc finger and BTB domain-containing prot	44.37				1								0	0	1	0	0.37390		KI-93 only	
sp O9B2A9 TIGAR_MOUSE	Fructose-2,6-bisphosphatase TIGAR	178.28				1								0	0	1	0	0.37390		KI-93 only	
sp O9OX51 PLEC_MOUSE	Plectin	151.81				1								0	0	1	0	0.37390		KI-93 only	
sp O9N5W3 SPKAP_MOUSE	A-kinase anchor protein SPKAP	258.58				1								0	0	1	0	0.37390		KI-93 only	
sp O9R0C3 TME2_MOUSE	Transmembrane emp24 domain-containing pr	59.01				1								0	0	1	0	0.37390		KI-93 only	
sp O91W00 SETD3_MOUSE	Histone-lysine N-methyltransferase setd3	90.35				1								0	0	1	0	0.37390		KI-93 only	
sp O35435 PYRD_MOUSE	Dihydroorotate dehydrogenase (quinone)	93.38				1								0	0	1	0	0.37390		KI-93 only	
sp O9C085 TM22_MOUSE	Mitochondrial import inner membrane transp	112				1								0	0	1	0	0.37390		KI-93 only	
sp O81016 CBG7_MOUSE	Guanine nucleotide-binding protein (G)beta	54.32				2								0	0	1	0	0.37390		KI-93 only	
sp O9Z2Z8 CL6A_MOUSE	Actin-like protein 6A	122.41				1		1						0	0	1	0	0.11624		KI-93 only	
sp O9WUT3 K56A2_MOUSE	Ribosomal protein S6 kinase alpha-2	75.64				1								0	0	1	0	0.37390		KI-93 only	
sp O91V09 IPYR2_MOUSE	Inorganic pyrophosphatase 2	83.89				1								0	0	1	0	0.37390		KI-93 only	
sp O9C0D5 ETU1_MOUSE	Elongation factor Tu GTP-binding domain-c	86.18				1								0	0	1	0	0.37390		KI-93 only	
sp O9CFE4 SCY12_MOUSE	SCY1-like protein 2	77.74				1								0	0	1	0	0.37390		KI-93 only	
sp O3U898 MYOV2_MOUSE	Myeloma-overexpressed gene 2 protein hor	71.25				1								0	0	1	0	0.37390		KI-93 only	
sp O90967 PAPS1_MOUSE	Bifunctional 3'-phosphoadenosine 5'-phosp	61.7		</																	

accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	Ki-93	Ki-92	pvalue	ratio	pvalue	ratio	pvalue	ratio
trjQ3UAS3/G3UAS3_MOUSE	Putative uncharacterized protein OS=Mus m	781.64	1	4	1	3	4	4	5	3	4	8	3	2	3	3	3	0.19235	1.83	0.09663	2.00	0.23221	2.17
sp Q02819 NUC1_MOUSE	Nucleobindin-1 OS=Mus musculus (Mouse)	347.2	1	2	1	3	2	1	3	3	3	3	3	4	3	3	3	0.41806	1.50	0.06061	2.25	0.01969	2.50
sp Q08B11 PRUNE_MOUSE	Prune OS=Mus musculus (Mouse)	746.56	1	2	1	1	1	3	1	1	1	2	3	2	1	2	3	0.22223	2.37	0.05223	2.00	0.05223	2.50
sp P81021 RAB5B_MOUSE	Ras-related protein Rab-5B OS=Mus musculus (Mouse)	738.82	1	1	1	1	3	2	6	3	2	3	5	3	3	3	3	0.70674	0.80	0.27792	2.00	0.17769	2.00
sp Q0D1K2 VATF_MOUSE	V-type proton ATPase subunit F OS=Mus musculus (Mouse)	262.28	1	1	1	1	3	1	3	2	1	3	2	1	3	3	3	0.39107	1.67	0.10538	2.00	0.08612	2.00
sp Q09247 IMPI_MOUSE	Mannose-6-phosphate isomerase OS=Mus musculus (Mouse)	431.28	1	1	1	1	2	2	1	2	1	2	2	2	2	3	3	0.65202	1.50	0.07888	2.50	0.37128	2.00
sp Q2L41 BZV2_MOUSE	Basic leucine zipper and WZ domain-containing protein OS=Mus musculus (Mouse)	307.81	1	1	1	1	2	2	3	2	1	1	2	2	2	2	2	0.68781	1.50	0.34853	2.50	0.12430	2.00
sp Q0LM14 NTSC_MOUSE	Nucleoside triphosphatase OS=Mus musculus (Mouse)	133.86	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.46474	2.00	0.04647	2.00	0.04647	2.00
sp Q0P4T2 UOS2_MOUSE	U5 small nuclear ribonucleoprotein 200 kDa OS=Mus musculus (Mouse)	729.79	1	1	1	1	1	1	1	1	1	1	2	2	1	3	3	0.99759	1.00	0.10121	3.00	0.05091	5.00
sp I47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus (Mouse)	124.65	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.99759	1.00	0.50267	2.00	0.08013	3.00
sp Q0K019 BCLF1_MOUSE	Bcl-2-associated transcription factor 1 OS=Mus musculus (Mouse)	173.04	1	1	1	1	1	1	2	1	1	1	1	1	1	1	2	0.94510	1.00	0.35515	3.00	0.46591	2.00
sp Q0C035 BZV1_MOUSE	Basic leucine zipper and WZ domain-containing protein OS=Mus musculus (Mouse)	394.28	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	0.94510	1.00	0.52166	2.00	0.44226	2.00
sp Q0T202 MT1_MOUSE	Metallothionein-1 OS=Mus musculus (Mouse)	146.28	1	1	1	1	1	2	1	1	1	1	2	2	3	3	3	0.43345	1.50	0.16684	2.00	0.16221	2.00
trjQ3U935/Q3U935_MOUSE	Putative uncharacterized protein OS=Mus musculus (Mouse)	334.95	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	0.97304	1.00	0.68457	2.00	0.48226	2.00
sp Q0H9W8 IGL05_MOUSE	IgLN family member 5 OS=Mus musculus (Mouse)	180.88	1	1	1	1	1	1	2	2	1	1	1	2	1	1	2	0.96951	1.00	0.88457	2.00	0.13680	3.00
sp Q0I0A7 DDX42_MOUSE	ATP-dependent RNA helicase DDX42 OS=Mus musculus (Mouse)	277.59	1	1	1	1	1	2	1	1	1	2	1	1	1	2	2	0.99676	1.00	0.86564	3.00	0.39668	3.00
sp Q0K821 NM1L_MOUSE	Nm1-like family domain-containing protein OS=Mus musculus (Mouse)	125.41	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	0.58441	2.00	0.47370	2.00	0.47370	2.00

Proteins mostly identified in the KI-scr sample with ratio>2:

accession	description	protein_set_score	Exp. from 01/02/2017												# Repl.	Exp. 01/02/2017								
			WT			Ki-93			Ki-92			Ki-93				Ki-93 / WT-scr	Ki-92 / WT-scr	Ki-93 / WT-scr	Ki-92 / WT-scr					
1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	WT	Ki-93	Ki-92	pvalue	ratio	pvalue	ratio	pvalue	ratio	
sp P05132 KAPCA_MOUSE	CAMP-dependent protein kinase catalytic subunit OS=Mus musculus (Mouse)	1235.28	6	6	4	10	12	11	12	2	4	10	2	2	3	3	3	3	0.00132	2.06	0.81905	1.13	0.8718	0.88
sp P24270 CATA_MOUSE	Catalase OS=Mus musculus (Mouse) GN=C	915.52	6	3	5	10	8	14	10	3	5	11	6	6	3	3	3	3	0.04811	2.29	0.51838	1.29	0.07027	1.64
sp P99026 PSB4_MOUSE	Proteasome subunit beta type-4 OS=Mus musculus (Mouse)	536.16	5	3	3	6	9	8	9	3	7	8	3	6	3	3	3	3	0.01786	2.09	0.17220	1.73	0.15307	1.55
sp P26043 RAD1_MOUSE	Radixin OS=Mus musculus (Mouse) GN=R	754.21	2	3	4	6	6	6	7	1	3	5	4	3	3	3	3	3	0.01299	2.00	0.17371	1.22	0.12673	1.33
sp Q0Z144 F3_MOUSE	Radix enhancer-binding protein 3 OS=Mus musculus (Mouse)	620.57	2	2	1	3	4	3	3	4	2	4	2	3	3	3	3	3	0.26328	2.00	0.06607	2.00	0.12625	1.25
trjB1AWE0 B1AWE0_MOUSE	Claudin light chain A OS=Mus musculus (Mouse)	529.43	3	3	3	8	6	4	4	4	1	4	3	2	3	3	3	3	0.02920	2.00	0.90038	1.00	0.52327	1.00
sp Q01V7R MLP3A_MOUSE	Microtubule-associated proteins 1A/1B light chain 3 OS=Mus musculus (Mouse)	305.94	2	3	3	4	6	6	3	2	5	5	1	4	3	3	3	3	0.01689	2.00	0.45354	1.25	0.47642	1.25
sp Q0BWT1 THM_MOUSE	3-ketoadipyl-CoA thiolase, mitochondrial OS=Mus musculus (Mouse)	1089.63	3	2	5	5	10	5	7	5	4	5	8	6	3	3	3	3	0.15926	2.00	0.12798	1.60	0.08200	1.90
sp Q0V5H5 EMIP_MOUSE	EMIP2-interacting protein OS=Mus musculus (Mouse)	713.91	2	2	3	5	6	3	3	4	2	4	2	3	3	3	3	3	0.37390	WT-scr only	0.53454	2.50	0.05897	3.50
sp P23931 FRIL1_MOUSE	Feritin light chain 1 OS=Mus musculus (Mouse)	467.27	4	4	1	4	4	10	8	2	5	5	1	3	3	3	3	3	0.26366	2.00	0.30556	1.67	0.85535	1.00
sp Q09K22 NEUA_MOUSE	N-acetylneuraminate cytidylyltransferase OS=Mus musculus (Mouse)	281.81	2	3	1	3	4	6	3	2	2	5	4	3	3	3	3	2	0.08997	2.17	0.40700	1.17	0.50198	1.50
sp Q0FR41 GNS_MOUSE	N-acetylneuraminate-6-sulfatase OS=Mus musculus (Mouse)	201.79	2	3	1	4	3	5	2	2	3	3	2	3	3	3	3	3	0.03073	2.40	0.18911	1.40	0.03883	1.60
sp Q0C071 AMPL_MOUSE	Cytosol aminopeptidase OS=Mus musculus (Mouse)	432.04	2	2	1	3	4	4	3	1	2	2	1	1	3	3	3	3	0.00921	2.00	0.64337	1.00	0.66877	0.80
sp Q0D005 GNAS_MOUSE	RAD1 dephosphorylation inhibitor 1 OS=Mus musculus (Mouse)	395.53	2	2	1	1	5	4	3	1	2	1	3	2	3	3	3	3	0.62503	0.80	0.62503	0.80	0.16689	1.40
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus (Mouse)	398.21	5	2	3	7	9	9	4	6	3	6	2	2	2	2	2	2	0.16740	2.71	0.62503	1.43	0.77088	0.71
sp Q09JF8 PSP1_MOUSE	PC4 and SFRS1-interacting protein OS=Mus musculus (Mouse)	886.27	3	3	3	3	4	6	7	1	1	4	1	1	2	3	3	3	0.16609	2.17	0.80039	1.33	0.91073	1.00
sp Q0D106 EERP44_MOUSE	Endoplasmic reticulum resident protein 44 OS=Mus musculus (Mouse)	450.38	3	2	3	3	5	6	5	1	2	2	3	3	3	3	3	3	0.07689	2.80	0.49983	1.60	0.24052	1.60
trjA0A0N5W5 A0A0N5W5_MOUSE	N-acetylneuraminate cytidylyltransferase OS=Mus musculus (Mouse)	98.03	2	2	3	3	3	3	3	2	1	4	2	2	2	2	2	2	0.07963	2.25	0.41635	1.50	0.57922	1.50
trjA0A0N5WC3 A0A0N5WC3_MOUSE	N-acetylneuraminate cytidylyltransferase OS=Mus musculus (Mouse)	98.03	2	2	3	3	3	3	3	2	1	4	2	2	2	2	2	2	0.07963	2.25	0.41635	1.50	0.57922	1.50
sp Q0ZVW6 IF2A_MOUSE	Eukaryotic translation initiation factor 2 subunit OS=Mus musculus (Mouse)	738.34	2	2	2	4	5	2	3	2	1	2	2	2	2	3	3	3	0.10592	2.75	0.58977	1.25	0.49505	1.25
sp P97820 M4K4_MOUSE	Mtogen-activated protein kinase kinase kinase OS=Mus musculus (Mouse)	539.88	2	1	3	3	6	3	3	1	2	4	2	2	3	3	3	3	0.16827	2.00	0.96981	1.00	0.18683	1.33
sp Q0JME2 MMN1_MOUSE	Mitogen-activated protein kinase 5 OS=Mus musculus (Mouse)	658.48	2	1	3	5	4	3	3	1	2	5	2	2	2	3	3	3	0.12320	2.00	0.86981	1.00	0.30029	1.50
sp Q0BLV1 PSMD5_MOUSE	26S proteasome non-ATPase regulatory subunit OS=Mus musculus (Mouse)	600.74	2	1	2	2	2	3	3	2	2	4	1	2	2	2	2	2	0.43039	2.00	0.53408	1.67	0.60061	1.67
sp Q07035 ATX2_MOUSE	Ataxin-2 OS=Mus musculus (Mouse) GN=A	520.43	2	1	1	2	3	2	2	1	1	1	2	2	2	3	1	2	0.31005	2.00	0.69382	0.67	0.86894	1.00
sp Q09JY8 LPP3_MOUSE	Lipid phosphate phosphohydrolase 3 OS=Mus musculus (Mouse)	288.01	2	1	1	1	4	2	2	1	2	2	2	2	2	2	2	2	0.28706	2.33	0.97943	1.00	0.72684	0.67
sp Q0JK48 SHL1_MOUSE	Endophilin-B1 OS=Mus musculus (Mouse)	459.95	1	2	1	1	2	5	2	2	2	2	1	1	2	3	1	3	0.29559	2.67	0.73981	0.67	0.49632	1.33
sp Q09J99 THM_MOUSE	3-mercaptopyruvate sulfurtransferase OS=Mus musculus (Mouse)	522.53	2	2	2	3	4	1	2	2	1	3	1	2	2	2	2	2	0.32888	2.00	0.65952	1.50	0.19192	1.25
sp P27545 CERS1_MOUSE	Ceramide synthase 1 OS=Mus musculus (Mouse)	207.92	3	1	3	3	2	2	2	2	1	3	2	2	2	3	2	2	0.27835	2.00	0.69501	1.25	0.73387	1.25
sp Q08759 UB3A_MOUSE	Ubiquitin-protein ligase E3A OS=Mus musculus (Mouse)	394.52	2	1	1	2	1	3	2	1	2	1	2	1	1	1	1	1	0.46624	2.00	0.72795	1.50	0.68821	1.50
sp Q01V64 ISOC1_MOUSE	Isocitrate dehydrogenase domain-containing protein OS=Mus musculus (Mouse)	330.11	1	3	3	6	4	3	4	2	2	6	3	2	2	2	2	2	0.62029	2.00	0.95504	1.00	0.61012	1.50
sp Q0D855 CQRT_MOUSE	Cytochrome b-c1 complex subunit 7 OS=Mus musculus (Mouse)	542.26	1	4	5	4	11	9	4	2	2	6	3	6	3	3	3	3	0.05965	2.14	0.64337	1.14	0.67312	1.29
sp P70189 MB1_MOUSE	Myosin subunit beta-1 OS=Mus musculus (Mouse)	1329.1	1	3	1	3	3	4	10	3	4	6	3	6	3	3	3	3	0.12581	2.40	0.69174	1.40		

Proteins mostly identified in the WT-scr sample with ratio>2:

accession	description	protein_set_score	Exp. from 01/02/2017												# Repl.	Exp. 01/02/2017									
			WT				K1-scr				K1-93					K1-scr / WT-scr		K1-93 / WT-scr							
			1	2	3	1	2	3	1	2	3	1	2	3		WT	K1-scr	ratio	WT	K1-93	ratio	WT	K1-93	ratio	
sp Q15841 FXR1_MOUSE	Fragile X mental retardation syndrome-relat	385.27	4	5	4	2	2	2	2	1	2	3	2	1	3	3	3	2	0.0008	0.46	0.03085	0.46	0.00670	0.23	
sp Q8BIE6 FRMA_MOUSE	FERM domain-containing protein 4A OS=M	428.9	2	3	3	3	1	2	1	2	1	1	1	1	1	3	2	3	2	0.23025	0.50	0.03679	0.50	0.01711	0.25
sp Q92254 PDE2A_MOUSE	cGMP-dependent 3',5'-cyclic phosphodiester	988.71	4	3	3	3	1	3	1	3	1	3	2	3	2	2	2	2	0.10475	0.40	0.08785	0.40	0.19818	0.50	
sp Q0KL02 TRIO_MOUSE	Triple functional domain protein OS=Musc	908.7	2	4	2	2	1	1	1	1	2	1	1	1	1	3	2	1	0.10490	0.38	0.03216	0.38	0.14884	0.50	
sp P61937 NFK2_MOUSE	Nuclear factor-kappa-B protein 2 OS=Muscu	192.49	3	3	2	2	2	2	2	1	2	2	2	2	2	1	1	1	0.13305	0.50	0.03390	0.50	0.05177	0.25	
sp P35922 FMR1_MOUSE	Fragile X mental retardation protein 1 homo	352.01	5	3	2	1	2	1	1	1	1	1	1	1	1	3	3	1	0.09150	0.40	0.03673	0.40	0.05527	0.20	
tr A2AJ7 A2AJ7_MOUSE	MC6130458 OS=Mus musculus (Mouse) G	328.13	3	3	1	2	1	1	1	1	1	1	1	1	1	3	1	3	2	0.15360	0.29	0.12395	0.29	0.11812	0.29
sp Q0AK09 PHF14_MOUSE	14 kDa phosphohistidine phosphatase OS	347.93	2	3	1	1	1	1	1	1	1	2	1	2	1	1	1	1	0.09923	0.33	0.06798	0.33	0.19755	0.33	
sp Q0C996 TM163_MOUSE	Transmembrane protein 163 OS=Mus muscu	136.74	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	0.25703	0.25	0.04527	0.25	0.25286	0.25	
sp Q0L456 QDE1_MOUSE	Cyclic-nucleoside diphosphate phosphodiester	167.97	3	1	2	1	2	1	1	1	1	1	1	1	1	3	2	1	0.24833	0.50	0.07761	0.37	0.09191	0.17	
sp B9EJA2 CTTB2_MOUSE	Corticactin-binding protein 2 OS=Mus muscu	402.27	2	1	1	1	1	1	1	1	1	1	1	1	1	3	2	1	0.21150	0.50	0.09239	0.25	0.10176	0.25	
sp P63248 PKA_MOUSE	cAMP-dependent protein kinase inhibitor al	143.27	2	1	1	1	1	1	1	1	1	1	1	1	1	3	2	2	0.22060	0.50	0.24653	0.50	0.10176	0.25	
sp Q0R5H1 UBP15_MOUSE	Ubiquitin carboxyl-terminal hydrolase 15 OS	83.16	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0.38533	0.33	0.16333	0.33	0.16333	0.33	
sp Q0Q272 GPC1_MOUSE	Colicoid domain-containing protein 177 C	155.85	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.35241	0.33	0.26361	0.33	0.46129	0.50	
sp Q0Z218 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit 1	122.85	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0.67949	0.50	0.65549	0.50	0.37990	WT-scr only	
sp Q0CC85 PABP2_MOUSE	Polyadenylate-binding protein 2 OS=Mus m	171.28	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.67949	0.50	0.72317	0.50	0.75820	0.50	
sp Q3UJH6 WNK2_MOUSE	Serine/threonine-protein kinase WNK2 OS=	114.95	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.64280	0.50	0.72317	0.50	0.37990	WT-scr only	
sp Q0JKN6 NOVA1_MOUSE	RNA-binding protein Nova-1 OS=Mus muscu	174.86	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.64280	0.50	0.37390	WT-scr only	0.73999	0.50	
sp Q0AKM3 OXRI_MOUSE	Oxidation resistance protein 1 OS=Mus mu	240.26	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.37390	WT-scr only	0.72317	0.50	0.37390	WT-scr only	
sp Q0H0A9 CNKR2_MOUSE	Connector enhancer of kinase suppressor C	160.91	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-scr only	0.37390	WT-scr only	0.62723	0.50
sp Q01VE0 S274_MOUSE	Long-chain fatty acid transport protein 4 C	452.26	1	3	5	3	1	1	1	1	1	1	1	1	1	3	2	1	0.27070	0.33	0.23817	0.33	0.19096	0.11	
sp Q092X9 NLGN2_MOUSE	Neurexin-2 OS=Mus musculus (Mouse) G	305.09	1	2	2	1	1	1	1	1	1	1	1	1	1	3	2	0	0.08162	0.40	0.00731	WT-scr only	0.00731	WT-scr only	
sp Q3UJH6 CO177_MOUSE	Coiled-coil domain-containing protein 177 C	119.53	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.01192	0.33	0.01192	0.33	0.01192	0.33	
sp Q0C8D3 VCP1_MOUSE	Deubiquitinating protein VCP1/315 OS=Mus	166.04	1	2	1	1	1	1	1	1	1	1	1	1	1	2	1	0	0.38072	0.33	0.15344	WT-scr only	0.45970	0.33	
sp P63248 TBCD_MOUSE	Tubulin-specific chaperone D OS=Mus mus	353.14	1	2	1	1	1	1	1	1	1	1	1	1	1	2	0	1	0.15344	WT-scr only	0.35814	0.33	0.15344	WT-scr only	
tr P70245 EBP_MOUSE	3-beta-hydroxysteroid-Delta(8),Delta(7)stero	47.77	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	0.12156	0.33	0.09556	0.33	0.00000	WT-scr only	
sp Q0P610 SNR40_MOUSE	US 53k nuclear ribonucleoprotein A0 4 kb; J	55.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.53515	0.50	0.49429	0.50	0.11633	WT-scr only	
tr F59P89 PVP_MOUSE	Protein Zc3h7b OS=Mus musculus (Mouse	55.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.53515	0.50	0.49429	0.50	0.11633	WT-scr only	
sp Q11136 PEPD_MOUSE	Xaa-Pro dipeptidase OS=Mus musculus (M	365.02	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.53515	0.50	0.60884	0.50	0.66668	0.50	
sp Q0D7A8 ARMC1_MOUSE	Armadillo repeat-containing protein 1 OS=	106.85	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.53515	0.50	0.60884	0.50	0.66668	0.50	
tr F7C897 F7C89_MOUSE	CAP-Gly domain-containing linker protein 1	201.92	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.47270	0.50	0.49429	0.50	0.52635	0.50	
sp Q0SS3M RH44_MOUSE	RhoGAP-activating protein 4 OS=Mus muscu	336.94	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.47270	0.50	0.49429	0.50	0.52635	0.50	
sp Q09KN9 EPN4_MOUSE	Clastrin interactor 1 OS=Mus musculus (M	164.74	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.49655	0.50	0.11633	WT-scr only	0.11633	WT-scr only	
sp Q0F2E8 TAOK1_MOUSE	Serine/threonine-protein kinase TAO1 OS=	69.25	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.11633	WT-scr only	0.35219	0.33	0.06379	0.50	
sp Q0P9U7 INW02_MOUSE	NACHT and WD repeat domain-containing p	154.86	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0.34148	0.33	0.16219	0.33	0.44622	0.33	
sp Q0B712 S4AT_MOUSE	Sodium bicarbonate cotransporter 3 OS=M	55.15	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.51472	0.50	0.58634	0.50	0.11616	WT-scr only	
sp Q09KX1 MLE2_MOUSE	Myeloid leukemia factor 2 OS=Mus muscu	129.99	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.51472	0.50	0.58634	0.50	0.11616	WT-scr only	
sp Q0P9B3 GALT2_MOUSE	Sulfatase N-acetylgalactosaminyltransfer	84.93	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.45451	0.50	0.47527	0.50	0.11616	WT-scr only	
sp Q0TEK5 VKORL_MOUSE	Vitamin K epoxide reductase complex subu	106.69	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.47466	0.50	0.56392	0.50	0.13637	0.50	
sp P52795 EFN1_MOUSE	Ephrin-B1 OS=Mus musculus (Mouse) GN=	38.54	1	2	2	2	1	1	1	1	1	1	1	1	1	2	0	1	0.11616	WT-scr only	0.11616	WT-scr only	0.64301	0.50	
sp Q09112 LANC1_MOUSE	Lancin-1 OS=Mus musculus (Mouse) GN=	244.51	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	0.24050	0.50	0.24050	0.50	0.48711	0.50	
sp Q02204 P5CR2_MOUSE	Pyruvate-5-carboxylase reductase 2 OS=M	135.56	3	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	0.59098	0.50	0.33338	0.25	0.38383	0.25	
sp P61087 UBE2K_MOUSE	Ubiquitin-conjugating enzyme E2 K OS=M	319.64	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.15120	WT-scr only	0.35349	0.33	0.36950	0.33	
tr D324C5 D324C5_MOUSE	Protein Ceif5 OS=Mus musculus (Mouse) C	123.27	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.69646	0.50	0.37390	WT-scr only	0.37390	WT-scr only	
sp P52479 UBP10_MOUSE	Ubiquitin carboxyl-terminal hydrolase 10 OS	189.71	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.67090	0.50	0.37390	WT-scr only	0.77848	0.50	
sp Q03398 PDE1_MOUSE	3',5'-cyclic phosphodiesterase 1 OS=Mus	114.15	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.37390	WT-scr only	0.47428	0.50	0.56585	0.50	
sp Q05483 CSK2_MOUSE	Cas kinase II subunit alpha' OS=Mus mu	254.63	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.52850	0.50	0.60146	0.50	0.11658	WT-scr only	
sp P62482 KCB2_MOUSE	Voltage-gated potassium channel subunit b	144.26	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.52850	0.50	0.57867	0.50	0.11658	WT-scr only	
sp Q02201 MARC2_MOUSE	Mitochondrial amidoxime reductase compone	229.77	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.52850	0.50	0.11658	WT-scr only	0.51712	0.50	
sp Q09079 CPE_MOUSE	Cationic protein 1 OS=Mus musculus (Mou	253.82	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.52850	0.50	0.57867	0.50	0.11658	WT-scr only	
sp Q04A48 UBP7_MOUSE	Ubiquitin carboxyl-terminal hydrolase 7 OS=	493.04	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.48750	0.50	0.11658	WT-scr only	0.51712	0.50	
sp Q04133 AOF4_MOUSE	Amine oxidase (flavin-containing) A OS=M	328.41	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.48750	0.50	0.11658	WT-scr only	0.11658	WT-scr only	
tr M0C9J9 M0C9J9_MOUSE	Protein Tmem78b OS=Mus musculus (Mo	64.67	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.11658	WT-scr only	0.57867	0.50	0.11658	WT-scr only	
sp Q0L0K0 SED1_MOUSE	SEC14 domain and spectrin repeat-contain	328.02	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.11658	WT-scr only	0.57867	0.50	0.11658	WT-scr only	
sp Q0C8Z5 SMC1A_MOUSE	Structural maintenance of chromosomes pr	144.72	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	0.37390	WT-scr only	0.71013	0.50	0.72094	0.50	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3														

accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	WT_0-93	WT_0-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp P28352 APEX1_MOUSE	DNA-(apurinic or apyrimidinic site) lyase OS	244.71	1	2	1	1	1	1	2	1	1	3	1	2	2	0.08215	0.25	0.79785	0.75	0.81207	1.00		
sp Q9WUJ1 CHIP_MOUSE	STP1 homology and U box-containing prot	262.29	1	2	1	1	1	1	3	1	1	2	1	2	3	0.34651	0.33	0.67150	1.33	0.36970	1.67		
sp Q55019 IMPCT_MOUSE	Protein IMPACT OS=Mus musculus (Mus)	206.1	1	2	2	1	1	1	1	1	1	1	1	2	2	0.15344	WT-wt only	0.91773	1.00	0.74503	0.67		
sp Q3C9V9 PUR9_MOUSE	Bifunctional protein biosynthesis protein PUF	491.4	1	2	1	1	1	1	2	3	2	1	1	2	0	0.15344	WT-wt only	0.92710	1.00	0.90979	1.00		
sp Q7M73 NDUAC_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	504.77	1	1	3	1	1	1	5	1	3	3	2	3	3	0.14448	0.20	0.33905	1.80	0.16220	1.60		
sp Q99L18 HGS_MOUSE	Hepatocyte growth factor-regulated tyrosine	317.61	1	1	1	1	1	1	1	2	1	1	3	3	1	0.08314	0.33	0.91815	1.00	0.59770	1.33		
sp Q62174 HNRLL_MOUSE	Heterogeneous nuclear ribonucleoprotein L	368.35	1	1	1	1	1	1	2	1	1	1	1	3	0	0.00000	WT-wt only	0.98875	1.00	0.65731	0.67		
sp Q3UKU3 CRUK3_MOUSE	Ubiquitin-like uncharacterized protein OS=Mus	154.54	1	1	1	1	1	1	1	1	1	1	1	3	0	0.00000	WT-wt only	0.98875	1.00	0.65731	0.67		
sp Q5DU25 IQEC2_MOUSE	IQ motif and SEC domain-containing protein	116.53	1	1	1	1	1	1	1	1	1	1	1	3	0	0.00000	WT-wt only	0.53068	0.67	0.65731	0.67		
sp Q9KJ81 MYG1_MOUSE	UPF0160 protein MYG1, mitochondrial OS	157.59	1	1	1	1	1	1	3	2	2	1	2	1	1	0.53515	0.50	0.78782	1.50	0.94411	1.00		
sp P12025 MK_MOUSE	Middle kinase OS=Mus musculus (Mouse) GN=M	113.84	1	1	1	1	1	1	1	1	1	1	1	2	1	0.53515	0.50	0.96234	1.00	0.89255	1.00		
sp P7E2AX FRZAX_MOUSE	Frizzled-related protein 1 OS=Mus m	174.67	1	1	1	1	1	1	2	2	1	1	1	2	1	0.50	0.50	0.97144	1.00	0.97144	1.00		
sp Q9G677 EXOC8_MOUSE	Exocyst subunit component 8 OS=Mus m	193.78	1	1	1	1	1	1	2	1	1	1	1	2	0	0.11633	WT-wt only	0.60271	1.50	0.87133	1.00		
sp P28063 PSB8_MOUSE	Proteasome subunit beta type-8 OS=Mus m	50.08	1	1	1	1	1	1	1	1	1	1	1	2	0	0.11633	WT-wt only	0.96234	1.00	0.98255	1.00		
sp Q30TLH PRC2_MOUSE	Protein PRC2 OS=Mus musculus (Mus)	203.68	1	1	1	1	1	1	1	1	1	1	1	2	1	0.51472	0.50	0.97826	1.00	0.90617	1.00		
sp Q96W12 PEF5_MOUSE	Peroxisomal targeting signal 1 receptor OS	168.27	1	1	1	1	1	1	1	1	1	1	1	2	0	0.45451	0.50	0.97826	1.00	0.90617	1.00		
sp Q9CAK1 C24T1_MOUSE	Activator transcription factor 7 homolog 1 (loc	73.12	1	1	1	1	1	1	1	1	1	1	1	2	0	0.11616	WT-wt only	0.97826	1.00	0.97826	1.00		
sp Q9D1L0 CHCH2_MOUSE	Coiled-coil helix-coiled-coil helix domain-con	43.11	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.99229	1.00		
sp Q98WQ2 VAC14_MOUSE	Protein VAC14 homolog OS=Mus musculus	191.47	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.99308	1.00		
sp Q9R146 AFPH_MOUSE	Acylamino-acid-releasing enzyme OS=Mus	105.09	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.99308	1.00		
sp P62322 LSME_MOUSE	Ub1 snRNP-associated Sm-like protein LSME	113.86	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.99308	1.00		
sp Q9R0G7 SPNS1_MOUSE	Protein spindler homolog 1 OS=Mus muscu	48.19	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.91525	1.00		
sp Q35691 PINN_MOUSE	Pinin OS=Mus musculus (Mouse) GN=Pnn	127.09	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96559	1.00	0.91525	1.00		
sp Q8J20 LINTA_MOUSE	Protein lin-7 homolog A OS=Mus musculus	254.8	1	2	2	1	1	1	3	1	1	2	2	2	3	0.40451	0.50	0.70222	1.25	0.90700	1.00		
sp P99029 OC9E_MOUSE	Cytochrome b-c1 complex subunit 6, mitoch	193.84	2	2	1	1	1	1	1	1	1	1	1	1	3	0.37568	0.33	0.80000	1.00	0.79859	1.00		
sp Q4JIM5 ABL2_MOUSE	Ablotin uncharacterized protein OS=Mus m	140.08	1	1	1	1	1	1	2	1	1	1	1	1	3	0.37568	0.33	0.80000	1.00	0.79859	1.00		
sp Q9CT10 RANB3_MOUSE	Ran-binding protein 3 OS=Mus musculus (M	241.55	1	1	1	1	1	1	2	1	1	1	1	2	2	0.48750	0.50	0.80004	1.00	0.79859	1.00		
sp Q9BCH1 INGEF_MOUSE	Ephexin-1 OS=Mus musculus (Mouse) GN=	451.11	1	1	1	1	1	1	2	1	1	1	1	2	0	0.11658	WT-wt only	0.56888	1.50	0.51885	1.50		
sp Q35857 TIM44_MOUSE	Mitochondrial import inner membrane transp	254.37	5	1	1	1	1	1	1	1	1	1	1	1	1	0.37390	WT-wt only	0.99012	1.00	0.98315	1.00		
sp Q9B0C3 S3F1_MOUSE	Solanum family 35 member F1 OS=Mus m	67.68	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.94927	1.00	0.98065	1.00		
sp Q90963 PAFA_MOUSE	Platelet-activating factor acetyltransferase O	40.98	1	1	1	1	1	1	1	1	1	1	1	1	0	0.37390	WT-wt only	0.96663	1.00	0.98065	1.00		
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	WT_0-93	WT_0-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
tr D3Y262 D3Y262_MOUSE	Unconventional myosin-Va OS=Mus muscu	3353.369	12	27	23	7	23	24	7	9	8	6	13	12	3	0.59991	0.87	0.05629	0.27	0.18386	0.50		
sp P31786 ACKP_MOUSE	Acy-CoA-binding protein OS=Mus muscu	556.82	7	16	3	6	9	3	7	4	4	10	2	3	3	0.51424	0.69	0.30399	0.42	0.40120	0.46		
sp Q9Q2E5 COP1_MOUSE	Cytochrome P-450 CYP1B1 OS=Mus muscu	621.21	6	5	4	2	2	2	2	2	2	2	2	2	3	0.37571	0.53	0.90761	0.60	0.64281	0.53		
sp Q12A2 SRP3_MOUSE	SLIT-ROBO Rho GTPase-activating protein	699.06	6	2	6	2	2	2	2	2	2	2	2	2	0	0.80408	1.25	0.21054	0.50	0.57822	0.50		
sp P99027 RLA2_MOUSE	60S acidic ribosomal protein P2 OS=Mus m	438.56	7	3	9	3	4	4	4	4	4	4	4	4	1	0.86116	1.20	0.44090	0.40	0.46042	0.40		
sp Q50542 SYUA_MOUSE	Alpha-synuclein OS=Mus musculus (Mouse)	507.69	5	13	1	4	4	2	2	5	1	1	3	2	3	0.43052	0.53	0.41642	0.42	0.32893	0.32		
sp Q60625 ICAM5_MOUSE	Intercellular adhesion molecule 5 OS=Mus	557.71	3	8	9	6	10	3	2	6	2	3	4	3	3	0.81016	0.95	0.28572	0.50	0.16397	0.35		
sp Q3UG14 Q3UG14_MOUSE	Ubiquitin-like uncharacterized protein OS=	145.94	4	6	5	4	4	4	3	4	3	3	3	2	1	0.80282	1.13	0.2457	0.40	0.63934	0.40		
sp Q9DCS9 NDUBA_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	659.61	2	6	3	6	6	3	4	1	1	3	2	3	2	0.48176	1.36	0.27486	0.45	0.29663	0.45		
sp Q60780 GAS7_MOUSE	Growth arrest-specific protein 7 OS=Mus m	633.39	4	3	6	7	6	4	4	1	2	1	2	3	2	0.47499	1.31	0.13865	0.38	0.03407	0.15		
sp Q50544 IBR_MOUSE	Active biphosphatase cluster region-related	612.47	4	3	4	6	6	4	3	1	1	2	3	3	2	0.14812	1.45	0.04806	0.45	0.19407	0.45		
sp Q9WU17 AR3_MOUSE	Diphosphoamino transferase 3 OS=Mus m	571.78	3	4	2	4	2	3	4	2	2	2	2	2	0	0.65330	0.13	0.92920	0.40	0.46281	0.40		
sp Q90631 GRB2_MOUSE	Growth factor receptor-bound protein 2 OS	523.77	3	4	4	2	3	2	3	2	3	2	3	2	1	0.35053	0.82	0.12726	0.45	0.01537	0.18		
sp Q9VD75 HIP1_MOUSE	Huntingtin-interacting protein 1 OS=Mus m	726.08	4	4	2	4	2	3	1	2	1	2	2	3	3	0.66931	0.90	0.06810	0.40	0.12633	0.40		
sp Q35382 EXOC4_MOUSE	Exocyst component 4 OS=Mus m	474.06	2	2	2	3	3	2	1	1	1	2	3	3	3	0.18724	1.33	0.00019	0.50	0.11391	0.33		
sp Q7TDD2 TPP9_MOUSE	Tubulin polymerization-promoting protein O	510.47	4	5	3	5	4	2	1	1	4	1	3	3	1	0.68860	0.92	0.03040	0.48	0.15251	0.50		
sp P91410 SRF3_MOUSE	SRF family transcription factor 3 OS=M	221.22	2	2	1	5	4	2	2	2	1	2	2	3	2	0.90113	0.57	0.04623	0.40	0.04623	0.40		
sp Q9BYM5 NLGN3_MOUSE	Neurigin-3 OS=Mus musculus (Mouse) GI	467.43	2	5	3	3	3	3	1	2	2	2	3	3	2	0.32121	0.75	0.07071	0.25	0.04933	0.17		
tr D3YV77 D3YV77_MOUSE	Protein Novx-2 OS=Mus musculus (Mouse)	320.7	5	2	2	2	3	4	4	1	1	1	3	3	2	0.89038	1.00	0.10480	0.22	0.30734	0.33		
sp Q91Y12 SNM4_MOUSE	Sorting nexin-4 OS=Mus musculus (Mouse)	584.07	3	2	2	2	2	2	2	1	1	1	1	1	1	0.22854	0.86	0.03468	0.14	0.01028	0.14		
sp Q9J4H6 NDU3_MOUSE	Cytochrome b-c1 complex subunit 3 OS=	660.91	2	1	1	3	1	1	1	1	3	1	2	2	0	0.39187	0.67	0.01947	0.40	0.01947	0.40		
sp Q88737 BSN_MOUSE	Protein bassoon OS=Mus musculus (Mus)	842.14	2	3	2	2	3	1	1	1	1	1	1	1	3	0.44177	1.71	0.02805	0.29	0.02825	0.29		
sp Q9DD03 RAB13_MOUSE	Ras-related protein Rab-1																						

sp P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus (Mouse) GN=C	2235.44	72	72	62	61	75	81	67	58	70	58	49	54	3	3	3	3	0.97041	1.05	0.98663	0.95	0.06549	0.78
sp P41042 TKT_MOUSE	Transketolase OS=Mus musculus (Mouse)	3070.63	72	63	76	74	69	81	66	63	71	51	55	51	3	3	3	3	0.90697	1.06	0.98804	0.95	0.26371	0.79
sp P44227 STMY1_MOUSE	Stathmin OS=Mus musculus (Mouse) GN=C	1974.47	72	70	38	38	36	34	67	47	52	74	33	34	3	3	3	3	0.73986	1.12	0.74409	1.04	0.56364	0.79
sp P18872 GNAO_MOUSE	Guanine nucleotide-binding protein (G <i>o</i>) subunit alpha-1 OS=Mus musculus (Mouse)	3103.13	72	85	85	75	82	79	64	69	65	61	72	3	3	3	3	3	0.28745	0.98	0.19479	0.82	0.25209	0.81
sp O08599 STXB1_MOUSE	Syntaxin-13 OS=Mus musculus (Mouse)	4381.2	71	86	89	81	91	83	68	63	68	81	73	59	3	3	3	3	0.87432	1.04	0.14623	0.81	0.83733	0.87
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus (Mouse)	2272.18	71	65	60	62	62	49	105	79	44	127	69	50	3	3	3	3	0.93989	1.06	0.43674	1.16	0.27538	1.26
sp Q1C513 DRC15_MOUSE	Putative uncharacterized protein OS=Mus musculus (Mouse)	4071	70	72	72	72	84	76	88	77	64	52	62	65	3	3	3	3	0.31767	1.08	0.17232	1.07	0.48848	0.84
sp P43252 PF2_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus (Mouse)	4127.70	70	72	69	69	69	73	70	77	63	52	56	55	3	3	3	3	0.38630	1.18	0.20107	1.12	0.19153	0.87
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus (Mouse)	2191.09	68	64	60	67	57	53	92	70	47	113	65	3	3	3	3	3	0.95904	1.03	0.47381	1.09	0.25354	1.19
sp A2A070 TBB1_MOUSE	Tubulin beta-1 chain OS=Mus musculus (Mouse)	604.49	67	51	57	50	55	60	60	53	55	54	53	60	3	3	3	3	0.35111	0.94	0.19299	0.96	0.53949	0.95
sp P42806 H4_MOUSE	Histone H4 OS=Mus musculus (Mouse)	1524.11	67	66	64	64	64	64	64	64	64	64	64	64	3	3	3	3	0.15212	0.91	0.14129	0.91	0.19429	0.89
sp Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus (Mouse)	1630.09	67	104	86	97	90	83	85	96	62	97	96	65	3	3	3	3	0.95443	1.05	0.94626	0.95	0.48084	1.00
sp Q02053 UBA1_MOUSE	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus (Mouse)	4244.72	66	71	68	61	74	76	70	59	72	62	63	69	3	3	3	3	0.66915	1.03	0.60200	0.98	0.43456	0.95
sp P10853 H2B1F_MOUSE	Histone H2B type 1-F/UL OS=Mus musculus (Mouse)	1615.7	66	105	86	95	90	84	54	67	60	96	95	64	3	3	3	3	0.97734	1.05	0.99515	1.04	0.52929	0.99
sp Q88723 ACTL7_MOUSE	Beta-actin-like protein 7 OS=Mus musculus (Mouse)	2196.23	64	81	77	71	76	54	61	60	75	47	60	78	3	3	3	3	0.22123	0.93	0.52819	0.85	0.83843	0.83
sp P15864 H12_MOUSE	Histone H1.12 OS=Mus musculus (Mouse)	1150.47	64	22	28	32	32	32	82	56	62	109	42	3	3	3	3	3	0.98133	1.00	0.74275	1.02	0.40055	1.17
sp Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus (Mouse)	1627.68	62	95	85	90	84	80	74	93	61	87	90	64	3	3	3	3	0.96563	1.05	0.98357	0.94	0.48536	1.00
sp Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus (Mouse)	1583	60	95	85	86	84	81	75	90	60	85	87	63	3	3	3	3	0.99182	1.05	0.99111	0.94	0.54793	0.98
sp P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus (Mouse)	1590.94	60	92	85	87	81	80	74	90	51	96	87	64	3	3	3	3	0.98612	1.05	0.95705	0.95	0.46409	1.00
sp Q8C027 H2B1F_MOUSE	Histone H2B type 1-F OS=Mus musculus (Mouse)	1543.56	55	90	85	81	81	81	68	88	60	78	85	63	3	3	3	3	0.94467	1.06	0.99311	0.94	0.54106	0.99
sp Q8C0V8 H133B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus (Mouse)	2707.711	58	79	68	68	70	63	68	58	55	57	54	48	3	3	3	3	0.50935	0.98	0.43526	0.88	0.25254	0.78
sp P19821 H143G_MOUSE	14-3-3 protein gamma OS=Mus musculus (Mouse)	2560.041	63	72	73	70	78	78	74	58	53	71	52	48	3	3	3	3	0.52367	0.99	0.38709	0.89	0.35441	0.82
sp P50516 VATA_MOUSE	V-type proton ATPase catalytic subunit A OS=Mus musculus (Mouse)	3286.76	61	67	61	68	77	68	62	45	53	58	51	52	3	3	3	3	0.70942	1.07	0.02565	0.85	0.29970	0.85
sp P50396 GDA_MOUSE	Rap GTP dissociation inhibitor alpha OS=Mus musculus (Mouse)	3418.31	55	66	59	55	68	59	53	52	54	56	51	49	3	3	3	3	0.51981	1.01	0.32222	0.88	0.76960	0.87
sp P50281 VATB2_MOUSE	V-type proton ATPase subunit B OS=Mus musculus (Mouse)	1937.99	57	64	60	61	61	57	60	61	61	61	61	61	3	3	3	3	0.98531	1.05	0.65631	0.95	0.25281	0.85
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus (Mouse)	2496.59	54	61	60	61	57	74	51	60	66	48	48	3	3	3	3	3	0.48456	1.00	0.29023	1.04	0.66007	0.92
sp P62874 GBB1_MOUSE	Guanine nucleotide-binding protein (G <i>i</i>) beta-1 OS=Mus musculus (Mouse)	2951.47	60	61	61	66	76	63	70	63	59	67	50	54	3	3	3	3	0.23162	1.13	0.04766	1.05	0.13135	0.94
sp P20122 VIME_MOUSE	Vimentin OS=Mus musculus (Mouse) GN=C	2787.57	51	37	55	68	45	93	83	40	78	73	44	83	3	3	3	3	0.29822	1.44	0.18952	1.41	0.12818	1.40
sp P50533 DLC_MOUSE	Disulfide isomerase OS=Mus musculus (Mouse)	2175.609	54	54	54	54	54	54	54	54	54	54	54	54	3	3	3	3	0.16273	1.18	0.20734	1.22	0.19134	1.22
sp Q5H28 OSH2B_MOUSE	isocitrate dehydrogenase (NADP) OS=Mus musculus (Mouse)	3016.47	59	54	55	53	62	67	56	45	64	47	39	54	3	3	3	3	0.66033	1.08	0.76730	0.98	0.63063	0.83
sp Q88844 DHC_MOUSE	isocitrate dehydrogenase (NADP) cytoplasmic isoform OS=Mus musculus (Mouse)	3016.47	59	54	55	53	62	67	56	45	64	47	39	54	3	3	3	3	0.66033	1.08	0.76730	0.98	0.63063	0.83
sp P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musculus (Mouse)	6085.921	60	43	40	39	65	65	58	47	51	42	31	46	3	3	3	3	0.58459	1.18	0.33628	1.09	0.74159	0.83
sp Q8R097 UOJ1_MOUSE	Ubiquitin carboxyl-terminal hydrolase isozyme 1 OS=Mus musculus (Mouse)	1960.23	62	51	54	58	60	64	62	50	50	41	52	3	3	3	3	3	0.64411	1.09	0.13179	0.97	0.63270	0.94
sp P27773 PDIA3_MOUSE	Protein disulfide-isomerase A3 OS=Mus musculus (Mouse)	2512.19	52	21	21	21	21	21	72	72	72	72	72	3	3	3	3	3	0.10489	1.01	0.07489	1.01	0.07489	1.01
sp P62259 H1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus (Mouse)	2298.8	40	52	49	41	55	57	59	36	43	54	34	44	3	3	3	3	0.77943	0.99	0.86400	0.98	0.73503	0.93
sp D5MR34 D5MR34_MOUSE	Tubulin beta 3 OS=Mus musculus (Mouse)	938.37	62	43	52	42	49	57	52	50	53	49	46	51	3	3	3	3	0.76518	1.01	0.75906	0.99	0.70808	0.93
sp Q3U1B1 Q3U1B1_MOUSE	Putative uncharacterized protein OS=Mus musculus (Mouse)	2422.72	53	52	52	55	66	56	60	54	50	59	45	46	3	3	3	3	0.18273	1.13	0.07877	1.04	0.08247	0.96
sp P20029 GRF7_MOUSE	Grb7 OS=Mus musculus (Mouse)	2023.38	59	60	50	50	50	50	63	65	65	65	65	65	3	3	3	3	0.99335	1.05	0.96335	1.05	0.26821	0.82
sp Q3U292 Q3U292_MOUSE	Putative uncharacterized protein OS=Mus musculus (Mouse)	1850.77	62	57	51	81	56	42	87	64	39	103	57	42	3	3	3	3	0.94965	1.05	0.91928	1.12	0.23237	1.19
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus (Mouse)	708.89	49	49	45	61	49	47	70	48	40	64	42	37	3	3	3	3	0.68280	1.10	0.32805	1.10	0.39959	1.00
sp Q89K0 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus (Mouse)	3506.08	37	51	49	48	54	54	55	41	57	49	42	47	3	3	3	3	0.40827	1.14	0.28214	1.12	0.23616	1.01
sp P17156 GRP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus (Mouse)	1658.99	55	52	55	49	57	49	45	52	52	42	50	52	3	3	3	3	0.17150	0.97	0.53358	0.93	0.22226	0.90
sp P28652 KCCB2_MOUSE	Calcium/calmodulin-dependent protein kinase beta OS=Mus musculus (Mouse)	2884.94	40	38	38	38	38	38	43	39	38	38	38	38	3	3	3	3	0.76244	1.01	0.76244	1.01	0.76244	1.01
sp P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial OS=Mus musculus (Mouse)	2994.14	42	45	46	42	44	45	45	40	43	40	46	37	3	3	3	3	0.20162	0.98	0.75123	0.96	0.67183	0.92
sp Q8R1M2 H2A_MOUSE	Histone H2A-J OS=Mus musculus (Mouse)	654.89	47	45	44	51	45	44	54	47	40	42	37	3	3	3	3	3	0.86651	1.03	0.25228	1.04	0.71890	0.90
sp P14152 HDC_MOUSE	Malate dehydrogenase, cytoplasmic OS=Mus musculus (Mouse)	1884.12	42	48	51	46	60	50	52	45	44	48	40	37	3	3	3	3	0.57409	1.11	0.46693	1.00	0.99099	0.89
sp Q8D061 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus (Mouse)	2477.81	42	48	48	48	48	48	48	48	48	48	48	48	3	3	3	3	0.58871	1.02	0.58871	1.02	0.58871	1.02
sp P46460 NSF_MOUSE	Vesicle-fusion ATPase OS=Mus musculus (Mouse)	2997.06	46	54	54	45	61	49	50	49	53	38	39	36	3	3	3	3	0.61776	1.01	0.60911	0.99	0.10150	0.73
sp Q1553 FSCN1_MOUSE	Fascin OS=Mus musculus (Mouse) GN=C	2681.931	44	47	39	44	52	50	49	37	47	44	37	40	3	3	3	3						

sp Q0B20 ATP0_MOUSE	ATP synthase subunit O, mitochondrial OS	1315.36	25	24	26	24	23	20	27	24	22	25	26	3	3	3	3	0.12715	0.89	0.94303	0.95	0.42531	0.97
sp P06843 FAA1_MOUSE	Eukaryotic initiation factor 4A1 OS=Mus mus	1655.42	25	24	21	26	25	27	27	24	24	25	26	3	3	3	3	0.36697	1.11	0.72809	0.99	0.19820	1.01
sp P03151 CFD_MOUSE	-complex protein 1 subunit delta OS=Mus	251.58	26	24	20	20	26	27	16	22	24	24	25	3	3	3	3	0.58154	0.98	0.92292	0.87	0.48243	0.94
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus muscu	1285.56	25	23	23	21	24	25	16	28	23	18	23	3	3	3	3	0.26624	0.99	0.94254	0.94	0.75040	0.92
sp P10630 F4A2_MOUSE	Eukaryotic initiation factor 4A1i OS=Mus m	1592.2	24	22	18	21	21	21	21	17	20	20	16	23	3	3	3	0.51482	0.98	0.63868	0.91	0.74342	0.92
sp Q0C213 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mito	1592.5	26	19	26	24	29	19	23	25	22	29	19	22	3	3	3	0.82109	1.01	0.78180	0.99	0.49512	0.99
sp P03355 PCBP1_MOUSE	Poly(C)binding protein 1 OS=Mus muscu	1227.62	16	16	14	15	16	12	20	17	14	14	22	3	3	3	3	0.22981	0.98	0.54707	1.07	0.36510	1.09
sp P17426 AR2A1_MOUSE	Ar2 domain-containing protein 1 OS=Mus	1476.76	25	21	25	25	22	22	22	22	22	22	22	3	3	3	3	0.28260	1.07	0.72177	1.00	0.28260	1.00
sp P03171 TCP2_MOUSE	T-complex protein 1 subunit zeta OS=Mus	1823.75	24	24	21	17	23	24	21	24	21	14	21	3	3	3	3	0.29266	0.94	0.37216	1.00	0.44261	0.81
sp P03001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1	887.79	25	21	21	24	23	22	20	22	23	18	22	20	3	3	3	0.85622	1.03	0.79911	0.97	0.88217	0.90
sp P17710 HKK1_MOUSE	Hekoxinase-1 OS=Mus musculus (Mouse)	2637.04	24	20	25	20	22	24	26	19	18	26	20	3	3	3	3	0.59993	0.96	0.93222	0.80	0.36854	0.84
sp Q01655 DOK1_MOUSE	Docking protein 1 OS=Mus musculus (Mou	1164.2	11	15	14	15	15	14	14	14	14	14	14	3	3	3	3	0.13366	1.41	0.03308	1.44	0.03366	1.44
sp P02922 EPZF0_MOUSE	Nucleoside diphosphate kinase OS=Mus r	860.91	19	20	19	20	21	25	20	23	23	24	20	3	3	3	3	0.89969	1.05	0.00372	1.17	0.34555	0.98
sp P05201 AACT_MOUSE	Aspartate aminotransferase, cytoplasmic O	1688.59	19	25	18	22	26	14	18	15	22	19	13	3	3	3	3	0.82338	1.00	0.53736	1.05	0.73105	0.84
sp Q13UM7 Q3UM7_MOUSE	Putative uncharacterized protein OS=Mus	1676.06	23	27	19	27	29	20	30	22	21	29	23	19	3	3	3	0.09508	1.23	0.35112	1.06	0.25465	1.03
sp Q0A16 THIO_MOUSE	Acetyl-CoA acetyltransferase, cytosolic OS	1558.24	25	21	25	21	28	27	21	22	28	18	17	3	3	3	3	0.88835	1.07	0.70551	1.00	0.21772	0.76
sp Q05W89 OSW89_MOUSE	Protein Rat-1a OS=Mus musculus (Mouse)	1596.53	25	22	27	20	26	19	19	19	18	19	18	3	3	3	3	0.29463	0.95	0.68925	0.95	0.33071	0.78
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mu	2185.8	16	16	16	17	20	22	19	17	17	14	19	3	3	3	3	0.07038	1.23	0.00681	1.10	0.16928	1.04
sp P08752 GNA2_MOUSE	Guanine nucleotide-binding protein (G <i>β</i>) su	1513.98	20	23	21	22	25	23	22	12	14	26	19	3	3	3	3	0.23677	1.09	0.10215	0.75	0.19384	0.98
sp P03178 TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=Mu	1967.26	25	22	21	14	24	24	16	19	19	23	17	3	3	3	3	0.35297	0.91	0.28981	0.81	0.35363	0.85
sp P00585 HZAZ_MOUSE	Histone H2AZ OS=Mus musculus (Mouse)	433.71	18	17	18	21	16	10	24	20	18	22	16	3	3	3	3	0.91783	1.06	0.02754	1.17	0.02681	1.06
sp P02821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musc	1573.59	27	25	26	20	20	26	18	19	23	18	15	3	3	3	3	0.42549	0.97	0.06814	0.81	0.30136	0.78
sp P56399 UBP5_MOUSE	Ubiquitin carboxyl-terminal hydrolase 5 OS	2002.94	15	18	20	19	24	25	16	14	13	14	15	3	3	3	3	0.13046	1.28	0.19480	0.81	0.93314	0.89
sp Q01900 PCBP2_MOUSE	Poly(C)binding protein 2 OS=Mus muscu	957.31	15	14	14	13	11	17	14	16	14	16	13	3	3	3	3	0.41649	0.93	0.55743	1.00	0.15873	1.07
sp Q0B033 AP2B1_MOUSE	AP-2 complex subunit beta OS=Mus muscu	2965.74	18	21	15	18	22	22	15	15	15	12	13	3	3	3	3	0.33373	1.15	0.18441	0.93	0.69123	0.94
sp Q05802 GPR4_MOUSE	Neutrophin receptor OS=Mus musculus (M	940.55	18	21	25	21	25	19	15	16	16	11	18	3	3	3	3	0.92696	1.05	0.01626	1.23	0.69013	0.95
sp Q13JL8 Q3TL8_MOUSE	Putative uncharacterized protein OS=Mus	1544.02	14	14	15	14	15	19	18	16	12	11	18	3	3	3	3	0.92696	1.05	0.01626	1.23	0.69013	0.95
sp Q02288 PDIa6_MOUSE	Protein disulfide-isomerase A6 OS=Mus m	1372.08	13	13	15	14	15	15	16	16	17	11	11	3	3	3	3	0.76327	0.107	0.01422	1.24	0.64924	0.98
sp Q09C22 ATPH_MOUSE	ATP synthase subunit e, mitochondrial OS	984.51	17	21	16	19	24	21	23	19	19	24	19	3	3	3	3	0.16647	1.19	0.04329	1.13	0.05103	1.11
sp P07765 H2AX_MOUSE	Histone H2AX OS=Mus musculus (Mouse)	593.44	22	17	15	18	17	19	21	22	12	29	17	3	3	3	3	0.59905	0.91	0.21484	0.87	0.18512	1.02
sp Q08809 DCI_MOUSE	Neuronal migration protein doublecortin OS	1375.84	23	21	21	23	22	24	25	20	19	21	17	3	3	3	3	0.83381	1.06	0.57601	0.98	0.60520	0.86
sp Q0BH59 CMC1_MOUSE	Calcium-binding mitochondrial carrier protei	2199.38	11	19	19	15	17	16	17	13	19	12	17	3	3	3	3	0.70548	0.98	0.91716	1.00	0.74365	0.94
sp Q09P71 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus	1194.46	24	28	18	22	27	26	30	21	18	25	14	17	3	3	3	0.84142	1.07	0.83961	0.99	0.49663	0.80
sp Q01758 NDKB_MOUSE	Nucleoside diphosphate kinase B OS=Mus	771.67	18	17	15	18	17	19	21	16	19	20	17	3	3	3	3	0.55236	1.10	0.05952	1.12	0.62216	0.96
sp P17879 HST1B_MOUSE	Heat shock 70 kDa protein 1 OS=Mus mu	1383.47	15	14	15	14	15	15	14	14	14	14	14	3	3	3	3	0.82051	0.98	0.64845	0.89	0.67895	0.78
sp Q01V12 BACH_MOUSE	Cytochrome c oxidase A thioester hydroly	1042.77	15	19	21	18	22	19	17	13	15	15	16	3	3	3	3	0.86284	1.07	0.25566	0.82	0.61255	0.95
sp Q0C28 SCRNI_MOUSE	Secam-1 OS=Mus musculus (Mouse) GN	1132.8	19	16	17	16	22	21	15	17	14	15	14	3	3	3	3	0.46951	1.13	0.60219	0.88	0.85919	0.87
sp Q03086 DHE3_BOVIN	Glutamate dehydrogenase 1, mitochondrial	1634.37	20	16	26	18	23	21	15	22	25	13	16	3	3	3	3	0.60967	0.95	0.15222	0.94	0.85258	0.87
sp Q01765 KNI_MOUSE	Kinesin heavy chain OS=Mus musculus (M	1976.89	17	15	14	15	19	19	12	16	15	17	15	3	3	3	3	0.44722	1.02	0.13464	0.87	0.18801	1.01
sp Q08FR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mu	1075.32	17	17	15	15	13	13	15	13	15	13	16	3	3	3	3	0.08323	0.90	0.23179	0.88	0.81531	0.90
sp Q020E5 FPP5_MOUSE	Farnesyl pyrophosphate synthase OS=Mus	1316.66	19	15	15	13	21	22	12	14	18	12	13	3	3	3	3	0.65215	1.14	0.82092	0.90	0.79258	0.84
sp P03011 RAB3A_MOUSE	Ras-related protein Rab-3A OS=Mus muscu	1342.37	16	19	15	12	21	20	18	15	17	18	12	3	3	3	3	0.97609	1.06	0.40347	1.00	0.70794	0.92
sp Q07XK5 Q3TK5_MOUSE	Putative uncharacterized protein OS=Mus	1947.04	22	14	14	17	23	24	28	16	18	11	16	3	3	3	3	0.35547	1.25	0.39624	1.18	0.94558	0.88
sp P03554 CAL_MOUSE	Calnexin OS=Mus musculus (Mouse) GN	1947.04	22	14	14	17	23	24	28	16	18	11	16	3	3	3	3	0.35547	1.25	0.39624	1.18	0.94558	0.88
sp Q01703 MATR3_MOUSE	Matrin-3 OS=Mus musculus (Mouse) GN=M	1984.35	26	22	15	20	28	26	22	22	23	25	23	3	3	3	3	0.51979	1.17	0.40757	1.06	0.56920	1.00
sp P47963 RL13_MOUSE	60S ribosomal protein L13 OS=Mus muscu	970.71	19	18	14	16	21	20	21	19	22	17	15	3	3	3	3	0.54915	1.12	0.06792	1.20	0.15555	1.06
sp Q01699 HS105_MOUSE	Heat shock protein 105 kDa OS=Mus musc	2701.64	15	15	15	15	16	23	15	16	16	16	15	3	3	3	3	0.33693	1.13	0.06717	1.20	0.07899	1.04
sp Q02K23 SDA_MOUSE	Sodium-dependent anion exchanger 1 OS=	1774.96	21	14	14	16	19	19	17	14	16	17	14	3	3	3	3	0.21446	1.02	0.13464	0.87	0.18512	1.02
sp Q0DBP5 PKCV_MOUSE	UMP-CMP kinase OS=Mus musculus (Mou	907.41	12	14	12	17	15	16	18	14	15	18	14	3	3	3	3	0.29120	1.16	0.04716	1.29	0.00039	1.24
sp Q0C208 Q0C208_MOUSE	ATP synthase subunit gamma OS=Mus m	1130.44	17	20	12	16	18	16	18	14	15	17	13	3	3	3	3	0.86872	1.02	0.92447	0.96	0.76888	0.92
sp P415591 COF2_MOUSE	Coflin-2 OS=Mus musculus (Mouse) GN=C	936.41	20	21	21	20	20	18	16	23	12	12	15	3	3	3	3	0.15391	0.94	0.84992	0.92	0.02932	0.83
sp P07300 NFYB_MOUSE	Neurofilin OS=Mus musculus (Mouse) G</																						

sp B0V2N1 PTFRS_MOUSE	Receptor-type tyrosine-protein phosphatase	1398.54	11	11	11	10	8	7	8	9	11	9	7	7	3	3	3	3	0.05277	0.76	0.47316	0.85	0.00121	0.70
sp P93029 PROX5_MOUSE	Peroxodioxin-5, mitochondrial OS=Mus mus	949.24	15	14	8	14	20	18	18	16	15	14	11	16	3	3	3	3	0.15602	1.41	0.08179	1.32	0.30103	1.11
sp Q6CA19 C2C19_MOUSE	Putative uncharacterized protein OS=Mus mu	1469.94	18	9	15	16	20	15	12	16	14	12	14	3	3	3	3	3	0.04977	1.40	0.65193	1.08	0.52882	1.00
sp Q1937 NPIM_MOUSE	Nucleophosmin OS=Mus musculus (Mouse)	1346.99	16	17	15	12	13	19	12	16	18	12	12	3	3	3	3	3	0.95180	1.05	0.28353	1.24	0.36034	1.11
sp P60879 SNP25_MOUSE	Synaptosomal-associated protein 25 OS=M	1217.66	18	20	6	14	13	14	17	23	17	16	19	10	3	3	3	3	0.74807	0.93	0.32694	1.30	0.66116	1.02
sp P55821 STM2_MOUSE	Stathmin-2 OS=Mus musculus (Mouse) GN	733.25	17	17	10	17	14	14	19	12	14	22	10	11	3	3	3	3	0.93661	1.02	0.69604	1.02	0.77437	0.98
sp A0A07WFL A0A07WFLP5_MOUSE	ATP-dependent RNA helicase A OS=Mus m	1978.97	15	15	10	15	15	12	9	15	15	16	13	3	3	3	3	3	0.45489	1.13	0.98030	0.95	0.06373	1.32
sp Q1301 CTNA2_MOUSE	Cytoskeleton-associated protein 2 OS=Mus	2523.03	15	15	10	12	15	12	15	14	15	15	13	3	3	3	3	3	0.45489	1.13	0.98030	0.95	0.06373	1.32
sp P1205 ARF3_MOUSE	ADP-ribosylation factor 3 OS=Mus muscu	1036.16	15	15	12	18	17	18	10	10	17	9	12	3	3	3	3	3	0.48302	1.18	0.22646	0.95	0.74281	0.95
sp Q17M9 HNRPO_MOUSE	Heterogeneous nuclear ribonucleoprotein C	1177.21	14	13	10	14	13	14	12	8	10	13	8	9	3	3	3	3	0.59172	1.11	0.23084	0.81	0.46455	0.81
sp P17777 PB_MOUSE	Prohibitin OS=Mus musculus (Mouse) GN	1317.46	11	12	7	13	11	14	11	6	6	13	9	9	3	3	3	3	0.27957	1.27	0.33555	0.77	0.35220	1.03
sp Q03092 TALDO_MOUSE	Tandemly repeated domain-containing pro	1108.4	11	10	8	12	10	11	11	6	10	15	15	3	3	3	3	3	0.49309	1.15	0.26530	0.81	0.46530	1.00
sp E9DA05 E9DA05_MOUSE	Glycogen synthase kinase-3 beta OS=Mus	784.86	16	12	9	12	11	8	9	9	9	11	11	3	3	3	3	3	0.80381	1.00	0.22999	0.70	0.78392	0.84
sp Q8E597 RTN3_MOUSE	Reticulon-3 OS=Mus musculus (Mouse) GN	1332.27	14	13	10	17	9	15	10	8	12	7	7	3	3	3	3	3	0.78638	1.11	0.27844	0.89	0.16784	0.70
sp Q8W74 VATG2_MOUSE	V-type proton ATPase subunit G 2 OS=Mu	967.35	14	13	7	14	14	9	9	12	5	14	15	6	3	3	3	3	0.75306	1.12	0.59735	0.79	0.58789	1.06
sp P64844 KRCB_MOUSE	Karyopherin class beta type OS=Mus musc	1432.23	14	13	9	11	13	9	9	14	9	9	11	3	3	3	3	3	0.91610	1.08	0.53780	0.78	0.56181	0.78
sp Q10U11 FUBP2_MOUSE	Far upstream element-binding protein 2 OS	116.16	15	16	10	10	10	14	11	14	9	12	7	8	3	3	3	3	0.53352	1.09	0.66536	0.97	0.70523	0.94
sp P10922 H10_MOUSE	Histone H1.0 OS=Mus musculus (Mouse) C	787.24	18	11	9	17	9	5	19	6	7	13	13	6	3	3	3	3	0.60083	0.82	0.70288	0.84	0.87546	0.84
sp Q191WQ3 SYCY_MOUSE	Thyrosine-tRNA ligase, cytoplasmic OS=Mu	1507.15	13	11	8	9	14	17	15	16	12	8	11	3	3	3	3	3	0.46321	1.25	0.09475	1.34	0.89269	0.91
sp P62897 CYC_MOUSE	Cytochrome c, somatic OS=Mus musculus i	932.62	14	17	8	9	15	13	14	12	7	15	8	3	3	3	3	3	0.67796	0.95	0.67574	0.85	0.64514	0.79
sp P53279 RAB5A_MOUSE	Ras-related protein Rab-5A OS=Mus muscu	788.99	11	11	10	14	11	12	9	10	12	7	11	3	3	3	3	3	0.65309	1.09	0.66536	0.97	0.70523	0.94
sp P28660 NCKP1_MOUSE	Nck-associated protein 1 OS=Mus muscu	1811.97	13	13	9	9	13	11	11	7	9	10	5	8	3	3	3	3	0.44823	0.94	0.18821	0.77	0.13832	0.66
sp P63028 TCTP_MOUSE	Translationally-controlled tumor protein OS	491.41	11	14	9	7	11	9	12	11	11	8	7	11	3	3	3	3	0.13681	0.79	0.61363	1.00	0.52199	0.76
sp P63094 GNAS2_MOUSE	Guanine nucleotide-binding protein G(s) su	704.81	11	13	10	10	13	10	8	7	9	13	8	9	3	3	3	3	0.42773	0.97	0.04226	0.71	0.90185	0.88
sp P14131 RS10_MOUSE	40S ribosomal protein S10 OS=Mus muscu	856.65	14	9	10	12	8	9	9	8	9	8	12	3	3	3	3	3	0.18977	0.79	0.18977	0.79	0.66512	0.79
sp P54022 RANG_MOUSE	Ras-related protein 51A OS=Mus muscu	483.94	11	11	11	11	11	11	9	8	9	10	4	3	3	3	3	3	0.81528	0.93	0.06610	1.01	0.91270	0.87
sp P62264 RS14_MOUSE	40S ribosomal protein S14 OS=Mus muscu	657.07	14	12	6	9	10	10	14	8	12	8	12	8	3	3	3	3	0.58097	0.91	0.89713	0.94	0.89713	0.91
sp Q17291 SUCB1_MOUSE	Succinyl-CoA ligase [ADP-forming] subunit	1014.48	11	11	9	7	9	6	10	8	9	10	6	8	3	3	3	3	0.02117	0.71	0.22328	0.87	0.21925	0.77
sp Q17522 MAP9_MOUSE	Microtubule-associated protein 6 OS=Mus i	1522.28	23	15	5	20	15	7	22	14	3	19	15	3	3	2	2	2	0.91269	0.98	0.90562	0.91	0.83701	0.79
sp Q0220M UBCL2_MOUSE	Ubiquitin carboxyl-terminal esterase (UCH	753.37	15	14	10	11	10	11	19	10	19	17	6	4	3	3	3	3	0.54171	1.22	0.84011	1.04	0.84011	1.04
sp Q3UNH4 GRIN_MOUSE	G-protein-regulated inducer of neurite out	1683.04	20	14	3	23	15	5	14	9	1	15	7	1	3	3	3	3	0.83374	1.16	0.56004	0.65	0.56371	0.62
sp Q0C244 NSFC1_MOUSE	NSFL-1 cofactor p47 OS=Mus musculus (M	887.46	12	11	3	9	12	6	11	6	6	8	4	3	3	3	3	3	0.99245	1.04	0.58894	0.88	0.75314	0.77
sp Q17073 OTU1_MOUSE	Ubiquitin thioesterase OTU1 OS=Mus mu	854.79	12	12	4	9	9	10	12	4	6	11	4	6	3	3	3	3	0.90031	1.00	0.61709	0.79	0.63494	0.75
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS	1248.79	16	9	17	13	11	17	15	17	24	14	16	15	3	3	3	3	0.83598	1.00	0.23394	1.37	0.34387	1.10
sp Q09L01 PARK7_MOUSE	Putative uncharacterized protein OS=Mus	896.13	10	10	11	13	15	19	11	7	10	13	6	4	3	3	3	3	0.89171	1.02	0.39137	0.81	0.89137	0.81
sp Q0CWS0 DDAH1_MOUSE	NG1(N)-O-dimethylarginine dimethylamino	1381.74	15	10	11	15	15	20	14	13	17	11	10	15	3	3	3	3	0.16023	0.39	0.19870	1.22	0.56376	1.00
sp Q19V55 O91V55_MOUSE	40S ribosomal protein S5 OS=Mus muscu	1318.97	12	10	11	12	14	16	14	11	8	12	10	12	3	3	3	3	0.11816	1.27	0.77219	1.00	0.14778	1.03
sp P01831 THY1_MOUSE	Thy1 membrane glycoprotein OS=Mus mu	440.31	12	10	11	11	14	13	15	14	10	13	8	9	3	3	3	3	0.30424	1.15	0.17507	1.18	0.91233	0.91
sp Q08Q02 Q8Q02_MOUSE	Putative uncharacterized protein OS=Mus	838.02	10	10	10	12	13	9	11	7	10	13	9	10	3	3	3	3	0.89373	0.62	0.95375	0.62	0.95375	0.62
sp H7B336 H7B336_MOUSE	Serine/threonine-protein kinase DCLK1 OS	863.8	12	10	11	12	12	11	6	12	13	9	10	3	3	3	3	3	0.87306	1.03	0.52619	0.83	0.85462	0.91
sp P61255 RL2B_MOUSE	60S ribosomal protein L26 OS=Mus muscu	914.88	11	9	11	13	17	12	9	7	11	11	9	10	3	3	3	3	0.11458	1.35	0.61105	0.87	0.35470	0.97
sp Q64522 JL2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus (f	371.21	15	10	12	12	9	8	12	13	5	11	13	9	3	3	3	3	0.22447	0.78	0.58978	0.81	0.92403	0.89
sp Q0C228 RS19_MOUSE	40S ribosomal protein S19 OS=Mus muscu	837.16	15	13	10	9	13	15	17	10	13	10	13	3	3	3	3	3	0.86201	1.03	0.36749	1.11	0.15511	1.03
sp P61585 DYL1_MOUSE	Dynamin light chain 1, cytoplasmic OS=Mu	1942.05	9	11	10	11	10	10	14	9	10	12	13	3	3	3	3	3	0.77447	0.81	0.77447	0.81	0.77447	0.81
sp P53994 RAB2A_MOUSE	Ras-related protein Rab-2A OS=Mus musc	1010.94	13	10	11	10	11	10	8	8	9	7	8	3	3	3	3	3	0.21728	0.91	0.10722	0.74	0.07464	0.65
sp P48758 CBR1_MOUSE	Carbonyl reductase [NADPH] 1 OS=Mus m	921.49	11	9	12	9	9	9	14	6	9	12	10	10	3	3	3	3	0.13270	0.84	0.75018	0.91	0.29009	1.00
sp Q19R14 PSPA1_MOUSE	Proteasome subunit alpha type 1 OS=Mus	1016.21	13	9	7	11	12	12	16	12	8	16	14	9	3	3	3	3	0.45681	1.21	0.33589	1.24	0.13885	1.34
sp P53550 PMA1_MOUSE	Phosphatase 1 OS=Mus musculus (Mouse)	830.76	14	13	10	11	11	13	13	10	11	13	11	10	3	3	3	3	0.84211	1.08	0.42216	0.91	0.42216	0.91
sp P11448 RL7_MOUSE	60S ribosomal protein L7 OS=Mus muscu	969.79	11	10	10	17	13	12	13	7	8	16	7	6	3	3	3	3	0.18312	1.35	0.65654	0.90	0.94176	0.94
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=	1166.06	11	8	9	11	13	13	16	10	8	12	10	10	3	3	3	3	0.08202	1.32	0.31377	1.21	0.03588	1.14
sp P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus muscu	930.13</																						

tfE907C9E907C9_MOUSE	Kinesin light chain 1	OS-Mus musculus (M	1625.7	8	7	8	11	10	11	7	4	6	9	5	8	3	3	3	3	0.03009	1.39	0.10120	0.74	0.66842	0.96
tfQ3U8V9Q3U8V_MOUSE	Putative uncharacterized protein	OS-Mus	977.81	9	9	10	11	9	9	10	7	8	7	6	8	3	3	3	3	0.94588	1.04	0.39827	0.89	0.49597	0.82
tfQ3J29J9M29J_MOUSE	Hydroxyethylglutaryl-CoA synthase, cytopl	OS-Mus	1677.67	9	10	8	12	13	6	12	9	9	10	9	3	3	3	3	3	0.25149	1.44	0.33597	1.24	0.18425	1.12
tfQ3N15N15N15_MOUSE	Spirosome RNA helicase Ddx3b	OS-M	920.49	9	7	7	8	12	13	8	8	7	11	8	6	3	3	3	3	0.12455	1.44	0.25607	1.17	0.04375	1.17
tfQ3JKK7TMO2D_MOUSE	Tropomodulin-2	OS-Mus musculus (M	866.17	9	9	9	9	11	11	11	6	6	7	11	8	3	3	3	3	0.11764	1.15	0.55312	0.89	0.07950	1.00
tfB8Q34B8Q34_MOUSE	Liprin-alpha 2	OS-Mus musculus (Mouse)	1425.91	10	6	7	6	13	11	9	6	5	4	5	3	3	3	3	3	0.46315	1.30	0.64959	0.87	0.10697	0.52
tfP46638R1B_MOUSE	Ras-related protein Rab-11B	OS-Mus mus	872.32	6	8	7	7	12	16	7	3	6	6	3	5	3	3	3	3	0.13890	1.57	0.28277	0.76	0.44069	0.76
tfP6R64Q6R1P_MOUSE	SH3 domain protein 1	OS-Mus muscu	1000.63	9	7	7	7	12	16	6	5	6	7	9	1	3	3	3	3	0.19635	1.28	0.29822	0.88	0.17628	0.28
tfQ3Y1WVSHL3_MOUSE	SH3 domain-binding glutamic acid-rich f	OS-Mus muscu	281.31	7	6	7	8	11	9	11	3	3	2	1	3	3	3	3	3	0.04128	1.40	0.82924	1.05	0.41075	0.65
tfQ3C9R8UCUR_MOUSE	Cytochrome b-c1 complex subunit Rheska	OS-Mus muscu	660.91	7	7	7	10	11	10	7	11	4	11	6	5	3	3	3	3	0.00036	1.08	0.74868	1.05	0.50608	1.05
tfQ3Y1L3Q3Y1L_MOUSE	Putative uncharacterized protein	OS-Mus	908.14	10	9	6	8	11	7	10	9	12	10	5	8	3	3	3	3	0.96274	1.04	0.17582	1.24	0.89886	0.92
tfE3K6Q4E3K6Q_MOUSE	Protein Rsp19	OS-Mus muscu	1962.38	9	7	7	7	12	16	6	5	6	7	9	3	3	3	3	3	0.79031	1.14	0.60302	0.82	0.60302	0.62
tfP9394QLOOC_MOUSE	Transcription elongation factor B polypept	OS-Mus muscu	611.13	7	8	7	6	11	9	9	7	7	10	4	9	3	3	3	3	0.49667	1.18	0.07943	1.05	0.54595	1.05
tfP6074RAC3_MOUSE	Ras-related G3 botulinum toxin substrate 3	OS-Mus muscu	619.83	9	9	10	9	12	10	8	7	6	8	5	6	3	3	3	3	0.55849	1.11	0.03304	0.75	0.03304	0.68
tfQ8X04P42B_MOUSE	Phosphatidylinositol 5-ophosphate 4-kinase I	OS-Mus muscu	915.03	7	9	9	9	12	10	6	7	5	9	7	10	3	3	3	3	0.15907	1.24	0.13060	0.72	0.28911	1.04
tfQ3C0W7ISNAG_MOUSE	Gamma-tubulin NSF attachment protein	OS-Mus muscu	1004.96	9	8	8	8	12	9	8	8	5	9	5	6	3	3	3	3	0.42562	1.21	0.89036	0.88	0.67119	0.83
tfQ8R01G2PLK4_MOUSE	Plexin-A4	OS-Mus musculus (GN=	1900.63	6	6	10	11	6	8	8	8	5	6	13	6	3	3	3	3	0.82224	1.18	0.09224	0.73	0.61696	1.09
tfQ8BH2QFA49A_MOUSE	Protein FAM9A	OS-Mus musculus (M	928.63	10	10	9	8	12	6	5	6	6	8	5	4	3	3	3	3	0.40123	0.90	0.00676	0.59	0.02444	0.59
tfQ3C0C2CY858_MOUSE	Cytochrome b5 type B	OS-Mus musculus (521.9	10	7	9	11	9	3	7	7	5	5	7	3	3	3	3	3	0.54337	1.12	0.24389	0.65	0.15030	0.65
tfQ3Z2Q6SEPT5_MOUSE	Septin-5	OS-Mus musculus (Mouse) GN=F	981.84	10	8	9	7	13	6	5	4	7	5	7	5	3	3	3	3	0.90908	1.04	0.02553	0.99	0.12812	0.63
tfQ3R795GLQ2_MOUSE	Glycosylase 2 subunit beta	OS-Mus muscu	632.29	8	7	8	7	11	11	9	11	7	4	6	3	3	3	3	3	0.45534	1.18	0.00727	1.41	0.27677	0.77
tfQ3U561Q3U56_MOUSE	Ribosomal protein OS-Mus musculus (M	OS-Mus muscu	506.04	9	6	8	10	9	12	14	7	9	9	7	4	3	3	3	3	0.18174	1.35	0.22600	1.30	0.88787	0.87
tfP32921SYWC_MOUSE	Tytophan-tRNA ligase, cytoplasmic OS=F	OS-Mus muscu	1291.1	9	8	8	8	9	12	10	8	6	11	9	7	3	3	3	3	0.46071	1.16	0.95856	0.96	0.12671	1.08
tfP70333HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H	OS-Mus muscu	794.72	10	8	8	8	11	10	8	10	8	7	10	3	3	3	3	3	0.95496	1.04	0.28996	1.04	0.71145	0.93
tfQ3D176RRL3_MOUSE	60S ribosomal protein L34	OS-Mus muscu	383.21	10	9	6	6	10	6	7	9	7	9	8	3	3	3	3	3	0.62847	0.92	0.78970	0.88	0.62599	0.96
tfQ3R328PSPC1_MOUSE	Alpha-tubulin class III	OS-Mus muscu	737.35	9	7	7	7	12	9	9	16	9	4	7	3	3	3	3	3	0.9395	1.36	0.11582	1.23	0.25965	0.73
tfQ3TQ5Q3TQ5_MOUSE	Putative uncharacterized protein	OS-Mus	611.52	9	6	6	8	7	11	8	6	9	4	4	7	3	3	3	3	0.46098	1.24	0.48217	1.10	0.48807	0.71
tfP62823RAB3C_MOUSE	Ras-related protein Rab-3C	OS-Mus muscu	599.69	10	9	8	8	10	8	12	12	12	8	5	7	3	3	3	3	0.35335	0.93	0.00423	1.33	0.15063	0.74
tfQ3C91VATG1_MOUSE	V-type proton ATPase subunit G1	OS-Mus muscu	959.97	9	8	6	8	9	9	13	12	8	9	9	4	3	3	3	3	0.51239	1.13	0.07910	1.43	0.77857	0.96
tfP3484HIF_MOUSE	Hydroxy-methylglutaryl-CoA lyase	OS-Mus muscu	554.31	10	9	7	7	10	10	16	9	11	15	8	3	3	3	3	3	0.19350	1.05	0.22055	1.05	0.22055	1.05
tfQ3E167DDX3_MOUSE	ATP-dependent RNA helicase DDX3	OS-Mus muscu	1413.91	9	9	8	7	10	10	14	7	14	7	10	10	3	3	3	3	0.88121	1.04	0.30516	1.23	0.37675	1.04
tfQ3Z204HNRFC_MOUSE	Heterogeneous nuclear ribonucleoproteins	OS-Mus muscu	1016.32	9	7	7	8	7	8	15	8	8	13	8	8	3	3	3	3	0.72036	1.00	0.18637	1.35	0.67069	1.26
tfQ3C9C1COX6_MOUSE	Cytochrome c oxidase subunit 6C	OS-Mus muscu	422.45	9	6	7	10	10	10	14	10	7	11	10	6	3	3	3	3	0.09360	1.36	0.14574	1.41	0.20479	1.23
tfQ3E0C3VFS3_MOUSE	Vacuolar protein sorting-associated protein	OS-Mus muscu	1667.53	9	7	9	9	8	9	11	4	9	8	8	4	3	3	3	3	0.35081	0.92	0.97748	0.96	0.64956	0.80
tfP70372ELAV1_MOUSE	ELAV-like protein L26	OS-Mus muscu	554.31	9	7	7	7	10	10	12	5	6	3	4	2	3	3	3	3	0.00194	1.08	0.49437	1.28	0.19487	0.72
tfQ4L64Q4L64_MOUSE	AMPA-selective glutamate receptor 2 flip ty	OS-Mus muscu	1267.62	6	6	6	6	6	6	12	2	3	11	2	3	3	3	3	3	0.46458	1.17	0.90406	0.94	0.66708	0.72
tfQ3JKD3SCAMS_MOUSE	Secretory carrier-associated membrane prot	OS-Mus muscu	181.08	8	8	8	7	8	7	9	11	9	7	8	8	3	3	3	3	0.01634	0.92	0.12507	1.21	0.45427	0.96
tfP12382PFKAL_MOUSE	ATP-dependent 6-phosphofruktokinase, liv	OS-Mus muscu	864.56	7	6	9	7	9	8	6	11	10	3	4	8	3	3	3	3	0.83582	1.09	0.38712	1.23	0.51125	0.68
tfQ3E93Q3E93_MOUSE	MG9927	OS-Mus musculus (Mouse) GN=	506.04	7	8	7	7	10	10	9	9	11	8	5	7	3	3	3	3	0.32074	1.04	0.07025	1.26	0.10765	0.87
tfQ3Q0Z0EIF3_MOUSE	Eukaryotic translation initiation factor 3	OS-Mus muscu	579.98	8	8	6	7	10	10	9	9	7	9	8	8	3	3	3	3	0.49691	1.17	0.36252	1.00	0.35638	1.04
tfQ8B6G8PHL2_MOUSE	Phytanoyl-CoA hydroxylase-interacting prot	OS-Mus muscu	707.6	8	8	8	8	7	10	6	9	7	6	8	8	3	3	3	3	0.96958	1.04	0.91928	0.92	0.74401	0.92
tfQ3J20Q3J20_MOUSE	14-3-3 protein sigma	OS-Mus musculus (M	385.59	10	10	9	8	8	8	6	9	6	7	8	9	3	3	3	3	0.05327	0.86	0.19971	0.72	0.69181	0.83
tfQ3U8Y7Q3U8Y_MOUSE	Putative uncharacterized protein	OS-Mus	1150.27	6	8	8	7	8	8	8	6	9	6	7	8	3	3	3	3	0.64801	1.10	0.42544	1.10	0.42256	1.00
tfP41105R2L_MOUSE	60S ribosomal protein L26	OS-Mus muscu	390.26	9	10	9	7	10	10	10	9	8	9	8	3	3	3	3	3	0.54005	0.97	0.08084	0.89	0.16618	0.72
tfQ3E127ADBP_MOUSE	TAR DNA-binding protein 43	OS-Mus muscu	920.33	10	8	6	9	8	10	6	9	9	6	8	3	3	3	3	3	0.31669	0.96	0.02970	1.13	0.39274	0.96
tfQ89L4FRTCC_MOUSE	tRNA-spirosome ligase RbcB homolog	OS-Mus muscu	719.5	7	8	6	7	9	9	7	8	8	10	5	8	3	3	3	3	0.19913	1.19	0.25718	1.10	0.28601	1.10
tfQ3Q901PSB1_MOUSE	Proteasome subunit beta type-1	OS-Mus	848.16	7	10	8	7	7	9	10	6	8	7	5	7	3	3	3	3	0.36350	0.92	0.97229	0.96	0.22616	0.76
tfP3032RST_MOUSE	40S ribosomal protein S7	OS-Mus muscu	504.06	7	9	7	6	9	9	9	10	8	6	5	7	3	3	3	3	0.97416	1.05	0.07165	1.26	0.37765	0.87
tfQ8BUV3GEFH_MOUSE	Gephyrin	OS-Mus musculus (Mouse) GN=F	735.52	9	10	6	9	8	8	8	7	8	8	5	5	3	3	3	3	0.80713	1.00	0.87028	0.92	0.25499	0.72
tfQ3E2W3JRL10_MOUSE	60S ribosomal protein L10	OS-Mus muscu	580.75	9	7	7	10	9	9	7	9	6	4	10	6	3	3	3	3	0.24937	1.22	0.98286	0.96	0.95868	0.87
tfP8E5U4SYG1_MOUSE	Ras/Rap GTPase-activating protein SynGAP	OS-Mus muscu	1116.16																						

sp Q810U4 NRCAM_MOUSE	Neuronal cell adhesion molecule	OS=Mus	756.47	8	5	5	9	6	8	7	9	10	3	6	8	3	3	3	3	0.40961	1.28	0.12693	1.44	0.79157	0.94
sp Q9918D DDAH2_MOUSE	NG(10C)-dimethylarginine dimethylaminohy	OS=Mus	822.33	7	3	4	8	8	9	5	6	9	6	4	9	3	3	3	3	0.06429	1.79	0.27530	1.43	0.30967	1.36
sp Q9WV02 RBMX_MOUSE	RNA-binding motif protein X chromosome 1	OS=Mus	584.85	10	5	6	10	6	9	9	6	8	15	4	3	3	3	3	3	0.51458	1.25	0.49655	1.16	0.49655	0.90
sp Q1VA93 QAVAR3_MOUSE	Protein kinase C OS=Mus musculus	OS=Mus	1253.63	8	4	5	6	8	4	1	7	7	4	4	5	5	3	3	3	0.99184	1.06	0.95356	0.88	0.82874	0.82
sp P61089 UBE2N_MOUSE	Ubiquitin-conjugating enzyme E2 N OS=M	OS=M	621.57	6	4	5	7	3	4	7	6	5	5	3	3	3	3	3	3	0.75563	0.93	0.16532	1.20	0.29433	0.73
sp Q3JHU0 AAK1_MOUSE	AP2-associated protein kinase 1 OS=Mus	OS=M	1032.19	7	3	3	6	3	3	7	3	1	6	3	2	3	3	3	3	0.80219	0.92	0.77592	0.85	0.85990	0.85
sp E9PVC5 EPFV2_MOUSE	Eukaryotic translation initiation factor 4 gam	OS=M	1335.39	7	5	3	8	5	5	3	8	9	4	2	3	3	3	3	3	0.64908	1.20	0.51140	1.13	0.85584	1.00
sp Q8KCS5 IFP2_MOUSE	Interferon-gamma OS=Mus musculus	OS=M	1421.24	6	3	6	3	6	3	2	4	3	14	2	3	3	3	3	3	0.48124	1.36	0.29232	1.07	0.48124	0.73
sp I4A0G2 DNT1 A0A0G2.DJNT	Microtubule-associated protein OS=Mus m	OS=M	956.66	8	3	2	10	4	1	14	3	1	1	10	2	1	3	3	3	0.87299	1.15	0.72488	1.38	0.56288	1.00
sp Q782A7 NP1L4_MOUSE	Nucleosome assembly protein 1-like 4 OS=	OS=M	839.15	10	4	4	4	5	12	8	13	8	9	7	8	6	3	3	3	0.52901	1.39	0.12202	1.67	0.43071	1.17
sp Q90YF9 NDRG3_MOUSE	Protein NDRG3 OS=Mus musculus	OS=M	838.63	7	3	2	5	7	6	6	6	2	4	7	3	3	3	3	3	0.34705	1.50	0.68990	1.17	0.58963	1.17
sp Q9C1W1 PAK2_MOUSE	Protein kinase PAK2 OS=Mus musculus	OS=M	814.44	6	4	3	2	10	4	4	4	3	7	4	4	1	4	3	3	0.42514	1.46	0.52737	1.01	0.52737	1.15
sp Q9C2D3 SYG_MOUSE	Glycine-tRNA synthetase OS=Mus musculus (M	OS=M	1210.6	10	3	3	5	9	6	5	6	6	6	6	4	3	3	3	3	0.72898	1.25	0.79295	1.06	0.79647	1.00
sp P62334 PRS1_MOUSE	26S proteasome regulatory subunit 10B OS=	OS=M	833.39	6	3	4	2	7	9	3	6	7	5	6	7	3	3	3	3	0.57927	1.38	0.16486	1.23	0.13410	1.38
sp P59999 ARPC4_MOUSE	Actin-related protein 2/3 complex subunit 4	OS=M	553.91	7	4	4	5	6	8	4	6	5	3	5	7	3	3	3	3	0.47486	1.27	0.80741	1.00	0.68531	1.00
sp P80033 PDIM4_MOUSE	Protein disulfide-isomerase A4 OS=Mus m	OS=M	1108.01	6	5	5	7	7	5	5	3	3	6	2	4	3	3	3	3	0.28116	1.36	0.44407	0.79	0.53661	0.86
sp Q9E125 P1B3_MOUSE	Platelet-activating factor acetylhydrolase IB	OS=M	449.77	6	9	7	7	7	7	5	3	3	5	4	4	3	3	3	3	0.78943	0.85	0.40937	0.65	0.69270	0.71
sp Q90972 RBBP4_MOUSE	Histone-binding protein RBBP4 OS=Mus m	OS=M	418.74	6	5	4	4	8	5	7	3	6	7	2	5	3	3	3	3	0.51012	1.31	0.44745	1.23	0.66519	1.08
sp Q86814 SAH3_MOUSE	Putative adenosylhomocysteinase 3 OS=N	OS=N	593.99	6	5	4	4	7	4	6	4	1	5	4	1	3	3	3	3	0.80261	1.00	0.45649	0.73	0.40058	0.67
sp Q8CA77 POM2L_MOUSE	Glucose 1,6-bisphosphate synthase OS=N	OS=N	1292.91	6	2	5	5	8	4	6	1	5	4	1	4	3	3	3	3	0.57170	1.31	0.89297	0.92	0.55408	0.69
sp Q90145 SC2A_MOUSE	Protein transposon protein Scs2A OS=Mus m	OS=M	1044.28	5	5	5	8	5	3	2	5	5	6	2	7	3	3	3	3	0.71440	1.13	0.16286	0.63	0.89763	0.94
sp Q9CR16 PP1D_MOUSE	Protein phosphatase 1 delta OS=Mus muscu	OS=M	757.83	6	5	4	5	7	5	5	5	3	7	4	5	3	3	3	3	0.63503	1.13	0.65698	0.87	0.30679	1.07
sp Q62318 TIF1_MOUSE	Transcription intermediary factor 1-beta OS=	OS=M	905.66	6	2	3	5	6	6	6	4	2	4	2	4	3	3	3	3	0.93596	1.00	0.79313	1.09	0.97890	0.91
sp Q8BMS1 ECH3_MOUSE	Triphunctional enzyme subunit alpha, mitoch	OS=M	1784.76	6	4	4	5	5	6	11	6	7	5	4	7	3	3	3	3	0.61492	1.14	0.04724	1.71	0.34676	1.14
sp Q9D019 SYRC_MOUSE	Arginine-tRNA ligase, cytoplasmic OS=Mus	OS=M	988.11	6	4	3	4	5	7	9	6	7	6	7	6	7	3	3	3	0.97214	1.07	0.24156	1.27	0.18491	1.33
sp Q9JUL0 GPD1L_MOUSE	Glycerol-3-phosphate dehydrogenase 1-like	OS=M	874.24	5	5	5	4	8	9	6	2	6	2	5	3	3	3	3	3	0.70383	0.80	0.66659	0.89	0.65439	0.88
sp Q91WU8 FUBP1_MOUSE	Far upstream element-binding protein 1 OS=	OS=M	855.56	6	5	2	2	4	7	2	2	5	3	5	3	3	3	3	3	0.90836	1.00	0.54244	0.69	0.55387	0.62
sp Q9VM18 IRG_MOUSE	Immunity-related GTPase family C protein 1	OS=M	55.57	6	3	3	4	3	3	5	6	2	4	3	2	3	3	3	3	0.50636	0.83	0.75185	1.08	0.59327	0.75
sp Q9T7M8 HUME1_MOUSE	E3 ubiquitin-protein ligase HUME1 OS=Mus	OS=M	921.66	6	3	2	4	5	3	3	4	4	4	6	4	3	3	3	3	0.91900	1.09	0.85612	1.00	0.45633	1.18
sp Q9NZL0 SOG3_MOUSE	Protein SOD3 OS=Mus musculus	OS=M	659.78	6	3	2	10	4	4	4	4	2	4	3	2	3	3	3	3	0.98834	1.07	0.79968	0.72	0.58218	1.14
sp Q9BFZ9 ERLN2_MOUSE	Erlin-2 OS=Mus musculus (Mouse) GN-Erlin	OS=M	659.78	8	4	4	4	4	4	4	4	4	3	4	6	3	3	3	3	0.32705	0.75	0.46781	0.75	0.88226	0.81
sp Q9ZZW0 DNPEP_MOUSE	Aspartyl aminopeptidase OS=Mus musculus	OS=M	865.13	7	2	4	2	5	4	4	4	4	4	4	4	3	3	3	3	0.60946	0.85	0.93544	0.92	0.89223	0.85
sp Q9WU33 PYGM_MOUSE	Glycogen phosphorylase, muscle form OS=	OS=M	503.23	6	4	2	3	4	2	3	3	2	2	2	6	3	3	3	3	0.42000	0.75	0.52666	0.75	0.34944	0.58
sp G9UX33 CSXK3_MOUSE	Sialoprotein reductase OS=Mus musculus (I	OS=M	675.57	6	2	3	4	5	4	1	3	6	2	2	6	3	3	3	3	0.74521	1.18	0.98457	0.91	0.93872	0.91
sp Q9V8F8 STUM_MOUSE	Protein stem homolog OS=Mus musculus (I	OS=M	185.28	6	2	3	5	8	6	4	3	3	3	2	4	3	3	3	3	0.40778	0.94	0.33287	0.82	0.82833	0.88
sp P35762 CDB1_MOUSE	CDB1 antigen OS=Mus musculus (Mouse) I	OS=M	275.93	6	2	1	4	4	4	7	3	2	5	3	3	3	3	3	3	0.62538	1.33	0.62583	1.33	0.96198	0.89
sp Q9JKC8 CEND1_MOUSE	Cell cycle exit and neuronal differentiation p	OS=M	577.39	6	4	2	13	5	1	8	1	9	1	9	1	2	2	2	2	0.58580	1.73	0.82441	0.82	0.94748	0.91
sp P63040 CPLX1_MOUSE	Complexin-1 OS=Mus musculus (Mouse) G	OS=M	253.75	7	5	5	7	8	11	1	4	5	2	4	5	2	2	2	2	0.96902	1.00	0.47209	1.67	0.84614	0.75
sp A2AGT5 CKAP5_MOUSE	Cytoskeleton-associated protein 5 OS=Mus m	OS=M	1027.57	6	3	3	5	2	2	9	3	2	2	2	1	2	3	3	3	0.82776	0.91	0.28776	0.73	0.62123	0.64
sp P56959 FUS_MOUSE	RNA-binding protein FUS OS=Mus musculus	OS=M	575.79	6	1	4	1	1	6	1	1	4	3	2	2	2	2	2	2	0.77557	1.00	0.97908	1.00	0.92617	1.00
sp Q9A065 CE170_MOUSE	Centromeres protein of 170 kDa OS=Mus m	OS=M	958.98	9	1	9	4	1	5	3	2	6	1	2	3	2	2	2	2	0.76521	1.40	0.98105	1.00	0.78958	0.70
sp E0CZ72 ECC27_MOUSE	Kinesin-like protein OS=Mus musculus (Mo	OS=M	1448.5	5	14	11	11	14	12	10	7	9	12	10	8	3	3	3	3	0.52866	1.23	0.75799	0.87	0.65276	1.00
sp P10655 CATR_MOUSE	Cathepsin B OS=Mus musculus (Mouse) G	OS=M	746.22	4	3	6	7	10	12	1	3	13	1	5	3	3	3	3	3	0.66733	1.28	0.80744	0.89	0.86465	1.06
sp Q908M3 CY1_MOUSE	Cytochrome c1 home protein OS=Mus muscu	OS=M	519.39	7	10	11	8	8	8	5	3	6	5	3	3	3	3	3	3	0.60714	0.82	0.60714	0.82	0.60714	0.82
sp Q9CFR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus muscu	OS=M	786.22	5	6	7	8	12	13	11	6	5	11	6	4	3	3	3	3	0.03310	1.83	0.38505	1.22	0.42578	1.17
sp Q9M8N0 CNRP1_MOUSE	R1 cannabinin receptor-interacting protein	OS=M	587.47	5	10	10	9	14	12	9	6	3	10	4	4	3	3	3	3	0.23582	1.40	0.40075	0.72	0.49863	0.72
sp Q90930 VDAC2_MOUSE	Voltage-dependent anion-selective channel	OS=M	813.13	3	6	10	8	9	9	13	4	7	12	4	4	3	3	3	3	0.42438	1.37	0.59119	1.26	0.70615	1.16
sp Q9C966 ROA_MOUSE	Retinol dehydrogenase 1 OS=Mus musculus	OS=M	402.56	4	3	6	7	10	16	9	3	2	5	6	6	6	6	6	6	0.50939	0.82	0.23193	0.82	0.50939	0.82
sp P53810 PIPNA_MOUSE	Phosphatidylinositol transfer protein alpha I	OS=M	793.04	5	9	6	9	10	6	10	2	7	2	5	3	3	3	3	3	0.44531	1.26	0.94987	0.95	0.43043	0.70
sp P35278 RAB5_MOUSE	Ras-related protein Rab-5 OS=Mus muscu	OS=M	986.83	5	9	10	6	6	9	10	5	6	5	5	6	3	3	3	3	0.50364	0.88	0.71154	0.88	0.31593	0.67
sp Q90737 CSK21_MOUSE	Casasin kinase II subunit alpha OS=Mus m	OS=M	788.2	3</																					

spi14685/PSM3_MOUSE	26S proteasome non-ATPase regulatory su	1140.19	5	5	3	2	10	10	5	4	6	6	3	4	3	3	3	3	0.36650	1.69	0.34017	1.15	0.61482	1.00
sp Q9D172/ESI1_MOUSE	E51 protein homolog, mitochondrial OS=M	381.48	4	4	4	4	6	7	4	4	2	6	3	2	3	3	3	3	0.13940	1.42	0.15669	0.83	0.99162	0.92
sp P73404/CHC1_MOUSE	Coactylate hydrolyase [NA2] subunit p8	687.04	4	4	4	4	6	7	4	4	2	6	3	1	3	3	3	3	0.11544	1.58	0.14600	0.73	0.75441	0.83
sp Q9Z0N1/IFZ2_MOUSE	Eukaryotic translation initiation factor 2 sub	812.94	5	5	3	6	6	5	4	5	5	5	2	3	3	3	3	3	0.56200	1.29	0.55711	1.00	0.85425	0.86
sp Q9JMA1/UBP1_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14 OS	1045.34	4	4	5	3	7	6	4	4	5	4	2	3	3	3	3	3	0.56924	1.23	0.70648	1.00	0.19689	0.69
sp Q9D6J6/INDU2_MOUSE	NADH dehydrogenase [ubiquinone] flavop	351.51	5	4	5	3	6	6	5	3	2	4	2	2	3	3	3	3	0.97103	1.07	0.21473	0.71	0.05889	0.57
sp P16054/KPCE_MOUSE	Protein kinase C epsilon type OS=Mus mus	856.3	5	5	4	3	8	8	3	3	3	4	4	2	3	3	3	3	0.28961	1.58	0.26556	0.75	0.80789	0.83
sp Q9R083/CHRB3_MOUSE	Chaperone protein 100 kDa OS=Mus mus	484.04	5	5	5	5	6	9	3	3	5	3	3	3	3	3	3	3	0.17440	1.67	0.26556	0.83	0.94923	0.67
sp Q9R086/IRB0_MOUSE	RNA-binding protein 3 OS=Mus musculus (M	337.73	5	5	2	5	6	9	3	3	2	5	5	4	3	3	3	3	0.17740	1.67	0.76560	0.83	0.27847	1.17
sp O70172/PI2A_MOUSE	Phosphatidylinositol 5-phosphate 4-kinase I	337.73	3	5	3	4	6	6	3	3	1	6	3	4	3	3	3	3	0.14189	1.45	0.25842	0.64	0.25567	1.18
sp Q70716/ANXA7_MOUSE	Annexin A7 OS=Mus musculus (Mouse) GN	707.73	2	5	4	2	6	6	4	4	4	5	3	3	2	2	2	2	0.64087	1.27	0.95950	0.73	0.47625	1.09
sp A2A4W7/A2A4W7_MOUSE	Annexin A2 OS=Mus musculus (Mouse) GN	802.84	5	4	4	4	6	6	7	7	6	7	5	4	3	3	3	3	0.64087	1.27	0.95950	0.73	0.47625	1.09
sp P94048/ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus muscu	676.46	4	5	4	3	6	5	8	2	2	6	2	5	3	3	3	3	0.92034	1.08	0.86949	0.92	0.71524	1.00
sp Q9I036/PAK3_MOUSE	Serine/threonine-protein kinase PAK 3 OS	932.32	5	4	3	3	8	5	6	4	4	5	7	4	3	3	3	3	0.49550	1.33	0.27732	1.17	0.20093	1.33
sp Q8BV05/PPME1_MOUSE	Protein phosphatase methyltransferase 1 OS	544.15	5	5	4	2	7	5	6	3	4	4	4	4	3	3	3	3	0.83343	1.00	0.82338	0.93	0.80658	0.86
sp Q9D085/NSA1_MOUSE	Alpha-soluble NSF attachment protein OS=M	864.94	3	3	3	5	7	3	6	2	2	5	2	3	3	3	3	3	0.16524	1.67	0.75842	1.11	0.41176	1.11
sp P51655/QPC4_MOUSE	Glycylase OS=Mus musculus (Mouse) GN	570.77	3	3	3	3	3	3	6	2	2	5	2	3	3	3	3	3	0.41149	1.33	0.98486	1.00	0.75092	0.79
sp Q9BQ21/HPCL4_MOUSE	Hippocampal-like protein 4 OS=Mus muscu	786.33	3	5	4	4	8	4	5	4	2	6	2	3	3	3	3	3	0.44555	1.33	0.87291	0.92	0.99379	0.92
sp P04925/PRIO_MOUSE	Major prion protein OS=Mus musculus (Mo	274.52	3	3	3	3	5	7	3	3	2	5	4	2	3	3	3	3	0.08685	1.55	0.29063	0.73	0.68731	1.00
sp Q9C089/QCR6_MOUSE	Histone h2-b1 complex subunit 8 OS=M	204.93	3	3	2	2	5	6	4	3	4	3	4	3	3	3	3	3	0.02333	1.88	0.07681	1.50	0.02622	1.38
sp Q9D123/VGLN_MOUSE	Vglin OS=Mus musculus (Mouse) GN=Htd	721.67	2	2	3	2	6	5	2	2	2	5	3	2	3	3	3	3	0.19499	1.66	0.59608	0.86	0.18593	1.43
sp Q9G073/RBBP7_MOUSE	Oocyte-binding protein RBBP7 OS=Mus m	371.66	3	3	3	2	7	2	3	4	4	4	2	3	3	3	3	3	0.78875	1.22	0.27743	1.22	0.63085	1.00
sp Q9C230/OLA1_MOUSE	Obg-like ATPase 1 OS=Mus musculus (Mo	697.27	4	3	4	5	6	3	4	4	4	3	1	4	3	3	3	3	0.44531	1.27	0.29329	1.09	0.55657	0.73
sp Q9I013/INFASC_MOUSE	Neurofascin OS=Mus musculus (Mouse) GF	707.91	3	3	4	4	6	4	5	2	3	4	1	1	3	3	3	3	0.17148	1.40	0.92155	1.00	0.29210	0.60
sp Q9C9V4/IGLOD4_MOUSE	Glyoxalase domain-containing protein 4 OS	699.22	3	3	5	5	7	5	3	1	2	4	1	3	3	3	3	3	0.12315	1.55	0.13869	0.55	0.52325	0.73
sp P48678/INNA_MOUSE	Insulin-like growth factor 1 OS=Mus muscu	810.12	3	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	0.09975	1.60	0.17137	0.37	0.32941	0.80
sp Q94010/CRK_MOUSE	Adaptor molecule crk OS=Mus musculus (M	396.15	2	4	2	2	3	6	5	1	4	2	2	3	2	2	2	2	0.13301	1.75	0.46661	0.63	0.70596	0.75
sp Q9D019/HRNL2_MOUSE	Heterogeneous nuclear ribonucleoprotein L	1009.1	4	4	3	4	6	5	4	8	3	3	2	3	3	3	3	3	0.09843	1.36	0.77397	1.00	0.19741	0.73
sp Q3U164/Q3U164_MOUSE	Putative uncharacterized protein OS=Mus m	550	4	4	3	4	5	6	6	6	5	4	6	5	3	3	3	3	0.12094	1.36	0.00999	1.55	0.11442	1.36
sp Q35226/PSMD4_MOUSE	26S proteasome non-ATPase regulatory su	565.88	5	5	5	5	5	5	6	6	6	6	6	6	6	6	6	6	0.16901	1.40	0.69801	1.40	0.27647	1.50
sp P92627/DL81_MOUSE	Dynamin light chain roadblock protein 1 OS=M	356.71	5	5	4	4	5	8	3	6	6	7	5	4	3	3	3	3	0.55644	1.21	0.59786	1.00	0.13944	1.14
sp Q9C092/FIS1_MOUSE	Mitochondrial fission 1 protein OS=Mus m	622.17	2	3	4	3	4	6	7	1	5	6	1	2	3	3	3	3	0.33273	1.44	0.47400	1.44	0.91299	1.00
sp P94089/ERH_MOUSE	Enhancer of rudimentary homolog OS=Mus	427.68	2	3	2	2	4	6	7	1	2	4	1	1	3	3	3	3	0.25337	1.71	0.59600	1.43	0.85447	0.86
sp Q9C233/RBM14_MOUSE	RNA-binding protein 14 OS=Mus musculus	637.43	5	5	2	2	3	3	8	1	1	5	4	1	3	3	3	3	0.50289	1.33	0.91968	1.11	0.69122	1.11
sp Q95029/PYC_MOUSE	Pyruvate carboxylase, mitochondrial OS=M	932.4	4	4	4	4	4	4	6	2	3	4	7	10	3	3	3	3	0.35545	1.95	0.05855	0.45	0.32941	0.80
sp Q9E020/MMSA_MOUSE	Methylmalonate-semialdehyde dehydrogen	591.56	5	5	4	5	4	7	4	5	8	3	5	7	3	3	3	3	0.64885	1.14	0.39202	1.21	0.50066	1.07
sp Q35136/NCAM2_MOUSE	Neural cell adhesion molecule 2 OS=Mus n	995.1	4	4	3	3	5	9	3	5	9	1	3	8	3	3	3	3	0.36153	1.55	0.29731	1.55	0.69317	1.09
sp Q8R191/NSG3_MOUSE	Synaptoglycin 3 OS=Mus musculus (Mouse	180.12	4	4	2	4	5	7	5	3	4	6	2	6	3	3	3	3	0.15588	1.60	0.31122	1.20	0.28931	1.40
sp Q9I213/PLC1_MOUSE	1-phosphatidylinositol 3-bisphosphate ph	177.46	4	4	4	4	4	4	3	3	4	3	3	3	3	3	3	3	0.52117	1.23	0.95238	1.00	0.27401	1.23
sp Q9T3X7/PSMD1_MOUSE	26S proteasome non-ATPase regulatory su	1111.44	3	4	4	2	5	6	4	3	4	3	4	3	3	3	3	3	0.73307	1.18	0.67991	1.00	0.82442	0.91
sp Q9R0P3/ESTD_MOUSE	S-formylglutathione hydrolase OS=Mus m	497.75	2	4	4	3	5	7	3	5	5	3	4	4	3	3	3	3	0.31780	1.50	0.30247	1.30	0.38187	1.10
sp P62267/RS23_MOUSE	40S ribosomal protein S23 OS=Mus muscu	391.53	4	3	3	3	4	2	3	3	3	5	3	3	3	3	3	3	0.68736	1.20	0.55021	1.10	0.41402	1.10
sp P23116/EIF3A_MOUSE	Eukaryotic translation initiation factor 3 sub	1364.08	5	5	4	3	4	6	4	3	3	3	5	2	2	3	3	3	0.55089	0.93	0.02037	0.71	0.19506	0.64
sp Q9R087/PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus musculus (Mouse) C	286.26	2	4	2	2	2	2	6	2	3	4	2	2	3	3	3	3	0.28537	1.71	0.25837	1.00	0.52941	0.80
sp Q9JUL5/CUL3_MOUSE	Cullin-3 OS=Mus musculus (Mouse) GN=C	823.51	3	2	2	2	2	2	3	2	1	2	2	2	2	2	2	2	0.38003	1.57	0.88609	0.86	0.88007	0.86
sp Q9D1D4/TMED4_MOUSE	Transmembrane emp24 domain-containin	445.73	4	5	2	2	4	4	6	7	6	3	3	4	3	3	3	3	0.64714	0.91	0.04235	1.73	0.86564	0.91
sp P93P44/ESPV4_MOUSE	ATPase inhibitor, mitochondrial OS=Mus m	379.47	4	4	5	4	3	5	6	3	7	4	2	5	3	3	3	3	0.28283	0.86	0.51104	1.14	0.63307	0.79
sp Q9ZNL5/ISG3_MOUSE	Interferon-stimulated gene 3 OS=Mus muscu	713.43	4	4	4	4	4	4	3	3	4	3	3	3	3	3	3	3	0.52117	1.23	0.95238	1.00	0.27401	1.23
sp P30416/FKBP4_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP4 (698.38	4	4	3	4	5	4	9	3	4	6	2	5	3	3	3	3	0.27219	1.18	0.32565	1.45	0.39764	1.18
sp P57776/EF1D_MOUSE	Protein elongation factor 1-delta OS=Mus mu	468.92	5	5	2	4	4	2	6	4	2	6	3	3	1	3	3	3	0.69481	0.91	0.72167	1.09	0.92192	0.91
sp Q9I0713/BAX_MOUSE	Apoptosis regulator BAX OS=Mus muscu	639.02	4	4	4	4	2	3	7	3	3	3	2	2	3	3	3	3	0.13125	0.69	0.93985	1.00	0.01799	0.54
sp Q9D028/VP59_MOUSE	Vacuolar protein sorting-associated protein	322.53	2	2	2	2	2	2	4	4	3	3	2	2	2	2	2	2	0.47328	1.25	0.40071	1.38	0.58760	0.75
sp P90967/ISOM_MOUSE	Isomerase OS=Mus musculus (Mouse)																							

sp Q9JMG7 HDGR3_MOUSE	Hepatoma-derived growth factor-related pro	289.37	3	1	2	1	1	2	3	1	2	2	2	2	2	0.76640	0.75	0.89330	0.75	0.95367	1.00
sp Q56926 TR150_MOUSE	Thyroid hormone receptor-associated protein	307.43	4	1	3	3	3	1	2	1	2	1	3	2	1	0.70133	0.80	0.98440	1.00	0.88375	0.60
sp Q3C0F9 SSRG_MOUSE	Transcobalamin-associated protein subunit gamma	144.05	2	1	1	1	1	1	1	1	1	1	2	3	3	0.69553	1.33	0.82677	0.67	0.91671	1.00
sp Q6BH66 JATL1_MOUSE	Atlastin-1 OS=Mus musculus (Mouse) GN=	594.54	2	1	1	1	2	3	1	1	1	1	1	2	1	0.94277	1.00	0.96440	1.00	0.72684	0.67
sp Q9R0H0 ACOX1_MOUSE	Peroxisomal acyl-coenzyme A oxidase 1 C	670.62	3	4	2	3	5	3	1	5	2	4	2	3	3	0.62686	1.43	0.68526	1.29	0.66580	1.14
sp G3X972 G3X972_MOUSE	Protein Sec24 OS=Mus musculus (Mouse)	495.05	2	4	4	4	2	1	3	1	3	3	1	2	3	0.44796	1.67	0.80777	0.83	0.70186	1.17
sp Q3C543 CENPY_MOUSE	Centromere protein V OS=Mus musculus (M	344.07	2	2	2	2	3	2	1	2	3	2	2	2	3	0.31088	1.75	0.80231	0.75	0.15151	1.75
sp Q3JUF7 COPR_MOUSE	Centromere subunit beta OS=Mus musculus	344.05	3	4	2	2	3	2	2	2	4	2	2	2	3	0.49456	1.40	0.84008	1.00	0.89150	0.60
sp Q17M36 CSPG5_MOUSE	Chondroitin sulfate proteoglycan 5 OS=Mu	449.78	3	2	3	5	1	3	1	2	1	2	1	2	3	0.45065	1.80	0.91992	1.00	0.95920	1.00
sp Q8BWY3 IERF1_MOUSE	Eukaryotic peptide chain release factor sub	342.29	2	2	2	2	2	1	2	1	2	2	2	3	2	0.76206	1.25	0.63754	1.25	0.93052	1.00
sp Q3C2W4 ACSLS3_MOUSE	Long-chain fatty acyl-CoA ligase 3 OS=M	569.18	3	1	2	1	4	1	5	1	1	1	2	2	2	0.90716	1.25	0.55264	1.75	0.90006	0.75
sp Q9P692 HM2_MOUSE	Nucleosome chromatin protein HM200	213.73	2	2	2	2	4	2	2	2	2	3	1	1	3	0.82539	1.40	0.82539	1.40	0.82539	0.60
sp Q3JZ22 SYN3_MOUSE	Synapsin-3 OS=Mus musculus (Mouse) GN	449.74	2	2	2	3	2	2	2	2	2	1	2	1	1	0.68028	1.67	0.76621	0.67	0.78864	0.67
sp O8997 JATOX1_MOUSE	Copper-storage protein ATOX1 OS=Mus	121.45	2	3	2	1	1	3	2	2	1	1	2	1	1	0.74873	1.50	0.82654	1.50	0.92924	1.00
sp Q3U9H9 GAGAP2_MOUSE	Arf-GAP with GTPase, ANK repeat and PH	377.84	2	1	2	1	1	2	1	1	2	1	2	2	1	0.76646	1.50	0.97860	1.00	0.99229	1.00
sp P17056 HMG21_MOUSE	High mobility group protein HMG-HMG-1 C	86.92	2	1	1	1	2	3	1	2	3	1	1	2	1	0.96818	1.00	0.96559	1.00	0.80194	1.50
sp Q81029 AP2B_MOUSE	Lamine-associated polypeptide 2 isoform	430.11	2	1	2	1	1	2	2	2	2	2	2	2	2	0.52394	1.00	0.76524	0.67	0.96350	1.00
sp Q8Z1F9 SAE2_MOUSE	SUMO-activating enzyme subunit 2 OS=M	531.95	4	2	2	1	3	1	1	3	3	1	1	2	2	0.78358	0.75	0.98402	1.00	0.84412	0.75
sp Q8BG51 MIRO1_MOUSE	Mitochondrial Rho GTPase 1 OS=Mus mus	341.2	2	1	2	2	1	1	2	1	2	1	2	2	1	0.77885	1.50	0.97860	1.00	0.99229	1.00
sp Q9Z051 BPN1_MOUSE	3'(2')5'-bisphosphate nucleotidase 1 OS=	395.57	3	1	1	1	1	2	2	2	1	2	1	2	2	0.72977	0.67	0.72061	1.33	0.88142	1.00
sp Q9N7F9 COPF_MOUSE	Cleavage and polyadenylation specificity fa	297.36	3	3	1	1	1	2	2	1	1	2	1	2	2	0.72977	0.67	0.92822	1.00	0.88142	1.00
sp P58395 CYB5_MOUSE	Cytochrome b5 OS=Mus musculus (Mouse)	346.26	2	1	3	3	1	2	2	2	2	1	1	2	1	0.82617	1.50	0.70632	1.50	0.91525	1.00
sp P63087 PP1G_MOUSE	Serine/threonine-protein phosphatase PP1-	1017.14	1	8	4	3	8	7	6	2	2	8	3	3	3	0.59164	1.38	0.70988	0.77	0.75848	1.08
sp Q55125 NIP51_MOUSE	Protein Nip5 homolog 1 OS=Mus muscu	465.74	1	6	5	4	6	3	6	3	2	4	3	3	3	0.94071	1.08	0.90868	0.92	0.88422	0.83
sp P62901 RL1_MOUSE	60S ribosomal protein L31 OS=Mus muscu	318.81	1	3	3	6	5	2	5	3	3	2	4	3	3	0.25670	1.86	0.72799	1.14	0.32564	1.29
sp Q3JAS2 Q3JAS2_MOUSE	Electron transfer flavoprotein-ubiquinone o	624.34	1	4	2	2	6	2	6	2	6	2	6	1	3	0.59933	1.43	0.68707	0.86	0.47620	1.14
sp Q921G7 ETFD_MOUSE	EH domain-containing protein 3 OS=M	1077.61	1	4	4	3	5	3	6	3	3	4	4	4	3	0.69502	1.22	0.42073	1.33	0.20769	1.33
sp Q921Y6 EH2_MOUSE	Valine-tRNA ligase OS=Mus musculus (Mo	757.47	1	2	5	4	4	3	5	4	3	3	1	4	3	0.56883	1.38	0.32634	1.50	0.86620	1.00
sp Q9P681 HMOX1_MOUSE	NAD(P)-dependent oxidoreductase OS=Mu	563.92	1	2	2	2	4	2	2	2	2	3	1	3	3	0.68552	1.63	0.82324	1.00	0.82324	1.00
sp Q9DBL1 ACDSB_MOUSE	Short-branched chain specific acyl-CoA deH	522.52	1	2	4	4	2	2	3	1	3	2	3	1	3	0.85275	1.14	0.95415	1.00	0.96355	0.86
sp Q9XJY5 COPD_MOUSE	Centromere subunit delta OS=Mus muscu	481.84	1	2	2	2	4	2	1	1	2	1	1	3	3	0.26121	1.60	0.52681	0.80	0.41271	1.33
sp B2R08 B2R08_MOUSE	Spectrin beta 1 OS=Mus musculus (Mouse)	388.79	1	2	2	3	3	2	3	1	2	1	2	1	2	0.13679	1.60	0.72018	0.80	0.42628	0.60
sp Q88741 GDAF1_MOUSE	Ganglioside-induced differentiation-associ	355.5	1	4	4	2	2	4	4	2	2	2	2	3	2	0.71836	0.89	0.53562	0.67	0.51559	0.67
sp Q9T023 ALX1_MOUSE	Putative tyrosine kinase class mu chain Va	622.17	1	2	3	4	2	1	1	3	3	1	1	3	3	0.54775	1.00	0.10889	1.00	0.35475	0.60
sp Q91086 ANFY1_MOUSE	Rabkynin-5 OS=Mus musculus (Mouse) C	304.88	1	2	2	3	1	2	2	3	1	2	2	3	2	0.70906	1.20	0.56920	1.20	0.83987	0.80
sp Q9COH3 INDUB5_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	154.62	1	2	3	1	3	3	5	2	2	3	1	3	3	0.83994	1.17	0.85143	1.17	0.58860	0.67
sp Q9Z09 DCTN5_MOUSE	Dynactin subunit 5 OS=Mus musculus (Mo	278.89	1	2	1	1	2	2	2	2	1	1	2	2	3	0.43271	0.80	0.86220	1.00	0.65413	1.00
sp Q7M0F3 G7M0F3_MOUSE	Glycylglycyl transferase class mu chain Va	171.62	1	2	2	2	2	2	2	1	1	2	2	2	2	0.92648	1.00	0.91612	1.00	0.73968	1.33
sp Q9R1R2 TPM1_MOUSE	Tropomyosin alpha-4 chain OS=Mus muscu	279.83	1	2	2	1	1	2	3	1	2	2	1	3	3	0.43271	0.80	0.86220	1.00	0.41271	0.60
sp E901Z0 E901Z0_MOUSE	Protein 4732456N10Rk OS=Mus muscu	308.35	1	3	2	1	5	2	2	6	2	1	4	3	2	0.96324	1.00	0.37489	1.00	0.60592	1.17
sp Q9D023 MPC2_MOUSE	Mitochondrial pyruvate carrier 2 OS=Mu	261.43	1	3	2	2	3	2	3	2	3	1	3	2	2	0.66908	0.83	0.77610	0.83	0.60063	0.67
sp P69566 RANB9_MOUSE	Ran-binding protein S24 OS=Mus muscu	172.9	1	2	2	2	1	1	1	1	2	3	2	2	2	0.29628	0.60	0.14585	0.60	0.55478	0.60
sp Q55100 GSD1_MOUSE	Dynactin-1 OS=Mus musculus (Mouse)	243.64	1	2	1	2	2	2	2	2	1	1	1	3	3	0.31439	1.00	0.31439	1.00	0.44858	0.60
sp Q92376 RU17_MOUSE	U1 small nuclear ribonucleoprotein 70 kDa	356.03	1	3	1	2	2	2	2	2	2	1	3	3	3	0.12857	1.50	0.06940	1.50	0.27277	1.50
sp Q90749 KHDIR1_MOUSE	KH domain-containing, RNA-binding, signal	485.03	1	3	1	2	4	3	1	5	3	1	3	3	3	0.20088	1.80	0.34418	1.80	0.26642	1.80
sp P65771 TYH3_MOUSE	Protein tyrosine kinase OS=Mus muscu	363.83	1	2	1	2	2	2	2	1	2	3	1	3	3	0.12857	1.50	0.39090	1.25	0.17001	1.75
sp P61957 AP151_MOUSE	AP-1 complex subunit 1 OS=Mus muscu	282.25	1	2	1	2	2	2	2	1	1	1	1	2	2	0.75476	1.75	0.91676	1.75	0.92924	1.00
sp Q9CWC3 RBMM8_MOUSE	RNA-binding protein 8A OS=Mus muscu	211.17	1	2	2	2	2	1	1	1	1	1	1	3	3	0.12857	1.50	0.44287	0.75	0.58760	0.75
sp F6ZU0 F6ZU0_MOUSE	Elongation factor 1-delta OS=Mus muscu	377.84	1	3	1	2	3	1	3	2	2	4	2	1	3	0.76757	1.20	0.29286	1.40	0.42599	1.40
sp Q9WV3 KCD12_MOUSE	BTB/POZ domain-containing protein KCD12	115.48	1	3	1	2	3	1	2	2	2	2	2	2	2	0.76757	1.20	0.79966	0.80	0.85312	0.80
sp P62849 RS2A1_MOUSE	40S ribosomal protein S24 OS=Mus muscu	311.53	1	3	1	4	2	2	2	1	2	1	2	1	3	0.62451	1.20	0.71563	0.80	0.75847	1.00
sp E90X22 E90X22_MOUSE	Ubiquitin-conjugating enzyme E2 OS=Mu	528.92	1	3	1	4	1	1	1	1	1	1	1	3	3	0.48952	1.00	0.48952	1.00	0.48952	0.60
sp Q9QUP5 HPLN1_MOUSE	Hyaluronan and proteoglycan link protein 1	777.79	1	3	1	2	1	1	4	1	2	1	1	3	2	0.48071	0.60	0.99789	1.00	0.54117	0.60
sp Q91074 PPM1G_MOUSE	Protein phosphatase 1G OS=Mus muscu	344.4	1	2	1	1	5	1	2	2	2	2	1	3	3	0.52851	1.75	0.09840	1.50	0.30971	1.25
sp Q8B2M2 SYLC_MOUSE	Leucine-tRNA ligase, cytoplasmic OS=Mu	830.91	1	3	1	1	4	1	2	2	3	1	2	3	3	0.84780	1.20	0.32418	1.40	0.60393	0.60
sp Q35114 H3CB2_MOUSE	3-methylcrotonyl-CoA carboxylase mu	260.32	1	3	1	1	4	1	1	1	1	3	1	3	3	0.80534	1.67	0.50534	1.67	0.42919	1.05
sp P35282 RAB21_MOUSE	Ras-related protein Rab-21 OS=Mus muscu	408.89	1	1	1	1	4	1	3	2	1	1	1	3	3	0.84780	1.20	0.57105	0.60	0.81058	0.80
sp Q8BT38 Q8BT38_MOUSE	Putative																				

Table S2. Gene Ontology classification of differentially expressed, rescued proteins.

Category	Term	Count	%	PValue	Proteins	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_M	GO:0000166	14	50	1.66E-06	Q9CW03, Q99020, Q91ZR1, Q921F4, P30	28	1936	17446	4.50568182	1.64E-04	1.64E-04	0.00183826
INTERPRO	IPRO27417:P	9	32.1428571	1.47E-05	Q9CW03, Q91ZR1, P21278, S4R232, P306	28	909	20594	7.28217822	0.00127464	0.00127464	0.01584308
UP_KEYWOR	Nucleotide-b	11	39.2857143	1.85E-05	P05132, Q9CW03, Q91ZR1, Q99PU5, P21	28	1754	22680	5.07981756	0.00203303	0.00203303	0.02090064
UP_KEYWOR	GTP-binding	6	21.4285714	4.04E-05	Q91ZR1, P21278, S4R232, P30677, P352E	28	332	22680	14.6385542	0.00443471	0.00221982	0.04564041
UP_SEQ_FE	nucleotide.pl	6	21.4285714	6.70E-05	Q91ZR1, P21278, S4R232, P30677, P352E	26	319	18012	13.0301423	0.006216	0.006216	0.07337298
GOTERM_M	GO:0005525	6	21.4285714	2.69E-04	Q91ZR1, P21278, S4R232, P30677, P352E	28	383	17446	9.76091011	0.02630855	0.01324195	0.29789629
UP_KEYWOR	Phosphoprot	19	67.8571429	4.48E-04	Q9DCN2, Q9CW03, Q99020, P21126, Q91	28	7617	22680	2.0204805	0.04813435	0.01630933	0.50540779
UP_KEYWOR	Acetylation	12	42.8571429	5.16E-04	Q9CYR6, Q9CW03, Q9DCN2, Q99020, Q9	28	3125	22680	3.1104	0.05519451	0.01409379	0.581459
UP_KEYWOR	Cytoplasm	14	50	7.04E-04	Q9DCN2, Q99020, P21126, P56371, P051	28	4404	22680	2.57493188	0.07452646	0.0153706	0.79234111
GOTERM_CC	GO:0005739	9	32.1428571	0.00165395	P05132, Q9DCN2, Q8BGH2, O89023, Q91	28	1721	19662	3.67224205	0.14551396	0.14551396	1.80307883
GOTERM_CC	GO:0070062	11	39.2857143	0.0019703	P05132, Q9DCN2, Q8BGH2, O89023, P24	28	2674	19662	2.88869003	0.1708572	0.08942722	2.1445667
UP_KEYWOR	Lipoprotein	6	21.4285714	0.00204304	P05132, Q9DCN2, Q91ZR1, P21278, S4R2	28	780	22680	6.23076923	0.20145504	0.0367998	2.28414508
GOTERM_M	GO:0003924	4	14.2857143	0.00401014	P21278, P30677, D3Y268, P56371	28	209	17446	11.924812	0.32820502	0.12418526	4.35387531
INTERPRO	IPRO00654:G	2	7.14285714	0.00523432	P21278, P30677	28	4	20594	367.75	0.36655495	0.20410739	5.51404488
GOTERM_CC	GO:0005737	17	60.7142857	0.00570778	Q9CW03, Q9DCN2, Q99020, P21126, P56	28	6631	19662	1.80027792	0.41945738	0.16578492	6.09812944
UP_SEQ_FE	short sequen	3	10.7142857	0.00842407	Q91ZR1, S4R232, P35283, P56371	26	100	18012	20.7830769	0.54468102	0.32522672	8.84538121
GOTERM_CC	GO:0005829	8	28.5714286	0.00876123	Q9CYR6, P05132, P21126, P21278, Q922I	28	1784	19662	3.14894299	0.56655248	0.18860163	9.21973172
UP_SEQ_FE	lipid moiety	3	10.7142857	0.01011654	Q91ZR1, S4R232, P35283, P56371	26	110	18012	18.8937063	0.61156522	0.27036437	10.5342867
GOTERM_CC	GO:0032593	2	7.14285714	0.01229368	Q91ZR1, S4R232, P56371	28	9	19662	156.047619	0.69122372	0.20945101	12.7131425
GOTERM_M	GO:0005515	13	46.4285714	0.01304464	Q9DCN2, Q9CW03, Q99020, O89023, A0	28	4092	17446	1.97945469	0.72744554	0.27745762	13.5378819
INTERPRO	IPRO01806:S	3	10.7142857	0.01326132	Q91ZR1, S4R232, P35283, P56371	28	134	20594	16.4664179	0.68696909	0.32101152	13.4356186
UP_SEQ_FE	domain:RRM	3	10.7142857	0.01350891	Q99020, Q921F4, P52912	26	128	18012	16.2367788	0.71773016	0.27110307	13.8341783
UP_SEQ_FE	domain:RRM	3	10.7142857	0.01350891	Q99020, Q921F4, P52912	26	128	18012	16.2367788	0.71773016	0.27110307	13.8341783
GOTERM_BF	GO:0060158	2	7.14285714	0.0137436	P21278, P30677	26	10	18082	139.092308	0.90618729	0.90618729	15.5490801
GOTERM_CC	GO:0048471	5	17.8571429	0.01401921	P05132, Q9WTX2, Q91ZR1, P24369, S4R2	28	692	19662	5.07380264	0.73848116	0.20031829	14.3747733
UP_KEYWOR	Prenylation	3	10.7142857	0.0149212	Q91ZR1, S4R232, P35283, P56371	28	157	22680	15.477707	0.80865936	0.21041111	15.6211807
KEGG_PATH	mmu05146:z	3	10.7142857	0.01853061	P05132, P21278, P30677	15	117	7691	13.1470085	0.74945815	0.74945815	17.7801684
INTERPRO	IPRO05225:S	3	10.7142857	0.01964105	Q91ZR1, S4R232, P35283, P56371	28	165	20594	13.3727273	0.82196502	0.35042944	19.296218
SMART	SM00275:SV	2	7.14285714	0.01978062	P21278, P30677	14	16	10425	93.0803571	0.258947	0.258947	12.9689304
COG_ONTO	Coenzyme m	2	7.14285714	0.02055046	Q8BHC4, Q922D8	5	11	2126	77.3090909	0.07970247	0.07970247	7.62193054
INTERPRO	IPRO01019:G	2	7.14285714	0.02077947	P21278, P30677	28	16	20594	91.9375	0.83908207	0.30606165	20.3033091
INTERPRO	IPRO11025:G	2	7.14285714	0.02077947	P21278, P30677	28	16	20594	91.9375	0.83908207	0.30606165	20.3033091
UP_KEYWOR	Magnesium	4	14.2857143	0.02341931	Q9CYR6, P21278, P30677, Q9CPY7	28	521	22680	6.21880998	0.92622747	0.27808373	23.4896967
UP_KEYWOR	Methylation	5	17.8571429	0.02577614	Q8BGH2, Q99020, Q91ZR1, S4R232, D3Y	28	960	22680	4.21875	0.94344595	0.27325031	25.5501458
GOTERM_M	GO:0044822	6	21.4285714	0.02612478	Q9WTX2, Q99020, P24369, Q921F4, P52E	28	1113	17446	3.35887563	0.9272508	0.4079401	25.4176864
GOTERM_CC	GO:0016020	16	57.1428571	0.02671011	Q9DCN2, P21126, Q91ZR1, Q921F4, Q8B	28	6998	19662	1.60551994	0.92361463	0.30748366	25.7395063
GOTERM_M	GO:0019001	2	7.14285714	0.02750716	P21278, P30677	28	18	17446	69.2301587	0.93679453	0.3688599	26.5821652
SMART	SM00360:RR	3	10.7142857	0.03195314	Q99020, Q921F4, P52912	14	229	10425	9.7551466	0.3856078	0.21616826	20.2109578
UP_KEYWOR	RNA-binding	4	14.2857143	0.03378888	Q9WTX2, Q99020, Q921F4, P52912	28	601	22680	5.39101498	0.9772006	0.31483947	32.1827649
GOTERM_M	GO:0031683	2	7.14285714	0.03800639	P21278, P30677	28	25	17446	49.8457143	0.97842024	0.42189507	34.900773
GOTERM_BF	GO:0030100	2	7.14285714	0.03802642	Q91ZR1, S4R232, P56371	26	28	18082	49.6758242	0.99867902	0.96365464	37.7140911
INTERPRO	IPRO00504:R	3	10.7142857	0.03950976	Q99020, Q921F4, P52912	28	241	20594	9.15560166	0.97001615	0.44262447	35.3168661
KEGG_PATH	mmu04020:c	3	10.7142857	0.04121417	P05132, P21278, P30677	15	1807	7691	8.54555556	0.95559836	0.78928302	35.6296644
GOTERM_BF	GO:0007264	3	10.7142857	0.04179136	Q91ZR1, S4R232, P35283, P56371	26	236	18082	8.84061278	0.99932442	0.91225453	40.6265678
UP_SEQ_FE	nucleotide.pl	5	17.8571429	0.04192923	P05132, Q9CW03, Q99PU5, Q8BHC4, Q9	26	963	18012	3.59693266	0.98138017	0.54918834	37.4322709
GOTERM_CC	GO:0005834	2	7.14285714	0.05092453	P21278, P30677	28	38	19662	36.9586466	0.99302457	0.46241596	43.7025512
INTERPRO	IPRO12677:N	3	10.7142857	0.0520625	Q99020, Q921F4, P52912	28	281	20594	7.85231317	0.99045372	0.48547687	43.8894472
UP_SEQ_FE	domain:RRM	2	7.14285714	0.06717819	Q921F4, P52912	26	50	18012	27.7107692	0.99844662	0.65968609	53.2941109
GOTERM_CC	GO:0030529	3	10.7142857	0.07099296	Q99020, Q921F4, P52912	28	320	19662	6.58325893	0.99908419	0.54035468	55.4894065
UP_KEYWOR	ATP-binding	5	17.8571429	0.07575569	P05132, Q9CW03, Q99PU5, Q8BHC4, Q9	28	1363	22680	2.97138665	0.9998276	0.54515037	58.9370112
KEGG_PATH	mmu00330:z	2	7.14285714	0.08566337	Q8CHT0, Q9CPY7	15	49	7691	20.9278912	0.99867611	0.89019613	60.8339399
KEGG_PATH	mmu00520:z	2	7.14285714	0.08566337	Q9CYR6, Q9DCN2	15	49	7691	20.9278912	0.99867611	0.89019613	60.8339399
GOTERM_M	GO:0019003	2	7.14285714	0.08888623	P35283, P56371	28	60	17446	20.7690476	0.99990053	0.68398258	64.3440741
UP_SEQ_FE	mutagenesis	4	14.2857143	0.08970462	P05132, Q9CW03, Q921F4, Q99PU5	26	772	18012	3.58947788	0.99984006	0.71311474	64.2604308
GOTERM_M	GO:0001664	2	7.14285714	0.09453329	P21278, P30677	28	64	17446	19.4709821	0.99994625	0.66457351	66.7172763