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Supplemental Information

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

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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: 20µm (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 µm. (B) Histogram of axon length of WT and KI-CGG. Results show the mean axon length ± SEM of 150 randomly selected cells for each condition from three independent cultures. Mann-Whitney test ***$p<0.001$.

Fig. S1

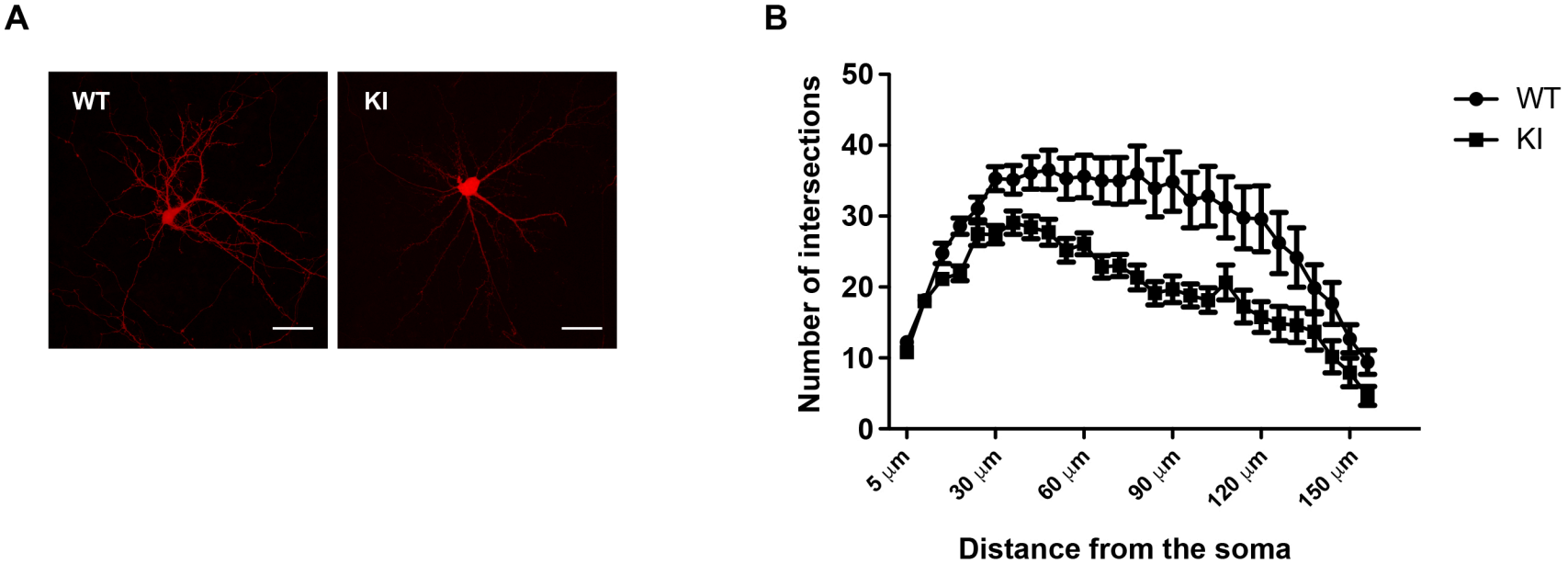

A
WT
KI
B
Number of intersections
50
40
30
20
10
0
5 μm
30 μm
60 μm
90 μm
120 μm
150 μm
Distance from the soma
WT
KI

Fig. S2

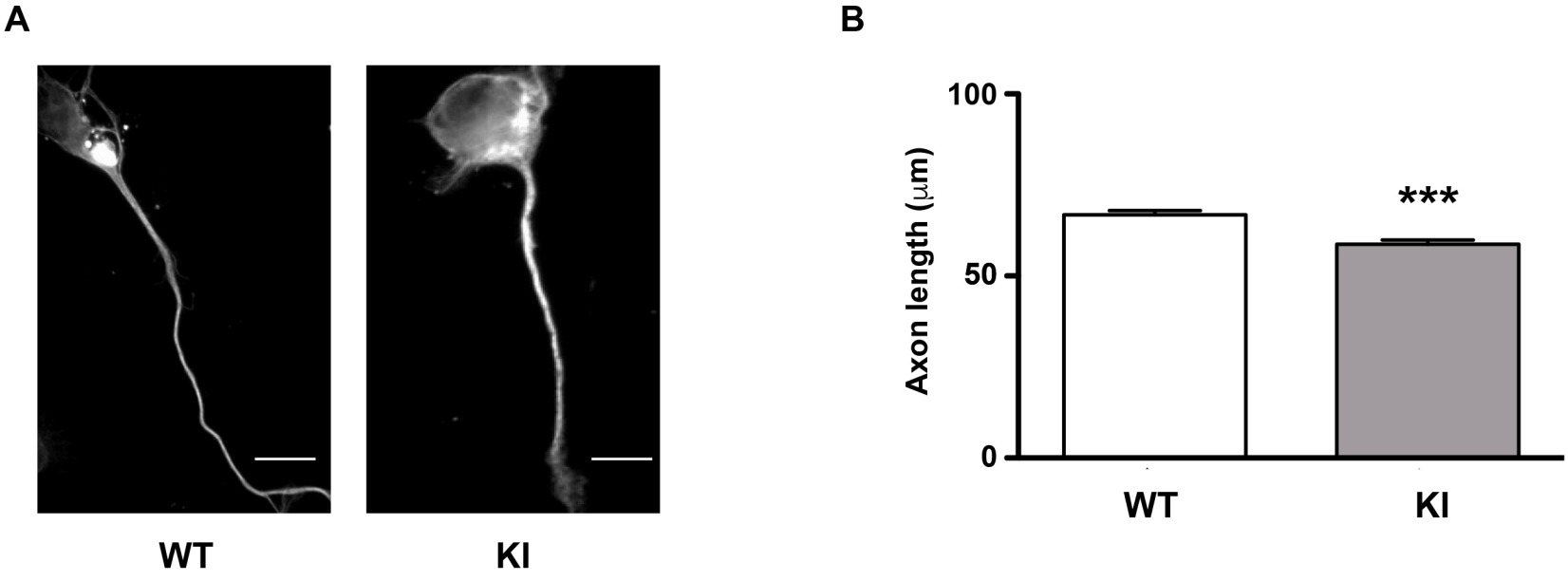


Table S1. Proteins idenified in the various samples by nanoLC MS/MS.

LEGEND:

Colour key	Meaning	Colour key	Meaning
ratio	KI-93 only, and ratio(KIscr/WT)>2	ratio	KI-93 only, and ratio(KI93/WT)>2
# Spectra	=1 spectrum in KI-scr samples	# Spectra	=1 spectrum in KI-93 samples
# Spectra	=2-5 spectra in KI-scr samples	# Spectra	=2-5 spectra in KI-93 samples
# Spectra	=6-10 spectra in KI-scr samples	# Spectra	=6-10 spectra in KI-93 samples
# 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	If contains "neuro*", "dendrit*", "axon*", "synap*"		

STATISTICS:

Columns EN, EP and ER

Student t-test between 2 conditions, with 3 replicates for each condition.

P-values returned by the t-test are listed before the corresponding ratios (columns EO, EQ and ES).

Data have been normalized before statistics.

p.value	<0.05
p.value	0.05-0.10

NO FILTER

Total number of proteins:

BASIC Spectral Count (Proline)

accession	description	protein_set_score	WT 1	WT 2	WT 3	KI-scr 1	KI-scr 2	KI-scr 3	KI-93 1	KI-93 2	KI-93 3	KI-82 1	KI-82 2	KI-82 3
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/µL) 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):

Exp. from 01/02/2017 — BASIC Spectral Count (Proline); Exp. 01/02/2017

accession	description	protein_set_score	WT 1	WT 2	WT 3	KI-scr 1	KI-scr 2	KI-scr 3	KI-93 1	KI-93 2	KI-93 3	KI-82 1	KI-82 2	KI-82 3	# Repl. WT	# Repl. KI-scr	# Repl. KI-93	# Repl. KI-82	KI-scr / WT-scr pvalue	KI-scr / WT-scr ratio	KI-93 / WT-scr pvalue	KI-93 / WT-scr ratio	KI-82 / WT-scr pvalue	KI-82 / WT-scr ratio
sp|Q6ZQ58|LARP1_MOUSE	La-related protein 1 OS=Mus musculus (Mc	209.47				3	2	1	1			1			0	3	1	1	0.03345	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|A2BH40|ARI1A_MOUSE	AT-rich interactive domain-containing protei	144.43				3	2		1			1			0	2	1	1	0.14063	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P0DN34|NDUB1_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	35.77				2	2			1			1	1	0	2	1	2	0.11728	KI-scr only	0.37390	KI-93 only	0.11630	KI-82 only
sp|Q9CQW1|YKT6_MOUSE	Synaptobrevin homolog YKT6 OS=Mus mu	442.81				2	1	2	2			1	1	1	0	3	1	3	0.01024	KI-scr only	0.37390	KI-93 only	0.00010	KI-82 only
sp|Q6PCX7|RGMA_MOUSE	Repulsive guidance molecule A OS=Mus m	102.65				2	1	1	1	1	1	2	1	1	0	3	3	3	0.02431	KI-scr only	0.00005	KI-93 only	0.00479	KI-82 only
sp|Q9DBZ5|EIF3K_MOUSE	Eukaryotic translation initiation factor 3 subu	153.19				2	1	1	1		3	2			0	3	2	1	0.02431	KI-scr only	0.22250	KI-93 only	0.37390	KI-82 only
sp|Q8VEK0|CC50A_MOUSE	Cell cycle control protein 50A OS=Mus mus	247.64				3	1		1			1			0	2	1	1	0.21775	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P24638|PPAL_MOUSE	Lysosomal acid phosphatase OS=Mus mus	102.66				2		1	1		1			1	0	2	2	1	0.16603	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q9R118|HTRA1_MOUSE	Serine protease HTRA1 OS=Mus musculus	130.96				2		1		1			2		0	2	1	1	0.16603	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|A2A699|F1712_MOUSE	Protein FAM171A2 OS=Mus musculus (Mo	485.37				4			2				2		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8VBW6|ULA1_MOUSE	NEDD8-activating enzyme E1 regulatory sul	213.87				1	3	2	1	1		2	2	1	0	3	2	3	0.01924	KI-scr only	0.11948	KI-93 only	0.00745	KI-82 only
tr|E9PX28|E9PX28_MOUSE	Protein Pcdh10 OS=Mus musculus (Mouse	221.95				1	1	3	1	1			1		0	3	2	1	0.06411	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|P62311|LSM3_MOUSE	U6 snRNA-associated Sm-like protein LSm3	160.88				1	1	1	2	1		1			0	3	2	1	0.00001	KI-scr only	0.14014	KI-93 only	0.37390	KI-82 only
sp|Q9DB50|AP1S2_MOUSE	AP-1 complex subunit sigma-2 OS=Mus mu	148.57				1	1	1	2		2	2	1		0	3	2	2	0.00001	KI-scr only	0.11834	KI-93 only	0.13722	KI-82 only
sp|P46414|CDN1B_MOUSE	Cyclin-dependent kinase inhibitor 1B OS=M	76.23				1	1	1	1	1	1	1	1	1	0	3	3	3	0.00001	KI-scr only	0.00005	KI-93 only	0.00010	KI-82 only
sp|Q8CIV8|TBCE_MOUSE	Tubulin-specific chaperone E OS=Mus mus	97.68				1	1	1		1	1		1		0	3	2	1	0.00001	KI-scr only	0.11624	KI-93 only	0.37390	KI-82 only
sp|Q8C522|ENDD1_MOUSE	Endonuclease domain-containing 1 protein	218.67				1	1		2	1	1	1			0	2	3	1	0.11728	KI-scr only	0.00595	KI-93 only	0.37390	KI-82 only
sp|Q03517|SCG2_MOUSE	Secretogranin-2 OS=Mus musculus (Mouse	197.8				1	1		5			1			0	2	1	1	0.11728	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9R0N3|SYT11_MOUSE	Synaptotagmin-11 OS=Mus musculus (Mou	54.01				1	1		1	1		1	1		0	2	2	2	0.11728	KI-scr only	0.11948	KI-93 only	0.12082	KI-82 only
sp|O08915|AIP_MOUSE	AH receptor-interacting protein OS=Mus mu	118.06				1	1		1	1			1		0	2	2	1	0.11728	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q9CXU9|EIF1B_MOUSE	Eukaryotic translation initiation factor 1b OS	72.41				1	1		1	1			1		0	2	2	1	0.11728	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q80WC7|AGFG2_MOUSE	Arf-GAP domain and FG repeat-containing	146.32				1	1		1			1			0	2	1	1	0.11728	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9D882|CJ035_MOUSE	Uncharacterized protein C10orf35 homolog	57.2				1	1		1			1			0	2	1	1	0.11728	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q922B1|MACD1_MOUSE	O-acetyl-ADP-ribose deacetylase MACROD	60.96				1		1	1		1	1			0	2	2	1	0.11661	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q9CQF0|RM11_MOUSE	39S ribosomal protein L11, mitochondrial C	76.19				1		1	1			1			0	2	1	1	0.11661	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q80ZF8|AGRB3_MOUSE	Adhesion G protein-coupled receptor B3 O	47.09				1		1	1			1			0	2	1	1	0.11661	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q3UHX2|HAP28_MOUSE	28 kDa heat- and acid-stable phosphoprote	454.99				1			2			2			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P55096|ABCD3_MOUSE	ATP-binding cassette sub-family D member	548.53				1			1	1	2		1	1	0	1	3	2	0.37390	KI-scr only	0.02146	KI-93 only	0.11630	KI-82 only
sp|Q99J36|THUM1_MOUSE	THUMP domain-containing protein 1 OS=M	103.47				1			1	1			1		0	1	2	1	0.37390	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|P52760|UK114_MOUSE	Ribonuclease UK114 OS=Mus musculus (M	99.92				1			1			2			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P49070|CAMLG_MOUSE	Calcium signal-modulating cyclophilin ligand	213.39				1			1			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|O08992|SDCB1_MOUSE	Syntenin-1 OS=Mus musculus (Mouse) GN	177.63				1			1			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q05186|RCN1_MOUSE	Reticulocalbin-1 OS=Mus musculus (Mouse	124.37				1				1			1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|B9EJ86|OSBL8_MOUSE	Oxysterol-binding protein-related protein 8	209.82				1					1			1	0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
tr|Q8R3C7|Q8R3C7_MOUSE	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1!	187.86					2	2	2	1			1		0	2	2	1	0.11626	KI-scr only	0.14014	KI-93 only	0.37390	KI-82 only
sp|Q6PDS3|SARM1_MOUSE	Sterile alpha and TIR motif-containing prote	478.44					2	2	2			1	1		0	2	1	2	0.11626	KI-scr only	0.37390	KI-93 only	0.12082	KI-82 only
sp|P46061|RAGP1_MOUSE	Ran GTPase-activating protein 1 OS=Mus	316.86					2	3	3				1		0	2	1	1	0.13468	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P08553|NFM_MOUSE	Neurofilament medium polypeptide OS=Mu	294.41					2	2	1		4	1		1	0	2	2	2	0.11626	KI-scr only	0.25340	KI-93 only	0.11916	KI-82 only
sp|Q8CIB5|FERM2_MOUSE	Fermitin family homolog 2 OS=Mus muscul	463.85					4	1	2	1	1		2		0	2	3	1	0.23368	KI-scr only	0.00595	KI-93 only	0.37390	KI-82 only
sp|Q9D0L7|ARM10_MOUSE	Armadillo repeat-containing protein 10 OS=	300.09					2	1	2		1	1	1	2	0	2	2	3	0.15432	KI-scr only	0.14329	KI-93 only	0.02240	KI-82 only
sp|Q9Z2D6|MECP2_MOUSE	Methyl-CpG-binding protein 2 OS=Mus mus	297.23					2		1	1		2	1		0	1	2	2	0.37390	KI-scr only	0.11948	KI-93 only	0.13722	KI-82 only
sp|Q8R0H9|GGA1_MOUSE	ADP-ribosylation factor-binding protein GGA	393.51					2		1		1	1	1		0	1	2	2	0.37390	KI-scr only	0.11834	KI-93 only	0.12082	KI-82 only
sp|Q9Z2C9|MTMR7_MOUSE	Myotubularin-related protein 7 OS=Mus mu	145.49					2			1	1		1		0	1	2	1	0.37390	KI-scr only	0.11624	KI-93 only	0.37390	KI-82 only
sp|Q9EPL8|IPO7_MOUSE	Importin-7 OS=Mus musculus (Mouse) GN=	689.61					1	2	3			2	1		0	2	1	2	0.16239	KI-scr only	0.37390	KI-93 only	0.13722	KI-82 only
sp|Q9CYI4|LUC7L_MOUSE	Putative RNA-binding protein Luc7-like 1 O	219.67					1	2	2					1	0	2	1	1	0.16239	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P0C027|NUD10_MOUSE	Diphosphoinositol polyphosphate phosphol	323.65					1	2	1	1	1			1	0	2	3	1	0.16239	KI-scr only	0.00005	KI-93 only	0.37390	KI-82 only
sp|O88736|DHB7_MOUSE	3-keto-steroid reductase OS=Mus musculu	126.73					1	2	1	1				1	0	2	2	1	0.16239	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q64152|BTF3_MOUSE	Transcription factor BTF3 OS=Mus musculu	108.7					1	2	1			1			0	2	1	1	0.16239	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|O08810|U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein	466.46					1	1	3	1		2			0	2	2	1	0.11626	KI-scr only	0.18328	KI-93 only	0.37390	KI-82 only
sp|Q8C570|RAE1L_MOUSE	mRNA export factor OS=Mus musculus (Mo	138.31					1	1	2		2		1		0	2	2	1	0.11626	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q9JMG1|EDF1_MOUSE	Endothelial differentiation-related factor 1 (	152.87					1	1	2			2			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
tr|E9Q107|E9Q107_MOUSE		32.95					1	1	2			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9CWM4|PFD1_MOUSE	Prefoldin subunit 1 OS=Mus musculus (Mou	195.14					1	1	1	2			2	1	0	2	2	2	0.11626	KI-scr only	0.17908	KI-93 only	0.16298	KI-82 only
sp|Q62288|TICN1_MOUSE	Testican-1 OS=Mus musculus (Mouse) GN=	46.52					1	1	1	1		1	1		0	2	2	2	0.11626	KI-scr only	0.11948	KI-93 only	0.12082	KI-82 only
sp|Q924T2|RT02_MOUSE	28S ribosomal protein S2, mitochondrial OS	45.32					1	1	1	1		1			0	2	2	1	0.11626	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q925E7|2ABD_MOUSE	Serine/threonine-protein phosphatase 2A 5	262.12					1	1	1	1		1			0	2	2	1	0.11626	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q05BC3|EMAL1_MOUSE	Echinoderm microtubule-associated protein-	69.59					1	1	1	1			1		0	2	2	1	0.11626	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|P08551|NFL_MOUSE	Neurofilament light polypeptide OS=Mus m	328.62					1	1	1		2	2			0	2	2	1	0.11626	KI-scr only	0.17504	KI-93 only	0.37390	KI-82 only
sp|Q02257|PLAK_MOUSE	Junction plakoglobin OS=Mus musculus (M	351.57					1	1	1		2	1		2	0	2	2	2	0.11626	KI-scr only	0.17504	KI-93 only	0.17801	KI-82 only
sp|Q6URW6|MYH14_MOUSE	Myosin-14 OS=Mus musculus (Mouse) GN=	409.38					1	1	1		1	1	2	3	0	2	2	3	0.11626	KI-scr only	0.11834	KI-93 only	0.03438	KI-82 only
sp|G5E870|TRIPC_MOUSE	E3 ubiquitin-protein ligase TRIP12 OS=Mu:	57.95					1	1	1		1	1			0	2	2	1	0.11626	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q8BU14|SEC62_MOUSE	Translocation protein SEC62 OS=Mus mus	141.23					1	1	1		1	1			0	2	2	1	0.11626	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|P61202|CSN2_MOUSE	COP9 signalosome complex subunit 2 OS=	400.7					1	1	1			2		1	0	2	1	2	0.11626	KI-scr only	0.37390	KI-93 only	0.14095	KI-82 only
sp|P41216|ACSL1_MOUSE	Long-chain-fatty-acid--CoA ligase 1 OS=Mu	285.75					1	1	1			2			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|O35900|LSM2_MOUSE	U6 snRNA-associated Sm-like protein LSm2	95.05					1	1	1			1	1	1	0	2	1	3	0.11626	KI-scr only	0.37390	KI-93 only	0.00010	KI-82 only
sp|P97823|LYPA1_MOUSE	Acyl-protein thioesterase 1 OS=Mus muscu	102.05					1	1	1			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q61686|CBX5_MOUSE	Chromobox protein homolog 5 OS=Mus mu	57.87					1	1	1			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8R123|FAD1_MOUSE	FAD synthase OS=Mus musculus (Mouse)	62.11					1	1	1			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P49442|INPP_MOUSE	Inositol polyphosphate 1-phosphatase OS:	327.21					1	1	1			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
tr|F7AA26|F7AA26_MOUSE	Protein Pakap OS=Mus musculus (Mouse)	200.47					1	1	1			1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P07356|ANXA2_MOUSE	Annexin A2 OS=Mus musculus (Mouse) GN	272.14					1	1	1					1	0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
tr|Q3TFD0|Q3TFD0_MOUSE	Serine hydroxymethyltransferase OS=Mus	293.89					1	1		2			1		0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9D554|SF3A3_MOUSE	Splicing factor 3A subunit 3 OS=Mus musc	153.95					1	1		1	1			2	0	2	2	1	0.11626	KI-scr only	0.11624	KI-93 only	0.37390	KI-82 only
sp|Q9CR60|GOT1B_MOUSE	Vesicle transport protein GOT1B OS=Mus	42.88					1	1		1		1			0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|O88958|GNPI1_MOUSE	Glucosamine-6-phosphate isomerase 1 OS	89.4					1	1			1			1	0	2	1	1	0.11626	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
tr|Q0VGU4|Q0VGU4_MOUSE	MCG18019 OS=Mus musculus (Mouse) GN	272.96					1		2	2			2		0	1	2	1	0.37390	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|Q9D0R2|SYTC_MOUSE	Threonine--tRNA ligase, cytoplasmic OS=M	514.27					1		2	1	1	2		2	0	1	3	2	0.37390	KI-scr only	0.00595	KI-93 only	0.11916	KI-82 only
sp|Q80UY2|KCMF1_MOUSE	E3 ubiquitin-protein ligase KCMF1 OS=Mu:	122.73					1		2		1	2			0	1	2	1	0.37390	KI-scr only	0.14329	KI-93 only	0.37390	KI-82 only
sp|Q811S7|UBIP1_MOUSE	Upstream-binding protein 1 OS=Mus muscu	40.82					1		1	1		1			0	1	2	1	0.37390	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
sp|A2AJI0|MA7D1_MOUSE	MAP7 domain-containing protein 1 OS=Mu	126.2					1		1	1				1	0	1	2	1	0.37390	KI-scr only	0.11948	KI-93 only	0.37390	KI-82 only
tr|A0PJG5|A0PJG5_MOUSE	Rbm15 protein OS=Mus musculus (Mouse)	46.95					1		1		1	1			0	1	2	1	0.37390	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q8R164|BPHL_MOUSE	Valacyclovir hydrolase OS=Mus musculus (	158.51					1		1		1	1			0	1	2	1	0.37390	KI-scr only	0.11834	KI-93 only	0.37390	KI-82 only
sp|Q8BLY2|SYTC2_MOUSE	Probable threonine--tRNA ligase 2, cytoplas	133.72					1		1			1	1		0	1	1	2	0.37390	KI-scr only	0.37390	KI-93 only	0.12082	KI-82 only
sp|Q3UZ39|LRRF1_MOUSE	Leucine-rich repeat flightless-interacting pro	85.72					1		1			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|O54781|SRPK2_MOUSE	SRSF protein kinase 2 OS=Mus musculus (	161.99					1		1				1	1	0	1	1	2	0.37390	KI-scr only	0.37390	KI-93 only	0.11630	KI-82 only
tr|Q8C845|Q8C845_MOUSE	EF-hand domain-containing protein D2 OS	249.18					1		1				1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q80Y24|PRIC2_MOUSE	Prickle-like protein 2 OS=Mus musculus (Mc	106.5					1			2			2		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8R5J9|PRAF3_MOUSE	PRA1 family protein 3 OS=Mus musculus (I	256.04					1			1			1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8JZY2|COMDA_MOUSE	COMM domain-containing protein 10 OS=M	41.78					1			1			1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8CIG0|DEP1A_MOUSE	DEP domain-containing protein 1A OS=Mu	39.02					1				1		1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9D1L9|LTOR5_MOUSE	Ragulator complex protein LAMTOR5 OS=I	147.07						1	2			2			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9CPU0|LGUL_MOUSE	Lactoylglutathione lyase OS=Mus musculu:	163.35						1	2			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P61327|MGN_MOUSE	Protein mago nashi homolog OS=Mus mus	71.75						1	2					1	0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q6PDG5|SMRC2_MOUSE	SWI/SNF complex subunit SMARCC2 OS=I	356.38						1	1	1	2	1			0	1	3	1	0.37390	KI-scr only	0.02146	KI-93 only	0.37390	KI-82 only
sp|Q9DB60|PGFS_MOUSE	Prostamide/prostaglandin F synthase OS=I	113.52						1	1			2			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9D1M4|MCA3_MOUSE	Eukaryotic translation elongation factor 1 ep	78.75						1	1			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|P16675|PPGB_MOUSE	Lysosomal protective protein OS=Mus mus	134.45						1	1			1			0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8BK67|RCC2_MOUSE	Protein RCC2 OS=Mus musculus (Mouse) (	127.94						1			1		1		0	1	1	1	0.37390	KI-scr only	0.37390	KI-93 only	0.37390	KI-82 only

Proteins only identified in 2 KI samples (KI-scr + KI-93):

Exp. from 01/02/2017 — BASIC Spectral Count (Proline); Exp. 01/02/2017

accession	description	protein_set_score	WT 1	WT 2	WT 3	KI-scr 1	KI-scr 2	KI-scr 3	KI-93 1	KI-93 2	KI-93 3	KI-82 1	KI-82 2	KI-82 3	# Repl. WT	# Repl. KI-scr	# Repl. KI-93	# Repl. KI-82	KI-scr / WT-scr pvalue	KI-scr / WT-scr ratio	KI-93 / WT-scr pvalue	KI-93 / WT-scr ratio	KI-82 / WT-scr pvalue	KI-82 / WT-scr ratio
sp|Q8BGH4|REEP1_MOUSE	Receptor expression-enhancing protein 1 (	244.44				2	1		3						0	2	1	0	0.17028	KI-scr only	0.37390	KI-93 only		
sp|O88746|TOM1_MOUSE	Target of Myb protein 1 OS=Mus musculus	156.55				1	2		1						0	2	1	0	0.14722	KI-scr only	0.37390	KI-93 only		
sp|Q8BHC4|DCAKD_MOUSE	Dephospho-CoA kinase domain-containing	147.07				1	1	1	1						0	3	1	0	0.00001	KI-scr only	0.37390	KI-93 only		
sp|Q9D379|HYEP_MOUSE	Epoxide hydrolase 1 OS=Mus musculus (M	234.58				1	1	1	1						0	3	1	0	0.00001	KI-scr only	0.37390	KI-93 only		
sp|Q8R3Z5|CACB1_MOUSE	Voltage-dependent L-type calcium channel	155.16				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q9CQE5|RGS10_MOUSE	Regulator of G-protein signaling 10 OS=Mu	41.82				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		

sp|O35972|RM23_MOUSE	39S ribosomal protein L23, mitochondrial C	49.71				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q8BGR6|ARL15_MOUSE	ADP-ribosylation factor-like protein 15 OS=	44.41				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q8R4R6|NUP53_MOUSE	Nucleoporin NUP53 OS=Mus musculus (Mc	35.48				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q8VBT0|TMX1_MOUSE	Thioredoxin-related transmembrane protein	85.48				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q6PHQ8|NAA35_MOUSE	N-alpha-acetyltransferase 35, NatC auxiliary	115.24				1	1		1						0	2	1	0	0.11728	KI-scr only	0.37390	KI-93 only		
sp|Q05512|MARK2_MOUSE	Serine/threonine-protein kinase MARK2 OS	278.66				1	1		1						0	2	1	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	2						0	2	1	0	0.11661	KI-scr only	0.37390	KI-93 only		
sp|P11531|DMD_MOUSE	Dystrophin OS=Mus musculus (Mouse) GN=	52.75				1		1	1	1	1				0	2	3	0	0.11661	KI-scr only	0.00005	KI-93 only		
sp|Q80V26|IMPA3_MOUSE	Inositol monophosphatase 3 OS=Mus mus	81.94				1			2		1				0	1	2	0	0.37390	KI-scr only	0.14329	KI-93 only		
sp|Q6P9Q6|FKB15_MOUSE	FK506-binding protein 15 OS=Mus muscul	63.91				1			2						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8C166|CPNE1_MOUSE	Copine-1 OS=Mus musculus (Mouse) GN=(	142.14				1			1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
tr|Q6ZWX2|Q6ZWX2_MOUSE	Thymosin, beta 4, X chromosome OS=Mus	48.74				1			1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|P49769|PSN1_MOUSE	Presenilin-1 OS=Mus musculus (Mouse) GN	37.89				1			1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q9D1G2|PMVK_MOUSE	Phosphomevalonate kinase OS=Mus musc	159.96					2	2			1				0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q6ZQ08|CNOT1_MOUSE	CCR4-NOT transcription complex subunit 1	236.17					2	1	2						0	2	1	0	0.15432	KI-scr only	0.37390	KI-93 only		
sp|Q8R2U6|NUDT4_MOUSE	Diphosphoinositol polyphosphate phosphoh	148.53					2	1		1	1				0	2	2	0	0.15432	KI-scr only	0.11624	KI-93 only		
sp|B9EKR1|PRPTZ_MOUSE	Receptor-type tyrosine-protein phosphatase	135.73					2		3	1					0	1	2	0	0.37390	KI-scr only	0.18328	KI-93 only		
tr|A9C473|A9C473_MOUSE	Protein A630010A05Rik (Fragment) OS=Mu	31.7					2		2						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|P70429|EVL_MOUSE	Ena/VASP-like protein OS=Mus musculus (	360.87					2		2						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q3UE37|UBE2Z_MOUSE	Ubiquitin-conjugating enzyme E2 Z OS=Mu	163.62					2		1		1				0	1	2	0	0.37390	KI-scr only	0.11834	KI-93 only		
sp|P53811|PIPNB_MOUSE	Phosphatidylinositol transfer protein beta is	174.35					2		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|P22315|HEMH_MOUSE	Ferrochelatase, mitochondrial OS=Mus mus	126.93					2		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q64737|PUR2_MOUSE	Trifunctional purine biosynthetic protein ade	223.96					1	2	1		2				0	2	2	0	0.16239	KI-scr only	0.17504	KI-93 only		
sp|P26039|TLN1_MOUSE	Talin-1 OS=Mus musculus (Mouse) GN=Tln	163.8					1	1	1		1				0	2	2	0	0.11626	KI-scr only	0.11834	KI-93 only		
tr|D4AFX7|D4AFX7_MOUSE	Protein Dnajc13 OS=Mus musculus (Mouse	128.46					1	1	1		1				0	2	2	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						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q8K1Z0|COQ9_MOUSE	Ubiquinone biosynthesis protein COQ9, mit	112.45					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q920A5|RISC_MOUSE	Retinoid-inducible serine carboxypeptidase	78.79					1	1	1						0	2	1	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						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q7TPV4|MBB1A_MOUSE	Myb-binding protein 1A OS=Mus musculus	303.45					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
tr|E9Q740|E9Q740_MOUSE	Protein Srp72 OS=Mus musculus (Mouse)	466.95					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q9WU28|PFD5_MOUSE	Prefoldin subunit 5 OS=Mus musculus (Mo	156.04					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q9CY27|TECR_MOUSE	Very-long-chain enoyl-CoA reductase OS=	200.24					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q5SVL6|RPGP2_MOUSE	Rap1 GTPase-activating protein 2 OS=Mus	43.76					1	1	1						0	2	1	0	0.11626	KI-scr only	0.37390	KI-93 only		
sp|Q8K0C4|CP51A_MOUSE	Lanosterol 14-alpha demethylase OS=Mus	334.38					1	1		1	1				0	2	2	0	0.11626	KI-scr only	0.11624	KI-93 only		
sp|Q9R1V7|ADA23_MOUSE	Disintegrin and metalloproteinase domain-c	69.29					1		2						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q3UH93|PLXD1_MOUSE	Plexin-D1 OS=Mus musculus (Mouse) GN=	64.86					1		1	1					0	1	2	0	0.37390	KI-scr only	0.11948	KI-93 only		
sp|P50544|ACADV_MOUSE	Very long-chain specific acyl-CoA dehydrog	276.89					1		1	1					0	1	2	0	0.37390	KI-scr only	0.11948	KI-93 only		
sp|Q8R313|EXOC6_MOUSE	Exocyst complex component 6 OS=Mus mu	70.99					1		1		1				0	1	2	0	0.37390	KI-scr only	0.11834	KI-93 only		
sp|Q8BNW9|KBTBB_MOUSE	Kelch repeat and BTB domain-containing p	65.66					1		1		1				0	1	2	0	0.37390	KI-scr only	0.11834	KI-93 only		
sp|Q3TDQ1|STT3B_MOUSE	Dolichyl-diphosphooligosaccharide--protein	140.56					1		1		1				0	1	2	0	0.37390	KI-scr only	0.11834	KI-93 only		
sp|Q8VHY0|CSPG4_MOUSE	Chondroitin sulfate proteoglycan 4 OS=Mu	65.04					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q9D7B6|ACAD8_MOUSE	Isobutyryl-CoA dehydrogenase, mitochondr	48					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q91X58|ZFN2B_MOUSE	AN1-type zinc finger protein 2B OS=Mus m	44.42					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q7TSY6|CELF4_MOUSE	CUGBP Elav-like family member 4 OS=Mus	127.95					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q04690|NF1_MOUSE	Neurofibromin OS=Mus musculus (Mouse)	205.39					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|P97372|PSME2_MOUSE	Proteasome activator complex subunit 2 O	112.16					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q9DB27|MCTS1_MOUSE	Malignant T-cell-amplified sequence 1 OS=	285.27					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q3UHK6|TEN4_MOUSE	Teneurin-4 OS=Mus musculus (Mouse) GN	96.83					1		1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8CH72|TRI32_MOUSE	E3 ubiquitin-protein ligase TRIM32 OS=Mu	50.98					1				1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|O35459|ECH1_MOUSE	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase	90.64					1				1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|O88983|STX8_MOUSE	Syntaxin-8 OS=Mus musculus (Mouse) GN	76.02					1				1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
tr|D3YWQ0|D3YWQ0_MOUSE	Diacylglycerol kinase OS=Mus musculus (M	146.89					1				1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8C0L0|TMX4_MOUSE	Thioredoxin-related transmembrane protein	239.26					1				1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8K3C3|LZIC_MOUSE	Protein LZIC OS=Mus musculus (Mouse) G	194.67						2	2						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q7TNR6|IGS21_MOUSE	Immunoglobulin superfamily member 21 OS	184.28						2	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q80Y17|L2GL1_MOUSE	Lethal(2) giant larvae protein homolog 1 O	101.38						1	1		1				0	1	2	0	0.37390	KI-scr only	0.11834	KI-93 only		
sp|Q99K01|PDXD1_MOUSE	Pyridoxal-dependent decarboxylase domain	50.61						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|P32233|DRG1_MOUSE	Developmentally-regulated GTP-binding pro	38.76						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q9CQ62|DECR_MOUSE	2,4-dienoyl-CoA reductase, mitochondrial C	106.01						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q6NZB0|DNJC8_MOUSE	DnaJ homolog subfamily C member 8 OS=	138.44						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|B2RXS4|PLXB2_MOUSE	Plexin-B2 OS=Mus musculus (Mouse) GN=	287.35						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q6GQS1|SCMC3_MOUSE	Calcium-binding mitochondrial carrier protein	104.92						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q9CQM5|TXD17_MOUSE	Thioredoxin domain-containing protein 17 (	108.04						1	1						0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q99LS3|SERB_MOUSE	Phosphoserine phosphatase OS=Mus mus	64.08						1		2	1				0	1	2	0	0.37390	KI-scr only	0.16207	KI-93 only		
sp|Q80SZ7|GBG5_MOUSE	Guanine nucleotide-binding protein G(I)/G(S	60.71						1		1					0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8R2Y8|PTH2_MOUSE	Peptidyl-tRNA hydrolase 2, mitochondrial C	151.02						1		1					0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q8BTM8|FLNA_MOUSE	Filamin-A OS=Mus musculus (Mouse) GN=I	423.12						1			1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		
sp|Q80X90|FLNB_MOUSE	Filamin-B OS=Mus musculus (Mouse) GN=I	77.32						1			1				0	1	1	0	0.37390	KI-scr only	0.37390	KI-93 only		

Proteins only identified in 2 KI samples (KI-scr + KI-82):

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q8BGH7|C42S2_MOUSE	CDC42 small effector protein 2 OS=Mus mu	108.11				2	1					1			0	2	0	1	0.17028	KI-scr only			0.37390	KI-82 only
sp|Q8BYK6|YTHD3_MOUSE	YTH domain-containing family protein 3 OS	119.55				2	1						2		0	2	0	1	0.17028	KI-scr only			0.37390	KI-82 only
sp|Q9D967|MGDP1_MOUSE	Magnesium-dependent phosphatase 1 OS	134.68				2								1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q3UHH2|S22AN_MOUSE	Solute carrier family 22 member 23 OS=Mu	74.83				2								1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q61425|HCDH_MOUSE	Hydroxyacyl-coenzyme A dehydrogenase, r	262.32				1	1	1				1			0	3	0	1	0.00001	KI-scr only			0.37390	KI-82 only
sp|P52912|TIA1_MOUSE	Nucleolysin TIA-1 OS=Mus musculus (Mous	88.49				1	1	1				1			0	3	0	1	0.00001	KI-scr only			0.37390	KI-82 only
sp|Q8VD63|TSYL4_MOUSE	Testis-specific Y-encoded-like protein 4 OS	74.52				1	1	1				1			0	3	0	1	0.00001	KI-scr only			0.37390	KI-82 only
sp|Q9DC37|MFSD1_MOUSE	Major facilitator superfamily domain-containi	51.8				1	1					1			0	2	0	1	0.11728	KI-scr only			0.37390	KI-82 only
sp|Q99NB9|SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musc	304.16				1	1					1			0	2	0	1	0.11728	KI-scr only			0.37390	KI-82 only
sp|P47941|CRKL_MOUSE	Crk-like protein OS=Mus musculus (Mouse)	61.31				1		1				1			0	2	0	1	0.11661	KI-scr only			0.37390	KI-82 only
sp|Q9DAU1|CNPY3_MOUSE	Protein canopy homolog 3 OS=Mus muscu	104.88				1		1				1			0	2	0	1	0.11661	KI-scr only			0.37390	KI-82 only
sp|Q8K0C9|GMDS_MOUSE	GDP-mannose 4,6 dehydratase OS=Mus n	157.59				1		1					1	1	0	2	0	2	0.11661	KI-scr only			0.11630	KI-82 only
sp|Q8BIQ5|CSTF2_MOUSE	Cleavage stimulation factor subunit 2 OS=I	41.19				1		1						1	0	2	0	1	0.11661	KI-scr only			0.37390	KI-82 only
sp|Q9D832|DNJB4_MOUSE	DnaJ homolog subfamily B member 4 OS=I	149.15				1						1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
tr|E9Q4N7|E9Q4N7_MOUSE	Protein Arid1b OS=Mus musculus (Mouse)	36.89				1						1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q61164|CTCF_MOUSE	Transcriptional repressor CTCF OS=Mus mu	65.38				1						1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q791T5|MTCH1_MOUSE	Mitochondrial carrier homolog 1 OS=Mus m	146.1				1							2		0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q7TPG7|F19A2_MOUSE	Protein FAM19A2 OS=Mus musculus (Mou	63.59				1							1		0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q8BH69|SPS1_MOUSE	Selenide, water dikinase 1 OS=Mus muscu	159.85				1								2	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|P70362|UFD1_MOUSE	Ubiquitin fusion degradation protein 1 homo	292.65					3	1				1	1	1	0	2	0	3	0.20065	KI-scr only			0.00010	KI-82 only
sp|Q61191|HCFC1_MOUSE	Host cell factor 1 OS=Mus musculus (Mous	222.05					2					1		1	0	1	0	2	0.37390	KI-scr only			0.11916	KI-82 only
sp|P19246|NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus	137.99					1	2				1			0	2	0	1	0.16239	KI-scr only			0.37390	KI-82 only
sp|Q60872|IF1A_MOUSE	Eukaryotic translation initiation factor 1A O	180.57					1	1				1	1		0	2	0	2	0.11626	KI-scr only			0.12082	KI-82 only
sp|Q8K4G5|ABLM1_MOUSE	Actin-binding LIM protein 1 OS=Mus muscu	165.73					1	1				1			0	2	0	1	0.11626	KI-scr only			0.37390	KI-82 only
sp|Q9D898|ARP5L_MOUSE	Actin-related protein 2/3 complex subunit 5-	49.27					1	1				1			0	2	0	1	0.11626	KI-scr only			0.37390	KI-82 only
sp|Q8C145|S39A6_MOUSE	Zinc transporter ZIP6 OS=Mus musculus (M	55.98					1	1				1			0	2	0	1	0.11626	KI-scr only			0.37390	KI-82 only
sp|Q920P5|KAD5_MOUSE	Adenylate kinase isoenzyme 5 OS=Mus mu	203.05					1	1					2	1	0	2	0	2	0.11626	KI-scr only			0.16298	KI-82 only
sp|Q91YE6|IPO9_MOUSE	Importin-9 OS=Mus musculus (Mouse) GN=	274.25					1	1					2		0	2	0	1	0.11626	KI-scr only			0.37390	KI-82 only
sp|Q8BXV2|BRI3B_MOUSE	BRI3-binding protein OS=Mus musculus (M	231.61					1	1					1		0	2	0	1	0.11626	KI-scr only			0.37390	KI-82 only
sp|Q8BHK1|NIPA1_MOUSE	Magnesium transporter NIPA1 OS=Mus mu	70.34					1					1	1	1	0	1	0	3	0.37390	KI-scr only			0.00010	KI-82 only
sp|P97822|AN32E_MOUSE	Acidic leucine-rich nuclear phosphoprotein 3	98.31					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q8C078|KKCC2_MOUSE	Calcium/calmodulin-dependent protein kinas	140.34					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q921M4|GOGA2_MOUSE	Golgin subfamily A member 2 OS=Mus mus	94.78					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q5RKR3|ISLR2_MOUSE	Immunoglobulin superfamily containing leuc	97.74					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q03173|ENAH_MOUSE	Protein enabled homolog OS=Mus muscul	66.63					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
tr|D3YZI9|D3YZI9_MOUSE	Protein Pgbd5 OS=Mus musculus (Mouse)	77.81					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q3TYX3|SMYD5_MOUSE	SET and MYND domain-containing protein 5	43.88					1					1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|P63080|GBRB3_MOUSE	Gamma-aminobutyric acid receptor subunit	294.08					1						1		0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q91XI1|DUS3L_MOUSE	tRNA-dihydrouridine(47) synthase [NAD(P)(	40.74					1						1		0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q5SNZ0|GRDN_MOUSE	Girdin OS=Mus musculus (Mouse) GN=Ccd	547.33						3				2			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q9D5T0|ATAD1_MOUSE	ATPase family AAA domain-containing prot	113.75						2					1		0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q9JJY3|NSMA2_MOUSE	Sphingomyelin phosphodiesterase 3 OS=M	193.47						1				1	3		0	1	0	2	0.37390	KI-scr only			0.23025	KI-82 only
sp|Q8K3X4|I2BPL_MOUSE	Interferon regulatory factor 2-binding protein	82						1				1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|P63046|ST4A1_MOUSE	Sulfotransferase 4A1 OS=Mus musculus (M	209.83						1				1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q8BKI2|TNR6B_MOUSE	Trinucleotide repeat-containing gene 6B pro	43.94						1				1			0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q3URS9|CCD51_MOUSE	Coiled-coil domain-containing protein 51 O	49.54						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|P17439|GLCM_MOUSE	Glucosylceramidase OS=Mus musculus (Mo	97.81						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q9DCG9|TR112_MOUSE	Multifunctional methyltransferase subunit TF	48.02						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q9D662|SC23B_MOUSE	Protein transport protein Sec23B OS=Mus	170.88						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q91ZW3|SMCA5_MOUSE	SWI/SNF-related matrix-associated actin-de	64.69						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only
sp|Q91VF2|HNMT_MOUSE	Histamine N-methyltransferase OS=Mus mu	61.39						1						1	0	1	0	1	0.37390	KI-scr only			0.37390	KI-82 only

Proteins only identified in 2 KI samples (KI-93 + KI-82):

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q922P8|T132A_MOUSE	Transmembrane protein 132A OS=Mus mu	180.06							2	1	1		1	1	0	0	3	2			0.00595	KI-93 only	0.11630	KI-82 only
sp|Q9ESW4|AGK_MOUSE	Acylglycerol kinase, mitochondrial OS=Mus	510.48							3	1		1	1	1	0	0	2	3			0.18328	KI-93 only	0.00010	KI-82 only
sp|Q8BGB5|LIMD2_MOUSE	LIM domain-containing protein 2 OS=Mus r	106.36							2			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9WUQ2|PREB_MOUSE	Prolactin regulatory element-binding protein	76.36							2			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8K400|STXB5_MOUSE	Syntaxin-binding protein 5 OS=Mus muscu	95.48							2			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|A3KGB4|TBC8B_MOUSE	TBC1 domain family member 8B OS=Mus m	38.42							2				1		0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q99NH0|ANR17_MOUSE	Ankyrin repeat domain-containing protein 1	100.71							1	1		1	1		0	0	2	2			0.11948	KI-93 only	0.12082	KI-82 only
tr|A2RTH5|A2RTH5_MOUSE	Leucine carboxyl methyltransferase 1 OS=I	110.11							1	1			1	1	0	0	2	2			0.11948	KI-93 only	0.11630	KI-82 only
sp|Q8CC35|SYNPO_MOUSE	Synaptopodin OS=Mus musculus (Mouse)	128.84							1	1			1		0	0	2	1			0.11948	KI-93 only	0.37390	KI-82 only
sp|Q9CWE0|MFR1L_MOUSE	Mitochondrial fission regulator 1-like OS=M	118.37							1	1				1	0	0	2	1			0.11948	KI-93 only	0.37390	KI-82 only
sp|Q99LY9|NDUS5_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	196.88							1		1		1	1	0	0	2	2			0.11834	KI-93 only	0.11630	KI-82 only
sp|Q99PG2|OGFR_MOUSE	Opioid growth factor receptor OS=Mus mus	123.77							1		1		1		0	0	2	1			0.11834	KI-93 only	0.37390	KI-82 only
sp|Q9R0P6|SC11A_MOUSE	Signal peptidase complex catalytic subunit	123.5							1		1			1	0	0	2	1			0.11834	KI-93 only	0.37390	KI-82 only
sp|Q9QYH6|MAGD1_MOUSE	Melanoma-associated antigen D1 OS=Mus	105.91							1			2			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9JKW0|AR6P1_MOUSE	ADP-ribosylation factor-like protein 6-interac	91.57							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only

sp|Q8BGU5|CCNY_MOUSE	Cyclin-Y OS=Mus musculus (Mouse) GN=C	69.24							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q3UVK0|ERMP1_MOUSE	Endoplasmic reticulum metallopeptidase 1	88.36							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8R3S6|EXOC1_MOUSE	Exocyst complex component 1 OS=Mus mu	78.77							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|P47802|MTX1_MOUSE	Metaxin-1 OS=Mus musculus (Mouse) GN=	117.26							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q7TNS2|MIC10_MOUSE	MICOS complex subunit Mic10 OS=Mus mu	38.03							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8JZN7|MIRO2_MOUSE	Mitochondrial Rho GTPase 2 OS=Mus mus	87.49							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q9JIP4|PANX1_MOUSE	Pannexin-1 OS=Mus musculus (Mouse) GN	190.92							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q2M3X8|PHAR1_MOUSE	Phosphatase and actin regulator 1 OS=Mu	50							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8BU31|RAP2C_MOUSE	Ras-related protein Rap-2c OS=Mus muscu	246.85							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8BP71|RFOX2_MOUSE	RNA binding protein fox-1 homolog 2 OS=I	111.35							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8BIF2|RFOX3_MOUSE	RNA binding protein fox-1 homolog 3 OS=I	123.13							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q6P5F6|S39AA_MOUSE	Zinc transporter ZIP10 OS=Mus musculus (	108.87							1			1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|P17809|GTR1_MOUSE	Solute carrier family 2, facilitated glucose tra	50.19							1				1		0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q922R1|CP070_MOUSE	UPF0183 protein C16orf70 homolog OS=M	36.57								1	1	1	1		0	0	2	2			0.11624	KI-93 only	0.12082	KI-82 only
sp|Q9ERR1|NDEL1_MOUSE	Nuclear distribution protein nudE-like 1 OS	93.23								1	1		2		0	0	2	1			0.11624	KI-93 only	0.37390	KI-82 only
sp|Q9CX56|PSMD8_MOUSE	26S proteasome non-ATPase regulatory su	302.28								1	1		1	2	0	0	2	2			0.11624	KI-93 only	0.15377	KI-82 only
sp|P97783|AF1Q_MOUSE	Protein AF1q OS=Mus musculus (Mouse) G	60.38								1	1		1	1	0	0	2	2			0.11624	KI-93 only	0.11630	KI-82 only
sp|Q61070|EI24_MOUSE	Etoposide-induced protein 2.4 OS=Mus mu	61.01								1	1		1		0	0	2	1			0.11624	KI-93 only	0.37390	KI-82 only
sp|Q9D773|RM02_MOUSE	39S ribosomal protein L2, mitochondrial OS	153.19								1		1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|O55128|SAP18_MOUSE	Histone deacetylase complex subunit SAP1	99.19								1		1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q8BZM1|GLMN_MOUSE	Glomulin OS=Mus musculus (Mouse) GN=G	67.37								1			1	1	0	0	1	2			0.37390	KI-93 only	0.11630	KI-82 only
sp|Q8C181|MBNL2_MOUSE	Muscleblind-like protein 2 OS=Mus musculu	33.4								1			1		0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q99LC2|CSTF1_MOUSE	Cleavage stimulation factor subunit 1 OS=I	111.25									2	1			0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q7TNV0|DEK_MOUSE	Protein DEK OS=Mus musculus (Mouse) G	77.88									1	1		2	0	0	1	2			0.37390	KI-93 only	0.17801	KI-82 only
sp|A2AQP0|MYH7B_MOUSE	Myosin-7B OS=Mus musculus (Mouse) GN=	89.87									1		1	2	0	0	1	2			0.37390	KI-93 only	0.15377	KI-82 only
sp|Q64727|VINC_MOUSE	Vinculin OS=Mus musculus (Mouse) GN=V	257.98									1		1		0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|Q3V1L4|5NTC_MOUSE	Cytosolic purine 5'-nucleotidase OS=Mus m	90.04									1			1	0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
sp|P47740|AL3A2_MOUSE	Fatty aldehyde dehydrogenase OS=Mus m	54.65									1			1	0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only
tr|F6RPJ9|F6RPJ9_MOUSE	Insulin-degrading enzyme OS=Mus muscul	274.08									1			1	0	0	1	1			0.37390	KI-93 only	0.37390	KI-82 only

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

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
tr|Q9D104|Q9D104_MOUSE	Signal recognition particle 19 kDa protein C	186				2	1								0	2	0	0	0.17028	KI-scr only				
sp|P12657|ACM1_MOUSE	Muscarinic acetylcholine receptor M1 OS=M	72.17				2									0	1	0	0	0.37390	KI-scr only				
sp|O89023|TPP1_MOUSE	Tripeptidyl-peptidase 1 OS=Mus musculus	110.6				1	1	1							0	3	0	0	0.00001	KI-scr only				
tr|A0AUM9|A0AUM9_MOUSE	Eif2b3 protein OS=Mus musculus (Mouse)	38.59				1	1	1							0	3	0	0	0.00001	KI-scr only				
sp|Q8VEH8|ERLEC_MOUSE	Endoplasmic reticulum lectin 1 OS=Mus mu	35.03				1	1								0	2	0	0	0.11728	KI-scr only				
sp|Q3UHC7|DAB2P_MOUSE	Disabled homolog 2-interacting protein OS	32.04				1	1								0	2	0	0	0.11728	KI-scr only				
sp|Q99MR6|SRRT_MOUSE	Serrate RNA effector molecule homolog OS	261.31				1	1								0	2	0	0	0.11728	KI-scr only				
sp|Q8BI08|MAL2_MOUSE	Protein MAL2 OS=Mus musculus (Mouse) (	101.56				1	1								0	2	0	0	0.11728	KI-scr only				
sp|Q9EQ80|NIF3L_MOUSE	NIF3-like protein 1 OS=Mus musculus (Mou	370.81				1		2							0	2	0	0	0.15096	KI-scr only				
sp|Q8K0B2|LMBD1_MOUSE	Probable lysosomal cobalamin transporter	116.41				1		1							0	2	0	0	0.11661	KI-scr only				
sp|Q8R0X7|SGPL1_MOUSE	Sphingosine-1-phosphate lyase 1 OS=Mus	101.95				1		1							0	2	0	0	0.11661	KI-scr only				
sp|Q08890|IDS_MOUSE	Iduronate 2-sulfatase OS=Mus musculus (M	75.3				1		1							0	2	0	0	0.11661	KI-scr only				
sp|Q8CI51|PDLI5_MOUSE	PDZ and LIM domain protein 5 OS=Mus mu	68.99				1									0	1	0	0	0.37390	KI-scr only				
tr|A0A0J9YUD5|A0A0J9YUD5_M	Protein Nup205 OS=Mus musculus (Mouse	32.66				1									0	1	0	0	0.37390	KI-scr only				
sp|O88271|CFDP1_MOUSE	Craniofacial development protein 1 OS=Mu	53.04				1									0	1	0	0	0.37390	KI-scr only				
sp|O55057|PDE6D_MOUSE	Retinal rod rhodopsin-sensitive cGMP 3',5'-c	42.37				1									0	1	0	0	0.37390	KI-scr only				
sp|Q9DCL8|IPP2_MOUSE	Protein phosphatase inhibitor 2 OS=Mus m	84.95				1									0	1	0	0	0.37390	KI-scr only				
sp|Q9CXY9|GPI8_MOUSE	GPI-anchor transamidase OS=Mus muscul	78.94				1									0	1	0	0	0.37390	KI-scr only				
tr|Q3UTE1|Q3UTE1_MOUSE	Putative uncharacterized protein OS=Mus	60.1				1									0	1	0	0	0.37390	KI-scr only				
sp|Q80U23|SNPH_MOUSE	Syntaphilin OS=Mus musculus (Mouse) GN	53.18				1									0	1	0	0	0.37390	KI-scr only				
sp|Q64096|MCF2L_MOUSE	Guanine nucleotide exchange factor DBS	43.2				1									0	1	0	0	0.37390	KI-scr only				
sp|Q6QD59|SEC20_MOUSE	Vesicle transport protein SEC20 OS=Mus r	38.28				1									0	1	0	0	0.37390	KI-scr only				
sp|Q8R0I4|TM2D2_MOUSE	TM2 domain-containing protein 2 OS=Mus	34.76				1									0	1	0	0	0.37390	KI-scr only				
sp|O70139|IPKG_MOUSE	cAMP-dependent protein kinase inhibitor ga	34.54				1									0	1	0	0	0.37390	KI-scr only				
sp|A3KGF7|PLCB2_MOUSE	1-phosphatidylinositol 4,5-bisphosphate ph	34.16				1									0	1	0	0	0.37390	KI-scr only				
sp|Q9CPW0|CNTP2_MOUSE	Contactin-associated protein-like 2 OS=Mu	33.26				1									0	1	0	0	0.37390	KI-scr only				
sp|Q8WTY4|CPIN1_MOUSE	Anamorsin OS=Mus musculus (Mouse) GN	32.91				1									0	1	0	0	0.37390	KI-scr only				
sp|Q3TZX8|NOL9_MOUSE	Polynucleotide 5'-hydroxyl-kinase NOL9 OS	32.03				1									0	1	0	0	0.37390	KI-scr only				
sp|Q70IV5|SYNEM_MOUSE	Synemin OS=Mus musculus (Mouse) GN=S	31.12				1									0	1	0	0	0.37390	KI-scr only				
sp|Q9D8C2|TSN13_MOUSE	Tetraspanin-13 OS=Mus musculus (Mouse)	30.73				1									0	1	0	0	0.37390	KI-scr only				
sp|Q6P2L7|CASC4_MOUSE	Protein CASC4 OS=Mus musculus (Mouse)	30.12				1									0	1	0	0	0.37390	KI-scr only				
sp|P00920|CAH2_MOUSE	Carbonic anhydrase 2 OS=Mus musculus (	76.29				1									0	1	0	0	0.37390	KI-scr only				
sp|Q3UVX5|GRM5_MOUSE	Metabotropic glutamate receptor 5 OS=Mu	335.63				1									0	1	0	0	0.37390	KI-scr only				
sp|Q09143|CTR1_MOUSE	High affinity cationic amino acid transporter	93.01				1									0	1	0	0	0.37390	KI-scr only				
tr|Q5DTQ9|Q5DTQ9_MOUSE	MKIAA0327 protein OS=Mus musculus (Mc	63.12				1									0	1	0	0	0.37390	KI-scr only				
sp|Q8R0A7|K0513_MOUSE	Uncharacterized protein KIAA0513 OS=Mu	169.92					2								0	1	0	0	0.37390	KI-scr only				
sp|Q8VCH6|DHC24_MOUSE	Delta(24)-sterol reductase OS=Mus muscul	138.09					2								0	1	0	0	0.37390	KI-scr only				
sp|Q3UHK1|MYCT_MOUSE	Proton myo-inositol cotransporter OS=Mus	168.41					2								0	1	0	0	0.37390	KI-scr only				
sp|P70122|SBDS_MOUSE	Ribosome maturation protein SBDS OS=Mu	44.29					1	1							0	2	0	0	0.11626	KI-scr only				
sp|P49962|SRP09_MOUSE	Signal recognition particle 9 kDa protein OS	55.67					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q8VD33|SGTB_MOUSE	Small glutamine-rich tetratricopeptide repea	42.46					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q9QUH0|GLRX1_MOUSE	Glutaredoxin-1 OS=Mus musculus (Mouse)	40.28					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q8BYR1|TYW4_MOUSE	tRNA wybutosine-synthesizing protein 4 OS	71.26					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q80XR2|AT2C1_MOUSE	Calcium-transporting ATPase type 2C memb	101.16					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q9CPT4|MYDGF_MOUSE	Myeloid-derived growth factor OS=Mus mus	101.17					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q9CQI7|RU2B_MOUSE	U2 small nuclear ribonucleoprotein B" OS=	217.02					1	1							0	2	0	0	0.11626	KI-scr only				
sp|P51807|DYLT1_MOUSE	Dynein light chain Tctex-type 1 OS=Mus mu	63.41					1	1							0	2	0	0	0.11626	KI-scr only				
sp|Q62092|NSG1_MOUSE	Neuron-specific protein family member 1 OS	79.03					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8VC30|TKFC_MOUSE	Triokinase/FMN cyclase OS=Mus musculus	120.85					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9Z315|SNUT1_MOUSE	U4/U6.U5 tri-snRNP-associated protein 1 C	97.71					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BK72|RT27_MOUSE	28S ribosomal protein S27, mitochondrial C	78.11					1								0	1	0	0	0.37390	KI-scr only				
sp|O54916|REPS1_MOUSE	RalBP1-associated Eps domain-containing	71.12					1								0	1	0	0	0.37390	KI-scr only				
sp|Q3UH68|LIMC1_MOUSE	LIM and calponin homology domains-contai	70.75					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8R3L5|SO3A1_MOUSE	Solute carrier organic anion transporter fam	40.47					1								0	1	0	0	0.37390	KI-scr only				
sp|Q6DFV3|RHG21_MOUSE	Rho GTPase-activating protein 21 OS=Mus	80.9					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9JIY5|HTRA2_MOUSE	Serine protease HTRA2, mitochondrial OS=	65.18					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CR29|CCD43_MOUSE	Coiled-coil domain-containing protein 43 OS	58.75					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9JIK5|DDX21_MOUSE	Nucleolar RNA helicase 2 OS=Mus musculu	45.92					1								0	1	0	0	0.37390	KI-scr only				
sp|Q62384|ZPR1_MOUSE	Zinc finger protein ZPR1 OS=Mus musculus	43.59					1								0	1	0	0	0.37390	KI-scr only				
sp|Q68FM6|PPR29_MOUSE	Protein phosphatase 1 regulatory subunit 2	42.39					1								0	1	0	0	0.37390	KI-scr only				
sp|Q91XF0|PNPO_MOUSE	Pyridoxine-5'-phosphate oxidase OS=Mus	42.28					1								0	1	0	0	0.37390	KI-scr only				
sp|A2A5R2|BIG2_MOUSE	Brefeldin A-inhibited guanine nucleotide-exc	38.88					1								0	1	0	0	0.37390	KI-scr only				
sp|Q6PFD5|DLGP3_MOUSE	Disks large-associated protein 3 OS=Mus m	38.41					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9D5V6|SYAP1_MOUSE	Synapse-associated protein 1 OS=Mus mu	38.03					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BT35|YB039_MOUSE	Uncharacterized protein LINC00116 homolo	35.86					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CRA4|MSMO1_MOUSE	Methylsterol monooxygenase 1 OS=Mus m	35.46					1								0	1	0	0	0.37390	KI-scr only				
tr|Q91Y09|Q91Y09_MOUSE	Protein Pcdhac2 OS=Mus musculus (Mous	33.97					1								0	1	0	0	0.37390	KI-scr only				
sp|O70324|MOT8_MOUSE	Monocarboxylate transporter 8 OS=Mus mu	33.33					1								0	1	0	0	0.37390	KI-scr only				
sp|Q6PGH0|UBTD2_MOUSE	Ubiquitin domain-containing protein 2 OS=I	33.13					1								0	1	0	0	0.37390	KI-scr only				
sp|Q99K90|TAB2_MOUSE	TGF-beta-activated kinase 1 and MAP3K7-I	32.95					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CWW6|PIN4_MOUSE	Peptidyl-prolyl cis-trans isomerase NIMA-inte	32.52					1								0	1	0	0	0.37390	KI-scr only				
sp|Q920Q2|REV1_MOUSE	DNA repair protein REV1 OS=Mus musculu	31.6					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8K296|MTMR3_MOUSE	Myotubularin-related protein 3 OS=Mus mu	31.3					1								0	1	0	0	0.37390	KI-scr only				
sp|Q80U56|AVL9_MOUSE	Late secretory pathway protein AVL9 homo	31.2					1								0	1	0	0	0.37390	KI-scr only				
sp|P84309|ADCY5_MOUSE	Adenylate cyclase type 5 OS=Mus musculu	30.55					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CQS4|S2546_MOUSE	Solute carrier family 25 member 46 OS=Mu	30.38					1								0	1	0	0	0.37390	KI-scr only				
tr|E9Q6P5|E9Q6P5_MOUSE	Protein Ttc7b OS=Mus musculus (Mouse) (	29.7					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8JZX4|SPF45_MOUSE	Splicing factor 45 OS=Mus musculus (Mous	29.58					1								0	1	0	0	0.37390	KI-scr only				
sp|Q5RJ54|ZSC26_MOUSE	Zinc finger and SCAN domain-containing pr	29.5					1								0	1	0	0	0.37390	KI-scr only				
tr|Q6R5F5|Q6R5F5_MOUSE	Putative uncharacterized protein OS=Mus m	29.48					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9WVG6|CARM1_MOUSE	Histone-arginine methyltransferase CARM1	29.46					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BVU5|NUDT9_MOUSE	ADP-ribose pyrophosphatase, mitochondria	29.13					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8K0X8|FEZ1_MOUSE	Fasciculation and elongation protein zeta-1	28.53					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9JKK8|ATR_MOUSE	Serine/threonine-protein kinase ATR OS=M	28.2					1								0	1	0	0	0.37390	KI-scr only				
sp|P09055|ITB1_MOUSE	Integrin beta-1 OS=Mus musculus (Mouse)	141.82					1								0	1	0	0	0.37390	KI-scr only				
sp|Q00915|RET1_MOUSE	Retinol-binding protein 1 OS=Mus musculus	81.55					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BSY0|ASPH_MOUSE	Aspartyl/asparaginyl beta-hydroxylase OS=	106.23					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9DAR7|DCPS_MOUSE	m7GpppX diphosphatase OS=Mus muscul	89.37					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CQ80|VPS25_MOUSE	Vacuolar protein-sorting-associated protein	119.5					1								0	1	0	0	0.37390	KI-scr only				
sp|Q3UUQ7|PGAP1_MOUSE	GPI inositol-deacylase OS=Mus musculus (	279.14					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9QXB9|DRG2_MOUSE	Developmentally-regulated GTP-binding pro	189.22					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9D8B4|NDUAB_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	127.48					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9EQI8|RM46_MOUSE	39S ribosomal protein L46, mitochondrial C	65.97					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BX94|OSBL2_MOUSE	Oxysterol-binding protein-related protein 2	47.02					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BIG7|CMTD1_MOUSE	Catechol O-methyltransferase domain-conta	114.11					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9D1K7|CT027_MOUSE	UPF0687 protein C20orf27 homolog OS=M	55.73					1								0	1	0	0	0.37390	KI-scr only				
sp|Q99KI3|EMC3_MOUSE	ER membrane protein complex subunit 3 C	97.9					1								0	1	0	0	0.37390	KI-scr only				
sp|Q9CPU4|MGST3_MOUSE	Microsomal glutathione S-transferase 3 OS	261.13					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8C8N2|SCAI_MOUSE	Protein SCAI OS=Mus musculus (Mouse) G	239.61					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8VBZ3|CLPT1_MOUSE	Cleft lip and palate transmembrane protein	263.74					1								0	1	0	0	0.37390	KI-scr only				
sp|Q4VAE3|TMM65_MOUSE	Transmembrane protein 65 OS=Mus muscu	82.34					1								0	1	0	0	0.37390	KI-scr only				
sp|L0N7N1|KIF14_MOUSE	Kinesin-like protein KIF14 OS=Mus muscul	69.77					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8K4Q0|RPTOR_MOUSE	Regulatory-associated protein of mTOR OS	98.24					1								0	1	0	0	0.37390	KI-scr only				
sp|Q8BRF7|SCFD1_MOUSE	Sec1 family domain-containing protein 1 OS	170.21					1								0	1	0	0	0.37390	KI-scr only				
sp|O70152|DPM1_MOUSE	Dolichol-phosphate mannosyltransferase su	88.91					1								0	1	0	0	0.37390	KI-scr only				
sp|Q7TN98|CPEB4_MOUSE	Cytoplasmic polyadenylation element-bindin	87.2					1								0	1	0	0	0.37390	KI-scr only				
tr|Q91XW9|Q91XW9_MOUSE	MCG133388, isoform CRA_f OS=Mus musc	62.07					1								0	1	0	0	0.37390	KI-scr only				
sp|A2A432|CUL4B_MOUSE	Cullin-4B OS=Mus musculus (Mouse) GN=C	78.11						2							0	1	0	0	0.37390	KI-scr only				
sp|Q9D071|MMS19_MOUSE	MMS19 nucleotide excision repair protein h	58.88						1							0	1	0	0	0.37390	KI-scr only				
sp|O35668|HAP1_MOUSE	Huntingtin-associated protein 1 OS=Mus m	83.85						1							0	1	0	0	0.37390	KI-scr only				
sp|Q91YR7|PRP6_MOUSE	Pre-mRNA-processing factor 6 OS=Mus mu	70.66						1							0	1	0	0	0.37390	KI-scr only				
sp|O88967|YMEL1_MOUSE	ATP-dependent zinc metalloprotease YME1	81.52						1							0	1	0	0	0.37390	KI-scr only				
sp|Q8BH55|THNS1_MOUSE	Threonine synthase-like 1 OS=Mus muscul	51.67						1							0	1	0	0	0.37390	KI-scr only				
sp|Q60759|GCDH_MOUSE	Glutaryl-CoA dehydrogenase, mitochondrial	45.3						1							0	1	0	0	0.37390	KI-scr only				
sp|P11352|GPX1_MOUSE	Glutathione peroxidase 1 OS=Mus musculu	45.22						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9EQP6|ARRC_MOUSE	Arrestin-C OS=Mus musculus (Mouse) GN=	41.17						1							0	1	0	0	0.37390	KI-scr only				
tr|F8VQ54|F8VQ54_MOUSE	Endoribonuclease Dicer OS=Mus musculus	35.55						1							0	1	0	0	0.37390	KI-scr only				

sp|Q9CYI0|NJMU_MOUSE	Protein Njmu-R1 OS=Mus musculus (Mouse	35.19						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9DC23|DJC10_MOUSE	DnaJ homolog subfamily C member 10 OS	33.44						1							0	1	0	0	0.37390	KI-scr only				
sp|Q6ZWQ0|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 muscu	32.05						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9DBR4|APBB2_MOUSE	Amyloid beta A4 precursor protein-binding f	31.92						1							0	1	0	0	0.37390	KI-scr only				
sp|Q3UDP0|WDR41_MOUSE	WD repeat-containing protein 41 OS=Mus	31.88						1							0	1	0	0	0.37390	KI-scr only				
sp|P37804|TAGL_MOUSE	Transgelin OS=Mus musculus (Mouse) GN=	31.86						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9DB15|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|Q7TSC3|NEK5_MOUSE	Serine/threonine-protein kinase Nek5 OS=M	29.79						1							0	1	0	0	0.37390	KI-scr only				
sp|Q8R1N4|NUDC3_MOUSE	NudC domain-containing protein 3 OS=Mus	141.89						1							0	1	0	0	0.37390	KI-scr only				
sp|Q5SUF2|LC7L3_MOUSE	Luc7-like protein 3 OS=Mus musculus (Mou	186.6						1							0	1	0	0	0.37390	KI-scr only				
sp|P60904|DNJC5_MOUSE	DnaJ homolog subfamily C member 5 OS=	311.67						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9JI90|RNF14_MOUSE	E3 ubiquitin-protein ligase RNF14 OS=Mus	263.19						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9D710|TMX2_MOUSE	Thioredoxin-related transmembrane protein	180.02						1							0	1	0	0	0.37390	KI-scr only				
sp|Q9Z0J0|NPC2_MOUSE	Epididymal secretory protein E1 OS=Mus m	63.99						1							0	1	0	0	0.37390	KI-scr only				
sp|Q8BR63|F177A_MOUSE	Protein FAM177A1 OS=Mus musculus (Mo	183.01						1							0	1	0	0	0.37390	KI-scr only				
sp|Q5SW19|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|Q9DAI2|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):

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q8K4R4|PITC1_MOUSE	Cytoplasmic phosphatidylinositol transfer pr	303.78							2	2	1				0	0	3	0			0.00715	KI-93 only		
sp|O35887|CALU_MOUSE	Calumenin OS=Mus musculus (Mouse) GN	434.64							4						0	0	1	0			0.37390	KI-93 only		
sp|Q8R4F1|NTNG2_MOUSE	Netrin-G2 OS=Mus musculus (Mouse) GN=	92.39							2						0	0	1	0			0.37390	KI-93 only		
sp|Q9CRD0|OCAD1_MOUSE	OCIA domain-containing protein 1 OS=Mus	147.41							2						0	0	1	0			0.37390	KI-93 only		
sp|Q9D6U8|F162A_MOUSE	Protein FAM162A OS=Mus musculus GN=F	107.03							2						0	0	1	0			0.37390	KI-93 only		
sp|P55088|AQP4_MOUSE	Aquaporin-4 OS=Mus musculus (Mouse) G	96.51							1	1	1				0	0	3	0			0.00005	KI-93 only		
sp|Q61290|CAC1E_MOUSE	Voltage-dependent R-type calcium channel	39.61							1	1	1				0	0	3	0			0.00005	KI-93 only		
sp|Q8R180|ERO1A_MOUSE	ERO1-like protein alpha OS=Mus musculus	146.71							1	1	1				0	0	3	0			0.00005	KI-93 only		
sp|O08842|GFRA2_MOUSE	GDNF family receptor alpha-2 OS=Mus mu	64.44							1	1					0	0	2	0			0.11948	KI-93 only		
sp|Q68ED7|CRTC1_MOUSE	CREB-regulated transcription coactivator 1	104.36							1	1					0	0	2	0			0.11948	KI-93 only		
sp|P55264|ADK_MOUSE	Adenosine kinase OS=Mus musculus (Mou	76.31							1		1				0	0	2	0			0.11834	KI-93 only		
sp|Q9WVE8|PACN2_MOUSE	Protein kinase C and casein kinase substra	101.97							1						0	0	1	0			0.37390	KI-93 only		
sp|P62500|T22D1_MOUSE	TSC22 domain family protein 1 OS=Mus m	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|Q9CRB2|NHP2_MOUSE	H/ACA ribonucleoprotein complex subunit 2	55.19							1						0	0	1	0			0.37390	KI-93 only		
sp|P42227|STAT3_MOUSE	Signal transducer and activator of transcript	107.81							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9D1I6|RM14_MOUSE	39S ribosomal protein L14, mitochondrial C	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|4EBP2_MOUSE	Eukaryotic translation initiation factor 4E-bin	70.75							1						0	0	1	0			0.37390	KI-93 only		
sp|Q62313|TGON1_MOUSE	Trans-Golgi network integral membrane prot	64.33							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BVI5|STX16_MOUSE	Syntaxin-16 OS=Mus musculus (Mouse) GI	61.94							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BI84|MIA3_MOUSE	Melanoma inhibitory activity protein 3 OS=M	60.44							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BM65|NYAP2_MOUSE	Neuronal tyrosine-phosphorylated phospho	58.06							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9R0M0|CELR2_MOUSE	Cadherin EGF LAG seven-pass G-type rece	52.45							1						0	0	1	0			0.37390	KI-93 only		
sp|P50429|ARSB_MOUSE	Arylsulfatase B OS=Mus musculus (Mouse)	48.93							1						0	0	1	0			0.37390	KI-93 only		
sp|Q7TSC1|PRC2A_MOUSE	Protein PRRC2A OS=Mus musculus (Mous	44.92							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9EQ06|DHB11_MOUSE	Estradiol 17-beta-dehydrogenase 11 OS=M	42.2							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8VEA4|MIA40_MOUSE	Mitochondrial intermembrane space import a	41.37							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9ERN0|SCAM2_MOUSE	Secretory carrier-associated membrane prot	39.89							1						0	0	1	0			0.37390	KI-93 only		
tr|Q0VBD0|Q0VBD0_MOUSE	Integrin beta OS=Mus musculus (Mouse) G	37.95							1						0	0	1	0			0.37390	KI-93 only		
sp|Q31125|S39A7_MOUSE	Zinc transporter SLC39A7 OS=Mus muscul	37.63							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9CQ00|TM261_MOUSE	Transmembrane protein 261 OS=Mus musc	37.04							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9QXV0|PCSK1_MOUSE	ProSAAS OS=Mus musculus (Mouse) GN=	36.66							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9CQX8|RT36_MOUSE	28S ribosomal protein S36, mitochondrial C	35.67							1						0	0	1	0			0.37390	KI-93 only		
sp|Q922U1|PRPF3_MOUSE	U4/U6 small nuclear ribonucleoprotein Prp3	34.28							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8CCP0|NEMF_MOUSE	Nuclear export mediator factor Nemf OS=M	33.26							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9D1H8|RM53_MOUSE	39S ribosomal protein L53, mitochondrial C	32.84							1						0	0	1	0			0.37390	KI-93 only		
sp|P97467|AMD_MOUSE	Peptidyl-glycine alpha-amidating monooxyg	32.82							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9WUN2|TBK1_MOUSE	Serine/threonine-protein kinase TBK1 OS=	32.72							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9EPE9|AT131_MOUSE	Manganese-transporting ATPase 13A1 OS	32.42							1						0	0	1	0			0.37390	KI-93 only		
sp|Q61337|BAD_MOUSE	Bcl2-associated agonist of cell death OS=M	31.86							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BWM0|PGES2_MOUSE	Prostaglandin E synthase 2 OS=Mus musc	31.59							1						0	0	1	0			0.37390	KI-93 only		
tr|E9Q7N9|E9Q7N9_MOUSE	Protein Dnah11 OS=Mus musculus GN=Dn	31.44							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8C7K6|PCYXL_MOUSE	Prenylcysteine oxidase-like OS=Mus muscu	201.14							1						0	0	1	0			0.37390	KI-93 only		
sp|Q91YH5|ATLA3_MOUSE	Atlastin-3 OS=Mus musculus GN=Atl3 PE=1	106.68							1						0	0	1	0			0.37390	KI-93 only		
sp|Q6P2B1|TNPO3_MOUSE	Transportin-3 OS=Mus musculus (Mouse) G	211.94							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8VHJ5|MARK1_MOUSE	Serine/threonine-protein kinase MARK1 OS	247.76							1						0	0	1	0			0.37390	KI-93 only		
sp|Q6DFW4|NOP58_MOUSE	Nucleolar protein 58 OS=Mus musculus (M	267.84							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8VED9|LEGL_MOUSE	Galectin-related protein OS=Mus musculus	83.26							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9CZB0|C560_MOUSE	Succinate dehydrogenase cytochrome b56	81.93							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BLV3|SL9A7_MOUSE	Sodium/hydrogen exchanger 7 OS=Mus m	80.5							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9WUK6|ZBT18_MOUSE	Zinc finger and BTB domain-containing prot	44.37							1						0	0	1	0			0.37390	KI-93 only		
sp|Q8BZA9|TIGAR_MOUSE	Fructose-2,6-bisphosphatase TIGAR OS=M	178.28							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9QXS1|PLEC_MOUSE	Plectin OS=Mus musculus (Mouse) GN=Ple	151.81							1						0	0	1	0			0.37390	KI-93 only		
sp|Q6NSW3|SPKAP_MOUSE	A-kinase anchor protein SPHKAP OS=Mus	256.58							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9R0Q3|TMED2_MOUSE	Transmembrane emp24 domain-containing	59.01							1						0	0	1	0			0.37390	KI-93 only		
sp|Q91WC0|SETD3_MOUSE	Histone-lysine N-methyltransferase setd3 C	90.35							1						0	0	1	0			0.37390	KI-93 only		
sp|O35435|PYRD_MOUSE	Dihydroorotate dehydrogenase (quinone), r	93.38							1						0	0	1	0			0.37390	KI-93 only		
sp|Q9CQ85|TIM22_MOUSE	Mitochondrial import inner membrane transl	112							1						0	0	1	0			0.37390	KI-93 only		
sp|Q61016|GBG7_MOUSE	Guanine nucleotide-binding protein G(I)/G(S	54.32								2					0	0	1	0			0.37390	KI-93 only		
sp|Q9Z2N8|ACL6A_MOUSE	Actin-like protein 6A OS=Mus musculus (M	122.41								1	1				0	0	2	0			0.11624	KI-93 only		
sp|Q9WUT3|KS6A2_MOUSE	Ribosomal protein S6 kinase alpha-2 OS=M	75.64								1					0	0	1	0			0.37390	KI-93 only		
sp|Q91VM9|IPYR2_MOUSE	Inorganic pyrophosphatase 2, mitochondria	83.89								1					0	0	1	0			0.37390	KI-93 only		
sp|Q8C0D5|ETUD1_MOUSE	Elongation factor Tu GTP-binding domain-c	86.18								1					0	0	1	0			0.37390	KI-93 only		
sp|Q8CFE4|SCYL2_MOUSE	SCY1-like protein 2 OS=Mus musculus (Mo	77.74								1					0	0	1	0			0.37390	KI-93 only		
sp|Q3U898|MYOV2_MOUSE	Myeloma-overexpressed gene 2 protein hor	71.25								1					0	0	1	0			0.37390	KI-93 only		
sp|Q60967|PAPS1_MOUSE	Bifunctional 3'-phosphoadenosine 5'-phosp	61.7								1					0	0	1	0			0.37390	KI-93 only		
sp|Q8R071|IP3KA_MOUSE	Inositol-trisphosphate 3-kinase A OS=Mus	44.2								1					0	0	1	0			0.37390	KI-93 only		
tr|Q9Z1R9|Q9Z1R9_MOUSE	MCG124046 OS=Mus musculus (Mouse) G	32.94								1					0	0	1	0			0.37390	KI-93 only		
sp|O09126|SEM4D_MOUSE	Semaphorin-4D OS=Mus musculus (Mouse	32								1					0	0	1	0			0.37390	KI-93 only		
sp|Q3U308|CTU2_MOUSE	Cytoplasmic tRNA 2-thiolation protein 2 OS	30.09								1					0	0	1	0			0.37390	KI-93 only		
tr|Q3T984|Q3T984_MOUSE	Putative uncharacterized protein OS=Mus	149.06								1					0	0	1	0			0.37390	KI-93 only		
sp|Q9Z0P5|TWF2_MOUSE	Twinfilin-2 OS=Mus musculus (Mouse) GN=	133.87								1					0	0	1	0			0.37390	KI-93 only		
tr|E9PVU0|E9PVU0_MOUSE	Unconventional myosin-VI OS=Mus muscul	229.96								1					0	0	1	0			0.37390	KI-93 only		
sp|Q8CIP4|MARK4_MOUSE	MAP/microtubule affinity-regulating kinase 4	96.32								1					0	0	1	0			0.37390	KI-93 only		
sp|P54731|FAF1_MOUSE	FAS-associated factor 1 OS=Mus musculus	60.54								1					0	0	1	0			0.37390	KI-93 only		
sp|Q9WVK8|CP46A_MOUSE	Cholesterol 24-hydroxylase OS=Mus muscu	180.57								1					0	0	1	0			0.37390	KI-93 only		
sp|Q8BGT5|ALAT2_MOUSE	Alanine aminotransferase 2 OS=Mus musc	115.4								1					0	0	1	0			0.37390	KI-93 only		
sp|Q80TK0|K1107_MOUSE	Uncharacterized protein KIAA1107 OS=Mu	87.32								1					0	0	1	0			0.37390	KI-93 only		
sp|Q569Z5|DDX46_MOUSE	Probable ATP-dependent RNA helicase DD	64.59									2				0	0	1	0			0.37390	KI-93 only		
sp|O08582|GTPB1_MOUSE	GTP-binding protein 1 OS=Mus musculus (	108.25									2				0	0	1	0			0.37390	KI-93 only		
sp|O08586|PTEN_MOUSE	Phosphatidylinositol 3,4,5-trisphosphate 3-p	144.7									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9CQ26|STABP_MOUSE	STAM-binding protein OS=Mus musculus (M	126.96									1				0	0	1	0			0.37390	KI-93 only		
sp|Q6PHS9|CA2D2_MOUSE	Voltage-dependent calcium channel subuni	88.75									1				0	0	1	0			0.37390	KI-93 only		
tr|Q6P8K4|Q6P8K4_MOUSE	AW551984 protein OS=Mus musculus (Mo	57.04									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9Z275|RLBP1_MOUSE	Retinaldehyde-binding protein 1 OS=Mus r	55.16									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9DBH5|LMAN2_MOUSE	Vesicular integral-membrane protein VIP36	52.84									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9JIA7|SPHK2_MOUSE	Sphingosine kinase 2 OS=Mus musculus (M	46.18									1				0	0	1	0			0.37390	KI-93 only		
sp|O08530|S1PR1_MOUSE	Sphingosine 1-phosphate receptor 1 OS=M	44.41									1				0	0	1	0			0.37390	KI-93 only		
sp|P49290|PERE_MOUSE	Eosinophil peroxidase OS=Mus musculus (	37.96									1				0	0	1	0			0.37390	KI-93 only		
sp|A2A8Z1|OSBL9_MOUSE	Oxysterol-binding protein-related protein 9	31.32									1				0	0	1	0			0.37390	KI-93 only		
sp|Q8VE92|RBM4B_MOUSE	RNA-binding protein 4B OS=Mus musculus	30.33									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9CR56|KBRS2_MOUSE	NF-kappa-B inhibitor-interacting Ras-like pro	29.79									1				0	0	1	0			0.37390	KI-93 only		
tr|D3Z1M8|D3Z1M8_MOUSE	Protein polybromo-1 OS=Mus musculus (M	29.11									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9QYB1|CLIC4_MOUSE	Chloride intracellular channel protein 4 OS=	260.08									1				0	0	1	0			0.37390	KI-93 only		
sp|Q6PFE7|TEFF1_MOUSE	Tomoregulin-1 OS=Mus musculus (Mouse)	140.79									1				0	0	1	0			0.37390	KI-93 only		
sp|O35607|BMPR2_MOUSE	Bone morphogenetic protein receptor type-2	116.44									1				0	0	1	0			0.37390	KI-93 only		
sp|Q9D880|TIM50_MOUSE	Mitochondrial import inner membrane transl	200.9									1				0	0	1	0			0.37390	KI-93 only		
sp|Q920B9|SP16H_MOUSE	FACT complex subunit SPT16 OS=Mus mu	69.61									1				0	0	1	0			0.37390	KI-93 only		
sp|Q3UU96|MRCKA_MOUSE	Serine/threonine-protein kinase MRCK alph	109.77									1				0	0	1	0			0.37390	KI-93 only		
sp|Q01065|PDE1B_MOUSE	Calcium/calmodulin-dependent 3',5'-cyclic n	169.06									1				0	0	1	0			0.37390	KI-93 only		
sp|P23591|FCL_MOUSE	GDP-L-fucose synthase OS=Mus musculus	141.2									1				0	0	1	0			0.37390	KI-93 only		

Proteins only identified in 1 KI sample (KI-82):

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|P70188|KIFA3_MOUSE	Kinesin-associated protein 3 OS=Mus musc	215.03										1	1		0	0	0	2					0.12082	KI-82 only
sp|Q69ZK0|PREX1_MOUSE	Phosphatidylinositol 3,4,5-trisphosphate-de	78.42										1			0	0	0	1					0.37390	KI-82 only
sp|Q08274|DMWD_MOUSE	Dystrophia myotonica WD repeat-containing	44.25										1			0	0	0	1					0.37390	KI-82 only
sp|Q9EQZ6|RPGF4_MOUSE	Rap guanine nucleotide exchange factor 4	42.59										1			0	0	0	1					0.37390	KI-82 only
sp|Q6PAM1|TXLNA_MOUSE	Alpha-taxilin OS=Mus musculus (Mouse) GI	38.27										1			0	0	0	1					0.37390	KI-82 only
sp|Q80X71|T106B_MOUSE	Transmembrane protein 106B OS=Mus mu	34.31										1			0	0	0	1					0.37390	KI-82 only
sp|Q5ND29|RILP_MOUSE	Rab-interacting lysosomal protein OS=Mus	30.75										1			0	0	0	1					0.37390	KI-82 only
sp|O88456|CPNS1_MOUSE	Calpain small subunit 1 OS=Mus musculus	94.83										1			0	0	0	1					0.37390	KI-82 only
sp|O88545|CSN6_MOUSE	COP9 signalosome complex subunit 6 OS=	89.98										1			0	0	0	1					0.37390	KI-82 only
sp|P08030|APT_MOUSE	Adenine phosphoribosyltransferase OS=M	118.16										1			0	0	0	1					0.37390	KI-82 only
sp|P26048|GBRA2_MOUSE	Gamma-aminobutyric acid receptor subunit	119.68										1			0	0	0	1					0.37390	KI-82 only
sp|Q9CZ04|CSN7A_MOUSE	COP9 signalosome complex subunit 7a OS	287.02										1			0	0	0	1					0.37390	KI-82 only
sp|Q9D517|PLCC_MOUSE	1-acyl-sn-glycerol-3-phosphate acyltransfera	122.2										1			0	0	0	1					0.37390	KI-82 only

sp|Q5XG69|F169A_MOUSE	Soluble lamin-associated protein of 75 kDa	176.74										1			0	0	0	1					0.37390	KI-82 only
sp|Q9D8U8|SNX5_MOUSE	Sorting nexin-5 OS=Mus musculus (Mouse)	96.61										1			0	0	0	1					0.37390	KI-82 only
sp|Q9Z2A0|PDPK1_MOUSE	3-phosphoinositide-dependent protein kina	40.97										1			0	0	0	1					0.37390	KI-82 only
sp|Q9CXZ1|NDUS4_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	45.64											1	1	0	0	0	2					0.11630	KI-82 only
sp|Q9CQU1|MFAP1_MOUSE	Microfibrillar-associated protein 1 OS=Mus	38.57											1	1	0	0	0	2					0.11630	KI-82 only
sp|Q8BMG7|RBGPR_MOUSE	Rab3 GTPase-activating protein non-catalyt	68.67											1		0	0	0	1					0.37390	KI-82 only
sp|Q9WV91|FPRP_MOUSE	Prostaglandin F2 receptor negative regulato	44.62											1		0	0	0	1					0.37390	KI-82 only
sp|P30875|SSR2_MOUSE	Somatostatin receptor type 2 OS=Mus mus	40.2											1		0	0	0	1					0.37390	KI-82 only
sp|P56857|CLD18_MOUSE	Claudin-18 OS=Mus musculus (Mouse) GN	36.83											1		0	0	0	1					0.37390	KI-82 only
sp|Q3TC72|FAHD2_MOUSE	Fumarylacetoacetate hydrolase domain-con	36.43											1		0	0	0	1					0.37390	KI-82 only
sp|Q9QYM9|TEFF2_MOUSE	Tomoregulin-2 OS=Mus musculus (Mouse)	31.8											1		0	0	0	1					0.37390	KI-82 only
sp|Q9DBF7|CWC25_MOUSE	Pre-mRNA-splicing factor CWC25 homolog	30.95											1		0	0	0	1					0.37390	KI-82 only
tr|F6RCC5|F6RCC5_MOUSE	Hepatocyte growth factor receptor OS=Mus	29.1											1		0	0	0	1					0.37390	KI-82 only
sp|Q8VFX2|O1444_MOUSE	Olfactory receptor 1444 OS=Mus musculus	28.08											1		0	0	0	1					0.37390	KI-82 only
sp|Q8VDN4|CCD92_MOUSE	Coiled-coil domain-containing protein 92 O	27.82											1		0	0	0	1					0.37390	KI-82 only
tr|B2RXC6|B2RXC6_MOUSE	DNA-directed RNA polymerase OS=Mus mu	27.53											1		0	0	0	1					0.37390	KI-82 only
sp|Q9CYH2|F213A_MOUSE	Redox-regulatory protein FAM213A OS=Mu	127.8											1		0	0	0	1					0.37390	KI-82 only
sp|Q9Z1J3|NFS1_MOUSE	Cysteine desulfurase, mitochondrial OS=M	152.37											1		0	0	0	1					0.37390	KI-82 only
sp|Q5F2E7|NUFP2_MOUSE	Nuclear fragile X mental retardation-interact	63.2											1		0	0	0	1					0.37390	KI-82 only
sp|Q6PB44|PTN23_MOUSE	Tyrosine-protein phosphatase non-receptor	338.38											1		0	0	0	1					0.37390	KI-82 only
sp|Q9D1F4|AKTS1_MOUSE	Proline-rich AKT1 substrate 1 OS=Mus mus	45.9											1		0	0	0	1					0.37390	KI-82 only
sp|P29351|PTN6_MOUSE	Tyrosine-protein phosphatase non-receptor	59.05												2	0	0	0	1					0.37390	KI-82 only
sp|Q5SXY1|CYTSB_MOUSE	Cytospin-B OS=Mus musculus (Mouse) GN	69.31												1	0	0	0	1					0.37390	KI-82 only
tr|B2RXL7|B2RXL7_MOUSE	Kidins220 protein OS=Mus musculus (Mou	57.39												1	0	0	0	1					0.37390	KI-82 only
sp|Q7TSK2|SEZ6_MOUSE	Seizure protein 6 OS=Mus musculus (Mous	49.39												1	0	0	0	1					0.37390	KI-82 only
sp|P10107|ANXA1_MOUSE	Annexin A1 OS=Mus musculus (Mouse) GN	40												1	0	0	0	1					0.37390	KI-82 only
sp|Q810U5|CCD50_MOUSE	Coiled-coil domain-containing protein 50 OS	38.91												1	0	0	0	1					0.37390	KI-82 only
sp|P15252|REF_HEVBR	Rubber elongation factor protein OS=Hevea	35.7												1	0	0	0	1					0.37390	KI-82 only
sp|Q04519|ASM_MOUSE	Sphingomyelin phosphodiesterase OS=Mu	145.38												1	0	0	0	1					0.37390	KI-82 only
sp|O54988|SLK_MOUSE	STE20-like serine/threonine-protein kinase	103.71												1	0	0	0	1					0.37390	KI-82 only
sp|P57724|PCBP4_MOUSE	Poly(rC)-binding protein 4 OS=Mus musculu	79.3												1	0	0	0	1					0.37390	KI-82 only
sp|Q6Y7W8|PERQ2_MOUSE	PERQ amino acid-rich with GYF domain-cor	160.52												1	0	0	0	1					0.37390	KI-82 only
sp|Q8BYK8|ZC3H6_MOUSE	Zinc finger CCCH domain-containing protein	32.58												1	0	0	0	1					0.37390	KI-82 only

Proteins only identified in the WT-scr samples:

			Exp. from 01/02/2017												Exp. 01/02/2017									
			BASIC Spectral Count (Proline)																					
			WT			KI-scr			KI-93			KI-82			# Repl.				KI-scr / WT-scr		KI-93 / WT-scr		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q8BJH1|ZC21A_MOUSE	Zinc finger C2HC domain-containing protein	199.67	2												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9D0M1|KPRA_MOUSE	Phosphoribosyl pyrophosphate synthase-as	133.67	1	1	1										3	0	0	0	0.00000	WT-scr only	0.00000	WT-scr only	0.00000	WT-scr only
sp|Q9DBR7|MYPT1_MOUSE	Protein phosphatase 1 regulatory subunit 1	48.48	1	1	1										3	0	0	0	0.00000	WT-scr only	0.00000	WT-scr only	0.00000	WT-scr only
sp|Q9WTP7|KAD3_MOUSE	GTP:AMP phosphotransferase AK3, mitoch	247.98	1	1											2	0	0	0	0.11633	WT-scr only	0.11633	WT-scr only	0.11633	WT-scr only
sp|O88689|PCDA4_MOUSE	Protocadherin alpha-4 OS=Mus musculus (	61.4	1	1											2	0	0	0	0.11633	WT-scr only	0.11633	WT-scr only	0.11633	WT-scr only
sp|P59016|VP33B_MOUSE	Vacuolar protein sorting-associated protein	35.95	1		1										2	0	0	0	0.11616	WT-scr only	0.11616	WT-scr only	0.11616	WT-scr only
sp|O88444|ADCY1_MOUSE	Adenylate cyclase type 1 OS=Mus musculu	41.96	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BMI3|GGA3_MOUSE	ADP-ribosylation factor-binding protein GGA	31.37	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8C0I1|ADAS_MOUSE	Alkyldihydroxyacetonephosphate synthase,	121.75	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|Q8R1X0|Q8R1X0_MOUSE	BC022960 protein OS=Mus musculus (Mou	31.48	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q6PAJ1|BCR_MOUSE	Breakpoint cluster region protein OS=Mus	96.25	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|O08688|CAN5_MOUSE	Calpain-5 OS=Mus musculus (Mouse) GN=	99.81	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BVP5|KC1G2_MOUSE	Casein kinase I isoform gamma-2 OS=Mus	46.09	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9DB34|CHM2A_MOUSE	Charged multivesicular body protein 2a OS	28.25	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|E9PVB3|CC175_MOUSE	Coiled-coil domain-containing protein 175 (	27.71	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P21460|CYTC_MOUSE	Cystatin-C OS=Mus musculus (Mouse) GN=	30.45	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9R1V6|ADA22_MOUSE	Disintegrin and metalloproteinase domain-c	122.68	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q69ZW3|EHBP1_MOUSE	EH domain-binding protein 1 OS=Mus mus	136.01	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P97494|GSH1_MOUSE	Glutamate--cysteine ligase catalytic subunit	44.22	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q99LP6|GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial OS	81.74	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R0N6|HOT_MOUSE	Hydroxyacid-oxoacid transhydrogenase, mit	27.44	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|Q1A4F7|Q1A4F7_MOUSE	Lectin-like transmembrane protein Nkrp1c (	27.11	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BH93|MISSL_MOUSE	MAPK-interacting and spindle-stabilizing prc	28.28	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q6PCZ4|MAGE1_MOUSE	Melanoma-associated antigen E1 OS=Mus	32.83	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9D8W7|OCAD2_MOUSE	OCIA domain-containing protein 2 OS=Mus	77.1	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q5SUR0|PUR4_MOUSE	Phosphoribosylformylglycinamidine synthase	33.49	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q80VD1|FA98B_MOUSE	Protein FAM98B OS=Mus musculus (Mouse	216.41	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|H3BJD0|H3BJD0_MOUSE	Protein Ppp1r9a OS=Mus musculus (Mouse	130.15	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|Q3TKC5|Q3TKC5_MOUSE	Putative uncharacterized protein OS=Mus	33.89	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R361|RFIP5_MOUSE	Rab11 family-interacting protein 5 OS=Mus	32.2	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9QUG9|GRP2_MOUSE	RAS guanyl-releasing protein 2 OS=Mus m	79.13	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9ESK9|RBCC1_MOUSE	RB1-inducible coiled-coil protein 1 OS=Mus	30.26	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9JM62|REEP6_MOUSE	Receptor expression-enhancing protein 6 (	27.31	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P59281|RHG39_MOUSE	Rho GTPase-activating protein 39 OS=Mus	82.56	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R4H2|ARHGC_MOUSE	Rho guanine nucleotide exchange factor 12	150.92	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9CY97|SSU72_MOUSE	RNA polymerase II subunit A C-terminal dor	29.4	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|D3YZU1|SHAN1_MOUSE	SH3 and multiple ankyrin repeat domains pi	39.69	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P61807|SNN_MOUSE	Stannin OS=Mus musculus (Mouse) GN=S	34.62	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8C079|STRP1_MOUSE	Striatin-interacting protein 1 OS=Mus musc	126.41	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q99K46|UBP11_MOUSE	Ubiquitin carboxyl-terminal hydrolase 11 OS	76.83	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P61961|UFM1_MOUSE	Ubiquitin-fold modifier 1 OS=Mus musculus	31.28	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BR90|CE051_MOUSE	UPF0600 protein C5orf51 homolog OS=Mu	29.42	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8VEJ9|VPS4A_MOUSE	Vacuolar protein sorting-associated protein	74.12	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8C1M2|ZN428_MOUSE	Zinc finger protein 428 OS=Mus musculus (	88.08	1												1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P05977|MYL1_MOUSE	Myosin light chain 1/3, skeletal muscle isofo	37.23		2											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|P50136|ODBA_MOUSE	2-oxoisovalerate dehydrogenase subunit al	74.63		1	1										2	0	0	0	0.11658	WT-scr only	0.11658	WT-scr only	0.11658	WT-scr only
sp|Q6ZPQ6|PITM2_MOUSE	Membrane-associated phosphatidylinositol t	202.99		1	1										2	0	0	0	0.11658	WT-scr only	0.11658	WT-scr only	0.11658	WT-scr only
sp|B0F2B4|NLGN4_MOUSE	Neuroligin 4-like OS=Mus musculus (Mouse	116.4		1	1										2	0	0	0	0.11658	WT-scr only	0.11658	WT-scr only	0.11658	WT-scr only
sp|Q3B7Z2|OSBP1_MOUSE	Oxysterol-binding protein 1 OS=Mus muscu	241.36		1	1										2	0	0	0	0.11658	WT-scr only	0.11658	WT-scr only	0.11658	WT-scr only
sp|Q99ME2|WDR6_MOUSE	WD repeat-containing protein 6 OS=Mus m	209.25		1	1										2	0	0	0	0.11658	WT-scr only	0.11658	WT-scr only	0.11658	WT-scr only
sp|Q60649|CLPB_MOUSE	Caseinolytic peptidase B protein homolog (	34.23		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BI72|CARF_MOUSE	CDKN2A-interacting protein OS=Mus musc	35.26		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9D486|CMIP_MOUSE	C-Maf-inducing protein OS=Mus musculus (	53.58		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9D4H8|CUL2_MOUSE	Cullin-2 OS=Mus musculus (Mouse) GN=Cu	246.76		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q99M87|DNJA3_MOUSE	DnaJ homolog subfamily A member 3, mitoc	101.71		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|O54865|GCYB1_MOUSE	Guanylate cyclase soluble subunit beta-1 (	545.22		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|E9Q4K7|E9Q4K7_MOUSE	Kinesin-like protein OS=Mus musculus (Mo	69.87		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BFZ2|LPPR1_MOUSE	Lipid phosphate phosphatase-related prote	50.78		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|O35683|NDUA1_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	61.88		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8C8T8|TSR2_MOUSE	Pre-rRNA-processing protein TSR2 homolog	39.39		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R1F6|HID1_MOUSE	Protein HID1 OS=Mus musculus (Mouse) G	35.07		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q91VH6|MEMO1_MOUSE	Protein MEMO1 OS=Mus musculus (Mouse	39.66		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
tr|A0A0A6YWM0|A0A0A6YWM0	Protein Pcdh9 OS=Mus musculus (Mouse)	96.08		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8VE37|RCC1_MOUSE	Regulator of chromosome condensation O	57.26		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9CQ88|TSN31_MOUSE	Tetraspanin-31 OS=Mus musculus (Mouse)	33.74		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BYI8|K1467_MOUSE	Uncharacterized protein KIAA1467 OS=Mu	75.9		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R307|VPS18_MOUSE	Vacuolar protein sorting-associated protein	126.66		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9R1Q9|VAS1_MOUSE	V-type proton ATPase subunit S1 OS=Mus	33.81		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q4VBE8|WDR18_MOUSE	WD repeat-containing protein 18 OS=Mus	42.05		1											1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9DCT1|AKCL2_MOUSE	1,5-anhydro-D-fructose reductase OS=Mus	37.79			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9CQN7|RM41_MOUSE	39S ribosomal protein L41, mitochondrial C	35.86			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9EPL2|CSTN1_MOUSE	Calsyntenin-1 OS=Mus musculus (Mouse) (	45.45			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8K1A6|C2D1A_MOUSE	Coiled-coil and C2 domain-containing protei	58.16			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8C863|ITCH_MOUSE	E3 ubiquitin-protein ligase Itchy OS=Mus m	40.21			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|O88630|GOSR1_MOUSE	Golgi SNAP receptor complex member 1 O	68.18			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q80U57|RIMS3_MOUSE	Regulating synaptic membrane exocytosis p	54.27			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q3U5Q7|CMPK2_MOUSE	UMP-CMP kinase 2, mitochondrial OS=Mus	66.69			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q91XD6|VPS36_MOUSE	Vacuolar protein-sorting-associated protein	37.67			1										1	0	0	0	0.37390	WT-scr only	0.37390	WT-scr only	0.37390	WT-scr only

Proteins mostly identified in all 3 KI samples with ratio>2 (KI-scr + KI-93 + KI-82):

			Exp. from 01/02/2017												Exp. 01/02/2017									
			BASIC Spectral Count (Proline)																					
			WT			KI-scr			KI-93			KI-82			# Repl.				KI-scr / WT-scr		KI-93 / WT-scr		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q62446|FKBP3_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP3 (	462.67	3	1		2	4	3	5	2	3	3	2	3	2	3	3	3	0.20979	2.25	0.13932	2.50	0.15133	2.00
sp|Q3UQS2|LSME1_MOUSE	Leucine-rich single-pass membrane protein	43.76	2			2		2	1	1	2	1	1	3	1	2	3	3	0.53700	2.00	0.38687	2.00	0.30054	2.50
sp|Q9CPW4|ARPC5_MOUSE	Actin-related protein 2/3 complex subunit 5	407.74	1	2	2	2	4	4	5	3	3	7	3	2	3	3	3	3	0.08549	2.00	0.01925	2.20	0.12835	2.40
sp|P19536|COX5B_MOUSE	Cytochrome c oxidase subunit 5B, mitochor	205.83	1	1		3	2	1	5		2	4			2	3	2	1	0.13834	3.00	0.30518	3.50	0.65023	2.00
sp|Q8BRK8|AAPK2_MOUSE	5'-AMP-activated protein kinase catalytic su	214.11	1	1		1	1	2	1		3	1	1	2	2	3	2	3	0.24678	2.00	0.50489	2.00	0.17768	2.00
sp|Q9DAW9|CNN3_MOUSE	Calponin-3 OS=Mus musculus (Mouse) GN	395.3	1		2			7	4	2	5	3	2	4	2	1	3	3	0.63254	2.33	0.06264	3.67	0.05915	3.00
sp|Q921M3|SF3B3_MOUSE	Splicing factor 3B subunit 3 OS=Mus musc	371.64	1		1	1	2	2	2	2	1	1	1	2	2	3	3	3	0.11271	2.50	0.09124	2.50	0.19125	2.00
sp|Q64310|SURF4_MOUSE	Surfeit locus protein 4 OS=Mus musculus (I	264.64	1			2	2	1	2		1	1	1	2	1	3	2	3	0.05589	5.00	0.36273	3.00	0.09130	4.00
sp|P12023|A4_MOUSE	Amyloid beta A4 protein OS=Mus musculus	199.66	1			2	2	1	1	2	1			3	1	3	3	1	0.05589	5.00	0.10961	4.00	0.52867	3.00
sp|P09528|FRIH_MOUSE	Ferritin heavy chain (Ferritin H subunit) (EC	144.36	1			2	3		1		1	2			1	2	2	1	0.23081	5.00	0.51266	2.00	0.68309	2.00
sp|Q9ER73|ELP4_MOUSE	Elongator complex protein 4 OS=Mus musc	181.87	1			2	1		2		1		2		1	2	2	1	0.39558	3.00	0.36273	3.00	0.61250	2.00
sp|P18608|HMGN1_MOUSE	Non-histone chromosomal protein HMG-14	126.25	1			3	1		4			4			1	2	1	1	0.36569	4.00	0.51777	4.00	0.50946	4.00
sp|Q6P9K8|CSKI1_MOUSE	Caskin-1 OS=Mus musculus (Mouse) GN=C	413.86	1			3	1		1	3	1	1	1		1	2	3	2	0.36569	4.00	0.16208	5.00	0.46591	2.00
sp|O70228|ATP9A_MOUSE	Probable phospholipid-transporting ATPase	430.13	1			2		1		1	1	1	1	1	1	2	2	3	0.38755	3.00	0.46107	2.00	0.08013	3.00
sp|Q80XU3|NUCKS_MOUSE	Nuclear ubiquitous casein and cyclin-depen	100.23	1			3			4			2			1	1	1	1	0.56042	3.00	0.51777	4.00	0.68309	2.00
tr|Q3UDL6|Q3UDL6_MOUSE	Putative uncharacterized protein OS=Mus	331.3	1			1	4	2	2	3	1		1	2	1	3	3	2	0.09359	7.00	0.07660	6.00	0.31942	3.00
sp|Q8VDP6|CDIPT_MOUSE	CDP-diacylglycerol--inositol 3-phosphatidyltr	194.35	1			1	2	2	3			3		1	1	3	1	2	0.04762	5.00	0.57660	3.00	0.32079	4.00
sp|Q9DCH4|EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subu	303.49	1			1	2	2	1	1	1	1	1	3	1	3	3	3	0.04762	5.00	0.10121	3.00	0.14552	5.00
sp|Q61771|KIF3B_MOUSE	Kinesin-like protein KIF3B OS=Mus muscul	403.99	1			1	2	1	4		1	1		2	1	3	2	2	0.10292	4.00	0.33286	5.00	0.36272	3.00
sp|Q8VDM6|HNRL1_MOUSE	Heterogeneous nuclear ribonucleoprotein U	427.92	1			1	1	1	2	1	2	1	1	2	1	3	3	3	0.14051	3.00	0.03800	5.00	0.09130	4.00
sp|P05532|KIT_MOUSE	Mast/stem cell growth factor receptor Kit OS	77.42	1			1	1	1	1	2	1	2	2	1	1	3	3	3	0.14051	3.00	0.10961	4.00	0.03744	5.00
sp|Q80Y86|MK15_MOUSE	Mitogen-activated protein kinase 15 OS=M	44.83	1			1	1	1	1	2	1	2	2		1	3	3	2	0.14051	3.00	0.10961	4.00	0.23685	4.00
sp|Q8K2H2|OTU6B_MOUSE	OTU domain-containing protein 6B OS=Mu	181.54	1			1	1	1	1	1	2		1	1	1	3	3	2	0.14051	3.00	0.10136	4.00	0.42068	2.00
sp|Q9CPR5|RM15_MOUSE	39S ribosomal protein L15, mitochondrial C	54.19	1			1	1	1		1	1	1	1	1	1	3	2	3	0.14051	3.00	0.46107	2.00	0.08013	3.00

sp|Q9CZS1|AL1B1_MOUSE	Aldehyde dehydrogenase X, mitochondrial	238.57	1			1	1	1		1	1		1	2	1	3	2	2	0.14051	3.00	0.46107	2.00	0.31942	3.00
sp|Q9CSN1|SNW1_MOUSE	SNW domain-containing protein 1 OS=Mus	157.16	1			1	1		2	1		1	1		1	2	2	2	0.54855	2.00	0.35515	3.00	0.46591	2.00
sp|F6ZDS4|TPR_MOUSE	Nucleoprotein TPR OS=Mus musculus (Mou	516.72	1				2	4	2	1	2	2		1	1	2	3	2	0.25139	6.00	0.03800	5.00	0.34101	3.00
sp|P62878|RBX1_MOUSE	E3 ubiquitin-protein ligase RBX1 OS=Mus	249.53	1				2	2	2	1		2			1	2	2	1	0.27034	4.00	0.35515	3.00	0.68309	2.00
sp|Q6PGD0|ARAID_MOUSE	All-trans retinoic acid-induced differentiation	111.03	1				2	1		2		1	1		1	2	1	2	0.40150	3.00	0.63776	2.00	0.46591	2.00
sp|Q6ZWY8|TYB10_MOUSE	Thymosin beta-10 OS=Mus musculus (Mou	50.85	1				2		3			3			1	1	1	1	0.71684	2.00	0.57660	3.00	0.56473	3.00
sp|Q8CCB4|VPS53_MOUSE	Vacuolar protein sorting-associated protein	368.25	1				2			1	1	3		2	1	1	2	2	0.71684	2.00	0.46107	2.00	0.20964	5.00
sp|P61290|PSME3_MOUSE	Proteasome activator complex subunit 3 O	236.97	1				1	1	2			1	1		1	2	1	2	0.57091	2.00	0.70178	2.00	0.46591	2.00
sp|P59325|IF5_MOUSE	Eukaryotic translation initiation factor 5 OS	262.68	1				1	1		2			4	1	1	2	1	2	0.57091	2.00	0.63776	2.00	0.32651	5.00
sp|P19324|SERPH_MOUSE	Serpin H1 OS=Mus musculus (Mouse) GN=	423.01		2	1	2	3	3	2	2	2	2	2	2	2	3	3	3	0.06504	2.67	0.11675	2.00	0.08825	2.00
sp|P28661|SEPT4_MOUSE	Septin-4 OS=Mus musculus (Mouse) GN=S	73.19		2		1	2	1	2		2	2	1	1	1	3	2	3	0.42855	2.00	0.48634	2.00	0.29777	2.00
sp|P35585|AP1M1_MOUSE	AP-1 complex subunit mu-1 OS=Mus musc	371.45		2			3	2	2	1	1	2	1	1	1	2	3	3	0.43352	2.50	0.34901	2.00	0.29777	2.00
sp|P15116|CADH2_MOUSE	Cadherin-2 OS=Mus musculus (Mouse) GN	722.08		1	1	2	3	4	5	2	3	2	3	2	2	3	3	3	0.02307	4.50	0.02437	5.00	0.03083	3.50
sp|P28798|GRN_MOUSE	Granulins OS=Mus musculus (Mouse) GN=	105.04		1		2			2			1	1		1	1	1	2	0.66021	2.00	0.68457	2.00	0.44226	2.00
sp|Q9CQF3|CPSF5_MOUSE	Cleavage and polyadenylation specificity fa	328.12		1		1	3	4	1		2	1	1	1	1	3	2	3	0.06536	8.00	0.36573	3.00	0.06802	3.00
sp|P45952|ACADM_MOUSE	Medium-chain specific acyl-CoA dehydroger	245.23		1		1	2	1	2			1	2		1	3	1	2	0.09274	4.00	0.68457	2.00	0.34858	3.00
sp|D3YZP9|CCDC6_MOUSE	Coiled-coil domain-containing protein 6 OS	394.22		1		1	1	2	4	1	1	1	2	1	1	3	3	3	0.10072	4.00	0.14897	6.00	0.09501	4.00
sp|A2AHC3|CAMP1_MOUSE	Calmodulin-regulated spectrin-associated p	126.45		1		1	1		1	1		1	1		1	2	2	2	0.52049	2.00	0.47695	2.00	0.44226	2.00
sp|Q9D289|TPC6B_MOUSE	Trafficking protein particle complex subunit	98.89		1		1	1			1	1		1	1	1	2	2	2	0.52049	2.00	0.43725	2.00	0.39923	2.00
sp|Q640N2|AR13B_MOUSE	ADP-ribosylation factor-like protein 13B OS	42.11		1		1		3	2			2			1	2	1	1	0.34038	4.00	0.68457	2.00	0.66673	2.00
sp|Q8BIJ6|SYIM_MOUSE	Isoleucine--tRNA ligase, mitochondrial OS=	394.82		1			2	2	2			2	1		1	2	1	2	0.25942	4.00	0.68457	2.00	0.31860	3.00
sp|Q8C167|PPCEL_MOUSE	Prolyl endopeptidase-like OS=Mus musculu	300.71		1				2		1	2		1	1	1	1	2	2	0.68498	2.00	0.32861	3.00	0.39923	2.00
sp|Q80X80|C2C2L_MOUSE	C2 domain-containing protein 2-like OS=Mu	335.14			2	3	2	2	4	1	1	1	2	1	1	3	3	3	0.12041	3.50	0.30560	3.00	0.35669	2.00
sp|Q5FWK3|RHG01_MOUSE	Rho GTPase-activating protein 1 OS=Mus	521.51			2	2	2	1		2	2	1	2	1	1	3	2	3	0.29949	2.50	0.47285	2.00	0.35669	2.00
sp|P52196|THTR_MOUSE	Thiosulfate sulfurtransferase OS=Mus mus	112.69			2	1		3	3	1	2	1		3	1	2	3	2	0.61020	2.00	0.18145	3.00	0.54728	2.00
sp|O08529|CAN2_MOUSE	Calpain-2 catalytic subunit OS=Mus muscu	631.28			2		1	3	1	1	2	2	2	1	1	2	3	3	0.63202	2.00	0.40254	2.00	0.20184	2.50
sp|P63216|GBG3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S	321.26			1	3	2	1	3	1		3	1		1	3	2	2	0.08498	6.00	0.33372	4.00	0.31726	4.00
tr|Q8R2K3|Q8R2K3_MOUSE	Single-stranded DNA-binding protein OS=M	272.12			1	2	1	2		1	2	2		2	1	3	2	2	0.06191	5.00	0.34732	3.00	0.24332	4.00
sp|Q9WTS4|TEN1_MOUSE	Teneurin-1 OS=Mus musculus (Mouse) GN	143.82			1	2	1		2		2	1		1	1	2	2	2	0.40296	3.00	0.25543	4.00	0.48921	2.00
sp|P24668|MPRD_MOUSE	Cation-dependent mannose-6-phosphate re	158.52			1	1	1	1	1		1	1		1	1	3	2	2	0.15088	3.00	0.52560	2.00	0.48921	2.00
sp|Q9QZE7|TSNAX_MOUSE	Translin-associated protein X OS=Mus mus	152.02			1	1	1	1	1		1	1		1	1	3	2	2	0.15088	3.00	0.52560	2.00	0.48921	2.00
sp|Q3KNM2|MARH5_MOUSE	E3 ubiquitin-protein ligase MARCH5 OS=M	118.79			1		1	1	2		1		2		1	2	2	1	0.58510	2.00	0.37023	3.00	0.61885	2.00
sp|Q9JLB0|MPP6_MOUSE	MAGUK p55 subfamily member 6 OS=Mus	255.94			1		1	1			2		1	1	1	2	1	2	0.58510	2.00	0.65614	2.00	0.43133	2.00
sp|Q80TB8|VAT1L_MOUSE	Synaptic vesicle membrane protein VAT-1 h	480.92			1			4	3			2	1	2	1	1	1	3	0.52176	4.00	0.58200	3.00	0.03352	5.00

Proteins mostly identified in 2 KI samples with ratio>2 (KI-scr + KI-93):

			Exp. from 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		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P26638|SYSC_MOUSE	Serine--tRNA ligase, cytoplasmic OS=Mus r	780.7	2	2	2	2	5	5	4	6	3	4	2	4	3	3	3	3	0.11313	2.00	0.07586	2.17	0.06052	1.67
tr|A0A087WNW3|A0A087WNW3	Kinectin OS=Mus musculus (Mouse) GN=K	1013.28	2	2		4	4	5	6	1	3	2	2	3	2	3	3	3	0.01802	3.25	0.23380	2.50	0.16661	1.75
sp|Q9D0R8|LSM12_MOUSE	Protein LSM12 homolog OS=Mus musculu	206.61	3	1		2	5	2	2	5	2	2	3		2	3	3	2	0.29632	2.25	0.27066	2.25	0.70367	1.25
sp|Q9CRB6|TPPP3_MOUSE	Tubulin polymerization-promoting protein fa	215.74	2	1		2	4		4	2		2	1		2	2	2	2	0.49842	2.00	0.45623	2.00	0.92559	1.00
sp|Q9CQS8|SC61B_MOUSE	Protein transport protein Sec61 subunit bet	189.27	2			1	1	2	3		1	2	1		1	3	2	2	0.46486	2.00	0.58085	2.00	0.67364	1.50
tr|Q32M04|Q32M04_MOUSE	Prps1l1 protein OS=Mus musculus (Mouse)	246.28	2				2	2	3	1	2	1	1		1	2	3	2	0.57091	2.00	0.17286	3.00	0.93079	1.00
sp|Q9D7G0|PRPS1_MOUSE	Ribose-phosphate pyrophosphokinase 1 C	485.45	2				2	2	3	1	2	1	1		1	2	3	2	0.57091	2.00	0.17286	3.00	0.93079	1.00
sp|Q99LD4|CSN1_MOUSE	COP9 signalosome complex subunit 1 OS=	438.2	2				2	2	2	1	1	3			1	2	3	1	0.57091	2.00	0.38442	2.00	0.80194	1.50
sp|O08585|CLCA_MOUSE	Clathrin light chain A OS=Mus musculus (M	475.81	1	1	2	7	5	3	5	3		4	2	1	3	3	2	3	0.05411	3.75	0.39992	2.00	0.24545	1.75
sp|P35235|PTN11_MOUSE	Tyrosine-protein phosphatase non-receptor	523.27	1	1	1	2	2	2	2	3	2	1	1	3	3	3	3	3	0.00015	2.00	0.03218	2.33	0.31920	1.67
sp|Q9DBR1|XRN2_MOUSE	5'-3' exoribonuclease 2 OS=Mus musculus	318.69	1		1	2	1	2	3		1	2			2	3	2	1	0.13066	2.50	0.51848	2.00	0.98271	1.00
sp|O35621|PMM1_MOUSE	Phosphomannomutase 1 OS=Mus muscul	223.36	1		1	1	2	2	1	2	1	1	1		2	3	3	2	0.11271	2.50	0.23261	2.00	0.90617	1.00
sp|Q3UGS4|F195B_MOUSE	Protein FAM195B OS=Mus musculus (Mou	117.56	1			2	2	2	2	2		1			1	3	2	1	0.00997	6.00	0.24831	4.00	0.99229	1.00
sp|Q9JKV1|ADRM1_MOUSE	Proteasomal ubiquitin receptor ADRM1 OS	267.16	1			2	1	2	2			1			1	3	1	1	0.05918	5.00	0.70178	2.00	0.99229	1.00
sp|Q3UJB9|EDC4_MOUSE	Enhancer of mRNA-decapping protein 4 O	413.54	1			2	1		2	2		1			1	2	2	1	0.39558	3.00	0.24831	4.00	0.99229	1.00
sp|P21126|UBL4A_MOUSE	Ubiquitin-like protein 4A OS=Mus musculus	134.25	1			1	2	2	1		1			1	1	3	2	1	0.04762	5.00	0.51266	2.00	0.91525	1.00
sp|Q9CW03|SMC3_MOUSE	Structural maintenance of chromosomes pr	107.9	1			1	2	2			2			1	1	3	1	1	0.04762	5.00	0.64890	2.00	0.91525	1.00
sp|Q3UTJ2|SRBS2_MOUSE	Sorbin and SH3 domain-containing protein	120.01	1			1	2	1	1	2		1			1	3	2	1	0.10292	4.00	0.37590	3.00	0.99229	1.00
sp|Q9Z1R2|BAG6_MOUSE	Large proline-rich protein BAG6 OS=Mus m	383.14	1			1	2		2			1			1	2	1	1	0.38552	3.00	0.70178	2.00	0.99229	1.00
sp|P56376|ACYP1_MOUSE	Acylphosphatase-1 OS=Mus musculus (Mo	199.17	1			1	1	1	2			1			1	3	1	1	0.14051	3.00	0.70178	2.00	0.99229	1.00
sp|Q9Z1Q2|ABHGA_MOUSE	Abhydrolase domain-containing protein 16A	46.11	1			1	1	1	1	1		1			1	3	2	1	0.14051	3.00	0.50267	2.00	0.99229	1.00
sp|Q9JLN9|MTOR_MOUSE	Serine/threonine-protein kinase mTOR OS	204.82	1			1	1		2	1	1			1	1	2	3	1	0.54855	2.00	0.07029	4.00	0.91525	1.00
sp|Q9D1Q4|DPM3_MOUSE	Dolichol-phosphate mannosyltransferase su	51.77	1				2		1		1			1	1	1	2	1	0.71684	2.00	0.51266	2.00	0.91525	1.00
sp|Q8CG72|ARHL2_MOUSE	Poly(ADP-ribose) glycohydrolase ARH3 OS	102.08	1				1	2	1	1	3	1			1	2	3	1	0.40463	3.00	0.15226	5.00	0.99229	1.00
sp|O88998|NOE1_MOUSE	Noelin OS=Mus musculus (Mouse) GN=Olfr	47.05	1				1	1	2			1			1	2	1	1	0.57091	2.00	0.70178	2.00	0.99229	1.00
sp|Q8BGS2|BOLA2_MOUSE	BolA-like protein 2 OS=Mus musculus (Mou	87.3	1				1	1	1	1		1			1	2	2	1	0.57091	2.00	0.50267	2.00	0.99229	1.00
sp|Q8BW41|PMGT2_MOUSE	Protein O-linked-mannose beta-1,4-N-acety	137.4	1				1	1	1	1		1			1	2	2	1	0.57091	2.00	0.50267	2.00	0.99229	1.00
sp|O35393|EFNB3_MOUSE	Ephrin-B3 OS=Mus musculus (Mouse) GN=	201	1				1	1		1	2			1	1	2	2	1	0.57091	2.00	0.34108	3.00	0.91525	1.00
sp|Q9D2N4|DTNA_MOUSE	Dystrobrevin alpha OS=Mus musculus (Mou	183.51		1		1	1	1	1	1	1	1			1	3	3	1	0.12048	3.00	0.08618	3.00	0.98315	1.00
sp|Q8BGX2|CS052_MOUSE	Uncharacterized protein C19orf52 homolog	203.64		1			1	1		1	2		1		1	2	2	1	0.54185	2.00	0.32861	3.00	0.86966	1.00
sp|Q8C052|MAP1S_MOUSE	Microtubule-associated protein 1S OS=Mus	478.51			1	2	1	1	2			1			1	3	1	1	0.13187	4.00	0.71022	2.00	0.98065	1.00
sp|P61963|DCAF7_MOUSE	DDB1- and CUL4-associated factor 7 OS=I	218.77			1	2	1		1		1	1			1	2	2	1	0.40296	3.00	0.52560	2.00	0.98065	1.00
sp|P48024|EIF1_MOUSE	Eukaryotic translation initiation factor 1 OS	104.88			1	1	1	1	1	1			1		1	3	2	1	0.15088	3.00	0.51533	2.00	0.90433	1.00
sp|Q0VE82|CPNE7_MOUSE	Copine-7 OS=Mus musculus (Mouse) GN=(	172.52			1	1	1			2	1			1	1	2	2	1	0.56228	2.00	0.35175	3.00	0.92666	1.00
sp|Q9DC50|OCTC_MOUSE	Peroxisomal carnitine O-octanoyltransferase	180.36			1		2	1	1	1		1			1	2	2	1	0.40977	3.00	0.51533	2.00	0.98065	1.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P97855|G3BP1_MOUSE	Ras GTPase-activating protein-binding prot	411.37	2	2		4	2	2	4	4	1	1			2	3	3	1	0.26621	2.00	0.21310	2.25	0.25286	0.25
tr|D3YXZ3|D3YXZ3_MOUSE	Kinesin light chain 2 OS=Mus musculus (M	549.8	1	1		2	3	3	3		1	1			2	3	2	1	0.01073	4.00	0.50254	2.00	0.52365	0.50
sp|Q9JJU8|SH3L1_MOUSE	SH3 domain-binding glutamic acid-rich-like p	337.98	1	1		2	1	2	4		1	1			2	3	2	1	0.11954	2.50	0.45410	2.50	0.52365	0.50
sp|Q9WUA6|AKT3_MOUSE	RAC-gamma serine/threonine-protein kinase	208.65	1		1	2	1	1	1	2	1	1			2	3	3	1	0.28730	2.00	0.23261	2.00	0.50359	0.50
sp|Q9QZI8|SERC1_MOUSE	Serine incorporator 1 OS=Mus musculus (M	117.01	1			1	2		1	1					1	2	2	0	0.38552	3.00	0.50267	2.00	0.37390	WT-scr only
sp|Q3UMR5|MCU_MOUSE	Calcium uniporter protein, mitochondrial OS	272.77	1				2			2	1				1	1	2	0	0.71684	2.00	0.34569	3.00	0.37390	WT-scr only
sp|Q9DCZ4|MIC26_MOUSE	MICOS complex subunit Mic26 OS=Mus mu	162.19	1				1	1	1	1	2				1	2	3	0	0.57091	2.00	0.10136	4.00	0.37390	WT-scr only
sp|Q8VHI6|WASF3_MOUSE	Wiskott-Aldrich syndrome protein family men	309.93		2		1	2	1	1	3	1	1			1	3	3	1	0.42855	2.00	0.31473	2.50	0.68938	0.50
sp|Q9R0P4|SMAP_MOUSE	Small acidic protein OS=Mus musculus (Mo	186.1		1		3	1		1	1					1	2	2	0	0.35674	4.00	0.47695	2.00	0.37390	WT-scr only
sp|Q9JLJ2|AL9A1_MOUSE	4-trimethylaminobutyraldehyde dehydrogen	434.4		1		1	3	3	2		1				1	3	2	0	0.04955	7.00	0.34771	3.00	0.37390	WT-scr only
sp|P41241|CSK_MOUSE	Tyrosine-protein kinase CSK OS=Mus mus	150.48		1		1	1	2	1		1				1	3	2	0	0.10072	4.00	0.48634	2.00	0.37390	WT-scr only
tr|F8VPU6|F8VPU6_MOUSE	Protein Usp9y OS=Mus musculus (Mouse)	297.99		1		1	1	1	1		1				1	3	2	0	0.12048	3.00	0.48634	2.00	0.37390	WT-scr only
sp|Q9D358|PPAC_MOUSE	Low molecular weight phosphotyrosine prot	273.58		1			3	4		1	1				1	2	2	0	0.18968	7.00	0.43725	2.00	0.37390	WT-scr only
tr|M1VHG6|M1VHG6_MOUSE	Metastasis-associated protein MTA1 isoform	186.79			1	1	1	2	2		2				1	3	2	0	0.11606	4.00	0.25543	4.00	0.37390	WT-scr only
tr|B2RWW6|B2RWW6_MOUSE	GCN1 general control of amino-acid synthe	271			1		1	1	2						1	2	1	0	0.58510	2.00	0.71022	2.00	0.37390	WT-scr only

Proteins mostly identified in 2 KI samples with ratio>2 (KI-scr + KI-82):

			Exp. from 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		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q99L04|DHRS1_MOUSE	Dehydrogenase/reductase SDR family mem	384.42	2	1	1	2	2	4	2	2	2	2	3	3	3	3	3	3	0.16456	2.00	0.09538	1.50	0.05405	2.00
sp|Q99KK7|DPP3_MOUSE	Dipeptidyl peptidase 3 OS=Mus musculus (	836.23	2	1	1	2	2	4	2	1		2	2	4	3	3	2	3	0.16456	2.00	0.63863	0.75	0.13120	2.00
sp|Q7TNC4|LC7L2_MOUSE	Putative RNA-binding protein Luc7-like 2 O	247.03	2	1		1	3	2	2		2	1	1	4	2	3	2	3	0.31237	2.00	0.70316	1.33	0.37799	2.00
sp|Q8BTI8|SRRM2_MOUSE	Serine/arginine repetitive matrix protein 2 C	408.94	2			3	3		3			2	3		1	2	1	2	0.34793	3.00	0.82564	1.50	0.38707	2.50
sp|Q9QYS9|QKI_MOUSE	Protein quaking OS=Mus musculus (Mouse	171.17	2			3	1			1	1	1	1	2	1	2	2	3	0.59745	2.00	0.92930	1.00	0.33952	2.00
sp|P70399|TP53B_MOUSE	Tumor suppressor p53-binding protein 1 O	299.38	2			1	3	2		1	1	3	1		1	3	2	2	0.22277	3.00	0.92930	1.00	0.53957	2.00
sp|O55142|RL35A_MOUSE	60S ribosomal protein L35a OS=Mus musc	210.96	1	2		3	2	1	3		2	5	1		2	3	2	2	0.31047	2.00	0.53196	1.67	0.53132	2.00
sp|Q99KV1|DJB11_MOUSE	DnaJ homolog subfamily B member 11 OS	291.12	1	1	1	3	1	2	2	1	1	3	2	1	3	3	3	3	0.19989	2.00	0.22141	1.33	0.08612	2.00
sp|Q9CYN2|SPCS2_MOUSE	Signal peptidase complex subunit 2 OS=M	233.49	1	1	1	1	3	4	2	1	2	4	2	1	3	3	3	3	0.13515	2.67	0.07873	1.67	0.12814	2.33
sp|P60229|EIF3E_MOUSE	Eukaryotic translation initiation factor 3 subu	582.58	1	1		1	2	2	1		1	2		2	2	3	2	2	0.10151	2.50	0.96234	1.00	0.37896	2.00
sp|Q8VH51|RBM39_MOUSE	RNA-binding protein 39 OS=Mus musculus	392.66	1		1		2	2	1		2		2	2	2	2	2	2	0.47497	2.00	0.63742	1.50	0.34629	2.00
sp|Q9D3P8|PLRKT_MOUSE	Plasminogen receptor (KT) OS=Mus muscu	142.28	1		1		3	2		1	1	2	1	1	2	2	2	3	0.38212	2.50	0.90349	1.00	0.13838	2.00
tr|Q91XH6|Q91XH6_MOUSE	Vesicle transport through interaction with t-S	375.09	1			2	1	1	1			2	1		1	3	1	2	0.12676	4.00	0.96559	1.00	0.33204	3.00
sp|Q9DC28|KC1D_MOUSE	Casein kinase I isoform delta OS=Mus mus	157.03	1			2	1		1				2		1	2	1	1	0.39558	3.00	0.96559	1.00	0.61250	2.00
sp|Q9D164|FXYD6_MOUSE	FXYD domain-containing ion transport regu	213.89	1			2			1			2			1	1	1	1	0.67625	2.00	0.96559	1.00	0.68309	2.00
sp|Q8C015|PAK7_MOUSE	Serine/threonine-protein kinase PAK 7 OS	132.77	1			2				1		1	1		1	1	1	2	0.67625	2.00	0.93674	1.00	0.46591	2.00
sp|P70297|STAM1_MOUSE	Signal transducing adapter molecule 1 OS	210.83	1			1	1	2	1			1		1	1	3	1	2	0.11083	4.00	0.96559	1.00	0.47715	2.00
sp|P46978|STT3A_MOUSE	Dolichyl-diphosphooligosaccharide--protein	177.48	1			1	1		1			1	1	1	1	2	1	3	0.54855	2.00	0.96559	1.00	0.08013	3.00
tr|A3KGR9|A3KGR9_MOUSE	Minor histocompatibility antigen H13 OS=M	124.67	1			1	1		1			1	1		1	2	1	2	0.54855	2.00	0.96559	1.00	0.46591	2.00
sp|Q920L1|FADS1_MOUSE	Fatty acid desaturase 1 OS=Mus musculus	83.4	1			1	1			1			1	1	1	2	1	2	0.54855	2.00	0.93674	1.00	0.42068	2.00
sp|Q8C0T5|SI1L1_MOUSE	Signal-induced proliferation-associated 1-lik	301.01	1				3			1		2			1	1	1	1	0.58627	3.00	0.93674	1.00	0.68309	2.00
sp|Q9CQV1|TIM16_MOUSE	Mitochondrial import inner membrane transl	126.52	1				1	1	1			1	1	1	1	2	1	3	0.57091	2.00	0.96559	1.00	0.08013	3.00
sp|Q8CGF7|TCRG1_MOUSE	Transcription elongation regulator 1 OS=M	48.18	1				1	1		1			1	1	1	2	1	2	0.57091	2.00	0.93674	1.00	0.42068	2.00
sp|Q99L43|CDS2_MOUSE	Phosphatidate cytidylyltransferase 2 OS=M	203.59		1		1	1	1		1		2	1	1	1	3	1	3	0.12048	3.00	0.91265	1.00	0.04961	4.00
sp|O35449|PRRT1_MOUSE	Proline-rich transmembrane protein 1 OS=M	56.49		1		1	1		1			1	1		1	2	1	2	0.52049	2.00	0.99012	1.00	0.44226	2.00
sp|O70318|E41L2_MOUSE	Band 4.1-like protein 2 OS=Mus musculus	276.15		1				2			1	2	1	1	1	1	1	3	0.68498	2.00	0.93075	1.00	0.04961	4.00
sp|O35344|IMA4_MOUSE	Importin subunit alpha-4 OS=Mus musculu	321.12			1	1	1	1	1			1	1		1	3	1	2	0.15088	3.00	0.95400	1.00	0.47760	2.00
sp|Q99P47|CNTP4_MOUSE	Contactin-associated protein-like 4 OS=Mu	83.76			1		1	1			1	1		1	1	2	1	2	0.58510	2.00	0.96663	1.00	0.48921	2.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q8BHE3|ATCAY_MOUSE	Caytaxin OS=Mus musculus (Mouse) GN=A	289.26	2			2	2		1			1	3		1	2	1	2	0.54855	2.00	0.65549	0.50	0.52767	2.00
tr|E9PV26|E9PV26_MOUSE	Protein Prr36 OS=Mus musculus (Mouse) G	196.17	1			1	1					2			1	2	0	1	0.54855	2.00	0.37390	WT-scr only	0.68309	2.00
sp|Q91Y86|MK08_MOUSE	Mitogen-activated protein kinase 8 OS=Mu	240.74	1					2				1	1		1	1	0	2	0.70221	2.00	0.37390	WT-scr only	0.46591	2.00
sp|P01942|HBA_MOUSE	Hemoglobin subunit alpha OS=Mus muscu	50.48		1		2						2		2	1	1	0	2	0.66021	2.00	0.37390	WT-scr only	0.23092	4.00
sp|Q80U28|MADD_MOUSE	MAP kinase-activating death domain protei	384.39		1		1	2	1					2		1	3	0	1	0.09274	4.00	0.37390	WT-scr only	0.59965	2.00
sp|P61620|S61A1_MOUSE	Protein transport protein Sec61 subunit alp	243.25		1		1	1					1	1		1	2	0	2	0.52049	2.00	0.37390	WT-scr only	0.44226	2.00
sp|Q99JP7|GGT7_MOUSE	Gamma-glutamyltransferase 7 OS=Mus mu	109.69			1	1	1					1	1		1	2	0	2	0.56228	2.00	0.37390	WT-scr only	0.47760	2.00

Proteins mostly identified in 2 KI samples with ratio>2 (KI-93 + KI-82):

			Exp. from 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		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q6R891|NEB2_MOUSE	Neurabin-2 OS=Mus musculus (Mouse) GN	952.05	3	2	1	4	6	1	7	3	3	6	4	2	3	3	3	3	0.36301	1.83	0.11801	2.17	0.11585	2.00
sp|Q8K2K6|AGFG1_MOUSE	Arf-GAP domain and FG repeat-containing	276.36	2	1		2	3		4	2		4	2		2	2	2	2	0.58762	1.67	0.45623	2.00	0.42297	2.00
sp|P63213|GBG2_MOUSE	Guanine nucleotide-binding protein G(I)/G(S	473.34	2		1			2	5	7	3	3	9	5	2	1	3	3	0.67540	0.67	0.04509	5.00	0.08216	5.67

tr|Q3UA53|Q3UA53_MOUSE	Putative uncharacterized protein OS=Mus ı	781.64	1	4	1	3	4	4	5	3	4	8	3	2	3	3	3	3	0.19235	1.83	0.09663	2.00	0.23221	2.17
sp|Q02819|NUCB1_MOUSE	Nucleobindin-1 OS=Mus musculus (Mouse)	347.2	1	2	1	3	2	1	3	3	3	3	3	4	3	3	3	3	0.41806	1.50	0.00601	2.25	0.01369	2.50
sp|Q8BIW1|PRUNE_MOUSE	Protein prune homolog OS=Mus musculus	748.56	1	2		1	4		3	1	2	3	2	2	2	2	3	3	0.66322	1.67	0.22131	2.00	0.05004	2.33
sp|P61021|RAB5B_MOUSE	Ras-related protein Rab-5B OS=Mus muscı	738.82	1	1	3		1	3	2	6	3	2	3	5	3	2	3	3	0.70674	0.80	0.22792	2.20	0.17769	2.00
sp|Q9D1K2|VATF_MOUSE	V-type proton ATPase subunit F OS=Mus ı	262.28	1	1	1	1	3	1	3	2	1	3	2	1	3	3	3	3	0.39107	1.67	0.10538	2.00	0.08612	2.00
sp|Q924M7|MPI_MOUSE	Mannose-6-phosphate isomerase OS=Mus	431.28	1	1		1		2	2	1	2	2	2		2	2	3	2	0.65202	1.50	0.07588	2.50	0.37128	2.00
sp|Q2L4X1|BZW2_MUSMM	Basic leucine zipper and W2 domain-contaiı	307.81	1	1			1	2	2		3	2	1	1	2	2	2	3	0.68781	1.50	0.34853	2.50	0.12430	2.00
sp|Q9JM14|NT5C_MOUSE	5'(3')-deoxyribonucleotidase, cytosolic type	133.86	1	1			1	1	1	2	1	3	1	2	2	2	3	3	0.93454	1.00	0.21647	2.00	0.06450	3.00
sp|Q6P4T2|U520_MOUSE	U5 small nuclear ribonucleoprotein 200 kDa	729.79	1			1			1	1	1	1	2	2	1	1	3	3	0.99759	1.00	0.10121	3.00	0.05091	5.00
sp|P47955|RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus ı	124.65	1			1			1	1		1	1	1	1	1	2	3	0.99759	1.00	0.50267	2.00	0.08013	3.00
sp|Q8K019|BCLF1_MOUSE	Bcl-2-associated transcription factor 1 OS=	173.04	1				1		2	1		1	1		1	1	2	2	0.94510	1.00	0.35515	3.00	0.46591	2.00
sp|Q9CQC6|BZW1_MOUSE	Basic leucine zipper and W2 domain-contaiı	394.28	1				1		1		1	1		1	1	1	2	2	0.94510	1.00	0.51266	2.00	0.47715	2.00
sp|P02802|MT1_MOUSE	Metallothionein-1 OS=Mus musculus (Mous	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	0.18221	2.00
tr|Q3U935|Q3U935_MOUSE	Putative uncharacterized protein OS=Mus ı	334.95		1		1			2			1	1		1	1	1	2	0.97304	1.00	0.68457	2.00	0.44226	2.00
sp|Q8HW98|IGLO5_MOUSE	IgLON family member 5 OS=Mus musculus	180.88		1			1		2			2	1		1	1	1	2	0.96951	1.00	0.68457	2.00	0.31860	3.00
sp|Q810A7|DDX42_MOUSE	ATP-dependent RNA helicase DDX42 OS=	277.59			1	1			1		2	1		2	1	1	2	2	0.99076	1.00	0.38564	3.00	0.36868	3.00
sp|Q8K2T1|NMRL1_MOUSE	NmrA-like family domain-containing protein '	128.41			1			1			2	1	1		1	1	1	2	0.95341	1.00	0.65614	2.00	0.47760	2.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P03930|ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus	99.57	2				1		2	1	1	2	2		1	1	3	2	0.64280	0.50	0.38442	2.00	0.46591	2.00
sp|Q58A65|JIP4_MOUSE	C-Jun-amino-terminal kinase-interacting prot	230.48	1						1	1	1		1	1	1	0	3	2	0.37390	WT-scr only	0.10121	3.00	0.42068	2.00
sp|O35593|PSDE_MOUSE	26S proteasome non-ATPase regulatory su	322.58	1						1	1		2			1	0	2	1	0.37390	WT-scr only	0.50267	2.00	0.68309	2.00
sp|Q9Z2D0|MTMR9_MOUSE	Myotubularin-related protein 9 OS=Mus mu	242.67	1						1		2	1	1	1	1	0	2	3	0.37390	WT-scr only	0.37901	3.00	0.08013	3.00
sp|Q9QX47|SON_MOUSE	Protein SON OS=Mus musculus (Mouse) G	95.09	1							3			2		1	0	1	1	0.37390	WT-scr only	0.53646	3.00	0.61250	2.00
sp|P47226|TES_MOUSE	Testin OS=Mus musculus (Mouse) GN=Tes	97.03	1							1	1	2	1	1	1	0	2	3	0.37390	WT-scr only	0.46107	2.00	0.05581	4.00
sp|O35215|DOPD_MOUSE	D-dopachrome decarboxylase OS=Mus mu	197.34		1					3		1	2			1	0	2	1	0.37390	WT-scr only	0.32616	4.00	0.66673	2.00
sp|Q9JJ28|FLII_MOUSE	Protein flightless-1 homolog OS=Mus musc	81.27		1					1		1	1	1	1	1	0	2	3	0.37390	WT-scr only	0.48634	2.00	0.06802	3.00
sp|Q9CZR8|EFTS_MOUSE	Elongation factor Ts, mitochondrial OS=Mu	100.94			1					1	1		1	1	1	0	2	2	0.37390	WT-scr only	0.47285	2.00	0.43133	2.00

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

			Exp. from 01/02/2017												Exp. 01/02/2017									
			BASIC Spectral Count (Proline)																					
			WT			KI-scr			KI-93			KI-82			# Repl.				KI-scr / WT-scr		KI-93 / WT-scr		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P05132|KAPCA_MOUSE	cAMP-dependent protein kinase catalytic sı	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	0.88718	0.88
sp|P24270|CATA_MOUSE	Catalase OS=Mus musculus (Mouse) GN=(	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 ı	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|RADI_MOUSE	Radixin OS=Mus musculus (Mouse) GN=Rc	754.21	2	3	4	6	6	6	7	1	3	5	4	3	3	3	3	3	0.01299	2.00	0.71371	1.22	0.12673	1.33
sp|Q9Z1X4|ILF3_MOUSE	Interleukin enhancer-binding factor 3 OS=ı	684.57	4	2	2	6	6	4	4	3	3	8	2		3	3	3	2	0.06607	2.00	0.30399	1.25	0.75964	1.25
tr|B1AWE0|B1AWE0_MOUSE	Clathrin light chain A OS=Mus musculus (M	529.43	3	3	3	8	6	4	4	4	1	4	3	2	3	3	3	3	0.09260	2.00	0.90038	1.00	0.52327	1.00
sp|Q91VR7|MLP3A_MOUSE	Microtubule-associated proteins 1A/1B light	305.94	2	3	3	4	6	6	3	2	5	5	1	4	3	3	3	3	0.01669	2.00	0.45354	1.25	0.47642	1.25
sp|Q8BWT1|THIM_MOUSE	3-ketoacyl-CoA thiolase, mitochondrial OS=	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|Q8VEH5|EPMIP_MOUSE	EPM2A-interacting protein 1 OS=Mus musc	713.91	2	2	3	5	6	3		3	4	2	4	2	3	3	2	3	0.07917	2.00	0.86231	1.00	0.49230	1.14
sp|P29391|FRIL1_MOUSE	Ferritin light chain 1 OS=Mus musculus (Mc	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	0.85635	1.00
sp|Q99KK2|NEUA_MOUSE	N-acylneuraminate cytidylyltransferase OS=	281.81	2	3	1	3	4	6	3	2	2	5		4	3	3	3	2	0.08997	2.17	0.47070	1.17	0.50198	1.50
sp|Q8BFR4|GNS_MOUSE	N-acetylglucosamine-6-sulfatase OS=Mus ı	201.79	2	2	1	4	3	5	2	2	3	3	2	3	3	3	3	3	0.03073	2.40	0.18911	1.40	0.03853	1.60
sp|Q9CPY7|AMPL_MOUSE	Cytosol aminopeptidase OS=Mus musculus	432.04	2	2	1	3	4	4	3	1	2	2	1	1	3	3	3	3	0.00921	2.20	0.53465	1.20	0.66877	0.80
sp|Q9DCJ5|NDUA8_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	395.3	2	2	1	1	5	4	2	1	1	2	3	2	3	3	3	3	0.26326	2.00	0.52503	0.80	0.16600	1.40
sp|P30681|HMGB2_MOUSE	High mobility group protein B2 OS=Mus mu	398.21	5	2		3	7	9	4		6	3		2	2	3	2	2	0.16740	2.71	0.66250	1.43	0.77068	0.71
sp|Q99JF8|PSIP1_MOUSE	PC4 and SFRS1-interacting protein OS=Mı	886.27	3	3		3	4	6	7	1		4	1	1	2	3	2	3	0.16609	2.17	0.80039	1.33	0.91073	1.00
sp|Q9D1Q6|ERP44_MOUSE	Endoplasmic reticulum resident protein 44 (	450.38	3	2		3	5	6	5	1	2	2	3	3	2	3	3	3	0.07669	2.80	0.49583	1.60	0.24052	1.60
tr|A0A0N4SW65|A0A0N4SW65_	N-acylneuraminate cytidylyltransferase OS=	98.03	2	2		3	3	3	3	2	1	4		2	2	3	3	2	0.07963	2.25	0.41635	1.50	0.57922	1.50
tr|A0A0N4SWC3|A0A0N4SWC3_	N-acylneuraminate cytidylyltransferase OS=	98.03	2	2		3	3	3	3	2	1	4		2	2	3	3	2	0.07963	2.25	0.41635	1.50	0.57922	1.50
sp|Q6ZWX6|IF2A_MOUSE	Eukaryotic translation initiation factor 2 subı	738.34	2	2		4	5	2	2	1	2	2	2	1	2	3	3	3	0.10592	2.75	0.58977	1.25	0.49505	1.25
sp|P97820|M4K4_MOUSE	Mitogen-activated protein kinase kinase kinı	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	0.31863	1.33
sp|Q9JM52|MINK1_MOUSE	Misshapen-like kinase 1 OS=Mus musculus	658.48	2	1	3	5	4	3	3	1	2	5	2	2	3	3	3	3	0.11230	2.00	0.96981	1.00	0.30029	1.50
sp|Q8BJY1|PSMD5_MOUSE	26S proteasome non-ATPase regulatory su	600.74	2	1		2	5	2	3	2		4	1		2	3	2	2	0.15439	3.00	0.53406	1.67	0.60060	1.67
sp|O70305|ATX2_MOUSE	Ataxin-2 OS=Mus musculus (Mouse) GN=A	520.43	2	1		2	3	1	2			1	2		2	3	1	2	0.31005	2.00	0.69382	0.67	0.86894	1.00
sp|Q99JY8|LPP3_MOUSE	Lipid phosphate phosphohydrolase 3 OS=	288.01	2	1		1	4	2	2		1	2			2	3	2	1	0.28706	2.33	0.99743	1.00	0.72684	0.67
sp|Q9JK48|SHLB1_MOUSE	Endophilin-B1 OS=Mus musculus (Mouse)	459.95	2	1		1	2	5			2	2	1	1	2	3	1	3	0.29559	2.67	0.79381	0.67	0.49632	1.33
sp|Q99J99|THTM_MOUSE	3-mercaptopyruvate sulfurtransferase OS=ı	562.53	2		2	3	4	1	2	1	3	1	2	2	2	3	3	3	0.32888	2.00	0.46592	1.50	0.51920	1.25
sp|P27545|CERS1_MOUSE	Ceramide synthase 1 OS=Mus musculus (ı	207.92	3		1	3	3	2	2	2	1	3	2		2	3	3	2	0.27635	2.00	0.69501	1.25	0.73387	1.25
sp|O08759|UBE3A_MOUSE	Ubiquitin-protein ligase E3A OS=Mus musc	394.52	2			1	2	1	2		1	2		1	1	3	2	2	0.46624	2.00	0.72795	1.50	0.68621	1.50
sp|Q91V64|ISOC1_MOUSE	Isochorismatase domain-containing protein	330.11	2				1	3			2		1	2	1	2	1	2	0.62029	2.00	0.95504	1.00	0.61012	1.50
sp|Q9D855|QCR7_MOUSE	Cytochrome b-c1 complex subunit 7 OS=M	342.26	1	3	3	6	5	4	4	2	2	6		3	3	3	3	2	0.05965	2.14	0.64337	1.14	0.67312	1.29
sp|P70168|IMB1_MOUSE	Importin subunit beta-1 OS=Mus musculus	1324.1	1	4	5	4	11	9	10		4	6	3	8	3	3	2	3	0.12581	2.40	0.69174	1.40	0.21639	1.70
sp|P51410|RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculı	521.21	1	3	1	3	3	4	3	2	3	4	1		3	3	3	2	0.09172	2.00	0.16818	1.60	0.94650	1.00
sp|Q6P8X1|SNX6_MOUSE	Sorting nexin-6 OS=Mus musculus (Mouse)	513.48	1	3	1	2	5	4	4	1	2	3	2	2	3	3	3	3	0.13645	2.20	0.50230	1.40	0.21210	1.40
sp|Q922D8|C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic	605.33	1	2	1	3	3	3	3			4			3	3	1	1	0.00809	2.25	0.72353	0.75	0.99803	1.00
sp|Q9ES28|ARHG7_MOUSE	Rho guanine nucleotide exchange factor 7	664.93	1	2	1	2	2	5		3	4		3	2	3	3	2	2	0.19358	2.25	0.40170	1.75	0.56516	1.25
sp|P62307|RUXF_MOUSE	Small nuclear ribonucleoprotein F OS=Mus	206.43	1	2		2	2	3	2	1	1	1	1	1	2	3	3	3	0.12151	2.33	0.55258	1.33	0.78899	1.00
sp|Q8BR92|PALM2_MOUSE	Paralemmin-2 OS=Mus musculus (Mouse) (	249.32	1	2		2	3	1	3			3			2	3	1	1	0.29248	2.00	0.97743	1.00	0.98954	1.00
sp|O35633|VIAAT_MOUSE	Vesicular inhibitory amino acid transporter (	432.39	1	3		1	4	5	2	2	2	3		2	2	3	3	2	0.25917	2.50	0.39110	1.50	0.71624	1.25
sp|Q9CQR6|PPP6_MOUSE	Serine/threonine-protein phosphatase 6 cat	397.65	1	1	1	2	3	2	2	1	2	2	2	1	3	3	3	3	0.00961	2.33	0.07873	1.67	0.07923	1.67
sp|Q99JF5|MVD1_MOUSE	Diphosphomevalonate decarboxylase OS=	327.06	1	1	1	2	3	2	3		2	2			3	3	2	1	0.00961	2.33	0.47506	1.67	0.63688	0.67
sp|O54983|CRYM_MOUSE	Ketimine reductase mu-crystallin OS=Mus ı	440.04	1	1	1	1	5		1	2		1	4		3	2	2	2	0.56979	2.00	0.91815	1.00	0.55208	1.67
sp|Q8K4Z3|NNRE_MOUSE	NAD(P)H-hydrate epimerase OS=Mus musc	274.74	1	1	1		3	3	1	1	1	2	2		3	2	3	2	0.41003	2.00	0.39275	1.00	0.55541	1.33
sp|Q8R404|MIC13_MOUSE	MICOS complex subunit MIC13 OS=Mus m	178.59	1	1		1	2	1	1		1	2	1		2	3	2	2	0.23659	2.00	0.96234	1.00	0.56462	1.50
sp|P24547|IMDH2_MOUSE	Inosine-5'-monophosphate dehydrogenase	305.06	1		2	2	1	3	1	1	2		1	1	2	3	3	2	0.33221	2.00	0.60159	1.33	0.77876	0.67
sp|Q7TT37|ELP1_MOUSE	Elongator complex protein 1 OS=Mus musc	513.58	1		1	1	1	2	2	1		2		1	2	3	2	2	0.26908	2.00	0.63719	1.50	0.60300	1.50
sp|O70378|EMC8_MOUSE	ER membrane protein complex subunit 8 C	224.72	1			1	1	1	1					1	1	3	1	1	0.14051	3.00	0.96559	1.00	0.91525	1.00
tr|A1L338|A1L338_MOUSE	Rapgef1 protein OS=Mus musculus (Mouse	81.27	1			1	1		1			1			1	2	1	1	0.54855	2.00	0.96559	1.00	0.99229	1.00
sp|A2A690|TANC2_MOUSE	Protein TANC2 OS=Mus musculus (Mouse)	137.87	1				1	2	1			1			1	2	1	1	0.40463	3.00	0.96559	1.00	0.99229	1.00
sp|Q8VCI5|PEX19_MOUSE	Peroxisomal biogenesis factor 19 OS=Mus	149.88	1				1	1	1			1			1	2	1	1	0.57091	2.00	0.96559	1.00	0.99229	1.00
sp|P42208|SEPT2_MOUSE	Septin-2 OS=Mus musculus (Mouse) GN=S	656.82		2	3	5	3	4	4	3	1	5	1	2	2	3	3	3	0.12479	2.40	0.42618	1.60	0.45241	1.60
sp|P70398|USP9X_MOUSE	Probable ubiquitin carboxyl-terminal hydrola	1327.75		3	2	4	4	3	5		2	6			2	3	2	1	0.11675	2.20	0.70464	1.40	0.88360	1.20
sp|O09167|RL21_MOUSE	60S ribosomal protein L21 OS=Mus muscu	374.14		3	2	4	2	4	1	1	2	2	3		2	3	3	2	0.23131	2.00	0.82374	0.80	0.86471	1.00
sp|Q99MN1|SYK_MOUSE	Lysine--tRNA ligase OS=Mus musculus (Mc	828.57		2	3	3	5	4		1	2	3		1	2	3	2	2	0.10228	2.40	0.63706	0.60	0.83155	0.80
sp|P60521|GBRL2_MOUSE	Gamma-aminobutyric acid receptor-associat	306.85		2	1	2	2	2	3	1	1	2			2	3	3	1	0.17368	2.00	0.42746	1.67	0.72794	0.67
sp|P48320|DCE2_MOUSE	Glutamate decarboxylase 2 OS=Mus musc	695.2		4		3	3	2	2		1	4	1	2	1	3	2	3	0.39419	2.00	0.84673	0.75	0.45637	1.75
sp|P06797|CATL1_MOUSE	Cathepsin L1 OS=Mus musculus (Mouse) (	142.02		2		2	2	1	3			2			1	3	1	1	0.25709	2.50	0.80384	1.50	0.98315	1.00
sp|Q921L3|TMCO1_MOUSE	Transmembrane and coiled-coil domain-con	247.44		3		1	4	1	3			2			1	3	1	1	0.52872	2.00	0.99012	1.00	0.80996	0.67
sp|Q8BK64|AHSA1_MOUSE	Activator of 90 kDa heat shock protein ATP	468.53		1	4	3	5	3	2		1	2		1	2	3	2	2	0.26072	2.20	0.63431	0.60	0.66632	0.60
sp|Q9JHI5|IVD_MOUSE	Isovaleryl-CoA dehydrogenase, mitochondri	392.18		1	2	3	1	2	4		1	3			2	3	2	1	0.33537	2.00	0.65231	1.67	0.99076	1.00
sp|P53986|MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus mı	154.28		1	1	1	2	1	2	1		1	1		2	3	2	2	0.24427	2.00	0.62026	1.50	0.88294	1.00
sp|Q8BFT9|SVOP_MOUSE	Synaptic vesicle 2-related protein OS=Mus	210.84		1	1		3	2	2	1		1	1		2	2	2	2	0.37324	2.50	0.62026	1.50	0.88294	1.00
sp|Q3TCN2|PLBL2_MOUSE	Putative phospholipase B-like 2 OS=Mus ı	172.94		1		2				1		1			1	1	1	1	0.66021	2.00	0.91265	1.00	0.98315	1.00
sp|Q99PL6|UBXN6_MOUSE	UBX domain-containing protein 6 OS=Mus	232.49		1		1	1	2	1					1	1	3	1	1	0.10072	4.00	0.99012	1.00	0.89145	1.00
sp|Q9ER88|RT29_MOUSE	28S ribosomal protein S29, mitochondrial (	163.06		1		1	1	1	1			1			1	3	1	1	0.12048	3.00	0.99012	1.00	0.98315	1.00
sp|Q80T41|GABR2_MOUSE	Gamma-aminobutyric acid type B receptor s	119.92		1		1		1	1			1			1	2	1	1	0.50939	2.00	0.99012	1.00	0.98315	1.00
sp|Q69ZH9|RHG23_MOUSE	Rho GTPase-activating protein 23 OS=Mus	80.75		1			2		1			1			1	1	1	1	0.69898	2.00	0.99012	1.00	0.98315	1.00
sp|Q9JHQ5|LZTL1_MOUSE	Leucine zipper transcription factor-like prote	228.03		1			1	2		1		1			1	2	1	1	0.38855	3.00	0.91265	1.00	0.98315	1.00
sp|P97315|CSRP1_MOUSE	Cysteine and glycine-rich protein 1 OS=Mu	186.13		1			1	1	1			1			1	2	1	1	0.54185	2.00	0.99012	1.00	0.98315	1.00
sp|Q9R0N5|SYT5_MOUSE	Synaptotagmin-5 OS=Mus musculus (Mous	237.89		1				2	1			1			1	1	1	1	0.68498	2.00	0.99012	1.00	0.98315	1.00
sp|Q61772|EPHA7_MOUSE	Ephrin type-A receptor 7 OS=Mus musculu	190.89			1	1	1	2		1		1			1	3	1	1	0.11606	4.00	0.94827	1.00	0.98065	1.00
tr|Q8C2W4|Q8C2W4_MOUSE	RIKEN cDNA 2610528K11, isoform CRA_b	167.53			1		1	1		1			1		1	2	1	1	0.58510	2.00	0.94827	1.00	0.90433	1.00
sp|Q5IRJ6|ZNT9_MOUSE	Zinc transporter 9 OS=Mus musculus (Mou	56.32			1		1	1			1			1	1	2	1	1	0.58510	2.00	0.96663	1.00	0.92666	1.00
sp|P70318|TIAR_MOUSE	Nucleolysin TIAR OS=Mus musculus (Mous	177.34			1			2			1			1	1	1	1	1	0.71065	2.00	0.96663	1.00	0.92666	1.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q9JJK2|LANC2_MOUSE	LanC-like protein 2 OS=Mus musculus (Mou	639.47	2	1		2	3	2				2	2		2	3	0	2	0.12819	2.33	0.16333	WT-scr only	0.63223	1.33
sp|O70311|NMT2_MOUSE	Glycylpeptide N-tetradecanoyltransferase 2	505.69	2		2	2	3	4	1	1		1	3	3	2	3	2	3	0.15551	2.25	0.43354	0.50	0.27865	1.75
tr|B2RY15|B2RY15_MOUSE	Tln2 protein OS=Mus musculus (Mouse) GI	1060.49	3		3	5	3	5		1		2		2	2	3	1	2	0.16428	2.17	0.20168	0.17	0.66483	0.67
tr|A0A0A6YXV8|A0A0A6YXV8_	Calmodulin-regulated spectrin-associated pı	182	2			1	2	1	1			1		1	1	3	1	2	0.46624	2.00	0.65549	0.50	0.94727	1.00
sp|Q3UHB1|NT5D3_MOUSE	5'-nucleotidase domain-containing protein 3	485.32	1	2		2	3	1	1			2			2	3	1	1	0.29248	2.00	0.35814	0.33	0.73384	0.67
sp|Q8K0U4|HS12A_MOUSE	Heat shock 70 kDa protein 12A OS=Mus ı	965.02	1	2		3	3	1				2	2		2	3	0	2	0.21602	2.33	0.15344	WT-scr only	0.61645	1.33
tr|Q3V3S8|Q3V3S8_MOUSE	Putative uncharacterized protein OS=Mus ı	235.86	1	1		1	2	1			1	1		1	2	3	1	2	0.23659	2.00	0.58585	0.50	0.89525	1.00
tr|A0A0A6YY83|A0A0A6YY83_I	Protein Pcdh7 OS=Mus musculus (Mouse)	141.43	1			1	2	1					1		1	3	0	1	0.10292	4.00	0.37390	WT-scr only	0.89308	1.00
sp|Q3TCJ1|F175B_MOUSE	BRISC complex subunit Abro1 OS=Mus mı	250.52	1			1	2					1			1	2	0	1	0.38552	3.00	0.37390	WT-scr only	0.99229	1.00
tr|A0A087WSA6|A0A087WSA6_	Protein Gm7356 OS=Mus musculus (Mous	33.22	1			1		1					1		1	2	0	1	0.53700	2.00	0.37390	WT-scr only	0.89308	1.00
sp|Q9CRD2|EMC2_MOUSE	ER membrane protein complex subunit 2 C	177.35	1				1	1						1	1	2	0	1	0.57091	2.00	0.37390	WT-scr only	0.91525	1.00
sp|Q4V9Z5|SE6L2_MOUSE	Seizure 6-like protein 2 OS=Mus musculus	189.45		1	2	3	3	2	1			2			2	3	1	1	0.08823	2.67	0.36172	0.33	0.71787	0.67
sp|Q8VDQ8|SIR2_MOUSE	NAD-dependent protein deacetylase sirtuin-	353.91		1	1	1	3	1	1			2			2	3	1	1	0.25263	2.50	0.48813	0.50	0.99802	1.00
sp|O70252|HMOX2_MOUSE	Heme oxygenase 2 OS=Mus musculus (Mc	248.91		1		1	2					1			1	2	0	1	0.36933	3.00	0.37390	WT-scr only	0.98315	1.00
sp|Q9CZJ2|HS12B_MOUSE	Heat shock 70 kDa protein 12B OS=Mus ı	109.99		1		1	1						1		1	2	0	1	0.52049	2.00	0.37390	WT-scr only	0.86966	1.00
sp|Q8K212|PACS1_MOUSE	Phosphofurin acidic cluster sorting protein 1	495.39		1		1		1				1			1	2	0	1	0.50939	2.00	0.37390	WT-scr only	0.98315	1.00
tr|Q80XU6|Q80XU6_MOUSE	Ogt protein OS=Mus musculus (Mouse) GN	264.81		1			2	1				1			1	2	0	1	0.38490	3.00	0.37390	WT-scr only	0.98315	1.00
sp|Q6NZC7|S23IP_MOUSE	SEC23-interacting protein OS=Mus muscul	55.87		1			1	1					1		1	2	0	1	0.54185	2.00	0.37390	WT-scr only	0.86966	1.00
sp|Q9CY50|SSRA_MOUSE	Translocon-associated protein subunit alphı	153.4		1			1	1						1	1	2	0	1	0.54185	2.00	0.37390	WT-scr only	0.89145	1.00
sp|Q9CYR6|AGM1_MOUSE	Phosphoacetylglucosamine mutase OS=Mı	177.46			1	2	2	2				1			1	3	0	1	0.01091	6.00	0.37390	WT-scr only	0.98065	1.00
sp|Q8BG18|NECA1_MOUSE	N-terminal EF-hand calcium-binding protein	160.57			1	1	1						1		1	2	0	1	0.56228	2.00	0.37390	WT-scr only	0.90433	1.00
sp|Q9WVA3|BUB3_MOUSE	Mitotic checkpoint protein BUB3 OS=Mus ı	312.05			1		1	3				1			1	2	0	1	0.37362	4.00	0.37390	WT-scr only	0.98065	1.00
sp|Q01279|EGFR_MOUSE	Epidermal growth factor receptor OS=Mus ı	123.5			1			2				1			1	1	0	1	0.71065	2.00	0.37390	WT-scr only	0.98065	1.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q8JZU2|TXTP_MOUSE	Tricarboxylate transport protein, mitochondr	512.45	3	2	3	5	5	6	7		3	1			3	3	2	1	0.00838	2.00	0.76542	1.25	0.00950	0.13
sp|O70589|CSKP_MOUSE	Peripheral plasma membrane protein CASK	912.39	2	2	2	2	3	7	1		5	1	1		3	3	2	2	0.27858	2.00	0.93664	1.00	0.02977	0.33
sp|P47758|SRPRB_MOUSE	Signal recognition particle receptor subunit	246.11	2	1		1	3	2	1	2				1	2	3	2	1	0.31237	2.00	0.93222	1.00	0.44308	0.33
sp|O35551|RABE1_MOUSE	Rab GTPase-binding effector protein 1 OS	628.84	3	1			3	5		2	1		1	1	2	2	2	2	0.51923	2.00	0.86183	0.75	0.62222	0.50
sp|Q6GQT9|NOMO1_MOUSE	Nodal modulator 1 OS=Mus musculus (Mou	400.81	2			2	2		2				1		1	2	1	1	0.54855	2.00	0.96559	1.00	0.75820	0.50
sp|P47708|RP3A_MOUSE	Rabphilin-3A OS=Mus musculus (Mouse) G	427.92	4			5	3			3			1		1	2	1	1	0.56270	2.00	0.91175	0.75	0.54365	0.25
sp|Q9CRY7|GDPD1_MOUSE	Glycerophosphodiester phosphodiesterase	226.72	1	1	1	2	3	2		2	2				3	3	2	0	0.00961	2.33	0.54761	1.33	0.00000	WT-scr only
sp|O70503|DHB12_MOUSE	Very-long-chain 3-oxoacyl-CoA reductase (	426.86	1	1	1	1	3	2	2	1	1			1	3	3	3	1	0.15188	2.00	0.22141	1.33	0.20028	0.33
sp|Q9CQ22|LTOR1_MOUSE	Ragulator complex protein LAMTOR1 OS=ı	121.84	1	1		2	1	1	1	1					2	3	2	0	0.26621	2.00	0.94262	1.00	0.11633	WT-scr only
sp|Q9ERB0|SNP29_MOUSE	Synaptosomal-associated protein 29 OS=ı	138.59	1	1		1	1	2	1	1				1	2	3	2	1	0.24678	2.00	0.94262	1.00	0.63679	0.50
sp|Q3UEB3|PUF60_MOUSE	Poly(U)-binding-splicing factor PUF60 OS=ı	399.98	1	1			2	4	1	1					2	2	2	0	0.34876	3.00	0.94262	1.00	0.11633	WT-scr only
tr|A2AE27|A2AE27_MOUSE	AMP deaminase 2 (Adenosine monophospl	158.14	1			2	2				1				1	2	1	0	0.26285	4.00	0.95504	1.00	0.37390	WT-scr only
sp|Q9CX30|YIF1B_MOUSE	Protein YIF1B OS=Mus musculus (Mouse)	55.28	1			1	1			1					1	2	1	0	0.54855	2.00	0.93674	1.00	0.37390	WT-scr only
sp|Q91VR8|BRK1_MOUSE	Protein BRICK1 OS=Mus musculus (Mouse	75.6	1			1		1		1					1	2	1	0	0.53700	2.00	0.93674	1.00	0.37390	WT-scr only
sp|Q9D823|RL37_MOUSE	60S ribosomal protein L37	32.89	1				2	1		1					1	2	1	0	0.40150	3.00	0.93674	1.00	0.37390	WT-scr only
sp|Q6PAR5|GAPD1_MOUSE	GTPase-activating protein and VPS9 doma	351.26	1				1	1	1						1	2	1	0	0.57091	2.00	0.96559	1.00	0.37390	WT-scr only
sp|Q8BNY6|NCS1_MOUSE	Neuronal calcium sensor 1 OS=Mus muscu	187.27	1				1	1	1						1	2	1	0	0.57091	2.00	0.96559	1.00	0.37390	WT-scr only
sp|Q9EPW0|INP4A_MOUSE	Type I inositol 3,4-bisphosphate 4-phospha	399.55		2	1	2	3	1	2	1	2		1		2	3	3	1	0.29598	2.00	0.30273	1.67	0.45435	0.33
sp|Q9DCT5|SDF2_MOUSE	Stromal cell-derived factor 2 OS=Mus musc	107.73		2	1	1	1	4		1	2	1			2	3	2	1	0.44948	2.00	0.88904	1.00	0.36950	0.33

tr|Q3U6W2|Q3U6W2_MOUSE	Putative uncharacterized protein OS=Mus m	221.34		3		3	3	1	1	1			1		1	3	2	1	0.33495	2.33	0.80603	0.67	0.62696	0.33
sp|Q9D0W5|PPIL1_MOUSE	Peptidyl-prolyl cis-trans isomerase-like 1 OS	116.46		2		3	1	1	3						1	3	1	0	0.35803	2.50	0.80384	1.50	0.37390	WT-scr only
sp|Q8CCT4|TCAL5_MOUSE	Transcription elongation factor A protein-like	213.39		2		3	1	1		2	1		1		1	3	2	1	0.35803	2.50	0.62737	1.50	0.77848	0.50
sp|Q9WUB4|DCTN6_MOUSE	Dynactin subunit 6 OS=Mus musculus (Mou	105.14		1	2	2	2	2	2	1		1			2	3	2	1	0.20621	2.00	0.99928	1.00	0.37685	0.33
sp|Q9DC16|ERGI1_MOUSE	Endoplasmic reticulum-Golgi intermediate co	316.43		1	1	1	2	2		1	2				2	3	2	0	0.10526	2.50	0.56688	1.50	0.11658	WT-scr only
sp|P56387|DYLT3_MOUSE	Dynein light chain Tctex-type 3 OS=Mus mu	202.31		1		1	2	1	1						1	3	1	0	0.09274	4.00	0.99012	1.00	0.37390	WT-scr only
sp|P58802|TB10A_MOUSE	TBC1 domain family member 10A OS=Mus	53.07		1		1	1		1						1	2	1	0	0.52049	2.00	0.99012	1.00	0.37390	WT-scr only
sp|Q9DC07|LNEBL_MOUSE	LIM zinc-binding domain-containing Nebulet	170.97		1			2		1						1	1	1	0	0.69898	2.00	0.99012	1.00	0.37390	WT-scr only
tr|A0A0A6YX97|A0A0A6YX97_I	N-terminal Xaa-Pro-Lys N-methyltransferase	70.32		1			1	1	1						1	2	1	0	0.54185	2.00	0.99012	1.00	0.37390	WT-scr only
sp|Q8R2U4|NTM1A_MOUSE	N-terminal Xaa-Pro-Lys N-methyltransferase	70.32		1			1	1	1						1	2	1	0	0.54185	2.00	0.99012	1.00	0.37390	WT-scr only
sp|P50428|ARSA_MOUSE	Arylsulfatase A OS=Mus musculus (Mouse)	64.57		1			1	1			1				1	2	1	0	0.54185	2.00	0.93075	1.00	0.37390	WT-scr only
tr|E0CXD4|E0CXD4_MOUSE	Protein Pcdh1 OS=Mus musculus (Mouse)	282.94			1	1	1	2	1						1	3	1	0	0.11606	4.00	0.95400	1.00	0.37390	WT-scr only
sp|Q8CJ61|CKLF4_MOUSE	CKLF-like MARVEL transmembrane domain	51.65			1	1	1	1	1						1	3	1	0	0.15088	3.00	0.95400	1.00	0.37390	WT-scr only
tr|Q3TFB5|Q3TFB5_MOUSE	Putative uncharacterized protein OS=Mus m	211.6			1		1	1			1				1	2	1	0	0.58510	2.00	0.96663	1.00	0.37390	WT-scr only
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q80TS3|AGRL3_MOUSE	Adhesion G protein-coupled receptor L3 O	264.18	1	1	1	2	2	3		1				1	3	3	1	1	0.01678	2.33	0.17665	0.33	0.20028	0.33
sp|Q8CH09|SUGP2_MOUSE	SURP and G-patch domain-containing prote	398.17	1			3	1								1	2	0	0	0.36569	4.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9WTX2|PRKRA_MOUSE	Interferon-inducible double-stranded RNA-d	195.12	1			1	2	2							1	3	0	0	0.04762	5.00	0.37390	WT-scr only	0.37390	WT-scr only
tr|Q8BRR9|Q8BRR9_MOUSE	Calcium/calmodulin-dependent 3',5'-cyclic n	413.06	1			1	2	1							1	3	0	0	0.10292	4.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9Z2G6|SE1L1_MOUSE	Protein sel-1 homolog 1 OS=Mus musculus	189.7	1			1	2								1	2	0	0	0.38552	3.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|P41778|PBX1_MOUSE	Pre-B-cell leukemia transcription factor 1 O	176.93	1			1		1							1	2	0	0	0.53700	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|P38585|TTL_MOUSE	Tubulin--tyrosine ligase OS=Mus musculus	39.5	1			1		1							1	2	0	0	0.53700	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8R3Q0|SARAF_MOUSE	Store-operated calcium entry-associated reg	71.56	1				2	1							1	2	0	0	0.40150	3.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8BPG6|SUMF2_MOUSE	Sulfatase-modifying factor 2 OS=Mus musc	38.23	1				1	1							1	2	0	0	0.57091	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|P54823|DDX6_MOUSE	Probable ATP-dependent RNA helicase DD	265.39	1					3							1	1	0	0	0.57687	3.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|O08917|FLOT1_MOUSE	Flotillin-1 OS=Mus musculus (Mouse) GN=F	685.8		2	2	2	2	4		1	1		1		2	3	2	1	0.25424	2.00	0.48650	0.50	0.30667	0.25
sp|Q9Z2Y8|PROSC_MOUSE	Proline synthase co-transcribed bacterial ho	250.11		2		1	5	3			1				1	3	1	0	0.14824	4.50	0.72778	0.50	0.37390	WT-scr only
sp|Q9CQZ6|NDUB3_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	63.25		1	1	2	2		1						2	2	1	0	0.44254	2.00	0.48813	0.50	0.11658	WT-scr only
sp|Q80Z38|SHAN2_MOUSE	SH3 and multiple ankyrin repeat domains pr	124.61		1		3	1								1	2	0	0	0.35674	4.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q8VE99|CC115_MOUSE	Coiled-coil domain-containing protein 115 C	41.51		1		1	1								1	2	0	0	0.52049	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q80TE7|LRRC7_MOUSE	Leucine-rich repeat-containing protein 7 OS	190.38		1			2								1	1	0	0	0.69898	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q80W47|WIPI2_MOUSE	WD repeat domain phosphoinositide-interac	172.5		1			2								1	1	0	0	0.69898	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|P22723|GBRG2_MOUSE	Gamma-aminobutyric acid receptor subunit	162.8		1			1	1							1	2	0	0	0.54185	2.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q9WTX6|CUL1_MOUSE	Cullin-1 OS=Mus musculus (Mouse) GN=Cu	403.02			1	1	2								1	2	0	0	0.39361	3.00	0.37390	WT-scr only	0.37390	WT-scr only
sp|Q6ZPU9|KBP_MOUSE	KIF1-binding protein OS=Mus musculus (M	190.86			1		1	1							1	2	0	0	0.58510	2.00	0.37390	WT-scr only	0.37390	WT-scr only

Proteins mostly identified in the KI-93 sample with ratio>2:

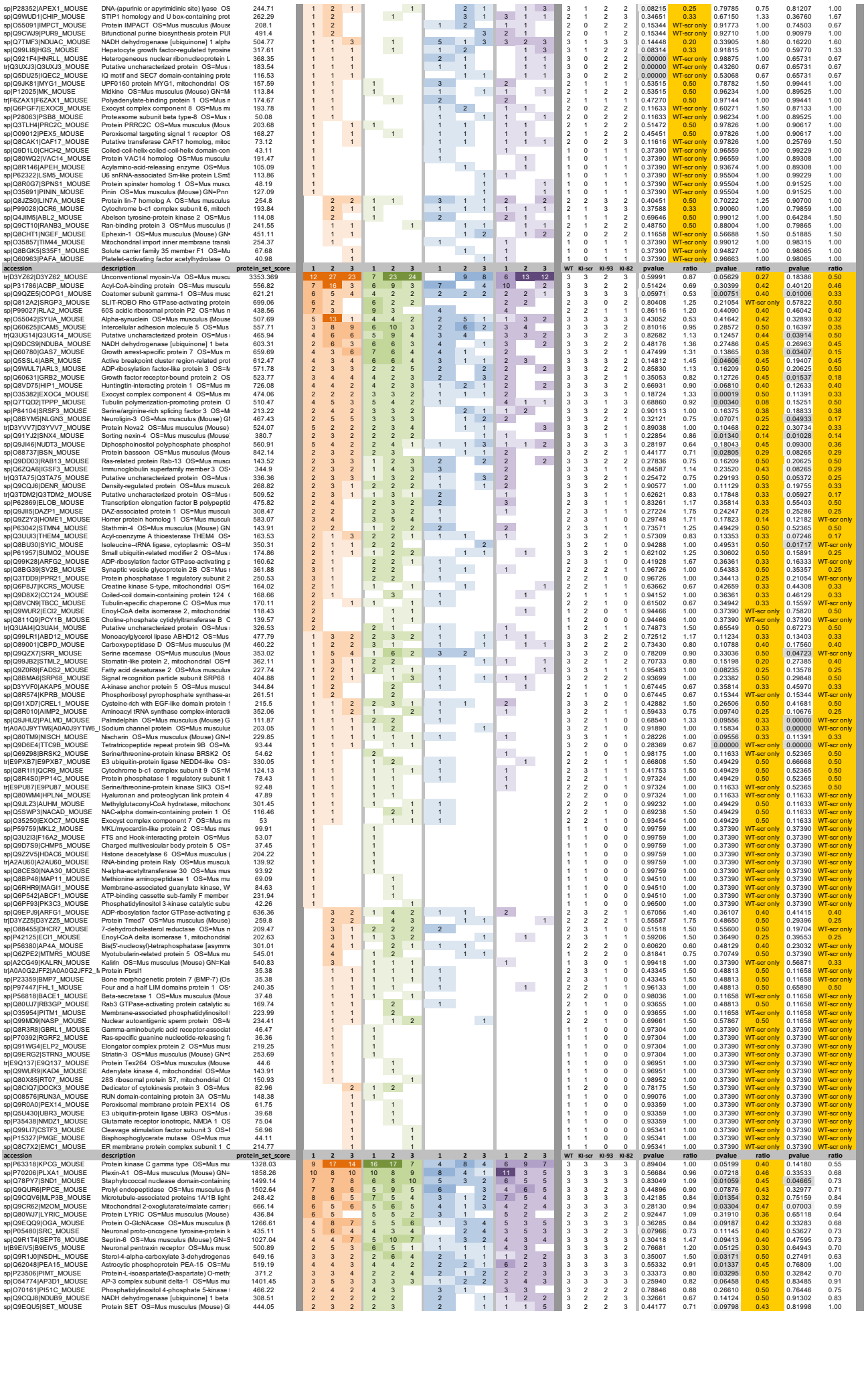
			Exp. from 01/02/2017 BASIC Spectral Count (Proline)												Exp. 01/02/2017									
			WT			KI-scr			KI-93			KI-82			# Repl.				KI-scr / WT-scr		KI-93 / WT-scr		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P46660|AINX_MOUSE	Alpha-internexin OS=Mus musculus (Mouse	1309.38	6	5	3	5	7	6	21	8	13	6	5	6	3	3	3	3	0.32689	1.29	0.03886	3.00	0.12931	1.21
sp|Q91WS0|CISD1_MOUSE	CDGSH iron-sulfur domain-containing protei	404.67	2	4	3	3	6	8	8	5	7	6	2	6	3	3	3	3	0.16887	1.89	0.00890	2.22	0.21518	1.56
sp|P31938|MP2K1_MOUSE	Dual specificity mitogen-activated protein kir	571.47	2	2	4	3	5	4	6	5	5	2	3	4	3	3	3	3	0.26088	1.50	0.01534	2.00	0.50356	1.13
tr|Q3UMG4|Q3UMG4_MOUSE	Putative uncharacterized protein OS=Mus m	569.7	2	2	1	2	2	1	7	2	5	2	1	1	3	3	3	3	0.89897	1.00	0.07916	2.80	0.66877	0.80
sp|P56391|CX6B1_MOUSE	Cytochrome c oxidase subunit 6B1 OS=Mu	219.9	2	1	1	2	2	2	2	5	1	2	3	2	3	3	3	3	0.17262	1.50	0.34593	2.00	0.09596	1.75
sp|P28741|KIF3A_MOUSE	Kinesin-like protein KIF3A OS=Mus muscul	348.42	2	1		1	2	1	3	2	1	1		1	2	3	3	2	0.70279	1.33	0.23766	2.00	0.71791	0.67
sp|Q8BFU3|RN214_MOUSE	RING finger protein 214 OS=Mus musculus	190.4	2	1		1	2		2	2	2	1	1		2	2	3	2	0.95265	1.00	0.13079	2.00	0.73746	0.67
sp|Q3UGC7|EI3JA_MOUSE	Eukaryotic translation initiation factor 3 subu	333.19	2	1			3	2	5	1		2	2		2	2	2	2	0.61288	1.67	0.56615	2.00	0.63223	1.33
sp|Q61187|TS101_MOUSE	Tumor susceptibility gene 101 protein OS=	267.37	2		1	2			2	2	2	2	1	1	2	1	3	3	0.72196	0.67	0.13662	2.00	0.51575	1.33
sp|Q8BH58|TIPRL_MOUSE	TIP41-like protein OS=Mus musculus (Mous	378.86	2		1		2	2	3	2	2	3	1		2	2	3	2	0.80889	1.33	0.08267	2.33	0.72715	1.33
sp|P32020|NLTP_MOUSE	Non-specific lipid-transfer protein OS=Mus m	303.49	2				1	2	3	1	1	1		1	1	2	3	2	0.77885	1.50	0.31339	2.50	0.94727	1.00
sp|P28474|ADHX_MOUSE	Alcohol dehydrogenase class-3 OS=Mus m	639.42	1	2	2	1	3	4	4	2	5	3		5	3	3	3	2	0.38920	1.60	0.09129	2.20	0.49592	1.60
tr|D3Z0V2|D3Z0V2_MOUSE	Rho guanine nucleotide exchange factor 7	470.12	1	2	1	1	2	3		5	3		4	2	3	3	2	2	0.40372	1.50	0.37500	2.00	0.48680	1.50
sp|O88952|LIN7C_MOUSE	Protein lin-7 homolog C OS=Mus musculus	398.28	1	3		1	2		5	2	2	2		2	2	2	3	2	0.73944	0.75	0.21066	2.25	0.89769	1.00
sp|Q922Q8|LRC59_MOUSE	Leucine-rich repeat-containing protein 59 C	538.19	1	1	5	5	3	3	6	3	5	4	2	3	3	3	3	3	0.50272	1.57	0.18854	2.00	0.54694	1.29
sp|Q8BL86|MBLC2_MOUSE	Metallo-beta-lactamase domain-containing p	309.08	1	1				2	1	2	3	1	1	1	2	1	3	3	0.97067	1.00	0.11557	3.00	0.22632	1.50
sp|A2AN08|UBR4_MOUSE	E3 ubiquitin-protein ligase UBR4 OS=Mus m	623.68	1		2	1	2	1	5	2	2	2			2	3	3	1	0.73911	1.33	0.11638	3.00	0.70616	0.67
sp|P26369|U2AF2_MOUSE	Splicing factor U2AF 65 kDa subunit OS=M	280.7	1			1			2		1			1	1	1	2	1	0.99759	1.00	0.36273	3.00	0.91525	1.00
sp|Q9JIX8|ACINU_MOUSE	Apoptotic chromatin condensation inducer i	94.28	1			1				1	1	1			1	1	2	1	0.99759	1.00	0.46107	2.00	0.99229	1.00
tr|Q9D4I9|Q9D4I9_MOUSE	RAB23, member RAS oncogene family, isof	258.62	1				1		2			1			1	1	1	1	0.94510	1.00	0.70178	2.00	0.99229	1.00
sp|Q9Z2W9|GRIA3_MOUSE	Glutamate receptor 3 OS=Mus musculus (M	294.11	1					1	1	1		1			1	1	2	1	0.96500	1.00	0.50267	2.00	0.99229	1.00
sp|Q9D2R0|AACS_MOUSE	Acetoacetyl-CoA synthetase OS=Mus musc	277.3		2			2	1	1	3	1		1	2	1	2	3	2	0.75363	1.50	0.31473	2.50	0.58254	1.50
sp|Q99PV0|PRP8_MOUSE	Pre-mRNA-processing-splicing factor 8 OS=	480.33		1	1	1	1	1	2	1	1	1	1		2	3	3	2	0.43345	1.50	0.16684	2.00	0.88294	1.00
sp|P62315|SMD1_MOUSE	Small nuclear ribonucleoprotein Sm D1 OS	99.72		1	1	1	1	1	2	1	1	1		1	2	3	3	2	0.43345	1.50	0.16684	2.00	0.90700	1.00
tr|Q923F1|Q923F1_MOUSE	Chloride channel, nucleotide-sensitive, 1A	165.86		1	1		1	2	2	1	1		1	1	2	2	3	2	0.69661	1.50	0.16684	2.00	0.79865	1.00
sp|Q80UM3|NAA15_MOUSE	N-alpha-acetyltransferase 15, NatA auxiliary	336.49		1	1			2	3		1	2	1		2	1	2	2	0.96289	1.00	0.50782	2.00	0.57240	1.50
sp|Q9WUP7|UCHL5_MOUSE	Ubiquitin carboxyl-terminal hydrolase isozym	225.56		1		1			1		1			1	1	1	2	1	0.97304	1.00	0.48634	2.00	0.89145	1.00
sp|Q7TPD3|ROBO2_MOUSE	Roundabout homolog 2 OS=Mus musculus	114.5		1			1				2			1	1	1	1	1	0.96951	1.00	0.63418	2.00	0.89145	1.00
sp|Q8BLR2|CPNE4_MOUSE	Copine-4 OS=Mus musculus (Mouse) GN=C	414.86			4	2	3	1	3	3	2	2	2	1	1	3	3	3	0.73910	1.50	0.36767	2.00	0.73963	1.25
sp|Q9WV80|SNX1_MOUSE	Sorting nexin-1 OS=Mus musculus (Mouse)	336.04			3		2	2	1	2	3	1	1		1	2	3	2	0.87320	1.33	0.40821	2.00	0.80656	0.67
sp|P48036|ANXA5_MOUSE	Annexin A5 OS=Mus musculus (Mouse) GN	365.26			1	1			3	1			1		1	1	2	1	0.99076	1.00	0.33372	4.00	0.90433	1.00
sp|Q8BT60|CPNE3_MOUSE	Copine-3 OS=Mus musculus (Mouse) GN=C	86.54			1			1		1	2			1	1	1	2	1	0.95341	1.00	0.34732	3.00	0.92666	1.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P46664|PURA2_MOUSE	Adenylosuccinate synthetase isozyme 2 O	554.18	2		2		1		2	4	3		4	3	2	1	3	2	0.22878	0.25	0.13999	2.25	0.41484	1.75
sp|O54879|HMGB3_MOUSE	High mobility group protein B3 OS=Mus mu	237.07	1	1		1			1	1	2			2	2	1	3	1	0.53515	0.50	0.20567	2.00	0.88421	1.00
sp|P70699|LYAG_MOUSE	Lysosomal alpha-glucosidase OS=Mus mus	291.5	1		1		1		2	2	2		2	1	2	1	3	2	0.45451	0.50	0.01606	3.00	0.53252	1.50
sp|Q8BL97|SRSF7_MOUSE	Serine/arginine-rich splicing factor 7 OS=M	294.86	1		1			1	2		4			2	2	1	2	1	0.47466	0.50	0.34323	3.00	0.90433	1.00
sp|P29595|NEDD8_MOUSE	NEDD8 OS=Mus musculus (Mouse) GN=Ne	61.89	1						2	1		1			1	0	2	1	0.37390	WT-scr only	0.35515	3.00	0.99229	1.00
sp|Q640R3|HECAM_MOUSE	Hepatocyte cell adhesion molecule OS=Mu	127.91	1						1	1			1		1	0	2	1	0.37390	WT-scr only	0.50267	2.00	0.89308	1.00
sp|Q8CJG0|AGO2_MOUSE	Protein argonaute-2 OS=Mus musculus (M	201.16		1	1				4	1	2			2	2	0	3	1	0.11658	WT-scr only	0.11114	3.50	0.89087	1.00
sp|Q9QZC2|PLXC1_MOUSE	Plexin-C1 OS=Mus musculus (Mouse) GN=	442		1	1				2	1	1	2	1		2	0	3	2	0.11658	WT-scr only	0.16684	2.00	0.57240	1.50
sp|Q99N87|RT05_MOUSE	28S ribosomal protein S5, mitochondrial O	126.81			2					2	2	2			1	0	2	1	0.37390	WT-scr only	0.47285	2.00	0.98065	1.00
sp|Q9Z140|CPNE6_MOUSE	Copine-6 OS=Mus musculus (Mouse) GN=C	147.61			1					1	2			1	1	0	2	1	0.37390	WT-scr only	0.34732	3.00	0.92666	1.00
sp|Q8JZW4|CPNE5_MOUSE	Copine-5 OS=Mus musculus (Mouse) GN=C	84.25			1					1	1			1	1	0	2	1	0.37390	WT-scr only	0.47285	2.00	0.92666	1.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q9WTL7|LYPA2_MOUSE	Acyl-protein thioesterase 2 OS=Mus muscu	316.42	1		1			1	1	2	1			1	2	1	3	1	0.47466	0.50	0.23261	2.00	0.61367	0.50
sp|A2BDX3|MOCS3_MOUSE	Adenylyltransferase and sulfurtransferase M	38.7	1						2						1	0	1	0	0.37390	WT-scr only	0.70178	2.00	0.37390	WT-scr only
sp|Q6P5H2|NEST_MOUSE	Nestin OS=Mus musculus (Mouse) GN=Nes	483.38	1						2						1	0	1	0	0.37390	WT-scr only	0.70178	2.00	0.37390	WT-scr only
sp|Q8C1W1|VASH1_MOUSE	Vasohibin-1 OS=Mus musculus (Mouse) GN	59.61	1						1	1	1				1	0	3	0	0.37390	WT-scr only	0.10121	3.00	0.37390	WT-scr only
sp|Q8BHL3|TB10B_MOUSE	TBC1 domain family member 10B OS=Mus	166.06	1							1	1				1	0	2	0	0.37390	WT-scr only	0.46107	2.00	0.37390	WT-scr only
sp|Q8CF66|LTOR4_MOUSE	Ragulator complex protein LAMTOR4 OS=M	61.26	1							1	1				1	0	2	0	0.37390	WT-scr only	0.46107	2.00	0.37390	WT-scr only
sp|P0C192|LRC4B_MOUSE	Leucine-rich repeat-containing protein 4B C	68.54		1					2						1	0	1	0	0.37390	WT-scr only	0.68457	2.00	0.37390	WT-scr only
sp|Q9D6Z1|NOP56_MOUSE	Nucleolar protein 56 OS=Mus musculus (M	315.77			1				3						1	0	1	0	0.37390	WT-scr only	0.58200	3.00	0.37390	WT-scr only
sp|Q61137|ASTN1_MOUSE	Astrotactin-1 OS=Mus musculus (Mouse) G	224.66			1				1		1				1	0	2	0	0.37390	WT-scr only	0.52560	2.00	0.37390	WT-scr only
sp|Q80VL1|TDRKH_MOUSE	Tudor and KH domain-containing protein C	246.31			1				1		1				1	0	2	0	0.37390	WT-scr only	0.52560	2.00	0.37390	WT-scr only
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q3ULD5|MCCB_MOUSE	Methylcrotonoyl-CoA carboxylase beta chai	343.46	1	1		1	1	1	3	1					2	3	2	0	0.41753	1.50	0.49395	2.00	0.11633	WT-scr only
sp|P97355|SPSY_MOUSE	Spermine synthase OS=Mus musculus (Mo	632.49	1		2	1	1		5	1	3		1		2	2	3	1	0.60186	0.67	0.16643	3.00	0.44622	0.33
sp|Q9WTP6|KAD2_MOUSE	Adenylate kinase 2, mitochondrial OS=Mus	232.03	1		2		1	3	5	1	3	1			2	2	3	1	0.83806	1.33	0.16643	3.00	0.36710	0.33
sp|Q07113|MPRI_MOUSE	Cation-independent mannose-6-phosphate	108.34	1			1			1	1					1	1	2	0	0.99759	1.00	0.50267	2.00	0.37390	WT-scr only
sp|Q2TBE6|P4K2A_MOUSE	Phosphatidylinositol 4-kinase type 2-alpha	45.59	1			1			1	1					1	1	2	0	0.99759	1.00	0.50267	2.00	0.37390	WT-scr only
sp|Q8K0D5|EFGM_MOUSE	Elongation factor G, mitochondrial OS=Mus	35.91	1			1			1		1				1	1	2	0	0.99759	1.00	0.51266	2.00	0.37390	WT-scr only
sp|P35293|RAB18_MOUSE	Ras-related protein Rab-18 OS=Mus muscu	319.46		1	1	1	1	1	2		2	1			2	3	2	1	0.43345	1.50	0.41247	2.00	0.51712	0.50
sp|Q8K009|AL1L2_MOUSE	Mitochondrial 10-formyltetrahydrofolate deh	222.46		1	1		2		2	1	1				2	1	3	0	0.93655	1.00	0.16684	2.00	0.11658	WT-scr only
sp|Q5DTT2|PSD1_MOUSE	PH and SEC7 domain-containing protein 1	228.94		1		1			2						1	1	1	0	0.97304	1.00	0.68457	2.00	0.37390	WT-scr only

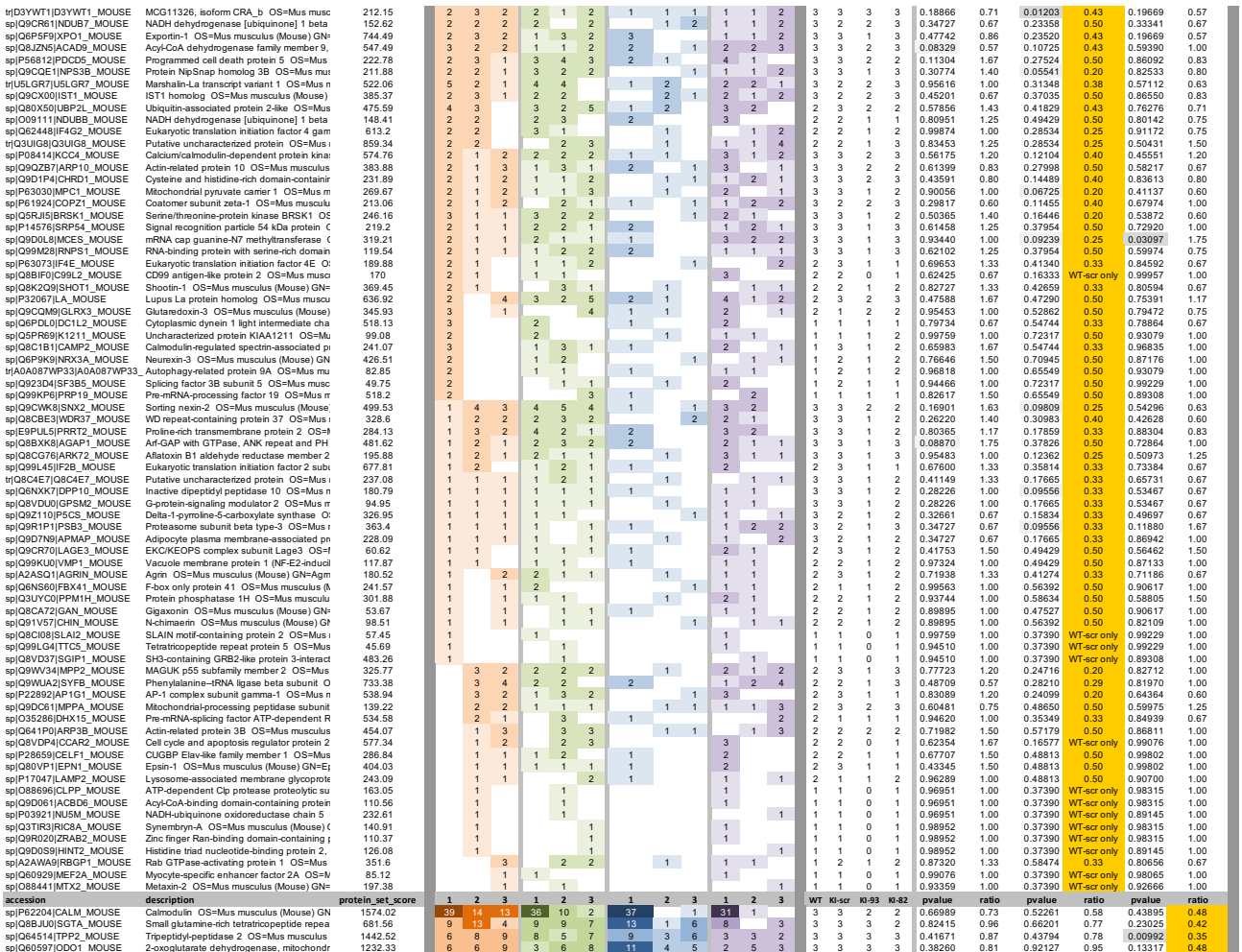
Proteins mostly identified in the KI-82 sample with ratio>2:

			Exp. from 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		KI-82 / WT-scr	
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P00493|HPRT_MOUSE	Hypoxanthine-guanine phosphoribosyltrans	528.96	2	2	2	1	4	4	3	2	1	4	4	5	3	3	3	3	0.42039	1.50	0.90182	1.00	0.00639	2.17
tr|Q3TDR9|Q3TDR9_MOUSE	Putative uncharacterized protein OS=Mus m	367.75	2			1	2				2	2	1	3	1	2	1	3	0.76646	1.50	0.95504	1.00	0.17290	3.00
sp|Q80UG5|SEPT9_MOUSE	Septin-9 OS=Mus musculus (Mouse) GN=S	455.56	2			1	1				2	2		3	1	2	1	2	0.96818	1.00	0.95504	1.00	0.39305	2.50
sp|O08579|EMD_MOUSE	Emerin OS=Mus musculus (Mouse) GN=Em	160.69	1	1			3		1		2	2	2		2	1	2	2	0.80728	1.50	0.61499	1.50	0.37128	2.00
sp|Q9D0T1|NH2L1_MOUSE	NHP2-like protein 1 OS=Mus musculus (Mo	118.93	1	1			1	1	1		1	1	2	1	2	2	2	3	0.93454	1.00	0.96234	1.00	0.19155	2.00
sp|Q3UH60|DIP2B_MOUSE	Disco-interacting protein 2 homolog B OS=	205.63	1			1				1		1	1		1	1	1	2	0.99759	1.00	0.93674	1.00	0.46591	2.00
sp|Q8CAE9|PDXL2_MOUSE	Podocalyxin-like protein 2 OS=Mus muscul	140.65	1			1					1	2	1	1	1	1	1	3	0.99759	1.00	0.95504	1.00	0.05581	4.00
tr|F7CFL3|F7CFL3_MOUSE	2'-5'-oligoadenylate synthase 2 (Fragment)	31.79	1			1					1		1	1	1	1	1	2	0.99759	1.00	0.95504	1.00	0.42068	2.00
tr|A2A5R8|A2A5R8_MOUSE	Double-stranded RNA-binding protein Stauf	181.48	1					1	1			1	1		1	1	1	2	0.96500	1.00	0.96559	1.00	0.46591	2.00
sp|A2ARZ3|FSIP2_MOUSE	Fibrous sheath-interacting protein 2	32.24	1					1			1		1	1	1	1	1	2	0.96500	1.00	0.95504	1.00	0.42068	2.00
tr|E9QPE7|E9QPE7_MOUSE	Myosin-11 OS=Mus musculus (Mouse) GN=	687.52		4	2	2	4	3	3	3	4	3	4	6	2	3	3	3	0.51498	1.50	0.26030	1.67	0.13552	2.17
sp|Q8VDD5|MYH9_MOUSE	Myosin-9 OS=Mus musculus (Mouse) GN=M	1996.37		4	4		7	8	2	3	5	3	4	11	2	2	3	3	0.50344	1.88	0.60859	1.25	0.26601	2.25
tr|G3UY52|G3UY52_MOUSE	Probable ubiquitin carboxyl-terminal hydrola	251.57		1		1			1			2			1	1	1	1	0.97304	1.00	0.99012	1.00	0.66673	2.00
tr|Q3TF18|Q3TF18_MOUSE	Poly [ADP-ribose] polymerase OS=Mus mu	164.46			2	1		1		1	2	2	1	1	1	2	2	3	0.96562	1.00	0.67399	1.50	0.34675	2.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q8R105|VP37C_MOUSE	Vacuolar protein sorting-associated protein	121.11	1						1			1		1	1	0	1	2	0.37390	WT-scr only	0.96559	1.00	0.47715	2.00
sp|B2RQC6|PYR1_MOUSE	CAD protein OS=Mus musculus (Mouse) GN	300.68	1						1				1	2	1	0	1	2	0.37390	WT-scr only	0.96559	1.00	0.31942	3.00
sp|Q9WV54|ASAH1_MOUSE	Acid ceramidase OS=Mus musculus (Mouse	291.12		1	1	1				1	2	1	2	2	2	1	2	3	0.52850	0.50	0.56688	1.50	0.09234	2.50
tr|E9PUF2|E9PUF2_MOUSE	Disks large-associated protein 4 OS=Mus m	168.58		1					1			2			1	0	1	1	0.37390	WT-scr only	0.99012	1.00	0.66673	2.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|Q61831|MK10_MOUSE	Mitogen-activated protein kinase 10 OS=M	199.65	1									1	1		1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.46591	2.00
sp|Q3UIZ8|MYLK3_MOUSE	Myosin light chain kinase 3 OS=Mus muscu	43.98	1									1	1		1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.46591	2.00
sp|Q6PDN3|MYLK_MOUSE	Myosin light chain kinase, smooth muscle C	43.98	1									1	1		1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.46591	2.00
sp|Q922Y1|UBXN1_MOUSE	UBX domain-containing protein 1 OS=Mus	79.92	1										1	1	1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.42068	2.00
sp|A2RT62|FXL16_MOUSE	F-box/LRR-repeat protein 16 OS=Mus mus	234.46		1								1		1	1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.45272	2.00
sp|Q08943|SSRP1_MOUSE	FACT complex subunit SSRP1 OS=Mus mu	67.52			1								1	1	1	0	0	2	0.37390	WT-scr only	0.37390	WT-scr only	0.43133	2.00
accession	**description**	**protein_set_score**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**WT**	**KI-scr**	**KI-93**	**KI-82**	**pvalue**	**ratio**	**pvalue**	**ratio**	**pvalue**	**ratio**
sp|P61079|UB2D3_MOUSE	Ubiquitin-conjugating enzyme E2 D3 OS=M	252.88	1	1		1	2		1			2	1	1	2	2	1	3	0.66808	1.50	0.49429	0.50	0.12430	2.00
sp|P70288|HDAC2_MOUSE	Histone deacetylase 2 OS=Mus musculus (	219.87	1	1		1		1			1	3		2	2	2	1	2	0.99232	1.00	0.58585	0.50	0.30865	2.50
sp|Q8CH25|SLTM_MOUSE	SAFB-like transcription modulator OS=Mus	128.08	1				1					2			1	1	0	1	0.94510	1.00	0.37390	WT-scr only	0.68309	2.00
sp|P62320|SMD3_MOUSE	Small nuclear ribonucleoprotein Sm D3 OS	188.02	1					1				1	2	2	1	1	0	3	0.96500	1.00	0.37390	WT-scr only	0.05091	5.00
sp|Q80U78|PUM1_MOUSE	Pumilio homolog 1 OS=Mus musculus (Mou	170.22		1	2	1	1	3			1	2	1	3	2	3	1	3	0.54066	1.67	0.41024	0.33	0.23929	2.00
sp|Q60634|FLOT2_MOUSE	Flotillin-2 OS=Mus musculus (Mouse) GN=F	652.07		1	1	1	1					2	3		2	2	0	2	0.96133	1.00	0.11658	WT-scr only	0.33304	2.50

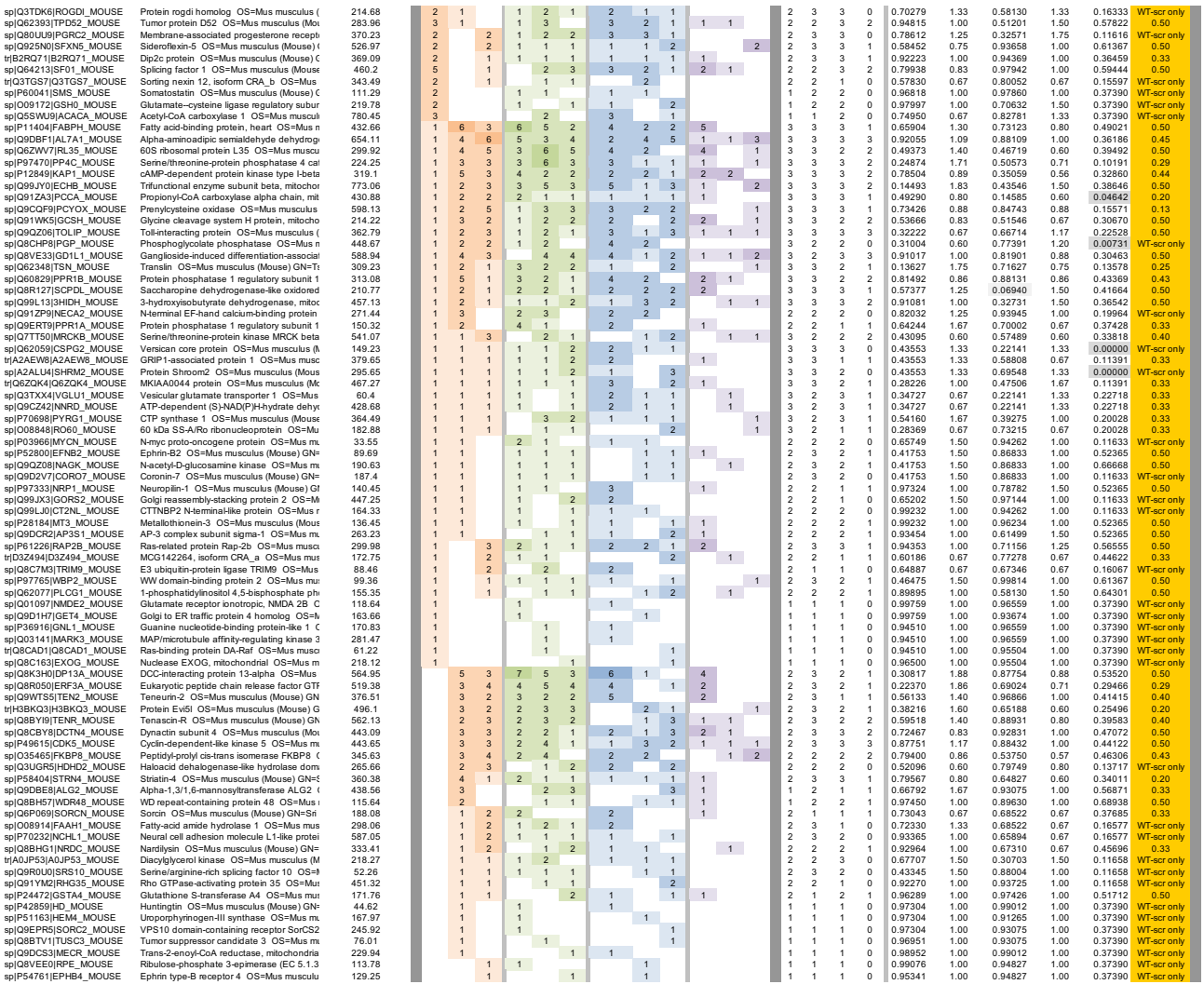
Proteins mostly identified in the WT-scr sample with ratio>2:

			Exp. from 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		KI-82 / WT-scr	
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q61584|FXR1_MOUSE	Fragile X mental retardation syndrome-relat	388.27	4	5	4	2	2	2	2	1	3	2	1		3	3	3	2	0.00068	0.46	0.03085	0.46	0.00670	0.23
sp|Q8BIE6|FRM4A_MOUSE	FERM domain-containing protein 4A OS=M	428.9	2	3	3	3	1		2	1	1	1		1	3	2	3	2	0.23205	0.50	0.03679	0.50	0.01711	0.25
sp|Q922S4|PDE2A_MOUSE	cGMP-dependent 3',5'-cyclic phosphodieste	988.71	4	3	3	3	1		3	1		3	2		3	2	2	2	0.10475	0.40	0.08785	0.40	0.19818	0.50
sp|Q0KL02|TRIO_MOUSE	Triple functional domain protein OS=Mus m	908.7	2	4	2	2	1				1	2	1	1	3	2	1	3	0.11903	0.38	0.03215	0.13	0.14884	0.50
sp|P61971|NTF2_MOUSE	Nuclear transport factor 2 OS=Mus muscul	192.49	3	3	2	2		2	1		2	2			3	2	2	1	0.13305	0.50	0.08380	0.38	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		3	3	1	2	0.09015	0.40	0.03673	0.10	0.05527	0.20
tr|A2AJ72|A2AJ72_MOUSE	MCG130458 OS=Mus musculus (Mouse) G	328.13	3	3	1	2			1	1	1		1	1	3	1	3	2	0.15360	0.29	0.12395	0.43	0.11812	0.29
sp|Q9DAK9|PHP14_MOUSE	14 kDa phosphohistidine phosphatase OS	347.93	2	3	1	1	1				1	2			3	2	1	1	0.09923	0.33	0.06798	0.17	0.19755	0.33
sp|Q8C996|TM163_MOUSE	Transmembrane protein 163 OS=Mus mus	136.74	2	2		1			1	1		1			2	1	2	1	0.25703	0.25	0.45227	0.50	0.25286	0.25
sp|Q9JL56|GDE1_MOUSE	Glycerophosphodiester phosphodiesterase	167.97	3	1	2	1	2				1		1		3	2	1	1	0.24833	0.50	0.07761	0.17	0.09121	0.17
sp|B9EJA2|CTTB2_MOUSE	Cortactin-binding protein 2 OS=Mus muscu	402.27	2	1	1	1	1		1			1			3	2	1	1	0.21150	0.50	0.09239	0.25	0.10176	0.25
sp|P63248|IPKA_MOUSE	cAMP-dependent protein kinase inhibitor al	143.27	2	1	1	1		1	1		1	1			3	2	2	1	0.22060	0.50	0.24653	0.50	0.10176	0.25
sp|Q8R5H1|UBP15_MOUSE	Ubiquitin carboxyl-terminal hydrolase 15 OS	83.16	2	1		1									2	1	0	0	0.38533	0.33	0.16333	WT-scr only	0.16333	WT-scr only
sp|Q9QZF2|GPC1_MOUSE	Glypican-1 OS=Mus musculus (Mouse) GN	155.85	2	1			1		1				1		2	1	1	1	0.35241	0.33	0.36361	0.33	0.46129	0.33
sp|Q9Z2I8|SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit	122.85	2			1			1						1	1	1	0	0.67949	0.50	0.65549	0.50	0.37390	WT-scr only
sp|Q8CCS6|PABP2_MOUSE	Polyadenylate-binding protein 2 OS=Mus n	171.28	2			1				1			1		1	1	1	1	0.67949	0.50	0.72317	0.50	0.75820	0.50
sp|Q3UH66|WNK2_MOUSE	Serine/threonine-protein kinase WNK2 OS	114.95	2				1			1					1	1	1	0	0.64280	0.50	0.72317	0.50	0.37390	WT-scr only
sp|Q9JKN6|NOVA1_MOUSE	RNA-binding protein Nova-1 OS=Mus musc	174.86	2				1							1	1	1	0	1	0.64280	0.50	0.37390	WT-scr only	0.73999	0.50
sp|Q4KMM3|OXR1_MOUSE	Oxidation resistance protein 1 OS=Mus mu	240.26	2							1					1	0	1	0	0.37390	WT-scr only	0.72317	0.50	0.37390	WT-scr only
sp|Q80YA9|CNKR2_MOUSE	Connector enhancer of kinase suppressor c	160.91	2									1			1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.67273	0.50
sp|Q91VE0|S27A4_MOUSE	Long-chain fatty acid transport protein 4 O	452.26	1	3	5	3				2	1		1		3	1	2	1	0.27070	0.33	0.23817	0.33	0.10906	0.11
sp|Q69ZK9|NLGN2_MOUSE	Neuroligin-2 OS=Mus musculus (Mouse) G	305.09	1	2	2		1	1							3	2	0	0	0.08162	0.40	0.00731	WT-scr only	0.00731	WT-scr only
sp|Q3UHB8|CC177_MOUSE	Coiled-coil domain-containing protein 177	119.63	1	2	1					1	1				3	0	2	0	0.01192	WT-scr only	0.29553	0.50	0.01192	WT-scr only
sp|Q8CDG3|VCIP1_MOUSE	Deubiquitinating protein VCIP135 OS=Mus	166.04	1	2		1							1		2	1	0	1	0.38072	0.33	0.15344	WT-scr only	0.45970	0.33
sp|Q8BYA0|TBCD_MOUSE	Tubulin-specific chaperone D OS=Mus mus	353.14	1	2					1						2	0	1	0	0.15344	WT-scr only	0.35814	0.33	0.15344	WT-scr only
sp|P70245|EBP_MOUSE	3-beta-hydroxysteroid-Delta(8),Delta(7)-isom	47.77	1	1	1	1			1						3	1	1	0	0.12156	0.33	0.09556	0.33	0.00000	WT-scr only
sp|Q6PE01|SNR40_MOUSE	U5 small nuclear ribonucleoprotein 40 kDa	63.25	1	1		1			1						2	1	1	0	0.53515	0.50	0.49429	0.50	0.11633	WT-scr only
tr|F8VPP8|F8VPP8_MOUSE	Protein Zc3h7b OS=Mus musculus (Mouse	55.32	1	1		1			1						2	1	1	0	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		2	1	1	1	0.53515	0.50	0.60884	0.50	0.66668	0.50
sp|Q9D7A8|ARMC1_MOUSE	Armadillo repeat-containing protein 1 OS=	106.85	1	1		1				1			1		2	1	1	1	0.53515	0.50	0.60884	0.50	0.66668	0.50
tr|F7CB97|F7CB97_MOUSE	CAP-Gly domain-containing linker protein 1	201.92	1	1			1		1			1			2	1	1	1	0.47270	0.50	0.49429	0.50	0.52365	0.50
sp|Q5SSM3|RHG44_MOUSE	Rho GTPase-activating protein 44 OS=Mus	336.04	1	1				1	1						2	1	1	0	0.49365	0.50	0.49429	0.50	0.11633	WT-scr only
sp|Q99KN9|EPN4_MOUSE	Clathrin interactor 1 OS=Mus musculus (Mo	164.74	1	1				1							2	1	0	0	0.49365	0.50	0.11633	WT-scr only	0.11633	WT-scr only
sp|Q5F2E8|TAOK1_MOUSE	Serine/threonine-protein kinase TAO1 OS=	69.25	1	1										1	2	0	0	1	0.11633	WT-scr only	0.11633	WT-scr only	0.63679	0.50
sp|Q6P5U7|NWD2_MOUSE	NACHT and WD repeat domain-containing	154.66	1		2		1		1				1		2	1	1	1	0.34146	0.33	0.35219	0.33	0.44622	0.33
sp|Q8BTY2|S4A7_MOUSE	Sodium bicarbonate cotransporter 3 OS=M	55.15	1		1	1				1					2	1	1	0	0.51472	0.50	0.58634	0.50	0.11616	WT-scr only
sp|Q99KX1|MLF2_MOUSE	Myeloid leukemia factor 2 OS=Mus muscul	129.99	1		1	1				1					2	1	1	0	0.51472	0.50	0.58634	0.50	0.11616	WT-scr only
sp|Q6PB93|GALT2_MOUSE	Polypeptide N-acetylgalactosaminyltransfera	84.93	1		1		1		1						2	1	1	0	0.45451	0.50	0.47527	0.50	0.11616	WT-scr only
sp|Q6TEK5|VKORL_MOUSE	Vitamin K epoxide reductase complex subu	106.69	1		1			1			1			1	2	1	1	1	0.47466	0.50	0.56392	0.50	0.61367	0.50
sp|P52795|EFNB1_MOUSE	Ephrin-B1 OS=Mus musculus (Mouse) GN=	38.54	1		1								1		2	0	0	1	0.11616	WT-scr only	0.11616	WT-scr only	0.64301	0.50
sp|O89112|LANC1_MOUSE	LanC-like protein 1 OS=Mus musculus (Mo	244.51		2	2	2			1			1	1		2	1	1	2	0.52850	0.50	0.24057	0.25	0.48711	0.50
sp|Q922Q4|P5CR2_MOUSE	Pyrroline-5-carboxylate reductase 2 OS=M	135.56		3	1	2			1					1	2	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			2	0	1	1	0.15120	WT-scr only	0.35349	0.33	0.36950	0.33
tr|D3Z4C5|D3Z4C5_MOUSE	Protein Celf5 OS=Mus musculus (Mouse) G	123.27		2		1									1	1	0	0	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		2				1					1		1	1	0	1	0.67090	0.50	0.37390	WT-scr only	0.77848	0.50
sp|Q03958|PFD6_MOUSE	Prefoldin subunit 6 OS=Mus musculus (Mo	114.15		2						1				1	1	0	1	1	0.37390	WT-scr only	0.74208	0.50	0.75958	0.50
sp|O54833|CSK22_MOUSE	Casein kinase II subunit alpha' OS=Mus m	254.63		1	1	1				1					2	1	1	0	0.52850	0.50	0.60146	0.50	0.11658	WT-scr only
sp|P62482|KCAB2_MOUSE	Voltage-gated potassium channel subunit b	144.26		1	1	1					1				2	1	1	0	0.52850	0.50	0.57867	0.50	0.11658	WT-scr only
sp|Q922Q1|MARC2_MOUSE	Mitochondrial amidoxime reducing compone	229.77		1	1	1						1			2	1	0	1	0.52850	0.50	0.11658	WT-scr only	0.51712	0.50
sp|O89079|COPE_MOUSE	Coatomer subunit epsilon OS=Mus muscul	253.82		1	1		1				1				2	1	1	0	0.46682	0.50	0.57867	0.50	0.11658	WT-scr only
sp|Q6A4J8|UBP7_MOUSE	Ubiquitin carboxyl-terminal hydrolase 7 OS	493.04		1	1			1				1			2	1	0	1	0.48750	0.50	0.11658	WT-scr only	0.51712	0.50
sp|Q64133|AOFA_MOUSE	Amine oxidase [flavin-containing] A OS=M	328.41		1	1			1							2	1	0	0	0.48750	0.50	0.11658	WT-scr only	0.11658	WT-scr only
tr|M0QWJ9|M0QWJ9_MOUSE	Protein Tmem178b OS=Mus musculus (Mo	64.67		1	1						1				2	0	1	0	0.11658	WT-scr only	0.57867	0.50	0.11658	WT-scr only
sp|Q80UK0|SESD1_MOUSE	SEC14 domain and spectrin repeat-contain	328.02		1	1							1			2	0	0	1	0.11658	WT-scr only	0.11658	WT-scr only	0.51712	0.50
sp|Q9CU62|SMC1A_MOUSE	Structural maintenance of chromosomes pr	144.72			2						1			1	1	0	1	1	0.37390	WT-scr only	0.70103	0.50	0.73096	0.50
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|P20108|PRDX3_MOUSE	Thioredoxin-dependent peroxide reductase	392.18	5	5	4	2	3	2	5		2	5	1	3	3	3	2	3	0.00297	0.50	0.16642	0.50	0.27848	0.64
sp|P70207|PLXA2_MOUSE	Plexin-A2 OS=Mus musculus (Mouse) GN=	964.64	3	4	5	2	2	1	3	1		3	3	2	3	3	2	3	0.02641	0.42	0.05967	0.33	0.24723	0.67
sp|Q8BNU0|ARMC6_MOUSE	Armadillo repeat-containing protein 6 OS=	612.99	2	1	3	2	1		1		1	2	2	1	3	2	2	3	0.28565	0.50	0.12914	0.33	0.85344	0.83
sp|O09131|GSTO1_MOUSE	Glutathione S-transferase omega-1 OS=M	476.48	3	1			2		2			5			2	1	1	1	0.53917	0.50	0.55685	0.50	0.87043	1.25
tr|B1APX2|B1APX2_MOUSE	Protein 5031439G07Rik OS=Mus musculu	174.34	2	1			1		1			2	1		2	1	1	2	0.35241	0.33	0.36361	0.33	0.92559	1.00
sp|Q9DD18|DTD1_MOUSE	D-tyrosyl-tRNA(Tyr) deacylase 1 OS=Mus m	178.34	2			1			1			2			1	1	1	1	0.67949	0.50	0.65549	0.50	0.99229	1.00
sp|Q8BFQ8|PDDC1_MOUSE	Parkinson disease 7 domain-containing pro	214.55	1	1	2	2				1	1		1	2	3	1	2	2	0.43114	0.50	0.31108	0.50	0.86295	0.75
sp|Q8JZM4|DNER_MOUSE	Delta and Notch-like epidermal growth facto	159.66	1	1	1	1				1			2		3	1	1	1	0.12156	0.33	0.17665	0.33	0.84141	0.67
tr|Q3TLE4|Q3TLE4_MOUSE	Putative uncharacterized protein OS=Mus	181.58	1	1		1			1			1	2		2	1	1	2	0.53515	0.50	0.49429	0.50	0.56221	1.50
sp|Q922J9|FACR1_MOUSE	Fatty acyl-CoA reductase 1 OS=Mus muscu	108.11	1	1		1			1				1	1	2	1	1	2	0.53515	0.50	0.49429	0.50	0.78745	1.00
tr|Q7TNY3|Q7TNY3_MOUSE	Calcipressin 1 large isoform OS=Mus musc	74.15	1	1		1				1		1	1		2	1	1	2	0.53515	0.50	0.60884	0.50	0.87133	1.00
sp|Q8K2Q0|COMD9_MOUSE	COMM domain-containing protein 9 OS=M	50.54	1									1			1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.99229	1.00
sp|Q99K51|PLST_MOUSE	Plastin-3 OS=Mus musculus (Mouse) GN=F	119.23	1										1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.89308	1.00
sp|Q9CR98|F136A_MOUSE	Protein FAM136A OS=Mus musculus (Mou	44.19	1										1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.89308	1.00
sp|Q99KN2|CIAO1_MOUSE	Probable cytosolic iron-sulfur protein assem	31.99	1										1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.89308	1.00
sp|Q80SU3|ZAR1_MOUSE	Zygote arrest protein 1 OS=Mus musculus	31.45	1										1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.89308	1.00
sp|P10711|TCEA1_MOUSE	Transcription elongation factor A protein 1	56.63	1											1	1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.91525	1.00
tr|A8DUK2|A8DUK2_MOUSE	Beta-globin OS=Mus musculus (Mouse) GN	297.48		1	3	2						3		3	2	1	0	2	0.58366	0.50	0.21310	WT-scr only	0.59445	1.50
sp|P53395|ODB2_MOUSE	Lipoamide acyltransferase component of br	168.11		1	2				1			1	1		2	0	1	2	0.16577	WT-scr only	0.36172	0.33	0.72674	0.67
sp|Q59J78|MIMIT_MOUSE	Mimitin, mitochondrial OS=Mus musculus (M	136.64		1	1	1							1	1	2	1	0	2	0.52850	0.50	0.11658	WT-scr only	0.79865	1.00
sp|Q91WV0|NC2B_MOUSE	Protein Dr1 OS=Mus musculus (Mouse) GN	67.42		1								1			1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.98315	1.00
sp|B1AZP2|DLGP4_MOUSE	Disks large-associated protein 4 OS=Mus n	230.75		1								1			1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.98315	1.00
sp|Q9R226|KHDR3_MOUSE	KH domain-containing, RNA-binding, signal	179.56		1									1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.86966	1.00
sp|P51906|EAA3_MOUSE	Excitatory amino acid transporter 3 OS=Mu	109.13		1									1		1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.86966	1.00
sp|Q7TN29|SMAP2_MOUSE	Stromal membrane-associated protein 2 OS	122.83			1									1	1	0	0	1	0.37390	WT-scr only	0.37390	WT-scr only	0.92666	1.00
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
tr|B2RXT3|B2RXT3_MOUSE	Ogdhl protein OS=Mus musculus (Mouse)	1178.5	6	9	6	2	4	4	9	6	6	1	3	5	3	3	3	3	0.01993	0.48	0.76247	1.00	0.10807	0.43
sp|P37040|NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=	888.6	5	4	2	2	1	1		5	3	1	2	2	3	3	2	3	0.06622	0.36	0.74114	0.73	0.15955	0.45
sp|Q9R0X4|ACOT9_MOUSE	Acyl-coenzyme A thioesterase 9, mitochond	317.19	2	2	1		1	1	3	1	1		1	1	3	2	3	2	0.07775	0.40	0.96314	1.00	0.17196	0.40
sp|Q64519|SDC3_MOUSE	Syndecan-3 OS=Mus musculus (Mouse) G	133.18	2	2					3			2			2	0	1	1	0.11633	WT-scr only	0.76454	0.75	0.52365	0.50
sp|Q9QXK3|COPG2_MOUSE	Coatomer subunit gamma-2 OS=Mus musc	245.51	3	1	2	1	1	1	1	1	2		1	2	3	3	3	2	0.14988	0.50	0.45307	0.67	0.42009	0.50
sp|Q80U49|C170B_MOUSE	Centrosomal protein of 170 kDa protein B	332.8	2	1		1				2					2	1	1	0	0.38533	0.33	0.81762	0.67	0.16333	WT-scr only
sp|Q60714|S27A1_MOUSE	Long-chain fatty acid transport protein 1 O	121.79	2	1					2		1				2	0	2	0	0.16333	WT-scr only	0.99743	1.00	0.16333	WT-scr only
sp|P35550|FBRL_MOUSE	rRNA 2'-O-methyltransferase fibrillarin OS=	236.88	2				1			1	1			1	1	1	2	1	0.64280	0.50	0.92930	1.00	0.73999	0.50
tr|J3QNT7|J3QNT7_MOUSE	Epsin-2 OS=Mus musculus (Mouse) GN=E	293.61	1	2	1	1	1		1	1	1	1	1		3	2	3	2	0.19769	0.50	0.44287	0.75	0.29848	0.50
sp|Q8C878|UBA3_MOUSE	NEDD8-activating enzyme E1 catalytic subu	312.96	1	2	1			1	1	1	2			1	3	1	3	1	0.08215	0.25	0.84272	1.00	0.13578	0.25
sp|Q8VCW8|ACSF2_MOUSE	Acyl-CoA synthetase family member 2, mito	351.72	1	1	4	1		2	2	2	2		1	2	3	2	3	2	0.41787	0.50	0.93721	1.00	0.54325	0.50
sp|Q8R3H7|HS2ST_MOUSE	Heparan sulfate 2-O-sulfotransferase 1 OS	228.1	1	1	1	1			1	1	1		1		3	1	3	1	0.12156	0.33	0.39275	1.00	0.22718	0.33
sp|Q9ERI6|RDH14_MOUSE	Retinol dehydrogenase 14 OS=Mus muscu	112.84	1	1	1	1			1		1				3	1	2	0	0.12156	0.33	0.40516	0.67	0.00000	WT-scr only
tr|Q3TRG0|Q3TRG0_MOUSE	Gene model 1604B, (NCBI) OS=Mus musc	76.69	1	1	1					1	1		1		3	0	2	1	0.00000	WT-scr only	0.53068	0.67	0.22718	0.33
sp|Q8BHJ5|TBL1R_MOUSE	F-box-like/WD repeat-containing protein TBL	79.22	1	1		1			1		1	1			2	1	2	1	0.53515	0.50	0.96234	1.00	0.52365	0.50
sp|O08919|NUMBL_MOUSE	Numb-like protein OS=Mus musculus (Mous	187.87	1	1			1		3						2	1	1	0	0.47270	0.50	0.78782	1.50	0.11633	WT-scr only
sp|Q9D6S7|RRFM_MOUSE	Ribosome-recycling factor, mitochondrial O	61.79	1	1			1		1	1	1	1			2	1	3	1	0.47270	0.50	0.29422	1.50	0.52365	0.50
sp|Q8BKV1|GPC2_MOUSE	Glypican-2 OS=Mus musculus (Mouse) GN	59.3	1		1	1			1	1			1		2	1	2	1	0.51472	0.50	0.97826	1.00	0.64301	0.50
sp|Q8BLN5|ERG7_MOUSE	Lanosterol synthase OS=Mus musculus (M	256.16	1		1	1				1	1				2	1	2	0	0.51472	0.50	0.90349	1.00	0.11616	WT-scr only
tr|A0A087WSS1|A0A087WSS1_	Protein 2310035C23Rik OS=Mus musculus	815.23	1		1		1			2	1		1		2	1	2	1	0.45451	0.50	0.58043	1.50	0.64301	0.50
sp|Q7TNM2|TRI46_MOUSE	Tripartite motif-containing protein 46 OS=M	344.48	1		1			1	1		1				2	1	2	0	0.47466	0.50	0.99814	1.00	0.11616	WT-scr only
tr|E9Q7G0|E9Q7G0_MOUSE	Protein Numa1 OS=Mus musculus (Mouse)	241.11	1		1				2			1			2	0	1	1	0.11616	WT-scr only	0.94793	1.00	0.50359	0.50
sp|Q61315|APC_MOUSE	Adenomatous polyposis coli protein OS=M	120.09	1						1						1	0	1	0	0.37390	WT-scr only	0.96559	1.00	0.37390	WT-scr only
sp|Q8CI32|BAG5_MOUSE	BAG family molecular chaperone regulator 5	107.97	1						1						1	0	1	0	0.37390	WT-scr only	0.96559	1.00	0.37390	WT-scr only
sp|P56213|ALR_MOUSE	FAD-linked sulfhydryl oxidase ALR OS=Mu	46.32	1						1						1	0	1	0	0.37390	WT-scr only	0.96559	1.00	0.37390	WT-scr only
sp|Q9D1P0|RM13_MOUSE	39S ribosomal protein L13, mitochondrial C	36.02	1						1						1	0	1	0	0.37390	WT-scr only	0.96559	1.00	0.37390	WT-scr only
sp|S4R1M9|OSB10_MOUSE	Oxysterol-binding protein-related protein 10	33.06	1						1						1	0	1	0	0.37390	WT-scr only	0.96559	1.00	0.37390	WT-scr only
sp|O08738|CASP6_MOUSE	Caspase-6 OS=Mus musculus (Mouse) GN	33.97	1							1					1	0	1	0	0.37390	WT-scr only	0.93674	1.00	0.37390	WT-scr only
sp|Q9CXJ4|ABCB8_MOUSE	ATP-binding cassette sub-family B member	54.11	1								1				1	0	1	0	0.37390	WT-scr only	0.95504	1.00	0.37390	WT-scr only
sp|P70202|LXN_MOUSE	Latexin OS=Mus musculus (Mouse) GN=Lx	177.56	1								1				1	0	1	0	0.37390	WT-scr only	0.95504	1.00	0.37390	WT-scr only
sp|Q99LG2|TNPO2_MOUSE	Transportin-2 OS=Mus musculus (Mouse)	211.27		2	3		1	1	1	1	1	1		1	2	2	3	2	0.33039	0.40	0.53483	0.60	0.38601	0.40
sp|Q9D2R6|COA3_MOUSE	Cytochrome c oxidase assembly factor 3 ho	115.39		2	1					1	1		1		2	0	2	1	0.15120	WT-scr only	0.73753	0.67	0.45435	0.33
sp|P59108|CPNE2_MOUSE	Copine-2 OS=Mus musculus (Mouse) GN=	180.18		1	2					2	1			1	2	0	2	1	0.16577	WT-scr only	0.90248	1.00	0.43919	0.33
sp|Q9ERR7|SEP15_MOUSE	15 kDa selenoprotein OS=Mus musculus (M	62.13		1					1						1	0	1	0	0.37390	WT-scr only	0.99012	1.00	0.37390	WT-scr only
sp|Q60960|IMA5_MOUSE	Importin subunit alpha-5 OS=Mus musculu	121.75		1					1						1	0	1	0	0.37390	WT-scr only	0.99012	1.00	0.37390	WT-scr only
sp|A2AG50|MA7D2_MOUSE	MAP7 domain-containing protein 2 OS=Mu	162.78		1						1					1	0	1	0	0.37390	WT-scr only	0.91265	1.00	0.37390	WT-scr only
sp|Q8C080|SNX16_MOUSE	Sorting nexin-16 OS=Mus musculus (Mous	96.55		1							1				1	0	1	0	0.37390	WT-scr only	0.93075	1.00	0.37390	WT-scr only
sp|Q9D6K8|FUND2_MOUSE	FUN14 domain-containing protein 2 OS=M	48.7		1							1				1	0	1	0	0.37390	WT-scr only	0.93075	1.00	0.37390	WT-scr only
sp|O70401|TSN6_MOUSE	Tetraspanin-6 OS=Mus musculus (Mouse)	33.22		1							1				1	0	1	0	0.37390	WT-scr only	0.93075	1.00	0.37390	WT-scr only
sp|Q922Q9|CHID1_MOUSE	Chitinase domain-containing protein 1 OS=	89.24			2		1			1	1				1	1	2	0	0.63587	0.50	0.94474	1.00	0.37390	WT-scr only
sp|Q3TBW2|RM10_MOUSE	39S ribosomal protein L10, mitochondrial C	84.71			1						1				1	0	1	0	0.37390	WT-scr only	0.96663	1.00	0.37390	WT-scr only
accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|Q6A0A9|F120A_MOUSE	Constitutive coactivator of PPAR-gamma-lik	542.58	2	4	4	3	2		3	3	1	3	3	1	3	2	3	3	0.19577	0.50	0.40966	0.70	0.52003	0.70
sp|Q04750|TOP1_MOUSE	DNA topoisomerase 1 OS=Mus musculus (	465.36	2	4	4	2	1	2	2	1	3	3	2	2	3	3	3	3	0.08296	0.50	0.25203	0.60	0.35310	0.70
sp|Q9D964|GATM_MOUSE	Glycine amidinotransferase, mitochondrial	389.25	2	3	3	2	1	1	2	2	1	1	2	3	3	3	3	3	0.04963	0.50	0.12911	0.63	0.70921	0.75
sp|O88291|ZN326_MOUSE	DBIRD complex subunit ZNF326 OS=Mus	347.4	3	2	3	3			3	3	4	2	5		3	1	3	2	0.19780	0.38	0.21750	1.25	0.98268	0.88
sp|P62071|RRAS2_MOUSE	Ras-related protein R-Ras2 OS=Mus musc	437.31	3	3	3	1	2	1	2	2	1	2	3	3	3	3	3	3	0.00370	0.44	0.02374	0.56	0.88914	0.89
sp|P30677|GNA14_MOUSE	Guanine nucleotide-binding protein subunit	410.02	2	4	2	1	1	1	2	1	4	4	2	3	3	3	3	3	0.04928	0.38	0.88974	0.88	0.40976	1.13
sp|Q3THG9|AASD1_MOUSE	Alanyl-tRNA editing protein Aarsd1 OS=Mu	347.54	2	2	2	1	1	1	1	1	2	2	2	3	3	3	3	3	0.00003	0.50	0.21497	0.67	0.22244	1.17
sp|Q8CHT0|AL4A1_MOUSE	Delta-1-pyrroline-5-carboxylate dehydrogen	435.58	3	2	4	1		1	2	3	2		2	3	3	2	3	2	0.02926	0.22	0.54007	0.78	0.45494	0.56
sp|O54829|RGS7_MOUSE	Regulator of G-protein signaling 7 OS=Mus	491.65	2	5	3		2	3	3	4	4	2	3	3	3	2	3	3	0.20482	0.50	0.56365	1.10	0.83124	0.80
sp|Q9Z2H2|RGS6_MOUSE	Regulator of G-protein signaling 6 OS=Mus	290.85	2	2	3		1	1	2	2	2	2	1	2	3	2	3	3	0.02366	0.29	0.59688	0.86	0.39208	0.71
sp|Q8BGH2|SAM50_MOUSE	Sorting and assembly machinery componen	427.86	2	2	3		1		2	3	1	3	1	2	3	1	3	3	0.01329	0.14	0.79778	0.86	0.82568	0.86
sp|Q91W39|NCOA5_MOUSE	Nuclear receptor coactivator 5 OS=Mus mu	258.5	3	1	2	1	1	1	2	2	2	2	1	4	3	3	3	3	0.14988	0.50	0.87331	1.00	0.62864	1.17
sp|Q9R008|KIME_MOUSE	Mevalonate kinase OS=Mus musculus (Mo	272.3	4	1	2	1		1	2	3	4	1	2	3	3	2	3	3	0.14990	0.29	0.48994	1.29	0.99221	0.86
sp|Q99020|ROAA_MOUSE	Heterogeneous nuclear ribonucleoprotein A	483.56	2	1	2			1	2	1	2	2	1	3	3	1	3	3	0.04589	0.20	0.90543	1.00	0.49446	1.20
sp|Q921W0|CHM1A_MOUSE	Charged multivesicular body protein 1a OS	136.72	2	1	2			1	2	1	1		2	1	3	1	3	2	0.04589	0.20	0.52743	0.80	0.59516	0.60
sp|P62862|RS30_MOUSE	40S ribosomal protein S30 OS=Mus muscu	97.22	2	1	1	2				4	2	2	3	2	3	1	2	3	0.43120	0.50	0.53869	1.50	0.09596	1.75
sp|P28271|ACOC_MOUSE	Cytoplasmic aconitate hydratase OS=Mus	441.84	2	1	1		1	1			5		1	2	3	2	1	2	0.19287	0.50	0.80421	1.25	0.86866	0.75
sp|P62996|TRA2B_MOUSE	Transformer-2 protein homolog beta OS=M	154.73	3	1			2		3			2	1	2	2	1	1	3	0.53917	0.50	0.78216	0.75	0.60403	1.25
sp|O35345|IMA7_MOUSE	Importin subunit alpha-7 OS=Mus musculu	195.98	2	1			1		2	2		1	1		2	1	2	2	0.35241	0.33	0.68774	1.33	0.73746	0.67
sp|O54984|ASNA_MOUSE	ATPase Asna1 OS=Mus musculus (Mouse)	420.7	2		1				1	1	3	1	2	1	2	0	3	3	0.15597	WT-scr only	0.46072	1.67	0.51247	1.33
sp|P30999|CTND1_MOUSE	Catenin delta-1 OS=Mus musculus (Mouse	812.58	1	2	3		1	2	3		3		3	1	3	2	2	2	0.25600	0.50	0.97862	1.00	0.77788	0.67
tr|E9Q8Z5|E9Q8Z5_MOUSE	Catenin delta-1 OS=Mus musculus (Mouse	827.54	1	2	3		1	2	3		3		3	1	3	2	2	2	0.25600	0.50	0.97862	1.00	0.77788	0.67

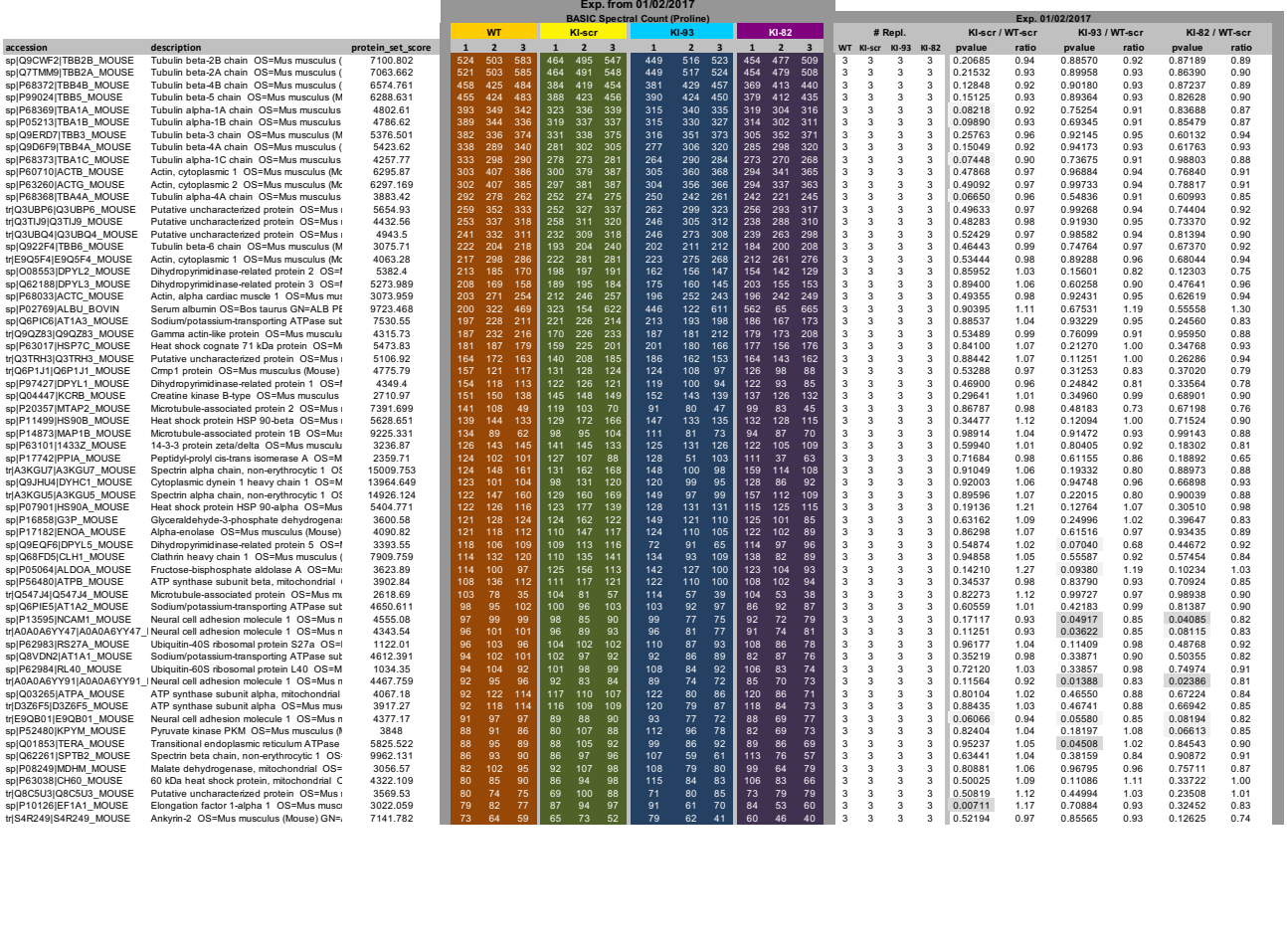


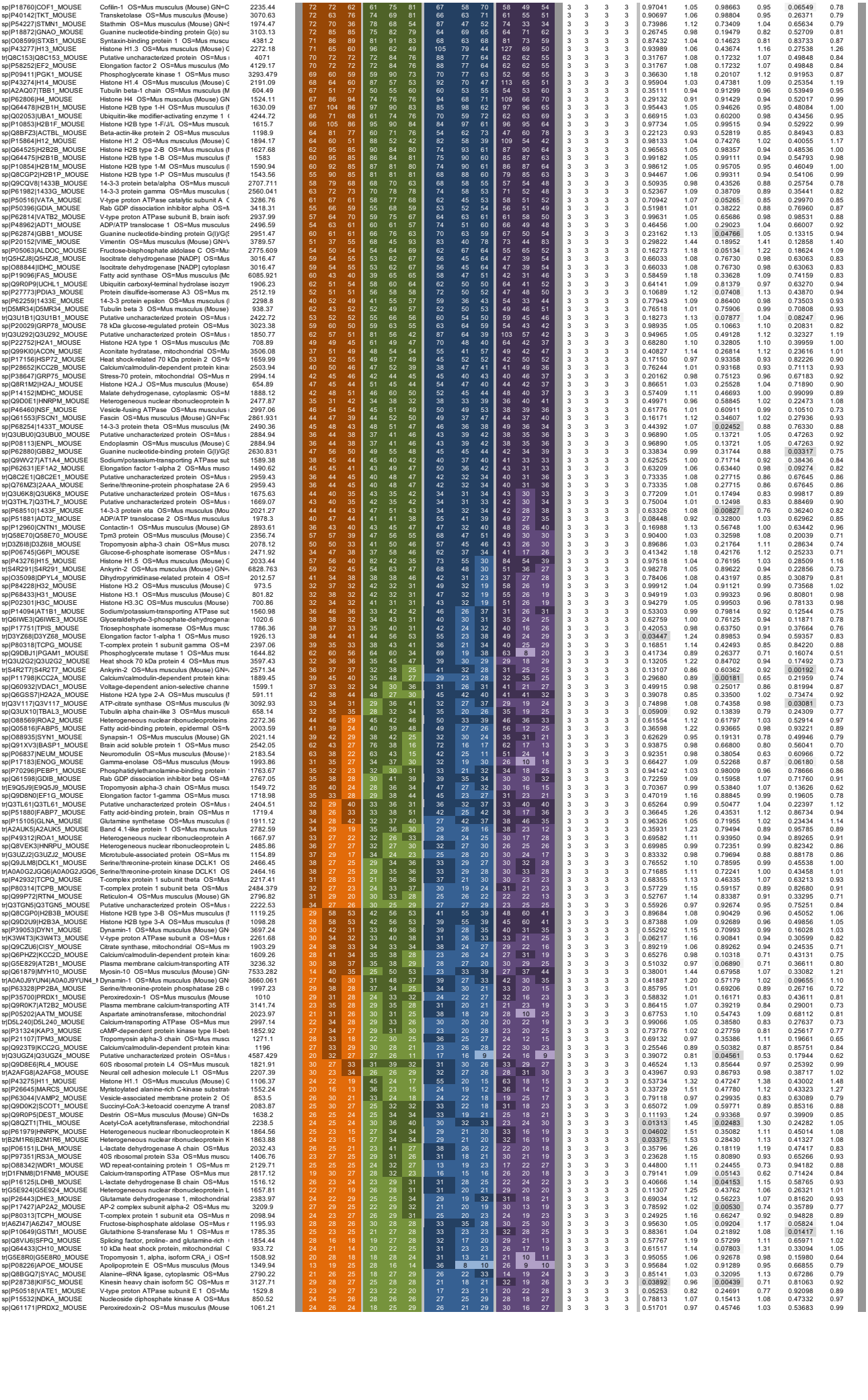


accession	description	protein_set_score	1	2	3	1	2	3	1	2	3	WT	KI-scr	KI-93	KI-82	pvalue	ratio	pvalue	ratio	pvalue	ratio
sp|P62204|CALM_MOUSE	Calmodulin OS=Mus musculus (Mouse) GN	1574.02	39	14	13	36	10	2	37		1	31	1			3	3	2	2	0.66989	0.73	0.52261	0.58	0.43895	0.48
sp|Q8BJU0|SGTA_MOUSE	Small glutamine-rich tetratricopeptide repea	681.56	9	13	4	9	9	7	13	1	6	8		3		3	3	3	2	0.82415	0.96	0.66201	0.77	0.23025	0.42
sp|Q64514|TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus	1442.52	6	8	9	8	5	7	9	3	6	3	3	2		3	3	3	2	0.41671	0.87	0.43794	0.78	0.00992	0.35
sp|Q60597|ODO1_MOUSE	2-oxoglutarate dehydrogenase, mitochondr	1232.33	6	6	9	3	6	8	11	4	5	2	5	3		3	3	3	3	0.38260	0.81	0.92127	0.95	0.13317	0.48
sp|Q9QUR7|PIN1_MOUSE	Peptidyl-prolyl cis-trans isomerase NIMA-inte	568.77	6	7	6	5	7	7	9	5	5	6	2	1		3	3	3	3	0.58144	1.00	0.82567	1.00	0.09680	0.47
sp|Q8K183|PDXK_MOUSE	Pyridoxal kinase OS=Mus musculus (Mouse	554.57	8	8	6	4	9	6	4	5	6	4	3	4		3	3	3	3	0.36735	0.86	0.12272	0.68	0.00828	0.50
sp|P48428|TBCA_MOUSE	Tubulin-specific chaperone A OS=Mus mus	413.39	7	6	3	3	6	4	4		6	5		2		3	3	2	2	0.42346	0.81	0.45404	0.63	0.19676	0.44
sp|Q92L5S|SEPT3_MOUSE	Neuronal-specific septin-3 OS=Mus musculu	512.42	7	5	6	5	6	5	3	4	4	4	2	2		3	3	3	3	0.24307	0.89	0.06976	0.61	0.02100	0.44
sp|P26883|FKB1A_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A	283.5	6	5	5	7	4	4	6	3	4	4	1	3		3	3	3	3	0.69245	0.94	0.32148	0.81	0.05971	0.50
sp|O70439|STX7_MOUSE	Syntaxin-7 OS=Mus musculus (Mouse) GN	619.81	7	3	3	6	5	4	9	4	3	2	1	1		3	3	3	3	0.78011	1.15	0.62363	1.23	0.10583	0.31
tr|Q570Z8|Q570Z8_MOUSE	MKIAA4114 protein OS=Mus musculus (Mo	793.66	6	5	2	7	3	2	5	3	1	3	2	1		3	3	3	3	0.84861	0.92	0.48086	0.69	0.18084	0.46
sp|F8VPU2|FARP1_MOUSE	FERM, RhoGEF and pleckstrin domain-cont	627.22	6	3	2	5	6	5	4	2	1	4		1		3	3	3	2	0.31610	1.45	0.42393	0.64	0.31425	0.45
sp|Q9R0Q7|TEBP_MOUSE	Prostaglandin E synthase 3 OS=Mus musc	381.15	6	3	4	3	3	6	5	1	4	2	1	3		3	3	3	3	0.69895	0.92	0.55840	0.77	0.14153	0.46
sp|Q68FF6|GIT1_MOUSE	ARF GTPase-activating protein GIT1 OS=M	587.55	6	4	1	2	4	3	6	3	2	3	2			3	3	3	2	0.62227	0.82	0.95162	1.00	0.34835	0.45
sp|Q3UPL0|SC31A_MOUSE	Protein transport protein Sec31A OS=Mus	1171.91	6		2	3	8		5	3	3	3	1			2	2	3	2	0.80352	1.38	0.57919	1.38	0.54703	0.50
sp|Q9DC69|NDUA9_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	761.6	4	11	10	7	7	4	6	4	5	5	3	4		3	3	3	3	0.33862	0.72	0.22907	0.60	0.15238	0.48
tr|A0A0A0MQA6|A0A0A0MQA6_MOUSE	Microtubule-actin cross-linking factor 1 OS=	4018.1	5	11	5	5	7	14	10	3	9	6	1	3		3	3	3	3	0.70165	1.24	0.82611	1.05	0.21692	0.48
sp|Q8BLQ9|CADM2_MOUSE	Cell adhesion molecule 2 OS=Mus musculu	570.76	5	8	7	8	5	8	5	4	8	4	3	2		3	3	3	3	0.99307	1.05	0.71285	0.85	0.02606	0.45
sp|P29758|OAT_MOUSE	Ornithine aminotransferase, mitochondrial	905.98	4	6	6	6	3	9	5	3	5	4	2	2		3	3	3	3	0.32784	1.13	0.42784	0.81	0.01655	0.44
sp|Q77TM8|CYFP1_MOUSE	Cytoplasmic FMR1-interacting protein 1 OS	898.11	5	10	7	4	9	9	7	4	6	5	3	2		3	3	3	3	0.85278	1.00	0.40739	0.77	0.07659	0.45
tr|Q3TJ95|Q3TJ95_MOUSE	Putative uncharacterized protein OS=Mus	551.55	5	7	4	12	10	2	7	2	1	4	2			3	3	3	2	0.48543	1.50	0.34506	0.63	0.08587	0.38
sp|Q08331|CALB2_MOUSE	Calretinin OS=Mus musculus (Mouse) GN=C	435.86	3	7	2	6	8	6	4	3	3	2	2	2		3	3	3	3	0.18672	1.67	0.77052	0.83	0.31005	0.50
sp|Q8R5H6|WASF1_MOUSE	Wiskott-Aldrich syndrome protein family mem	678.3	5	7	5	6	6	3	8	3	3	3	3	2		3	3	3	3	0.49223	0.88	0.58615	0.82	0.01740	0.47
sp|O55106|STRN_MOUSE	Striatin OS=Mus musculus (Mouse) GN=Str	737.71	4	7	3	2	7	3	3	4	2	2	4			3	3	3	2	0.63575	0.86	0.33300	0.64	0.26998	0.43
sp|Q9DCD0|6PGD_MOUSE	6-phosphogluconate dehydrogenase, decа	919.46	5	6	5	5	5	6	5	3	6		3	5		3	3	3	2	0.58750	1.00	0.68333	0.88	0.29217	0.50
sp|Q791V5|MTCH2_MOUSE	Mitochondrial carrier homolog 2 OS=Mus m	431.31	4	6	5	5	4	4	4	2	4	4	2	1		3	3	3	3	0.29168	0.87	0.13641	0.67	0.06257	0.47
sp|Q62108|DLG4_MOUSE	Disks large homolog 4 OS=Mus musculus (	436.21	5	6	4	3	5	2	3	3	2	3	3			3	3	3	2	0.11438	0.67	0.02170	0.53	0.08935	0.40
sp|Q8VBV7|CSN8_MOUSE	COP9 signalosome complex subunit 8 OS=	380.84	5	3	7	2	4	4	2	5	2	1	3	2		3	3	3	3	0.23704	0.67	0.36219	0.60	0.14218	0.40
sp|P28658|ATX10_MOUSE	Ataxin-10 OS=Mus musculus (Mouse) GN=	833.09	4	3	4	2	6	7	5	3	4			4		3	3	3	1	0.51800	1.36	0.42778	1.09	0.26640	0.36
sp|P62484|ABI2_MOUSE	Abl interactor 2 OS=Mus musculus (Mouse	546.56	5	4	2	5	6	3	6	4		2	1			3	3	3	2	0.53915	1.27	0.90513	0.91	0.06876	0.27
sp|P23818|GRIA1_MOUSE	Glutamate receptor 1 OS=Mus musculus (M	763.65	2	5	5	5	7	5	7	1	2	6				3	3	3	1	0.28042	1.42	0.74519	0.83	0.41751	0.50
tr|Q8R5L1|Q8R5L1_MOUSE	Complement component 1 Q subcomponen	335	3	5	4	5	6	5	5	2	2	3	2	1		3	3	3	3	0.12408	1.33	0.39982	0.75	0.07627	0.50
sp|P12658|CALB1_MOUSE	Calbindin OS=Mus musculus (Mouse) GN=C	722.56	3	5	4	3	7	3	4	3	2	1	2	1		3	3	3	3	0.94617	1.08	0.29142	0.75	0.02510	0.33
sp|P47738|ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial O	636.52	3	3	5	5	6	5	2	3	3	1	1	1		3	3	3	3	0.14275	1.45	0.40240	0.73	0.02582	0.27
tr|A0A087WRS3|A0A087WRS3_MOUSE	Abl interactor 2 OS=Mus musculus (Mouse	535.7	5	4	2	5	6	3	5	4	4		2	1		3	3	2	2	0.53915	1.27	0.76745	0.82	0.06876	0.27
sp|Q8K2C9|HACD3_MOUSE	Very-long-chain (3R)-3-hydroxyacyl-CoA del	438.26	2	4	2	2	6	5	2	1	3	1	1	2		3	3	3	3	0.30279	1.63	0.57266	0.75	0.20705	0.50
sp|Q9CYT6|CAP2_MOUSE	Adenylyl cyclase-associated protein 2 OS=	528.45	3	4	2	4	6	1	2	3	1	1	2			3	3	3	2	0.74224	1.22	0.37716	0.67	0.10852	0.33
sp|P56546|CTBP2_MOUSE	C-terminal-binding protein 2 OS=Mus musc	346.31	2	3	5	4	3	6	2		4	4	1			3	3	2	2	0.56351	1.30	0.46967	0.60	0.34244	0.50
sp|Q9JMH9|MY18A_MOUSE	Unconventional myosin-XVIIIa OS=Mus mu	1440.01	4	4	4	2	2	4	6	3	2	1	3	1		3	3	3	3	0.07966	0.67	0.82286	0.92	0.08115	0.42
sp|P45376|ALDR_MOUSE	Aldose reductase OS=Mus musculus (Mou	712.27	5	4	5	5	5	4	8		3		1			3	3	2	1	0.71392	1.00	0.65768	0.79	0.00189	0.07
sp|Q80TL4|PHF24_MOUSE	PHD finger protein 24 OS=Mus musculus (M	426.75	4	5	2	3	5	4	3	2	2	3	1	1		3	3	3	3	0.87926	1.09	0.22732	0.64	0.14324	0.45
tr|A0A087WNW8|A0A087WNW8_MOUSE	CLIP-associating protein 1 OS=Mus muscu	849.76	3	5	2	4	3	4	3	3	2	3	1			3	3	3	2	0.82090	1.10	0.60948	0.80	0.18444	0.40
sp|Q9DCC4|P5CR3_MOUSE	Pyrroline-5-carboxylate reductase 3 OS=M	343.37	4	2	4	5	3	5	3	2	4	1	2	1		3	3	3	3	0.47299	1.30	0.84919	0.90	0.10180	0.40
sp|P56382|ATP5E_MOUSE	ATP synthase subunit epsilon, mitochondri	136.7	4	3	3	3	2	3	3	4	2		2	3		3	3	3	2	0.20776	0.80	0.86201	0.90	0.29715	0.50
sp|Q9DBG6|RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein	841.34	4	4	4	3	3	3	2	3	2			4		3	3	3	1	0.00073	0.75	0.03315	0.58	0.20028	0.33
sp|Q9WUM3|COR1B_MOUSE	Coronin-1B OS=Mus musculus (Mouse) GN	484.97	2	5	4	3	2	5	3	3	1	3	2			3	3	3	2	0.71918	0.91	0.33192	0.64	0.10565	0.45
sp|Q9CPQ8|ATPA1_MOUSE	ATP synthase subunit alpha-1, mitochondrial OS	291.06	5	4	5	4	5	4	5	1	3	2	3	1		3	3	3	3	0.90390	0.93	0.22016	0.64	0.04897	0.43
sp|Q8CGK3|LONM_MOUSE	Lon protease homolog, mitochondrial OS=I	647.99	2	3	5	3	4	4	4	1	4	2	1	1		3	3	3	3	0.89871	1.10	0.86369	0.90	0.12424	0.40
sp|Q9WU78|PDC6I_MOUSE	Programmed cell death 6-interacting protein	799.34	2	2	2	3	5	3	5	1	1	3				3	3	3	1	0.05315	1.83	0.80431	1.17	0.36841	0.50
tr|A0A087WPM2|A0A087WPM2_MOUSE	MCG5343 OS=Mus musculus (Mouse) GN=	358.3	2	2	2	3	3	3	3	1	1	1	2			3	3	3	2	0.00099	1.50	0.61624	0.83	0.30533	0.50
sp|Q9D7X3|DUS3_MOUSE	Dual specificity protein phosphatase 3 OS=	273.33	2	2	2	2	2	2	1	1	2	1	1			3	3	3	2	0.28226	1.00	0.21497	0.67	0.02977	0.33
tr|Q3TMX5|Q3TMX5_MOUSE	Arginine-rich, mutated in early stage tumors	233.08	2	3	2	2	3	2		2	2		1	1		3	3	2	2	0.79133	1.00	0.35533	0.57	0.03726	0.29
sp|Q6ZQI3|MLEC_MOUSE	Malectin OS=Mus musculus (Mouse) GN=M	251.83	3	2	4	4	3	1	4	1	2	3	1			3	3	3	2	0.70355	0.89	0.54742	0.78	0.20581	0.44
sp|Q8CHG7|RPGF2_MOUSE	Rap guanine nucleotide exchange factor 2	299.68	3	2	2	2	1	2	2	2	4			1	2	3	3	2	2	0.21315	0.71	0.89494	0.86	0.21279	0.43
sp|P54822|PUR8_MOUSE	Adenylosuccinate lyase OS=Mus musculus	291.85	2	4	2	1	2	2	3	2	2	2	1	1		3	3	3	2	0.18338	0.63	0.75981	0.88	0.05618	0.25
sp|Q8BG81|PDIP3_MOUSE	Polymerase delta-interacting protein 3 OS=	242.08	4	2	2	1	2	3	2	2	3	1	2	1		3	3	3	2	0.41277	0.75	0.60374	0.75	0.14835	0.38
sp|Q9CR00|PSMD9_MOUSE	26S proteasome non-ATPase regulatory su	401.05	4	2	2	1	2	4	4	2	1	3				3	3	3	1	0.68126	0.88	0.79290	0.88	0.23573	0.38
sp|P02798|MT2_MOUSE	Metallothionein-2 OS=Mus musculus (Mous	139.41	2	2	2	1	1	3	2	2	2	1				3	3	3	1	0.54176	0.83	0.39275	1.00	0.00747	0.17
sp|Q8BWG8|ARRB1_MOUSE	Beta-arrestin-1 OS=Mus musculus (Mouse)	290.11	4	2	2		2	3	3	2	2	3				3	2	3	1	0.35386	0.63	0.75354	0.88	0.23573	0.38
sp|Q8CGF6|WDR47_MOUSE	WD repeat-containing protein 47 OS=Mus	863.56	2	3	4		4	3	3	1	3	1	1			3	2	3	2	0.53545	0.78	0.54790	0.78	0.03443	0.22
sp|Q8VE47|UBA5_MOUSE	Ubiquitin-like modifier-activating enzyme 5	289.11	3	5	1	2	3	2	2	4	2	2	1	1		3	3	3	3	0.54435	0.78	0.95700	0.89	0.25608	0.44
sp|Q9Z2I0|LETM1_MOUSE	LETM1 and EF-hand domain-containing pro	582.82	2	3	1	1	2	1	3	1	4	1		1		3	3	3	2	0.29990	0.67	0.49626	1.33	0.12635	0.33
tr|Q80ZX0|Q80ZX0_MOUSE	Protein Sec24b OS=Mus musculus (Mouse	297.84	2	2	1	1	1	1	2	1						3	3	2	2	0.09035	0.60	0.36332	0.60	0.13674	0.40
sp|P59017|B2L13_MOUSE	Bcl-2-like protein 13 OS=Mus musculus (Mo	188.57	2	2	1	1	1	1	1		2	1	1			3	3	2	2	0.09035	0.60	0.43778	0.60	0.13674	0.40
sp|P62743|AP2S1_MOUSE	AP-2 complex subunit sigma OS=Mus mus	163.94	3	3	3	3	3	3	3	3	3	3				2	3	3	2	0.41753	1.50	0.70842	0.67	0.52365	0.50
sp|Q99MN9|PCCB_MOUSE	Propionyl-CoA carboxylase beta chain, mito	563.99	3	4		3	3	2	1	2	2	1	1	1		2	3	3	2	0.79921	0.86	0.68200	0.71	0.27658	0.29
sp|P63054|PCP4_MOUSE	Purkinje cell protein 4 OS=Mus musculus (M	188.49	4	3		4	2	1	3	1	1	1				3	2	3	1	0.98216	1.00	0.66654	0.71	0.18766	0.14
tr|F2Z3U3|F2Z3U3_MOUSE	Protein Raph1 OS=Mus musculus (Mouse)	189.07	2	2		2		1	3	2		2				2	2	2	1	0.73139	0.75	0.73892	1.25	0.52365	0.50
sp|P61222|ABCE1_MOUSE	ATP-binding cassette sub-family E member	529.23	2	2			3	1	1	1	2					2	2	3	0	0.93449	1.00	0.89084	1.00	0.11633	WT-scr only
sp|Q91V09|WDR13_MOUSE	WD repeat-containing protein 13 OS=Mus	363.18	2	1	2	3		3	3	1		1				3	2	2	1	0.80419	1.20	0.71182	0.80	0.05077	0.20
sp|Q9Z130|HNRDL_MOUSE	Heterogeneous nuclear ribonucleoprotein D	685.93	4	1	3	1	4	3	2	1	3	2		2		3	3	3	2	0.87343	1.00	0.62242	0.75	0.34695	0.50
sp|Q9CQC7|NDUB4_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta	210.83	2	1	2	1	2	2	2	1		1	1			3	3	2	2	0.82510	1.00	0.36405	0.60	0.14691	0.40
sp|Q91ZJ5|UGPA_MOUSE	UTP--glucose-1-phosphate uridylyltransferas	484.16	3	1	2	1	3	2	3		2	2				3	3	2	1	0.86470	1.00	0.76144	0.83	0.20326	0.33
sp|Q08875|ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2	312.42	2	1	1	2	3	1	4	2			1			3	3	2	1	0.41617	1.50	0.58564	1.50	0.15891	0.25
sp|Q62189|SNRPA_MOUSE	U1 small nuclear ribonucleoprotein A OS=M	318.97	3	1	1	2	2		3	1	1		1			3	2	3	1	0.69640	0.80	0.98569	1.00	0.18674	0.20
sp|Q9QXT0|CNPY2_MOUSE	Protein canopy homolog 2 OS=Mus muscu	341.7	2	1	1	2	1	4	2	1	2	1		1		3	3	3	2	0.37439	1.75	0.43276	1.25	0.28977	0.50
sp|Q8VHR5|P66B_MOUSE	Transcriptional repressor p66-beta OS=Mu	106.14	2	1	1	2	1	1	2	1		2				3	3	2	1	0.93440	1.00	0.63863	0.75	0.41663	0.50
sp|P60840|ENSA_MOUSE	Alpha-endosulfine OS=Mus musculus (Mou	131.88	2	1	1	1	2	1	1	1	2	1		1		3	3	3	2	0.86737	1.00	0.87166	1.00	0.28977	0.50
sp|Q8BME9|CBLN4_MOUSE	Cerebellin-4 (Cerebellin-like glycoprotein 1)	41.53	2	1	1	1		2	2	1	2			2		3	2	3	1	0.59600	0.75	0.43276	1.25	0.55936	0.50
sp|Q9QYF1|RDH11_MOUSE	Retinol dehydrogenase 11 OS=Mus musculu	311.15	2	1	1		2	3	2	2	2		1			3	2	3	1	0.82365	1.25	0.09538	1.50	0.15891	0.25
sp|Q9CS42|PRPS2_MOUSE	Ribose-phosphate pyrophosphokinase 2 O	294.01	2	1	1		2	2	1	1	1	1	1			3	2	3	2	0.89250	1.00	0.46781	0.75	0.30865	0.50

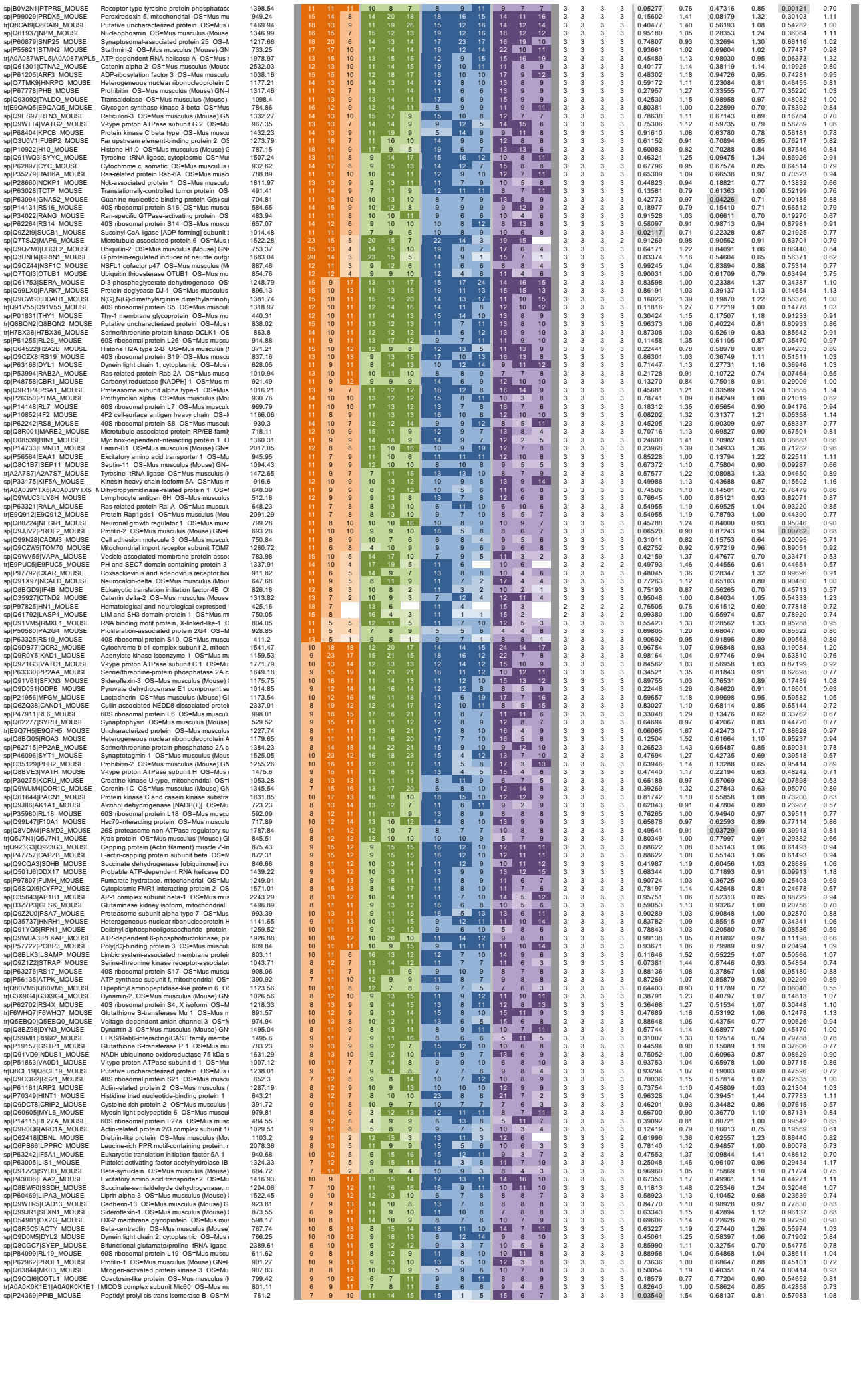


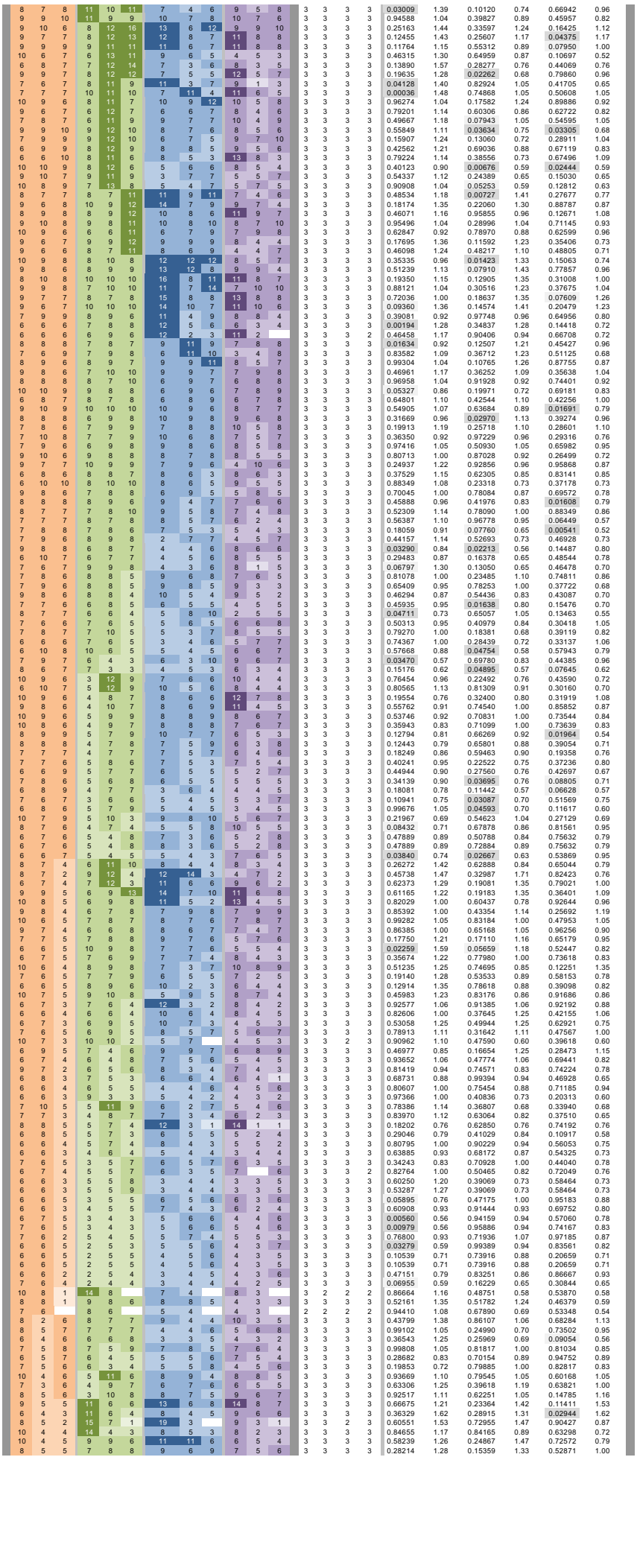
Other proteins:

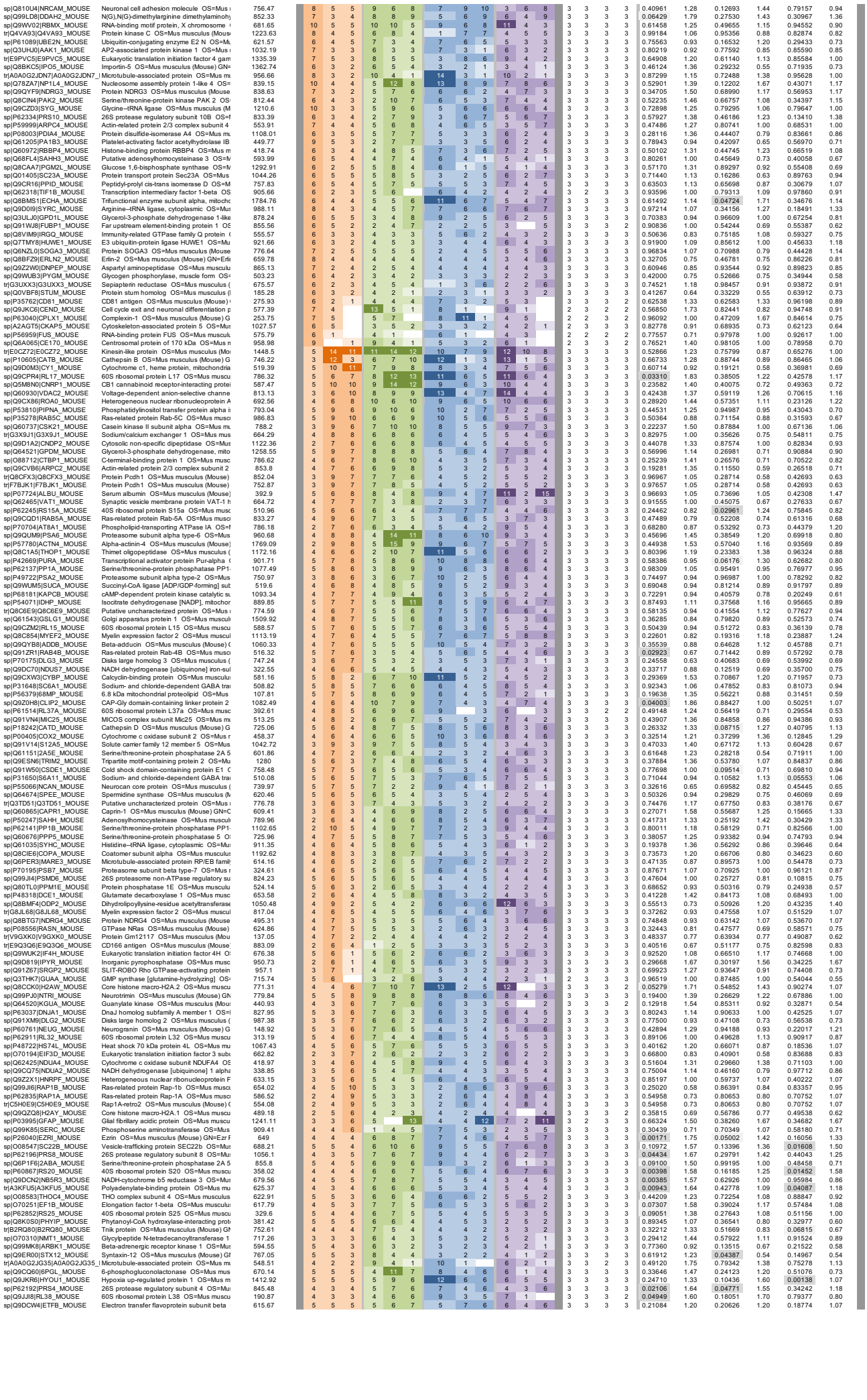




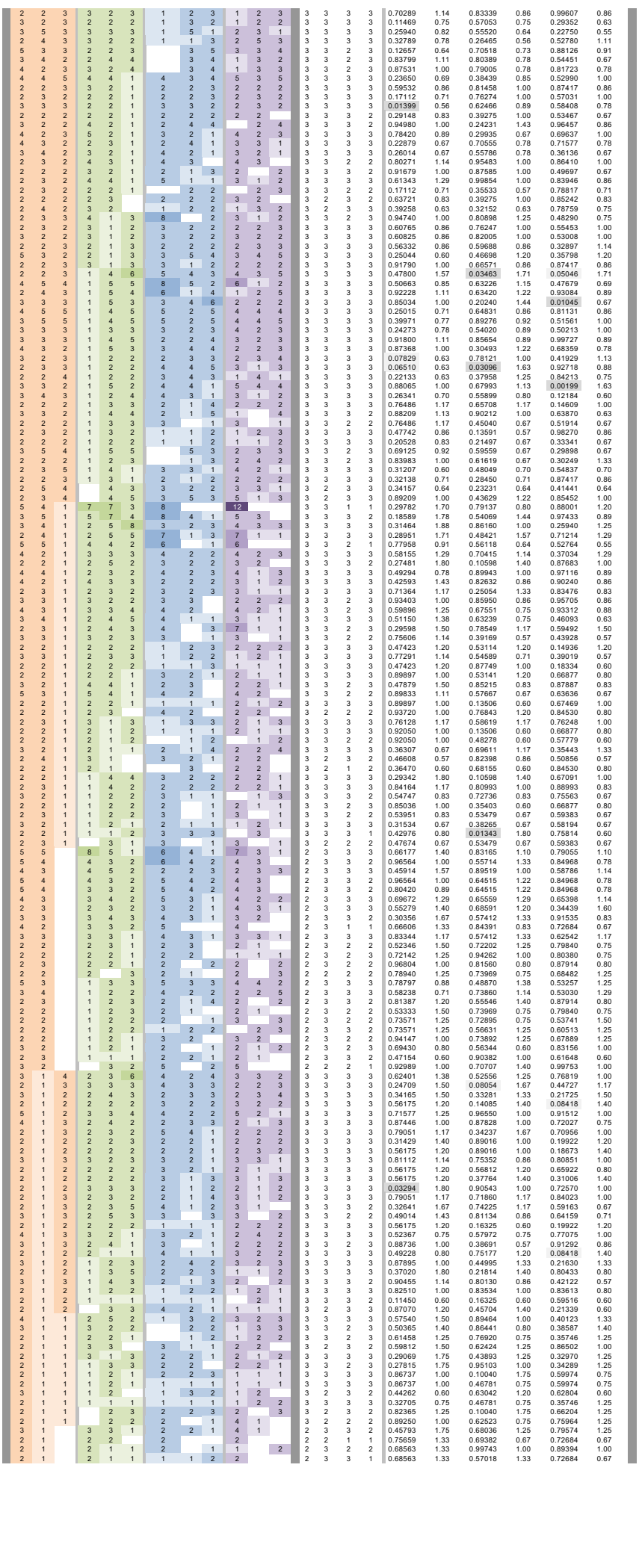
sp|Q9DB20|ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS	1315.36	25	24	26	24	23	20	20	27	24	22	25	26	3	3	3	3	0.12715	0.89	0.94303	0.95	0.42531	0.97
sp|P60843|IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=Mus mu	1655.42	25	24	21	26	25	27	27	18	24	25	20	26	3	3	3	3	0.36697	1.11	0.72809	0.99	0.19820	1.01
sp|P80315|TCPD_MOUSE	T-complex protein 1 subunit delta OS=Mus	2510.58	26	29	23	29	30	26	27	14	27	24	24	25	3	3	3	3	0.58154	1.09	0.62292	0.87	0.48243	0.94
sp|P27659|RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculu	1285.56	25	23	23	21	24	25	16	28	23	18	23	24	3	3	3	3	0.26624	0.99	0.94254	0.94	0.75040	0.92
sp|P10630|IF4A2_MOUSE	Eukaryotic initiation factor 4A-II OS=Mus m	1592.2	24	22	18	21	21	21	21	17	20	20	16	23	3	3	3	3	0.51482	0.98	0.63368	0.91	0.75432	0.92
sp|Q9CZ13|QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitoch	1592.5	26	19	26	24	29	19	23	25	22	29	19	22	3	3	3	3	0.82109	1.01	0.78180	0.99	0.49512	0.99
sp|P60335|PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculu	1227.62	15	15	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|AP2A1_MOUSE	AP-2 complex subunit alpha-1 OS=Mus mu	2914.76	23	29	18	25	29	28	22	26	22	28	22	21	3	3	3	3	0.36026	1.17	0.68740	1.00	0.29661	1.01
sp|P80317|TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus	1823.75	24	24	21	17	23	25	24	21	24	21	14	21	3	3	3	3	0.29266	0.94	0.37216	1.00	0.44261	0.81
sp|P63001|RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1	886.79	25	21	21	24	23	22	20	22	23	18	22	20	3	3	3	3	0.85622	1.03	0.79911	0.97	0.86217	0.90
sp|P17710|HXK1_MOUSE	Hexokinase-1 OS=Mus musculus (Mouse) (	2637.04	24	30	25	30	22	24	26	19	18	26	20	20	3	3	3	3	0.59993	0.96	0.09322	0.80	0.36854	0.84
sp|Q61656|DDX5_MOUSE	Probable ATP-dependent RNA helicase DD	1648.2	11	13	13	15	19	18	22	12	16	19	16	20	3	3	3	3	0.01136	1.41	0.08308	1.35	0.00646	1.49
tr|E9PZF0|E9PZF0_MOUSE	Nucleoside diphosphate kinase OS=Mus m	860.91	19	20	19	20	20	21	25	20	23	23	14	20	3	3	3	3	0.89969	1.05	0.00372	1.17	0.38455	0.98
sp|P05201|AATC_MOUSE	Aspartate aminotransferase, cytoplasmic O	1688.59	19	25	18	22	26	14	28	15	22	19	13	20	3	3	3	3	0.82338	1.00	0.58736	1.05	0.73105	0.84
tr|Q3UMT7|Q3UMT7_MOUSE	Putative uncharacterized protein OS=Mus	1676.06	23	27	19	27	29	29	30	22	21	29	23	19	3	3	3	3	0.09508	1.23	0.35112	1.06	0.25465	1.03
sp|Q8CAY6|THIC_MOUSE	Acetyl-CoA acetyltransferase, cytosolic OS	1558.24	25	21	25	21	28	27	21	22	28	18	17	19	3	3	3	3	0.88835	1.07	0.70551	1.00	0.21772	0.76
tr|Q5SW88|Q5SW88_MOUSE	Protein Rab1a OS=Mus musculus (Mouse)	1588.53	27	25	27	20	29	26	26	19	19	28	15	19	3	3	3	3	0.28463	0.95	0.06825	0.81	0.30877	0.78
sp|P11983|TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus	2185.6	16	16	16	17	20	22	19	17	17	17	14	19	3	3	3	3	0.07038	1.23	0.00661	1.10	0.18928	1.04
sp|P08752|GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) sub	1513.98	20	23	21	22	25	23	22	12	14	26	19	18	3	3	3	3	0.23677	1.09	0.10215	0.75	0.19364	0.98
sp|P80316|TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=M	1967.26	25	22	21	14	24	24	16	19	20	23	17	18	3	3	3	3	0.35297	0.91	0.28981	0.81	0.53583	0.85
sp|P0C0S6|H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus (Mouse)	433.71	18	17	18	21	16	19	24	20	18	22	16	18	3	3	3	3	0.91783	1.06	0.02754	1.17	0.02261	1.06
sp|P62821|RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musc	1573.59	27	25	26	20	30	26	26	18	19	28	15	18	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	18	3	3	3	3	0.13046	1.28	0.19480	0.81	0.93314	0.89
sp|Q61990|PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=Mus musculu	957.31	15	15	14	13	11	17	14	16	14	16	13	18	3	3	3	3	0.41649	0.93	0.55743	1.00	0.15873	1.07
sp|Q9DBG3|AP2B1_MOUSE	AP-2 complex subunit beta OS=Mus muscu	2965.74	18	21	15	18	22	22	22	15	13	21	12	18	3	3	3	3	0.33373	1.15	0.81841	0.93	0.69123	0.94
sp|P35802|GPM6A_MOUSE	Neuronal membrane glycoprotein M6-a OS	940.55	18	22	21	25	21	19	25	15	16	24	11	18	3	3	3	3	0.86647	1.07	0.72069	0.92	0.83385	0.87
tr|Q3TJL8|Q3TJL8_MOUSE	Putative uncharacterized protein OS=Mus	1544.02	14	14	15	14	16	15	19	18	16	12	11	18	3	3	3	3	0.92696	1.05	0.01626	1.23	0.69013	0.95
sp|Q922R8|PDIA6_MOUSE	Protein disulfide-isomerase A6 OS=Mus mu	1372.08	13	13	15	14	15	15	18	16	17	11	11	18	3	3	3	3	0.76327	1.07	0.01422	1.24	0.64924	0.98
sp|Q9DCX2|ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS	984.51	17	21	16	19	24	21	23	19	19	24	19	17	3	3	3	3	0.16647	1.19	0.04329	1.13	0.05103	1.11
sp|P27661|H2AX_MOUSE	Histone H2AX OS=Mus musculus (Mouse)	597.44	22	19	17	24	15	14	22	24	12	23	19	17	3	3	3	3	0.59085	0.91	0.81484	1.00	0.18532	1.02
sp|O88809|DCX_MOUSE	Neuronal migration protein doublecortin OS	1375.84	23	21	21	23	22	24	25	20	19	21	18	17	3	3	3	3	0.83381	1.06	0.57601	0.98	0.60520	0.86
sp|Q8BH59|CMC1_MOUSE	Calcium-binding mitochondrial carrier protein	2199.38	11	19	19	15	17	16	17	13	19	12	17	17	3	3	3	3	0.70548	0.98	0.79176	1.00	0.74365	0.94
sp|Q99PT1|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	3	0.84142	1.07	0.83961	0.99	0.49663	0.80
sp|Q01768|NDKB_MOUSE	Nucleoside diphosphate kinase B OS=Mus	717	18	17	15	19	17	19	21	16	19	20	11	17	3	3	3	3	0.55236	1.10	0.05532	1.12	0.62216	0.96
sp|P17879|HS71B_MOUSE	Heat shock 70 kDa protein 1B OS=Mus mu	638.47	17	19	18	15	20	18	14	17	17	15	17	16	3	3	3	3	0.28051	0.98	0.66485	0.89	0.87895	0.89
sp|Q91V12|BACH_MOUSE	Cytosolic acyl coenzyme A thioester hydrola	1042.77	15	19	21	18	22	19	17	13	15	21	15	16	3	3	3	3	0.86284	1.07	0.25566	0.82	0.61255	0.95
sp|Q9CZC8|SCRN1_MOUSE	Secernin-1 OS=Mus musculus (Mouse) GN	1132.8	19	16	17	16	22	21	15	17	14	15	14	16	3	3	3	3	0.46951	1.13	0.60219	0.88	0.85919	0.87
sp|P00366|DHE3_BOVIN	Glutamate dehydrogenase 1, mitochondrial	1634.37	20	16	26	18	18	23	21	15	22	25	13	16	3	3	3	3	0.60967	0.95	0.91522	0.94	0.85258	0.87
sp|Q61768|KINH_MOUSE	Kinesin-1 heavy chain OS=Mus musculus (	1978.89	17	15	14	14	15	19	12	16	12	17	13	16	3	3	3	3	0.95920	1.04	0.64732	0.87	0.18801	1.00
sp|Q8BFR5|EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mu	1075.32	17	17	15	15	16	13	15	13	15	15	13	16	3	3	3	3	0.08323	0.90	0.23179	0.88	0.81531	0.90
sp|Q920E5|FPPS_MOUSE	Farnesyl pyrophosphate synthase OS=Mus	1316.66	19	15	15	13	21	22	12	14	18	12	13	16	3	3	3	3	0.65215	1.14	0.82092	0.90	0.79258	0.84
sp|P63011|RAB3A_MOUSE	Ras-related protein Rab-3A OS=Mus musc	1342.37	16	19	15	12	21	20	18	15	17	18	12	16	3	3	3	3	0.97609	1.06	0.40347	1.00	0.70974	0.92
tr|Q3TXE5|Q3TXE5_MOUSE	Putative uncharacterized protein OS=Mus	1947.04	22	14	15	17	23	24	28	16	16	18	11	16	3	3	3	3	0.35547	1.25	0.39624	1.18	0.94558	0.88
sp|P35564|CALX_MOUSE	Calnexin OS=Mus musculus (Mouse) GN=C	1947.04	22	14	15	17	23	24	28	16	16	18	11	16	3	3	3	3	0.35547	1.25	0.39624	1.18	0.94558	0.88
sp|Q8K310|MATR3_MOUSE	Matrin-3 OS=Mus musculus (Mouse) GN=M	1986.35	26	22	15	20	28	26	22	22	23	25	23	15	3	3	3	3	0.51979	1.17	0.47057	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	21	19	22	17	15	3	3	3	3	0.54915	1.12	0.06792	1.20	0.15555	1.06
sp|Q61699|HS105_MOUSE	Heat shock protein 105 kDa OS=Mus musc	2701.64	15	15	15	15	20	16	23	15	16	16	16	15	3	3	3	3	0.33693	1.13	0.06717	1.20	0.07289	1.04
sp|Q8K2B3|SDHA_MOUSE	Succinate dehydrogenase [ubiquinone] flav	1774.94	18	24	19	21	23	24	27	15	21	21	15	15	3	3	3	3	0.44346	1.11	0.61364	1.03	0.52349	0.84
sp|Q9DBP5|KCY_MOUSE	UMP-CMP kinase OS=Mus musculus (Mous	907.41	12	14	12	12	17	15	16	18	15	18	14	15	3	3	3	3	0.29120	1.16	0.04716	1.29	0.00039	1.24
tr|Q8C2Q8|Q8C2Q8_MOUSE	ATP synthase subunit gamma OS=Mus mu	1130.44	17	20	12	16	18	16	18	14	15	17	13	15	3	3	3	3	0.86872	1.02	0.92447	0.96	0.76868	0.92
sp|P45591|COF2_MOUSE	Cofilin-2 OS=Mus musculus (Mouse) GN=C	936.41	20	21	21	20	18	20	18	16	23	12	12	15	3	3	3	3	0.15391	0.94	0.84992	0.92	0.02932	0.63
sp|P97300|NPTN_MOUSE	Neuroplastin OS=Mus musculus (Mouse) G	804.07	14	28	24	29	23	18	20	19	18	20	19	14	3	3	3	3	0.93248	1.06	0.67060	0.86	0.68297	0.80
sp|P16627|HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus	617.51	18	19	19	18	18	18	15	18	18	15	19	14	3	3	3	3	0.10701	0.96	0.80301	0.91	0.90340	0.86
sp|Q9D6R2|IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alp	1076.87	23	24	21	22	24	17	27	19	18	27	17	14	3	3	3	3	0.27698	0.93	0.84970	0.94	0.71801	0.85
tr|B7FAU8|B7FAU8_MOUSE	Guanosine diphosphate (GDP) dissociation	1023.11	17	20	20	15	19	14	12	17	17	15	16	14	3	3	3	3	0.07095	0.84	0.40437	0.81	0.33704	0.79
sp|P25444|RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculu	900.74	14	12	13	12	12	14	16	11	16	13	16	14	3	3	3	3	0.41048	0.97	0.28381	1.10	0.18428	1.10
sp|P48453|PP2BB_MOUSE	Serine/threonine-protein phosphatase 2B c	1695.68	19	22	14	17	16	14	15	16	16	16	15	14	3	3	3	3	0.23236	0.85	0.53096	0.85	0.59429	0.82
sp|P61264|STX1B_MOUSE	Syntaxin-1B OS=Mus musculus (Mouse) GI	1328.21	20	19	16	22	15	13	14	13	16	13	13	14	3	3	3	3	0.53331	0.91	0.13163	0.78	0.11628	0.73
sp|O55143|AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium	2861.44	14	24	19	19	30	19	22	16	14	17	21	13	3	3	3	3	0.55110	1.19	0.80103	0.91	0.91351	0.89
sp|O08749|DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial	1513.7	23	25	26	23	19	19	19	20	18	21	18	13	3	3	3	3	0.07753	0.82	0.06213	0.77	0.09331	0.70
tr|A2ALL9|A2ALL9_MOUSE	Calcium-transporting ATPase OS=Mus mus	1860.6	18	18	21	19	21	18	17	13	14	12	18	13	3	3	3	3	0.71095	1.02	0.05719	0.77	0.49050	0.75
sp|P62754|RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculu	1177.13	18	19	21	20	21	19	15	15	17	18	17	13	3	3	3	3	0.84869	1.03	0.19129	0.81	0.56142	0.83
sp|Q9Z1W8|AT12A_MOUSE	Potassium-transporting ATPase alpha chain	578.91	18	19	17	21	19	17	18	17	16	19	16	13	3	3	3	3	0.90296	1.06	0.97705	0.94	0.98034	0.89
sp|P62918|RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculu	790.27	16	17	21	24	21	20	19	18	16	16	16	13	3	3	3	3	0.34442	1.20	0.77690	0.98	0.67721	0.83
tr|E9Q1G8|E9Q1G8_MOUSE	Septin-7 OS=Mus musculus (Mouse) GN=S	1529.8	18	16	19	15	24	24	15	16	15	17	11	13	3	3	3	3	0.45942	1.19	0.44312	0.87	0.19503	0.77
sp|Q9CQQ7|AT5F1_MOUSE	ATP synthase F(0) complex subunit B1, mit	925.88	14	17	19	13	16	12	20	14	18	16	11	13	3	3	3	3	0.11631	0.82	0.48807	1.04	0.37699	0.80
sp|Q60864|STIP1_MOUSE	Stress-induced-phosphoprotein 1 OS=Mus	2270.52	27	25	19	23	27	26	27	18	21	22	16	12	3	3	3	3	0.83536	1.07	0.82759	0.93	0.19105	0.70
sp|Q80XN0|BDH_MOUSE	D-beta-hydroxybutyrate dehydrogenase, mi	1102.52	11	18	13	14	17	16	16	12	15	13	16	12	3	3	3	3	0.62908	1.12	0.59982	1.02	0.57430	0.98
sp|Q9QYC0|ADDA_MOUSE	Alpha-adducin OS=Mus musculus (Mouse)	2141.29	21	15	21	18	20	19	21	18	15	19	15	12	3	3	3	3	0.69768	1.00	0.95349	0.95	0.53661	0.81
sp|Q9CXW4|RL11_MOUSE	60S ribosomal protein L11 OS=Mus muscu	555.93	17	15	13	14	16	13	18	11	15	16	15	12	3	3	3	3	0.37053	0.96	0.86297	0.98	0.50611	0.96
sp|P84091|AP2M1_MOUSE	AP-2 complex subunit mu OS=Mus muscul	1806.73	18	21	19	22	27	24	18	14	19	17	14	12	3	3	3	3	0.01438	1.26	0.43886	0.88	0.05045	0.74
sp|Q64436|ATP4A_MOUSE	Potassium-transporting ATPase alpha chain	372.45	18	15	12	14	14	15	13	14	17	14	14	12	3	3	3	3	0.50112	0.96	0.81281	0.98	0.93988	0.89
sp|P19783|COX41_MOUSE	Cytochrome c oxidase subunit 4 isoform 1,	734.44	11	26	27	15	15	14	20	16	15	16	13	12	3	3	3	3	0.23368	0.69	0.54341	0.80	0.31938	0.64
sp|P29387|GBB4_MOUSE	Guanine nucleotide-binding protein subunit	1250.26	16	16	16	15	21	19	13	12	15	13	13	12	3	3	3	3	0.30890	1.15	0.21389	0.83	0.17373	0.79
sp|Q62420|SH3G2_MOUSE	Endophilin-A1 OS=Mus musculus (Mouse)	1081.85	15	14	11	12	16	17	18	16	13	11	12	12	3	3	3	3	0.58543	1.13	0.11753	1.18	0.99272	0.88
sp|Q99JY9|ARP3_MOUSE	Actin-related protein 3 OS=Mus musculus (	1555.7	13	15	13	13	20	27	22	12	11	21	14	11	3	3	3	3	0.21525	1.46	0.53224	1.10	0.21129	1.12
sp|Q8VEM8|MPCP_MOUSE	Phosphate carrier protein, mitochondrial O	1152.74	15	23	18	20	25	19	30	15	16	22	13	11	3	3	3	3	0.52689	1.14	0.60144	1.09	0.64887	0.82
sp|P28663|SNAB_MOUSE	Beta-soluble NSF attachment protein OS=	1520.86	18	18	13	18	21	16	22	15	13	20	13	11	3	3	3	3	0.56826	1.12	0.67565	1.02	0.98918	0.90
sp|P47962|RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculu	1246.86	20	18	14	16	21	16	19	16	14	16	13	11	3	3	3	3	0.81459	1.02	0.94484	0.94	0.29788	0.77
sp|Q61548|AP180_MOUSE	Clathrin coat assembly protein AP180 OS=	1566.84	22	23	13	27	28	16	27	21	17	27	12	11	3	3	3	3	0.51862	1.22	0.39070	1.12	0.85655	0.86
sp|Q9D6M3|GHC1_MOUSE	Mitochondrial glutamate carrier 1 OS=Mus	1169.97	11	17	13	11	16	14	17	11	11	16	12	11	3	3	3	3	0.73771	1.00	0.97292	0.95	0.60651	0.95
sp|P35979|RL12_MOUSE	60S ribosomal protein L12 OS=Mus muscu	629.05	12	15	12	12	15	16	13	13	12	12	11	11	3	3	3	3	0.58951	1.10	0.69265	0.97	0.90232	0.87
sp|Q99KJ8|DCTN2_MOUSE	Dynactin subunit 2 OS=Mus musculus (Mo	1599.56	16	17	14	21	21	20	23	20	18	18	16	10	3	3	3	3	0.01381	1.32	0.00565	1.30	0.74409	0.94
sp|P14206|RSSA_MOUSE	40S ribosomal protein SA OS=Mus muscul	912.4	14	13	12	11	11	12	17	13	11	15	12	10	3	3	3	3	0.03540	0.87	0.37281	1.05	0.49551	0.95
sp|P40124|CAP1_MOUSE	Adenylyl cyclase-associated protein 1 OS=	1621.71	15	16	15	14	18	16	16	12	12	13	11	10	3	3	3	3	0.86528	1.04	0.08562	0.87	0.00826	0.74
sp|Q64332|SYN2_MOUSE	Synapsin-2 OS=Mus musculus (Mouse) GN	1788.52	17	23	16	20	23	14	17	18	11	21	19	9	3	3	3	3	0.88556	1.02	0.47103	0.82	0.95673	0.88
sp|Q02248|CTNB1_MOUSE	Catenin beta-1 OS=Mus musculus (Mouse)	1767.77	15	17	14	15	17	16	19	14	15	21	12	8	3	3	3	3	0.92417	1.04	0.15168	1.04	0.94516	0.89
sp|P63024|VAMP3_MOUSE	Vesicle-associated membrane protein 3 OS	567.73	13	19	14	18	12	11	12	12	11	11	12	8	3	3	3	3	0.51841	0.89	0.15975	0.76	0.18931	0.67
sp|Q8CAQ8|MIC60_MOUSE	MICOS complex subunit Mic60 OS=Mus mu	2234.71	16	25	21	21	21	23	19	14	13	22	13	7	3	3	3	3	0.97786	1.05	0.15098	0.74	0.31924	0.68
sp|Q11011|PSA_MOUSE	Puromycin-sensitive aminopeptidase OS=M	2334.27	12	17	17	13	19	19	16	17	17	14	10	19	3	3	3	3	0.73901	1.11	0.32246	1.09	0.80608	0.93
tr|Q6GT24|Q6GT24_MOUSE	Peroxiredoxin 6 OS=Mus musculus (Mouse	1191.46	13	16	18	18	18	19	28	15	15	22	9	16	3	3	3	3	0.34001	1.17	0.29818	1.23	0.67224	1.00
sp|Q8K1M6|DNM1L_MOUSE	Dynamin-1-like protein OS=Mus musculus (	2442.93	14	14	16	15	19	19	21	15	16	20	10	15	3	3	3	3	0.16337	1.20	0.05124	1.18	0.45953	1.02
tr|Q3U4P3|Q3U4P3_MOUSE	Putative uncharacterized protein OS=Mus	2363.76	13	13	15	14	18	18	21	14	15	20	9	14	3	3	3	3	0.15772	1.22	0.07130	1.22	0.46741	1.05
tr|E9PUD2|E9PUD2_MOUSE	Dynamin-1-like protein OS=Mus musculus (	2262.29	11	11	14	12	18	18	19	14	14	17	9	14	3	3	3	3	0.18147	1.33	0.03843	1.31	0.27212	1.11
sp|P61164|ACTZ_MOUSE	Alpha-centractin OS=Mus musculus (Mouse	1067.64	12	12	17	11	21	16	23	15	13	17	10	13	3	3	3	3	0.66642	1.17	0.24296	1.24	0.64328	0.98
sp|O55131|SEPT7_MOUSE	Septin-7 OS=Mus musculus (Mouse) GN=S	1470.51	17	14	18	15	23	23	14	14	14	15	9	12	3	3	3	3	0.32186	1.24	0.41742	0.86	0.19389	0.73
sp|P61294|RAB6B_MOUSE	Ras-related protein Rab-6B OS=Mus musc	962.39	14	16	12	12	20	15	16	13	11	16	8	12	3	3	3	3	0.68357	1.12	0.98425	0.95	0.76910	0.86
sp|O55022|PGRC1_MOUSE	Membrane-associated progesterone recept	903	16	19	19	20	19	22	20	19	15	19	7	12	3	3	3	3	0.39060	1.13	0.61189	1.00	0.26087	0.70
sp|P47857|PFKAM_MOUSE	ATP-dependent 6-phosphofructokinase, mu	1681.58	12	14	13	14	19	16	16	13	12	12	7	11	3	3	3	3	0.06827	1.26	0.14229	1.05	0.26682	0.77
sp|P29341|PABP1_MOUSE	Polyadenylate-binding protein 1 OS=Mus n	1596.64	17	16	13	16	22	22	23	12	16	22	9	10	3	3	3	3	0.10734	1.30	0.41647	1.11	0.92412	0.89
sp|Q9QUI0|RHOA_MOUSE	Transforming protein RhoA OS=Mus muscu	905.49	16	12	16	17	17	17	18	16	11	17	8	10	3	3	3	3	0.41698	1.16	0.69621	1.02	0.51999	0.80
sp|Q61166|MARE1_MOUSE	Microtubule-associated protein RP/EB famil	1452.61	24	14	13	22	20	18	26	13	12	19	9	9	3	3	3	3	0.61744	1.18	0.92890	1.00	0.48112	0.73
sp|Q9QYR6|MAP1A_MOUSE	Microtubule-associated protein 1A OS=Mus	2968.44	21	16	13	18	25	20	20	11	12	22	10	7	3	3	3	3	0.29367	1.26	0.59132	0.86	0.62121	0.78
sp|Q8BP67|RL24_MOUSE	60S ribosomal protein L24 OS=Mus muscu	709.37	19	13	13	16	12	13	14	14	11	13	10	6	3	3	3	3	0.50917	0.91	0.61686	0.87	0.20405	0.64
sp|P14211|CALR_MOUSE	Calreticulin OS=Mus musculus (Mouse) GN	1727.01	18	15	16	17	17	13	20	11	18	11	4	13	3	3	3	3	0.48636	0.96	0.79752	1.00	0.13841	0.57
tr|Q66JR8|Q66JR8_MOUSE	Ptms protein OS=Mus musculus (Mouse) G	949.3	20	20	13	20	21	15	22	12	17	16	3	8	3	3	3	3	0.93973	1.06	0.97749	0.96	0.12656	0.51
sp|P09103|PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus muscu	1745.69	18	14	15	17	18	28	14	13	22	10	11	14	3	3	3	3	0.28542	1.34	0.66930	1.04	0.37951	0.74
sp|O08788|DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus (Mo	2644.43	13	13	13	12	13	17	16	11	14	10	13	12	3	3	3	3	0.82248	1.08	0.23728	1.05	0.83709	0.90
sp|P63085|MK01_MOUSE	Mitogen-activated protein kinase 1 OS=Mu	1485.02	14	19	22	15	19	14	13	11	10	18	16	15	3	3	3	3	0.31537	0.87	0.06271	0.62	0.96463	0.89
sp|Q9EPN1|NBEA_MOUSE	Neurobeachin OS=Mus musculus (Mouse)	2993.8	23	19	11	18	23	11	20	11	9	21	14	8	3	3	3	3	0.82519	0.98	0.42737	0.75	0.73883	0.81
tr|B1AQX9|B1AQX9_MOUSE	SRC kinase-signaling inhibitor 1 OS=Mus m	2324.17	15	14	13	16	20	12	13	12	6	16	11	5	3	3	3	3	0.58992	1.14	0.22947	0.74	0.51466	0.76
sp|Q9QXS6|DREB_MOUSE	Drebrin OS=Mus musculus (Mouse) GN=Db	1891.75	11	15	11	14	23	15	15	12	8	16	10	7	3	3	3	3	0.17300	1.41	0.96616	0.95	0.96841	0.89
tr|A2AEG6|A2AEG6_MOUSE	Glycoprotein m6b, isoform CRA_g OS=Mus	1100.73	12	19	14	20	19	12	14	15	6	19	9	6	3	3	3	3	0.69485	1.13	0.49659	0.78	0.54622	0.76
tr|Q3US81|Q3US81_MOUSE	Glycoprotein m6b, isoform CRA_f OS=Mus	1014.26	13	19	13	21	17	11	14	15	6	20	9	6	3	3	3	3	0.83996	1.09	0.49065	0.78	0.61790	0.78
sp|B2RSH2|GNAI1_MOUSE	Guanine nucleotide-binding protein G(i) sub	1397.24	16	19	17	20	22	20	23	8	12	28	12	15	3	3	3	3	0.03453	1.19	0.52177	0.83	0.51658	1.06
sp|Q91ZX7|LRP1_MOUSE	Prolow-density lipoprotein receptor-related p	2988.659	14	13	20	12	15	16	19	9	16	19	16	14	3	3	3	3	0.46378	0.91	0.89421	0.94	0.37135	1.04
sp|Q99K48|NONO_MOUSE	Non-POU domain-containing octamer-bindir	1631.88	15	11	14	16	18	15	15	9	14	23	14	8	3	3	3	3	0.23717	1.23	0.95563	0.95	0.48578	1.13
tr|Q3TMM5|Q3TMM5_MOUSE	Putative uncharacterized protein OS=Mus	1573.05	15	11	14	15	15	14	13	9	14	21	14	8	3	3	3	3	0.70143	1.10	0.73210	0.90	0.53005	1.08
sp|P60766|CDC42_MOUSE	Cell division control protein 42 homolog OS	731.85	11	18	20	24	19	22	19	9	13	20	7	12	3	3	3	3	0.26839	1.33	0.57257	0.84	0.64978	0.80
sp|P61922|GABT_MOUSE	4-aminobutyrate aminotransferase, mitocho	1735.91	12	15	22	12	17	14	15	10	14	15	7	13	3	3	3	3	0.45057	0.88	0.46347	0.80	0.42734	0.71
sp|P62827|RAN_MOUSE	GTP-binding nuclear protein Ran OS=Mus	764.27	15	20	14	13	16	16	15	7	13	14	10	12	3	3	3	3	0.28250	0.92	0.18346	0.71	0.16044	0.73
sp|Q9R111|GUAD_MOUSE	Guanine deaminase OS=Mus musculus (M	1653.59	14	22	12	15	21	15	13	10	12	13	9	13	3	3	3	3	0.93741	1.06	0.25812	0.73	0.40786	0.73
sp|P21550|ENOB_MOUSE	Beta-enolase OS=Mus musculus (Mouse) (	788.79	16	14	11	14	15	14	15	10	11	13	9	11	3	3	3	3	0.98611	1.05	0.53118	0.88	0.44333	0.80
sp|Q8CI94|PYGB_MOUSE	Glycogen phosphorylase, brain form OS=M	2449.65	17	13	11	12	15	18	17	9	16	12	7	11	3	3	3	3	0.80698	1.10	0.75483	1.02	0.32696	0.73
sp|Q8BHN3|GANAB_MOUSE	Neutral alpha-glucosidase AB OS=Mus mu	1583.16	11	11	12	13	14	14	15	8	12	11	6	11	3	3	3	3	0.03795	1.21	0.65282	1.03	0.63250	0.82
sp|Q921M7|FA49B_MOUSE	Protein FAM49B OS=Mus musculus (Mouse	1293.53	13	15	14	17	15	16	13	9	12	13	7	10	3	3	3	3	0.30646	1.14	0.09841	0.81	0.10291	0.71
sp|P35486|ODPA_MOUSE	Pyruvate dehydrogenase E1 component su	1415.52	12	23	15	16	20	17	14	9	15	9	16	10	3	3	3	3	0.94013	1.06	0.39919	0.76	0.52599	0.70
sp|P62270|RS18_MOUSE	40S ribosomal protein S18 OS=Mus muscu	865.98	12	15	13	12	14	16	13	10	14	10	8	14	3	3	3	3	0.99096	1.05	0.83569	0.93	0.63983	0.80
sp|Q9DC51|GNAI3_MOUSE	Guanine nucleotide-binding protein G(k) sul	873.53	12	15	14	16	16	14	16	7	9	21	11	11	3	3	3	3	0.43999	1.12	0.30578	0.78	0.45573	1.05
sp|Q7TQF7|AMPH_MOUSE	Amphiphysin OS=Mus musculus (Mouse) G	1643.93	17	19	15	19	17	16	23	8	10	16	13	8	3	3	3	3	0.82643	1.02	0.49313	0.80	0.24688	0.73
sp|P62908|RS3_MOUSE	40S ribosomal protein S3 OS=Mus musculu	1373.31	22	17	14	18	14	13	14	10	10	18	7	10	3	3	3	3	0.34185	0.85	0.07545	0.64	0.24498	0.66
sp|P12970|RL7A_MOUSE	60S ribosomal protein L7a OS=Mus muscu	1257.87	13	19	11	21	22	16	22	7	8	20	9	6	3	3	3	3	0.18103	1.37	0.72725	0.86	0.73862	0.81
sp|P63158|HMGB1_MOUSE	High mobility group protein B1 OS=Mus mu	953.85	18	15	12	14	16	20	14	4	22	14	8	10	3	3	3	3	0.71753	1.11	0.87264	0.89	0.20494	0.71
sp|P62281|RS11_MOUSE	40S ribosomal protein S11 OS=Mus muscu	694.79	15	12	11	13	15	16	9	13	12	11	10	9	3	3	3	3	0.39448	1.16	0.82819	0.89	0.36943	0.79
sp|Q9CR57|RL14_MOUSE	60S ribosomal protein L14 OS=Mus muscu	683.14	15	13	12	17	16	14	10	12	8	14	11	8	3	3	3	3	0.32588	1.18	0.19904	0.75	0.58357	0.83
sp|Q8CHC4|SYNJ1_MOUSE	Synaptojanin-1 OS=Mus musculus (Mouse)	1711.89	12	17	13	15	16	14	5	7	10	9	8	12	3	3	3	3	0.80774	1.07	0.05112	0.52	0.22620	0.69
tr|A0A0A6YX73|A0A0A6YX73_I	cAMP-dependent protein kinase type II-alph	1355.41	18	13	12	16	11	10	15	15	17	11	12	15	3	3	3	3	0.44134	0.86	0.37913	1.09	0.95377	0.88
tr|Q7M6W1|Q7M6W1_MOUSE	Reticulon OS=Mus musculus (Mouse) GN=	747.12	17	17	16	16	17	8	18	14	14	13	10	13	3	3	3	3	0.26512	0.82	0.35007	0.92	0.03217	0.72
sp|Q9Z0E0|NCDN_MOUSE	Neurochondrin OS=Mus musculus (Mouse)	1897.7	19	18	19	16	15	9	16	12	9	19	18	13	3	3	3	3	0.06717	0.71	0.02713	0.66	0.94368	0.89
sp|O35295|PURB_MOUSE	Transcriptional activator protein Pur-beta O	1168.62	11	17	13	14	15	8	11	15	9	13	13	8	3	3	3	3	0.52261	0.90	0.69241	0.85	0.76132	0.83
tr|Q14BH8|Q14BH8_MOUSE	Cacna2d1 protein OS=Mus musculus (Mou	2067.48	13	21	26	21	18	7	14	14	7	28	14	6	3	3	3	3	0.41641	0.77	0.16927	0.58	0.73280	0.80
sp|Q8K0T0|RTN1_MOUSE	Reticulon-1 OS=Mus musculus (Mouse) GN	1043.85	20	16	11	20	15	6	17	11	9	11	6	8	3	3	3	3	0.64519	0.87	0.41682	0.79	0.08158	0.53
sp|P21279|GNAQ_MOUSE	Guanine nucleotide-binding protein G(q) su	2059.83	16	15	21	14	14	10	14	10	13	15	15	10	3	3	3	3	0.11036	0.73	0.12933	0.71	0.47315	0.77
sp|Q9D0J8|PTMS_MOUSE	Parathymosin OS=Mus musculus (Mouse) (	757.55	20	17	12	22	18	10	23	6	14	19	4	7	3	3	3	3	0.95288	1.02	0.75046	0.88	0.30560	0.61
sp|P62761|VISL1_MOUSE	Visinin-like protein 1 OS=Mus musculus (M	1262.67	12	14	13	12	14	9	11	10	8	15	8	6	3	3	3	3	0.25260	0.90	0.03263	0.74	0.36820	0.74
sp|P28667|MRP_MOUSE	MARCKS-related protein OS=Mus musculu	1022.71	17	17	11	18	14	10	12	9	10	17	10	7	3	3	3	3	0.66174	0.93	0.09079	0.69	0.47409	0.76
sp|O89053|COR1A_MOUSE	Coronin-1A OS=Mus musculus (Mouse) GN	1128.61	12	15	12	13	16	9	13	8	7	14	7	6	3	3	3	3	0.67155	0.97	0.10136	0.72	0.23237	0.69
sp|Q8BRT1|CLAP2_MOUSE	CLIP-associating protein 2 OS=Mus muscu	2095.55	14	11	11	20	9	12	9	11	10	15	11	7	3	3	3	3	0.75893	1.14	0.44112	0.83	0.91731	0.92
sp|Q91V41|RAB14_MOUSE	Ras-related protein Rab-14 OS=Mus muscu	1105.42	15	15	15	8	18	18	19	12	17	17	12	20	3	3	3	3	0.70017	0.98	0.33661	1.07	0.26712	1.09
sp|Q8R0Y6|AL1L1_MOUSE	Cytosolic 10-formyltetrahydrofolate dehydro	2465.9	11	15	13	9	19	20	13	15	19	7	12	14	3	3	3	3	0.54319	1.23	0.23255	1.21	0.95607	0.85
sp|Q8BMK4|CKAP4_MOUSE	Cytoskeleton-associated protein 4 OS=Mus	1915.31	14	13	15	10	12	17	13	8	13	12	8	12	3	3	3	3	0.45927	0.93	0.28260	0.81	0.25235	0.76
tr|Q50HX0|Q50HX0_MOUSE	RAB14 protein OS=Mus musculus (Mouse)	1025.89	14	13	13	6	12	12	14	8	15	16	10	17	3	3	3	3	0.08890	0.75	0.85876	0.93	0.29038	1.08
sp|Q6PHN9|RAB35_MOUSE	Ras-related protein Rab-35 OS=Mus muscu	566.89	11	12	12	8	12	13	14	8	10	12	5	11	3	3	3	3	0.38671	0.94	0.67207	0.91	0.58138	0.80
sp|P61027|RAB10_MOUSE	Ras-related protein Rab-10 OS=Mus muscu	893	17	15	14	10	11	14	10	12	14	11	8	14	3	3	3	3	0.03804	0.76	0.27141	0.78	0.27445	0.72
sp|Q9D394|RUFY3_MOUSE	Protein RUFY3 OS=Mus musculus (Mouse)	1372.56	11	12	14	10	14	14	10	6	12	10	9	10	3	3	3	3	0.82433	1.03	0.29604	0.76	0.30648	0.78
sp|Q9D1G1|RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus muscu	907.42	12	11	13	8	13	10	12	7	8	12	8	10	3	3	3	3	0.17316	0.86	0.10960	0.75	0.48421	0.83







sp|P14685|PSMD3_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|ES1_MOUSE	ES1 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	0.51669	0.83	0.99162	0.92
sp|P70404|IDHG1_MOUSE	Isocitrate dehydrogenase [NAD] subunit ga	687.04	4	4	4	4	8	7	4	3	2	6	3	1	3	3	3	3	0.11544	1.58	0.14600	0.75	0.79541	0.83
sp|Q9Z0N1|IF2G_MOUSE	Eukaryotic translation initiation factor 2 subu	812.94	4	5	5	3	9	6	5	4	5	5	2	5	3	3	3	3	0.56200	1.29	0.59571	1.00	0.85425	0.86
sp|Q9JMA1|UBP14_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	0.16969	0.69
sp|Q9D6J6|NDUV2_MOUSE	NADH dehydrogenase [ubiquinone] flavopr	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	3	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|Q9D8B3|CHM4B_MOUSE	Charged multivesicular body protein 4b OS	480.04	4	5	4	5	8	9	3	4	3	3	3	2	3	3	3	3	0.06429	1.69	0.24923	0.77	0.04704	0.62
sp|O89086|RBM3_MOUSE	RNA-binding protein 3 OS=Mus musculus (	360.08	5	5	2	5	6	9	3	2	5	5	5	4	3	3	3	3	0.17740	1.67	0.76560	0.83	0.27847	1.17
sp|O70172|PI42A_MOUSE	Phosphatidylinositol 5-phosphate 4-kinase	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|Q07076|ANXA7_MOUSE	Annexin A7 OS=Mus musculus (Mouse) GN	707.73	2	5	4	2	6	6	4		4	4	5	3	3	3	2	3	0.64087	1.27	0.59550	0.73	0.47625	1.09
tr|A2AWI7|A2AWI7_MOUSE	Endophilin-B2 OS=Mus musculus (Mouse)	802.84	5	4	5	3	6	5	7	8	5	7	5	5	3	3	3	3	0.75347	1.00	0.10549	1.43	0.03234	1.21
sp|P84084|ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus musculu	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|Q61036|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|Q8BVQ5|PPME1_MOUSE	Protein phosphatase methylesterase 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|Q9DB05|SNAA_MOUSE	Alpha-soluble NSF attachment protein OS=	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|GPC4_MOUSE	Glypican-4 OS=Mus musculus (Mouse) GN	570.77	3	3	3	3	6	3	7	2		5	2		3	3	2	2	0.41149	1.33	0.98486	1.00	0.73508	0.78
sp|Q8BGZ1|HPCL4_MOUSE	Hippocalcin-like protein 4 OS=Mus musculu	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 (Mou	274.52	3	5	3	5	7	5	3	3	2	5	4	2	3	3	3	3	0.08685	1.55	0.29063	0.73	0.68731	1.00
sp|Q9CQ69|QCR8_MOUSE	Cytochrome b-c1 complex subunit 8 OS=M	204.93	3	3	2	5	6	4	5	4	3	4	3	4	3	3	3	3	0.02333	1.88	0.04761	1.50	0.02622	1.38
sp|Q8VDJ3|VIGLN_MOUSE	Vigilin OS=Mus musculus (Mouse) GN=Hdlb	721.67	2	2	3	2	6	5	2	2	2	5	3	2	3	3	3	3	0.19499	1.86	0.59688	0.86	0.18593	1.43
sp|Q60973|RBBP7_MOUSE	Histone-binding protein RBBP7 OS=Mus m	371.66	3	4	2	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|Q9CZ30|OLA1_MOUSE	Obg-like ATPase 1 OS=Mus musculus (Mou	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|Q810U3|NFASC_MOUSE	Neurofascin OS=Mus musculus (Mouse) GN	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	0.29224	0.60
sp|Q9CPV4|GLOD4_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	0.12915	1.55	0.13869	0.55	0.53235	0.73
sp|P48678|LMNA_MOUSE	Prelamin-A/C OS=Mus musculus (Mouse) G	810.12	3	5	2	5	6	5	5		3	7		2	3	3	2	2	0.09975	1.60	0.71737	0.80	0.93471	0.90
sp|Q64010|CRK_MOUSE	Adapter molecule crk OS=Mus musculus (M	396.15	2	4	2	3	6	5	4		1	4		2	3	3	2	2	0.13301	1.75	0.46961	0.63	0.70596	0.75
sp|Q00PI9|HNRL2_MOUSE	Heterogeneous nuclear ribonucleoprotein U	1009.1	4	4	3	4	6	5		4	8	3	2	3	3	3	2	3	0.09483	1.36	0.77397	1.09	0.19741	0.73
tr|Q3ULG4|Q3ULG4_MOUSE	Putative uncharacterized protein OS=Mus	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	0.11142	1.36
sp|O35226|PSMD4_MOUSE	26S proteasome non-ATPase regulatory su	565.88	3	4	3	4	4	6	6	6	5	4	6	5	3	3	3	3	0.16901	1.40	0.00567	1.70	0.07647	1.50
sp|P62627|DLRB1_MOUSE	Dynein light chain roadblock-type 1 OS=Mu	356.71	5	5	4	4	5	8	6	3	6	7	5	4	3	3	3	3	0.55644	1.21	0.59786	1.07	0.13944	1.14
sp|Q9CQ92|FIS1_MOUSE	Mitochondrial fission 1 protein OS=Mus mu	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|P84089|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	0.59060	1.43	0.85347	0.86
sp|Q8C2Q3|RBM14_MOUSE	RNA-binding protein 14 OS=Mus musculus	637.43	5	2	2	3	3	6	8	1	1	5	4	1	3	3	3	3	0.59289	1.33	0.91968	1.11	0.69132	1.11
sp|Q05920|PYC_MOUSE	Pyruvate carboxylase, mitochondrial OS=M	932.4	3	4	4	3	5	9	5	6	9	4	7	10	3	3	3	3	0.36545	1.55	0.08599	1.82	0.12357	1.91
sp|Q9EQ20|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|O35136|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|SNG3_MOUSE	Synaptogyrin-3 OS=Mus musculus (Mouse)	380.12	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|Q9Z1B3|PLCB1_MOUSE	1-phosphatidylinositol 4,5-bisphosphate ph	1775.46	4	5	4	3	5	8	3	5	4	3	5	8	3	3	3	3	0.62117	1.23	0.98238	0.92	0.37401	1.23
sp|Q3TXS7|PSMD1_MOUSE	26S proteasome non-ATPase regulatory su	1111.44	3	4	4	2	5	6	4	3	4	3	3	4	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 mu	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	4	2	6	3	3	5	3	3	5	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 subu	1364.08	5	5	4	3	4	6	4	3	3	5	2	2	3	3	3	3	0.55089	0.93	0.02037	0.71	0.19506	0.64
sp|O08807|PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus musculus (Mouse	286.26	2	3	2	2	4	6	4	2	3	4	2	2	3	3	3	3	0.25337	1.71	0.20635	1.29	0.35533	1.14
sp|Q9JLV5|CUL3_MOUSE	Cullin-3 OS=Mus musculus (Mouse) GN=Cu	823.51	3	2	2	3	2	6	3	2	1	2	2	2	3	3	3	3	0.38003	1.57	0.68609	0.86	0.88007	0.86
sp|Q9D1D4|TMEDA_MOUSE	Transmembrane emp24 domain-containing	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
tr|E9PV44|E9PV44_MOUSE	ATPase inhibitor, mitochondrial OS=Mus m	379.47	4	5	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|Q2NL51|GSK3A_MOUSE	Glycogen synthase kinase-3 alpha OS=Mu	713.43	4	4	5	5	5	3	7	4	4	7	2	3	3	3	3	3	0.81298	1.00	0.36674	1.15	0.99045	0.92
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	Elongation factor 1-delta OS=Mus musculu	468.92	4	5	2	4	4	2	6	4	2	6	3	1	3	3	3	3	0.69481	0.91	0.72167	1.09	0.99212	0.91
sp|Q07813|BAX_MOUSE	Apoptosis regulator BAX OS=Mus musculu	639.02	4	4	5	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|Q9QZ88|VPS29_MOUSE	Vacuolar protein sorting-associated protein	322.53	2	4	2	3	3	4	6	2	3	2	2	2	3	3	3	3	0.47328	1.25	0.40071	1.38	0.58760	0.75
sp|P09671|SODM_MOUSE	Superoxide dismutase [Mn], mitochondrial	330.48	2	3	3	3	4	4	6	3	3	4	2	1	3	3	3	3	0.11027	1.38	0.15777	1.50	0.89607	0.88
sp|P62774|MTPN_MOUSE	Myotrophin OS=Mus musculus (Mouse) GN	270.46	4	4	2	5	3	3	6	1	3	5	2	2	3	3	3	3	0.83056	1.10	0.97352	1.00	0.96836	0.90
sp|P18572|BASI_MOUSE	Basigin OS=Mus musculus (Mouse) GN=Bs	473.14	5	5	3	4	4	2	4	6	6	2	2	5	3	3	3	3	0.28180	0.77	0.28816	1.23	0.57021	0.69
tr|B1AQZ0|B1AQZ0_MOUSE	Septin-8 OS=Mus musculus (Mouse) GN=S	459.52	4	3	2	4	5	4	3	6	3	4	3	3	3	3	3	3	0.13983	1.44	0.39326	1.33	0.26777	1.11
sp|Q9ER72|SYCC_MOUSE	Cysteine--tRNA ligase, cytoplasmic OS=Mu	749.17	5	4	4	3	4	4	2	6	4	3	3	2	3	3	3	3	0.11462	0.85	0.98544	0.92	0.06743	0.62
sp|Q8K3J1|NDUS8_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	268.64	4	3	3	4	2	3	2	6	4	4	4	4	3	3	3	3	0.58411	0.90	0.52148	1.20	0.05744	1.20
sp|Q62095|DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y OS=	861.29	5	5	5	4	4	5	5	3	10	2	7	8	3	3	3	3	0.05883	0.87	0.58973	1.20	0.51246	1.13
sp|P15209|NTRK2_MOUSE	BDNF/NT-3 growth factors receptor OS=Mu	463.39	5	3	4	2	3	4	3	4	6	4	4	4	3	3	3	3	0.21809	0.75	0.63671	1.08	0.48083	1.00
sp|Q9WVK4|EHD1_MOUSE	EH domain-containing protein 1 OS=Mus m	980.12	5	5	5	3	4	5	5	3	6	3	4	4	3	3	3	3	0.07428	0.80	0.92258	0.93	0.28396	0.73
sp|Q6P5E4|UGGG1_MOUSE	UDP-glucose:glycoprotein glucosyltransfera	924.74	3	3	5	5	4	3	5	2	6	4	1	1	3	3	3	3	0.88226	1.09	0.59337	1.18	0.25679	0.55
sp|Q8C0C7|SYFA_MOUSE	Phenylalanine--tRNA ligase alpha subunit	701.9	2	4	4	2	4	2	3	5	5	6	5	3	3	3	3	3	0.40119	0.80	0.30247	1.30	0.15015	1.40
tr|A2AFQ2|A2AFQ2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2	757.86	4	4	4	3	4	4	5	2	4	6	3	4	3	3	3	3	0.09619	0.92	0.80268	0.92	0.28882	1.08
sp|Q60692|PSB6_MOUSE	Proteasome subunit beta type-6 OS=Mus r	284.8	4	3	3	5	5	4	5	3	3	6	3	3	3	3	3	3	0.09430	1.40	0.46105	1.10	0.27824	1.20
sp|Q06185|ATP5I_MOUSE	ATP synthase subunit e, mitochondrial OS	247.06	4	4	3	4	5	4	5	3	3	6	3	2	3	3	3	3	0.27219	1.18	0.79494	1.00	0.76020	1.00
sp|P59279|RAB2B_MOUSE	Ras-related protein Rab-2B OS=Mus musc	480.35	5	3	5	5	5	3	4	2	3	6	3	3	3	3	3	3	0.84067	1.00	0.22128	0.69	0.96655	0.92
sp|P52503|NDUS6_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	263.42	3	4	2	2	2	4	5	2	2	6	2	2	3	3	3	3	0.61540	0.89	0.93463	1.00	0.65427	1.11
sp|Q91WD5|NDUS2_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	705.59	4	2	2	3	5	4	4	2	2	6	1	1	3	3	3	3	0.24048	1.50	0.93329	1.00	0.94729	1.00
sp|P14869|RLA0_MOUSE	60S acidic ribosomal protein P0 OS=Mus m	786.01	4	4	3	4	5	5	4	2	2	5	5	6	3	3	3	3	0.09027	1.27	0.19852	0.73	0.02370	1.45
sp|Q60900|ELAV3_MOUSE	ELAV-like protein 3 OS=Mus musculus (Mo	554.62	4	4	2	2	3	4	2	2	4	3	4	6	3	3	3	3	0.59039	0.90	0.66700	0.80	0.27639	1.30
sp|Q3TWW8|SRSF6_MOUSE	Serine/arginine-rich splicing factor 6 OS=M	359.87	4	5	3	3	3	5	3	2	4	3	2	6	3	3	3	3	0.57449	0.92	0.36976	0.75	0.89977	0.92
sp|Q9CS84|NRX1A_MOUSE	Neurexin-1 OS=Mus musculus (Mouse) GN	854.37	3	3	3	2	4	4	3	4	3	4	4	4	3	3	3	3	0.81149	1.11	0.34084	1.11	0.00676	1.33
sp|P26231|CTNA1_MOUSE	Catenin alpha-1 OS=Mus musculus (Mouse	511.84	4	5	3	5	3	5	3	3	4	3	4	4	3	3	3	3	0.83964	1.08	0.55423	0.83	0.77614	0.92
sp|Q91VR5|DDX1_MOUSE	ATP-dependent RNA helicase DDX1 OS=M	809.08	4	2	4	3	5	4	2	2	5	4	3	4	3	3	3	3	0.63879	1.20	0.92051	0.90	0.37425	1.10
sp|P61750|ARF4_MOUSE	ADP-ribosylation factor 4 OS=Mus musculu	687.81	5	4	4	2	5	2	4	2	4	4	3	4	3	3	3	3	0.17974	0.69	0.30264	0.77	0.69887	0.85
sp|Q9JKB1|UCHL3_MOUSE	Ubiquitin carboxyl-terminal hydrolase isozym	535.23	5	3	4	3	3	5	2	2	4	4	3	4	3	3	3	3	0.58398	0.92	0.30710	0.67	0.86750	0.92
sp|Q8QZY1|EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subu	733.82	4	2	3	2	4	3	4	4	2	4	3	4	3	3	3	3	0.82018	1.00	0.62320	1.11	0.17514	1.22
sp|Q921H8|THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS	591.05	5	2	5	4	5	3	3	5	5	3	3	4	3	3	3	3	0.85357	1.00	0.67689	1.08	0.85414	0.83
sp|Q9QZQ1|AFAD_MOUSE	Afadin OS=Mus musculus (Mouse) GN=Mllt	889.35	4	4	2	5	4	5	4	3	5	3	3	4	3	3	3	3	0.20339	1.40	0.36755	1.20	0.57408	1.00
sp|Q8R464|CADM4_MOUSE	Cell adhesion molecule 4 OS=Mus musculu	441.66	5	5	4	3	2	3	3	2	5	3	2	4	3	3	3	3	0.01095	0.57	0.33504	0.71	0.16327	0.64
sp|Q9EPU0|RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=M	806.25	3	4	2	2	3	2	5	2	4	3	2	4	3	3	3	3	0.25627	0.78	0.42708	1.22	0.65151	1.00
sp|Q6ZWU9|RS27_MOUSE	40S ribosomal protein S27 OS=Mus muscu	226.59	3	5	5	5	5	5	4	3	3	5	4	3	3	3	3	3	0.54696	1.15	0.28383	0.77	0.85359	0.92
sp|Q8C0M9|ASGL1_MOUSE	Isoaspartyl peptidase/L-asparaginase OS=	469.85	4	4	4	4	4	4	3	4	4	2	4	3	3	3	3	3	0.28226	1.00	0.89428	0.92	0.58720	0.75
sp|Q8BX10|PGAM5_MOUSE	Serine/threonine-protein phosphatase PGA	382.38	3	5	4	3	3	2	5	4	2	2	4	3	3	3	3	3	0.08278	0.67	0.87291	0.92	0.64949	0.75
tr|A0A087WQA5|A0A087WQA5_	TAR DNA-binding protein 43 OS=Mus mus	341.48	2	3	3	3	5	2	5	4	3	5	3	3	3	3	3	3	0.58872	1.25	0.05258	1.50	0.06407	1.38
sp|P11031|TCP4_MOUSE	Activated RNA polymerase II transcriptional	521.45	4	3	5	4	4	4	3	2	4	4	3	3	3	3	3	3	0.77426	1.00	0.39903	0.75	0.69700	0.83
sp|Q9CQ54|NDUC2_MOUSE	NADH dehydrogenase [ubiquinone] 1 subu	228.76	2	3	4	4	4	4	2	3	3	3	3	3	3	3	3	3	0.26270	1.33	0.86210	0.89	0.56611	1.00
sp|P27601|GNA13_MOUSE	Guanine nucleotide-binding protein subunit	282.19	3	3	3	3	3	2	2	3	3	3	3	3	3	3	3	3	0.26598	0.89	0.79395	0.89	0.14609	1.00
sp|Q9EST5|AN32B_MOUSE	Acidic leucine-rich nuclear phosphoprotein	276.63	3	2	2	3	3	3	3	2	3	3	3	3	3	3	3	3	0.21407	1.29	0.36599	1.14	0.05862	1.29
sp|A2A8L5|PTPRF_MOUSE	Receptor-type tyrosine-protein phosphatase	398.74	2	3	3	2	3	2	2	2	2	3	3	3	3	3	3	3	0.34192	0.88	0.19367	0.75	0.13229	1.13
sp|Q9CY57|CHTOP_MOUSE	Chromatin target of PRMT1 protein OS=Mu	295.19	4	2	2	2	2	3	3	2	3	2	3	3	3	3	3	3	0.58119	0.88	0.87239	1.00	0.66354	1.00
sp|P51859|HDGF_MOUSE	Hepatoma-derived growth factor OS=Mus r	313.76	2	5	3	4	3	5	5	2	4	4	2	3	3	3	3	3	0.62834	1.20	0.68479	1.10	0.97843	0.90
sp|Q9D892|ITPA_MOUSE	Inosine triphosphate pyrophosphatase OS	487.06	4	4	4	2	4	2	3	2	4	4	2	3	3	3	3	3	0.05865	0.67	0.26055	0.75	0.21528	0.75
sp|P61082|UBC12_MOUSE	NEDD8-conjugating enzyme Ubc12 OS=Mu	353.78	3	3	2	4	4	5	5	3	3	4	2	3	3	3	3	3	0.02760	1.63	0.10393	1.38	0.27807	1.13
sp|Q9QXL2|KI21A_MOUSE	Kinesin-like protein KIF21A OS=Mus muscu	736.8	5	4	3	2	4	3	3	4	2	4	2	3	3	3	3	3	0.18766	0.75	0.42412	0.75	0.41214	0.75
sp|Q91YR1|TWF1_MOUSE	Twinfilin-1 OS=Mus musculus (Mouse) GN=	609.42	2	3	2	2	3	3	5	2	3	3	2	3	3	3	3	3	0.61644	1.14	0.22112	1.43	0.18150	1.14
sp|B2RUJ5|APBA1_MOUSE	Amyloid beta A4 precursor protein-binding f	202.53	3	3	4	4	2	2	2	3	3	2	2	3	3	3	3	3	0.41234	0.80	0.48485	0.80	0.32842	0.70
tr|S4R1M4|S4R1M4_MOUSE	Ankyrin-2 OS=Mus musculus (Mouse) GN=	482.5	2	3	3	2	3	4	4	4	2	2	2	3	3	3	3	3	0.78479	1.13	0.33402	1.25	0.99208	0.88
sp|P11438|LAMP1_MOUSE	Lysosome-associated membrane glycoprote	258.57	2	3	3	3	3	4	4	2	2	2	2	3	3	3	3	3	0.31965	1.25	0.89764	1.00	0.99208	0.88
sp|Q9Z0X1|AIFM1_MOUSE	Apoptosis-inducing factor 1, mitochondrial	338.96	3	3	2	3	2	4	4	2	2	3	4	2	3	3	3	3	0.75129	1.13	0.88582	1.00	0.40561	1.13
sp|P32037|GTR3_MOUSE	Solute carrier family 2, facilitated glucose tra	557.85	4	4	4	4	4	3	3	4	2	4	3	2	3	3	3	3	0.24777	0.92	0.31546	0.75	0.26580	0.75
sp|O55137|ACOT1_MOUSE	Acyl-coenzyme A thioesterase 1 OS=Mus r	461.39	4	2	3	3	2	4	4	5	3	3	3	2	3	3	3	3	0.87531	1.00	0.26365	1.33	0.99653	0.89
sp|Q6ZQ73|CAND2_MOUSE	Cullin-associated NEDD8-dissociated protei	109.23	3	3	3	2	3	4	3	3	2	3	3	2	3	3	3	3	0.77140	1.00	0.62466	0.89	0.96454	0.89
sp|Q9CRB9|MIC19_MOUSE	MICOS complex subunit Mic19 OS=Mus mu	393.44	3	3	2	3	4	2	3	3	2	3	3	2	3	3	3	3	0.75850	1.13	0.75383	1.00	0.50153	1.00
sp|Q6PH08|ERC2_MOUSE	ERC protein 2 OS=Mus musculus (Mouse)	387.67	4	4	4	5	4	5	3	3	2	2	3	2	3	3	3	3	0.34292	1.17	0.02981	0.67	0.06786	0.58
tr|A0A0G2JF97|A0A0G2JF97_M	Proteasome subunit alpha type-5 OS=Mus	195.33	3	2	2	3	5	2	3	3	2	2	3	2	3	3	3	3	0.38619	1.43	0.38863	1.14	0.60452	1.00
sp|Q9Z1P6|NDUA7_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	344.99	3	3	3	5	3	2	4	5	2	4	2	2	3	3	3	3	0.82520	1.11	0.43067	1.22	0.91058	0.89
sp|Q8VEH3|ARL8A_MOUSE	ADP-ribosylation factor-like protein 8A OS=	464.93	4	2	2	4	2	3	4	2	2	4	2	2	3	3	3	3	0.82084	1.13	0.93329	1.00	0.77163	1.00
sp|Q9CQH7|BT3L4_MOUSE	Transcription factor BTF3 homolog 4 OS=M	281.03	2	4	2	5	3	3	3	3	4	3	2	2	3	3	3	3	0.40819	1.38	0.29852	1.25	0.95865	0.88
sp|Q9CR95|NECP1_MOUSE	Adaptin ear-binding coat-associated protein	414.99	2	2	3	3	5	3	4	3	2	3	2	2	3	3	3	3	0.16148	1.57	0.26674	1.29	0.56443	1.00
sp|Q99KB8|GLO2_MOUSE	Hydroxyacylglutathione hydrolase, mitochor	322.64	3	4	4	4	5	4	3	2	2	3	2	2	3	3	3	3	0.31584	1.18	0.03336	0.64	0.04973	0.64
sp|Q9QYJ0|DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=	444.05	3	2	2	2	4	3	2	3	2	2	2	2	3	3	3	3	0.44219	1.29	0.79455	1.00	0.88007	0.86
sp|P62889|RL30_MOUSE	60S ribosomal protein L30 OS=Mus muscu	440.22	5	4	3	3	3	3	4	2	2	4	4	1	3	3	3	3	0.12088	0.75	0.17959	0.67	0.64602	0.75
sp|Q9ESN9|JIP3_MOUSE	C-Jun-amino-terminal kinase-interacting prot	791.33	4	4	2	4	5	2	2	4	2	3	4	1	3	3	3	3	0.87024	1.10	0.69780	0.80	0.83591	0.80
sp|Q9Z0R4|ITSN1_MOUSE	Intersectin-1 OS=Mus musculus (Mouse) G	623.24	2	3	4	4	4	4	3	2	2	3	2	1	3	3	3	3	0.26270	1.33	0.42220	0.78	0.38242	0.67
sp|Q62283|TSN7_MOUSE	Tetraspanin-7 OS=Mus musculus (Mouse)	152.68	3	2	2	3	2	3	3	3	3	2	2	1	3	3	3	3	0.68249	1.14	0.09583	1.29	0.42315	0.71
sp|P47809|MP2K4_MOUSE	Dual specificity mitogen-activated protein kir	282.69	2	2	2	3	5	2	4	2	2	2	2	1	3	3	3	3	0.20785	1.67	0.22141	1.33	0.76814	0.83
sp|O35685|NUDC_MOUSE	Nuclear migration protein nudC OS=Mus m	407.87	2	2	3	3	5	4	3	3	2	4	2		3	3	3	2	0.06592	1.71	0.41281	1.14	0.88045	0.86
sp|Q8CIG8|ANM5_MOUSE	Protein arginine N-methyltransferase 5 OS=	368.13	2	2	2	2	3	2	3	2	3	3	2		3	3	3	2	0.46458	1.17	0.05491	1.33	0.85242	0.83
sp|P68037|UB2L3_MOUSE	Ubiquitin-conjugating enzyme E2 L3 OS=M	462.12	2	2	2	3	4	3	5	2	2	5	1	3	3	3	3	3	0.00878	1.67	0.27004	1.50	0.31416	1.50
sp|Q3THS6|METK2_MOUSE	S-adenosylmethionine synthase isoform typ	390.51	3	4	4	3	4	5	4	2	3	4	1	3	3	3	3	3	0.83509	1.09	0.37570	0.82	0.46071	0.73
sp|Q60899|ELAV2_MOUSE	ELAV-like protein 2 OS=Mus musculus (Mo	527.35	3	4	2	3	3	5	2	2	5	3	1	3	3	3	3	3	0.55720	1.22	0.85844	1.00	0.67757	0.78
sp|Q9CPQ3|TOM22_MOUSE	Mitochondrial import receptor subunit TOM2	506.28	3	5	3	3	3	4	4	2	2	3	1	2	3	3	3	3	0.52302	0.91	0.31560	0.73	0.13587	0.55
tr|E0CZ50|E0CZ50_MOUSE	Protein NDRG4 OS=Mus musculus (Mouse	222.77	2	3	2	2	2	3	2	3	2	2	1	2	3	3	3	3	0.82836	1.00	0.76195	1.00	0.35411	0.71
sp|Q3UMC0|SPAT5_MOUSE	Spermatogenesis-associated protein 5 OS	50.81	2	3	3	2	2	2	2	2	2	2	1	2	3	3	3	3	0.08749	0.75	0.19367	0.75	0.16239	0.63
tr|Q9CTB9|Q9CTB9_MOUSE	Putative uncharacterized protein OS=Mus	287.32	2	4	3	2	3	4	5	3	2	5	1	1	3	3	3	3	0.85446	1.00	0.63974	1.11	0.72030	0.78
sp|O88531|PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus m	396.37	3	5	3	3	3	5	4	2	3	4	1	1	3	3	3	3	0.86990	1.00	0.51190	0.82	0.23847	0.55
sp|Q8VCM8|NCLN_MOUSE	Nicalin OS=Mus musculus (Mouse) GN=Ncl	304.63	2	2	3	3	2	2	2	2	2	2	1	1	3	3	3	3	0.86783	1.00	0.59688	0.86	0.12722	0.57
sp|O35609|SCAM3_MOUSE	Secretory carrier-associated membrane prot	407.64	2	3	3	3	3	2	4	2	2	4	1		3	3	3	2	0.82165	1.00	0.89764	1.00	0.48906	0.63
sp|Q91W90|TXND5_MOUSE	Thioredoxin domain-containing protein 5 O	448.06	2	4	2	3	2	3	4	3	5	1	2	2	3	3	3	3	0.91568	1.00	0.14647	1.50	0.41604	0.63
sp|Q9D3D9|ATPD_MOUSE	ATP synthase subunit delta, mitochondrial	260.62	4	4	3	3	2	4	2	5	4	1	2	3	3	3	3	3	0.28878	0.82	0.78885	1.00	0.17301	0.55
sp|Q8CBW3|ABI1_MOUSE	Abl interactor 1 OS=Mus musculus (Mouse)	648.37	3	3	4	4	4	2	4	5	3	1	3	3	3	3	3	3	0.85141	1.00	0.33467	1.20	0.57171	0.70
sp|Q9ERS2|NDUAD_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha	387.34	3	3	3	3	3	4	4	3	3	1	5	3	3	3	3	3	0.60310	1.11	0.03590	1.11	0.72070	1.00
sp|Q61207|SAP_MOUSE	Prosaposin OS=Mus musculus (Mouse) GN	540.42	3	3	3	4	4	4	3	4	5	1		6	3	3	3	2	0.00386	1.33	0.17357	1.33	0.89873	0.78
sp|Q78IK2|USMG5_MOUSE	Up-regulated during skeletal muscle growth	260.28	3	4	5	2	3	3	5	2	1	5	2	3	3	3	3	3	0.09120	0.67	0.34821	0.67	0.73580	0.83
sp|Q61206|PA1B2_MOUSE	Platelet-activating factor acetylhydrolase IB	371.17	3	2	2	4	4	2	3	2	1	4	1	1	3	3	3	3	0.31703	1.43	0.68609	0.86	0.84514	0.86
sp|Q9QUJ7|ACSL4_MOUSE	Long-chain-fatty-acid--CoA ligase 4 OS=Mu	768.39	3	4	3	3	5	3	3	3	1	1	3	2	3	3	3	3	0.81659	1.10	0.30456	0.70	0.30851	0.60
sp|Q9D1T0|LIGO1_MOUSE	Leucine-rich repeat and immunoglobulin-like	287.54	2	2	2	2	3	3	3	5		2	4	3	3	3	2	3	0.10875	1.33	0.63643	1.33	0.15557	1.50
sp|Q9CQW2|ARL8B_MOUSE	ADP-ribosylation factor-like protein 8B OS=	469.65	5	5	4	5	4	4	5	1	2	6	2	3	3	3	3	3	0.39990	0.93	0.14709	0.57	0.56842	0.79
sp|P26041|MOES_MOUSE	Moesin OS=Mus musculus (Mouse) GN=Ms	342.74	2	2	3	3	3	4	4	1	2	3	3	3	3	3	3	3	0.16129	1.43	0.97731	1.00	0.06975	1.29
sp|Q9DCT2|NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sul	686.81	2	4	4	3	4	5	3	1	4	3	2	3	3	3	3	3	0.60076	1.20	0.66138	0.80	0.67773	0.80
tr|Q32P00|Q32P00_MOUSE	Chromobox homolog 3 (Drosophila HP1 gar	634.01	4	3	4	2	3	3	2	1	4	3	2	2	3	3	3	3	0.07058	0.73	0.31807	0.64	0.07133	0.64
sp|Q8BP92|RCN2_MOUSE	Reticulocalbin-2 OS=Mus musculus (Mouse	651.56	4	2	4	2	5	5	3	1	3	2	2	2	3	3	3	3	0.73923	1.20	0.38897	0.70	0.21339	0.60
sp|O88543|CSN3_MOUSE	COP9 signalosome complex subunit 3 OS=	504.45	4	3	3	3	3	3	3	1	2	4	4	3	3	3	3	3	0.26475	0.90	0.10258	0.60	0.20500	1.10
sp|P54923|ADPRH_MOUSE	[Protein ADP-ribosylarginine] hydrolase OS	393.27	2	3	3	3	2	2	2	1	3	3	1	3	3	3	3	3	0.46315	0.88	0.47670	0.75	0.92718	0.88
sp|P63082|VATL_MOUSE	V-type proton ATPase 16 kDa proteolipid su	317.95	5	3	3	4	3	2	4	1	2	5	1	1	3	3	3	3	0.44671	0.82	0.27441	0.64	0.44450	0.64
sp|Q925I1|ATAD3_MOUSE	ATPase family AAA domain-containing prot	510.06	2	3	2	3	3	2	2	1	1	3	3	1	3	3	3	3	0.63433	1.14	0.06871	0.57	0.72452	1.00
sp|Q3UHD6|SNX27_MOUSE	Sorting nexin-27 OS=Mus musculus (Mous	372.16	2	3	2	2	3	3	2	1	1	2	1	2	3	3	3	3	0.61644	1.14	0.06871	0.57	0.35411	0.71
sp|Q9R1T2|SAE1_MOUSE	SUMO-activating enzyme subunit 1 OS=Mu	472.11	3	3	2	2	4	3	4	1		5		1	3	3	2	2	0.77058	1.13	0.42890	0.63	0.71152	0.75
sp|Q8BUK6|HOOK3_MOUSE	Protein Hook homolog 3 OS=Mus musculu	590.49	2	2	2	2	3	2	3		2	1	1	2	3	3	2	3	0.46458	1.17	0.72497	0.83	0.33341	0.67
sp|Q9QYA2|TOM40_MOUSE	Mitochondrial import receptor subunit TOM4	321.53	2	2	2	2	2	2	3		1	3	1		3	3	2	2	0.28226	1.00	0.45040	0.67	0.52960	0.67
sp|Q9D1E6|TBCB_MOUSE	Tubulin-folding cofactor B OS=Mus muscul	548.2	2	3	2	2	4	4	5			3		1	3	3	1	2	0.26044	1.43	0.66482	0.71	0.36384	0.57
sp|P62274|RS29_MOUSE	40S ribosomal protein S29 OS=Mus muscu	111.84	4	4	4	5	5	4	1	5	5	3	3	1	3	3	3	3	0.29675	1.17	0.98226	0.92	0.14218	0.58
sp|Q8K341|ATAT_MOUSE	Alpha-tubulin N-acetyltransferase 1 OS=Mu	284.7	3	2	2	2	2	2	1	2	2	2	1	2	3	3	3	3	0.29133	0.86	0.38942	0.71	0.38045	0.71
sp|P51174|ACADL_MOUSE	Long-chain specific acyl-CoA dehydrogenas	722.79	2	3	5	2	4	4	1	2	4	1	2	4	3	3	3	3	0.85852	1.00	0.58372	0.70	0.68915	0.70



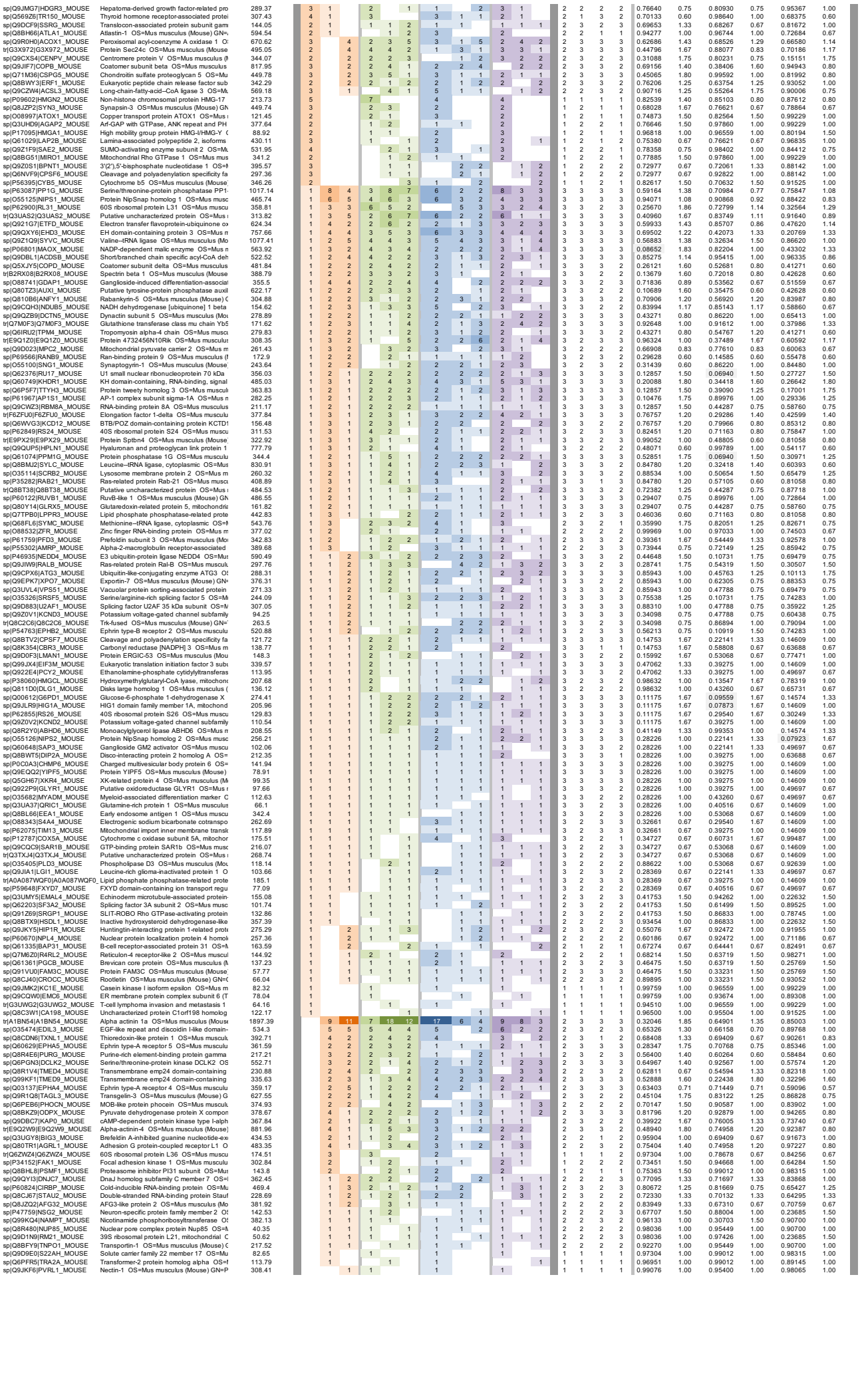


Table S2. Gene Ontology classification of differentially expressed, rescued proteins.

Category	Term	Count	%	PValue	Proteins	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_MI	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	IPR027417:P	9	32.1428571	1.47E-05	Q9CW03, Q91ZR1, P21278, S4R232, P30	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, P352	28	332	22680	14.6385542	0.00443471	0.00221982	0.04564041
UP_SEQ_FEA	nucleotide pl	6	21.4285714	6.70E-05	Q91ZR1, P21278, S4R232, P30677, P352	26	319	18012	13.0301423	0.006216	0.006216	0.07337298
GOTERM_MI	GO:0005525	6	21.4285714	2.69E-04	Q91ZR1, P21278, S4R232, P30677, P352	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_MI	GO:0003924	4	14.2857143	0.00401014	P21278, P30677, D3YZ68, P56371	28	209	17446	11.924812	0.32820502	0.12418526	4.35387531
INTERPRO	IPR000654: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_FEA	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, Q922	28	1784	19662	3.14894299	0.56655248	0.18860163	9.21973172
UP_SEQ_FEA	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_MI	GO:0005515	13	46.4285714	0.01304464	Q9DCN2, Q9CW03, Q99020, O89023, A0A	28	4092	17446	1.97945469	0.72744554	0.27745762	13.5378819
INTERPRO	IPR001806:S	3	10.7142857	0.01326132	Q91ZR1, S4R232, P35283, P56371	28	134	20594	16.4664179	0.68696909	0.32101152	13.4356186
UP_SEQ_FEA	domain:RRM	3	10.7142857	0.01350891	Q99020, Q921F4, P52912	26	128	18012	16.2367788	0.71773016	0.27110307	13.8341783
UP_SEQ_FEA	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:A	3	10.7142857	0.01853061	P05132, P21278, P30677	15	117	7691	13.1470085	0.74945815	0.74945815	17.7801684
INTERPRO	IPR005225:S	3	10.7142857	0.01964105	Q91ZR1, S4R232, P35283, P56371	28	165	20594	13.3727273	0.82196502	0.35042944	19.296218
SMART	SM00275:SM	2	7.14285714	0.01978062	P21278, P30677	14	16	10425	93.0803571	0.258947	0.258947	12.9689304
COG_ONTOL	Coenzyme m	2	7.14285714	0.02055046	Q8BHC4, Q922D8	5	11	2126	77.3090909	0.07970247	0.07970247	7.62193054
INTERPRO	IPR001019:G	2	7.14285714	0.02077947	P21278, P30677	28	16	20594	91.9375	0.83908207	0.30606165	20.3033091
INTERPRO	IPR011025: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_MI	GO:0044822	6	21.4285714	0.02612478	Q9WTX2, Q99020, P24369, Q921F4, P52	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_MI	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_MI	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	IPR000504: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	180	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_FEA	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	IPR012677:N	3	10.7142857	0.0520625	Q99020, Q921F4, P52912	28	281	20594	7.85231317	0.99045372	0.48547687	43.8894472
UP_SEQ_FEA	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:A	2	7.14285714	0.08566337	Q8CHT0, Q9CPY7	15	49	7691	20.9278912	0.99867611	0.89019613	60.8339399
KEGG_PATH	mmu00520:A	2	7.14285714	0.08566337	Q9CYR6, Q9DCN2	15	49	7691	20.9278912	0.99867611	0.89019613	60.8339399
GOTERM_MI	GO:0019003	2	7.14285714	0.08888623	P35283, P56371	28	60	17446	20.7690476	0.99990053	0.68398258	64.3440741
UP_SEQ_FEA	mutagenesis	4	14.2857143	0.08970462	P05132, Q9CW03, Q921F4, Q99PU5	26	772	18012	3.58947788	0.99984006	0.71311474	64.2604308
GOTERM_MI	GO:0001664	2	7.14285714	0.09453329	P21278, P30677	28	64	17446	19.4709821	0.99994625	0.66457351	66.7172763