

Supplemental Materials to:

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Huntingtin protein interactions altered by polyglutamine expansion as determined by quantitative proteomic analysis

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Supplemental figures and tables legends

Figure S1. The IPA network diagram, including Htt, showing proteins related to DNA Metabolism, Energy Production, Neurological Disorder and Cell Cycle, based on the protein data set shown in Table S1 (CV<0.35 between duplicate samples). Proteins identified as 50Q preferential interactors are shown in red; 20Q preferential interactors are shown in green; proteins equally present in both 50Q and 20Q IPs are shown in yellow; Htt is shown in purple; proteins that were not detected by us, but fit into the network are shown in white.

Figure S2. Merged two top networks, defined by IPA as most significantly enriched in differential Htt interactors (based on the proteins shown in Table S1), includes proteins related to Gene Expression, RNA post transcriptional modifications and Protein Synthesis. Proteins identified as 50Q preferential interactors are shown in red; 20Q preferential interactors are shown in green; proteins that were not detected by us, but fit into the network are shown in white.

Table S1. Htt differential interactors. Proteins identified with median iTRAQ ratios >1.2 or <0.8 between Htt-50Q and Htt-20Q were considered as differential interactors. Only proteins with coefficient of variation (CV) less than 0.35 (calculated from iTRAQ ratios between 2 parallel biological replicates) are shown.

Table S2. Htt most significant differential interactors. Proteins most significantly changed in abundance between normal and expanded Htt complexes with ANOVA p-value less than 0.05 are shown

Description	Accession	observation	MW (kDa)	calc. pI	%coverage	# PSMs	# Peptides	AS: 115/114	115-114 mean	115-114 STDEV	115-114 CV	AS: 115/114 Count	AS: 116/114	AS: 116/114 Count	AS: 117/114	AS: 117/114 Count	116-117 MEAN	116-117 STDEV	116-117 CV
thioredoxin-related transmembrane protein 4 precursor [Mus musculus]	112817607	2	37.1	4.37	9.25	9	2	1.117	1.059	0.083	0.078	5	2.253	5	2.175	5	2.214	0.1	0.025
immunity-related GTPase family M protein [Mus musculus]	6680351	2	46.5	8.28	3.91	2	1	0.956	0.978	0.031	0.032	1	2.617	1	1.796	1	2.207	0.6	0.263
protein CYR61 precursor [Mus musculus]	6753594	2	41.7	8.12	2.64	2	1	1.298	1.149	0.211	0.183	1	1.887	1	2.419	1	2.153	0.4	0.175
atlastin-2 isoform 2 [Mus musculus]	119372304	2	46.8	5.95	3.64	3	1	1.302	1.151	0.213	0.185	1	1.917	1	1.941	1	1.929	0.0	0.009
receptor-type tyrosine-kinase phosphatase kappa precursor [Mus musculus]	6679561	2	164.1	5.95	0.82	2	1	0.880	0.940	0.085	0.090	1	1.824	1	2.025	1	1.925	0.1	0.074
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor [Mus musculus]	23346461	2	52.6	6.99	2.59	2	1	1.184	1.092	0.130	0.119	1	1.611	1	2.145	1	1.878	0.4	0.201
voltage-dependent anion-selective channel protein 1 [Mus musculus]	6755963	2	30.7	8.54	12.37	13	3	1.447	1.224	0.316	0.259	2	1.920	2	1.762	2	1.841	0.1	0.061
peptidyl-RNA hydrolase 2 [Mus musculus]	149363634	2	19.5	7.42	19.89	18	2	1.041	1.020	0.029	0.028	8	1.571	8	2.011	8	1.791	0.3	0.174
mitochondrial import inner membrane translocase subunit TIM50 precursor [Mus musculus]	22094989	2	39.8	8.13	4.82	6	1	1.139	1.069	0.098	0.092	3	1.965	3	1.578	3	1.771	0.3	0.154
prolactin regulatory element-binding protein [Mus musculus]	158749640	2	45.4	8.76	11.27	6	4	1.015	1.008	0.011	0.011	4	1.403	4	2.134	4	1.768	0.5	0.292
ATP-dependent metalloprotease YME1L1 [Mus musculus]	7305635	2	80.0	8.97	2.52	2	2	1.580	1.290	0.410	0.318	2	1.470	2	1.948	2	1.709	0.3	0.198
60S ribosomal protein L7-like 1 [Mus musculus]	27754134	2	28.5	10.64	13.01	8	3	1.358	1.179	0.253	0.215	3	2.009	3	1.400	3	1.704	0.4	0.253
nuclear valosin-containing protein-like [Mus musculus]	33468981	2	94.4	6.35	5.26	17	4	1.477	1.238	0.337	0.272	1	1.405	1	1.915	1	1.660	0.4	0.217
E3 ubiquitin-protein ligase UBR5 isoform 2 [Mus musculus]	163310753	2	308.1	5.83	1.00	6	2	1.596	1.298	0.422	0.325	3	1.825	3	1.457	3	1.641	0.3	0.158
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 [Mus musculus]	21312012	2	20.0	8.46	27.91	7	4	1.389	1.194	0.275	0.230	6	1.685	6	1.567	6	1.626	0.1	0.052
importin-4 [Mus musculus]	19745156	2	119.2	5.03	2.87	5	3	1.007	1.004	0.005	0.005	3	1.402	3	1.835	3	1.619	0.3	0.189
integrin beta-1 precursor [Mus musculus]	4504394	2	88.2	5.94	4.51	5	3	0.684	0.842	0.223	0.265	4	1.645	4	1.592	4	1.618	0.0	0.023
vesicle-associated membrane protein-associated protein A [Mus musculus]	94721328	2	27.8	8.40	10.04	5	2	1.636	1.318	0.449	0.33	3	1.616	3	1.544	3	1.580	0.1	0.032
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 [Mus musculus]	21624617	2	20.1	9.39	12.14	3	2	1.395	1.198	0.280	0.233	2	1.624	2	1.531	2	1.577	0.1	0.042
LAG1 longevity assurance homolog 2 [Mus musculus]	22095015	2	45.0	8.75	4.21	3	1	0.669	0.835	0.234	0.280	1	1.307	1	1.845	1	1.576	0.4	0.241
zinc transporter SLC39A7 [Mus musculus]	118150668	2	50.6	6.87	2.73	2	1	0.848	0.924	0.108	0.117	2	1.279	2	1.822	2	1.551	0.4	0.248
very long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Mus musculus]	23956084	2	70.8	8.75	3.05	1	1	1.295	1.148	0.209	0.182	1	1.483	1	1.612	1	1.547	0.1	0.059
serum paraoxonase/arylesterase 2 [Mus musculus]	34303979	2	39.6	5.83	5.93	5	2	0.722	0.861	0.197	0.228	3	1.226	3	1.816	3	1.521	0.4	0.274
chitobiosylphosphodolichol beta-mannosyltransferase [Mus musculus]	148277043	2	54.4	8.37	5.39	5	2	0.657	0.828	0.243	0.293	2	1.232	2	1.793	2	1.513	0.4	0.263
oxysterol-binding protein-related protein 1 [Mus musculus]	52345396	2	107.7	6.44	2.95	4	2	1.182	1.091	0.129	0.118	2	1.522	2	1.502	2	1.512	0.0	0.009
ATPase, Ca++ translocase, slow twitch 2 isoform a [Mus musculus]	158639579	2	114.8	5.34	21.17	96	23	0.897	0.949	0.073	0.075	34	1.226	35	1.795	35	1.511	0.4	0.266
mitochondrial rho GTPase 1 isoform 1 [Mus musculus]	31559891	2	72.2	6.49	4.44	3	3	0.883	0.942	0.083	0.088	2	1.261	2	1.757	2	1.509	0.4	0.233
protein unc-84 homolog B [Mus musculus]	168693641	2	78.1	6.90	3.86	4	2	1.561	1.281	0.397	0.212	2	1.584	2	1.499	2	1.499	0.1	0.081
vesicle-fusing ATPase [Mus musculus]	31543349	2	82.6	6.95	3.36	4	3	1.482	1.241	0.341	0.274	2	1.669	2	1.322	2	1.495	0.2	0.164
mannosyl-oligosaccharide glucosidase [Mus musculus]	31981106	2	91.8	9.00	3.00	4	2	0.905	0.952	0.067	0.07	2	1.329	2	1.660	2	1.494	0.2	0.157
caprin-1 isoform c [Mus musculus]	162329568	2	76.6	5.12	4.34	3	3	1.170	1.085	0.120	0.111	3	1.828	3	1.142	3	1.485	0.5	0.326
nuclear MIF4G domain-containing protein 1 [Mus musculus]	134288861	2	95.9	8.87	1.64	2	1	1.620	1.310	0.438	0.335	2	1.463	2	1.501	2	1.482	0.0	0.018
mediator of RNA polymerase II transcription subunit 27 [Mus musculus]	76253678	2	35.3	9.31	4.82	2	1	1.612	1.306	0.433	0.331	1	1.756	1	1.206	1	1.481	0.4	0.263
NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial precursor [Mus musculus]	21312950	2	24.7	9.92	7.59	2	2	1.532	1.266	0.376	0.297	2	1.645	2	1.315	2	1.480	0.2	0.158
CTP synthase 1 [Mus musculus]	172072613	2	66.6	6.58	14.21	17	7	1.458	1.229	0.324	0.264	10	1.217	10	1.698	10	1.457	0.3	0.234
nucleoporin NUP188 homolog [Mus musculus]	38678526	2	196.6	7.01	4.66	27	9	0.835	1.167	0.237	0.103	11	1.121	11	1.776	11	1.449	0.5	0.319
PREDICTED: similar to nuclear pore-targeting complex component of 58 kDa isoform 1 [Mus musculus]	149250822	2	57.9	5.68	13.04	14	6	1.236	1.118	0.167	0.149	6	1.421	6	1.465	6	1.443	0.0	0.022
probable RNA-binding protein 19 [Mus musculus]	30794154	2	106.0	6.57	1.58	4	1	1.473	1.236	0.334	0.270	2	1.158	2	1.725	2	1.442	0.4	0.278
activator of 90 kDa heat shock protein ATPase homolog 1 [Mus musculus]	22122515	2	38.1	5.53	5.62	2	1	1.468	1.234	0.331	0.268	1	1.471	1	1.403	1	1.437	0.0	0.034
splicing factor 3B subunit 4 [Mus musculus]	23346437	2	44.3	8.56	4.72	4	2	1.043	1.022	0.031	0.030	2	1.477	2	1.390	2	1.433	0.1	0.043
PREDICTED: similar to translocin-associated protein alpha, muscle specific [Mus musculus]	82950283	2	31.2	4.45	2.92	3	1	0.729	0.865	0.191	0.221	2	1.200	2	1.665	2	1.432	0.3	0.230
integrator complex subunit 1 [Mus musculus]	160948597	2	245.0	6.28	4.10	17	6	1.422	1.211	0.299	0.197	9	1.265	9	1.579	9	1.422	0.2	0.156
receptor tyrosine-kinase erbB-2 precursor [Mus musculus]	54873610	2	138.5	5.97	0.88	1	1	1.594	1.297	0.420	0.324	1	1.508	1	1.335	1	1.422	0.1	0.086
immature colon carcinoma transcript 1 protein [Mus musculus]	19387848	2	20.3	10.65	7.91	2	1	1.591	1.295	0.418	0.323	1	1.077	1	1.418	1	1.418	0.5	0.340
RIKEN cDNA 2700050L05 isoform 1 [Mus musculus]	22122451	2	66.2	7.31	2.56	10	2	1.534	1.267	0.378	0.298	1	1.485	1	1.342	1	1.413	0.1	0.071
thyroid receptor-interacting protein 13 [Mus musculus]	110625724	2	48.3	5.86	8.56	8	3	1.203	1.101	0.143	0.143	4	1.062	4	1.759	4	1.410	0.5	0.350
heterogeneous nuclear ribonucleoprotein A/B isoform 2 [Mus musculus]	6754222	2	30.8	7.91	18.25	9	4	1.309	1.154	0.218	0.189	4	1.491	4	1.329	4	1.410	0.1	0.081
cytochrome c1, heme protein, mitochondrial [Mus musculus]	13385006	2	35.3	9.16	14.15	6	3	1.374	1.187	0.265	0.223	5	1.121	5	1.398	5	1.281	0.4	0.281
fatty aldehyde dehydrogenase [Mus musculus]	75677435	2	53.9	8.35	10.33	13	5	1.817	1.099	0.129	0.142	4	1.223	4	1.570	4	1.397	0.2	0.176
interferon-stimulated 20 kDa exonuclease-like 2 [Mus musculus]	29244084	2	41.0	9.98	3.53	2	1	0.910	1.095	0.134	0.123	1	1.323	1	1.469	1	1.396	0.1	0.074
tuffin-interacting protein 11 [Mus musculus]	10190660	2	96.2	5.90	1.19	3	1	1.604	1.302	0.427	0.328	2	1.435	2	1.357	2	1.396	0.1	0.039
DNA-directed RNA polymerase 1 subunit RPA43 [Mus musculus]	27545207	2	36.7	6.21	5.76	4	1	1.631	1.316	0.446	0.339	2	1.729	2	1.062	2	1.395	0.5	0.338
ATPase family AAA domain-containing protein 1 [Mus musculus]	31560168	2	40.7	6.90	6.93	11	2	1.188	1.094	0.133	0.121	1	1.075	1	1.709	1	1.392	0.4	0.322
ras GTPase-activating protein-binding protein 1 [Mus musculus]	7305075	2	51.8	5.59	6.24	2	2	1.395	1.198	0.279	0.233	2	1.455	2	1.325	2	1.390	0.1	0.066
ribosome biogenesis protein WDR12 [Mus musculus]	10946614	2	47.3	5.60	13.00	8	5	1.350	1.175	0.247	0.210	4	1.460	4	1.316	4	1.388	0.1	0.074
ATP synthase subunit beta, mitochondrial precursor [Mus musculus]	31980648	2	56.3	5.34	32.70	89	16	1.060	1.030	0.043	0.042	49	1.112	49	1.664	49	1.388	0.4	0.281
V-type proton ATPase 116 kDa subunit a isoform 2 [Mus musculus]	83627707	2	98.1	6.64	2.10	3	2	0.657	0.828	0.243	0.293	1	1.578	1	1.191	1	1.385	0.3	0.198
beta-catenin [Mus musculus]	6671684	2	85.4	5.86	2.30	6	2	1.347	1.173	0.245	0.209	1	1.508	1	1.261	1	1.385	0.2	0.126
transportin-3 [Mus musculus]	54312056	2	104.1	5.57	1.30	2	1	1.263	1.132	0.186	0.165	1	1.063	1	1.705	1	1.384	0.5	0.328
fatty acyl-CoA reductase 1 [Mus musculus]	74096448	2	59.4	9.19	10.49	24	5	1.191	1.095	0.135	0.123	4	1.093	4	1.673	4	1.383	0.4	0.296
aspartyl/asparanyl beta-hydroxylase isoform 1 [Mus musculus]	125628659	2	83.0	5.08	10.12	11	6	0.947	0.974	0.037	0.038	4	1.680	4	1.085	4	1.383	0.4	0.304
DNA repair protein REV1 [Mus musculus]	40254551	2	137.3	8.54	0.56	4	1	1.065	1.032	0.046	0.044	2	1.191	2	1.574	2	1.376	0.3	0.196
polycomb protein Suz12 isoform 1 [Mus musculus]	40353214	2	83.0	8.81	2.70	3	2	1.511	1.256	0.362	0.288	1	1.512	1	1.240	1	1.376	0.2	0.140
monocarboxylate transporter 1 [Mus musculus]	6677995	2	53.2	7.47	8.92	4	3	0.689											

serine/threonine-protein kinase SRPK2 [Mus musculus]	47059480	2	76.8	4.91	4.25	2	2	1.495	1.248	0.350	0.281	2	1.483	2	1.172	2	1.328	0.2	0.166
60S acidic ribosomal protein P2 [Mus musculus]	83745120	2	11.6	4.54	85.22	105	6	1.472	1.236	0.333	0.270	35	1.266	35	1.385	36	1.326	0.1	0.063
ATP synthase subunit alpha, mitochondrial precursor [Mus musculus]	6680748	2	59.7	9.19	26.94	76	15	0.759	0.880	0.170	0.193	51	1.218	51	1.431	51	1.325	0.2	0.114
programmed cell death protein 2 [Mus musculus]	120407033	2	38.3	5.38	4.66	2	1	1.572	1.286	0.404	0.314	1	1.514	1	1.132	1	1.323	0.3	0.204
U3 small nucleolar RNA-associated protein 14 homolog A [Mus musculus]	51889716	2	87.2	9.20	6.26	12	4	1.428	1.214	0.303	0.249	7	1.387	7	1.258	7	1.323	0.1	0.069
casein kinase I isoform delta isoform 2 [Mus musculus]	20544147	2	46.8	9.64	4.40	2	2	1.406	1.203	0.287	0.239	1	1.619	1	1.023	1	1.321	0.4	0.319
probable ATP-dependent RNA helicase DDX10 [Mus musculus]	189491668	2	100.7	7.75	1.26	2	1	1.570	1.285	0.403	0.314	1	1.554	1	1.086	1	1.320	0.3	0.251
60 kDa heat shock protein, mitochondrial [Mus musculus]	183396771	2	60.9	6.18	15.71	12	6	1.291	1.146	0.206	0.180	5	1.207	6	1.432	6	1.319	0.2	0.121
cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor [Mus musculus]	6753498	2	19.5	9.23	10.65	2	1	1.182	1.091	0.118	0.118	1	1.366	1	1.269	1	1.317	0.1	0.052
hypothetical protein LOC74847 [Mus musculus]	197116351	2	47.4	5.96	1.38	11	4	1.263	1.132	0.186	0.164	5	1.401	5	1.233	5	1.317	0.1	0.090
PREDICTED: similar to optic atrophy 1 (autosomal dominant) [Mus musculus]	149267809	2	95.7	6.76	5.94	12	1	1.131	1.065	0.092	0.087	4	1.292	4	1.336	4	1.314	0.0	0.024
kinectin [Mus musculus]	144922638	2	152.4	5.90	24.94	70	30	0.879	0.939	0.086	0.091	40	1.235	40	1.383	41	1.309	0.1	0.080
PREDICTED: hypothetical protein [Mus musculus]	149263967	2	24.9	6.42	4.11	2	1	0.958	0.979	0.030	0.030	1	1.138	1	1.480	1	1.309	0.2	0.185
transducin beta-like protein 3 [Mus musculus]	30102935	2	88.2	6.81	3.87	6	3	1.347	1.174	0.246	0.209	5	1.164	5	1.451	5	1.308	0.2	0.155
chromodomain-helicase-DNA-binding protein 1-like [Mus musculus]	13386044	2	101.4	6.64	1.67	2	1	1.459	1.230	0.325	0.264	1	1.538	1	1.076	1	1.307	0.3	0.250
hypothetical protein LOC69612 [Mus musculus]	31981558	2	54.1	6.79	3.09	2	1	1.426	1.213	0.301	0.248	1	1.542	1	1.069	1	1.305	0.3	0.256
nucleolar protein 6 [Mus musculus]	118026904	2	129.1	6.79	3.04	5	3	1.354	1.177	0.251	0.213	3	1.239	3	1.371	3	1.305	0.1	0.072
PREDICTED: hypothetical protein [Mus musculus]	149251053	2	23.3	9.99	38.03	25	8	0.812	0.906	0.133	0.147	14	1.248	13	1.360	14	1.304	0.1	0.061
hypothetical protein LOC72722 [Mus musculus]	139948818	2	55.0	8.95	18.64	14	6	1.647	1.323	0.457	0.346	4	1.081	4	1.527	4	1.304	0.3	0.242
exosome complex exonuclease RRP41 [Mus musculus]	29611663	2	26.2	6.15	22.45	11	4	1.577	1.288	0.408	0.317	6	1.576	6	1.030	6	1.303	0.4	0.296
mRNA turnover protein 4 homolog [Mus musculus]	37537520	2	27.4	8.28	36.55	17	10	1.588	1.294	0.416	0.321	8	1.548	8	1.056	8	1.302	0.3	0.267
A-kinase anchor protein 8 [Mus musculus]	31560394	2	76.2	5.14	1.60	4	2	0.855	0.927	0.103	0.111	2	1.369	2	1.233	2	1.301	0.1	0.074
PREDICTED: hypothetical protein [Mus musculus]	149253631	2	11.4	9.74	18.45	2	1	1.235	1.118	0.166	0.149	1	1.127	1	1.473	1	1.300	0.2	0.188
vam6/Vps39-like protein isoform 2 [Mus musculus]	30578384	2	100.6	7.12	1.37	2	1	1.547	1.274	0.387	0.304	1	1.497	1	1.100	1	1.298	0.3	0.217
PREDICTED: similar to fibrillarin isoform 1 [Mus musculus]	149251501	2	34.3	10.24	37.92	75	12	1.198	1.099	0.140	0.127	41	1.281	41	1.310	41	1.296	0.0	0.016
trinuclotide repeat-containing gene 6B protein isoform 2 [Mus musculus]	159110982	2	187.9	6.81	1.86	3	2	1.294	1.147	0.208	0.181	2	1.425	2	1.162	2	1.294	0.2	0.144
exportin-5 [Mus musculus]	24429570	2	136.9	5.82	6.64	10	4	1.253	1.127	0.179	0.159	4	0.981	3	1.606	4	1.293	0.4	0.341
stress-70 protein, mitochondrial [Mus musculus]	162461907	2	73.4	6.07	28.28	89	18	1.011	1.006	0.008	0.008	57	1.254	57	1.325	57	1.290	0.1	0.039
coiled-coil domain-containing protein 50 isoform 2 [Mus musculus]	71043970	2	33.7	7.11	4.48	5	2	1.047	1.024	0.034	0.032	2	1.302	2	1.271	2	1.287	0.0	0.017
ubiquitin-conjugating enzyme E2 Q1 [Mus musculus]	170172548	2	46.1	5.10	1.90	1	1	1.576	1.288	0.407	0.316	1	1.000	1	1.573	1	1.286	0.4	0.315
39S ribosomal protein L13, mitochondrial [Mus musculus]	21312936	2	20.7	9.35	13.48	4	2	1.336	1.168	0.237	0.203	2	1.535	2	1.037	2	1.286	0.4	0.274
mitochondrial inner membrane protein [Mus musculus]	70608131	2	83.8	6.61	15.98	25	11	1.298	1.149	0.211	0.183	15	1.207	15	1.362	15	1.284	0.1	0.086
coatomer subunit beta [Mus musculus]	15426055	2	107.0	6.00	19.20	41	13	1.311	1.155	0.220	0.190	19	1.088	20	1.477	20	1.282	0.3	0.215
alpha-soluble NSF attachment protein [Mus musculus]	13385392	2	33.2	5.45	5.08	1	1	0.711	0.856	0.204	0.139	1	1.131	1	1.433	1	1.282	0.2	0.166
thyroid hormone receptor-associated protein 3 [Mus musculus]	68533246	2	108.1	10.17	2.31	2	2	1.308	1.154	0.218	0.229	2	1.314	2	1.250	2	1.282	0.0	0.035
PREDICTED: hypothetical protein [Mus musculus]	82994972	2	22.2	10.11	8.42	9	3	1.222	1.111	0.157	0.141	1	1.395	1	1.165	1	1.280	0.2	0.127
ephrin type-A receptor 2 precursor [Mus musculus]	32484983	2	108.8	6.23	2.76	4	2	0.727	0.863	0.193	0.224	3	1.458	3	1.275	3	1.275	0.3	0.203
cytochrome P450 20A1 [Mus musculus]	74271886	2	52.1	6.95	8.44	6	3	1.050	1.025	0.036	0.035	3	1.039	3	1.508	3	1.274	0.3	0.260
PREDICTED: similar to fibrous sheath-interacting protein 2 [Mus musculus]	149249474	2	725.4	6.29	0.43	15	5	0.731	0.866	0.190	0.216	6	1.057	6	1.488	6	1.273	0.3	0.239
AP-1 complex subunit gamma-1 [Mus musculus]	56744242	2	92.7	6.80	3.03	4	2	1.514	1.257	0.364	0.289	1	1.185	1	1.352	1	1.270	0.1	0.095
PREDICTED: similar to EF-hand Ca2+ binding protein p22 [Mus musculus]	149249669	2	21.4	5.10	5.64	4	1	1.093	1.046	0.066	0.063	3	1.147	3	1.395	3	1.270	0.2	0.136
steroid regulatory element-binding protein cleavage-activating protein [Mus musculus]	156938291	2	139.5	7.08	0.94	1	1	1.229	1.115	0.162	0.145	1	1.121	1	1.416	1	1.269	0.2	0.165
protein VAC14 homolog [Mus musculus]	31542488	2	88.0	6.13	4.86	22	3	1.261	1.130	0.184	0.161	13	1.253	13	1.281	13	1.267	0.0	0.015
PREDICTED: similar to GTP-binding protein (smg p21B) [Mus musculus]	149261508	2	20.8	5.78	25.54	6	1	1.042	1.021	0.030	0.029	1	1.224	1	1.305	1	1.264	0.1	0.045
neuropilin-2 isoform 6 precursor [Mus musculus]	116686144	2	101.4	5.81	1.11	1	4	0.759	0.879	0.171	0.194	1	0.979	1	1.550	1	1.264	0.4	0.319
28S ribosomal protein S22, mitochondrial [Mus musculus]	13384904	2	41.2	8.56	9.19	4	3	0.992	0.996	0.006	0.006	3	1.464	3	1.064	3	1.264	0.3	0.224
U4/U6 small nuclear ribonucleoprotein Prp4 [Mus musculus]	55925589	2	58.3	7.28	14.40	13	6	1.592	1.246	0.348	0.279	7	1.546	7	1.567	7	1.263	0.4	0.317
exosome complex exonuclease MTR3 [Mus musculus]	30794378	2	28.4	6.11	14.65	4	2	1.469	1.234	0.332	0.269	1	1.176	1	1.347	1	1.261	0.1	0.096
PREDICTED: similar to leucine rich repeat containing 47 [Mus musculus]	149253441	2	63.6	8.35	10.52	7	4	1.467	1.233	0.330	0.268	4	1.320	4	1.203	4	1.261	0.1	0.066
mannosyl-oligosaccharide 1,2-alpha-mannosidase IB [Mus musculus]	6754620	2	72.8	8.28	2.65	2	1	1.294	1.147	0.208	0.181	1	1.196	1	1.324	1	1.260	0.1	0.072
T-complex protein 1 subunit beta [Mus musculus]	126521835	2	57.4	6.40	30.65	39	14	1.309	1.155	0.219	0.199	21	1.449	22	1.069	22	1.259	0.3	0.213
amine and glutamate-rich protein 1 [Mus musculus]	134152669	2	32.9	10.36	2.21	4	1	1.389	1.194	0.275	0.230	2	1.038	2	1.478	2	1.258	0.3	0.247
ADP-ribosylation factor-like protein 8B [Mus musculus]	13385518	2	21.5	8.43	22.04	4	3	0.883	0.941	0.083	0.088	1	1.491	1	1.025	1	1.258	0.3	0.262
lactadherin isoform 2 [Mus musculus]	113865977	2	47.1	7.05	23.24	19	9	0.999	1.000	0.001	0.001	13	0.963	13	1.551	13	1.257	0.4	0.331
T-complex protein 1 subunit delta [Mus musculus]	6753322	2	58.0	8.02	12.43	48	7	1.150	1.075	0.106	0.099	27	1.281	27	1.232	27	1.257	0.0	0.027
protein diaphanous homolog 3 [Mus musculus]	9789931	2	133.6	7.61	5.81	14	6	1.545	1.273	0.386	0.303	9	1.189	9	1.324	9	1.257	0.1	0.076
ATP synthase subunit b, mitochondrial precursor [Mus musculus]	78214312	2	28.9	9.06	6.25	3	2	0.817	0.909	0.219	0.142	2	1.098	2	1.414	2	1.256	0.2	0.178
ran-binding protein 10 [Mus musculus]	40804757	2	70.0	6.68	2.16	2	1	1.574	1.287	0.406	0.315	1	1.334	1	1.174	1	1.254	0.1	0.090
survival of motor neuron-related-splicing factor 30 [Mus musculus]	27369569	2	26.7	7.82	2.52	1	1	0.782	0.891	0.154	0.173	1	1.383	1	1.123	1	1.253	0.2	0.146
multidrug resistance protein 1 [Mus musculus]	6755046	2	140.9	8.34	2.90	6	4	0.947	0.974	0.037	0.038	3	1.486	3	1.015	3	1.251	0.3	0.266
short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Mus musculus]	31982522	2	44.9	8.47	10.68	7	4	1.187	1.093	0.132	0.121	5	1.484	5	1.484	5	1.249	0.3	0.265
probable ATP-dependent RNA helicase DDX27 [Mus musculus]	124249330	2	85.9	9.25	2.63	3	2	1.479	1.239	0.338	0.273	2	1.357	2	1.136	2	1.246	0.2	0.125
mediator of RNA polymerase II transcription subunit 8 isoform 2 [Mus musculus]	29366816	2	25.9	6.90	5.13	2	1	1.560	1.280	0.396	0.309	1	1.242	1	1.251	1	1.246	0.0	0.005
PREDICTED: hypothetical protein [Mus musculus]	149257810	2	29.9	10.56	35.34	122	14	1.444	1.222	0.314	0.257	47	1.451	47	1.038	47	1.244	0.3	0.235
nucleolar protein 16 [Mus musculus]	30519925	2	21.1	9.91	15.17	13	3	1.174	1.087	0.123	0.113	6	1.252	6	1.234	6	1.243	0.	

leucine-rich repeat and WD repeat-containing protein 1 [Mus musculus]	166851848	2	71.5	7.87	2.01	3	1	1.086	1.043	0.061	0.058	2	1.448	2	1.009	2	1.228	0.3	0.253
intraflagellar transport protein 20 homolog [Mus musculus]	9506865	2	15.2	5.12	11.36	1	1	1.558	1.279	0.394	0.308	1	1.312	1	1.144	1	1.228	0.1	0.097
SWI/SNF complex subunit SMARCC1 [Mus musculus]	112421097	2	122.8	5.73	12.59	24	12	1.604	1.302	0.427	0.328	6	1.390	6	1.066	6	1.228	0.2	0.186
calcium-binding mitochondrial carrier protein Aralar2 [Mus musculus]	7657583	2	74.4	8.60	6.51	8	3	1.047	1.023	0.033	0.032	6	1.015	6	1.439	6	1.227	0.3	0.244
ribosome biogenesis regulatory protein homolog [Mus musculus]	227908779	2	41.5	10.77	7.40	5	3	0.739	0.870	0.184	0.212	4	1.129	4	1.139	4	1.224	0.1	0.110
zinc finger MYM-type protein 2 [Mus musculus]	37959742	2	154.5	6.37	1.31	2	2	1.346	1.173	0.245	0.209	2	1.331	2	1.117	2	1.224	0.2	0.124
small protein rich in amine and glycine [Mus musculus]	31981251	2	23.8	12.26	5.80	3	1	1.335	1.168	0.237	0.203	2	1.240	2	1.207	2	1.224	0.0	0.019
ATP-dependent RNA helicase DDX51 [Mus musculus]	40538825	2	70.3	9.47	7.20	5	3	1.361	1.180	0.255	0.216	3	1.392	3	1.055	3	1.223	0.2	0.195
PREDICTED: similar to splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) [Mus musculus]	149262253	2	27.7	10.36	8.06	2	2	1.497	1.248	0.351	0.281	2	1.177	2	1.270	2	1.223	0.1	0.054
cytosolic Fe-S cluster assembly factor NUBP2 [Mus musculus]	6754908	2	29.5	6.52	3.27	1	1	1.189	1.095	0.134	0.122	1	1.205	1	1.240	1	1.222	0.0	0.020
PREDICTED: similar to H+ ATP synthase [Mus musculus]	149262632	2	14.2	10.01	5.15	4	1	0.807	0.904	0.136	0.151	3	1.155	3	1.286	3	1.221	0.1	0.076
nucleolar GTP-binding protein 1 [Mus musculus]	31560110	2	74.1	9.52	0.95	2	1	1.101	1.051	0.071	0.068	1	1.228	1	1.209	1	1.218	0.0	0.011
la-related protein 4 isoform 2 [Mus musculus]	124358932	2	79.6	6.51	8.36	9	4	1.200	1.100	0.142	0.129	4	1.418	4	1.016	4	1.217	0.3	0.233
telomere-associated protein RIF1 [Mus musculus]	146231944	2	267.0	5.60	3.71	13	8	0.882	0.941	0.083	0.089	8	0.937	8	1.496	8	1.217	0.4	0.325
MK167 FHA domain-interacting nucleolar phosphoprotein [Mus musculus]	224809384	2	36.2	10.24	5.36	1	1	0.781	0.891	0.155	0.173	1	0.961	1	1.470	1	1.216	0.4	0.296
poly(A) binding protein, cytoplasmic 4 isoform 2 [Mus musculus]	22507391	2	67.8	9.50	10.24	12	5	1.229	1.114	0.162	0.145	4	1.102	4	1.328	4	1.215	0.2	0.132
signal recognition particle receptor subunit alpha [Mus musculus]	27229036	2	69.6	8.95	17.14	43	12	0.631	0.816	0.261	0.320	28	0.981	28	1.449	28	1.215	0.3	0.273
PREDICTED: hypothetical protein [Mus musculus]	149271689	2	23.1	4.09	3.48	1	1	1.014	1.007	0.010	0.010	1	1.169	1	1.261	1	1.215	0.1	0.054
HEAT repeat-containing protein 3 [Mus musculus]	40789301	2	74.3	5.01	7.22	10	5	0.802	0.901	0.140	0.155	7	1.171	7	1.258	7	1.214	0.1	0.051
serine/arginine repetitive matrix protein 2 [Mus musculus]	126157504	2	283.4	12.09	0.54	2	1	1.452	1.226	0.319	0.260	1	1.265	1	1.160	1	1.213	0.1	0.061
histone H2B type 1-H [Mus musculus]	30061387	2	13.9	10.32	60.32	123	10	0.684	0.842	0.223	0.265	2	1.008	2	1.211	2	1.211	0.3	0.236
PREDICTED: similar to HistH2b protein [Mus musculus]	149264032	2	13.9	10.32	60.32	123	10	0.684	0.842	0.223	0.265	2	1.413	2	1.008	2	1.211	0.3	0.236
eukaryotic translation initiation factor 4 gamma 1 isoform b [Mus musculus]	56699434	2	175.2	5.38	6.59	23	8	1.457	1.228	0.323	0.263	7	1.059	7	1.360	7	1.210	0.2	0.176
ferritin heavy chain [Mus musculus]	6753912	2	21.1	5.88	3.85	2	1	0.742	0.871	0.182	0.209	2	1.273	2	1.143	2	1.208	0.1	0.076
SHC-transforming protein 1 isoform b [Mus musculus]	15778828	2	51.4	7.08	2.77	2	1	0.985	0.992	0.011	0.011	2	1.152	2	1.264	2	1.208	0.1	0.065
T-complex protein 1 subunit alpha B [Mus musculus]	110625624	2	60.4	6.16	31.12	52	15	1.243	1.122	0.172	0.153	29	1.189	29	1.227	29	1.208	0.0	0.022
dna) homolog subfamily 1 precursor [Mus musculus]	7106295	2	63.8	8.97	5.25	10	2	0.900	0.950	0.071	0.075	3	0.997	3	1.419	3	1.208	0.3	0.247
putative ribosomal RNA methyltransferase NOP2 [Mus musculus]	15896689	2	86.9	9.19	7.81	11	6	1.100	1.050	0.071	0.067	9	1.038	9	1.378	9	1.208	0.2	0.199
plakophilin-4 isoform 2 [Mus musculus]	147899467	2	126.7	8.95	1.57	3	2	1.021	1.011	0.015	0.015	1	1.239	1	1.176	1	1.207	0.0	0.037
phosphatidylserine decarboxylase proenzyme [Mus musculus]	126722757	2	45.9	9.57	3.45	2	1	0.979	0.989	0.015	0.015	1	1.123	1	1.289	1	1.206	0.1	0.097
PDS5, regulator of cohesion maintenance, homolog B [Mus musculus]	6695886	2	164.3	8.50	15.98	44	22	1.008	1.004	0.006	0.006	23	1.067	23	1.344	23	1.206	0.2	0.163
PREDICTED: similar to Probable ATP-dependent RNA helicase DDX46 (DEAD box protein 46) [M	149264152	2	110.3	7.39	4.81	12	5	1.281	1.141	0.199	0.174	7	1.087	7	1.324	7	1.206	0.2	0.139
gap junction alpha-1 protein [Mus musculus]	6753992	2	43.0	8.76	3.93	4	1	0.687	0.843	0.221	0.263	2	1.450	2	0.961	2	1.205	0.3	0.287
serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform [Mus mus	8394027	2	65.3	5.11	13.75	14	7	1.329	1.165	0.233	0.200	9	0.956	9	1.453	9	1.205	0.4	0.292
60S acidic ribosomal protein P0 [Mus musculus]	6671569	2	34.2	6.25	42.59	144	11	1.243	1.121	0.172	0.153	90	1.234	91	1.174	91	1.204	0.0	0.035
3-keto-steroid reductase [Mus musculus]	87162470	2	37.3	6.73	3.59	1	1	1.394	1.197	0.279	0.233	1	1.281	1	1.122	1	1.202	0.1	0.094
182 kDa tankyrase-1-binding protein [Mus musculus]	124486923	0.5	181.7	4.88	7.15	16	8	1.332	1.166	0.235	0.201	9	0.678	9	0.921	9	1.099	0.2	0.214
tyrosine-protein kinase Sgk269 [Mus musculus]	157909795	0.5	191.0	6.87	4.09	12	6	1.415	1.208	0.294	0.243	7	0.703	7	0.892	7	0.798	0.1	0.167
family with sequence similarity 48, member A [Mus musculus]	9910330	0.5	59.6	7.08	1.32	1	1	0.916	0.908	0.130	0.143	1	0.736	1	0.859	1	0.798	0.1	0.109
U4/U6.U5 tri-snRNP-associated protein 1 [Mus musculus]	124244096	0.5	90.8	5.82	7.44	10	6	1.000	1.000	0.000	0.000	6	0.791	6	0.802	6	0.797	0.0	0.010
protein ECT2 [Mus musculus]	6681261	0.5	83.6	8.59	2.85	3	2	0.724	0.862	0.195	0.226	2	0.797	2	0.795	2	0.796	0.0	0.002
40S ribosomal protein S7 [Mus musculus]	6755376	0.5	22.1	10.10	34.54	51	7	0.900	0.950	0.071	0.075	22	0.736	22	0.796	22	0.796	0.1	0.107
cAMP-dependent protein kinase type II-alpha regulatory subunit [Mus musculus]	22550094	0.5	45.6	4.93	4.23	2	2	1.076	1.038	0.054	0.052	1	0.785	1	0.801	1	0.793	0.0	0.014
ctron Rho-interacting kinase [Mus musculus]	124487319	0.5	235.2	6.57	1.12	3	2	0.996	0.998	0.003	0.003	2	0.737	2	0.846	2	0.792	0.1	0.097
E1A binding protein p300 [Mus musculus]	94421034	0.5	263.1	8.54	2.32	4	3	0.761	0.880	0.169	0.192	1	0.639	1	0.942	1	0.791	0.2	0.271
TRIO and F-actin-binding protein isoform 5 [Mus musculus]	88501743	0.5	218.1	7.75	9.86	44	16	1.245	1.122	0.173	0.154	25	0.806	25	0.776	25	0.791	0.0	0.027
tubulin beta-2A chain [Mus musculus]	33859488	0.5	49.9	4.89	53.48	286	19	0.860	0.930	0.099	0.106	10	0.796	10	0.784	10	0.790	0.0	0.011
DNA damage-binding protein 1 [Mus musculus]	7657011	0.5	126.8	5.26	17.54	49	16	0.723	0.861	0.196	0.227	25	0.780	25	0.800	25	0.790	0.0	0.018
guanine nucleotide-binding protein (G1)/G(S)/G(T) subunit beta-2 [Mus musculus]	13937391	0.5	37.3	6.00	12.35	20	4	0.603	0.802	0.281	0.350	13	0.979	13	0.601	13	0.790	0.3	0.338
multidrug resistance-associated protein 1 [Mus musculus]	6678848	0.5	171.1	7.36	1.37	15	2	0.721	0.861	0.197	0.229	3	0.908	3	0.671	3	0.790	0.2	0.212
spectrin beta chain, brain 1 [Mus musculus]	117938332	0.5	274.1	5.58	36.94	272	78	1.414	1.207	0.293	0.242	141	0.641	141	0.936	142	0.788	0.2	0.265
C2 domain-containing protein 2-like [Mus musculus]	88900515	0.5	76.3	7.21	6.09	9	3	0.681	0.840	0.226	0.269	3	0.827	3	0.749	3	0.788	0.1	0.071
protein NEDD1 [Mus musculus]	171543875	0.5	71.2	7.84	3.18	2	1	0.961	0.980	0.028	0.028	1	0.839	1	0.736	1	0.788	0.1	0.093
alpha-parvin [Mus musculus]	31982526	0.5	42.3	5.95	1.61	1	1	0.692	0.846	0.218	0.257	1	0.653	1	0.919	1	0.786	0.2	0.240
protein Shroom2 [Mus musculus]	125347788	0.5	165.2	6.70	1.82	4	2	1.203	1.102	0.144	0.131	2	0.794	2	0.776	2	0.785	0.0	0.016
rab11 family-interacting protein 5 isoform 2 [Mus musculus]	55743143	0.5	69.5	9.07	1.55	2	1	0.668	0.834	0.235	0.282	1	0.762	1	0.805	1	0.783	0.0	0.039
serine/threonine-protein kinase 12 [Mus musculus]	51317394	0.5	39.4	9.44	3.48	1	1	1.015	1.008	0.011	0.011	1	0.903	1	0.662	1	0.783	0.2	0.218
eukaryotic translation initiation factor 3 subunit K [Mus musculus]	21312044	0.5	25.1	4.93	19.72	11	4	0.982	0.991	0.013	0.013	8	0.763	8	0.799	8	0.781	0.0	0.033
eukaryotic translation initiation factor 3 subunit L [Mus musculus]	51093840	0.5	66.6	6.44	31.56	74	18	0.749	0.875	0.177	0.203	48	0.633	49	0.927	49	0.780	0.2	0.266
exosome complex exonuclease RRP46 [Mus musculus]	20070392	0.5	25.2	7.56	3.83	1	1	0.890	0.945	0.078	0.082	1	0.788	1	0.772	1	0.780	0.0	0.015
dedicator of cytokinesis protein 1 [Mus musculus]	88853584	0.5	214.9	7.62	5.36	13	9	0.862	0.931	0.098	0.105	9	0.715	9	0.845	9	0.780	0.1	0.118
activity-dependent neuroprotector homeobox protein [Mus musculus]	90093349	0.5	124.2	6.86	2.89	4	3	0.937	0.969	0.044	0.046	3	0.780	3	0.778	3	0.779	0.0	0.002
carnitine O-palmitoyltransferase 1, liver isoform [Mus musculus]	162287142	0.5	88.2	8.62	2.98	5	2	0.988	0.994	0.009	0.009	3	0.757	3	0.800	3	0.778	0.0	0.039
leucine zipper protein 1 [Mus musculus]	119433663	0.5	119.2	7.99	30.62	90	28	0.906	0.953	0.067	0.070	52	0.901	52	0.656	52	0.778	0.2	0.223
microtubule-actin cross-linking factor 1 [Mus musculus]	169234940	0.5	619.1	5.44	2.34	17	9	0.976											

death-associated protein kinase 3 [Mus musculus]	6681133	0.5	51.4	8.70	14.51	8	6	0.967	0.983	0.024	0.024	7	0.750	7	0.778	7	0.764	0.0	0.026
WD repeat-containing protein 82 [Mus musculus]	148223079	0.5	35.1	7.69	15.34	6	4	0.983	0.992	0.012	0.012	4	0.738	4	0.790	4	0.764	0.0	0.048
3,2-trans-enoyl-CoA isomerase, mitochondrial precursor [Mus musculus]	31981810	0.5	32.2	8.98	21.80	13	5	0.832	0.916	0.119	0.130	8	0.794	8	0.733	8	0.764	0.0	0.057
tropomyosin alpha-4 chain [Mus musculus]	47894398	0.5	28.5	4.68	62.90	196	24	1.244	1.122	0.172	0.154	107	0.889	107	0.638	108	0.764	0.2	0.233
kinesin-like protein KIF3A [Mus musculus]	34328138	0.5	80.1	6.54	1.71	2	1	0.996	0.998	0.003	0.003	2	0.801	2	0.725	2	0.763	0.1	0.071
AP-3 complex subunit mu-2 [Mus musculus]	170763483	0.5	46.9	7.56	3.59	4	2	0.721	0.860	0.198	0.230	2	0.604	2	0.916	2	0.760	0.2	0.291
myosin-XVIIa [Mus musculus]	22094119	0.5	230.8	6.16	26.29	120	50	1.046	1.023	0.032	0.032	71	0.905	72	0.614	72	0.759	0.2	0.271
serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C [Mus musculus]	27370168	0.5	115.0	6.54	1.49	2	1	0.774	0.887	0.160	0.180	1	0.768	1	0.751	1	0.759	0.0	0.016
procollagen C-proteinase enhancer protein [Mus musculus]	125490382	0.5	50.1	8.41	4.49	4	2	1.078	1.039	0.055	0.053	3	0.656	3	0.862	3	0.759	0.1	0.192
EH domain-binding protein 1 [Mus musculus]	154240710	0.5	136.2	5.39	10.61	26	12	1.485	1.243	0.343	0.276	16	0.808	16	0.708	16	0.758	0.1	0.093
filamin-C [Mus musculus]	124487139	0.5	290.9	5.95	11.92	253	31	0.951	0.976	0.035	0.035	18	0.740	18	0.775	18	0.757	0.0	0.033
PREDICTED: hypothetical protein [Mus musculus]	149257848	0.5	10.1	9.76	8.33	1	1	0.880	0.940	0.085	0.091	1	0.759	1	0.752	1	0.755	0.0	0.006
ATP-binding cassette sub-family A member 13 [Mus musculus]	116292744	0.5	568.5	6.52	0.24	13	2	1.023	1.011	0.016	0.016	5	0.691	5	0.817	5	0.754	0.1	0.118
AP-2 complex subunit alpha-1 isoform b [Mus musculus]	116256510	0.5	105.4	7.66	16.65	64	17	0.677	0.838	0.228	0.272	16	0.818	16	0.690	16	0.754	0.1	0.121
SECIS-like 2 [Mus musculus]	226371698	0.5	94.1	6.39	2.96	3	2	1.129	1.065	0.091	0.086	2	0.815	2	0.693	2	0.754	0.1	0.114
patatin-like phospholipase domain-containing protein 7 [Mus musculus]	225007615	0.5	150.4	6.92	1.11	1	1	1.024	1.012	0.017	0.017	1	0.810	1	0.695	1	0.753	0.1	0.109
coronin-1B [Mus musculus]	6753494	0.5	53.9	5.78	10.33	15	5	1.066	1.033	0.047	0.045	10	0.808	10	0.696	10	0.752	0.1	0.105
probable ATP-dependent RNA helicase DHX40 [Mus musculus]	144926009	0.5	88.5	8.63	1.54	2	1	1.018	1.009	0.013	0.013	1	0.850	1	0.655	1	0.752	0.1	0.183
paraspeckle component 1 [Mus musculus]	225543409	0.5	58.7	6.67	1.34	1	1	1.166	1.083	0.117	0.108	1	0.676	1	0.828	1	0.752	0.1	0.143
PREDICTED: triple functional domain (PTPRF interacting) [Mus musculus]	149264663	0.5	347.7	6.35	1.80	11	5	0.947	0.973	0.038	0.039	6	0.741	6	0.753	6	0.747	0.0	0.011
uveal autoantigen with coiled-coil domains and ankyrin repeats [Mus musculus]	28077007	0.5	160.8	7.20	9.06	22	11	0.831	0.915	0.120	0.131	12	0.855	12	0.639	12	0.747	0.2	0.205
6-phosphofruktokinase, liver type [Mus musculus]	31560653	0.5	85.3	7.17	13.46	18	8	0.898	0.949	0.072	0.076	10	0.904	10	0.587	10	0.745	0.2	0.301
KN motif and ankyrin repeat domain-containing protein 2 [Mus musculus]	160333753	0.5	90.2	5.55	0.83	5	1	1.087	1.043	0.061	0.059	3	0.716	3	0.773	3	0.744	0.0	0.054
CCR4-NOT transcription complex subunit 3 [Mus musculus]	21222717	0.5	81.9	6.20	4.66	5	3	1.096	1.048	0.068	0.065	3	0.615	3	0.871	3	0.743	0.2	0.244
ankyrin repeat domain protein 17 isoform b [Mus musculus]	40549395	0.5	246.5	6.70	2.21	4	3	0.882	0.941	0.084	0.089	2	0.638	2	0.848	2	0.743	0.1	0.199
protein SMG7 isoform 3 [Mus musculus]	53828718	0.5	126.5	8.69	1.59	2	1	0.983	0.991	0.012	0.012	1	0.573	1	0.908	1	0.741	0.2	0.320
polymerase delta-interacting protein 3 [Mus musculus]	30519969	0.5	46.1	10.05	23.33	21	8	1.191	1.095	0.135	0.123	10	0.824	10	0.654	11	0.739	0.1	0.163
80 kDa MCM3-associated protein [Mus musculus]	109627648	0.5	217.2	6.61	1.67	3	2	1.045	1.023	0.032	0.031	2	0.752	2	0.721	2	0.737	0.0	0.030
protein flightless-1 homolog [Mus musculus]	11528490	0.5	144.7	6.06	20.14	79	24	0.894	0.947	0.075	0.079	50	0.836	50	0.631	50	0.734	0.1	0.197
dna) homolog subfamily C member 3 precursor [Mus musculus]	31245263	0.5	57.4	5.85	18.65	21	8	0.693	0.846	0.217	0.257	7	0.657	7	0.808	7	0.732	0.1	0.146
heat shock-related 70 kDa protein 2 [Mus musculus]	50345978	0.5	69.6	5.67	17.85	176	14	0.624	0.812	0.266	0.327	1	0.839	1	0.624	1	0.731	0.2	0.208
electron transfer flavoprotein subunit alpha, mitochondrial precursor [Mus musculus]	227500281	0.5	35.0	8.38	15.32	8	3	1.604	0.802	0.280	0.350	5	0.757	5	0.704	5	0.730	0.0	0.052
transcription factor 4 isoform b [Mus musculus]	145386522	0.5	71.1	7.01	1.35	1	1	0.507	1.253	0.358	0.286	1	0.746	1	0.714	1	0.730	0.0	0.032
hypothetical protein LOC67267 [Mus musculus]	13385560	0.5	16.3	9.19	11.76	2	1	0.711	0.855	0.204	0.239	1	0.839	1	0.618	1	0.729	0.2	0.214
pericentriolar material 1 protein [Mus musculus]	170763496	0.5	228.7	5.01	5.14	17	9	0.890	0.945	0.078	0.082	12	0.750	12	0.707	12	0.728	0.0	0.042
condensin-2 complex subunit H2 isoform b [Mus musculus]	153792292	0.5	68.0	4.81	5.51	4	2	0.938	0.969	0.044	0.045	3	0.665	3	0.786	3	0.725	0.1	0.118
DNA-directed RNA polymerase II subunit RPB1 [Mus musculus]	6677795	0.5	213.3	7.43	1.66	4	2	0.610	0.805	0.276	0.343	2	0.604	2	0.846	2	0.725	0.2	0.236
protein C20orf11 homolog [Mus musculus]	58037443	0.5	26.8	10.97	2.63	1	1	0.798	0.899	0.143	0.159	1	0.739	1	0.711	1	0.725	0.0	0.028
serine/threonine-protein kinase D1 [Mus musculus]	153945802	0.5	102.0	6.58	3.70	4	3	0.711	0.856	0.204	0.239	2	0.844	2	0.605	2	0.725	0.2	0.234
protein phosphatase 1 regulatory subunit 12A [Mus musculus]	95772123	0.5	111.7	5.60	21.61	38	17	0.761	0.880	0.169	0.192	21	0.875	21	0.566	21	0.721	0.2	0.303
pleckstrin homology domain-containing family G member 3 [Mus musculus]	167621502	0.5	148.4	5.68	2.39	3	3	0.709	0.855	0.205	0.240	3	0.861	3	0.578	3	0.719	0.2	0.278
dynactin subunit 2 [Mus musculus]	28076935	0.5	44.1	5.26	9.45	7	3	0.753	0.877	0.175	0.199	2	0.875	2	0.562	2	0.719	0.2	0.308
melanoma-associated antigen D1 [Mus musculus]	9789935	0.5	85.6	7.50	4.52	4	3	0.792	0.896	0.147	0.164	3	0.628	3	0.808	3	0.718	0.1	0.178
cytochrome b-c1 complex subunit 9 [Mus musculus]	37574048	0.5	7.4	9.19	26.56	2	1	1.011	1.005	0.008	0.008	1	0.637	1	0.796	1	0.716	0.1	0.157
formin-like protein 3 [Mus musculus]	38708163	0.5	117.1	6.67	8.46	20	9	0.656	0.828	0.243	0.279	7	0.740	7	0.686	7	0.713	0.0	0.054
leucine-rich repeat flightless-interacting protein 1 isoform 1 [Mus musculus]	162417949	0.5	79.2	4.82	23.18	41	14	0.855	0.927	0.103	0.111	19	0.730	19	0.697	19	0.713	0.0	0.032
leucine-rich repeat and calponin homology domain-containing protein 3 precursor [Mus musculus]	124486939	0.5	86.3	7.03	13.50	24	8	0.899	0.949	0.072	0.076	14	0.889	14	0.537	14	0.713	0.2	0.350
interferon-stimulated gene 20 kDa protein [Mus musculus]	15805028	0.5	20.6	8.75	4.42	1	1	1.411	1.206	0.291	0.241	1	0.612	1	0.812	1	0.712	0.1	0.199
cysteine-rich protein 2 [Mus musculus]	13195646	0.5	22.7	8.63	5.77	1	1	0.967	0.983	0.023	0.024	1	0.635	1	0.789	1	0.712	0.1	0.153
nck-associated protein 1 [Mus musculus]	28395023	0.5	128.7	6.62	11.52	29	12	0.647	0.824	0.249	0.303	20	0.696	20	0.727	21	0.712	0.0	0.030
eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 2 [Mus musculus]	194018533	0.5	68.5	5.21	4.88	12	4	0.631	0.816	0.261	0.320	3	0.692	3	0.724	3	0.708	0.0	0.033
rho GTPase-activating protein 21 isoform 2 [Mus musculus]	203097667	0.5	215.7	7.64	0.26	1	1	0.966	0.983	0.024	0.025	1	0.679	1	0.737	1	0.708	0.0	0.057
lethal(2) ant larva protein homolog 2 [Mus musculus]	144922656	0.5	114.3	7.46	5.94	9	5	0.686	0.843	0.222	0.263	5	0.831	5	0.584	5	0.707	0.2	0.247
vacuolar protein sorting-associated protein 13C [Mus musculus]	122114537	0.5	419.8	6.81	1.01	10	3	1.102	1.051	0.072	0.068	2	0.801	2	0.613	2	0.707	0.1	0.188
dedicator of cytokinesis 7 [Mus musculus]	78191789	0.5	237.9	6.79	16.40	98	30	1.017	1.009	0.012	0.012	48	0.762	48	0.646	48	0.704	0.1	0.117
A-kinase anchor protein 2 isoform 2 [Mus musculus]	78711834	0.5	97.1	5.19	1.59	3	1	1.236	1.118	0.167	0.149	1	0.746	1	0.660	1	0.703	0.1	0.087
PTB domain-containing enigma1 adapter protein 1 [Mus musculus]	164518895	0.5	34.4	7.90	6.58	4	2	0.779	0.890	0.156	0.175	2	0.643	2	0.760	2	0.701	0.1	0.119
stress-induced-phosphoprotein 1 [Mus musculus]	14389431	0.5	62.5	6.80	1.84	2	1	0.714	0.857	0.202	0.236	1	0.656	1	0.745	1	0.700	0.1	0.090
proteasome subunit alpha type-6 [Mus musculus]	6755198	0.5	27.4	6.86	14.23	8	3	0.681	0.841	0.225	0.268	5	0.795	5	0.604	5	0.699	0.1	0.193
dynein light chain 2, cytoplasmic [Mus musculus]	18087731	0.5	10.3	7.37	20.22	4	2	0.802	0.901	0.140	0.155	3	0.635	3	0.759	3	0.697	0.1	0.126
glucocorticoid receptor [Mus musculus]	121247453	0.5	87.1	6.35	2.90	3	2	0.790	0.895	0.166	0.166	2	0.539	2	0.849	2	0.694	0.2	0.316
protein phosphatase 1 regulatory subunit 12C [Mus musculus]	124249341	0.5	84.6	6.00	12.15	19	7	1.222	1.111	0.157	0.141	11	0.751	11	0.635	11	0.693	0.1	0.118
phosphorylase b kinase regulatory subunit alpha, liver isoform [Mus musculus]	27370156	0.5	138.4	6.37	1.46	2	1	1.212	1.106	0.150	0.136	1	0.642	1	0.742	1	0.692	0.1	0.102
leucine-rich repeat flightless-interacting protein 1 isoform 3 [Mus musculus]	162417952	0.5	48.9	5.57	14.25	10	6	0.696	0.848	0.215	0.253	1	0.815	1	0.568	1	0.691	0.2	0.253

cytoskeleton-associated protein 2-like [Mus musculus]	31712008	0.5	82.9	9.69	2.55	4	2	0.869	0.935	0.093	0.099	1	0.653	1	0.588	1	0.620	0.0	0.075
amyotrophic lateral sclerosis 2 chromosomal reon candidate gene 4 protein homolog isoform 2 (I	83715982	0.5	44.6	6.48	4.47	2	1	0.861	0.931	0.098	0.106	1	0.586	1	0.637	1	0.612	0.0	0.059
tropomyosin beta chain [Mus musculus]	11875203	0.5	32.8	4.70	70.07	349	34	0.771	0.885	0.162	0.183	78	0.706	78	0.504	78	0.605	0.1	0.236
SLIT-ROBO Rho GTPase-activating protein 2 [Mus musculus]	157951723	0.5	120.7	6.64	20.92	41	16	0.912	0.956	0.062	0.065	24	0.596	24	0.592	24	0.594	0.0	0.004
tight junction protein ZO-2 [Mus musculus]	160333863	0.5	131.2	6.79	21.34	65	24	0.692	0.846	0.218	0.258	44	0.659	44	0.527	44	0.593	0.1	0.157
nuclear factor 1 B-type isoform 3 [Mus musculus]	148747370	0.5	47.4	8.87	2.62	1	1	0.789	0.895	0.149	0.167	1	0.627	1	0.543	1	0.585	0.1	0.101
PREDICTED: similar to ribosomal protein S17 [Mus musculus]	149261791	0.5	15.8	9.54	50.72	54	6	0.657	0.829	0.242	0.292	2	0.525	2	0.629	2	0.577	0.1	0.127
keratin, type II cytoskeletal 2 oral [Mus musculus]	85701680	0.5	62.8	8.43	5.56	41	5	0.699	0.850	0.213	0.250	12	0.614	12	0.524	12	0.569	0.1	0.113
collagen alpha-1(XII) chain [Mus musculus]	111074529	0.5	333.1	5.80	17.45	136	45	0.725	0.862	0.195	0.226	84	0.589	84	0.531	85	0.560	0.0	0.073
ras GTPase-activating-like protein IQGAP2 [Mus musculus]	118344444	0.5	180.4	5.64	3.75	28	6	0.674	0.837	0.231	0.276	6	0.489	6	0.612	6	0.551	0.1	0.157
keratin, type II cytoskeletal 79 [Mus musculus]	22164776	0.5	57.5	7.69	5.27	33	4	0.651	0.826	0.247	0.299	10	0.446	10	0.650	10	0.548	0.1	0.263
keratin Kb40 [Mus musculus]	145580629	0.5	112.2	7.97	2.62	41	4	0.615	0.807	0.272	0.337	18	0.494	18	0.583	18	0.538	0.1	0.117
PREDICTED: similar to Snrpf protein [Mus musculus]	94372795	0.5	13.3	7.28	4.88	1	1	0.684	0.842	0.223	0.265	1	0.432	1	0.625	1	0.529	0.1	0.259
keratin, type I cytoskeletal 42 [Mus musculus]	154090941	0.5	50.1	5.16	6.19	6	4	0.832	0.916	0.119	0.130	1	0.579	1	0.463	1	0.521	0.1	0.158
long-chain-fatty-acid-CoA ligase 4 isoform 2 [Mus musculus]	75992925	0.5	74.3	8.00	2.69	2	1	0.902	0.951	0.069	0.073	1	0.410	1	0.624	1	0.517	0.2	0.292
probable RNA-binding protein 18 isoform 1 [Mus musculus]	13385930	0.5	21.6	9.44	6.84	7	2	0.807	0.903	0.136	0.151	1	0.466	1	0.563	1	0.515	0.1	0.133
liprin-alpha-3 [Mus musculus]	161016786	0.5	133.3	5.64	0.84	2	1	1.563	1.282	0.398	0.311	1	0.407	1	0.574	1	0.490	0.1	0.241
epidermal growth factor receptor pathway substrate 8 [Mus musculus]	75677397	0.5	91.7	7.65	3.29	5	3	0.622	0.811	0.267	0.330	2	0.354	2	0.403	2	0.478	0.1	0.224
acetyl-CoA carboxylase 1 [Mus musculus]	125656173	0.5	265.1	6.39	4.78	12	8	0.974	0.987	0.018	0.019	6	0.411	6	0.388	6	0.400	0.0	0.040

Gene name	Entrez Gene Name	Accession	MW [kDa]	calc. pl	ΣCoverage	Σ# PSMs	Σ# Peptides	A5: 115/114	A5: 115/114 Count	A5: 116/114	A5: 116/114 Count	A5: 117/114	A5: 117/114 Count	mean 117-116	P value
TMX4	thioredoxin-related transmembrane protein 4	112817607	37.1	4.37	9.25	9	2	1.117	5	2.253	5	2.175	5	2.214	0.013
IRGM	immunity-related GTPase family, M	6680351	46.5	8.28	3.91	2	1	0.956	1	2.617	1	1.796	1	2.207	0.054
PTPRK	protein tyrosine phosphatase, receptor type, K	6679561	164.1	5.95	0.82	2	1	0.880	1	1.824	1	2.025	1	1.925	0.008
PTRH2	peptidyl-HRNA hydrolase 2	149363634	19.5	7.42	19.89	18	2	1.041	8	1.571	8	2.011	8	1.791	0.054
TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. c	22094989	39.8	8.13	4.82	6	1	1.139	3	1.965	3	1.578	3	1.771	0.011
MOGS	mannosyl-oligosaccharide glucosidase	31981106	91.8	9.00	3.00	4	2	0.905	2	1.329	2	1.660	2	1.494	0.053
CAPRN1	cell cycle associated protein 1	162329568	76.6	5.12	4.34	3	3	1.170	3	1.828	3	1.142	3	1.485	0.045
SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transp	6677995	53.2	7.47	8.92	4	3	0.689	3	1.327	3	1.415	3	1.371	0.022
ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, carr	163838648	30.2	8.84	41.97	59	13	0.873	33	1.236	33	1.464	33	1.350	0.030
AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	6755004	66.7	9.17	5.72	5	2	1.002	2	1.314	2	1.377	2	1.345	0.006
KTN1	kinesin 1 (kinesin receptor)	144922638	152.4	5.90	24.94	70	30	0.879	40	1.235	40	1.383	41	1.309	0.015
HSPA9	heat shock 70kDa protein 9 (mortalin)	162461907	73.4	6.07	26.28	89	18	1.011	57	1.254	57	1.325	57	1.290	0.048
Gm2835	predicted gene 2835	149271689	23.1	4.09	3.48	1	1	1.014	1	1.169	1	1.261	1	1.215	0.035
HEATR3	HEAT repeat containing 3	40789301	74.3	5.01	7.22	10	5	0.802	7	1.171	7	1.258	7	1.214	0.016
SHC1	SHC (Src homology 2 domain containing) transforming protein	15778828	51.4	7.08	2.77	2	1	0.985	2	1.152	2	1.264	2	1.208	0.035
SART1	squamous cell carcinoma antigen recognized by T cells	124244096	90.8	5.82	7.44	10	6	1.000	6	0.791	6	0.802	6	0.797	0.037
RPS7	ribosomal protein S7	6755376	22.1	10.10	34.54	51	7	0.900	22	0.736	22	0.855	22	0.796	0.051
PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	22550094	45.6	4.93	4.23	2	2	1.076	1	0.785	1	0.801	1	0.793	0.037
ADNP	activity-dependent neuroprotector homeobox	90093349	124.2	6.86	2.89	4	3	0.937	3	0.780	3	0.778	3	0.779	0.051
VAT1	vesicle amine transport protein 1 homolog (T. californica)	33859662	43.1	6.37	9.61	6	3	0.947	5	0.797	5	0.760	5	0.778	0.047
MED19	mediator complex subunit 19	21313194	26.2	9.88	6.56	2	1	0.939	1	0.750	1	0.804	1	0.777	0.022
UBTF	upstream binding transcription factor, RNA polymerase I	113205053	85.0	5.55	3.44	7	2	0.682	4	0.745	4	0.786	4	0.765	0.004
DAPK3	death-associated protein kinase 3	6681133	51.4	8.70	14.51	8	6	0.967	7	0.750	7	0.778	7	0.764	0.024
KIF3A	kinesin family member 3A	34328138	80.1	6.54	1.71	2	1	0.996	2	0.801	2	0.725	2	0.763	0.048
MCM3AP	minichromosome maintenance complex component 3 associat	109627648	217.2	6.61	1.67	3	2	1.045	2	0.752	2	0.721	2	0.737	0.021
ARHGAP21	Rho GTPase activating protein 21	203097667	215.7	7.64	0.26	1	1	0.966	1	0.679	1	0.737	1	0.708	0.011
LLGL1	lethal giant larvae homolog 1 (Drosophila)	6678696	112.3	6.48	2.61	2	2	1.094	2	0.660	2	0.714	2	0.687	0.026
FLNB	filamin B, beta	145966915	276.4	5.69	22.46	245	54	1.211	72	0.657	72	0.714	72	0.686	0.054
CSDA	cold shock domain protein A	20806532	30.7	9.63	17.81	29	5	0.936	2	0.655	2	0.656	2	0.655	0.003
CKAP2L	cytoskeleton associated protein 2-like	31712008	82.9	9.69	2.55	4	2	0.869	1	0.653	1	0.588	1	0.620	0.040
RBM18	RNA binding motif protein 18	13385930	21.6	9.44	6.84	7	2	0.807	1	0.466	1	0.563	1	0.515	0.049
ACACA	acetyl-CoA carboxylase alpha	125656173	265.1	6.39	4.78	12	8	0.974	6	0.411	6	0.388	6	0.400	0.050
MCCC2	methylcrotonoyl-CoA carboxylase 2 (beta)	73622267	61.3	8.00	6.39	5	3	0.568	3	0.180	3	0.185	3	0.183	0.053