Peptidomics and Secretomics of the Mammalian Peripheral Sensory-Motor System

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Supplementary Material

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Calibration of regional release

When collecting release from semi-intact preparations (see Figure S1), the amount of material collected usually precludes LC-MS measurement and MALDI MS-based MS/MS measurements. An issue is that even with SPE sample collection, the direct MALDI MS produced numerous low intensity peaks; accurately assigning these peaks can be problematic. Thus, we acquired MALDI MS (with limited LC-FT MS information on release), and LC-FT MS characterization of the contents of the system. We performed a three-stage calibration approach for the compounds detected using SPE and MALDI MS. We then compared the different datasets using the higher accuracy (but with poorer detection limit) datasets to identify and even to calibrate the direct MALDI MS spectra. We internally calibrated the spectra using several ubiquitously observed compounds, including well-recognized and consistently observed DHB matrix ions in the low molecular mass region and thymosin beta 4 ions in the higher mass region. Peptides from neurofilament 3, medium (2328.158 Da Acetyl-SYTLDSLGNPSAYRRVTETR, and 3094.667 Da VEAPKLKVQHKFVEEIIEETKVEDEK) and vimentin (2335.160 Da) proteins were chosen as additional standards. Most spectra were recalibrated in more defined mass windows.

As a result of the MALDI MS dataset evaluations, 198 different *m/z* entries were selected as putative peptides present in releasate from all studied regions. The selective nature of choosing mass spectra for high quality calibration restricted the number of compounds assigned; in all cases, we had between 50 and 116 peaks of acceptable quality in each spectrum. The identities of 160 peptides were assigned in our MALDI MS dataset by matching the *m/z*s with corresponding information in the FT MS identification results (Table S4). Perhaps not surprisingly, there are several instances where more than one identification assignment can be made for a detected *m/z*. For such cases, whenever possible, we assigned isobaric peptides to those from proteins that already have been confirmed. For example, 68 matches to neurofilament protein-related peptides represent a large group of related peptides. However, peptides related to medium neurofilament 3 (P12839) and uncharacterized peptide G3V7S2 indicate two possible assignments to the same molecules. A BLAST search demonstrates a 95% homology between P12839 and G3V7S2 (http://www.uniprot.org/blast/uniprot/B201505242FZDO96J1N). Nine peptide pairs with the same *m/z*s were found that originated from either G3V7S2 or P12839, suggesting an inability to distinguish the protein source for these peptides.

The detection of multiple peptides originating from the same protein family increases the confidence in their assignment. In our dataset, there are several peaks that have tentative assignments that match others from the same protein family (similar to peptide mass fingerprinting). For example, myelin-related proteins such as myelin basic protein and myelin protein P0 are likely the source of 39 peptides. Additional putative peptides entries include: vimentin (13), tubulin-related proteins (4), thymosin beta 4 and 10 (7), hemoglobin-related (6), caveolin 1 (2), and gamma-synuclein (2). There are many other peptides observed via MALDI MS that match the FT MS data by *m/z,* and additional peaks that have no match (Table S4).

As a last point, many of our assignments are for peptides that are expected or previously reported to be in these tissues. For example, isolated semi-intact preparations of DRGs were used in the experiments. When isolating our samples, nerves had to be cut, creating a nerve injury model. Therefore, the release of neurofilament protein-related peptides is expected since neurofilament proteins are markers of neurite outgrowth. Interestingly, although G3V7S2 is listed as an uncharacterized protein in the UniProt database, the expression of G3V7S2 is high in the brain (the Expression Atlas, http://www.ebi.ac.uk/gxa/genes/ENSRNOG00000013916). In addition, a 1.6 log2-fold increase in the G3V7S2 RNA level was reported in DRGs two weeks after L5 spinal nerve ligation (the Expression Atlas, http://www.ebi.ac.uk/gxa/genes/ ENSRNOG00000013916). However, the opposite effect was observed for the RNA levels in the case of the intraorbital nerve damage. Unfortunately, there is no information on the expression of neurofilament 3, medium (P12839) in the database. Only peptides associated with the light (68–70 kDa) and the medium (145–160 kDa), but not the heavy (200–220 kDa), neurofilament proteins were observed, indicating differences in their localization and/or processing. Another protein frequently observed in our dataset is vimentin, an intermediate filament protein expressed by neurons and glia, including Schwann cells [1, 2]. Vimentin is involved in axonogenesis and peripheral nerve injury response, induced in Schwann cells after nerve injury, and its phosphorylation controls axon outgrowth [1, 3]. Vimentin RNA levels decrease in DRGs 2 weeks after L5 spinal nerve ligation (the Expression Atlas, http://www.ebi.ac.uk/gxa/genes/ ENSRNOG00000013916).

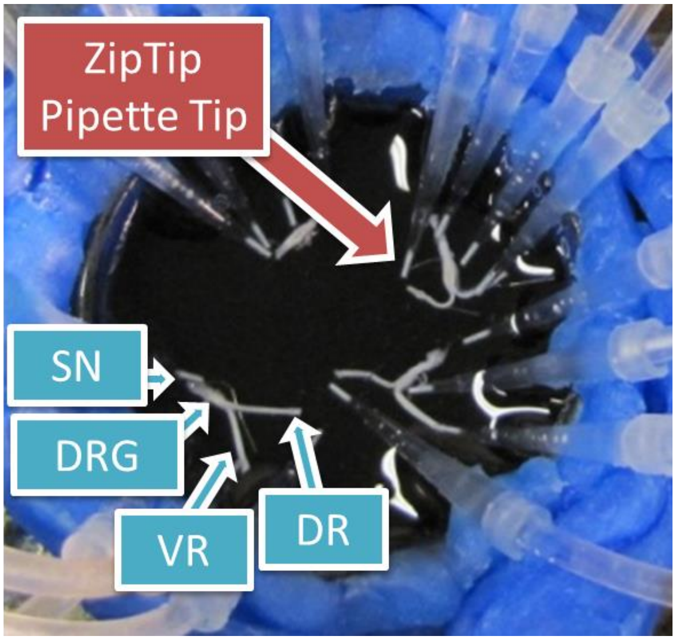

Figure S1. Experimental schematic for investigation of regional release from mammalian peripheral sensory-motor structures, including the L4 dorsal root ganglion (DRG), ventral root (VR), dorsal root (DR), and spinal nerve (SN). A cured Sylgard-filled glass Petri dish with dentist's wax affixed on the walls was used as the experimental chamber. DRGs and attached nerves were pinned down to the Sylgard surface and C18 ZipTip pipette tips (Millipore) mounted in close proximity to the investigated anatomical region. Four different experiments were performed (4 animals and 8 L4 ganglia) at 36 ^{o}C.

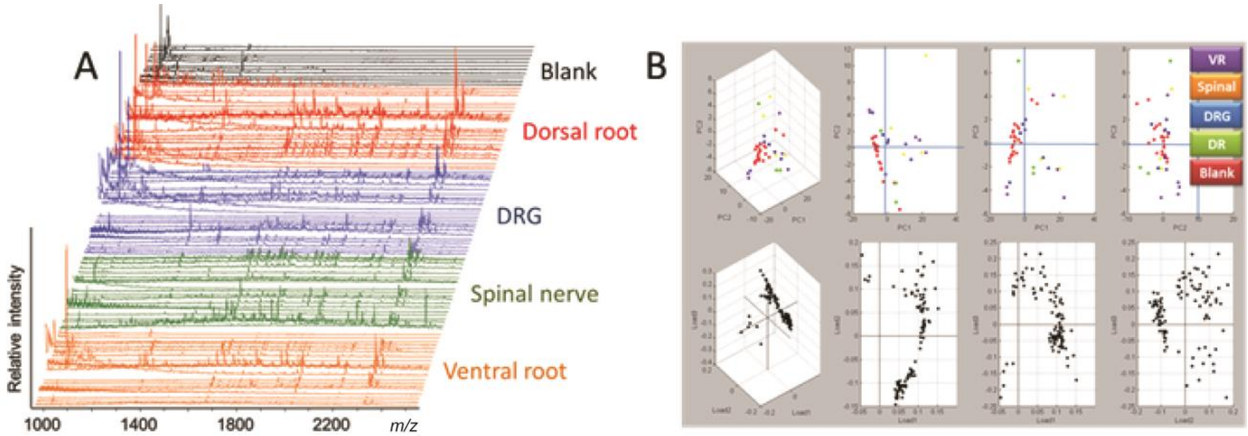

Figure S2. Metabolite and peptide profiles are similar for releasates from the studies regions of the mammalian peripheral sensory-motor system. **A.** Representative mass spectra of peptide profiles of releasates collected four experiments. **B.** Principal component analysis of the data set.

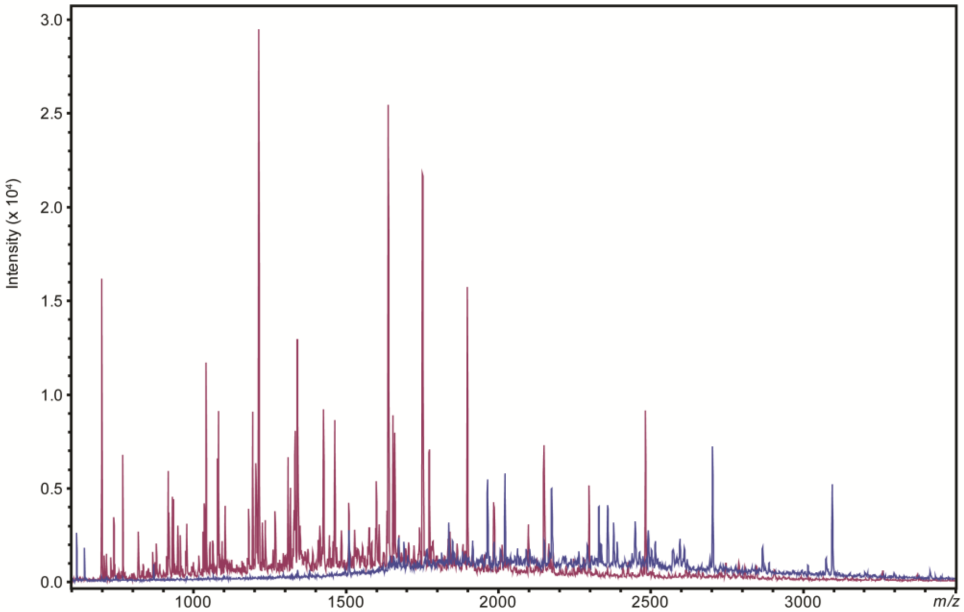

Figure S3. Mass spectra comparing peaks from stimulation collections from cluster (maroon) and culture (blue). Although a number of signals in the peptide range were observed for both samples, few peaks overlap.

Table S1. Peptides identified from tissue extracts from the LC-FTMS measurements assigned using PEAKS software.

Precursor	Accession number	Peptide sequence	Score (-10logP)	Mass (Da)	Mass error (ppm)
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	F.LFRDGDILGKYVD	30.94	1509.78	-5
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	F.RDGDILGKYVD	30.75	1249.63	-1
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFL.P	44.81	1078.59	-0.4
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPL.F	41.07	1288.73	0.7
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDR.V	49.45	1706.93	-2.6
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRV.L	51.12	1805.99	-2.8
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLV.E	38.81	2018.15	0.6
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVE.R	43.39	2147.19	0.4
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVER.S	51.94	2303.29	0.1
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERS.A	56.6	2390.32	-2.2
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERSA.A	27.12	2461.36	-1
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERSAA.E	36.39	2532.4	-1.1
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERSAAET.V	34.09	2762.49	-2.8
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERSAAETV.T	26.28	2861.56	-0.1
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.A(+42.01)GQAFRKFLPLFDRVLVERSAAETVTKGGIMLPEKSQGKVLQA.T	19.81	4727.59	-1.9
10 kDa heat shock protein mitochondrial	sp|P26772|CH10_RAT	M.AGQAFRK(+42.01)FLPLFDRVLVERSAAETVTKGGIMLPEKSQGKVLQA(-.98).T	19.49	4726.61	-6.7
40S ribosomal protein S12	tr|Q6PDW1|Q6PDW1_RAT	M.A(+42.01)EEGIAAGGVMDVNTALQEVLKTALIHDGLAR.G	21.79	3303.71	-0.1
40S ribosomal protein S12	tr|Q6PDW1|Q6PDW1_RAT	M.A(+42.01)EEGIAAGGVMDVNTALQEVLKTALIHDGLARGIRE.A	27.29	3758.96	0.1
40S ribosomal protein S12	tr|Q6PDW1|Q6PDW1_RAT	M.A(+42.01)EEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREA.A	35.06	3830	-2.5
40S ribosomal protein S12	tr|Q6PDW1|Q6PDW1_RAT	M.A(+42.01)EEGIAAGGVMDVNTALQEVLKT.A	41.56	2357.18	-0.6
40S ribosomal protein S12	tr|Q6PDW1|Q6PDW1_RAT	M.A(+42.01)EEGIAAGGVMDVNTALQEVLKTALIHDGL.A	38.92	3076.58	0.3
40S ribosomal protein S19	sp|P17074|RS19_RAT	L.AKHKELAPYDEN.W	20.56	1413.69	-0.2
40S ribosomal protein S21	sp|P05765|RS21_RAT	A.IRRMGESDDSILRLAKADGIVSKNF	44.41	2790.48	0.4
40S ribosomal protein S21	sp|P05765|RS21_RAT	A.KADGIVSKNF	43.13	1077.58	0

40S ribosomal protein S21	sp|P05765|RS21_RAT	G.AIRRMGESDDSILRLAKADGIVSKNF	18.85	2861.52	-2.5
40S ribosomal protein S21	sp|P05765|RS21_RAT	L.AKADGIVSKNF	48.89	1148.62	-0.8
40S ribosomal protein S21	sp|P05765|RS21_RAT	M(+42.01)QNDAGEFVDLYVPRKC(-.98)(-1.01).S	18.95	2023.94	-7.7
40S ribosomal protein S21	sp|P05765|RS21_RAT	M(+42.01)QNDAGEFVDLYVPRKC.S	44.17	2025.93	0.8
40S ribosomal protein S21	sp|P05765|RS21_RAT	M.GESDDSILRLAKADGIVSKNF	24.87	2234.15	0.6
40S ribosomal protein S21	sp|P05765|RS21_RAT	R.MGESDDSILRLAKADGIVSKNF	44.35	2365.19	-2.1
40S ribosomal protein S21	sp|P05765|RS21_RAT	R.RMGESDDSILRLAKADGIVSKNF	45.11	2521.3	-2.2
40S ribosomal protein S21	sp|P05765|RS21_RAT	K.ADGIVSKNF	19.47	949.487	-2
40S ribosomal protein S21	tr|D3ZSE0|D3ZSE0_RAT	M(+42.01)QNDAGEFVDLYVPRK(-.98).C	35.68	1921.94	-0.4
40S ribosomal protein S28	sp|P05765|RS21_RAT	M(+42.01)QNDAGEFVDLYVPRK.C	40.97	1922.92	-3.1
40S ribosomal protein S28	sp|P62859|RS28_RAT	F.MDDTSRSIIRNVKGPVREGDVLTLLESEREARRLR	25.92	4066.18	-0.6
40S ribosomal protein S28	sp|P62859|RS28_RAT	I.RNVKGPVREGDVLTLLESEREARRLR	34.07	3047.71	-1.3
40S ribosomal protein S28	sp|P62859|RS28_RAT	L.TLLESEREARRLR	20.44	1627.91	-0.4
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIK.L	37.75	1215.63	-1.5
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKL.A	36.19	1328.71	-1
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKLA.R	28.27	1399.75	-0.4
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKLAR.V	44.41	1555.85	-1.3
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKLARVTKV.L	28.65	1983.13	-3.6
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKLARVTKVLG.R	18.45	2153.24	0.1
40S ribosomal protein S28	sp|P62859|RS28_RAT	M(+42.01)DTSRVQPIKLARVTKVLGR.T	50.46	2309.34	-1.3
40S ribosomal protein S28	sp|P62859|RS28_RAT	N.VKGPVREGDVLTLLESEREARRLR	17.24	2777.56	0.4
40S ribosomal protein S28	sp|P62859|RS28_RAT	T.SRSIIRNVKGPVREGDVLTLLESEREARRLR	26.51	3604.04	-0.6
40S ribosomal protein S28	sp|P62859|RS28_RAT	T.SRSIIRNVKGPVREGDVLTLLESEREARRLR(-.98)	21.19	3603.06	-6.4
40S ribosomal protein S28	sp|P62859|RS28_RAT	V.KGPVREGDVLTLLESEREARRLR	22.15	2678.49	-0.6
40S ribosomal protein S28	sp|P62859|RS28_RAT	V.RVEFMDDTSRSIIRNVKGPVREGDVLTLLESEREARRLR	31.56	4597.46	0.9
40S ribosomal protein S28	sp|P62859|RS28_RAT	E.GDVLTLLESEREARRLR	19.94	2012.11	-1.7
40S ribosomal protein S28	sp|P62859|RS28_RAT	V.EFMDDTSRSIIRNVKGPVREGDVLTLLESEREARRLR	16.6	4342.29	-2.2
40S ribosomal protein S30	tr|Q5BJN7|Q5BJN7_RAT	G.KVHGSLARAGKVRGQ.T	17.39	1562.91	-0.5
40S ribosomal protein S30	tr|Q5BJN7|Q5BJN7_RAT	G.KVHGSLARAGKVRGQTPKVAKQEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS	15.6	6643.82	-1.2
40S ribosomal protein SA	sp|P38983|RSSA_RAT	M.S(+42.01)GGLDVLQMKEEDVLK.F	33.71	1801.91	-0.7

40S ribosomal protein SA	sp|P38983|RSSA_RAT	M.S(+42.01)GGLDVLQMKEEDVLKFLAAGTHL.G	37.04	2612.35	-0.7
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFA.K	19.02	1502.76	0.4
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAK.A	29.43	1630.85	-2
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAKA.L	29.13	1701.89	-4.7
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAKAL.A	41.26	1814.97	1.3
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAKALA.N	19.71	1886.01	-2.3
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAKALAN.V	15.89	2000.05	1.3
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.AGVNVEPFWPGLFAKALANV.N	32.35	2099.12	0.9
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	A.GVNVEPFWPGLFAKAL.A	40.57	1743.93	-1.9
60S acidic ribosomal protein P1	sp|P19944|RLA1_RAT	K.AAGVNVEPFWPGLFAKAL.A	34.58	1886.01	-1.4
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	F.GIRAKRAKEAAEQDVEK.K	25.96	1898.03	1
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	F.GIRAKRAKEAAEQDVEKK.K	18.75	2026.13	-0.7
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	F.GIRAKRAKEAAEQDVEKKK	41.31	2154.22	0.6
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	G.IRAKRAKEAAEQDVEKKK	44.88	2097.2	0.4
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	I.RNVYKKEKARAITEEEKN.F	15.96	2205.19	-2.7
60S ribosomal protein L13	tr|D3ZD02|D3ZD02_RAT	L.KLATQLTGPVMPI.R	32.19	1367.78	-0.5
60S ribosomal protein L3	sp|P21531|RL3_RAT	F.MGPLKKDRIAKEEGA	51.09	1641.89	-0.5
60S ribosomal protein L31	sp|P62902|RL31_RAT	F.KNLQTVNVDEN	42.52	1272.63	-0.8
60S ribosomal protein L31	sp|P62902|RL31_RAT	P.AKKGGEKKKGRSAINEVVTRE.Y	40.81	2284.3	-0.9
60S ribosomal protein L31	sp|P62902|RL31_RAT	P.AKKGGEKKKGRSAINEVVTREY.T	28.59	2447.36	-1.5
60S ribosomal protein L31	sp|P62902|RL31_RAT	Y.RIRVRLSRKRNEDEDSPNKLY.T	21.61	2643.43	-2.3
Ab2-162	tr|Q7TP54|Q7TP54_RAT	G.VAQASLGEYLFERLTLKHD	29.03	2189.15	-1.2
Ac1873	tr|Q7TQ70|Q7TQ70_RAT	E.FIEAGGDIR.G	26.56	976.498	-1
Ac1873	tr|Q7TQ70|Q7TQ70_RAT	T.ADTGTTSEFIEAGGDIR.G	38.35	1738.8	-3.9
Ac1873	tr|Q7TQ70|Q7TQ70_RAT	Y.KMADEAASEAHQEGDTRTTKRGRART.M	33.15	2872.4	-2.7
Ac2-246	tr|Q7TPJ6|Q7TPJ6_RAT	L.GSSKTDLFYERKKYGFKKR	28.3	2337.26	-0.7
Acidic leucine-rich nuclear phosphoprotein 32 family member A	sp|P49911|AN32A_RAT	L.SGNKIKDLSTIEPLKKLENL.K	27.91	2239.28	-2
Acidic leucine-rich nuclear phosphoprotein 32 family member A	sp|P49911|AN32A_RAT	M(+42.01)EMDKRIYLEL.R	42.78	1481.73	-0.4
Acidic leucine-rich nuclear phosphoprotein 32 family member A	sp|P49911|AN32A_RAT	M(+42.01)EMDKRIYLELRNRTPSDVKEL.V	27.3	2777.42	0.2
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	L.AGRDLTDYLMKILTERGYSF.V	28.51	2348.18	-0.9

Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	L.DLAGRDLTDYLMKILTERGYSF.V	38.14	2576.29	-1.3
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	M.RLDLAGRDLTDY.L	17.9	1406.72	-2.2
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	M.SGGTTMYPGIADRMQKEITAL.A	25.89	2239.1	-2.2
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	Y.PIEHGIITNWDDMEKIWHH.T	35.15	2370.12	-2.2
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	Y.PIEHGIITNWDDMEKIWHHTF.Y	20.24	2618.24	-0.3
Actin alpha skeletal muscle	sp|P68136|ACTS_RAT	Y.PIEHGIITNWDDMEKIWHHTFYNEL.R	23.79	3137.47	-2.4
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	C.DVDIRKDLYANTVL.S	30.9	1633.87	0.7
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	F.TTTAEREIVRDIKEKLCYV.A	21.3	2266.2	0.6
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	G.MGQKDSYVGDEAQSKRGILT.L	18.46	2182.07	0.4
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	L.DLAGRDLTDYLMKILTE.R	31.1	1966.01	1.4
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	L.DLAGRDLTDYLMKILTERGYS.F	25.21	2429.23	-3.9
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	L.RVAPEEHPVLLTEA.P	38.78	1559.83	-0.2
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	L.SGGTTMYPGIADRMQKEITAL.A	18.15	2239.1	-1.5
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	V.D(+42.01)IRK(+42.01)DLYANTVLS(+79.97)G.G	15.62	1727.81	2.5
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	V.GMGQKDSYVGDEAQSKRGILTL.K	21.1	2352.17	0.7
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	M.D(+42.01)DDIAALVVDNGSGMCK.A	21.61	1763.77	0.1
Actin cytoplasmic 1	sp|P60711|ACTB_RAT	Y.ALPHAILRL.D	24.91	1002.63	-0.3
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	A.PLNPKANREKMTQIMF.E	15.93	1917	-2.9
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	C.DVDIRKDLYANTVLSGGTTMYPGIADRMQKEITAL.A	21.35	3854.95	-1
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.AGRDLTDYLMKILTERGYSF.T	28.51	2348.18	-0.9
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.DLAGRDLTDYLM(+15.99)KILTE.R	21.64	1982	-0.3
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.DLAGRDLTDYLMKILTERGYSF.T	38.14	2576.29	-1.3
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.DLAGRDLTDYLMKILTERGYSFTTT.A	24.88	2879.44	3.5
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.PHAILRL.D	24.09	818.513	-0.5
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.RLDLAGRDLTDY.L	17.9	1406.72	-2.2
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.RVAPEEHPVLLTE.A	32.02	1488.79	0.4
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.RVAPEEHPVLLTEAPLNPKANREKMTQIMF.E	24.56	3458.82	-7.8
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.RVAPEEHPVLLTEAPLNPKANREKMTQIMFETF(-.98).N	21.76	3834.99	-5
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	L.RVAPEEHPVLLTEAPLNPKANREKMTQIMFETF.N	21.44	3835.98	-0.4
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	M.E(+42.01)EEIAALVIDNGSGMCK.A	30.57	1819.83	0.9
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	V.APEEHPVLLTEA.P	19.66	1304.66	-0.5
Actin cytoplasmic 2	sp|P63259|ACTG_RAT	Y.NELRVAPEEHPVLL.T	28.24	1614.87	0.7
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	A.TVGDVNTDRPGLLDL.K	41.18	1583.82	0

Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	F.KQATVGDVNTDRPGLLDL.K	42.24	1911.01	-2.5
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	G.TSKENAMKTYVEKVEELKKKYGI	36.4	2715.45	-0.8
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	K.GTSKENAMKTYVEKVEELKKKYGI	36.89	2772.47	-1.6
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	K.TYVEKVEELKKKYGI	42.41	1826.02	-0.5
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	L.KGTSKENAMKTYVEKVEELKKKYGI	27.27	2900.57	-0.7
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.KTYVEKVEELKKKYGI	36.19	1954.11	-2.6
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKR.L	42.43	1634.79	0.2
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRL.K	32.3	1747.87	-1.1
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLK.T	19.91	1875.97	-0.1
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTD.E	33.26	2418.2	0.4
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEM(+15.99)LF.I	15.17	3083.48	1.4
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEM.L	41.73	2807.33	-2
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEML.F	21.49	2920.41	-0.9
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLF.I	24.77	3067.48	-1.4
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLFIY.S	15.71	3343.63	2.5
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLFIYSH.F	25.22	3567.72	1.2
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLFIYSHF.K	47.66	3714.79	-2.7
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLFIYSHFKQA.T	49.74	4041.98	-2.7
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.S(+42.01)QADFDKAAEEVKRLKTQPTDEEMLFIYSHFKQATVGDVNTDRPGLLDL.K	21.67	5607.78	-3.6
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.SQADFDK(+42.01)AAEEVKRLKTQPTDEEMLFI.Y	16.36	3180.56	-1.9
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.SQADFDK(+42.01)AAEEVKRLKTQPTDEEMLFIYS(-.98).H	16.1	3429.68	6.2
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	M.SQADFDK(+42.01)AAEEVKRLKTQPTDEEMLFIYSHFKQ(-.98).A	16.18	3969.96	-1.1
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	N.AMKTYVEKVEELKKKYGI	34.95	2156.19	0.9
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	T.VGDVNTDRPGLLDL.K	34.48	1482.77	0.4
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	V.EELKKKYGI	33.18	1106.63	-0.7
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	V.GDVNTDRPGLLDL.K	21.79	1383.7	-1.8
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	Y.VEKVEELKKKYG.I	32.46	1448.82	0.5
Acyl-CoA-binding protein	sp|P11030|ACBP_RAT	Y.VEKVEELKKKYGI	46.23	1561.91	-0.5
Adducin 3 (Gamma) isoform CRA_b	tr|D3ZCH7|D3ZCH7_RAT	F.RTPSFLKKNKKKEKVEA	45.61	2030.2	-2.6

AHNAK 1	tr|Q38PG2|Q38PG2_RAT	I.KAPKISMPNIDL.N	41.69	1325.74	-1.2
AHNAK 1	tr|Q38PG2|Q38PG2_RAT	N.APDVDVQGPDWHL.K	32.08	1447.67	1
A-kinase anchor protein 12	sp|Q5QD51|AKA12_RAT	F.KKSKEDDLETAEKRKEQE.A	26.36	2190.11	-2.1
A-kinase anchor protein 12	sp|Q5QD51|AKA12_RAT	K.AQAEEDLQEPKGDLAES	30.05	1828.83	1.4
A-kinase anchor protein 12	sp|Q5QD51|AKA12_RAT	D.TTVTQTAEAVEKVIETVVISETG.E	35.6	2404.26	-1.1
A-kinase anchor protein 12	tr|E9PU09|E9PU09_RAT	S.VAVIDGTRAVTSVEERSPSWISASVTEPLE.H	25.28	3184.63	1.7
AKT1 substrate 1 (Proline-rich) (Predicted) isoform CRA_d	tr|D3ZH75|D3ZH75_RAT	M.A(+42.01)SGRPEELWEAVVGAAERFRARTGTEL.V	24.82	2999.52	-0.3
Alpha II spectrin	tr|C9EH87|C9EH87_RAT	M(+42.01)DPSGVKVLETAEDIQERRQQVLD.R	28.45	2797.39	0.2
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	A.PSWIDTGLSEMRM.E	40.19	1521.7	-0.1
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	F.FGEHLLESDLFSTATSL.S	19.93	1865.9	-2.4
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.DVKHFSPEEL.K	26.23	1199.58	-0.6
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.ESDLFSTATSLSPFYLRPPSFLRA.P	16.86	2701.38	0.9
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFL.R	18.62	1322.7	1.9
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFLRA.P	33.31	1549.84	-2.2
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFLRAPSWIDTGL.S	19.21	2419.27	0.6
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFLRAPSWIDTGLSEM(-.98).R	25.89	2765.4	2.9
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFLRAPSWIDTGLSEM.R	51.11	2766.38	0.6
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SPFYLRPPSFLRAPSWIDTGLSEMRM.E	22.44	3053.53	-1.1
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	L.SSDGVLTVNGPRKQASGPERTIPITREEKPAVTAAPKK	22.14	3985.17	-0.9
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	M(+42.01)DIAIHHPW.I	24.22	1160.54	1
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	M(+42.01)DIAIHHPWIRR.P	25.79	1585.83	-0.4
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	M(+42.01)DIAIHHPWIRRPFFPFHSPSRLFDQF.F	27	3435.72	-1.7
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	M(+42.01)DIAIHHPWIRRPFFPFHSPSRLFDQFFGEHLL.E	17.6	4132.08	-12.8
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	Q.ASGPERTIPITREEKPAVTAAPKK	15.22	2546.42	-0.3
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	R.PFFPFHSPSRLFDQFFGEH.L	30.62	2338.1	-0.1
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	R.PFFPFHSPSRLFDQFFGEHL.L	33.13	2451.18	-1.4
Alpha-crystallin B chain	sp|P23928|CRYAB_RAT	V.NGPRKQASGPERTIPITREEKPAVTAAPKK	20.13	3226.79	0.2
Alpha-internexin	sp|P23565|AINX_RAT	K.TEKSTIEEITTSSSQKM	52.57	1898.91	1.5
Alpha-synuclein	sp|P37377|SYUA_RAT	M(+42.01)DVFMKGLSKAKEGVVA.A	32.87	1850.96	-7.4
Alpha-synuclein	sp|P37377|SYUA_RAT	M(+42.01)DVFMKGLSKAKEGVVAA.A	48.06	1922	-0.8
Alpha-synuclein	sp|P37377|SYUA_RAT	M(+42.01)DVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLY.V	27.37	4081.16	0.4

Alpha-synuclein	sp|P37377|SYUA_RAT	M(+42.01)DVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTV(-.98).A	15.22	5659.05	6.7
Alpha-synuclein	sp|P37377|SYUA_RAT	M(+42.01)DVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTV.A	16.74	5660.03	0.8
Alpha-synuclein	sp|P37377|SYUA_RAT	Y.VGSKTKEGVVHGVTTV.A	32.07	1596.88	-0.2
Alpha-synuclein	tr|Q3LVE5|Q3LVE5_RAT	A.AEKTKQGVAEAAGKTKEGV.L	45.83	1901.02	1.9
Alpha-synuclein	tr|Q3LVE5|Q3LVE5_RAT	M(+42.01)DVFMKGLSK.A	40.84	1196.59	-3.6
Annexin A1	sp|P07150|ANXA1_RAT	M.A(+42.01)MVSEFLKQA.C	37.89	1164.58	-1.5
Annexin A2	sp|P07150|ANXA1_RAT	M.A(+42.01)MVSEFLKQACYIEKQE.Q	50.97	2057.98	-2.4
Annexin A2	sp|Q07936|ANXA2_RAT	M.S(+42.01)TVHEILCKLSLEGDH.S	34.18	1821.89	-0.4
Annexin A3	sp|P07150|ANXA1_RAT	M.A(+42.01)MVSEFLKQACYIEKQEQEYVQAVK.S	20.92	3003.47	0.9
Annexin A4	sp|P07150|ANXA1_RAT	M.A(+42.01)MVSEFLKQACYIEKQEQEYVQAVKSY.K	44.35	3253.57	-2.2
Annexin A6	sp|P48037|ANXA6_RAT	M.A(+42.01)KIAQGAMYRG.S	20.67	1206.62	-1.3
AP2-associated protein kinase 1	sp|P0C1X8|AAK1_RAT	V.SDPFIPLQVPDAPEKLIEGL.K	20.03	2177.16	-3.7
Apolipoprotein C-II	tr|G3V8D4|G3V8D4_RAT	A.GIFTDQLLTLLKGE	35.38	1546.86	-4.1
Apolipoprotein C-II	tr|G3V8D4|G3V8D4_RAT	G.TEEDDPGSSALLDTVQEHL.F	37.71	2054.93	0.2
Apolipoprotein C-II	tr|G3V8D4|G3V8D4_RAT	Y.AGIFTDQLLTLLKGE	36.82	1617.9	-0.7
Apolipoprotein C-III	sp|P06759|APOC3_RAT	A.DEGEGSLLLGSMQGYMEQASKTVQDALS.S	36.56	2943.35	2.4
ATP synthase subunit e mitochondrial	sp|P29419|ATP5I_RAT	M.VPPVQVSPLIKF.G	38.56	1322.8	-1.8
ATP synthase subunit e mitochondrial	sp|P29419|ATP5I_RAT	M.VPPVQVSPLIKFGRYS.A	29.21	1786.01	-1
ATP synthase subunit e mitochondrial	sp|P29419|ATP5I_RAT	M.VPPVQVSPLIKFGRYSALILGMAYG.A	17.2	2675.49	2.7
ATP synthase subunit e mitochondrial	sp|P29419|ATP5I_RAT	M.VPPVQVSPLIKFGRYSALILGMAYGAKRY.S	33.03	3193.78	-0.3
ATP synthase subunit epsilon mitochondrial	sp|P29418|ATP5E_RAT	M.VAYWRQAGLSYIRFSQICAKAVRDALKTEFKANAEKTSGTSIKTVKIKKE	34.55	5632.07	-0.2
ATP synthase subunit epsilon mitochondrial	sp|P29418|ATP5E_RAT	G.TSIKTVKIKKE	20.07	1273.8	-0.4
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	D.PKFEVLDKPQS	31.85	1286.69	0.5
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.KLKQMYGKGEMDKFPT.F	26.61	1899.96	0.2
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.NFEDPKFEVLDKPQS	33.27	1791.87	-1.9
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.NKELDPVQKLFLDKI.R	22.88	1799.02	-1
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.NKELDPVQKLFLDKIRE.Y	26.48	2084.16	0.9
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.NKELDPVQKLFLDKIREY.K	53.28	2247.23	0

ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.NKELDPVQKLFLDKIREYKAKRL.A	36.79	2843.64	-2.1
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	F.PTFNFEDPKFEVLDKPQS	15.84	2137.04	9.6
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	L.ASGGPVDTGPEYQQEVDREL.F	53.16	2145.98	-3.3
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	Y.GKGEMDKFPTFNFEDPKFEVLDKPQS	18.28	3029.45	0.2
ATP synthase-coupling factor 6 mitochondrial	sp|P21571|ATP5J_RAT	Y.KAKRLASGGPVDTGPEYQQEVDREL.F	45.34	2742.39	2.4
ATPase H transporting lysosomal V1 subunit G1	tr|B2GUV5|B2GUV5_RAT	M.A(+42.01)SQSQGIQQLLQAEKRAAEKV.S	20.97	2324.24	-0.1
ATPase H+ transporting V1 subunit G isoform 2	tr|Q8R2H0|Q8R2H0_RAT	M.A(+42.01)SQSQGIQQLLQAEKRAAEKV.A	20.97	2324.24	-0.1
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	A.ALKKHHEDEIDHHSKEIER.L	32.23	2350.18	0.8
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	A.LKKHHEDEIDHHSKEIER.L	24.64	2279.14	3.1
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	D.SGAGSIREAGGAFGKREKAEEDR.Y	41.35	2377.17	-0.2
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	L.AALKKHHEDEIDHHSKEIER.L	55.56	2421.21	-0.1
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	L.KKHHEDEIDHHSKEIER.L	34.73	2166.06	-0.7
ATPase inhibitor mitochondrial	sp|Q03344|ATIF1_RAT	Y.FREKTREQLAALKKHHEDEIDHHSKEIER.L	36.83	3608.86	-0.2
Band 3 anion transport protein	sp|P23562|B3AT_RAT	M.G(+42.01)DMQDHEKVLEIPDRDS(+79.97)EEELEHVIEQIAY.R	27.87	3687.63	-1.4
Band 3 anion transport protein	sp|P23562|B3AT_RAT	M.G(+42.01)DMQDHEKVLEIPDRDS(+79.97)EEELEHVIEQIAYRDLD(-.98).I	16.98	4185.88	-4.5
Band 3 anion transport protein	sp|P23562|B3AT_RAT	M.G(+42.01)DMQDHEKVLEIPDRDS(+79.97)EEELEHVIEQIAYRDLD.I	31.38	4186.87	-2.1
Basic transcription factor 3	tr|Q5U3Y8|Q5U3Y8_RAT	I.M(+42.01)NQEKLAKLQAQVR.I	39.43	1697.92	0.9
B-cell leukemia/lymphoma 11B isoform CRA_a	tr|D4A0W4|D4A0W4_RAT	G.P(+42.01)EPEDDEDEEEEEEELLLENESRPESSFSM(+15.99)DSELGRGRENGGGVPPGVAGAGAAAAAL.A	23.43	6083.67	-8.7
Beta-2-microglobulin	sp|P07151|B2MG_RAT	A.IQKTPQIQV.Y	24.43	1053.62	-0.7
Beta-2-microglobulin	sp|P07151|B2MG_RAT	A.IQKTPQIQVY.S	36.61	1216.68	0.3
Beta-glo	tr|Q6PDU6|Q6PDU6_RAT	M.VHLTDAE.K	22.62	783.376	-0.2
Beta-glo	tr|Q6PDU6|Q6PDU6_RAT	M.VHLTDAEKA.T	32.22	982.508	0
Beta-glo	tr|Q6PDU6|Q6PDU6_RAT	M.VHLTDAEKATV.N	34.24	1182.62	0
Beta-glo	tr|Q6PDU6|Q6PDU6_RAT	M.VHLTDAEKATVNGLWGKVNPVEIGAES.L	20.36	2833.46	1.7
Beta-glo	tr|Q6PDU6|Q6PDU6_RAT	M.VHLTDAEKATVNGLWGKVNPVEIGAESL.A	39.83	2946.54	0.3
Beta-synuclein	sp|Q63754|SYUB_RAT	M(+42.01)DVFMKGLSMAKEGVVAAAEKTKQGVTE.A	40.25	2996.5	-2.1
Beta-synuclein	sp|Q63754|SYUB_RAT	M(+42.01)DVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLY.V	26.83	4186.14	-3

Breast carcinoma-amplified sequence 1 homolog	sp|Q3ZB98|BCAS1_RAT	D.PVSIGPVGKSK	29.84	1067.63	-0.5
Breast carcinoma-amplified sequence 1 homolog	sp|Q3ZB98|BCAS1_RAT	G.GFLKGLGPKRMLDAQVQTDPVSIGPVGKSK	37.31	3122.73	0.7
Breast carcinoma-amplified sequence 1 homolog	sp|Q3ZB98|BCAS1_RAT	K.GLGPKRMLDAQVQTDPVSIGPVGKSK	38.1	2677.46	-2.1
Breast carcinoma-amplified sequence 1 homolog	sp|Q3ZB98|BCAS1_RAT	M.S(+42.01)FFKTLVSPNK.T	42.98	1308.71	-0.9
Calcitonin gene-related peptide 1	sp|P01256|CALCA_RAT	R.SC(-1.01)NTATC(-1.01)VTHRLAGLLSRSGGVVKDNFVPTNVGSEAF(-.98).G	29.65	3803.88	1.6
Calcitonin gene-related peptide 1	sp|P01256|CALCA_RAT	R.SGGVVKDNFVPTNVGSEAF(-.98).G	17.39	1921.95	-1.4
Calcitonin gene-related peptide 1	sp|P01256|CALCA_RAT	R.SC(-1.01)NTATC(-1.01)VTHRLAGLLSR.S	29.67	1899.94	-3
Calcitonin gene-related peptide 1	sp|P01256|CALCA_RAT	S.RSGGVVKDNFVPTNVGSEAF(-.98).G	20.98	2078.05	-1
Calcitonin OS=Rattus norvegicus	sp|P01257|CALC_RAT	A.VPLRSTLESSPGMAT.L	30.62	1544.79	-2.6
Calcitonin OS=Rattus norvegicus	sp|P01257|CALC_RAT	A.VPLRSTLESSPGMATLSEEEARLLAALVQN.Y	20.59	3181.67	1.7
Calcitonin OS=Rattus norvegicus	sp|P01257|CALC_RAT	A.VPLRSTLESSPGMATLSEEEARLLAALVQNY.M	37.03	3344.73	-3.9
Calcitonin OS=Rattus norvegicus	sp|P01257|CALC_RAT	A.VPLRSTLESSPGMATLSEEEARLLAALVQNYM.Q	27.94	3475.77	-3.2
Calcitonin OS=Rattus norvegicus	sp|P01257|CALC_RAT	A.VPLRSTLESSPGMATLSEEEARLLAALVQNYMQM.K	33.9	3734.87	-2.7
Calpain small subunit 1	tr|M0RD20|M0RD20_RAT	M(+42.01)FLVNSFLKGGGGGGGGGGLGGGLG.N	26.92	2164.07	-2.3
Calpain small subunit 1	tr|M0RD20|M0RD20_RAT	M(+42.01)FLVNSFLKGGGGGGGGGGLGGGLGN.V	28.49	2278.12	-0.4
Calpain small subunit 1	tr|M0RD20|M0RD20_RAT	M(+42.01)FLVNSFLKGGGGGGGGGG.L	26.85	1709.82	0.2
Calpain small subunit 1	tr|M0RD20|M0RD20_RAT	M(+42.01)FLVNSFLKGGGGGGGGGGLG.G	41.02	1879.93	-2.7
CAP-Gly domain-containing linker protein 2	tr|G3V949|G3V949_RAT	G.LDKEKSLSEQK(+42.01)(-.98).R	23.14	1344.72	-7.1
Catenin beta-1	sp|Q9WU82|CTNB1_RAT	M.A(+42.01)TQADLMELDMAMEPDRKAAVSHWQQ.Q	35.15	3013.37	-1.5
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	K.HEAGDVM(+15.99)GGHAIR.I	28.78	1364.63	0
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	K.HEAGDVMGGHAIR.I	27.15	1348.63	-0.4
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	N.LPESFDAREQW.S	41.92	1376.64	-0.5
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	S.VSDSEKEIMAEIYKNGPVE.G	37.72	2137.02	-1.7
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	T.SYSVSDSEKEIMAEIYKNGPVEGAFT.V	20.41	2850.33	-3.1
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	W.NVDWGDNGFFK.I	22.56	1297.57	-0.9
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	W.NVDWGDNGFFKIL.R	18.89	1523.74	-0.5
Cathepsin B	tr|Q6IN22|Q6IN22_RAT	Y.SVSDSEKEIMAEIYKNGPVE.G	19.41	2224.06	-1.4
Cathepsin D	tr|Q6P6T6|Q6P6T6_RAT	L.PVFDNLMK.Q	22.38	962.49	-0.8
Cathepsin D	tr|Q6P6T6|Q6P6T6_RAT	L.PVFDNLMKQKLVEKN.I	25.22	1801.98	0.1

Cathepsin D	tr|Q6P6T6|Q6P6T6_RAT	L.PVFDNLMKQKLVEKNIFS.F	35.75	2149.16	-0.1
Cathepsin D	tr|Q6P6T6|Q6P6T6_RAT	L.PVFDNLMKQKLVEKNIFSF.Y	44.71	2296.23	-1.2
Cathepsin L1	sp|P07154|CATL1_RAT	N.KDKYWLVKN.S	27.92	1192.66	0.3
Cathepsin L1	sp|P07154|CATL1_RAT	N.KDKYWL.V	17.5	851.454	0.6
Cathepsin L1	sp|P07154|CATL1_RAT	V.AMDASHPSLQFY.S	23.49	1365.6	-0.4
Caveolin 1	tr|Q8R4A2|Q8R4A2_RAT	M.S(+42.01)GGKYVDSEGHL.Y	43.52	1289.59	-1.4
Caveolin 1	tr|Q8R4A2|Q8R4A2_RAT	M.S(+42.01)GGKYVDSEGHLY.T	43.78	1452.65	-1.3
Caveolin 1	tr|Q8R4A2|Q8R4A2_RAT	M.S(+42.01)GGKYVDSEGHLYTVPIREQG.N	40.95	2333.13	-4.2
Caveolin 1	tr|Q8R4A2|Q8R4A2_RAT	M.S(+42.01)GGKYVDSEGHLYTVPIREQGNIY.K	28.31	2723.32	2.8
Caveolin 1	tr|Q8R4A2|Q8R4A2_RAT	M.S(+42.01)GGKYVDSEGHLYTVPIREQGNIYKPNN.K	34.56	3176.55	-0.9
Chaperonin 10	tr|P97601|P97601_RAT	M.AGQAFRK(+42.01)FLPLFDRVLVERSAAETVTKGGIMLPEKSQGKVLQA.T	19.85	4727.59	0.3
Chymase	sp|P50339|CMA1_RAT	A.KLTLGVGTLPL.S	31.37	1110.7	0.3
Cofilin-1	sp|P45592|COF1_RAT	M.A(+42.01)SGVAVSDGVIKVFNDMKVRKS.S	18.7	2348.25	-4.1
Cofilin-1	sp|P45592|COF1_RAT	S.SKDAIKKKLTGIKH.E	16.78	1565.96	1.1
Cofilin-1	sp|P45592|COF1_RAT	V.FNDMKVRKSSTPEEVKKRKKAV.L	22.11	2604.45	-0.2
Cofilin-1	sp|P45592|COF1_RAT	M.A(+42.01)SGVAVSDGVIKVFNDMKV.R	43.01	1977.02	0.1
Cofilin-1	sp|P45592|COF1_RAT	M.A(+42.01)SGVAVSDGVIKVFNDMKVR.K	35.46	2133.13	-0.2
Collagen alpha-2(I) chain	tr|F1LS40|F1LS40_RAT	D.FGFEGDFYR.A	25.84	1136.49	1.1
Collagen alpha-2(I) chain	tr|F1LS40|F1LS40_RAT	F.GFEGDFYR.A	31.52	989.424	-0.6
Collagen alpha-2(I) chain	tr|F1LS40|F1LS40_RAT	G.FEGDFYR.A	22.01	932.403	0.6
Collagen alpha-2(I) chain	tr|F1LS40|F1LS40_RAT	G.GGYDFGFEGDFYRA.D	26.84	1599.66	-0.3
Collagen alpha-2(I) chain	tr|F1LS40|F1LS40_RAT	Y.DFGFEGDFYR.A	19.26	1251.52	2.1
Complement C3	tr|M0RBJ7|M0RBJ7_RAT	R.SSPTVFRLLWESGSLLR.S	25.31	1947.06	-0.1
Complexin-1	sp|P63041|CPLX1_RAT	M(+42.01)EFVMKQALGGATKDMGK.M	50.25	1982.96	-0.9
Complexin-1	sp|P63041|CPLX1_RAT	M(+42.01)EFVMKQALGGATKDMGKMLGGDEEKD.P	41.55	2957.36	-1.3
Copper transport protein ATOX1	sp|Q9WUC4|ATOX1_RAT	A.TLNKTGKAVSYLGPK	41.4	1575.9	-0.2
Copper transport protein ATOX1	sp|Q9WUC4|ATOX1_RAT	L.NKTGKAVSYLGPK	34.38	1361.77	-1.1
Creatine kinase mitochondrial 1 ubiquitous	tr|Q5BJT9|Q5BJT9_RAT	M.A(+42.01)GPFSRLLSARPGLKLLALAGAGSLAAGILLRPESVRA.A	27.34	3811.23	0.4
Creatine kinase M-type	sp|P00564|KCRM_RAT	F.TLDDVIQTGVDNPGHPF.I	26.06	1823.87	-0.6
Creatine kinase M-type	sp|P00564|KCRM_RAT	Y.NKLRDKETPSGFTLDDVIQTGVDNPGHPF.I	20.37	3196.58	-1.9
Cysteine-rich protein 1	sp|P63255|CRIP1_RAT	M.PKC(-1.01)PKC(-1.01)DKEVYFAER.V	18.61	1809.85	0.5
Cysteine-rich protein 1	sp|P63255|CRIP1_RAT	M.PKC(-1.01)PKC(-1.01)DKEVYFAERVT.S	38.73	2009.97	0.2

Cysteine-rich protein 2	sp|P36201|CRIP2_RAT	Y.IYDKDPEGTVQP	22.22	1360.65	0.4
Cysteine-rich protein 2	sp|P36201|CRIP2_RAT	Y.IYEKPPTEAPQVTGPIEVPVVRTEERKTS.G	19.97	3249.72	1
Cysteine-rich protein 2	sp|P36201|CRIP2_RAT	M.A(+42.01)SKC(-1.01)PKC(-1.01)DKTVYFAEKV.S	33.76	1955.95	-1.5
Cysteine-rich protein 2	sp|P36201|CRIP2_RAT	M.A(+42.01)SKC(-1.01)PKC(-1.01)DKTVYFAEKVSSL.G	37.4	2243.1	-0.3
Cytochrome b-c1 complex subunit 7	tr|B2RYS2|B2RYS2_RAT	A.AGFNKLGL.M	16.12	818.465	-0.5
Cytochrome b-c1 complex subunit 7	tr|B2RYS2|B2RYS2_RAT	M.A(+42.01)GRPAVAASSKWLDGF.R	34.68	1673.85	-1.1
Cytochrome b-c1 complex subunit 7	tr|B2RYS2|B2RYS2_RAT	M.A(+42.01)GRPAVAASSKWLDGFRKWYYNA.A	36.74	2655.33	-3
Cytochrome b-c1 complex subunit Rieske mitochondrial	sp|P20788|UCRI_RAT	A.TRPLVATVGLNVPASVRY.S	27.88	1912.09	0.1
Cytochrome b-c1 complex subunit Rieske mitochondrial	sp|P20788|UCRI_RAT	R.PLVATVGLNVPASVRY.S	37.93	1654.94	-0.5
Cytochrome b-c1 complex subunit Rieske mitochondrial	sp|P20788|UCRI_RAT	V.GLNVPASVRY.S	34.46	1074.58	0
Cytochrome b-c1 complex subunit Rieske mitochondrial	sp|P20788|UCRI_RAT	L.SGQAATRPLVATVGLNVPASVRY.S	41.28	2326.28	3.2
Cytochrome b-c1 complex subunit Rieske mitochondrial	sp|P20788|UCRI_RAT	M(+42.01)LSVAARSGPFAPVLSATSR.G	29.29	2059.09	-3.9
Cytochrome c oxidase subunit 2	tr|Q8SEZ5|Q8SEZ5_RAT	L.EMVPLKYFENWSASMI	39.24	1943.92	-2.8
Cytochrome c oxidase subunit 2	tr|Q9QWQ4|Q9QWQ4_RAT	M.A(+42.01)NLERTFIAIKPDGV.Q	20.71	1684.91	-2.1
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	E.LRPTLNELGISTPEELGLDKV	29.96	2293.25	0.3
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	I.QELRPTLNEL.G	20.08	1211.65	1.2
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	I.QELRPTLNELGISTPEELGLDK.V	15.94	2451.29	0.2
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	I.QELRPTLNELGISTPEELGLDKV	19.06	2550.35	2
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	L.GISTPEELGLDKV	36.09	1356.71	0
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	L.NDFASAVRILEV.V	47.53	1332.7	0
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	L.VGYDLVPEPKIIDA.A	30.74	1527.82	-0.6
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	L.VPEPKIIDA.A	31.82	980.554	0.2
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	Y.DLVPEPKIIDAALRA.C	21	1619.92	-0.4
Cytochrome c oxidase	sp|P11240|COX5A_RAT	Y.FNKPDIDAWEL.R	25.95	1346.65	0.1

subunit 5A mitochondrial					
Cytochrome c oxidase subunit 5A mitochondrial	sp|P11240|COX5A_RAT	Y.VIQELRPTLNELGISTPEELGLDKV	28.88	2762.51	2.3
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	F.HNPHMNPLPTGYEDE	53.28	1749.74	-1.1
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	L.FHNPHMNPLPTGYEDE	50.78	1896.81	-1
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	M.SSGAHGEEGSARIWKA.L	45.54	1641.79	-0.7
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	M.SSGAHGEEGSARIWKALT.Y	37.86	1855.92	-0.7
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	M.SSGAHGEEGSARIWKALTY.F	47.08	2018.98	-1.2
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	M.SSGAHGEEGSARIWKALTYFV.A	25.35	2265.12	-2.7
Cytochrome c oxidase subunit 6A1 mitochondrial	sp|P10818|CX6A1_RAT	N.PHMNPLPTGYEDE	21.22	1498.64	0.7
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	C.PVSWVSAWDDRIAEGTFPGKI	25.14	2330.17	3.7
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKNY.K	45.04	1363.73	-1.7
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKNYKT.A	38.36	1592.88	-1.7
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKNYKTAPF.D	23.66	1908.04	-1.8
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKNYKTAPFDSRFPNQNQT.K	35.43	3095.57	-14.3
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKNYKTAPFDSRFPNQNQTKNC(-1.01)WQNYLDFHRC(-.98).E	18.51	4801.32	-5
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	S.AWDDRIAEGTFPGKI	22.15	1674.84	-6
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	V.SAWDDRIAEGTFPGKI	23.34	1761.87	1.2
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	V.SWVSAWDDRIAEGTFPGKI	37.25	2134.05	-2.2
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	W.DDRIAEGTFPGKI	28.76	1417.72	0.3
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	W.VSAWDDRIAEGTFPGKI	28.46	1860.94	0
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKI.K	24.66	958.533	-0.7
Cytochrome c oxidase subunit 6B1	tr|D3ZD09|D3ZD09_RAT	M.A(+42.01)EDIKTKIKN.Y	37.66	1200.67	-0.6
Cytochrome c oxidase subunit 8B mitochondrial	sp|P16221|COX8B_RAT	R.ISSKPAKSPTSAMDQAVGMSVIIAGFMVPAGWVLSHLESYKRSSAA	31.07	4762.43	-0.4
Dihydropyrimidinase-related protein 2	sp|P47942|DPYL2_RAT	S.SAKTSPAKQQAPPVRNLHQSGFSLS.G	31.39	2635.38	3.2
Dihydropyrimidinase-related protein 2	sp|P47942|DPYL2_RAT	S.SAKTSPAKQQAPPVRNLHQSGFSLSG.A	38.7	2692.4	0.3

Dihydropyrimidinase-related protein 2	sp|P47942|DPYL2_RAT	S.SAKTSPAKQQAPPVRNLHQSGFSLSGAQIDDNIPRRTTQRIV.A	34.01	4569.43	1.3
Dihydropyrimidinase-related protein 2	sp|P47942|DPYL2_RAT	S.SAKTSPAKQQAPPVRNLH.Q	24.22	1929.05	-0.2
Dihydropyrimidinase-related protein 2	sp|P47942|DPYL2_RAT	V.APPGGRANITSLG	32.08	1209.65	-0.7
EF-hand domain-containing protein D2	sp|Q4FZY0|EFHD2_RAT	M.A(+42.01)TDELASKLSR.R	33.08	1231.64	0.4
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	A.VGVIKAVDKKAAG.A	36.6	1254.77	-0.5
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	A.VGVIKAVDKKAAGAGKVTK.S	36.54	1839.13	-1.2
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	A.VGVIKAVDKKAAGAGKVTKSAQKAQKA.K	45.92	2651.58	0.9
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	A.VGVIKAVDKKAAGAGKVTKSAQKAQKAK	24.37	2779.68	0.6
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	G.VIKAVDKKAAGAGKVTKSAQKAQKAK	23.55	2623.59	-0.1
Elongation factor 1-alpha	tr|F1M6C2|F1M6C2_RAT	Y.KIGGIGTVPVGRVETGVLKPGMVVT.F	37.75	2463.42	-1.3
Elongation factor 1-alpha 1	sp|P62632|EF1A2_RAT	Y.KIGGIGTVPVGRVETGILRPGMVVT.F	21.86	2505.45	0.5
Elongation factor 1-alpha 1	sp|P62630|EF1A1_RAT	Y.TLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKEVST.Y	18.48	3965.08	-1.1
Elongation factor 1-delta	sp|Q68FR9|EF1D_RAT	M.A(+42.01)TNFLMHEKIWFDKF.K	39.04	1967.96	-1
Enthoprotin	tr|Q6DGF2|Q6DGF2_RAT	M(+42.01)LNMWKVREL.V	34.71	1360.7	-1.7
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	C.VRSIQADGL.V	30.53	957.524	0.1
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	C.VVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI	23.28	3848.8	-0.1
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	L.VWGSSKLVPVGY.G	21.51	1290.7	-1.4
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVL.N	40.03	1414.78	-1.2
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVLND.Y	33.46	1643.85	1.2
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVLNDY.L	31.1	1806.92	1.5
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVLNDYL.A	53.38	1920	-0.7
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVLNDYLADKSYIEGY.V	16.58	2946.47	2.7
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQVLNDYLADKSYIEGYVPSQADVAVFEAI.S	26.45	4273.15	-0.7
Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	E.DDKVGTDMLEEQITAFEDYVQSMDVAAFNKI	32.3	3521.62	2.1

Eukaryotic translation elongation factor 1 beta 2	tr|B5DEN5|B5DEN5_RAT	M.GFGDLKTPAGLQV.L	39.15	1301.7	0
Eukaryotic translation initiation factor 1	tr|B0K008|B0K008_RAT	I.GLAKDDQLKVHGF	43.28	1426.76	0.1
Eukaryotic translation initiation factor 4B	tr|Q5RKG9|Q5RKG9_RAT	F.LGNLPYDVTEDSIKDFFRGL.N	30.51	2298.15	-3.5
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	Q.LKPRTVATPLNQVANPNSAIFGGARPREEVVQKEQE	37.02	3943.1	0
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	R.TVATPLNQVANPNSAIFGGARPREEVVQKEQE	25.82	3448.77	-1.6
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	T.PLNQVANPNSAIFGGARPREE.V	15.17	2236.13	0
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	T.PLNQVANPNSAIFGGARPREEVVQKEQE	32.09	3076.57	-3.4
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	V.ATPLNQVANPNSAIFGGARPREEVVQKEQE	27.49	3248.65	-4.1
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	V.QGDIDAIFKDLSIRSV.R	45.2	1775.94	-1.7
Eukaryotic translation initiation factor 4H	sp|Q5XI72|IF4H_RAT	Y.VGNLPFNTVQGDIDAIFKDLSIRSV.R	37.56	2717.44	-2.8
Fatty acid-binding protein epidermal	sp|P55053|FABP5_RAT	M.A(+42.01)SLKDLEGKWRL.V	38.64	1456.8	-0.4
Fibrinogen alpha chain	tr|F7EUB6|F7EUB6_RAT	Y.KMADEAASEAHQEGDTRTTKRGRARTM.R	28.61	3003.44	-0.5
Fibrinogen beta chain	sp|P14480|FIBB_RAT	A.ATTDSDKVDLSIAR.G	54.85	1490.76	-0.2
Fibrinogen beta chain	sp|P14480|FIBB_RAT	A.TTDSDKVDLSIAR.G	31.53	1419.72	-2.3
Fibrinogen beta chain	sp|P14480|FIBB_RAT	L.V(+42.01)QTQAAT(+79.97)TDSDKVDLSIAR.G	16.13	2140	-7.2
Fibrinogen beta chain	sp|P14480|FIBB_RAT	R.GHRPVDRRKEEPPSLRPAPPPISGGGYRARPAK.V	24.5	3600.96	1.2
Fibrinogen beta chain	sp|P14480|FIBB_RAT	Y.LIQPDTSSKPY.R	39.74	1247.64	-0.1
Fibrinogen gamma chain	sp|P02680|FIBG_RAT	F.RVGPESDKYRLT.Y	40.13	1419.75	-0.5
Fibrinogen gamma chain	sp|P02680|FIBG_RAT	Y.KEGFGHLSPTGTTEF.W	38.06	1606.76	-3.1
Fructose-bisphosphate aldolase A	sp|P05065|ALDOA_RAT	C.PLLKPWALTF.S	34.43	1184.7	-0.6
Fructose-bisphosphate aldolase A	sp|P05065|ALDOA_RAT	L.KAWGGKKENLKAAQEE.Y	45.98	1785.94	-1.9
Fructose-bisphosphate aldolase A	sp|P05065|ALDOA_RAT	P.EQK(+42.01)KELADIA.H	16.23	1185.62	-0.9
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKL.P	19.94	701.432	2
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEF.K	17.77	1383.7	-1.3
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKF.P	53.62	1658.87	-1.8
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRL.N	39.38	2139.15	-0.1
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNM.E	44.78	2384.23	1.6
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNME.A	48.53	2513.27	1.5
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNMEA.I	32.34	2584.31	0.7
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNMEAI.N	34.07	2697.39	-0.5
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNMEAINY.M	16.19	2974.5	-0.7

Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNMEAINYM.A	34.6	3105.54	6.9
Galectin-1	sp|P11762|LEG1_RAT	A.DLTIKLPDGHEFKFPNRLNMEAINYMA.A	28.83	3176.58	-1.5
Galectin-1	sp|P11762|LEG1_RAT	A.SNLNLKPGECLKV.R	23.57	1413.76	-0.1
Galectin-1	sp|P11762|LEG1_RAT	A.SNLNLKPGECLKVRGELAPDAKSFVL.N	17.44	2797.52	0
Galectin-1	sp|P11762|LEG1_RAT	C.NSKDDGTWGTEQRETAFPFQPGSITEV.C	30.11	2996.38	-0.4
Galectin-1	sp|P11762|LEG1_RAT	E.LAPDAKSFVL.N	34.23	1059.6	-1.1
Galectin-1	sp|P11762|LEG1_RAT	E.LAPDAKSFVLNL.G	21.91	1286.72	0.5
Galectin-1	sp|P11762|LEG1_RAT	F.DQADLTIKLPDGHEF.K	32.11	1697.83	-0.8
Galectin-1	sp|P11762|LEG1_RAT	F.DQADLTIKLPDGHEFKFPNRL.N	32.83	2453.27	1.7
Galectin-1	sp|P11762|LEG1_RAT	F.KFPNRLNMEAIN.Y	15.2	1445.74	1
Galectin-1	sp|P11762|LEG1_RAT	F.KFPNRLNMEAINYM.A	27.42	1739.85	-10.5
Galectin-1	sp|P11762|LEG1_RAT	F.PNRLNMEAINYM.A	15.76	1464.69	0.1
Galectin-1	sp|P11762|LEG1_RAT	L.APDAKSFVL.N	33.45	946.512	-0.3
Galectin-1	sp|P11762|LEG1_RAT	L.APDAKSFVLNL.G	38.82	1173.64	-0.7
Galectin-1	sp|P11762|LEG1_RAT	L.HFNPRFN.A	20.18	930.446	-0.1
Galectin-1	sp|P11762|LEG1_RAT	L.HFNPRFNAH.G	39.43	1138.54	-0.7
Galectin-1	sp|P11762|LEG1_RAT	L.KVRGELAPDAKSFVL.N	31.48	1628.92	-1.1
Galectin-1	sp|P11762|LEG1_RAT	L.KVRGELAPDAKSFVLNL.G	36.35	1856.05	-1.3
Galectin-1	sp|P11762|LEG1_RAT	L.KVRGELAPDAKSFVLNLGKDSNNL.C	22.79	2584.4	-8.5
Galectin-1	sp|P11762|LEG1_RAT	L.NLGKDSNNLC(-1.01)LHFNPRFNAHGDANTIVC(-1.01).N	15.84	3081.43	-2.5
Galectin-1	sp|P11762|LEG1_RAT	L.NLKPGECLKV.R	19.35	1099.61	-0.7
Galectin-1	sp|P11762|LEG1_RAT	L.NLKPGECLKVRGELAPDAKSFVLNL.G	16.97	2710.48	-1.4
Galectin-1	sp|P11762|LEG1_RAT	L.PDGHEFKFPNRL.N	34.31	1455.73	-1
Galectin-1	sp|P11762|LEG1_RAT	L.PDGHEFKFPNRLNMEAINYM.A	16.83	2422.12	-3.5
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)C(-1.01)GLVASNLNLKPGEC(-1.01)LKVRGELAPDAKSF.V	15.27	3139.62	0.7
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)C(-1.01)GLVASNLNLKPGEC(-1.01)LKVRGELAPDAKSFVL.N	32.82	3351.77	-1.5
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)C(-1.01)GLVASNLNLKPGEC(-1.01)LKVRGELAPDAKSFVLNL.G	18.97	3578.9	-0.4
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)CGLVASNLNLKPGECLKVRGE.L	23.17	2312.2	0.1
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)CGLVASNLNLKPGECLKVRGELAPDAKSFVLNL.G	36.71	3580.91	-0.9
Galectin-1	sp|P11762|LEG1_RAT	N.SKDDGTWGTEQRETAFPFQPGSITEV.C	17.81	2882.34	0.3
Galectin-1	sp|P11762|LEG1_RAT	R.GELAPDAKSFVLNL.G	15.52	1472.79	-0.7
Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSF.V	17.68	1189.61	-1.5

Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSFV.L	29.28	1288.68	-0.1
Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSFVL.N	34.92	1401.76	-1.9
Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSFVLN.L	36.58	1515.8	0.3
Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSFVLNL.G	32.69	1628.89	-1.1
Galectin-1	sp|P11762|LEG1_RAT	V.RGELAPDAKSFVLNLGKDSNNL.C	46.84	2357.23	-0.9
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)CGLVASNLNLKPGECLK.V	23.41	1870.96	1.5
Galectin-1	sp|P11762|LEG1_RAT	M.A(+42.01)CGLVASNLNLKPGECLKV.R	27.99	1970.03	-0.6
Gamma-enolase	sp|P07323|ENOG_RAT	M.S(+42.01)IQKIWAR.E	23.69	1042.59	-1.2
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	G.VVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	50.71	3296.53	-1.1
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)(+15.99)DVFKKGFSIAR.E	37.4	1455.75	0.6
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKK.G	33.99	808.415	-0.5
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKG.F	30.41	865.437	-0.5
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGF.S	37.87	1012.51	-0.9
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFS.I	35.51	1099.54	-0.6
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSI.A	39.86	1212.62	-1.5
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIA.R	39.96	1283.66	-0.9
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAR.E	43.61	1439.76	-0.2
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVG.A	26.38	1880.98	-0.4
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGA.V	31.79	1952.02	0.4
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEK.T	64.02	2308.22	0
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTE(-.98).A	36.78	3050.62	-10.3
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTE.A	41.45	3051.61	0.1
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTEA(-.98).A	16.08	3121.66	-6.1
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTEA.A	46.78	3122.64	-1.2
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTEAAEKTKEGV.M	19.57	3965.09	0.3
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTEAAEKTKEGVM.Y	39.21	4096.13	-5.7
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSIAREGVVGAVEKTKQGVTEAAEKTKEGVMY.V	53.02	4259.2	0.1
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	M.DVFKKGFSIAR.E	15.77	1266.71	-1.9
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	N.TVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	23.55	5139.49	0.7
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	S.SVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	35.55	5439.63	0.3

Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	T.KTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	17.15	4767.28	-2.5
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	T.TGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	32.06	3454.6	0.7
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	T.VATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	39.03	5038.44	3.8
Gamma-synuclein	tr|F1LQ96|F1LQ96_RAT	V.TTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	33.58	3555.64	-0.3
Gamma-synuclein	sp|Q63544|SYUG_RAT	A.REGVVGAVEKTKQGVTEAAEKTKEGV.M	24.67	2699.45	-0.5
Gamma-synuclein	sp|Q63544|SYUG_RAT	N.TVATKTVEEAENIVVTTGVVR.K	19.97	2215.21	2.6
Glia maturation factor beta	sp|Q63228|GMFB_RAT	I.RNTEDLTEEWLREKLGFFH	49.28	2419.19	-0.9
Glial fibrillary acidic protein beta	tr|A1E251|A1E251_RAT	S.SETMVRGHGPTRHLG.T	27.7	1633.81	-1.1
Glial fibrillary acidic protein beta	tr|A1E251|A1E251_RAT	Y.ASSETMVRGHGPTRHLG.T	36.67	1791.88	-0.8
Glyceraldehyde-3-phosphate dehydrogenase	tr|D3ZKR3|D3ZKR3_RAT	A.STGAAKAVGKVIPELNGKLTGMA.F	18.08	2212.22	-0.4
Glyceraldehyde-3-phosphate dehydrogenase	tr|D3ZKR3|D3ZKR3_RAT	M.AFRVPTPNVSVVDL.T	29.52	1512.83	-3.3
Glyceraldehyde-3-phosphate dehydrogenase testis-specific	sp|Q9ESV6|G3PT_RAT	F.RVPTPNVSVVDL.T	17.04	1294.72	0.1
Glyceraldehyde-3-phosphate dehydrogenase testis-specific	sp|Q9ESV6|G3PT_RAT	S.STGAAKAVGKVIPELNGKLTGMA.F	18.08	2212.22	-0.4
Guanine nucleotide-binding protein subunit beta-4	tr|D4A752|D4A752_RAT	M.S(+42.01)ELEQLRQEAEQLR.N	21.36	1769.89	1.1
H2-K region expressed gene 2 rat orthologue	tr|Q6MGC4|Q6MGC4_RAT	M.A(+42.01)ELIQKKLQGEVEK.Y	30.82	1653.93	0.1
H2-K region expressed gene 2 rat orthologue	tr|Q6MGC4|Q6MGC4_RAT	M.A(+42.01)ELIQKKLQGEVEKY.Q	25.87	1816.99	-0.3
H2-K region expressed gene 2 rat orthologue	tr|Q6MGC4|Q6MGC4_RAT	M.A(+42.01)ELIQKKLQGEVEKYQQL.Q	36.14	2186.19	-0.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.APAFSRAL.N	37.34	831.46	-0.1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.APAFSRALNR.Q	36.6	1101.6	-0.6
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.APAFSRALNRQL.S	15.58	1342.75	-2.6
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEW.S	28.65	1248.59	1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQW(-.98).F	20.97	1648.78	-1.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQW.F	37.31	1649.76	-1.6
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWF.S	50.27	1796.83	-2.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWFS.S	49.58	1883.86	-1.1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWFSS.A	36.75	1970.9	4.1

Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWFSSA.G	40.49	2041.93	-8.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWFSSAGWPGYVRPLPAATAEGPAAV.T	16.46	4002.95	8.8
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.FGVPRFPDEWSQWFSSAGWPGYVRPLPAATAEGPAAVTL.A	33.8	4217.08	-4.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	A.GWPGYVRPLPAATAEGPAAVTL.A	44.55	2193.16	-2.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.DQAFGVPRFPDEWSQWF.S	35.17	2110.95	2.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.GVPRFPDEW.S	18.16	1101.52	-0.1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.GVPRFPDEWSQW.F	32.96	1502.69	-0.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.GVPRFPDEWSQWFS.S	25.49	1736.79	-1.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.GVPRFPDEWSQWFSSA.G	28.58	1894.86	0.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.SSAGWPGYVRPLPAATAEGPAAV.T	16.31	2224.13	-3.1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	F.SSAGWPGYVRPLPAATAEGPAAVTL.A	65.73	2438.26	-0.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.AAPAFSRALNRQL.S	20.83	1413.78	-1.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.AAPAFSRALNRQLSSGVSEIRQTADRW.R	32	2986.55	1.5
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.AAPAFSRALNRQLSSGVSEIRQTADRWRVSL.D	15.59	3441.83	-1.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.DVNHFAPEELTVKT.K	22.43	1598.79	-7.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.FDQAFGVPRFPDEWSQWF.S	17.64	2258.02	5.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.FDQAFGVPRFPDEWSQWFS.S	24.97	2345.05	-4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.NRQLSSGVSEIRQTADRWRVSL.D	19.86	2557.35	-0.8
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.RSPSWEPFRDWYPAHSRL.F	33.04	2286.11	0.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.RSPSWEPFRDWYPAHSRLFDQA.F	26.3	2747.3	8.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPF.S	27.56	945.503	-0.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFS.L	29.85	1032.54	-0.6
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSL.L	25.52	1145.62	-0.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLL.R	22.25	1258.7	0.1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLR.S	38.36	1414.8	1.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRS.P	38	1501.84	-1.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRSPSWEPFRDWYPAHS.R	27.9	3257.62	0.9
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRSPSWEPFRDWYPAHSR.L	26.6	3413.72	0
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRSPSWEPFRDWYPAHSRL(-.98).F	20.19	3525.82	-5.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRSPSWEPFRDWYPAHSRL.F	34.93	3526.8	-0.6

Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	M.T(+42.01)ERRVPFSLLRSPSWEPFRDWYPAHSRLFD.Q	24.07	3788.9	-1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	R.QLSSGVSEIRQTADRWRVSL.D	30.93	2287.2	0.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	S.AGWPGYVRPLPAAT.A	16.29	1454.77	-1.8
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	S.AGWPGYVRPLPAATAEGPAAVTL.A	41.3	2264.2	1
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	S.PSWEPFRDWYPAHS.R	28.77	1773.79	-0.6
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	S.PSWEPFRDWYPAHSRLFDQA.F	20.94	2504.17	1.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	S.SAGWPGYVRPLPAATAEGPAAVTL.A	50.35	2351.23	-10.5
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	V.PFSLLRS.P	24.07	818.465	0.4
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	V.PFSLLRSPSWEPFRDWYPAHS.R	21.96	2574.24	-4.3
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	V.PFSLLRSPSWEPFRDWYPAHSRLFDQA.F	23.65	3304.62	0.8
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	V.PRFPDEWSQWF.S	18.26	1493.67	-2.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	W.FSSAGWPGYVRPLPAATAEGPAAVTL.A	43.39	2585.33	-0.7
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	W.SQWFSSAGWPGYVRPLPAATAEGPAAVTL.A	31.33	2986.5	-3.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.AAPAFSRAL.N	33.63	902.497	0.2
Heat shock 27kDa protein 1	tr|G3V913|G3V913_RAT	L.AAPAFSRALNR.Q	27.71	1172.64	-1.4
Heat shock 70kDa protein 12A (Predicted) isoform CRA_a	tr|D3ZC55|D3ZC55_RAT	M.A(+42.01)DKEAGGGDAGPRETAPTSA.Y	60.28	1898.86	-1.6
Heat shock 70kDa protein 12A (Predicted) isoform CRA_a	tr|D3ZC55|D3ZC55_RAT	M.A(+42.01)DKEAGGGDAGPRETAPTSAY.S	56.66	2061.92	-3.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.ADHVEDLPGALSTL.S	20.45	1436.71	-2.5
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.ADHVEDLPGALSTLSDLHAHKL.R	34.33	2338.19	0
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.ADHVEDLPGALSTLSDLHAHKLRVDPV.N	36.45	2904.51	-0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.ADHVEDLPGALSTLSDLHAHKLRVDPVN.F	28.85	3018.55	-0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.C(+42.01)(-1.01)HHPGDFTPAM(+15.99)HASLDKFLASVSTVLTSKYR	15.34	3472.68	4.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.HGKKVADALAKA.A	34.58	1207.7	1.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.MHASLDKFLASVSTVLTSKYR	48.83	2353.25	0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.SLDKFLASV.S	29.45	978.539	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.SLDKFLASVSTVL.T	22.85	1378.77	-2.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.SLDKFLASVSTVLTSKYR	59.45	2014.11	-2.1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	A.SVSTVLTSKYR	37.49	1239.68	0
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	C.HHPGDFTPAMHASLDKFLASVSTVLTSKYR	50.61	3312.67	-3.7

Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	D.FTPAMHASLDKFLASVSTVLTSKYR	37.06	2769.45	2.5
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	D.PVNFKFLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSKYR	22.78	5198.67	-2.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.AAFPTTKTY.F	42.01	998.507	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.LASVSTVLTSKYR	32.45	1423.8	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.PTTKTYFSHIDVSPGSAQVKAHGKKV.A	30.71	2782.48	-1.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKK.V	31.2	1844.99	0
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKKV.A	38.48	1944.05	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKKVADA.L	35.97	2201.16	-0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKKVADAL.A	23.78	2314.24	-0.5
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKKVADALAK.A	38.67	2513.37	-1.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.SHIDVSPGSAQVKAHGKKVADALAKA.A	16.18	2584.41	-0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.T(+42.01)(+79.97)PAM(+15.99)HASLDK(+42.01)FLASVSTVLTSKYR	31.84	2802.37	2.9
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.TPAMHASLDKFLASVSTVLTSKYR	58.07	2622.38	0.1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	G.DFTPAMHASLDKFLASVSTVLTSKYR	24.97	2884.48	-0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.ASLDKFLASVSTVL.T	28.46	1449.81	-4.1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.ASLDKFLASVSTVLTSKYR	61.66	2085.15	-1.1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.HPGDFTPAMHASLDK.F	36.47	1622.75	-0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.HPGDFTPAMHASLDKFLASVSTVLTSKYR	56.51	3175.61	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.PGDFTPAMHASLDKFLASVSTVL.T	16.3	2403.21	0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	H.PGDFTPAMHASLDKFLASVSTVLTSKYR	51.07	3038.55	-0.9
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.ACHHPGDFTPAMHASLDK.F	41.59	1933.86	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.AKAADHVEDLPGALSTL.S	27.94	1706.88	-1.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.AKAADHVEDLPGALSTLSDLHAH.K	23.91	2367.18	0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.AKAADHVEDLPGALSTLSDLHAHKL.R	15.1	2608.36	0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.ASVSTVLTSKYR	40.83	1310.72	0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.QRMFAAFPTTKTY.F	20.76	1560.78	-0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.RVDPVNFKFL.S	29.31	1233.69	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.RVDPVNFKFLSH.C	34.57	1457.78	-0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.RVDPVNFKFLSHCL.L	37.68	1673.87	0

Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.RVDPVNFKFLSHCLLV.T	23.04	1886.02	-0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.RVDPVNFKFLSHCLLVTL.A	16.52	2100.16	0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.SDLHAHKLRVDPV.N	35.96	1485.81	-0.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.SDLHAHKLRVDPVN.F	40.56	1599.85	-0.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.SDLHAHKLRVDPVNFKFLSH.C	33	2359.25	-0.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.VTLAC(-1.01)HHPGDFTPAMHASLDKFLASVSTVLTSKYR	29.88	3798.91	-2.5
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	L.VTLACHHPGDFTPAMHASLDKFLASVSTVLTSKYR	34.22	3799.92	3.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.FAAFPTTKT.Y	19.55	982.512	0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.FAAFPTTKTYF.S	26.31	1292.64	2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.HASLDKFLASVSTVLTSKYR	40.49	2222.21	0
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNI.K	29.87	1074.56	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNIKN(-.98).C	32.57	1315.71	-1.2
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNIKNCWGKIGGHGGEYGEEAL.Q	20.56	3060.46	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNIKNCWGKIGGHGGEYGEEALQR.M	30.67	3344.62	-0.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNIKNCWGKIGGHGGEYGEEALQRMF.A	17.83	3622.73	0.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	M.VLSADDKTNIKNCWGKIGGHGGEYGEEALQRMFAAFPTTKTY.F	19.43	4603.23	-2.8
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	P.G(+42.01)DFTPAM(+15.99)HASLDK(+42.01)FLASVSTVLTSKYR	23.55	3041.52	14.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	P.GDFTPAMHASLDKFLASVSTVLTSKYR	22.06	2941.5	3.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	S.HIDVSPGSAQVKAHGKKV.A	32.46	1857.02	-2.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	S.LDKFLASVSTVLTSKYR	20.99	1927.08	0.1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	T.LAC(-1.01)HHPGDFTPAMHASLDKFLASVSTVLTSKYR	49.19	3598.79	-4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALST.L	41.86	1963.99	1.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALSTLSDLHAH.K	19.25	2737.37	1.4
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALSTLSDLHAHK.L	31.27	2865.46	-0.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALSTLSDLHAHKL.R	39.72	2978.55	-0.7
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALSTLSDLHAHKLRVDPV.N	29.31	3544.86	-1
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.ADALAKAADHVEDLPGALSTLSDLHAHKLRVDPVN.F	26.24	3658.91	-1.6
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	V.NFKFLSHC.L	22.38	994.47	-0.1

Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	Y.FSHIDVSPGSAQVKAHGKKV.A	26.93	2091.12	-0.3
Hemoglobin alpha adult chain 2	tr|B1H216|B1H216_RAT	F.AAFPTTKTYF.S	23.04	1145.58	0.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	D.KFLASVSTVLTSKYR	34.84	1698.97	-1.2
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	D.PVNFKFL.S	32.68	863.491	2.8
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	D.PVNFKFLSHC(-1.01)LLVTLAC(-1.01)HHPGDFTPAMHASLDKFLASVSTVLTSKYR	23.15	5196.65	-2.5
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	F.SHIDVSPGSAQVKAH.G	30.96	1531.77	0.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	F.SHIDVSPGSAQVKAHG.K	23.84	1588.8	-0.5
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	F.TPAM(+15.99)HASLDKFLASVSTVLTSKYR	43.72	2638.38	-0.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	G.DFTPAM(+15.99)HASLDKFLASVSTVLTSKYR	33.42	2900.47	-1.8
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	K.FLASVSTVLTSKYR	32.18	1570.87	-2
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	L.DKFLASVSTVLTSKYR	39.59	1813.99	-0.6
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	L.SADDKTNIKN(-.98).C	24.89	1103.56	-0.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	L.SADDKTNIKN.C	29.54	1104.54	-0.8
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	L.SHC(-1.01)LLVTLAC(-1.01)HHPGDFTPAMHASLDKFLASVSTVLTSKYR	23.91	4351.17	-2
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIK(+42.01)N(-.98).C	17.61	1357.72	-1.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIK(+42.01)NCWG(-.98).K	22.3	1703.83	14
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIK.N	33.57	1202.65	-0.2
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIKN.C	36.68	1316.69	-0.6
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIKNCWGK(+42.01)IGG(-.98).H	16.71	2059.05	10.3
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIKNCWGK(+42.01)IGGHG(-.98).G	18.35	2253.13	9.8
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	M.VLSADDKTNIKNCWGK(+42.01)IGGHGG(-.98).E	28.7	2310.15	10
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	S.TVLTSKYR	29.69	966.55	-0.3
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	T.PAMHASLDKFLASVSTVLTSKYR	31.63	2521.34	-0.7
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	T.VLTSKYR	21.41	865.502	0.1
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	V.LSADDKTNIK.N	16.85	1103.58	-1.4
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	V.LSADDKTNIKN.C	25.38	1217.63	-0.2
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	V.LTSKYR	19.02	766.434	-0.5
Hemoglobin subunit alpha-1/2	sp|P01946|HBA_RAT	V.STVLTSKYR	31.44	1053.58	-0.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.AFQKVVAGVASALAHKYH	42.81	1896.04	-1.2

Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.AVNGLWGKVNPDDVGGEAL.G	28.08	1909.95	3.4
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.FQKVVAGVASALAHKYH	35.81	1825	-0.9
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.GVASALAHKYH	36	1152.6	-0.4
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.LAHKYH	23.77	767.408	-0.4
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.Q(-17.03)AAFQKVVAGVASALAHKYH	40.78	2078.11	-0.9
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.SAIMGNPKVKAHGKKVINAFNDGLKHLDNLKG.T	19.68	3413.87	0
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	A.SALAHKYH	32.01	925.477	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	C.AQAAFQKVVAGVASALAHK.Y	38.2	1866.05	-1.9
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	C.AQAAFQKVVAGVASALAHKYH	49.86	2166.17	-0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	C.DKLHVDPENFRLLGNMIVIVLGHHL.G	30.02	2878.56	0.9
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	D.PENFRLLGNMIVIVLGHHLGKEF.T	30.8	2632.43	0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.GDLSSASAIMGNPKVKAHGKKV.I	28.77	2194.19	0.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.NDGLKHLDNL.K	23.25	1137.58	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.NDGLKHLDNLKGT.F	36.32	1423.74	-0.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.NDGLKHLDNLKGTFAHL.S	23.62	1891.99	-1.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.NDGLKHLDNLKGTFAHLSEL.H	20.7	2221.15	-0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.Q(-17.03)KVVAGVASALAHKYH	38.05	1660.9	-3.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.QKVVAGVASALAHKYH	43.19	1677.93	-0.5
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.RLLGNMIVI.V	22.25	1027.62	-0.7
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	F.RLLGNMIVIVLGHHL.G	32.77	1684	-0.6
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	G.KKVINAFNDGLKHLDNLKG.T	19.45	2123.19	0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	G.VASALAHKYH	33.83	1095.58	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	H.GKKVINAFNDGLKHLDNLKG.T	23.41	2180.21	-1.6
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	I.NAFNDGLKHLDNLKGT.F	32.08	1755.89	0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	I.NAFNDGLKHLDNLKGTFA.H	34.09	1974	-0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	K.VVAGVASALAHKYH	21.71	1421.78	-0.9
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.G(+42.01)KEFTPC(-1.01)AQAAFQKVVAGVASALAHKYH	26.75	2969.51	14.6
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.GHHLGK(+42.01)EFTPC(-1.01)AQAAFQKVVAGVASALAHKYH	36.3	3413.73	13.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.GRLLVVYPW.T	31.54	1101.63	-2.1

Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.GRLLVVVYPWTQRYFDSF.G	27.04	2146.1	0.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.HVDPENFRLLGNMIVI.V	25.54	1865.98	-3.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.HVDPENFRLLGNMIVIVLGHHL.G	45.02	2522.36	-0.5
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	L.TDAEKAAVNGLWGKVNPDDVGGEALGR.L	28.49	2738.36	-0.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEK.A	25.96	911.471	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKA.A	32.22	982.508	0
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAA.V	37.33	1053.55	-0.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAV.N	37.22	1152.61	-0.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVN.G	48.92	1266.66	-1.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNG(-.98).L	34.67	1322.69	-1.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNG.L	38.14	1323.68	-0.7
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGL.W	28.03	1436.76	-2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLW.G	34.9	1622.84	-1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWG.K	42	1679.86	-1.3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGK.V	41.76	1807.96	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVN.P	33.22	2021.07	1.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVG.G	19.41	2504.27	-0.6
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGG.E	45.09	2561.29	-7.4
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGE.A	20.32	2690.33	0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEA(-.98).L	38.15	2760.38	-3.1
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEAL(-.98).G	22.34	2873.47	-0.7
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEAL.G	39.52	2874.45	0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEALG.R	31.31	2931.47	-3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEALGR.L	22.03	3087.57	-3
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEALGRLLVVYPWTQR.Y	32.85	4343.28	3.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	M.VHLTDAEKAAVNGLWGKVNPDDVGGEALGRLLVVYPWTQRY.F	16.64	4506.34	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	Q.KVVAGVASALAHKYH	40.25	1549.87	-0.7
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	S.ALAHKYH	27.49	838.445	-0.8
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	V.AGVASALAHKYH	34.11	1223.64	-1.7

Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	V.ASALAHKYH	39.39	996.514	0
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	V.INAFNDGLKHLDNLKGT.F	19.9	1868.97	-0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	V.INAFNDGLKHLDNLKGTFAHL.S	18.01	2337.22	-1.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	Y.PWTQRYFDSF.G	16.3	1345.61	0.2
Hemoglobin subunit beta-1	sp|P02091|HBB1_RAT	Q.AAFQKVVAGVASALAHKYH	25.96	1967.07	-1.6
Hemoglobin subunit beta-2	sp|P02091|HBB1_RAT	N.AFNDGLKHLDNLKG.T	19.33	1540.8	0.5
Hemoglobin subunit beta-2	sp|P11517|HBB2_RAT	M.VHLTDAEKATV.S	34.24	1182.62	0
Hemoglobin subunit beta-2	sp|P11517|HBB2_RAT	M.VHLTDAEKATVS.G	23.24	1269.66	-1.1
Hemoglobin subunit beta-2	sp|P11517|HBB2_RAT	M.VHLTDAEKATVSG.L	42.01	1326.68	-1.1
Hepatoma-derived growth factor-related protein 3	sp|Q923W4|HDGR3_RAT	L.PEGAVKPPANKYPIFFF.G	27.19	1921.01	-1.2
Heterochromatin protein 1-binding protein 3	sp|Q6P747|HP1B3_RAT	M.A(+42.01)TDMSQGELIHPKALPLIVG.A	39.87	2131.13	-1.3
Heterogeneous nuclear ribonucleoproteins A2/B1	tr|F1LM82|F1LM82_RAT	F.DDHDPVDKIVL.Q	21.8	1264.63	0.7
High mobility group nucleosomal binding domain 2	tr|Q4KLJ0|Q4KLJ0_RAT	M.PKRKAEGDAKGDKAKVKDEPQRRSARLS.A	40.41	3120.72	-1
High mobility group protein B1	sp|P63159|HMGB1_RAT	C.REEHKKKHPDASVNF.S	28.61	1820.93	-0.6
High mobility group protein B1	sp|P63159|HMGB1_RAT	M.SAKEKGKFEDMAKADKAR.Y	48.75	2009.04	-0.4
High mobility group protein B1	sp|P63159|HMGB1_RAT	W.KTMSAKEKGKFEDMAKADKAR.Y	26.63	2369.22	0.9
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.RAKGKPDAAKKGVVKAEKSKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDD(-.98).E	25.35	6080.64	-4.5
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.RAKGKPDAAKKGVVKAEKSKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDD.E	56	6081.62	-2
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.RAKGKPDAAKKGVVKAEKSKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE	73.48	6210.67	0.3
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.RAKGKPDAAKKGVVKAEKSKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE(-.98)	52.04	6209.68	-5.1
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.EREMKTYIPPKGETKKKFKDPNAPKRPPS.A	40.74	3396.83	-0.2
High mobility group protein B1	sp|P63159|HMGB1_RAT	Y.EREMKTYIPPKGETKKKFKDPNAPKRPPSA.F	33.26	3467.87	0.3
High mobility group protein B2	sp|P52925|HMGB2_RAT	M.SAKEKSKFEDLAKSDKAR.Y	50.98	2037.09	0.3
High mobility group protein B2	sp|P52925|HMGB2_RAT	Y.RAKGKSEVGKKGPGRPTGSKKKNEPEDEEEEEEEEEDDEDEEEEDEDEE	44.07	5504.37	-0.5
High mobility group protein B2	sp|P52925|HMGB2_RAT	Y.RAKGKSEVGKKGPGRPTGSKKKNEPEDEEEEEEEEEDDEDEEEEDED.E	22.48	5246.29	0.7

High mobility group protein B2	sp|P52925|HMGB2_RAT	Y.RAKGKSEVGKKGPGRPTGSKKKNEPEDEEEEEEEEEDDEDEEEEDEDEE(-.98)	38.07	5503.39	-3.3
Histidine triad nucleotide-binding protein 1	sp|P62959|HINT1_RAT	F.HDISPQAPTHFLVIPKKHISQI.S	24.32	2505.39	0.7
Histidine triad nucleotide-binding protein 1	sp|P62959|HINT1_RAT	M.A(+42.01)DEIAKAQVAQPGGDTIFGKII.R	34.48	2283.21	-1.7
Histidine triad nucleotide-binding protein 1	sp|P62959|HINT1_RAT	M.A(+42.01)DEIAKAQVAQPGGDTIFGKIIRKEIPAKIIFEDDRCLAF(-.98).H	18.35	4427.37	-12.4
Histone H1.4	sp|P15865|H14_RAT	L.KKALAAAGYDVEKNNSR.I	35.55	1833.97	-1.7
Histone H1.4	sp|P15865|H14_RAT	M.S(+42.01)ETAPAAPAAPAPAEKTPIKKKAR.K	19.24	2442.36	-0.3
Histone H1.4	sp|P15865|H14_RAT	M.S(+42.01)ETAPAAPAAPAPAEKTPIKKKARKAAGGAKRKASGPPV.S	25.89	3818.16	0.3
Histone H1.4	sp|P15865|H14_RAT	V.SELITKAVAASKERSGVS.L	47.79	1832	-1
Histone H1.4	sp|P15865|H14_RAT	V.SELITKAVAASKERSGVSLA.A	32.76	2016.12	-0.2
Histone H1.4	sp|P15865|H14_RAT	V.SELITKAVAASKERSGVSLAA.L	22.59	2087.16	-0.2
Histone H1.4	sp|P15865|H14_RAT	A.ALKKALAAAGYDVEKNNSR.I	36.12	2018.09	0.3
Histone H1.4	sp|P15865|H14_RAT	R.KASGPPVSELITKAVAASKERSGVSL.A	17.79	2581.44	-6
Histone H1t	sp|P06349|H1T_RAT	MSETAPAASST.L	17.11	1051.45	7.5
Histone H2A	tr|D3ZXP3|D3ZXP3_RAT	A.TVGPKAPAGGKKASQASQEY	46.22	1974.02	0
Histone H2A type 1	sp|P02262|H2A1_RAT	L.AAVLEYLTAEILELAGNAARDNKKTRIIPRHL.Q	15.13	3559	-1.2
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	I.AQGGVLPNIQAVLLPKKTESHHKAKGK	34.13	2848.64	-1.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	I.RNDEELNKLLGRVTI.A	27.8	1768.98	1.7
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.AGNAARDNKKTRIIPRHL.Q	35.44	2030.16	0.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.ELAGNAARDNKKTRIIPR.H	19.31	2022.14	-0.1
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.LRKGNYAERVGAGAPV.Y	15.26	1656.91	0.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.QLAIRNDEELNKLLGRVTI.A	16.5	2194.24	0.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	M.S(+42.01)GRGKQGGKARAKAKSRSSRAGLQFPVG.R	15	2883.6	-1.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	I.RNDEELNKLLGRVT.I	38.89	1655.9	-1.8
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.AAVLEYLTAEILELAGNAARDNKKTR.I	31.47	2829.53	0
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.AGNAARDNKKTRIIPRHLQ.L	28.81	2158.22	0
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	L.QLAIRNDEELNKLLGRVT.I	28.15	2081.16	0
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	M.S(+42.01)GRGKQGGKARAKAKSRSSRAG.L	22.74	2242.25	-1.3
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	M.S(+42.01)GRGKQGGKARAKAKSRSSRAGLQFPVGRVH.R	20.79	3275.83	0.8
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	Q.AVLLPKKTESHHKAKGK	19.33	1871.11	0.2
Histone H2A type 1-C	sp|P0C169|H2A1C_RAT	R.KGNYAERVGAGAPV.Y	37.01	1387.72	0
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	H.RLLRKGNYAERVGAGAPV.Y	16.32	1926.09	-0.2

Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	I.RNDEELNKLLGKVT.I	41.33	1627.89	-3.3
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	I.RNDEELNKLLGKVTI.A	32.39	1740.97	-0.1
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.AIRNDEELNKLLGKVTI.A	24.67	1925.09	8.6
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.ELAGNAARDNKKTRIIPRHL.Q	18.78	2272.29	-1.4
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.QLAIRNDEELNKLLGKVT.I	20.73	2053.15	-1
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.QLAIRNDEELNKLLGKVTI.A	26.6	2166.24	0.2
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.TAEILELAGNAARDNKKTRIIPRHL.Q	19.41	2799.58	1.4
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	L.TAEILELAGNAARDNKKTRIIPRHLQLA.I	21.99	3111.76	5.2
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.AAVLEYLTAEILELAGNAARDNKKTR.I	31.47	2829.53	0
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.AAVLEYLTAEILELAGNAARDNKKTRIIPRHL.Q	15.13	3559	-1.2
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.S(+42.01)GRGKQGGKARAKAKSRSSRAGLQFPVGRVHR.L	20.78	3431.93	-1.7
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.S(+42.01)GRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKG.N	17.22	3999.32	-1.7
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.SGRGK(+42.01)QGGKARAKAKSRSSRAGLQFPVG.R	15.61	2883.6	-0.8
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	M.SGRGK(+42.01)QGGKARAKAKSRSSRAGLQFPVGRVH.R	18.8	3275.83	0.5
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	N.IQAVLLPKKTESHHKAKG.K	30.78	1984.16	-1.7
Histone H2A type 2-A	sp|P0CC09|H2A2A_RAT	Y.LTAEILELAGNAARDNKKTRIIPRHL.Q	21.65	2912.67	-0.9
Histone H2A type 3	sp|Q4FZT6|H2A3_RAT	L.RKGNYSERVGAGAPV.Y	17.97	1559.82	-1
Histone H2B	tr|G3V8B3|G3V8B3_RAT	A.VRLLLPGELAKHAVSEGTKAVTKYTSSK	40.47	2982.69	-4.8
Histone H2B	tr|G3V8B3|G3V8B3_RAT	E.GTKAVTKYTSSK	31.74	1269.69	-0.4
Histone H2B	tr|G3V8B3|G3V8B3_RAT	E.LAKHAVSEGTKAVTKYTSSK	16.68	2105.15	-2.6
Histone H2B	tr|G3V8B3|G3V8B3_RAT	E.RIAGEASRLAH.Y	23.94	1179.65	0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.ERIAGEASRLAH.Y	30.89	1308.69	0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASR.L	47.77	1575.8	-0.2
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRL.A	47.55	1688.88	-0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRLAH.Y	41.14	1896.98	-2.6
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRLAHY.N	47.03	2060.04	-0.8
Histone H2B	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRLAHYNKR.S	36.17	2458.28	-2.4
Histone H2B	tr|G3V8B3|G3V8B3_RAT	G.ELAKHAVSEGTKAVTKYTSSK	24.58	2234.19	-0.1
Histone H2B	tr|G3V8B3|G3V8B3_RAT	G.TKAVTKYTSSK	31.04	1212.67	0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	H.AVSEGTKAVTKYTSSK	27.89	1655.87	0
Histone H2B	tr|G3V8B3|G3V8B3_RAT	K.HAVSEGTKAVTKYTSSK	61.95	1792.93	0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	L.AKHAVSEGTKAVTKYTSSK	20.62	1992.06	-0.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	L.LPGELAKHAVSEGTKAVTK.Y	65.97	1935.08	-0.7
Histone H2B	tr|G3V8B3|G3V8B3_RAT	L.LPGELAKHAVSEGTKAVTKYTSSK	52.26	2501.35	-1.2

Histone H2B	tr|G3V8B3|G3V8B3_RAT	M.PEPAKSAPAPKKGSKKAVTKAQKKD.G	39.39	2589.5	-0.5
Histone H2B	tr|G3V8B3|G3V8B3_RAT	N.DIFERIAGEASRLAH.Y	26.26	1683.87	-1.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	P.GELAKHAVSEGTKAVTK.Y	48.36	1724.94	-2.2
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.NDIFERIAGEASR.L	33.28	1476.73	-3.2
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.NDIFERIAGEASRLAH.Y	38.36	1797.91	3.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.NDIFERIAGEASRLAHY.N	50.08	1960.98	-2.2
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.RLLLPGELAK.H	32.58	1108.7	-0.8
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.RLLLPGELAKHAVSEGTKAVTK.Y	64.25	2317.35	-6.1
Histone H2B	tr|G3V8B3|G3V8B3_RAT	V.RLLLPGELAKHAVSEGTKAVTKYTSSK	47.59	2883.62	0.7
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.KVLKQVHPDTGISSK.A	23.57	1635.93	-11.3
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.KVLKQVHPDTGISSKAMG.I	24.08	1895.03	-1.5
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.KVLKQVHPDTGISSKAMGI.M	29.19	2008.11	-0.7
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.KVLKQVHPDTGISSKAMGIMNS.F	64.27	2340.23	-1.4
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.KVLKQVHPDTGISSKAMGIMNSF.V	29.24	2487.3	-1.9
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.NKRSTITSREIQT.A	18.08	1532.83	0.2
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.NKRSTITSREIQTA.V	15.98	1603.86	-0.6
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.NKRSTITSREIQTAV.R	24.68	1702.93	-1.1
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.NKRSTITSREIQTAVR.L	50.79	1859.03	-0.6
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.VYKVLKQVHPDTGISSKAMGI.M	39.03	2270.25	-0.8
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.VYKVLKQVHPDTGISSKAMGIMNS.F	22.79	2602.36	0.5
Histone H2B	tr|G3V8B3|G3V8B3_RAT	Y.VYKVLKQVHPDTGISSKAMGIMNSF.V	29.09	2749.43	2.3
Histone H2B	tr|Q9Z2Q9|Q9Z2Q9_RAT	M.PDPAKSAPAPKKGSKKAVTKVQKKD.G	38.21	2603.51	-0.7
Histone H2B	tr|D3ZNH4|D3ZNH4_RAT	E.LAKHAVSEGTKAVTKYTSSK.I	16.68	2105.15	-2.6
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	A.KHAVSEGTKAVTKYTSSK	30.52	1921.03	-0.3
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	F.ERIAGEASRLAHY.N	27.12	1471.75	-0.3
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	F.VNDIFERI.A	32.74	1004.53	4.2
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	I.MNSFVNDIFER.I	15.56	1370.63	-1
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	L.KQVHPDTGISSKAMGIMNS.F	16.33	1999.98	-1.9
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	L.LLPGELAKHAVSEGTKAVTKYTSSK	16.45	2614.43	-0.2
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	L.LPGELAKHAVSEGTKAVTKY.T	31.45	2098.14	-2.6
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	T.AVRLLLPGELAKHAVSEGTKAVTKYTSSK	20.23	3053.72	-1.6
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	V.RLLLPGELA.K	17.45	980.602	0
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	V.RLLLPGELAKHAV.S	38.19	1415.86	-0.6

Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	V.RLLLPGELAKHAVSEGTKAVT.K	20.29	2189.25	0.5
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	Y.NKRSTITSREIQTAVRL.L	35.31	1972.12	0
Histone H2B	tr|D3ZWM5|D3ZWM5_RAT	Y.VYKVLKQVHPDTGISSKAMGIMNSFV.N	28	2848.5	-7.2
Histone H2B	tr|D4A817|D4A817_RAT	V.RLLLPGELAKHA.V	32.38	1316.79	-0.7
Histone H2B	tr|D4A817|D4A817_RAT	V.RLLLPGELAKHAVSEGTKAVTKY.T	18	2480.41	-0.2
Histone H3	tr|D3ZJ08|D3ZJ08_RAT	A.RTKQTARKSTGGK(+42.01)APRK(+42.01)QLATK(+42.01)AARKSAPATGGVKKPHRYRPGTVAL.R	18.15	5107.92	12.8
Histone H3	tr|D3ZJ08|D3ZJ08_RAT	L.REIRRYQKSTEL.L	26.39	1577.86	-1
Histone H3	tr|D3ZK97|D3ZK97_RAT	F.QRLVREIAQDF.K	20.07	1373.74	0
Histone H3	tr|D3ZK97|D3ZK97_RAT	L.IRKLPF.Q	15.49	772.496	0.2
Histone H3	tr|B0BMY8|B0BMY8_RAT	H.AKRVTIMPKDIQLARRIRGERA	25.48	2577.51	-0.7
Histone H3	tr|D3ZJ08|D3ZJ08_RAT	L.LIRKLPF.Q	20.81	885.58	0.5
Histone H4	sp|P62804|H4_RAT	A.MDVVYALKRQGRTLYGFGG	18.86	2130.1	-0.2
Histone H4	sp|P62804|H4_RAT	D.VVYALKRQGRTLYGFGG	19.88	1884.04	-1.5
Histone H4	sp|P62804|H4_RAT	G.RTLYGFGG	31.39	869.44	-0.6
Histone H4	sp|P62804|H4_RAT	I.RDAVTYTEHAKRKTVTA.M	20.64	1946.03	-6
Histone H4	sp|P62804|H4_RAT	I.SGLIYEETRGVLK.V	18.61	1463.8	-0.1
Histone H4	sp|P62804|H4_RAT	I.YEETRGVLK.V	18.1	1093.58	-0.5
Histone H4	sp|P62804|H4_RAT	K.TVTAMDVVYALKRQGRTLYGFGG	28.06	2502.31	-0.7
Histone H4	sp|P62804|H4_RAT	Q.GRTLYGFGG	30.84	926.461	-1.9
Histone H4	sp|P62804|H4_RAT	R.QGRTLYGFGG	37.11	1054.52	-0.1
Histone H4	sp|P62804|H4_RAT	V.FLENVIRDAVTYTEHAKRKTVT.A	18.04	2590.39	0.8
Histone H4	sp|P62804|H4_RAT	V.FLENVIRDAVTYTEHAKRKTVTA.M	23.88	2661.42	1.6
Histone H4	sp|P62804|H4_RAT	Y.TEHAKRKTVTAM(+15.99)DV.V	47.77	1601.82	-1.5
Histone H4	sp|P62804|H4_RAT	Y.TEHAKRKTVTAM(+15.99)DVVY.A	50.73	1863.95	-2.7
Histone H4	sp|P62804|H4_RAT	Y.TEHAKRKTVTAMDVVYALKRQGRTLYGFGG	31.6	3352.78	-0.8
Histone H4	tr|B0BMY8|B0BMY8_RAT	M.ARTKQTARKSTGGKAPRKQLA.T	22.59	2253.31	0.8
Histone H4	sp|P62804|H4_RAT	Y.ALKRQGRTLY.G	16.89	1204.7	0.3
Histone H4	sp|P62804|H4_RAT	Y.ALKRQGRTLYGFGG	33.07	1522.84	-0.2
Histone H5	tr|B0BMY8|B0BMY8_RAT	M.ARTKQTARKSTGGK(+42.01)APRKQLA.T	24.09	2295.32	-0.1
Histone H6	tr|B0BMY8|B0BMY8_RAT	D.IQLARRIRGERA	16.67	1437.86	-0.2
Interferon regulatory factor 3	tr|Q5XIB0|Q5XIB0_RAT	M.G(+42.01)TPKPLILPWLVSQL.D	24.64	1703	-2
L-gulonolactone oxidase	sp|P10867|GGLO_RAT	G.THNTGIKH.G	24.67	906.467	-0.4
Lumican	sp|P51886|LUM_RAT	A.SLKGLKSLEYLDL.S	18.52	1477.84	5.7

Lumican	sp|P51886|LUM_RAT	F.DVKSFCKILGPLS.Y	23.87	1405.76	-0.3
Lumican	sp|P51886|LUM_RAT	F.NQMSKLPAGLPT.S	17.46	1255.66	-0.7
Lumican	sp|P51886|LUM_RAT	F.NQMSKLPAGLPTSLLT.L	24.63	1669.91	-2.1
Lumican	sp|P51886|LUM_RAT	L.DNNKITNIPDEYFNR.F	50.28	1851.88	-0.9
Lumican	sp|P51886|LUM_RAT	L.ILDHNLLENSKIKGKV.F	36.97	1820.05	0
Lumican	sp|P51886|LUM_RAT	L.KSIPTVNENLEN.Y	31.42	1356.69	-0.1
Lumican	sp|P51886|LUM_RAT	L.KSVPMVPPGIK.Y	18.94	1151.67	-0.2
Lumican	sp|P51886|LUM_RAT	L.QHNQLKEEAVSASLKGLKSLE.Y	23.86	2308.24	1.1
Lumican	sp|P51886|LUM_RAT	L.QWLILDHNLLENSKIKGKV.F	22.11	2247.27	-0.2
Lumican	sp|P51886|LUM_RAT	L.SFNQMSKLPAGLPTSLLT.L	30.85	1904.01	0.9
Lumican	sp|P51886|LUM_RAT	L.SFNQMSKLPAGLPTSLLTL.Y	28.54	2017.09	0.4
Lumican	sp|P51886|LUM_RAT	M.SKLPAGLPTSLLTL.Y	26.94	1409.85	-2.6
Lumican	sp|P51886|LUM_RAT	M.SKLPAGLPTSLLTLY.L	39.67	1572.91	-0.8
Lumican	sp|P51886|LUM_RAT	Y.LDNNKITNIPDEY.F	27.66	1547.75	-2.4
Lumican	sp|P51886|LUM_RAT	Y.LDNNKITNIPDEYFNR.F	21.28	1964.96	0.5
Lumican	sp|P51886|LUM_RAT	Y.LDNNKITNIPDEYFNRFTGLQ.Y	32.9	2511.24	-0.6
Lumican	sp|P51886|LUM_RAT	Y.NKLKSIPTVNENLEN.Y	48.11	1711.91	0
Lumican	sp|P51886|LUM_RAT	Y.YLEVNKLEK.F	35.98	1134.63	-0.8
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	L.AQATGKPAQYIAVHVVPDQL.M	51.61	2105.13	-2.3
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	L.HISPDRVYINYY.D	38.49	1538.75	-3.8
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	M.PMFIVNTNVPRA.S	20.93	1357.72	-1
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	M.PMFIVNTNVPRASVPEGFLSELT(+79.97)QQLAQAT(+79.97)GK(+42.01)(-.98).P	15.3	3643.75	12.9
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	M.PMFIVNTNVPRASVPEGFLSELTQQL.A	34.05	2886.49	-1.9
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	N.TNVPRASVPEGFLSELTQQL.A	28.24	2185.14	-1.5
Macrophage migration inhibitory factor	sp|P30904|MIF_RAT	V.PRASVPEGFLSELTQQL.A	38.99	1870.98	-9.3
Mast cell protease 1	sp|P09650|MCPT1_RAT	A.HLEITTERG.Y	46.01	1054.54	-0.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	A.HLEITTERGY.K	36.29	1217.6	-0.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	A.VDVIPLPQPSDF.L	26.76	1325.69	0.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	C.RAAGWGQTGVTKPTSNT.L	33.02	1730.87	-0.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	E.IIGGVESRPHSRP.Y	23.01	1403.76	0.4
Mast cell protease 1	sp|P09650|MCPT1_RAT	E.IIGGVESRPHSRPY.M	22.39	1566.83	4.3
Mast cell protease 1	sp|P09650|MCPT1_RAT	F.TRISPYVPW.I	16.01	1117.59	-0.4
Mast cell protease 1	sp|P09650|MCPT1_RAT	I.GGVESRPHSRPY.M	17.15	1340.66	-1.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	I.IGGVESRPHSRPY.M	18.72	1453.74	0
Mast cell protease 1	sp|P09650|MCPT1_RAT	I.KVEKQIVHPNYN.F	35.87	1467.78	0
Mast cell protease 1	sp|P09650|MCPT1_RAT	L.GVHDVSKTESTQQKIKVEKQIVHPN.Y	38.12	2828.51	-0.7

Mast cell protease 1	sp|P09650|MCPT1_RAT	L.GVHDVSKTESTQQKIKVEKQIVHPNYN(-.98).F	25.56	3104.64	-7.1
Mast cell protease 1	sp|P09650|MCPT1_RAT	L.GVHDVSKTESTQQKIKVEKQIVHPNYN.F	53.48	3105.62	-1.3
Mast cell protease 1	sp|P09650|MCPT1_RAT	L.LKLQKKAKVTPA.V	30.15	1323.86	-0.2
Mast cell protease 1	sp|P09650|MCPT1_RAT	T.LGVHDVSKTESTQQK.I	42.93	1655.85	-1.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	T.LGVHDVSKTESTQQKIKVEKQIVHPNYN.F	24.73	3218.7	-0.6
Mast cell protease 1	sp|P09650|MCPT1_RAT	V.DVIPLPQPSDF.L	20.27	1226.62	-0.1
Mast cell protease 1	sp|P09650|MCPT1_RAT	V.HDVSKTESTQQKIKVEKQIVHPN.Y	20.76	2672.42	-4.3
Mast cell protease 1	sp|P09650|MCPT1_RAT	V.HDVSKTESTQQKIKVEKQIVHPNYN.F	31.89	2949.53	-0.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	V.TLGVHDVSKTESTQQK.I	15.13	1756.9	0.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	V.TLGVHDVSKTESTQQKIKVEKQIVHPNYN.F	29.03	3319.75	-0.2
Mast cell protease 1	sp|P09650|MCPT1_RAT	W.GQTGVTKPTSNTLREVKQR.I	16.53	2099.14	0.2
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.KGDSGGPLVCAGVAHGIVS.Y	17.46	1722.87	1.9
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.NFQVCVGSPRK.I	30.21	1233.63	-0.4
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.NFQVCVGSPRKIRSA.Y	21.96	1660.88	-0.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.NFYSNLHDI.M	34.46	1121.51	-0.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.NFYSNLHDIM.L	29.52	1252.55	0.7
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.SNLHDIM(+15.99).L	23.7	844.375	-0.4
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.SNLHDIM.L	32.2	828.38	-0.8
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.SNLHDIMLL.K	15.35	1054.55	-0.3
Mast cell protease 1	sp|P09650|MCPT1_RAT	Y.SNLHDIMLLK.L	27.52	1182.64	-1.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	R.AAGWGQTGVTKPTSNT.L	51.13	1574.77	-1.5
Mast cell protease 1	sp|P09650|MCPT1_RAT	R.AAGWGQTGVTKPTSNTLREVKQR.I	34.9	2484.32	0.2
Microtubule associated protein 1A	tr|Q63330|Q63330_RAT	K.KEEGRKEEKKDAKKDEKRKDTKPEVKKLSKPDL.K	41.72	3937.2	0
Microtubule-associated protein	tr|A0JN25|A0JN25_RAT	A.TLADEVSASLAKQGL	28.35	1501.8	-3.2
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	A.ALKPKVAKKEEPTKKEPI.A	25.87	2033.22	-0.4
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	A.SPKKKESVEKAMKTTTTPEVK.A	18.66	2346.28	0.4
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	E.KTPKVESKEKVIVKKDKPGKVE.S	22.6	2493.49	0.9
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	E.SKPSVTEKEVPSKEEQSPVKAEVAEKAA.T	29.78	2981.56	-2.6
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	K.ASQVEKTPKVESKEKVIVKKDKPGKVE.S	41.92	3007.73	2.2
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	K.ATRGEEKDKETKNAANASASKSVKTA.T	55.26	2691.38	-0.8
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	L.KDAKKEVKKDEKKEVKKEEKEPKKEIKK.I	17.45	3424	0.4
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	L.KKDEKPKKEEAKKEIKKEIKKEEKKE.L	19.54	3224.87	0
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	L.KKDEKPKKEEAKKEIKKEIKKEEKKEL.K	26.63	3337.95	0.6

Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	L.SDTKKPAALKPKVAKKEEPTKKEPI.A	39.73	2760.61	-2.2
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	S.M(+42.01)VDPEALAIEQNLGKAL.K	22.23	1852.96	-0.9
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	S.M(+42.01)VDPEALAIEQNLGKALK.K	45.43	1981.06	-2.4
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	T.RTPEVSGYTYEKTERSR.R	28.8	2058.01	-0.3
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	T.SSFPEPTTDDVSPSLHAEVG.S	39.61	2070.94	0
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	Y.KHM(+15.99)DPPPAPM(+15.99)QDRSPSPRHPDVS.M	24.91	2610.21	-0.9
Microtubule-associated protein 1B	sp|P15205|MAP1B_RAT	Y.KHMDPPPAPMQDRSPSPRHPDVS.M	34.81	2578.22	-1.1
Microtubule-associated protein 1B	tr|F1LRL9|F1LRL9_RAT	A.SEKVQSLE.G	29.88	918.466	-0.8
Microtubule-associated protein 1B	tr|F1LRL9|F1LRL9_RAT	D.PPPAPMQDRSPSPRHPDVS.M	31.13	2067	-0.7
Microtubule-associated protein 1B	tr|F1LRL9|F1LRL9_RAT	K.E(-18.01)T(+79.97)PLKDAKKEVKKDEKKEVKKEE.K	23.69	2817.49	8.4
Microtubule-associated protein 1B	tr|F1LRL9|F1LRL9_RAT	K.KEVKKETPLKDAKKEVKKDEKKEVKKEE.K	30.48	3367.93	0.8
Microtubule-associated protein 1B	tr|F1LRL9|F1LRL9_RAT	K.KSTPLSDTKKPAALKPKVAKKEEPTKKEPIAAGKLKDKGKVKVIKKEGKTTE.A	31.82	5624.33	-2.2
Microtubule-associated protein 4	sp|Q5M7W5|MAP4_RAT	E.AEPYDDIVGETVEKTEFIPLL.D	34.88	2377.19	2
Microtubule-associated protein 4	sp|Q5M7W5|MAP4_RAT	E.PPPEIEGEIKRDFMAALE.A	32.61	2041.02	2.8
Microtubule-associated protein 4	sp|Q5M7W5|MAP4_RAT	R.TSPSKPSSAPALRPGPKTTPTISKATSPSTL.V	19.62	3062.66	0.8
Microtubule-associated protein 4	sp|Q5M7W5|MAP4_RAT	T.ADLSRSKTTSASSVKRNTTPTG.A	17.47	2264.17	0.3
Microtubule-associated protein 4	sp|Q5M7W5|MAP4_RAT	E.AEPYDDIVGETVEKTE.F	40.96	1793.82	-1.2
Microtubule-associated protein RP/EB family member 1	sp|Q66HR2|MARE1_RAT	L.SKPKKPLGSGSAAPQRPIATQRTT.A	43.06	2476.39	-1.4
Myc box-dependent-interacting protein 1	tr|D4ABS7|D4ABS7_RAT	M.A(+42.01)EMGSKGVTAGKIASNVQKKLT.R	27.66	2259.23	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	A.SDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	22.41	4330.21	1.7
Myelin basic protein S	sp|P02688|MBP_RAT	A.STMDHARHGFLPRH.R	31.29	1660.8	-1.3
Myelin basic protein S	sp|P02688|MBP_RAT	A.STMDHARHGFLPRHRDTGILD.S	29.03	2431.19	-3
Myelin basic protein S	sp|P02688|MBP_RAT	D.AQGTLSKIFKLGGRDSRSGSPMARR	20.13	2675.44	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	D.ENPVVHFFKNIVTPR.T	22.08	1795.97	-0.3
Myelin basic protein S	sp|P02688|MBP_RAT	D.SHTRTTHYGSLPQK.S	30.35	1611.81	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	D.SIGRFFSGDR.G	18.41	1140.57	-1.3
Myelin basic protein S	sp|P02688|MBP_RAT	D.SRSGSPMARR	24.12	1103.56	-2.7
Myelin basic protein S	sp|P02688|MBP_RAT	D.TGILDSIGR.F	29.56	930.513	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	D.TGILDSIGRF.F	45.86	1077.58	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	D.TGILDSIGRFF.S	38.48	1224.65	0
Myelin basic protein S	sp|P02688|MBP_RAT	D.TGILDSIGRFFSG.D	31.61	1368.7	-1.8

Myelin basic protein S	sp|P02688|MBP_RAT	D.TGILDSIGRFFSGDR.G	43.17	1639.83	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	F.FKNIVTPR.T	34.17	973.571	0
Myelin basic protein S	sp|P02688|MBP_RAT	F.FKNIVTPRTPPPSQGKGR.G	16.36	1979.11	-0.2
Myelin basic protein S	sp|P02688|MBP_RAT	F.FKNIVTPRTPPPSQGKGRGLS.L	22.34	2236.24	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	F.FKNIVTPRTPPPSQGKGRGLSLSR.F	26.45	2592.46	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	F.GYGGRASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	15.34	4891.48	-3.5
Myelin basic protein S	sp|P02688|MBP_RAT	F.KNIVTPR.T	22.96	826.502	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	F.KNIVTPRTPPPSQGKGRGL.S	20.29	2002.14	-0.2
Myelin basic protein S	sp|P02688|MBP_RAT	F.KNIVTPRTPPPSQGKGRGLS.L	26.12	2089.18	-0.6
Myelin basic protein S	sp|P02688|MBP_RAT	F.KNIVTPRTPPPSQGKGRGLSLS.R	33.12	2289.29	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	F.KNIVTPRTPPPSQGKGRGLSLSR.F	21.58	2445.39	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	F.LPRHRDTGILDSIGR.F	42.54	1704.94	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	F.LPRHRDTGILDSIGRF.F	15.41	1852.01	0
Myelin basic protein S	sp|P02688|MBP_RAT	F.LPRHRDTGILDSIGRFFSGDR.G	15.6	2414.26	-1.6
Myelin basic protein S	sp|P02688|MBP_RAT	G.AYDAQGTLSKIFKLGGRDSRSGSPMARR	16.05	3024.57	-2.6
Myelin basic protein S	sp|P02688|MBP_RAT	G.FKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	17.62	3356.75	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	G.FLPRHRDTG.I	18.57	1097.57	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	G.FLPRHRDTGILD.S	30.28	1438.77	-1.6
Myelin basic protein S	sp|P02688|MBP_RAT	G.FLPRHRDTGILDSIGRF.F	16.78	1999.08	-2.8
Myelin basic protein S	sp|P02688|MBP_RAT	G.FLPRHRDTGILDSIGRFFSGDR.G	32.03	2561.33	-3.5
Myelin basic protein S	sp|P02688|MBP_RAT	G.GRASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	17.92	4614.37	-11.1
Myelin basic protein S	sp|P02688|MBP_RAT	G.GRDSRSGSPMARR	19.36	1431.71	-0.5
Myelin basic protein S	sp|P02688|MBP_RAT	G.ILDSIGRF.F	35.08	919.513	0.2
Myelin basic protein S	sp|P02688|MBP_RAT	G.RDSRSGSPMARR	27.46	1374.69	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	G.SKYLATASTMDH.A	28.72	1323.61	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	G.SKYLATASTMDHAR.H	22.17	1550.75	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	G.SLPQKSQRTQDENPVVH.F	47.63	1961.99	-1.5
Myelin basic protein S	sp|P02688|MBP_RAT	G.SLPQKSQRTQDENPVVHF.F	39.94	2109.06	-2.6
Myelin basic protein S	sp|P02688|MBP_RAT	G.SLPQKSQRTQDENPVVHFF.K	34.68	2256.13	-1.5
Myelin basic protein S	sp|P02688|MBP_RAT	G.SLPQKSQRTQDENPVVHFFKNIV.T	43.3	2710.42	-3.1
Myelin basic protein S	sp|P02688|MBP_RAT	G.SLPQKSQRTQDENPVVHFFKNIVTPR.T	54.93	3064.62	-1.3
Myelin basic protein S	sp|P02688|MBP_RAT	G.TLSKIFKLG.G	26.91	1005.62	0.4
Myelin basic protein S	sp|P02688|MBP_RAT	G.TLSKIFKLGGRDSRSGSPMARR	20.95	2419.32	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	H.ARHGFLPR.H	32.11	952.536	0.1

Myelin basic protein S	sp|P02688|MBP_RAT	H.ARHGFLPRHRD.T	23.11	1360.72	0.6
Myelin basic protein S	sp|P02688|MBP_RAT	H.ARHGFLPRHRDTGILD.S	18.36	1859.99	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	H.ARHGFLPRHRDTGILDSIGR.F	21.51	2273.23	-0.3
Myelin basic protein S	sp|P02688|MBP_RAT	H.ARHGFLPRHRDTGILDSIGRFFSGDR.G	17.97	2982.54	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	H.FFKNIVTPR.T	42.39	1120.64	-0.6
Myelin basic protein S	sp|P02688|MBP_RAT	H.GFLPRHRDTGILDSIGRFFSGDR.G	23.8	2618.35	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	H.RDTGILDSIGR.F	29.04	1201.64	-1
Myelin basic protein S	sp|P02688|MBP_RAT	H.RDTGILDSIGRFFSGDR.G	43.58	1910.96	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	H.TRTTHYGSLPQK.S	26.33	1387.72	-1.4
Myelin basic protein S	sp|P02688|MBP_RAT	I.GRFFSGDR.G	27.71	940.452	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	K.Q(-17.03)SRSPLPSH.A	16.5	990.488	0.2
Myelin basic protein S	sp|P02688|MBP_RAT	K.SAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	17.03	3837	1.2
Myelin basic protein S	sp|P02688|MBP_RAT	K.SQRTQDENPVVH.F	25.46	1408.67	-1.8
Myelin basic protein S	sp|P02688|MBP_RAT	K.SQRTQDENPVVHFFKNIVTPR.T	50.46	2511.3	-0.4
Myelin basic protein S	sp|P02688|MBP_RAT	K.YLATASTM(+15.99)DHAR.H	24.93	1351.62	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	L.PQKSQRTQDENPVVH.F	33.64	1761.88	0.4
Myelin basic protein S	sp|P02688|MBP_RAT	L.SKIFKLGGRDSR.S	15.62	1362.77	0.2
Myelin basic protein S	sp|P02688|MBP_RAT	L.SKIFKLGGRDSRSGSPMARR	16.02	2205.19	-1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)S(+79.97)QKRPSQRHGSKYLATASTMDH.A	16.55	2678.24	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)S(+79.97)QKRPSQRHGSKYLATASTMDHAR.H	36.41	2905.38	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)S(+79.97)QKRPSQRHGSKYLATASTMDHARHG.F	15.79	3099.46	1.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)S(+79.97)QKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIG.R	17.93	4777.35	0.4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPS(+79.97)QRHGSKY(+79.97)LATASTMDHAR.H	16.07	2985.34	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPS(+79.97)QRHGSKYLATA.S	21.3	2107.03	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPS(+79.97)QRHGSKYLATASTMDHARHGFLPRHRDTG.I	20.07	4179.02	-3
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPS(+79.97)QRHGSKYLATASTMDHARHGFLPRHRDTGILD.S	18.87	4520.21	-4.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHG.S	21.85	1292.67	-1.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGS(+79.97)KYLATASTMDHARH.G	27.04	3042.44	-3.6
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKY.L	33.53	1670.86	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYL.A	30.56	1783.94	0.4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLA.T	27.47	1854.98	-0.4

Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLAT.A	28.49	1956.03	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATA.S	35.42	2027.07	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATAS.T	25.2	2114.1	-2
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATAST.M	16.33	2215.15	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)D.H	19.99	2477.21	-1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DH.A	28.69	2614.27	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHA.R	39.7	2685.3	-0.2
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHAR.H	42.87	2841.41	-1.2
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARH.G	23.51	2978.46	0.4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHG.F	18.15	3035.49	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGF.L	24.74	3182.55	-3.6
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPR.H	30.56	3548.79	4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPRH.R	18.29	3685.85	-2.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPRHRD.T	30.98	3956.98	3.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPRHRDTG.I	30.32	4115.05	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPRHRDTGILD.S	30.37	4456.24	0.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM(+15.99)DHARHGFLPRHRDTGILDSIG.R	15.65	4713.38	-3.5
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTM.D	17.73	2346.19	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMD.H	21.05	2461.21	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDH.A	39.96	2598.27	-1.2
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHA.R	37.49	2669.31	-1.2
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHAR.H	41.6	2825.41	-0.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARH.G	31.18	2962.47	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHG(-.98).F	16.87	3018.51	-6.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHG.F	29.15	3019.49	-0.4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGF.L	38.07	3166.56	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFL.P	24.09	3279.64	-0.5

Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPR.H	31.13	3532.8	-2.4
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRH.R	40.89	3669.86	-3.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHR.D	40.74	3825.96	1.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRD.T	27.36	3940.98	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDT.G	17.24	4042.03	-6
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTG.I	30.9	4099.05	0.5
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGIL.D	28.42	4325.22	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILD.S	34.06	4440.25	-2.1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDS.I	27.69	4527.28	-1
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIG.R	33.05	4697.39	-2.6
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRF.F	19.36	5000.56	0.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFF.S	20	5147.62	0
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFSG.D	18.78	5291.68	-2.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.A(+42.01)SQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFSGDRGAPKRG.S	16.44	6129.13	-0.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.AS(+79.97)QKRPSQRHGSK(+42.01)YLATASTMDHA.R	15.59	2749.28	1
Myelin basic protein S	sp|P02688|MBP_RAT	M.ASQK(+42.01)RPS(+79.97)QRHGSKYLATASTM(+15.99)DH.A	17.93	2694.23	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	M.ASQK(+42.01)RPSQRHGSKY(+79.97)LATASTMDHARHGFLPRHRD.T	17.16	4020.95	0.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.ASQK(+42.01)RPSQRHGSKYLATASTMDH(-.98).A	35.87	2597.29	-7.8
Myelin basic protein S	sp|P02688|MBP_RAT	M.ASQKRPSQRHGSK(+42.01)YLATASTMDHAR(-.98).H	29.06	2824.43	-14.3
Myelin basic protein S	sp|P02688|MBP_RAT	N.PVVHFFKNIVTPR.T	38	1552.89	-1.8
Myelin basic protein S	sp|P02688|MBP_RAT	P.QKSQRT(+79.97)QDENPVVHFFKNIVTPR.T	21.02	2847.42	-8.2
Myelin basic protein S	sp|P02688|MBP_RAT	P.RHRDTGILD.S	26.79	1081.56	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	Q.DENPVVHFFKNIV.T	44.64	1556.8	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	Q.DENPVVHFFKNIVTPR.T	45.91	1911	-0.3
Myelin basic protein S	sp|P02688|MBP_RAT	Q.GTLSKIFKLGGRDSRSGSPMARR	23.5	2476.34	-0.2

Myelin basic protein S	sp|P02688|MBP_RAT	Q.RTQDENPVVHFFKNIVTPR.T	54.58	2296.21	-2.4
Myelin basic protein S	sp|P02688|MBP_RAT	Q.SRSPLPSH.A	22.41	879.456	-0.8
Myelin basic protein S	sp|P02688|MBP_RAT	R.DTGILDSIGR.F	39.36	1045.54	-1
Myelin basic protein S	sp|P02688|MBP_RAT	R.DTGILDSIGRF.F	43.71	1192.61	-0.2
Myelin basic protein S	sp|P02688|MBP_RAT	R.DTGILDSIGRFF.S	37.82	1339.68	-1.3
Myelin basic protein S	sp|P02688|MBP_RAT	R.DTGILDSIGRFFSGDR.G	30.43	1754.86	-7.8
Myelin basic protein S	sp|P02688|MBP_RAT	R.GAPKRGSGKVPWLKQSRSPLPSH.A	18.27	2469.37	-1.7
Myelin basic protein S	sp|P02688|MBP_RAT	R.GLSLSRF.S	26.23	778.434	-0.5
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGFLPR.H	36.89	725.397	0.5
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGFLPRHRDTGILDSIGR.F	28.62	2046.09	-1.5
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGFLPRHRDTGILDSIGRFFSGDR.G	42.9	2755.41	-2.3
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGSKYLATASTM(+15.99)DH.A	35.5	1533.69	0.3
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGSKYLATASTM(+15.99)DHAR.H	42.45	1760.83	1.1
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGSKYLATASTM(+15.99)DHARHG.F	18.32	1954.91	2.7
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGSKYLATASTMDH.A	49.14	1517.69	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	R.HGSKYLATASTMDHAR.H	54.57	1744.83	0.7
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGIL.D	21.73	810.435	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGILD.S	23.33	925.462	0.6
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGILDS.I	26.2	1012.49	-0.1
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGILDSIGR.F	44.08	1338.7	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGILDSIGRFFSGDR.G	45.33	2048.02	-2.6
Myelin basic protein S	sp|P02688|MBP_RAT	R.HRDTGILDSIGRFFSGDRGAPK.R	25.79	2401.23	1.2
Myelin basic protein S	sp|P02688|MBP_RAT	R.TPPPSQGKGRGL.S	35.41	1193.65	0.1
Myelin basic protein S	sp|P02688|MBP_RAT	R.TPPPSQGKGRGLS.L	31.93	1280.68	-0.4
Myelin basic protein S	sp|P02688|MBP_RAT	R.TPPPSQGKGRGLSLS.R	21.14	1480.8	-0.9
Myelin basic protein S	sp|P02688|MBP_RAT	R.TTHYGSLPQKSQR.T	30.7	1501.76	0.7
Myelin basic protein S	sp|P02688|MBP_RAT	S.KIFKLGGRDSRSGSPMA.R	19.81	1805.96	-0.3
Myelin basic protein S	sp|P02688|MBP_RAT	S.KIFKLGGRDSRSGSPMARR	18.13	2118.16	0
Myelin basic protein S	sp|P02688|MBP_RAT	T.M(+42.01)DHARHGFLPRHRDTGILDSIGRFFSG.D	16.63	3136.55	-1
Myelin basic protein S	sp|P02688|MBP_RAT	Y.GSLPQKSQRTQDENPVVH.F	39.98	2019.01	-1.1
Myelin basic protein S	sp|P02688|MBP_RAT	Y.GSLPQKSQRTQDENPVVHF.F	21.91	2166.08	-1.9
Myelin basic protein S	sp|P02688|MBP_RAT	Y.GSLPQKSQRTQDENPVVHFF.K	16.77	2313.15	-2.3
Myelin basic protein S	sp|P02688|MBP_RAT	Y.KSAHKGFKGAYDAQGTLSK.I	54.18	1993.04	-1
Myelin basic protein S	sp|P02688|MBP_RAT	Y.LATASTMDHARHGFLPRHRDTGILDSIGR.F	16.66	3200.64	0
Myelin protein P0	sp|P06907|MYP0_RAT	A.IVVYTDREVYGAVG.S	24.26	1539.79	-0.8
Myelin protein P0	sp|P06907|MYP0_RAT	A.IVVYTDREVYGAVGSQVTLH(-.98).C	31.82	2204.16	-0.9

Myelin protein P0	sp|P06907|MYP0_RAT	A.KGQPYIDEV.G	34.56	1047.52	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	A.MLDHSRST.K	27.06	945.434	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	A.MLDHSRSTKAA.S	38.98	1215.6	-1.1
Myelin protein P0	sp|P06907|MYP0_RAT	A.MLDHSRSTKAASEKKSKGLGESRKDKK	25.45	3001.61	-3.8
Myelin protein P0	sp|P06907|MYP0_RAT	A.SEKKSKGLGESRKDKK	29.39	1804.02	-1
Myelin protein P0	sp|P06907|MYP0_RAT	D.HS(+79.97)RSTKAASEKKSKGLG.E	27.74	1850.94	0.1
Myelin protein P0	sp|P06907|MYP0_RAT	D.HS(+79.97)RSTKAASEKKSKGLGESRKDKK	19.04	2722.42	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	D.HSRSTKAASEKKS(+79.97)KGL(-.98).G	25.06	1792.93	9.3
Myelin protein P0	sp|P06907|MYP0_RAT	D.HSRSTKAASEKKSKGLG.E	45.96	1770.97	-0.6
Myelin protein P0	sp|P06907|MYP0_RAT	D.HSRSTKAASEKKSKGLGESRKDKK	35.94	2642.46	-1.1
Myelin protein P0	sp|P06907|MYP0_RAT	D.SSKRGRQTPVLYAM(+15.99)LDHSRSTKAASEKKSKGLGESRKDKK	21.64	4461.4	2.3
Myelin protein P0	sp|P06907|MYP0_RAT	D.SSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	17.99	4445.4	1.1
Myelin protein P0	sp|P06907|MYP0_RAT	E.KGKFHKSSKDSSKRGRQTPVLY.A	25.48	2533.39	-1
Myelin protein P0	sp|P06907|MYP0_RAT	F.HYAKGQPYIDEVGT.F	16.27	1576.75	0.2
Myelin protein P0	sp|P06907|MYP0_RAT	F.HYAKGQPYIDEVGTF.K	26.65	1723.82	-1.9
Myelin protein P0	sp|P06907|MYP0_RAT	G.RQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	22.99	3930.12	1.8
Myelin protein P0	sp|P06907|MYP0_RAT	G.RQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK(-.98)	17.81	3929.14	-6.1
Myelin protein P0	sp|P06907|MYP0_RAT	H.SRSTKAASEKKSKGLG.E	39.06	1633.91	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	H.SRSTKAASEKKSKGLGESRKDKK	36.14	2505.4	-0.6
Myelin protein P0	sp|P06907|MYP0_RAT	K.GKFHKSSKDSSKRGRQTPVL.Y	28.72	2242.23	-0.9
Myelin protein P0	sp|P06907|MYP0_RAT	K.GKFHKSSKDSSKRGRQTPVLY.A	35.37	2405.29	-2.8
Myelin protein P0	sp|P06907|MYP0_RAT	K.SKGLGESRKDKK	18.38	1331.75	-0.3
Myelin protein P0	sp|P06907|MYP0_RAT	K.SSKDSSKRGRQTPVLY.A	23.52	1807.95	0.4
Myelin protein P0	sp|P06907|MYP0_RAT	K.SSKDSSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	30.46	4862.59	-3.7
Myelin protein P0	sp|P06907|MYP0_RAT	K.SSKDSSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK(-.98)	21.36	4861.61	-4
Myelin protein P0	sp|P06907|MYP0_RAT	L.YAM(+15.99)LDHSRSTKAASEKKSKGLGESRKDKK	19.56	3251.7	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	L.YAMLDHSRSTKAA.S	38.64	1449.7	-2
Myelin protein P0	sp|P06907|MYP0_RAT	L.YAMLDHSRSTKAASEKKSKGLG.E	15.79	2364.22	-0.6
Myelin protein P0	sp|P06907|MYP0_RAT	L.YAMLDHSRSTKAASEKKSKGLGESRKDKK	24.07	3235.71	0.1
Myelin protein P0	sp|P06907|MYP0_RAT	M.LDHSRSTK.A	31.01	942.488	-0.3
Myelin protein P0	sp|P06907|MYP0_RAT	M.LDHSRSTKAA.S	27.97	1084.56	-0.9
Myelin protein P0	sp|P06907|MYP0_RAT	M.LDHSRSTKAASEKKSKGLG.E	46.68	1999.08	0

Myelin protein P0	sp|P06907|MYP0_RAT	M.LDHSRSTKAASEKKSKGLGESRKDKK	25.96	2870.57	-1.9
Myelin protein P0	sp|P06907|MYP0_RAT	Q.TPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	23.43	3645.96	-1.8
Myelin protein P0	sp|P06907|MYP0_RAT	R.GRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	16.78	3987.14	-0.3
Myelin protein P0	sp|P06907|MYP0_RAT	R.STKAASEKKSKGLGESRKDKK	32.86	2262.27	-1
Myelin protein P0	sp|P06907|MYP0_RAT	R.STKAASEKKSKGLGESRKDKK(+42.01)(-.98)	19.54	2303.29	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	R.YQPEGGRDAISIFHY.A	30.58	1751.83	-1.1
Myelin protein P0	sp|P06907|MYP0_RAT	S.KDSSKRGRQTPVLY.A	15.11	1633.89	-1.8
Myelin protein P0	sp|P06907|MYP0_RAT	S.SKDSSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	25.05	4775.56	-2
Myelin protein P0	sp|P06907|MYP0_RAT	S.SKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	15.33	4358.37	2.6
Myelin protein P0	sp|P06907|MYP0_RAT	T.KAASEKKSKGLGESRKDKK	29.89	2074.19	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	V.GTFKERIQW.V	36.35	1163.61	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	V.LYAM(+15.99)LDHSRSTKAASEKKSKGLGESRKDKK	30.56	3364.79	0.3
Myelin protein P0	sp|P06907|MYP0_RAT	V.LYAMLDHSRSTKAASEKKSKGLGESRKDKK	17.95	3348.79	0.8
Myelin protein P0	sp|P06907|MYP0_RAT	W.RYQPEGGRDAISIFH.Y	23.53	1744.86	1.9
Myelin protein P0	sp|P06907|MYP0_RAT	W.RYQPEGGRDAISIFHY.A	22.53	1907.93	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	W.RYQPEGGRDAISIFHYA.K	30.16	1978.96	-0.9
Myelin protein P0	sp|P06907|MYP0_RAT	W.RYQPEGGRDAISIFHYAKGQPYIDEV(-.98).G	18.79	3007.49	-7.2
Myelin protein P0	sp|P06907|MYP0_RAT	W.RYQPEGGRDAISIFHYAKGQPYIDEV.G	33.85	3008.48	9.6
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHS(+79.97)RSTKAASEKKSKGLG.E	30.15	2297.12	-2.1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRST.K	27.69	1032.47	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTK.A	19.77	1160.56	-0.8
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAA.S	35.49	1302.64	-0.3
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKS(+79.97)KGL(-.98).G	15.03	2239.11	10.2
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKS.K	25.2	1861.93	-0.6
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKSKGLG.E	41.52	2217.15	-4
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKSKGLGE.S	21.08	2346.2	-3
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKSKGLGESRKDK.K	27.2	2960.55	-2.1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AM(+15.99)LDHSRSTKAASEKKSKGLGESRKDKK	33.67	3088.64	-2.2
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSR.S	24.6	828.391	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRS(+79.97)TKAASEKKSKGLG.E	17.24	2281.13	-0.1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRS.T	21.86	915.423	-0.4
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRST(+79.97)KAASEKKSKGLGESRKDKK	19.84	3152.61	-0.1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRST.K	32.91	1016.47	-0.4

Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTK.A	35.55	1144.57	-0.7
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAA.S	41.77	1286.64	-1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEK.K	41.64	1630.81	-1.4
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKK.S	41.13	1758.9	-0.7
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKS(+79.97)KGL(-.98).G	24.19	2223.12	8.5
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKS.K	41.17	1845.94	-1.1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKSK(+42.01)GLG(-.98).E	25.66	2242.19	-0.8
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKSKG.L	23.7	2031.05	-1
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKSKGLG.E	43.84	2201.16	-1.4
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKSKGLGESR.K	47.08	2573.33	-1.2
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AMLDHSRSTKAASEKKSKGLGESRKDKK	18.44	3072.65	-2.2
Myelin protein P0	sp|P06907|MYP0_RAT	Y.QPEGGRDAISIFHY.A	21.08	1588.76	-6.2
Myelin protein P0	sp|P06907|MYP0_RAT	Y.QPEGGRDAISIFHYA.K	19.73	1659.8	-0.5
Myelin protein P0	sp|P06907|MYP0_RAT	K.AASEKKSKGLGESRKDKK	23.47	1946.09	-0.6
Myelin protein P0	sp|P06907|MYP0_RAT	Y.AKGQPYIDEV.G	37.09	1118.56	-0.6
Myeloid-associated differentiation marker	sp|Q6VBQ5|MYADM_RAT	M.PVTVTRTTITTTS.S	27.82	1376.75	-2.1
Myeloperoxidase (Mapped)	tr|D3ZGE2|D3ZGE2_RAT	F.TNAFRYGHTLIQPF.M	20.06	1663.85	-3.7
Myocardial ischemic preconditioning associated protein 7	tr|Q1EG89|Q1EG89_RAT	M(+42.01)(+15.99)DDLDALLADLESTTSHISKR.P	32.35	2388.15	-2.2
Myocardial ischemic preconditioning associated protein 7	tr|Q1EG89|Q1EG89_RAT	M(+42.01)DDLDALLADLESTTSHISKR.P	29.85	2372.15	-2
Myocardial ischemic preconditioning associated protein 7	tr|Q1EG89|Q1EG89_RAT	M(+42.01)DDLDALLADLESTTSHISK.R	45.77	2216.05	-1.2
Myopalladin	tr|D4A7X7|D4A7X7_RAT	S.S(+42.01)PPTTSAT.I	20.68	802.371	11
Myosin heavy polypeptide 9 non-muscle	tr|G3V6P7|G3V6P7_RAT	F.VVTRRIVRKGTGDCS(+79.97)DEEVDGKADGADAKAAE	41.58	3397.59	0
Myosin heavy polypeptide 9 non-muscle	tr|G3V6P7|G3V6P7_RAT	F.VVTRRIVRKGTGDCSDEEVDGKADGADAKAAE	32.03	3317.63	1.3
Myosin light chain 1/3 skeletal muscle isoform	sp|P02600|MYL1_RAT	L.SQVGDVLRALGTNPTNAEVKKV.L	29.99	2295.25	-0.8
Myosin light chain 1/3 skeletal muscle isoform	sp|P02600|MYL1_RAT	M.A(+42.01)PKKDVKKPAAAAPAPAPAPAPAPAKPKEEKID.L	32.69	3311.86	10.9
Myosin light chain 1/3 skeletal muscle isoform	sp|P02600|MYL1_RAT	M.A(+42.01)PKKDVKKPAAAAPAPAPAPAPAPAKPKEEKIDL.S	26.07	3424.94	11.4
Myosin light chain 1/3 skeletal muscle isoform	sp|P02600|MYL1_RAT	M.APK(+42.01)KDVKKPAAAAPAPAPAPAPAPAKPKEEKIDLSAIKIEF.S	29.16	4213.39	10.2
Myosin light polypeptide 6	sp|Q64119|MYL6_RAT	V.LDFEHFLPMLQTV.A	24.7	1588.8	-0.9
Myosin regulatory light chain 2 skeletal muscle isoform	sp|P04466|MLRS_RAT	F.AAMGRLNVKNEELDAMMKEASGPIN.F	41.18	2688.3	0.7

Myosin regulatory light chain 2 skeletal muscle isoform	sp|P04466|MLRS_RAT	F.SMFDQTQIQEFKEA.F	25.84	1700.77	-1.4
Myosin regulatory light chain 2 skeletal muscle isoform	sp|P04466|MLRS_RAT	F.TVIDQNRDGIIDKEDLRDTFAAMGRLN.V	32.44	3075.54	0.2
Myosin regulatory light chain 2 skeletal muscle isoform	sp|P04466|MLRS_RAT	Q.FLEELLTTQCDR.F	17.04	1466.71	1.3
Myosin regulatory light chain 2 skeletal muscle isoform	sp|P04466|MLRS_RAT	Y.KNICYVITHGDAKDQE	20.68	1832.87	0.1
Myosin regulatory light polypeptide 9	sp|Q64122|MYL9_RAT	F.AMFDQSQIQEFKEA.F	29.46	1670.76	-2.9
N(G) N(G)-dimethylarginine dimethylaminohydrolase 2	sp|Q6MG60|DDAH2_RAT	M.G(+42.01)TPGEGLGRCSHALIRGVPESL.A	29	2247.14	-0.3
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	D.KGLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPEDKAAKGDK	26.31	4509.28	-1.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	D.Q(-17.03)KDSQPSEKAPEDKAAKGDK	27.9	2139.04	-0.6
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	D.SQPSEKAPEDKAAKGDK	23.27	1784.89	-1.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	F.AGYIDKVRQLEAHNRSLEGEAAALRQQQAGRAAMGEL.Y	15.18	4007.05	9.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	F.GGADALLGAPFAPLHGGGSLHY.A	16.41	2077.04	-1.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	F.HSWARTSVSSVS.A	16.01	1302.63	-1.1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.AARGQLRLEQEHLLEDIAHVR.Q	32.14	2453.33	-0.9
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.AGGTRSAAGSSSGFHSWARTSVSSVS.A	29.26	2496.17	-3.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.APFAPLHGGGSLHY.A	38.62	1422.7	-1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.APFAPLHGGGSLHYALS.R	21.49	1693.86	-0.7
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.APFAPLHGGGSLHYALSRKAG.A	19.33	2106.11	1.1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.APFAPLHGGGSLHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	24.99	4584.28	0.7
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	G.G(+42.01)SLHYALSRKAGAGGTRSAAGSSS(+79.97)GFHS(+79.97)WART.S	16.24	3392.52	-0.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	H.GGGSLHYALSR.K	41.13	1116.57	-1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	H.GGGSLHYALSRKAGAGGTR.S	30.03	1814.95	0.5
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	H.GGGSLHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	34.09	3850.88	0.1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	H.YALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	21.75	3342.65	-1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	L.GAPFAPLHGGGSLH.Y	28.68	1316.66	-1.7
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	L.GAPFAPLHGGGSLHY.A	36.6	1479.73	-1.6

Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	L.GAPFAPLHGGGSLHYALSRKAGAGGTR.S	17.9	2605.36	1.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	L.HGGGSLHYALSRKAGAGGTR.S	22.36	1952.01	1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)(+15.99)MSFGGADALLGAPFAPLHGGGSLHY.A	42.93	2631.22	-2.4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALL.G	30.43	1153.51	-1.1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLH.G	29.29	1943.93	-0.6
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLHGGGSLH.Y	42.45	2452.17	-2.7
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLHGGGSLHY.A	59.01	2615.23	-3.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLHGGGSLHYALSR.K	51.99	3042.48	-1.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLHGGGSLHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	35.95	5776.8	3.4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLH.G	26.87	1681.85	-0.1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLH.Y	30.14	2190.09	0
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHY.A	58.41	2353.15	-1.7
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYA.L	37.46	2424.19	-3.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYAL.S	30.4	2537.27	-2.9
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYALS.R	39.03	2624.3	-11.4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYALSR.K	29.34	2780.4	-1.4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS(-.98).A	19.56	5513.74	-0.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	M.S(+42.01)FGGADALLGAPFAPLHGGGSLHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	34.45	5514.72	0.5
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	MMS(+79.97)FGGADALLGAPFAPLH.G	21.05	1981.88	9.3
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	P.FAPLHGGGSLHY.A	33.33	1254.61	-1
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	P.FAPLHGGGSLHYALSRKAGAGGTR.S	31.69	2380.25	0.5
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	R.EIRAQLEGHTVQ.S	33.6	1379.72	-0.8
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	R.KAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	24.77	2752.33	-3.3
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	R.SAAGSSSGFHSWAR.T	46.9	1406.63	-0.6
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	R.SAAGSSSGFHSWARTSVSSVS.A	22.6	2053.95	-0.3
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	S.KKPEEKPKMEAKAKEEDKGLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPEDKAAKGDK	18.58	6505.31	1.3
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	S.RKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	25.15	2908.43	-0.7

Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	Y.ALSRKAGAGGTRSAAGSSSGFHS.W	29.21	2119.05	-2.4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	Y.ALSRKAGAGGTRSAAGSSSGFHSWAR.T	26.85	2532.27	-0.2
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	Y.ALSRKAGAGGTRSAAGSSSGFHSWARTS.V	15.41	2720.35	0.9
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	Y.ALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS(-.98).A	19.63	3178.6	4
Neurofilament heavy polypeptide	tr|F1LRZ7|F1LRZ7_RAT	Y.ALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVS.A	39.64	3179.58	-3.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.E(+42.01)GRLMEARK(+42.01)GADEAALARAEL.E	18.62	2340.19	-5.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.FPAYYTSHVQEEQ.S	33.21	1597.7	-0.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.FPAYYTSHVQEEQSEVEETIEATK.A	30.81	2814.29	-3.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.FPAYYTSHVQEEQSEVEETIEATKAEEAK.D	30.65	3342.54	6.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.RAFPAYYTSHVQE.E	38.86	1567.74	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.RAFPAYYTSHVQEEQSEVEETIEATK.A	53.2	3041.43	-3.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.RAFPAYYTSHVQEEQSEVEETIEATKAEEAK(-.98).D	31.73	3568.7	-6.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.RAFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	30.26	3569.68	-3.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	A.YYTSHVQEEQSEVEETIEATKAEEAK.D	24.8	3027.38	-0.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	C.RGMNEALEKQLQELEDKQNADISAMQDTINKLENELRSTKSEMAR.Y	33.48	5204.55	-10.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	D.AKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAKKKD	42.32	4124.81	-0.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	D.TKESEEEEKKEESAGEEQAAKKKD	46.27	2736.29	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.AAKDESEDAKEEEGGEGEEEDT(+79.97)KESEEEEKKEESAGEEQAAKKKD	36.39	5050.12	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.AAKDESEDAKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAKKKD	17.06	4970.16	-2.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.DAKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAKKKD	24.57	4239.84	0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.EQSEVEETIEATKAEEAK.D	49.26	2019.95	-1.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.NLDLSQVAAISNDLK.S	17.64	1599.85	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TIEATKAEEAK.D	40.23	1189.62	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVR.S	24.4	1150.66	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSG.Y	24.16	1294.71	-0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYS.T	15.82	1544.81	-1.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYSTA.R	22.9	1716.89	-0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYSTAR.S	31.5	1872.99	-0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYSTARS.A	24.12	1960.02	-1.6

Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYSTARSAY.S	18.74	2194.12	0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	E.TPRVHISSVRSGYSTARSAYSSY.S	26.64	2531.25	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQ.S	25.13	937.462	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQSSSY.L	35.34	1361.62	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQSSSYLMSA(-.98).R	21.06	1762.83	10.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQSSSYLMSA.R	37.92	1763.81	1.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQSSSYLMSAR.A	38.39	1919.92	-0.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.GRSAYSGLQSSSYLMSARAFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	36.76	5315.48	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.IERVHELEQQNKVLEAELLVLRQKHSEPSR.F	23.35	3606.96	1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	F.SYEPYFSTSYKRRY.V	34.56	1845.87	0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.GEGEEEDTKESEEEEKKEESAGEEQAAKKKD	16.2	3481.53	0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SITSGYSQSSQVFGR.S	48.49	1602.76	-3.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SITSGYSQSSQVFGRSA.Y	49.99	1760.83	0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SITSGYSQSSQVFGRSAYSGLQ.S	51.31	2309.09	4.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SLM(+15.99)PSLENLDLSQVAAISNDLK.S	47.59	2373.21	-4.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SLMPSLENLDLSQ.V	27.78	1445.71	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	G.SLMPSLENLDLSQVAAISNDLK.S	55.15	2357.21	-7.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	H.VQEEQSEVEETIEATK.A	55.2	1847.86	-1.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	H.VQEEQSEVEETIEATKAEEAK.D	37.36	2376.12	-1.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	K.SIRTQEKAQLQDLNDR.F	26.35	1913.99	-0.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	L.DLSQVAAISNDLK.S	21.51	1372.72	-2.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	L.MPSLENLDLSQVAAISNDLK.S	39.74	2157.1	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	L.SQVAAISNDLK.S	19.85	1144.61	0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.PSLENLDLSQVAAISNDLK.S	46.59	2026.06	-1.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKR.R	41.69	1889.85	-2.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRR.Y	20.38	2045.95	-2.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRY.V	26.04	2209.01	-0.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRYVE.T	24.71	2437.12	-2.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRYVETPR.V	16.28	2791.32	-3.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRYVETPRVH.I	26.02	3027.45	-0.5

Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRYVETPRVHISSVR.S	15.42	3569.77	0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.S(+42.01)SFSYEPYFSTSYKRRYVETPRVHISSVRSGYSTARSAYSSY.S	28.96	4950.36	3.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SARAFPAYY.T	18.36	1044.5	-1.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SARAFPAYYTSHVQEEQSEVEETIEATK(-.98).A	33.36	3198.51	-9.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SARAFPAYYTSHVQEEQSEVEETIEATK.A	41.95	3199.49	1.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SARAFPAYYTSHVQEEQSEVEETIEATKAEEAK(-.98).D	32.1	3726.76	-6.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SARAFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	49.54	3727.75	2.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	M.SSFSYEPYFSTSYKRRY.V	18.16	2167	-0.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	P.SLENLDLSQVAAISNDLK.S	46.97	1929.01	-6.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	P.YFSTSYKRRY.V	17	1369.68	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SEVEETIEATK.A	24.77	1234.59	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SEVEETIEATKAEEAK.D	56.99	1762.85	-0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSAR.A	33.33	1000.46	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAY.Y	17.44	1549.72	-2.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAYY.T	29.6	1712.79	0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAYYTS.H	32.85	1900.87	-0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAYYTSH.V	35.74	2037.93	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAYYTSHVQEEQSEVEETIEATK.A	19.35	3867.78	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.SSSYLMSARAFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	46.12	4396.03	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.VFGRSAYSG.L	34.16	942.456	0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Q.VFGRSAYSGLQ.S	50.24	1183.6	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.AFPAYYTSHVQEEQSEVEETIEATK.A	53.61	2885.32	-2.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.AFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	25.03	3413.58	-1.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.RSYSSSSGSLMPSLENLDLSQVAAISNDLK.S	29.94	3168.56	-3.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.RYVETPRVHISSVR.S	36.1	1697.93	0.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.SGYSTARSAY.S	27.92	1061.48	0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.SGYSTARSAYSSY.S	41.72	1398.61	-1.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.SGYSTARSAYSSYSAPVS.S	40.45	1839.83	0.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	R.YVETPRVHISSVR.S	36.67	1541.83	-0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.APVSSSLSVRRSYSSSSG.S	47.98	1812.9	-2.1

Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.FSYEPYFSTSYKRRY.V	30.03	1992.94	1.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.GSLMPSLENLDLSQVAAISNDLK.S	53.74	2414.24	0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.HVQEEQSEVEETIEATK.A	59.99	1984.92	-0.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.HVQEEQSEVEETIEATKAEEAK.D	71.43	2513.18	-1.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.LENLDLSQVAAISNDLK.S	44.2	1841.97	-1.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.LMPSLENLDLSQVAAISNDLK.S	44.84	2270.18	-3.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.QVAAISNDLK.S	33.71	1057.58	-1.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SGSLMPSLENLDLSQVAAISNDLK.S	54.19	2501.27	-2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SLSVRR.S	18.13	716.429	-0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SLSVRRS.Y	19.64	803.461	-0.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SLSVRRSYSSSSG.S	33.29	1371.67	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SQVFGRSAYSGLQ.S	25.49	1398.69	-2.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	S.SSLSVRRSYSSSSG.S	46.21	1458.71	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.PRVHISSVR.S	30.57	1049.61	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGR.S	48.59	1301.6	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSA.Y	38.12	1459.67	-1.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSAY.S	32.99	1622.73	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSAYSGLQ(-.98).S	20.16	2006.94	-1.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSAYSGLQ.S	59.27	2007.93	-0.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSAYSGLQS.S	49.73	2094.96	-3.8
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SGYSQSSQVFGRSAYSGLQSSSYLMSAR.A	22.56	2990.38	-3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	T.SHVQEEQSEVEETIEATKAEEAK.D	33.24	2600.21	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	V.ETPRVHISSVR.S	20.77	1279.7	0
Neurofilament light polypeptide	sp|P19527|NFL_RAT	V.FGRSAYSGLQ.S	15.69	1084.53	-0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.EPYFSTSYKRRY.V	28.03	1595.77	0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.FSTSYKRRYVETPRVHISSVR.S	19.9	2567.37	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.KRRYVETPRVH.I	34.25	1439.81	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.KRRYVETPRVHISSVR.S	20.77	1982.13	0.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.LMSARAFPAYYTSHVQEEQSEVEETIEATKAEEAK.D	25.45	3971.87	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVR.R	44.43	1088.58	-0.2

Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRR.S	46.23	1244.68	-0.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRS.Y	24.76	1331.72	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRSY.S	27.52	1494.78	-2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRSYSSS.S	38.42	1755.88	-0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRSYSSSS.G	15.24	1842.91	-7.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRSYSSSSG.S	42.08	1899.93	-0.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SQSSQVFGRSAYSGLQ.S	39.49	1700.81	-0.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SSSSGSLMPSLENLDLSQVAAISNDLK.S	51.88	2762.36	-1.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SSYSAPVSSSLSVRR.S	24.75	1581.81	-1.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SSYSAPVSSSLSVRRS.Y	26.26	1668.84	-3.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SSYSAPVSSSLSVRRSY.S	25.33	1831.91	-1.2
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.SSYSAPVSSSLSVRRSYSSSSG.S	28.67	2237.06	-1.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQS(+79.97)EVEETIEATKAEEAK.D	25.11	2781.22	-2.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEE.T	20.7	1529.65	-1.9
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEETIE.A	21.79	1872.82	0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEETIEATK(-.98).A	31.74	2172.02	-7.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEETIEATK.A	34.7	2173	-1.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEETIEATKAEEAK(+42.01)(-.98).D	32.81	2742.28	-0.7
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.TSHVQEEQSEVEETIEATKAEEAK.D	65.78	2701.26	-0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHIS.S	41.91	1036.57	0
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISS.V	31.6	1123.6	-1.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVR.S	34.7	1378.77	-1.6
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSG.Y	44.49	1522.82	-3.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYS.T	40.77	1772.92	0
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYST.A	26.31	1873.96	-0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTA.R	48.51	1945	-1.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTAR.S	33.15	2101.1	-1.3
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTARS.A	34.19	2188.13	0.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTARSA.Y	18.5	2259.17	0.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTARSAY.S	40.13	2422.24	-1.3

Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.VETPRVHISSVRSGYSTARSAYSSY.S	20.2	2759.36	-2.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQS(+79.97)EVEETIEATKAEEAK.D	24.55	2944.29	1.1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQSEVEETIE.A	19.72	2035.89	-1.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQSEVEETIEATK.A	40.55	2336.07	-2.4
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQSEVEETIEATKAEEA.K	17.78	2736.22	-4.5
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQSEVEETIEATKAEEAK(+42.01)(-.98).D	27.05	2905.35	-1
Neurofilament light polypeptide	sp|P19527|NFL_RAT	Y.YTSHVQEEQSEVEETIEATKAEEAK.D	45.12	2864.32	-0.3
Neurofilament medium polypeptide	sp|P12839|NFM_RAT	P.SAYRRVPTETRSSFSRVS.G	15.85	2085.07	-0.1
Neurofilament medium polypeptide	sp|P12839|NFM_RAT	Y.QDTIQQLENELRGTKWEMAR.H	24.25	2445.21	-5.3
Neurofilament medium polypeptide	sp|P12839|NFM_RAT	Y.QDTIQQLENELRGTKWEMARH.L	18.86	2582.27	2.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	A.IVKEVTQGD	24.58	987.524	-0.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	A.LAPRLAYSSAMLSS.A	32.68	1465.76	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	A.TKYITKSVTVTQK.V	36.04	1495.86	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	D.DKVVVTKKVEKIT.S	15.93	1485.91	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	D.VSPAEEKKGEDRSDDKVVVTKKVEKIT(-.98).S	21.96	3012.65	-6.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	D.VSPAEEKKGEDRSDDKVVVTKKVEKIT.S	57.29	3013.63	-3.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	E.AAEQNKEAIRSAKEEIAEYRRQLQ.S	29.64	2830.47	1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	E.EIIEETKVEDEK.S	42.38	1460.72	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	E.IIEETKVEDEK.S	44.91	1331.68	-1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	F.LRSNHEEEVADLLAQIQASHITVERKDYLK.T	15.88	3504.83	-2.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	F.VEEIIEETKVEDEK.S	48.19	1688.84	-1.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	G.SPSTVSSSYKRSA.L	22.55	1355.67	-0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.AIVKEVTQGD	18.04	1058.56	-1.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSK.I	16.87	1101.61	-3.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSKIQK.T	36.89	1470.85	0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSKIQKTK.V	34.21	1699.99	-0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSKIQKTKVE.A	23.94	1928.11	-1.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSKIQKTKVEAPK.L	18.24	2224.29	-1.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	H.RQPSVTISSKIQKTKVEAPKLK.V	16.46	2465.47	-0.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	I.SSKIQKTK.V	25.84	918.55	-0.6

Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	I.SSKIQKTKVEAPKLK.V	39.83	1684.02	0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.FVEEIIEETKVEDEK.S	24.38	1835.9	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.LKVQHKFVEEIIEETKVEDEK.S	38.57	2569.36	10.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALK.E	18.21	847.465	-1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALKEIR.S	31.02	1245.69	-1.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALKEIRSQ.L	27.59	1460.78	-1.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALKEIRSQLE.C	39.05	1702.91	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALKEIRSQLEC(-1.01)HSDQNMHQAEEWFKC(-1.01)R.Y	19.49	3830.76	-12.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.TDISTALKEIRSQLECH.S	37.17	1942.98	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLK.V	23.64	783.485	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLKV.Q	33.32	882.554	-0.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLKVQ.H	39.79	1010.61	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLKVQHK.F	15.99	1275.77	-0.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLKVQHKFVEEIIEETKVEDEK(-.98).S	16.22	3092.68	-7.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEAPKLKVQHKFVEEIIEETKVEDEK.S	44.13	3093.66	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VEEHEETFEEKLVSTKKVEKVT.S	68.78	2617.35	-1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VQHKFVEEIIEETKVEDEK(+42.01)(-.98).S	30.87	2369.21	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	K.VQHKFVEEIIEETKVEDEK.S	36.91	2328.18	-0.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	L.APRLAYSSAMLSS.A	21.47	1352.68	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	L.KVQHKFVEEIIEETKVEDEK.S	18.73	2456.28	-1.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	L.YTHRQPSVTISSK.I	35.62	1502.78	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	L.YTHRQPSVTISSKIQKTK.V	57.41	2101.16	-1.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRR.V	32.13	1740.84	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTET.R	15.06	2171.05	-1.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETR.S	17.14	2327.15	-2.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRS.S	32.67	2414.18	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRSS.F	15.09	2501.21	-0.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRSSF.S	26.69	2648.28	-1.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRSSFSR.V	40.87	2891.42	-0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRSSFSRVS.G	42.93	3077.52	-1.7

Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	M.S(+42.01)YTLDSLGNPSAYRRVTETRSSFSRVSGSPSSGFRSQSW.S	23.97	4341.08	-1.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	P.LYTHRQPSVTISSKIQKTK.V	22.06	2214.25	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	P.SSGFRSQSWSRGSPSTVS.S	41.79	1898.89	-1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Q.HKFVEEIIEETKVEDEK.S	33.18	2101.06	-0.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Q.KVEEHEETFEEKLVSTKKVEKVT.S	37.3	2745.44	0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.GSPSTVSSSYKRSAL.A	39.68	1525.77	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.GSPSTVSSSYKRSALAPR.L	28.75	1849.96	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.GSPSTVSSSYKRSALAPRLA.Y	25.33	2034.09	0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.GSPSTVSSSYKRSALAPRLAYSSAMLSS.A	26.48	2860.44	-3.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.RVTETRSSFSRVS.G	27.38	1510.79	0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SALAPRLA.Y	26.22	797.476	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SALAPRLAY.S	19.15	960.539	-1.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SALAPRLAYSSAMLS.S	40.33	1536.8	-0.7
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SALAPRLAYSSAMLSS.A	32.33	1623.83	1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SSFSRVS.G	22.34	768.377	-0.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SSFSRVSGSPSSGFRSQSWSRGSPSTVS.S	40.82	2890.36	-4.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.SSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSA.L	17.6	3669.75	-1.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	R.VTETRSSFSRVS.G	26.06	1354.68	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSW.S	46.63	1281.57	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSR.G	34.51	1524.71	-1.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPST.V	34.9	1953.89	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVS.S	16.24	2139.99	-0.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSS.Y	28.96	2314.06	-4.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYK.R	35.95	2605.22	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKR.S	38.67	2761.32	0
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRS.A	41.16	2848.35	-1.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRSA.L	39.37	2919.39	-0.4
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRSAL.A	28.93	3032.47	-3.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRSALAPR.L	23.42	3356.66	2.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAY.S	29.37	3703.85	-5.1

Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.GSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSA.M	21.99	3948.95	4.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.HAIVKEVTQGD	48.14	1195.62	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.SGFRSQSWSRGSPST.V	25.71	1625.75	-2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.SKIQKTKVEAPKLK.V	30.87	1596.99	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.SSYKRSALAPRL.A	36.62	1347.76	-0.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.SSYKRSALAPRLA.Y	34.42	1418.8	0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	S.SSYKRSALAPRLAY.S	15.11	1581.86	-1.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.GPLYTHRQPSVTIS.S	35.86	1554.82	-2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.GPLYTHRQPSVTISSK.I	42.7	1769.94	-1.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.GPLYTHRQPSVTISSKIQKTK.V	68.33	2368.32	-0.9
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.HRQPSVTISSKIQKTK.V	39.46	1837.05	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SEGGDGATKYITK.S	48	1325.65	-0.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SEGGDGATKYITKSVTVTQK.V	64.47	2069.06	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SEGGDGATKYITKSVTVTQKVEEHEETFEEKLVSTKKVEKVT.S	36.47	4668.4	0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SEGGDGATKYITKSVTVTQKVEEHEETFEEKLVSTKKVEKVTSHAIVKEVTQGD	16.08	5933.04	-1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SEGGDGATKYITKSVTVTQKVEEHEETFEEKLVSTKKVEKVTSHAIVKEVTQGD(-.98)	17.37	5932.06	-9.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.SHAIVKEVTQGD	52.07	1282.65	-0.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	T.VTQKVEEHEETFEEKLVSTKKVEKVT.S	36.1	3073.62	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	V.STKKVEKVTSHAIVKEVTQGD	34.93	2283.24	1.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	W.SRGSPSTVSSSYKRSAL.A	37.66	1768.91	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	W.SRGSPSTVSSSYKRSALAPR.L	30.12	2093.1	-0.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	W.SRGSPSTVSSSYKRSALAPRLA.Y	29.37	2277.22	-4.6
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.ITKSVTVTQK.V	36.94	1103.66	-2.2
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.KRSALAPRL.A	16.56	1010.63	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.KRSALAPRLA.Y	20.8	1081.67	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.LEQQNKEIEAEIHALRQKQASHAQLGDAYDQEIREL.R	15.29	4201.12	1.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.RRVTETRSSFSRVS.G	40.45	1666.89	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTIS.S	26.69	1124.59	1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSK.I	47.48	1339.72	-0.6

Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSKIQKTK.V	45.41	1938.1	-0.1
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSKIQKTKVE.A	18.75	2166.21	-0.5
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSKIQKTKVEAPK(-.98).L	23.03	2461.41	-5.8
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSKIQKTKVEAPK.L	50.21	2462.4	-0.3
Neurofilament medium polypeptide	tr|G3V7S2|G3V7S2_RAT	Y.THRQPSVTISSKIQKTKVEAPKLK.V	29.28	2703.58	-0.3
Noncompact myelin-associated protein	tr|M0R3T9|M0R3T9_RAT	G.SQQPAAVTSDPADVPVETR	42	1966.96	-1.1
Noncompact myelin-associated protein	tr|M0R3T9|M0R3T9_RAT	D.PADVPVETR	23.24	982.508	-0.2
Nuclear transport factor 2	sp|P61972|NTF2_RAT	M.G(+42.01)DKPIWEQIGSSFIQHYY.Q	23.35	2209.05	-0.7
Nuclear transport factor 2	sp|P62282|RS11_RAT	F.NVLKVTKAAGTKKQFQK.F	19.58	1888.13	-1
Nuclear transport factor 2	sp|P62282|RS11_RAT	M.A(+42.01)DIQTERAYQKQPTIF.Q	31.45	1949.98	-2.8
Nuclear transport factor 2	sp|P61972|NTF2_RAT	M.G(+42.01)DKPIWEQIGSSFIQH.Y	34.14	1882.92	-2
Nuclear transport factor 2	sp|P61972|NTF2_RAT	M.G(+42.01)DKPIWEQIGSSFIQHY.Y	41.88	2045.98	-4
Nucleophosmin	sp|P13084|NPM_RAT	F.RMTDQEAIQDLWQWRKSL	44.96	2303.15	-0.8
Nucleoside diphosphate kinase alpha isoform	tr|Q9QWQ4|Q9QWQ4_RAT	M.A(+42.01)NLERTFIAIKPDGVQR.G	29.22	1969.07	-1.5
Nucloside diphosphate kinase	tr|Q6LCQ4|Q6LCQ4_RAT	M.A(+42.01)NSERTFIAIKPDGV.Q	21.22	1658.86	-0.7
Osteocalcin	sp|P04640|OSTCN_RAT	G.FQDAYKRIYGTTV	38.96	1560.79	0.2
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	F.TGNLIEDIEDGTFSK.L	28.91	1637.78	-2
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	F.TGNLIEDIEDGTFSKL.S	32.26	1750.86	2.3
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	L.DFTGNLIEDIEDGTFSK.L	31.86	1899.87	1.1
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	L.K(+42.01)(+42.01)RLPTGS(-.98).Y	15.57	840.482	0.6
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	N.K(+42.01)(+42.01)IKK(+42.01)LTAKDFADM(+15.99)PNLRRLDFTGNLIEDIEDGTFSKL.S	18.56	4394.28	-3.3
Osteoglycin	tr|D3ZVB7|D3ZVB7_RAT	Y.IRERMEEIR.L	23.57	1230.65	-0.2
Peptidyl-prolyl cis-trans isomerase	tr|G3V6L9|G3V6L9_RAT	M.A(+42.01)AAVPQRAWTVEQL.R	18.37	1580.83	-0.2
Peptidyl-prolyl cis-trans isomerase	tr|G3V6L9|G3V6L9_RAT	M.A(+42.01)AAVPQRAWTVEQLRS.E	43.11	1823.96	-0.1
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	C.FELFADKVPKTAENFRAL.S	29.03	2095.11	-1.9
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	C.QGGDFTRHNGTGGKSIYGEKF.E	15.89	2255.07	-0.7
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	C.QGGDFTRHNGTGGKSIYGEKFEDENFILKH.T	21.63	3380.62	-4.8
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	C.QGGDFTRHNGTGGKSIYGEKFEDENFILKHTGPGILSM.A	20.35	4137	-0.4
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.ADKVPKTAENF.R	28.31	1218.62	-0.8
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.ADKVPKTAENFRAL.S	37.53	1558.85	-1.1

Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.EDENFILKHTGPGILSM.A	53.55	1899.94	-0.1
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.ELFADKVPKTAENFRAL.S	20	1948.04	0.6
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.GKVKEGMSIVEA.M	23.13	1246.66	-2.2
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.GKVKEGMSIVEAMER.F	23.69	1662.84	-0.6
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.RALSTGEKGFGYKGSS.F	28.5	1643.83	-0.2
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	F.RALSTGEKGFGYKGSSF.H	22.89	1790.9	1.4
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	H.NGTGGKSIYGEKFEDENFILKHTGPGILSM.A	36.16	3238.6	0.7
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	L.KHTGPGILSM.A	46.17	1039.55	-2.3
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	M.V(+42.01)NPTVFFDITADGEPLGR.V	20.23	1988.98	1.5
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	M.V(+42.01)NPTVFFDITADGEPLGRVC.F	15.8	2191.06	-1
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	M.VNPTVFFDITADGEPLGR.V	37.15	1946.97	7.6
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	M.VNPTVFFDITADGEPLGRV(-.98).C	24.18	2045.06	-1.2
Peptidyl-prolyl cis-trans isomerase A	sp|P10111|PPIA_RAT	M.VNPTVFFDITADGEPLGRVC.F	38.51	2149.05	3.3
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	F.DVELLKLE	28.8	957.538	-1.5
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	M.GVQVETISSGDGRTFPKRGQT(-.98).C	25.96	2218.15	-1.1
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	Y.TGMLEDGKKFDSSRDRNKPF.K	22.71	2327.13	-0.4
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	L.VFDVELLKLE	35.07	1203.68	0.2
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	M.SVGQRAKLIISPDYAYGATGHPGIIPPHATL.V	26.62	3199.71	-5.2
Peptidyl-prolyl cis-trans isomerase FKBP1A	sp|Q62658|FKB1A_RAT	V.FDVELLKLE	30.37	1104.61	-0.7
Periaxin	tr|G3V8D2|G3V8D2_RAT	L.KIPEVELVTPGAQETEKVTSGVKPSGLQVSTTRQVVAEGQEGAQRVSSLG.I	24.89	5160.73	8.9
Periaxin	tr|G3V8D2|G3V8D2_RAT	L.PDIQLPKVPEMKL.P	34.02	1506.85	0.2
Periaxin	tr|G3V8D2|G3V8D2_RAT	L.PKVPEMTMPDIRLPEVQL.P	21.76	2092.11	-1.6
Periaxin	tr|G3V8D2|G3V8D2_RAT	L.PTLGLGAPAAPAVEPPTTGIQVPQVEL.P	17.28	2622.43	-1.9
Periaxin	tr|G3V8D2|G3V8D2_RAT	L.PTLKMPSFGISV.A	21.93	1275.69	-0.4
Periaxin	tr|G3V8D2|G3V8D2_RAT	R.MPTFGLSLLESRPSGPEAAAESKLKLPTLK.M	16	3167.73	-1.9
Periaxin	tr|G3V8D2|G3V8D2_RAT	V.KLPKIPDMAVPDVRL.P	28.7	1690.98	0.3
Periaxin	tr|G3V8D2|G3V8D2_RAT	Y.EDALRLLQC.A	28.38	1059.54	0
Periaxin	sp|Q63425|PRAX_RAT	A.AAPPSRKAKSEAEVA.T	23.79	1510.81	-1.9
Periaxin	sp|Q63425|PRAX_RAT	A.EGQEGAQRVSSLG.I	47.37	1316.63	0.1
Periaxin	sp|Q63425|PRAX_RAT	D.AQLPSGKVEVAGAE.S	25.84	1354.71	-4.9

Periaxin	sp|Q63425|PRAX_RAT	E.AIAGQLKIPEVE.L	20.68	1266.72	0.7
Periaxin	sp|Q63425|PRAX_RAT	E.LDVGLGHEAQAGETAKSEGGLK.L	24.38	2166.09	-1.6
Periaxin	sp|Q63425|PRAX_RAT	E.SRPSGPEVAAESKLKLPTLK.M	28.08	2107.2	2.9
Periaxin	sp|Q63425|PRAX_RAT	F.GLARAKEGIETGEKVKSPKLR.L	29.2	2266.31	-0.3
Periaxin	sp|Q63425|PRAX_RAT	F.KLPKMTVPKLG.K	44.09	1210.75	-0.5
Periaxin	sp|Q63425|PRAX_RAT	F.SETAAPGSARIEGTQAAA.I	39.02	1686.82	-0.7
Periaxin	sp|Q63425|PRAX_RAT	F.SRLRRGLKADAVKGPVPAAPAR.R	20.3	2285.36	-0.1
Periaxin	sp|Q63425|PRAX_RAT	G.HEAQAGETAKSEGGLK.L	32.11	1611.79	-0.6
Periaxin	sp|Q63425|PRAX_RAT	G.KGWGWDGKVKMPKLK.M	43.12	1756.98	0.9
Periaxin	sp|Q63425|PRAX_RAT	G.KVTKPGEAGIEVPDK.L	36.15	1566.86	0.4
Periaxin	sp|Q63425|PRAX_RAT	G.KVTKPGEAGIEVPDKLLILPC.L	15.5	2219.26	-0.6
Periaxin	sp|Q63425|PRAX_RAT	G.LSGPKAVKAEVEGPGRATKLK.V	26.99	2135.24	0.1
Periaxin	sp|Q63425|PRAX_RAT	G.TEVARVGVPSL.S	24.99	1126.63	-0.3
Periaxin	sp|Q63425|PRAX_RAT	G.TEVARVGVPSLS.L	18.55	1213.67	-1.1
Periaxin	sp|Q63425|PRAX_RAT	G.TPADLAPVDVEFSFPKF.S	50.26	1878.94	-1.6
Periaxin	sp|Q63425|PRAX_RAT	G.TPADLAPVDVEFSFPKFS.R	49.39	1965.97	-1
Periaxin	sp|Q63425|PRAX_RAT	G.TPADLAPVDVEFSFPKFSR.L	26.22	2122.07	-1
Periaxin	sp|Q63425|PRAX_RAT	G.TPADLAPVDVEFSFPKFSRL.R	15.7	2235.16	0.6
Periaxin	sp|Q63425|PRAX_RAT	K.ADAVKGPVPAAPARR.R	30.82	1474.84	-0.1
Periaxin	sp|Q63425|PRAX_RAT	K.ADAVKGPVPAAPARRRLQ.L	30.81	1872.08	-0.4
Periaxin	sp|Q63425|PRAX_RAT	K.MPSFGLSRGKEAEIQDGRVSPGEKLE.A	24.7	2816.41	0.6
Periaxin	sp|Q63425|PRAX_RAT	L.ESRPSGPEVAAESKLKLPTLK.M	26.69	2236.24	-0.9
Periaxin	sp|Q63425|PRAX_RAT	L.KIPEVELVTPGAQETEKVTSGVKPSGLQVSTTRQVVA.E	16.07	3862.11	-2.4
Periaxin	sp|Q63425|PRAX_RAT	L.KLPKVPEMTMPDIRLPEVQL.P	35.69	2333.29	-0.8
Periaxin	sp|Q63425|PRAX_RAT	L.PKAPEAAIPDVQLPEVQL.P	28.29	1914.05	-5.6
Periaxin	sp|Q63425|PRAX_RAT	L.PKVPEMAVPDVPLPELQL.P	28.77	1971.08	1
Periaxin	sp|Q63425|PRAX_RAT	L.RVREVAEEAQVAR.M	33.7	1511.82	0.1
Periaxin	sp|Q63425|PRAX_RAT	M(+42.01)EARSRSAEELR.R	20.41	1475.72	-0.1
Periaxin	sp|Q63425|PRAX_RAT	M(+42.01)EARSRSAEELRRAELVEI.I	17.14	2286.18	-0.3
Periaxin	sp|Q63425|PRAX_RAT	P.ADLAPVDVEFSFPKF.S	18.61	1680.84	-5
Periaxin	sp|Q63425|PRAX_RAT	P.RFGVRGKEATEAKVVKGS(+79.97)PEAKAKGPRLR.M	25.87	3201.76	1
Periaxin	sp|Q63425|PRAX_RAT	Q.SLSPVKKKKMVIGTLG.T	33.47	1685.03	-0.2
Periaxin	sp|Q63425|PRAX_RAT	R.MPTFGLSLLESRPSGPEVA.A	39.17	1987.01	0
Periaxin	sp|Q63425|PRAX_RAT	R.MPTFGLSLLESRPSGPEVAAESKLKLPTLK.M	31.45	3195.76	-3.1
Periaxin	sp|Q63425|PRAX_RAT	R.RGLKADAVKGPVPAAPARR.R	28.27	1929.14	0.1

Periaxin	sp|Q63425|PRAX_RAT	S.FPRFGVRGKEATEAKVVK.G	19.62	2018.14	0.3
Periaxin	sp|Q63425|PRAX_RAT	S.FPRFGVRGKEATEAKVVKGS (+79.97)PEAKAKGPRLR.M	21.43	3445.88	-0.3
Periaxin	sp|Q63425|PRAX_RAT	S.FPRFGVRGKEATEAKVVKGS PEAKAKGPRLR.M	19.19	3365.92	-1.4
Periaxin	sp|Q63425|PRAX_RAT	S.LSPVKKKKMVIGTLG.T	15.33	1598	-0.4
Periaxin	sp|Q63425|PRAX_RAT	T.AAPGSARIEGTQAAAI	24.6	1482.78	-1.3
Periaxin	sp|Q63425|PRAX_RAT	V.AGGDLLVGEGIFKMPTVTV. P	21.55	1903.01	-8.8
Periaxin	sp|Q63425|PRAX_RAT	V.AGPEVKAPKGPEVKLPKVPE IKL.P	18.64	2423.45	4.2
Periaxin	sp|Q63425|PRAX_RAT	V.KLPKIPDMAVPDVRLPELQL. P	15.56	2271.3	-1.1
Peripherin	sp|P21807|PERI_RAT	F.GPPPSLSPGAFSYSSSSR.F	33.73	1779.84	-3
Peripherin	sp|P21807|PERI_RAT	F.GPPPSLSPGAFSYSSSSRF.S	23.68	1926.91	0.5
Peripherin	sp|P21807|PERI_RAT	F.GPPPSLSPGAFSYSSSSRFSSS R.L	21.72	2344.11	-6.2
Peripherin	sp|P21807|PERI_RAT	M.S(+42.01)HHSSGLRSSISST.S	23.9	1483.7	-0.8
Peripherin	sp|P21807|PERI_RAT	M.S(+42.01)HHSSGLRSSISSTS. Y	51.15	1570.73	-1.3
Peripherin	sp|P21807|PERI_RAT	M.S(+42.01)HHSSGLRSSISSTSY .R	59.12	1733.8	-1.1
Peripherin	sp|P21807|PERI_RAT	M.S(+42.01)HHSSGLRSSISSTSY RR.T	19.49	2046	-1.1
Peripherin	sp|P21807|PERI_RAT	M.S(+42.01)HHSSGLRSSISSTSY RRTF.G	16.29	2294.12	0
Peripherin	sp|P21807|PERI_RAT	N.Q(-17.03)EFLATRSNEKQELQELND RFANFIEKVRFLEQQN(-.98).A	16.53	4293.16	-3.8
Peripherin	sp|P21807|PERI_RAT	R.TIETRDGEKVVTESQKEQHS ELDKSSIHSY	36.01	3459.68	-2
Peripherin	tr|F1M7P4|F1M7P4_RAT	F.GPPPSLSPGAFSYSSSSRFSSS RLLG.S	17.09	2627.3	-1.2
Peripherin	tr|F1M7P4|F1M7P4_RAT	G.SGSPSSSARLG.S	25.39	1004.49	0.2
Peripherin	tr|F1M7P4|F1M7P4_RAT	M.PSSASMSHHSSGLR.S	30.75	1439.66	-0.2
Peripherin	tr|F1M7P4|F1M7P4_RAT	M.PSSASMSHHSSGLRSSISSTS Y.R	34.58	2252.01	-0.7
Peripherin	tr|F1M7P4|F1M7P4_RAT	M.PSSASMSHHSSGLRSSISSTS YRRT.F	17.07	2665.26	0.6
Peripherin	tr|F1M7P4|F1M7P4_RAT	M.PSSASMSHHSSGLRSSISSTS YRRTF.G	24.98	2812.33	0.6
Peripherin	tr|F1M7P4|F1M7P4_RAT	M.S(+42.01)HHSSGLRSSISSTSY RRT.F	19.93	2147.05	-3.2
Peroxiredoxin-2	sp|P35704|PRDX2_RAT	I.PLLADVTKSLSQNY.G	36.36	1547.82	-0.6
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	A.PIKVGDTIPSVEV.F	37.85	1352.76	-1
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	A.PIKVGDTIPSVEVF.E	39.62	1499.82	-1
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	C.SLAPNILSQL	27.78	1054.6	-3.6
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	L.LADPTGAFGKETDLLLDDSL VSLFGNRR.L	15.18	3019.56	-0.9
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	M.APIKVGDTIPSVEV.F	25.09	1423.79	-2
Peroxiredoxin-5 mitochondrial	sp|Q9R063|PRDX5_RAT	M.APIKVGDTIPSVEVF.E	18.59	1570.86	-1.6

Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	A.EWDDSVPKLHDQLAGK	24.78	1836.9	0.3
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	F.Q(-17.03)AEWDDSVPKLHDQLAGK	17.06	2018.97	-5.9
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	F.QAEWDDSVPKLHDQLAGK	21.9	2036	-0.6
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	G.PLSLQEVDEPPQHAL.R	25.08	1671.85	-0.7
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.DPGKLYTL.V	26.45	905.486	0.6
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.RVDYGGVTVDELGKVLTPTQVMNR.P	31.21	2646.38	2.2
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.RVDYGGVTVDELGKVLTPTQVMNRPSSISWDGLDPGKLYTL.V	17.84	4476.3	-1.8
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.VLTDPDAPSRKDPKFREWHH.F	18.42	2430.22	-1.9
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.VLTDPDAPSRKDPKFREWHHFL.V	19.55	2690.37	-1.2
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	L.VLTDPDAPSRKDPKFREWHHFLVV.N	30.73	2888.51	-1
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHAL.R	27.6	2613.27	-0.3
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALR.V	21.46	2769.37	-1.4
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRV.D	21.41	2868.44	-2.5
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRVDY.G	22.19	3146.53	1.1
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRVDYGGVTVDELGKVLTPTQVMNR.P	34.41	5241.64	-0.2
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRVDYGGVTVDELGKVLTPTQVMNRPSSISW.D	31.53	5898.95	0.9
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRVDYGGVTVDELGKVLTPTQVMNRPSSISWDGLDPGKLY.T	18.59	6857.43	-0.8
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQEVDEPPQHALRVDYGGVTVDELGKVLTPTQVMNRPSSISWDGLDPGKLYTL.V	23.82	7071.56	-3.2
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.KGNDISSGTVLSEY.V	18.25	1468.7	1.6
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.KGNDISSGTVLSEYVGSGPPKDTGLHR.Y	26.53	2770.39	-3.7
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.KGNDISSGTVLSEYVGSGPPKDTGLHRY.V	34.23	2933.45	-1.8
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	N.RPSSISWDGLDPGKLYTL.V	37.63	2004.03	-0.3
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	Q.AEWDDSVPKLHDQLAGK	19.96	1907.94	-1.4
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	R.PSSISWDGLDPGKLYTL.V	39.85	1847.93	0.1
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	V.DYGGVTVDELGKVLTPTQV.M	30.18	1990.03	-1.9
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	W.AGPLSLQEVDEPPQHAL.R	39	1799.91	-2.7

Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	W.DDSVPKLHDQLAGK	38.04	1521.78	-1.3
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSL.Q	29.15	1369.69	-1.4
Phosphatidylethanolamine-binding protein 1	sp|P31044|PEBP1_RAT	M.A(+42.01)ADISQWAGPLSLQE.V	20.82	1626.79	-2.6
Plasmolipin	sp|P47987|PLLP_RAT	M.A(+42.01)EFPSKVSTRT.S	45	1263.65	-1.2
Plasmolipin	sp|P47987|PLLP_RAT	M.A(+42.01)EFPSKVSTRTS.S	37.43	1350.68	-0.7
Plasmolipin	sp|P47987|PLLP_RAT	M.A(+42.01)EFPSKVSTRTSSPAQG.V	32.41	1790.88	-1.6
Plectin 4	tr|Q6S3A1|Q6S3A1_RAT	Q.EAGILSMEELQRLT.Q	34.9	1588.81	-1.7
Polymerase I and transcript release factor	sp|P85125|PTRF_RAT	G.TRLVPVERREKLK.T	21.88	1622.99	-0.4
Polymerase I and transcript release factor	sp|P85125|PTRF_RAT	K.TSRDKLRKSFTPDHVVYARSKTAVY.K	16.69	2924.56	-3.1
Polymerase I and transcript release factor	sp|P85125|PTRF_RAT	M(+42.01)EDVTLHIVERPYS.G	38.13	1729.83	-1
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	E.KTRLKTKENLEKTRHTLEK.R	23.7	2352.36	0.5
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	F.HVKKIREGEVEV.L	36.06	1421.8	-1.6
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	G.TRLVPVERREKLKTSRDKLR.K	20.12	2479.48	1.2
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	K.RSGLRRVDDFKKA.F	22.92	1546.87	-5.6
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	L.KTKENLEKTRHTLEK.R	27.87	1854.03	-1.7
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	L.KTKENLEKTRHTLEKR.M	26.57	2010.13	-0.3
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	L.SLLDKIIGAVDQI.Q	29.22	1383.8	-0.3
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	L.SLLDKIIGAVDQIQ.L	33.66	1511.86	-3.5
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	L.SLLDKIIGAVDQIQL.T	41.15	1624.94	0.1
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	M(+42.01)EDVTLHIVERPY.S	52.5	1642.8	0.2
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	S.GLRRVDDFKKA.F	22.68	1303.74	-1.8
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	T.RLVPVERREKLK.T	15.15	1521.95	0.2
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	V.ERREKLKTSRDKLRKSFTPDHV.V	21.05	2725.51	0.2
Polymerase I and transcript release factor	tr|G3V8L9|G3V8L9_RAT	V.RGSLERQAGQIKKLEV.N	17.05	1811.04	0.3
Polypyrimidine tract binding protein 1 isoform CRA_c	tr|D3ZB30|D3ZB30_RAT	M(+42.01)DGIVPDIAVGTKRGSDELF.S	21.96	2161.07	-8.4
Polyubiquitin	tr|Q63654|Q63654_RAT	E.STLHLVLRLRGG.M	15.72	1320.8	0.4
Polyubiquitin	tr|Q63654|Q63654_RAT	MQIFVKTL.T	28.15	978.557	-1.3
Polyubiquitin	tr|Q63654|Q63654_RAT	MQIFVKTLTGK.T	23.04	1264.72	-0.5
Prefoldin 1	tr|D3ZX38|D3ZX38_RAT	M.A(+42.01)ASVDLELKKAFTEL.Q	50.62	1675.9	-2.2
Prefoldin 1	tr|D3ZX38|D3ZX38_RAT	M.A(+42.01)ASVDLELKKAFTELQA.K	48.86	1875	-3.2
Prefoldin 1	tr|D3ZX38|D3ZX38_RAT	M.A(+42.01)ASVDLELKKAFTELQAKVIDTQQKVKL.A	23.45	3155.78	-9.7

Prohibitin	sp|P67779|PHB_RAT	M.A(+42.01)AKVFESIGKFGLA.L	47.28	1478.81	-2.7
Prohibitin	sp|P67779|PHB_RAT	M.A(+42.01)AKVFESIGKFGLALA.V	31.42	1662.93	-0.6
Proprotein convertase subtilisin/kexin type 1 inhibitor	tr|G3V6X7|G3V6X7_RAT	R.AVPRGEAAGAVQELARALAHLLEAERQE(-.98).R	20.87	2953.58	-6.5
Proprotein convertase subtilisin/kexin type 1 inhibitor	tr|G3V6X7|G3V6X7_RAT	R.AVPRGEAAGAVQELARALAHLLEAERQE.R	23.26	2954.57	-1.3
Proprotein convertase subtilisin/kexin type 1 inhibitor	tr|G3V6X7|G3V6X7_RAT	R.SLSAASAPLAETSTPLRL.R	43.72	1783.97	-3.2
Protachykinin-1	sp|P06767|TKN1_RAT	R.ALNSVAYERSAMQNYE.R	26.19	1844.84	-2.4
Protachykinin-1	sp|P06767|TKN1_RAT	R.DADSSIEKQVALLKALYGHGQIS.H	30.86	2442.28	-2.1
Protachykinin-1	sp|P06767|TKN1_RAT	R.DADSSIEKQVALLKALYGHGQISH.K	17.69	2579.33	-1.2
Proteasome subunit alpha type	tr|Q6P9V6|Q6P9V6_RAT	M(+42.01)FLTRSEYDRGVNTFSPEGRLFQVEY.A	32.61	3182.51	3.2
Proteasome subunit alpha type-5	sp|P34064|PSA5_RAT	Q.VEYAIEGHKLGSTAIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGC(-.98)(-1.01).A	19.28	5618.89	14.2
Proteasome subunit beta type-7	sp|Q9JHW0|PSB7_RAT	V.TPLELEVLEEIVQTMDTS	23.63	2046.01	-1.5
Protein Abracl	tr|D3ZSL2|D3ZSL2_RAT	M(+42.01)NVEHEVNLLVEEIHRL.G	42.05	2115.08	-0.3
Protein Acin1	tr|E9PST5|E9PST5_RAT	M.A(+42.01)ELEEVTLDGKPLQALRV.T	33.65	2022.1	-2.4
Protein Btf3l4	tr|D4A3I4|D4A3I4_RAT	M(+42.01)NQEKLAKLQAQVR.I	39.43	1697.92	0.9
Protein C8orf37 homolog	sp|Q6AY71|CH037_RAT	M.A(+42.01)KDLDELLDEVETKF.C	40.11	1805.89	-0.5
Protein Col6a3	tr|D4A115|D4A115_RAT	G.SVQELSELSETVLETLH.D	21.76	1912.96	-4.7
Protein DEK	sp|Q6AXS3|DEK_RAT	Y.NRPGTVSSLKKNVGQ.F	28.83	1583.87	-0.2
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	D.RPAPQFERASSKRVS.R	16.72	1714.92	-2.4
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	E.VKVEVREEK.S	18.77	1114.63	0
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	E.VKVEVREEKS.A	23.31	1201.67	-0.1
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	H.KETELAEEGED	23.46	1248.54	0.1
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	K.SSAEIQPAEQVRKDKEEEVIQDIQEEKLE.G	29.57	3396.69	-2.8
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	M.T(+42.01)TEVASASEVKKGSD.P	27.87	1549.75	-0.7
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	M.T(+42.01)TEVASASEVKKGSDPSGAD.A	29.11	1976.92	-0.2
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	M.T(+42.01)TEVASASEVKKGSDPSGADAHKEKAKEVVENE.Q	49.77	3468.69	-1.1
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	T.TTHITKTVKGGIS.E	31.98	1341.76	-1.1
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	E.GGAAKRETKEVQT.S	31.52	1373.73	-0.8
Protein Epb4.1l2	tr|D3ZAY2|D3ZAY2_RAT	E.GGAAKRETKEVQTSELK.A	17.88	1830.98	-1.6
Protein Hlcs	tr|D4AA38|D4AA38_RAT	F.NLETYRQNL.Q	22.06	1149.58	10.2

Protein Hmg1l1	tr|D3ZCR3|D3ZCR3_RAT	I.GDVAKKLGEM(+15.99).W	21.71	1062.54	-0.3
Protein Hmg1l1	tr|D3ZCR3|D3ZCR3_RAT	M.GKGDPKKPRGKMSSYAF.F	20.16	1852.96	1.6
Protein LOC100359642	tr|M0RCH6|M0RCH6_RAT	M.S(+42.01)VFGKLFGAGGGKAGKGGPTPQEA.I	23.37	2259.16	-0.4
Protein LOC100359642	tr|M0RCH6|M0RCH6_RAT	M.S(+42.01)VFGKLFGAGGGKAGKGGPTPQEAIQR.L	47.5	2656.41	-0.4
Protein LOC100359642	tr|M0RCH6|M0RCH6_RAT	M.S(+42.01)VFGKLFGAGGGKAGKGGPTPQEAIQRL.R	26.57	2769.49	-4.6
Protein LOC100360645	tr|G3V9Z2|G3V9Z2_RAT	G.MQIFVKTL.T	28.15	978.557	-1.3
Protein LOC100360645	tr|G3V9Z2|G3V9Z2_RAT	G.MQIFVKTLTGK.T	23.04	1264.72	-0.5
Protein LOC100360872	tr|M0R9F5|M0R9F5_RAT	L.LLPS(+79.97)GAGAEEIIGGVESIPHSRPYMAHLKITTEK(+42.01)GYVTFC(-1.01)GGFLISR.Q	18.67	5122.56	-4.3
Protein LOC100362339	tr|D4A6G6|D4A6G6_RAT	F.SRGSKSVARRVLQA.L	30.7	1513.88	-0.4
Protein LOC100362339	tr|D4A6G6|D4A6G6_RAT	M.PGVTVKDVNQQEFVRAL.A	40.93	1899.02	-0.9
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	A.ALGGNSNPSAKDIKKILDSV.G	15.53	2026.11	-2.5
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	L.AALGGNSNPSAKDIKKILDSV.G	15.71	2097.14	-0.8
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	L.NGKNIEDVIAQGVGKL.A	25.47	1653.9	-1
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	L.NGKNIEDVIAQGVGKLASVPAGGAVAV.S	18.52	2533.39	-1.8
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	MRYVASYLL.A	16.74	1114.58	-0.4
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	MRYVASYLLAAL.G	26.93	1369.74	-0.4
Protein LOC100362751	tr|D4A4D5|D4A4D5_RAT	V.GIEADDERLNKVISEL.N	22.6	1799.93	2.9
Protein LOC100911178	tr|D4A054|D4A054_RAT	H.LDFKHVVFGFVKDGMDTVRKIESFGSPK(+42.01)GSVSRRIC(-1.01)ITEC(-1.01)GQ.L	15.35	4712.37	14.6
Protein LOC100911178	tr|D4A054|D4A054_RAT	L.KHTGPGLLSM.A	40.92	1039.55	-0.1
Protein LOC100912106	tr|D4ADF5|D4ADF5_RAT	M.A(+42.01)DEELEALRKQRLAELQ.A	23.29	2053.08	-0.2
Protein LOC361414	tr|D3ZE32|D3ZE32_RAT	M.A(+42.01)KEGVEKAEETE.Q	32.74	1360.64	-1
Protein LOC361414	tr|D3ZE32|D3ZE32_RAT	M.A(+42.01)KEGVEKAEETEQMIEKETS.K	26.94	2307.08	0
Protein LOC686807	tr|M0R665|M0R665_RAT	I.KALVKPQAVKPKM(+15.99)PKGSSRKLSR.L	27.78	2549.53	-0.6
Protein Mapk1ip1	tr|D3ZNX9|D3ZNX9_RAT	T.PNMPLPELPRPYGA.P	24.11	1550.79	-2.8
Protein Mapk1ip1	tr|D3ZNX9|D3ZNX9_RAT	V.PSGPAGAPPMPGGPHSY.H	24.77	1575.71	-0.2
Protein Mapk1ip1	tr|D3ZNX9|D3ZNX9_RAT	V.PSGPAGAPPMPGGPHSYH	39.84	1712.77	4.6
Protein Mpo	tr|D3ZYH8|D3ZYH8_RAT	F.VRWLPAEYEDGISLPF.G	41.49	1890.95	-5.8
Protein Mrps36	tr|M0R776|M0R776_RAT	K.PMSQEEMEFIQRGGPE	37.13	1863.81	1.2
Protein Naca	tr|M0R9L0|M0R9L0_RAT	R.ALKNNSNDIVNAIMELTM	20.01	1989.99	-0.4
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.ANDPMIPAALLPFRG.S	24.58	1581.83	-0.9
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.ANDPMIPAALLPFRGSLIFQ.V	15.1	2170.16	-1.9

Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.PLRPVPADV.P	37.75	962.555	-0.6
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.PLRPVPADVPLPTTL.E	35.11	1584.92	5.5
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.PLRPVPADVPLPTTLEPRIVMGEET.C	18.62	2726.47	6.9
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	L.PLRPVPADVPLPTTLEPRIVMGEETC.Q	19	2829.48	-0.7
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	M.PGEAAGAELPLPEAGGSGSRTDLPCDAAIATILKGDQREPHGLTPGPSPLALTFL(-.98).S	23.48	5430.79	-10.8
Protein Nacad	tr|F1M6E5|F1M6E5_RAT	M.PGEAAGAELPLPEAGGSGSRTDLPCDAAIATILKGDQREPHGLTPGPSPLALTFL.S	22.65	5431.77	-0.1
Protein NDRG1	sp|Q6JE36|NDRG1_RAT	M.S(+42.01)RELHDVDLAEVKPLVEKGESITG.L	27.96	2662.38	-1.5
Protein NDRG1	sp|Q6JE36|NDRG1_RAT	M.S(+42.01)RELHDVDLAEVKPLVE.K	29.75	1990.04	-1.1
Protein NDRG1	sp|Q6JE36|NDRG1_RAT	M.S(+42.01)RELHDVDLAEVKPLVEKGES.I	22.46	2391.23	-2.8
Protein Ppp1r1c	tr|D3ZSW2|D3ZSW2_RAT	M(+42.01)EPNSPKKIQF.A	32.68	1359.69	-0.7
Protein Ppp1r1c	tr|D3ZSW2|D3ZSW2_RAT	M(+42.01)EPNSPKKIQFAV.P	19.25	1529.79	-0.6
Protein RGD1564606	tr|F1LT35|F1LT35_RAT	L.APDYDALDVANKIGII	27.3	1686.88	-0.6
Protein S100-A10	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNEGDKFKLNKT.E	33.72	3547.83	4.7
Protein S100-A10	sp|P05943|S10AA_RAT	C.NDYFVVHMKQKK	15.41	1535.79	-0.5
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQM(+15.99)EHAMET.M	16.18	1175.46	-1.5
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQM(+15.99)EHAMETM(+15.99).M	21.32	1322.49	-2.2
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQMEHAME.T	33.73	1058.42	-0.8
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQMEHAMETM.M	38.25	1290.5	-0.4
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQMEHAMETMML.T	23.48	1534.63	0.9
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQMEHAMETMMLT.F	25.79	1635.68	-3.5
Protein S100-A10	sp|P05943|S10AA_RAT	M.PSQMEHAMETMMLTF.H	19.84	1782.75	-1.9
Protein S100-A11	sp|Q6B345|S10AB_RAT	C.HESFLQTSQKRI	37.8	1472.77	2.5
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFH.K	41.02	1837.96	0.9
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHK.Y	42.55	1966.05	-2.4
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKY.S	47.43	2129.12	8.9
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYS.G	26.25	2216.15	0.5
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSG.N	43.98	2273.17	-1.5
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNE.G	24.77	2516.25	-0.8
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNEG.D	28.45	2573.28	-6.5
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNEGD.K	16.97	2688.3	-0.9
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNEGDKFKLNK.T	22.5	3446.78	0.1
Protein S100-A4	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGNEGDKFKLNKTEL.K	25.64	3789.96	-3.9

Protein S100-A8	sp|P50115|S10A8_RAT	Y.HNYSGIKGNHHAL.Y	53.57	1446.71	-1.4
Protein S100-A8	sp|P50115|S10A8_RAT	Y.HNYSGIKGNHHALY.R	48.55	1609.77	-2.9
Protein S100-A8	sp|P50115|S10A8_RAT	M.A(+42.01)TELEKALSNVIEVY.H	15.7	1719.89	-1.6
Protein S100-A9	sp|P05942|S10A4_RAT	M.A(+42.01)RPLEEALDVIVSTFHKYSGN.E	22.87	2387.21	-2.3
Protein S100-A9	sp|P50116|S10A9_RAT	M.A(+42.01)AKTGSQLERSISTIINVFHQY.S	47.57	2504.3	-0.5
Protein S100-A9	sp|P50116|S10A9_RAT	M.AAK(+42.01)TGSQLERSISTIINVFHQ.Y	17.91	2341.24	1.2
Protein S100-A9	sp|P50116|S10A9_RAT	M.A(+42.01)AKTGSQLERSISTIINV.F	25.52	1929.05	-3.2
Protein S100-A9	sp|P50116|S10A9_RAT	M.A(+42.01)AKTGSQLERSISTIINVFHQ.Y	32.99	2341.24	-0.6
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFH.Q	40.13	1742.89	-0.4
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQ.Y	43.28	1870.95	-0.9
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQY.S	54.64	2034.01	-3.2
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGRE.G	35.89	2463.21	-0.9
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREG.D	48.18	2520.23	-8
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREGD.K	45.74	2635.26	2
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREGDK(-.98).H	21.57	2762.37	-0.3
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREGDK.H	32.67	2763.35	-0.4
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREGDKH.K	20.22	2900.41	-1.7
Protein S100-B	sp|P04631|S100B_RAT	M.S(+42.01)ELEKAMVALIDVFHQYSGREGDKHKLKK.S	30.77	3397.78	-1.4
Protein Sec61b	tr|B2RZD1|B2RZD1_RAT	M.PGPTPSATNVGSSGRSPSKAVAAR.A	33.92	2251.17	-1.1
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	A.VEQNTLQEFLKLA	26.43	1531.82	-0.3
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	F.VEAVEQNTLQEFLKLA	24.75	1830.97	-1.5
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	L.QEFLKLA	15.61	847.48	-0.2
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	M.S(+42.01)GLRVYSTSVTGSREI.K	30.91	1752.9	-0.1
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	M.S(+42.01)GLRVYSTSVTGSREIKSQQSEVTRILDGKRIQY.Q	30.1	3883.06	1.1
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	M.S(+42.01)GLRVYSTSVTGSREIKSQQSEVTRILDGKRIQYQL.V	22.63	4124.2	0.8
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	M.S(+42.01)GLRVYSTSVTGSREIKSQQSEVTRILDGKRIQYQLVDISQDNALRDEMRTL.A	23.22	5981.1	-2.1
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	N.TLQEFLKLA	37.84	1061.61	-0.6
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	T.SVTGSREIKSQQSEVTRILDGKRIQYQLVDISQDNALRDEMRTL.A	23.27	5075.64	2.8
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	Y.STSVTGSREIKSQQSEVTR.I	25.09	2079.06	0
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	Y.STSVTGSREIKSQQSEVTRILDGKRIQ.Y	32.27	3002.61	-0.3
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	Y.STSVTGSREIKSQQSEVTRILDGKRIQY.Q	21.57	3165.67	0.5

Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	L.AGNPKATPPQIVNGDH.Y	25.92	1614.81	-1.8
Protein Sh3bgrl3	tr|B2RZ27|B2RZ27_RAT	V.EQNTLQEFLKLA	21.1	1432.76	-0.7
Protein Tex15	tr|D3ZYB8|D3ZYB8_RAT	G.SSVCVASNATK(+42.01)QV.V	15.46	1334.65	-11.4
Protein Tex15	tr|D3ZYB8|D3ZYB8_RAT	Y.G(+42.01)SSAINVNGTVQHT(+79.97)H.S	15.49	1642.71	8.6
Protein Thoc4	tr|D3ZXH7|D3ZXH7_RAT	M.A(+42.01)DKMDMSLDDIIKL.N	36.81	1648.81	-1.3
Protein Tmsbl1	tr|P97563|P97563_RAT	M.S(+42.01)DKPDLSEVETFDKSKLKKTNTEEKNTLPSKETIQQEKEYNQRS	35.83	5211.61	-5.9
Protein Tns1	tr|F1LN42|F1LN42_RAT	D.PNQPASAIVNFVSKVMLSAGQKR	27.3	2441.32	3.3
Protein Tns1	tr|F1LN42|F1LN42_RAT	F.DDHDPVDKIVLQKY.H	40.55	1683.85	5.1
Protein Tns1	tr|F1LN42|F1LN42_RAT	F.ETTEESLRNYYEQW.G	21.2	1846.8	-3.1
Protein Tsc22d2	tr|D3ZDW3|D3ZDW3_RAT	A.M(+42.01)DLVKSHLMYAVREEVEVLKEQI.K	33.73	2800.45	-1.9
Protein Tubb4a	tr|B4F7C2|B4F7C2_RAT	G.GGTGSGMGTLLISKIREEFPDRIMNTF.S	41.82	2926.47	-6
Protein Txndc17	tr|B0K010|B0K010_RAT	M.A(+42.01)TFEEVSVLGFEEFDKAVKE.H	41.89	2315.12	-0.9
Protein Txndc17	tr|B0K010|B0K010_RAT	M.A(+42.01)TFEEVSVLGFEEFDKAVKEHQGKTIF.A	35.46	3126.55	-2.7
Protein Txndc17	tr|B0K010|B0K010_RAT	M.A(+42.01)TFEEVSVLGFEEFDKAVKEHQGKTIFA.F	29.86	3197.59	-3.1
Protein Zmynd15	tr|D4A1E1|D4A1E1_RAT	S.SLPRLQSLRVP.A	23.5	1264.76	-4.4
Purkinje cell protein 4	sp|P63055|PCP4_RAT	M.S(+42.01)ERQSAGATNGKDKTSGDNDGQKKVQEEFDIDMDAPETERAAVAIQSQFRKFQKKKAGSQS	21.69	6714.26	-0.6
Purkinje cell protein 4	sp|P63055|PCP4_RAT	Q.SQFRKFQKKKAGSQS	32.87	1753.96	-0.6
RCG23287 isoform CRA_a	tr|Q6PED0|Q6PED0_RAT	E.STLHLVLRLRGG.A	15.72	1320.8	0.4
RCG45400	tr|G3V7C6|G3V7C6_RAT	E.ATGGKYVPRAVLVDLEPGTMDSVR.S	35.1	2530.32	0.2
RCG45400	tr|G3V7C6|G3V7C6_RAT	MREIVHLQA.G	31.73	1095.59	-1.6
Receptor expression-enhancing protein 5	sp|B2RZ37|REEP5_RAT	A.TVNLLGDEKKST	24.17	1303.7	-0.8
Reticulon-4	tr|F1LQN3|F1LQN3_RAT	D.SPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERKPAAGLS.A	19.99	5930.63	2.4
Reticulon-4	sp|Q9JK11|RTN4_RAT	M.KESLTEVSETVAQHKEERLS.A	26.28	2299.17	-0.3
RGD1562416 protein	tr|B0BN59|B0BN59_RAT	M.A(+42.01)GAAEDVRLLFGAGVRA.A	26.79	1713.92	-1.2
Ribosomal protein S5 isoform CRA_b	tr|B0BN81|B0BN81_RAT	Y.AIKKKDELERVAKSNR	40.33	1884.09	-2.2
RNA-binding motif single-stranded-interacting protein 1	sp|Q5PQP1|RBMS1_RAT	L.PLSMDEQELENMLKPFGQVISTRVL.R	40.81	2873.47	0.4
S100 calcium binding protein A6	tr|B2GVB1|B2GVB1_RAT	A.FLGALALIYNEALK	35	1534.88	3
S100 calcium binding protein A6	tr|B2GVB1|B2GVB1_RAT	E.YVAFLGALALIYNEALK	28.44	1868.04	1
Scg2 protein	tr|Q6P7R4|Q6P7R4_RAT	R.Q(-17.03)APYDNLNDKDQELGEYLARMLVKYPELMNTNQL.K	30.43	4008.92	-5.8

Scg2 protein	tr|Q6P7R4|Q6P7R4_RAT	R.TNEIVEEQYTPQSLATLESVFQELGKLTGPSNQ.K	27.94	3649.8	-0.6
Serine/arginine-rich splicing factor 2	sp|Q6PDU1|SRSF2_RAT	M.S(+42.01)YGRPPPDVEGMTSLKVDNL.T	47.24	2216.08	-2.4
Serine/arginine-rich splicing factor 2	sp|Q6PDU1|SRSF2_RAT	M.S(+42.01)YGRPPPDVEGMTSLKVDNLTY.R	45.65	2480.19	-3.2
Serine/arginine-rich splicing factor 2	sp|Q6PDU1|SRSF2_RAT	S.R(+42.01)S(+79.97)RSRSRSRSRSRYSRSKSRSRTRS(+79.97)RSR.S	15.87	3685.86	-3.2
Serum albumin	sp|P02770|ALBU_RAT	A.TEGPNLVARSKEALA	36.09	1554.84	-3.2
Serum albumin	sp|P02770|ALBU_RAT	F.AEITKLATDVTKINKEC(-1.01)CHGDLLEC(-1.01)ADDRAELAK.Y	21.75	3713.81	1.9
Serum albumin	sp|P02770|ALBU_RAT	F.AKTC(-1.01)VADENAENC(-1.01)DKSIHT.L	15.13	2045.88	0
Serum albumin	sp|P02770|ALBU_RAT	F.HSDICTLPDKEKQIKKQTA.L	31.93	2182.14	0.2
Serum albumin	sp|P02770|ALBU_RAT	F.LGHYLHEVARRHPY.F	38.32	1746.91	1
Serum albumin	sp|P02770|ALBU_RAT	F.PNAEFAEITKL.A	36.65	1231.64	-0.1
Serum albumin	sp|P02770|ALBU_RAT	L.AEFQPLVEEPKNLVKTNCEL.Y	18.77	2300.17	-0.2
Serum albumin	sp|P02770|ALBU_RAT	L.AELVKHKPKATEDQLKT.V	37.23	1935.08	0.2
Serum albumin	sp|P02770|ALBU_RAT	L.AELVKHKPKATEDQLKTV.M	23.38	2034.15	-0.4
Serum albumin	sp|P02770|ALBU_RAT	L.ATDVTKINKEC(-1.01)C(-1.01)HGDLLECADDRAELAK.Y	28.22	3058.42	-0.2
Serum albumin	sp|P02770|ALBU_RAT	L.GEYGFQNAVLVR.Y	26.3	1351.69	0.6
Serum albumin	sp|P02770|ALBU_RAT	L.GHYLHEVARRHPY.F	35.53	1633.82	0.4
Serum albumin	sp|P02770|ALBU_RAT	M.SQRFPNAEFAEITK.L	38.01	1636.82	-4.2
Serum albumin	sp|P02770|ALBU_RAT	R.EAHKSEIAHRF.K	32.88	1323.67	0.3
Serum albumin	sp|P02770|ALBU_RAT	R.EAHKSEIAHRFKDLGEQH.F	26.51	2131.06	-6.3
Serum albumin	sp|P02770|ALBU_RAT	R.EAHKSEIAHRFKDLGEQHF.K	27.81	2278.12	-0.1
Serum albumin	sp|P02770|ALBU_RAT	R.EAHKSEIAHRFKDLGEQHFKGLV.L	20.17	2675.39	-0.4
Serum albumin	sp|P02770|ALBU_RAT	R.FPNAEFAEITKL.A	34.54	1378.71	-3.7
Serum albumin	sp|P02770|ALBU_RAT	V.DETYVPKEF.K	25.66	1126.52	-1.6
Serum albumin	sp|P02770|ALBU_RAT	V.DETYVPKEFKAET.F	18.6	1555.74	-1.5
Serum albumin	sp|P02770|ALBU_RAT	Y.EEHIKLVQEVTDF.A	32.12	1585.8	-0.8
Serum albumin	sp|P02770|ALBU_RAT	Y.EKLGEYGFQNAVLVR.Y	38.33	1721.91	0.1
Serum albumin	sp|P02770|ALBU_RAT	Y.EYSRRHPDYSVS.L	42.68	1494.69	-1.3
Serum albumin	sp|P02770|ALBU_RAT	Y.LSAILNRLCVLHEKTPV.S	28.88	1905.09	0.3
Serum albumin	sp|P02770|ALBU_RAT	Y.TQKAPQVSTPTLVEA.A	43.8	1568.84	4.6
Serum deprivation-response protein	sp|Q66H98|SDPR_RAT	M.G(+42.01)EDAAQAEKFQHPNT.D	46.07	1683.75	-2.3
Stathmin	sp|P13668|STMN1_RAT	A.KLERLREKDKHVEEVRKNKESKDPADETEAD	28.66	3720.9	-0.3
Stathmin	sp|P13668|STMN1_RAT	E.RLREKDKHVEEVRKNKESKDPADETEAD	32.92	3350.68	-2.6
Stathmin	sp|P13668|STMN1_RAT	E.RLREKDKHVEEVRKNKESKDPADETEAD(-.98)	29.29	3349.7	-7.3
Stathmin	sp|P13668|STMN1_RAT	F.SKMAEEKLTHKMEANKEN.R	49.17	2117.02	-0.3

Stathmin	sp|P13668|STMN1_RAT	K.LERLREKDKHVEEVRKNKESKDPADETEAD	25.88	3592.81	-0.7
Stathmin	sp|P13668|STMN1_RAT	L.REKDKHVEEVRKNKESKDPADETEAD	38.55	3081.5	-1.4
Stathmin	sp|P13668|STMN1_RAT	M.A(+42.01)SSDIQVKELEKRASGQ.A	18.46	1886.97	-0.7
Stathmin	sp|P13668|STMN1_RAT	M.A(+42.01)SSDIQVKELEKRASGQA.F	52.95	1958.01	-1.4
Stathmin	sp|P13668|STMN1_RAT	M.A(+42.01)SSDIQVKELEKRASGQAF.E	39.23	2105.08	4.5
Stathmin	sp|P13668|STMN1_RAT	M.A(+42.01)SSDIQVKELEKRASGQAFEL.I	44.3	2347.2	-1.2
Stathmin	sp|P13668|STMN1_RAT	M.A(+42.01)SSDIQVKELEKRASGQAFELI.L	15.46	2460.29	0
Stathmin	sp|P13668|STMN1_RAT	M.AAKLERLREKDKHVEEVRKNKESKDPADETEAD	31.27	3862.98	-0.7
Stathmin	sp|P13668|STMN1_RAT	M.AAKLERLREKDKHVEEVRKNKESKDPADETEAD(-.98)	26.54	3861.99	-2.7
Stathmin	sp|P13668|STMN1_RAT	M.ASSDIQVK(+42.01)ELEKRASGQAFELILSPR.S	15.37	2913.56	-1.4
Stathmin	sp|P13668|STMN1_RAT	R.EKDKHVEEVRKNKESKDPADETEAD	40.2	2925.4	-1.7
Stathmin	sp|P13668|STMN1_RAT	R.EKDKHVEEVRKNKESKDPADETEAD(-.98)	25.72	2924.41	-7.8
Stathmin	sp|P13668|STMN1_RAT	R.LREKDKHVEEVRKNKESKDPADETEAD	36.17	3194.58	2.7
Syntenin-1	sp|Q9JI92|SDCB1_RAT	M.S(+42.01)LYPSLEDLKVDKVIQAQTA.S	33.01	2259.2	-4.9
Thioredoxin	sp|P11232|THIO_RAT	A.AGDKLVVVDF.S	19.54	1061.58	-0.4
Thioredoxin	sp|P11232|THIO_RAT	M.VKLIESKEAFQEAL.A	42.42	1603.88	-0.9
Thioredoxin	sp|P11232|THIO_RAT	M.VKLIESKEAFQEALAAAGDKL.V	40.74	2230.22	-1.8
Thioredoxin	sp|P11232|THIO_RAT	M.VKLIESKEAFQEALAAAGDKLVVVDF.S	16.46	2789.52	4.8
Thymosin beta-10	sp|P63312|TYB10_RAT	D.KPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS	23.79	4705.45	-2.5
Thymosin beta-10	sp|P63312|TYB10_RAT	E.TIEQEKRSEIS	34.65	1318.67	-1.4
Thymosin beta-10	sp|P63312|TYB10_RAT	F.DKAKLKKTETQEKNTLPT.K	16.29	2072.15	-5.6
Thymosin beta-10	sp|P63312|TYB10_RAT	K.LKKTETQEKNTLPTKETIEQEKRSEIS	64.05	3187.69	-2
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDM(+15.99)GEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS	50.65	4949.52	-2.7
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIAS(+79.97)FDKAKLKKTETQEKNTLPTKETIEQEKRSEIS	22.28	5013.49	0.6
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLKKTETQEKN.T	58.73	2963.49	-0.7
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLKKTETQEKNTLPT(+79.97)KET(+79.97)IE.Q	21.07	4135.97	-7.6
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLKKTETQEKNTLPTK(+42.01)ETIEQEKRSEIS(-.98)	30.65	4974.55	-0.3
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSE.I	17.38	4733.41	-12.1

Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS	50.69	4933.52	-3.4
Thymosin beta-10	sp|P63312|TYB10_RAT	M.ADK(+42.01)PDMGEIASFDKAKLKKTE.T	17.02	2363.2	-0.7
Thymosin beta-10	sp|P63312|TYB10_RAT	M.ADK(+42.01)PDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEKRSEIS(-.98)	23.91	4932.54	-4.7
Thymosin beta-10	sp|P63312|TYB10_RAT	N.TLPTKETIEQEKRSE.I	20.36	1787.93	-0.2
Thymosin beta-10	sp|P63312|TYB10_RAT	N.TLPTKETIEQEKRSEIS	47.49	1988.04	-1.3
Thymosin beta-10	sp|P63312|TYB10_RAT	T.KETIEQEKRSEIS	34.4	1575.81	0.1
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAK.L	46.9	1763.84	-1.9
Thymosin beta-10	sp|P63312|TYB10_RAT	M.A(+42.01)DKPDMGEIASFDKAKLK.K	36.95	2005.02	-4.1
Thymosin beta-4	sp|P62329|TYB4_RAT	D.KPDMAEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	18.25	4716.42	-2.1
Thymosin beta-4	sp|P62329|TYB4_RAT	E.KFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	23.66	3803	0.6
Thymosin beta-4	sp|P62329|TYB4_RAT	E.KNPLPSKETIEQEKQAGES	54.08	2112.07	0
Thymosin beta-4	sp|P62329|TYB4_RAT	E.TQEKNPLPSKETIEQEKQAGES	43.95	2470.22	-0.8
Thymosin beta-4	sp|P62329|TYB4_RAT	F.DKSKLKKTETQEKNPLPSKETIEQEKQAGES	59.29	3527.83	-2.7
Thymosin beta-4	sp|P62329|TYB4_RAT	K.KTETQEKNPLPSKETIEQEKQAGES	66.79	2828.4	-2.3
Thymosin beta-4	sp|P62329|TYB4_RAT	K.LKKTETQEKNPLPSKETIEQEKQAGES	54.94	3069.58	-3.8
Thymosin beta-4	sp|P62329|TYB4_RAT	K.NPLPSKETIEQEKQAGES	36.96	1983.97	-2.1
Thymosin beta-4	sp|P62329|TYB4_RAT	K.SKLKKTETQEKNPLPSKETIEQEKQAGES	29.72	3284.71	-2.3
Thymosin beta-4	sp|P62329|TYB4_RAT	K.TETQEKNPLPSKETIEQEKQAGES	46.74	2700.31	0.6
Thymosin beta-4	sp|P62329|TYB4_RAT	M(+42.01)(+15.99)SDKPDM(+15.99)AEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	15.87	5123.52	3.8
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDM(+15.99)AEIEK.F	30.18	1319.59	-0.2
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDM(+15.99)AEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	26.71	4976.48	-4.3
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEK.F	32.77	1303.6	-0.5
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKF.D	35.66	1450.66	-1.4
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFD.K	31.18	1565.69	-0.5
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDK.S	41.28	1693.79	-1.1
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSK.L	43.42	1908.91	-1.4
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLK.K	28.19	2150.09	0.4
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKK.T	33.38	2278.19	0.2
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTE.T	35.99	2508.28	-0.9
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTET.Q	39.31	2609.33	-0.6

Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTETQE.K	32.19	2866.43	-0.6
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTETQEKNPLPS.K	18.84	3502.79	-1.3
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTETQEKNPLPSK(+42.01)ETIEQEKQAGES(-.98)	27.98	5001.51	-1.2
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	28.94	4960.49	2.9
Thymosin beta-4	sp|P62329|TYB4_RAT	M.S(+42.01)DKPDMAEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES(-.98)	22.53	4959.5	-8.2
Thymosin beta-4	sp|P62329|TYB4_RAT	M.SDK(+42.01)PDMAEIEKFDKS(+79.97)KLKKTETQEKNPLPSKETIEQEKQAGES	21.32	5040.45	1
Thymosin beta-4	sp|P62329|TYB4_RAT	M.SDK(+42.01)PDMAEIEKFDKSKLKK(-.98).T	21	2277.2	-14.9
Thymosin beta-4	sp|P62329|TYB4_RAT	M.SDK(+42.01)PDMAEIEKFDKSKLKKTETQEKNPLPSK(+42.01)ETIEQEKQAGES	16.67	5002.5	0.7
Thymosin beta-4	sp|P62329|TYB4_RAT	M.SDKPDMAEIEKFDKS(+79.97)KLKKTETQEKNPLPSKETIEQEKQAGES	15.33	4998.44	5.1
Thymosin beta-4	sp|P62329|TYB4_RAT	M.SDKPDMAEIEKFDKSKLKKTETQEKNPLPSKETIEQEKQAGES	25.78	4918.48	0.3
Thymosin beta-4	sp|P62329|TYB4_RAT	N.PLPSKETIEQEKQAGES	57.99	1869.93	-2.1
Thymosin beta-4	sp|P62329|TYB4_RAT	T.QEKNPLPSKETIEQEKQAGES	29.85	2369.17	-0.4
Thymosin beta-4	sp|P62329|TYB4_RAT	F.DKSKLKKTETQEKNPLPSKET.I	36.19	2428.32	3.5
Transforming growth factor beta-1-induced transcript 1 protein	sp|Q99PD6|TGFI1_RAT	M(+42.01)EDLDALLSDLETTTSHMSRLG.A	50.28	2476.15	-3.1
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	A.RGGNIGDGGGAADRVINQILTEMDGM.S	23.09	2616.24	-0.2
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	A.RGGNIGDGGGAADRVINQILTEMDGMSTKKNVFIIGA.T	19.76	3774.91	2.3
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	A.TNRPDIIDPAILRPGRLDQLIYIPLPDEKSRVAILKA.N	15.51	4179.39	-0.4
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	C.QANFISIKGPELL.T	30.5	1428.8	-0.3
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	L.PLRHPALFKAIGVKPPRGI.L	41.01	2066.26	-1.9
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	L.SQSNPSALRETVVEVPQVTWEDIGGLEDVKRELQEL.V	18.66	4050.05	-2.8
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	L.VQYPVEHPDKFLKF.G	31.02	1745.91	-2.9
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	M.A(+42.01)SGADSKGDDLSTAILKQ.K	38.38	1817.9	-4

Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	R.PDIIDPAILRPGRLDQLIYI.P	28.18	2290.3	-3
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	V.PQVTWEDIGGLEDVKRELQEL.V	28.34	2453.24	-2.1
Transitional endoplasmic reticulum ATPase	sp|P46462|TERA_RAT	Y.PVEHPDKFLKF.G	45.18	1355.72	-1.3
Transmembrane protein 41B	sp|Q5FVN2|TM41B_RAT	Y.MLSYLVGRP.V	24.92	1034.56	5.4
Tropomyosin alpha-1 chain	sp|P04692|TPM1_RAT	M(+42.01)DAIKKKMQMLK.L	25.78	1505.81	0
Tropomyosin alpha-3 chain	sp|Q63610|TPM3_RAT	M.A(+42.01)GSTTIEAVKRKIQVLQ.Q	26.03	1883.08	-0.3
Tropomyosin alpha-4 chain	sp|P09495|TPM4_RAT	I.QEMQLKEAKHIAEEADRKYEEVARKLV.I	29.66	3240.69	-0.5
Tropomyosin alpha-4 chain	sp|P09495|TPM4_RAT	M.A(+42.01)GLNSLEAVKRKIQA.L	16.95	1638.94	0
Tropomyosin alpha-4 chain	sp|P09495|TPM4_RAT	M.A(+42.01)GLNSLEAVKRKIQALQ.Q	27.08	1880.08	0.2
Troponin I fast skeletal muscle	tr|F8WG17|F8WG17_RAT	Y.DMEVKVQKSSKELEDMNQK.L	50.27	2265.1	-0.3
Troponin I fast skeletal muscle	sp|P27768|TNNI2_RAT	F.DLRGKFKRPPLRRVR.M	28.22	1893.16	-1.4
Troponin I fast skeletal muscle	sp|P27768|TNNI2_RAT	L.FDLRGKFKRPPLRRVR.M	32	2040.23	-0.1
Troponin I fast skeletal muscle	sp|P27768|TNNI2_RAT	M.G(+42.01)DEEKRNRAITARRQHLKSV.M	17.15	2405.3	0
Troponin I fast skeletal muscle	sp|P27768|TNNI2_RAT	W.RKNIEEKSGMEGRKKMFESES	29.02	2499.22	0
Troponin I fast skeletal muscle	tr|F8WG17|F8WG17_RAT	C.KQLHAKIDAAEEEK.Y	36.94	1608.85	0.2
Troponin I fast skeletal muscle	tr|F8WG17|F8WG17_RAT	M.SADAMLKALLGSKHK.V	26.62	1568.87	0.6
Troponin I fast skeletal muscle	tr|F8WG17|F8WG17_RAT	Y.DMEVKVQKSSKELEDMNQKL.F	31.79	2378.18	1
Troponin T fast skeletal muscle	sp|P09739|TNNT3_RAT	L.RSRIDQAQKHSKKAGATAKGKVGGRWK	25.23	2948.66	-0.3
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	A.TYAPVISAEKAY.H	31.12	1311.67	0.3
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	A.VFVDLEPTVIDEVR.T	17.09	1629.86	-0.7
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	D.LEPTVIDEVR.T	17.46	1169.63	-0.3
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	F.HPEQLITGKEDAANN.Y	33.32	1635.79	-0.6
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	F.HPEQLITGKEDAANNY.A	50.78	1798.85	-1.8
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	F.VDLEPTVIDEVR.T	34.27	1383.72	0.7
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	G.AGKHVPRAVFVDLEPTVIDEVR.T	29.37	2446.33	-3.2
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	M.LSNTTAIAEAWARLD.H	19.38	1630.83	-3.5
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	P.RAVFVDLEPTVIDEVR.T	23.53	1857	-1
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Q.VSTAVVEPYNSILTTHTT.L	43.92	1931.98	-0.7
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	R.AVFVDLEPTVIDEVR.T	25.91	1700.9	-0.6
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	R.FDGALNVDLTEFQTNLVPYPRIHFPLA.T	20.16	3086.59	-3.8
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	T.YAPVISAEKAYHEQLS.V	36.3	1804.9	-0.6

Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	V.P(+42.01)KDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPT(+79.97)VVPGGDLAKVQRAVC.M	18.16	5731.98	4.3
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.APVISAEKAYHEQ.L	24.57	1441.72	-1.5
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.APVISAEKAYHEQLS.V	47.98	1641.84	-0.8
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.ARGHYTIGKEIIDLVLDRIRKL.A	38.64	2578.51	-0.6
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.QPPTVVPGGDLAKVQR.A	26.92	1660.93	-0.2
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.QPPTVVPGGDLAKVQRA.V	33.97	1731.96	-1.4
Tubulin alpha-1A chain	sp|P68370|TBA1A_RAT	Y.RGDVVPKDVNAAIATIKTKRTIQ.F	27.38	2493.44	-5
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	A.TYAPVISAEKAYHEQ.L	38.06	1705.83	-0.9
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	A.TYAPVISAEKAYHEQL.S	39.56	1818.92	-1.2
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	A.TYAPVISAEKAYHEQLS.V	41.36	1905.95	-1
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	A.TYAPVISAEKAYHEQLSVAEITN.A	18.2	2533.27	-1.1
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	D.IERPTYTNLNR.L	28.85	1375.72	-1.6
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	E.KDYEEVGVDSVEGEGEEEGEEY	35.47	2475.99	-0.8
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	L.VPYPRIHFPLA.T	24.25	1308.73	-1.3
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	N.SILTTHTTLEH.S	30.56	1251.65	-1.1
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	R.TGTYRQLFHPEQLITGKEDAANNY.A	25.65	2765.34	-1.7
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	S.AEKAYHEQLSVAEITN.A	17.1	1801.88	-2.3
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	T.YAPVISAEKAYHEQL.S	33.77	1717.87	-0.2
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	V.FVDLEPTVIDEVR.T	36.11	1530.79	-0.1
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	Y.Q(-17.03)PPTVVPGGDLAKVQR.A	23.32	1643.9	-1
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	Y.RQLFHPEQLITGKEDAANN.Y	20.48	2180.1	-4.3
Tubulin alpha-1B chain	sp|Q6P9V9|TBA1B_RAT	Y.RQLFHPEQLITGKEDAANNY.A	36.07	2343.16	-1.8
Tubulin alpha-3 chain	sp|Q68FR8|TBA3_RAT	Y.RQLFHPEQLITGKEDAANNYARGHYTIGK(+42.01)EIVDLVLDRIRK(+42.01)LADLC(-1.01)T.G	18.43	5475.86	7.2
Tubulin alpha-8 chain	sp|Q6AY56|TBA8_RAT	R.IRKLTDACS(+79.97)GLQGFLIFHS(+79.97)FGGGTGSGFTSLLMERL.S	15.95	3975.88	-9.3
Tubulin alpha-8 chain	sp|Q6AY56|TBA8_RAT	R.IRKLT(+79.97)DACS(+79.97)GLQGFLIFHSFGGGTGSGFTSLLMERL.S	19.32	3975.88	-1.2
Tubulin alpha-8 chain	sp|Q6AY56|TBA8_RAT	Y.APIVSAEKAYHEQLS(-.98).V	18.51	1640.85	2
Tubulin beta-2A chain	sp|P85108|TBB2A_RAT	F.SVMPSPKVSDTVVEPY.N	32.74	1733.85	-2
Tubulin beta-2A chain	sp|P85108|TBB2A_RAT	F.SVMPSPKVSDTVVEPYNA.T	25.44	1918.93	-5.3
Tubulin beta-2A chain	sp|P85108|TBB2A_RAT	F.SVMPSPKVSDTVVEPYNATLSVHQL.V	22.01	2697.37	-1.3
Tubulin beta-2A chain	sp|P85108|TBB2A_RAT	L.T(+42.01)QQMFDSKNM(+15.99)MAACDPRHGRYLTVAAIFRGR(-.98).M	15.77	3627.74	-11.8
Tubulin beta-2A chain	sp|P85108|TBB2A_RAT	W.AKGHYTEGAELVDSVLDVVRKE.S	15.38	2414.24	-8.8

Tubulin beta-3 chain	sp|Q4QRB4|TBB3_RAT	G.GGTGSGMGTLLISK.V	39.32	1277.66	-1.5
Tubulin beta-3 chain	sp|Q4QRB4|TBB3_RAT	H.SLGGGTGSGMGTLLISK.V	36.81	1534.8	-1.4
Tubulin beta-3 chain	sp|Q4QRB4|TBB3_RAT	W.AKGHYTEGAELVDSVLDVVRKE.C	15.38	2414.24	-8.8
Tubulin beta-3 chain	sp|Q4QRB4|TBB3_RAT	W.AKGHYTEGAELVDSVLDVVRKEC(-1.01)ENC(-1.01)D.C	24.14	2976.36	-2.1
Tubulin beta-4B chain	sp|Q6P9T8|TBB4B_RAT	A.DLRKLAVNMVPFPRLHF.F	48.74	2052.15	-1.2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	A.DLRKLAVNMVPFPRLHFF.M	43.39	2199.21	0.2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	E.ATGGKYVPRAILVDLEPGTMDSVR.S	31.27	2544.34	0.8
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.GQSGAGNNWAKGHYTEGAELVDSVLDVVR.K	34.36	3028.46	-9.3
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.SVVPSPKVSDTVVEPYN.A	46.62	1815.93	-1.4
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.SVVPSPKVSDTVVEPYNA.T	28.71	1886.96	-1.9
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.SVVPSPKVSDTVVEPYNATL.S	34.22	2101.09	-1.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.SVVPSPKVSDTVVEPYNATLSVHQL.V	20.88	2665.4	-3.9
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.SVVPSPKVSDTVVEPYNATLSVHQLVE.N	16.78	2893.51	-4.7
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.VFGQSGAGNNWAKGHYTEGAELVDSVLDVV.R	38.37	3118.5	0
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	F.VFGQSGAGNNWAKGHYTEGAELVDSVLDVVR.K	34.37	3274.6	-1.7
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	G.GGTGSGMGTLLISK.I	39.32	1277.66	-1.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	G.GGTGSGMGTLLISKI.R	15.93	1390.75	-8.3
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	G.GGTGSGMGTLLISKIREEYPDRIMNTF.S	47.07	2942.46	-0.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	G.SGMGTLLISKIREEYPDRIMNTF.S	45.13	2670.35	-1.9
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	H.SLGGGTGSGMGTLLISK.I	36.81	1534.8	-1.4
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	H.SLGGGTGSGMGTLLISKIREEYPDRIMNTF.S	21.15	3199.6	-0.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	H.YTEGAELVDSVLDVVR.K	28.92	1763.89	-0.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	K.IREEYPDRIMNT.F	17.87	1535.74	-2.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	K.LTTPTYGDLNHLVS.A	19.07	1529.77	0.2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	K.LTTPTYGDLNHLVSATMSGVT.T	24.78	2177.07	-3.1
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	K.LTTPTYGDLNHLVSATMSGVTT.C	34.46	2278.12	-4.1
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	L.KLTTPTYGDLNHLVSA.T	33.79	1728.9	0.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	L.THSLGGGTGSGMGTLLISKIREEYPDRIMNTF.S	44.48	3437.71	2.8
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	L.TTPTYGDLNHLVSATMSGVTT.C	36.61	2165.03	0.7
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	L.TVPELTQQVFDAKNM.M	30.59	1719.85	-0.2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	M.REIVHIQA.G	21.88	964.545	0
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	MREIVHI.Q	17.29	896.49	0.3
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	MREIVHIQA.G	31.73	1095.59	-1.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	MREIVHIQAGQ(-.98).C	26.9	1279.68	-0.5

Tubulin beta-5 chain	sp|P69897|TBB5_RAT	MREIVHIQAGQ.C	22.46	1280.67	1
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	R.AILVDLEPGTMDSVR.S	37.54	1614.83	-2.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	R.GRMSMKEVDEQMLNVQNK(+42.01)NSS(+79.97)YFVEWIPNNVKT.A	15.14	4036.85	6.9
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	R.SGPFGQIFRPDNF.V	34.7	1480.71	-2.3
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	R.SGPFGQIFRPDNFVF.G	29.42	1726.85	-0.1
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	R.SGPFGQIFRPDNFVFGQSGAGNNW.A	40.71	2598.2	-0.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	S.GPFGQIFRPDNF.V	34.73	1393.68	1.6
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	T.HSLGGGTGSGMGTLLISKIREEYPDRIMNT.F	21.38	3189.59	-2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	T.HSLGGGTGSGMGTLLISKIREEYPDRIMNTF.S	22.14	3336.66	-2.1
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	T.TPTYGDLNHLVSATMSGVTT.C	39.11	2063.98	-1.7
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	V.RSGPFGQIFRPDNFVFGQSGAGNNW.A	18.41	2754.31	-3.8
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVV.R	19.89	2001.01	-0.4
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVVR.K	28.02	2157.11	-1.7
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVVRKE.A	15.38	2414.24	-8.8
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVVRKEAES.C	26.27	2701.36	8.2
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVVRKEAESC(-1.01)DC(-1.01)L.Q	22	3133.47	-2.4
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	W.AKGHYTEGAELVDSVLDVVRKEAESCD.C	23.38	2919.39	-0.5
Tubulin beta-5 chain	sp|P69897|TBB5_RAT	Y.TEGAELVDSVLDVVR.K	19.32	1600.83	-4.6
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	F.KKALEELATKR.F	34.68	1285.77	0.3
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	F.SKVKAKSARVINYEE.F	17.66	1720.95	-0.9
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	M.A(+42.01)ASTDIAGLEESFRKFA.I	27.1	1853.92	1.4
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	M.A(+42.01)ASTDIAGLEESFRKFAI.H	27.68	1967	-2.1
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	M.A(+42.01)ASTDIAGLEESFRK.F	39.18	1635.81	-2.6
Tubulin polymerization-promoting protein family member 3	sp|Q5PPN5|TPPP3_RAT	M.A(+42.01)ASTDIAGLEESFRKF.A	44.7	1782.88	0.2
Tyrosine-protein kinase receptor	tr|G3V6A0|G3V6A0_RAT	E.GRHIYIY.V	20.74	920.487	9.9
Ubiquitin A-52 residue ribosomal protein fusion product 1	tr|Q6P7R7|Q6P7R7_RAT	E.STLHLVLRLRGG.I	15.72	1320.8	0.4
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	C.GTIGLIHAV.A	28.26	879.518	-0.9

Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	F.PLTAQHENFRKKQIEEL.K	19.6	2080.11	-0.5
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	F.PLTAQHENFRKKQIEELKGQEVSPKVYFM.K	16.7	3473.81	0.5
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	L.KPMEINPEMLNKVLAKLGVAGQWRF.A	33.99	2868.55	-4.1
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	M(+15.99)QLKPMEINPEMLNKVLAKLGVAGQWRF.A	23.97	3256.73	-6.4
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	MQLKPMEINPEML.N	33.78	1572.77	-2
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	MQLKPMEINPEMLNKVLAK.L	22.44	2226.19	1.7
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	MQLKPMEINPEMLNKVLAKL.G	32.94	2339.28	-1.5
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	MQLKPMEINPEMLNKVLAKLGVAGQWRF.A	41.58	3240.73	1.9
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	P.M(+42.01)EINPEMLNKVLAKL.G	27.86	1783.96	-4.3
Ubiquitin carboxyl-terminal hydrolase isozyme L1	sp|Q00981|UCHL1_RAT	L.KPMEINPEMLNKVLAKL.G	42.96	1967.09	-1.2
Ubiquitin-like-conjugating enzyme ATG3	sp|Q6AZ50|ATG3_RAT	M(+42.01)QNVINTVKGKALEV.A	30.43	1684.92	1.4
Uncharacterized protein	tr|M0R3Z1|M0R3Z1_RAT	G.YEEAEGQILERLIEKES.Q	20.02	2035.01	-0.9
Uncharacterized protein	tr|M0RD14|M0RD14_RAT	M.PKPDSEAGTAFIQTQQL.H	28.75	1829.92	-0.5
Uncharacterized protein	tr|D3ZET5|D3ZET5_RAT	M.GFVKVVKNKA.Y	24.55	1088.67	-0.6
Uncharacterized protein	tr|D4A5H3|D4A5H3_RAT	M.A(+42.01)DQLTEEQIAEFKEAFSLFDKDG.D	31.51	2672.25	-0.1
Uncharacterized protein	tr|D4A5H3|D4A5H3_RAT	M.A(+42.01)DQLTEEQIAEFKEAFSLFDKDGDG.T	33.2	2844.3	-4.9
Uncharacterized protein	tr|D4A5H3|D4A5H3_RAT	M.A(+42.01)DQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMR.S	30.6	4175.03	-5.6
Uncharacterized protein	tr|F1LWR6|F1LWR6_RAT	G.M(+42.01)QKGDLFKAEY.V	24.86	1370.65	0.7
Uncharacterized protein	tr|F1LWR6|F1LWR6_RAT	G.M(+42.01)QKGDLFKAEYV.F	19.04	1469.72	-1.4
Uncharacterized protein	tr|F1M3Q4|F1M3Q4_RAT	D.PGDSDIIRSMPEQTGEK	26.11	1858.87	0.3
Uncharacterized protein	tr|F8WFR3|F8WFR3_RAT	C.PLLKPWAL.T	25.3	936.58	-0.7
Uncharacterized protein	tr|M0R5B4|M0R5B4_RAT	L.AKVQRAVCMLRNT(+79.97)TAIAEAWARLDHKFDPM(+15.99)YAK(+42.01)R.A	15.55	4098.03	-2.2
Uncharacterized protein	tr|M0R734|M0R734_RAT	F.KQKQKEEQKKLEEL.K	41.39	1785	-0.8
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	A.EGPEVDVSLPKADL.D	17.21	1467.75	0.1

Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	A.PKISMPNIDL.N	28.17	1126.61	0.4
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	D.APDVDVQGPDWHL.K	32.08	1447.67	1
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	F.KAPKISMPNIDL.N	38.35	1325.74	0.3
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	H.KISMPDVGLNL.K	21.25	1185.64	-0.1
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	I.KGPKVDIDVPDVDVQGPDWHL.K	18.67	2328.18	1
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	K.GPKFKMPEMNIKAPKIS.M	21.39	1915.04	0.2
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	L.KGPGVDLPSVDL.S	21.21	1195.64	-0.3
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	L.KMPKVKMPK.F	23.38	1085.65	-2.4
Uncharacterized protein	tr|M0R9D5|M0R9D5_RAT	M.NIKAPKISMPNIDL.N	37.32	1552.86	-1.6
Uncharacterized protein	tr|M0RAX7|M0RAX7_RAT	F.KDAASVDKVLEL.K	21.43	1286.71	0.1
Uncharacterized protein	tr|M0RC66|M0RC66_RAT	V.NAEGSVDTVFSQVCTYLDSLK	28.01	2275.07	-0.6
Vesicle-associated membrane protein-associated protein B	sp|Q9Z269|VAPB_RAT	M.A(+42.01)KVEQVLSLEPQHEL.K	42.91	1760.93	-6.4
Vesicle-associated membrane protein-associated protein B	sp|Q9Z269|VAPB_RAT	M.A(+42.01)KVEQVLSLEPQHELK.F	19.25	1889.03	-0.8
Vesicle-associated membrane protein-associated protein B	sp|Q9Z269|VAPB_RAT	M.A(+42.01)KVEQVLSLEPQHELKF.R	37.16	2036.09	-1.5
Vesicle-associated membrane protein-associated protein B	sp|Q9Z269|VAPB_RAT	M.A(+42.01)KVEQVLSLEPQHELKFRGPFTDVVTT.N	29.71	3109.64	3.8
Vesicle-associated membrane protein-associated protein B	sp|Q9Z269|VAPB_RAT	M.A(+42.01)KVEQVLSLEPQHELKFRGPFTDVVTTNL.K	25.89	3336.77	-3.7
Vimentin	sp|P31000|VIME_RAT	A.AKNLQEAEEWYKSKFADLS.E	28.24	2256.11	-0.7
Vimentin	sp|P31000|VIME_RAT	A.AKNLQEAEEWYKSKFADLSE.A	29.2	2385.15	-0.6
Vimentin	sp|P31000|VIME_RAT	A.ANYQDTIGRLQDEIQNM.K	32.09	2007.93	-1.4
Vimentin	sp|P31000|VIME_RAT	A.RLDLERKVESLQEEIA.F	20.95	1927.04	-1.1
Vimentin	sp|P31000|VIME_RAT	A.YVTRSSAVRLR.S	31.52	1306.75	-1.1
Vimentin	sp|P31000|VIME_RAT	C.EVDALKGTNESLERQMREMEENF.A	27.77	2754.26	-1.3
Vimentin	sp|P31000|VIME_RAT	D.GQVINETSQHHDDLE	31.65	1720.77	-0.4
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTH.S	24.4	880.465	0.5
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKR.T	19.18	1251.69	-4.9
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKRT.L	40.38	1352.74	-0.9
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKRTL.L	55.52	1465.83	-0.8
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKRTLLIKTVETRDG.Q	44.47	2578.44	-1
Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKRTLLIKTVETRDGQVINETSQ.H	19.06	3477.88	-1.1

Vimentin	sp|P31000|VIME_RAT	E.SLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	17.12	4224.18	6.1
Vimentin	sp|P31000|VIME_RAT	F.ANYIDKVRFLEQQNKILLAELEQL.K	22.42	2887.58	-1.8
Vimentin	sp|P31000|VIME_RAT	F.GGSGTSSRPSSNRSYVTT.S	30.4	1799.84	-1.1
Vimentin	sp|P31000|VIME_RAT	F.GGSGTSSRPSSNRSYVTTSTRT.Y	28.85	2245.07	0.9
Vimentin	sp|P31000|VIME_RAT	F.KNTRTNEKVELQELNDR.F	33.09	2086.08	-0.6
Vimentin	sp|P31000|VIME_RAT	F.KNTRTNEKVELQELNDRFANYIDKV(-.98).R	17.03	3035.58	-0.2
Vimentin	sp|P31000|VIME_RAT	F.KNTRTNEKVELQELNDRFANYIDKV.R	17.8	3036.56	-2.8
Vimentin	sp|P31000|VIME_RAT	F.SLADAINTEFKNTRTNEKVELQEL.N	27.02	2762.41	1.1
Vimentin	sp|P31000|VIME_RAT	F.SLADAINTEFKNTRTNEKVELQELNDRFANYIDKV.R	27.26	4098.07	-1.7
Vimentin	sp|P31000|VIME_RAT	F.SSLNLRETNLE.S	27.54	1274.65	-0.7
Vimentin	sp|P31000|VIME_RAT	F.SSLNLRETNLESLPLVDTHSK.R	35.79	2352.23	-2.7
Vimentin	sp|P31000|VIME_RAT	F.SSLNLRETNLESLPLVDTHSKRT.L	28.32	2609.38	-1.9
Vimentin	sp|P31000|VIME_RAT	F.SSLNLRETNLESLPLVDTHSKRTL.L	31.15	2722.46	-1.1
Vimentin	sp|P31000|VIME_RAT	F.SSLNLRETNLESLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	19.61	5480.81	3.5
Vimentin	sp|P31000|VIME_RAT	G.GSGTSSRPSSNRSYVTT.S	18.67	1742.82	-0.4
Vimentin	sp|P31000|VIME_RAT	G.Q(-17.03)VINETSQHHDDLE	45.75	1646.72	-1.3
Vimentin	sp|P31000|VIME_RAT	G.QVINETSQHHDDLE	45.84	1663.74	-2
Vimentin	sp|P31000|VIME_RAT	G.SALRPSTSRS.L	28.03	1060.56	-0.4
Vimentin	sp|P31000|VIME_RAT	G.SALRPSTSRSLY.S	21.6	1336.71	-0.2
Vimentin	sp|P31000|VIME_RAT	G.SALRPSTSRSLYSSSPGGAYVTR.S	17.68	2399.22	-3.8
Vimentin	sp|P31000|VIME_RAT	G.SALRPSTSRSLYSSSPGGAYVTRSSAVRLR.S	21	3168.68	0.3
Vimentin	sp|P31000|VIME_RAT	G.TSSRPSSNRSYVTT.S	26.64	1541.74	-0.3
Vimentin	sp|P31000|VIME_RAT	H.SKRTLLIKTVETRDGQVINETSQHHDDLE	21.31	3361.72	0
Vimentin	sp|P31000|VIME_RAT	H.SKRTLLIKTVETRDGQVINETSQHHDDLE(-.98)	22.88	3360.74	-6.3
Vimentin	sp|P31000|VIME_RAT	I.KTVETRDGQVINETSQ.H	28.02	1803.9	-0.6
Vimentin	sp|P31000|VIME_RAT	I.KTVETRDGQVINETSQHHDDLE	59.55	2550.19	-1.7
Vimentin	sp|P31000|VIME_RAT	K.RTLLIKTVETRDGQVINETSQ.H	39.84	2400.3	0.2
Vimentin	sp|P31000|VIME_RAT	K.RTLLIKTVETRDGQVINETSQHHDDLE	52.03	3146.6	-2.5
Vimentin	sp|P31000|VIME_RAT	K.TVETRDGQVINETSQ.H	38.46	1675.8	-2.4
Vimentin	sp|P31000|VIME_RAT	K.TVETRDGQVINETSQHHDDLE	61.95	2422.1	-2.8
Vimentin	sp|P31000|VIME_RAT	L.IKTVETRDGQVINETSQ.H	56.46	1916.98	-1.5
Vimentin	sp|P31000|VIME_RAT	L.IKTVETRDGQVINETSQHHDDLE	38.89	2663.28	-0.8
Vimentin	sp|P31000|VIME_RAT	L.LIKTVETRDG.Q	28.06	1130.63	-0.7

Vimentin	sp|P31000|VIME_RAT	L.LIKTVETRDGQVINETSQ.H	62.62	2030.06	-3.4
Vimentin	sp|P31000|VIME_RAT	L.LIKTVETRDGQVINETSQHHDDLE	51.08	2776.36	-2.2
Vimentin	sp|P31000|VIME_RAT	L.NDRFANYIDKV.R	28.7	1353.67	-1.6
Vimentin	sp|P31000|VIME_RAT	L.NDRFANYIDKVRFLEQ.Q	25.2	2027.02	-0.4
Vimentin	sp|P31000|VIME_RAT	L.NLRETNLESLPLVDTHSKRTL.L	25.11	2435.31	2.4
Vimentin	sp|P31000|VIME_RAT	L.NLRETNLESLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	21.72	5193.67	-1.4
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSL.N	28.44	873.46	0.4
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSLNL.R	27.41	1100.59	0.2
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSLNLRETNLE.S	46.18	1842.95	-3.1
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSLNLRETNLES.L	24.32	1929.98	-1.7
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSLNLRETNLESL.P	55.74	2043.06	0.2
Vimentin	sp|P31000|VIME_RAT	L.PLPNFSSLNLRETNLESLPLVDTHSKRT.L	16.04	3177.68	0.1
Vimentin	sp|P31000|VIME_RAT	L.PLVDTHSKRTL.L	46.9	1265.71	-0.8
Vimentin	sp|P31000|VIME_RAT	L.PLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	30.77	4024.06	1
Vimentin	sp|P31000|VIME_RAT	L.QDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKV.R	16.01	4789.35	-6.7
Vimentin	sp|P31000|VIME_RAT	L.RETNLESLPLVDTHSKRTL.L	16.09	2208.19	-2
Vimentin	sp|P31000|VIME_RAT	L.RETNLESLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	23.16	4966.54	-2
Vimentin	sp|P31000|VIME_RAT	L.RSSMPGVRLL.Q	28.31	1114.63	-0.5
Vimentin	sp|P31000|VIME_RAT	M.FGGSGTSSRPSSNRSYVTT.S	38.79	1946.91	-1.6
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYR.R	32.32	1257.6	-1.4
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRM(+15.99)FGGSGTSSRPSSNRSYVTTSTRTY.S	16.95	4097.92	-2.4
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRM.F	26.16	1544.74	0.2
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRS.Y	27.4	3009.41	-0.9
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTT.S	33.09	3473.63	-1.5
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTST.R	20.86	3661.71	-0.7
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTR.T	19.01	3817.81	-4
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRT(-.98).Y	18.53	3917.88	-8
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRT.Y	18.42	3918.86	-2
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRTY(-.98).S	15.96	4080.94	1.4
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRTY.S	39.44	4081.93	0

Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRTYS.L	17.9	4168.96	-0.3
Vimentin	sp|P31000|VIME_RAT	M.S(+42.01)TRSVSSSSYRRMFGGSGTSSRPSSNRSYVTTSTRTYSLG.S	29.11	4339.06	-2.4
Vimentin	sp|P31000|VIME_RAT	N.TEFKNTRTNEK.V	26.52	1366.68	-1.4
Vimentin	sp|P31000|VIME_RAT	P.GGAYVTRSSAVRLR.S	38.24	1491.83	-0.8
Vimentin	sp|P31000|VIME_RAT	Q.QNKILLAELEQL.K	28.58	1410.81	-3.8
Vimentin	sp|P31000|VIME_RAT	Q.VINETSQHHDDLE	46.98	1535.69	-0.7
Vimentin	sp|P31000|VIME_RAT	R.ETNLESLPLVDTHSKRTLLIKTVETRDGQVINETSQHHDDLE	16.5	4810.44	0.8
Vimentin	sp|P31000|VIME_RAT	R.RMFGGSGTSSRPSSNRSYVTT.S	20.96	2234.05	-2.4
Vimentin	sp|P31000|VIME_RAT	R.SLYSSSPGGAYVTR.S	25.35	1443.7	-1.9
Vimentin	sp|P31000|VIME_RAT	R.SSAVRLR.S	22.64	787.466	-0.3
Vimentin	sp|P31000|VIME_RAT	R.SSAVRLRSSMPGVR.L	15.78	1501.81	-0.7
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRL.L	30.7	845.443	-0.4
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLL.Q	36.1	958.527	-0.3
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVD.F	34.44	1502.74	-2
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDF.S	27.64	1649.81	-0.5
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSL.A	27.88	1849.92	-1.9
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSLA.D	41.4	1920.96	2.4
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSLAD.A	33.53	2035.99	-7.8
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSLADA.I	28.64	2107.03	5
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSLADAIN(-.98).T	15.38	2333.17	-7.4
Vimentin	sp|P31000|VIME_RAT	R.SSMPGVRLLQDSVDFSLADAIN.T	40.63	2334.15	-4.9
Vimentin	sp|P31000|VIME_RAT	R.SYVTTSTRTYSLG.S	22.9	1434.7	-0.6
Vimentin	sp|P31000|VIME_RAT	R.TLLIKTVETRDGQVINETSQHHDDLE	51.82	2990.49	-1.9
Vimentin	sp|P31000|VIME_RAT	S.LPLVDTHSKRTL.L	27.09	1378.79	-0.4
Vimentin	sp|P31000|VIME_RAT	S.PGGAYVTRSSAVRLR.S	20.65	1588.88	-0.5
Vimentin	sp|P31000|VIME_RAT	S.SAVRLR.S	17.41	700.434	-0.1
Vimentin	sp|P31000|VIME_RAT	S.SLNLRETNLE.S	23.73	1187.61	-0.6
Vimentin	sp|P31000|VIME_RAT	S.SMPGVRL.L	25.16	758.411	0
Vimentin	sp|P31000|VIME_RAT	S.SMPGVRLL.Q	24.2	871.495	-0.4
Vimentin	sp|P31000|VIME_RAT	S.SMPGVRLLQDSVDF.S	32.81	1562.78	2.6
Vimentin	sp|P31000|VIME_RAT	S.SMPGVRLLQDSVDFSLA.D	16.94	1833.93	-2
Vimentin	sp|P31000|VIME_RAT	S.SMPGVRLLQDSVDFSLADAIN.T	37.97	2247.12	6.5
Vimentin	sp|P31000|VIME_RAT	S.SPGGAYVTR.S	30.58	906.456	-0.2
Vimentin	sp|P31000|VIME_RAT	S.SPGGAYVTRSSAVR.L	28.37	1406.73	0.4
Vimentin	sp|P31000|VIME_RAT	S.SPGGAYVTRSSAVRLR.S	37.66	1675.91	-1.7

Vimentin	sp|P31000|VIME_RAT	S.SSPGGAYVTRSSAVR.L	15.77	1493.76	-1.7
Vimentin	sp|P31000|VIME_RAT	S.SSPGGAYVTRSSAVRLR.S	38.92	1762.94	-0.8
Vimentin	sp|P31000|VIME_RAT	T.AALRDVRQQYESVA.A	22.8	1604.83	-12
Vimentin	sp|P31000|VIME_RAT	T.LLIKTVETRDGQVINETSQHHDDLE	22.79	2889.45	1.4
Vimentin	sp|P31000|VIME_RAT	T.RDGQVINETSQHHDDLE	21.87	1991.89	-2.3
Vimentin	sp|P31000|VIME_RAT	T.STRTYSLGSALRPSTSRS.L	30.59	1925.99	0.6
Vimentin	sp|P31000|VIME_RAT	T.VETRDGQVINETSQ.H	41.54	1574.75	-4.4
Vimentin	sp|P31000|VIME_RAT	T.VETRDGQVINETSQHHDDLE	52.48	2321.05	-1.3
Vimentin	sp|P31000|VIME_RAT	V.QIDVDVSKPDLTAALRDVRQQ.Y	18.23	2366.26	-0.4
Vimentin	sp|P31000|VIME_RAT	V.RFLEQQNKILLAELEQL.K	20.55	2084.16	0.8
Vimentin	sp|P31000|VIME_RAT	Y.RKLLEGEESRISL.P	35.33	1528.86	-0.2
Vimentin	sp|P31000|VIME_RAT	Y.RRM(+15.99)FGGSGTSSRPSSNRSYVTT.S	18.3	2406.15	-1.1
Vimentin	sp|P31000|VIME_RAT	Y.RRMFGGSGTSSRPSSNRSYVTT.S	32.11	2390.15	-1.1
Vimentin	sp|P31000|VIME_RAT	Y.RRMFGGSGTSSRPSSNRSYVTTSTRT.Y	43.1	2835.38	0
Vimentin	sp|P31000|VIME_RAT	Y.RRMFGGSGTSSRPSSNRSYVTTSTRTY.S	45.15	2998.44	-0.6
Vimentin	sp|P31000|VIME_RAT	Y.RRMFGGSGTSSRPSSNRSYVTTSTRTYSLG.S	22.49	3255.58	-0.2
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPST.S	28.1	987.535	-0.8
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTS.R	15.31	1074.57	-0.6
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTSR.S	23.44	1230.67	-0.4
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTSRS.L	30.99	1317.7	-0.9
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTSRSLY.S	24.25	1593.85	-0.6
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTSRSLYSSSPGGAYVTRSSAVRL(-.98).R	18.24	3268.73	-7.7
Vimentin	sp|P31000|VIME_RAT	Y.SLGSALRPSTSRSLYSSSPGGAYVTRSSAVRLR.S	15.44	3425.81	-0.3
Vimentin	sp|P31000|VIME_RAT	Y.SSSPGGAYVTR.S	20.45	1080.52	-0.6
Vimentin	sp|P31000|VIME_RAT	Y.SSSPGGAYVTRSSAVR.L	33.65	1580.79	-1.3
Vimentin	sp|P31000|VIME_RAT	Y.SSSPGGAYVTRSSAVRLR.S	17.64	1849.98	-0.4
Voltage-dependent T-type calcium channel subunit alpha-1G	tr|F1M9P2|F1M9P2_RAT	L.E(-18.01)GWVDIMYFVMDAHS(+79.97)FYNFIYFILLIIVGSFFMINLCLVVI(-.98).A	20.84	4955.44	5.7
Zero beta-globin	tr|Q63011|Q63011_RAT	A.QAAFQKVVAGVASALAHKYH	40.35	2095.13	-1.5
Zero beta-globin	tr|Q63011|Q63011_RAT	E.FTPSAQAAFQKVVAGVASALAHKYH	44.75	2598.37	-1.9
Zero beta-globin	tr|Q63011|Q63011_RAT	F.QKVVAGVASAL.A	28.89	1041.62	-0.4
Zero beta-globin	tr|Q63011|Q63011_RAT	F.QKVVAGVASALAHK.Y	33.66	1377.81	-0.3
Zero beta-globin	tr|Q63011|Q63011_RAT	F.RLLGNMIV.I	21.92	914.537	-0.8
Zero beta-globin	tr|Q63011|Q63011_RAT	F.RLLGNMIVI.M	22.25	1027.62	-0.7
Zero beta-globin	tr|Q63011|Q63011_RAT	F.TPSAQAAFQKVVAGVASALAHKYH	59.74	2451.3	-1.5

Zero beta-globin	tr|Q63011|Q63011_RAT	G.HHLGKEFTPSAQAAFQKVVAG(-.98).V	20.2	2221.18	12.1
Zero beta-globin	tr|Q63011|Q63011_RAT	G.HHLGKEFTPSAQAAFQKVVAGVASALAHKYH	25.86	3299.73	1.2
Zero beta-globin	tr|Q63011|Q63011_RAT	G.KEFTPSAQAAFQKVVAGVASALAHKYH	33.04	2855.51	-1
Zero beta-globin	tr|Q63011|Q63011_RAT	H.HLGKEFTPSAQAAFQKVVAGVASALAHKYH	39.05	3162.67	0
Zero beta-globin	tr|Q63011|Q63011_RAT	K.EFTPSAQAAFQKVVAGVASALAHKYH	34.78	2727.41	-0.8
Zero beta-globin	tr|Q63011|Q63011_RAT	L.ASLLIVYPWTQRYFSKF.G	15.14	2118.13	-1.1
Zero beta-globin	tr|Q63011|Q63011_RAT	L.GKEFTPSAQAAFQKVVAGVASAL.A	27.56	2276.22	2.8
Zero beta-globin	tr|Q63011|Q63011_RAT	L.GKEFTPSAQAAFQKVVAGVASALAHKY.H	33.76	2775.47	-1.1
Zero beta-globin	tr|Q63011|Q63011_RAT	L.GKEFTPSAQAAFQKVVAGVASALAHKYH	51.5	2912.53	-1.2
Zero beta-globin	tr|Q63011|Q63011_RAT	L.HVDPENFRLLGNMIVI.M	25.54	1865.98	-3.2
Zero beta-globin	tr|Q63011|Q63011_RAT	L.HVDPENFRLLGNMIVIMMGHHL.G	21.08	2572.29	-5.2
Zero beta-globin	tr|Q63011|Q63011_RAT	M.GHHLGKEFTPSAQAAFQKVVAGVASALAHKYH	25.19	3356.75	-1
Zero beta-globin	tr|Q63011|Q63011_RAT	Q.KVVAGVASALAHK.Y	33.38	1249.75	0.1
Zero beta-globin	tr|Q63011|Q63011_RAT	S.AQAAFQKVVAGVASALAHK.Y	38.2	1866.05	-1.9
Zero beta-globin	tr|Q63011|Q63011_RAT	S.AQAAFQKVVAGVASALAHKYH	49.86	2166.17	-0.2
Zero beta-globin	tr|Q63011|Q63011_RAT	V.VAGVASALAHKYH	15.45	1322.71	-0.4
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAE.K	22.62	783.376	-0.2
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAEK.A	25.96	911.471	-0.8
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAEKA.T	32.22	982.508	0
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAEKATV.N	34.24	1182.62	0
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAEKATVNGLWGKVNPVEIGAES.L	20.36	2833.46	1.7
Zero beta-globin	tr|Q63011|Q63011_RAT	VHLTDAEKATVNGLWGKVNPVEIGAESL.A	39.83	2946.54	0.3

Table S2. Peptides exclusively identified from tissue Extracts using ProSight.

Precursor	**Accession number**	**Peptide sequence**	**p score**	**Mass (Da)**	**Mass error (ppm)**
Zinc finger protein with KRAB and SCAN domains 1	F8WFK5	KEFGEKREQQGRVIERQQKNPEEK	4.96E-12	2969.56	5.1
Zero beta-1 globin	Q62669	IVIMMGHHLGKEFTPSAQAAFQKVVAGVASALAHKYH	4E-44	3944.07	-0.52
Voltage-dependent L-type calcium channel subunit alpha-1D	E9PU62	FERPRGYHHPQGF	5.35E-08	1626.79	5.62
Vimentin	P31000	SSMPGVRLLQDSVDFSLADAINTEFKNTRTNEKVELQEL	2.32E-23	4394.22	1.6
Vimentin	G3V8C3	SSSSYRRMFGGSGTSSRPSSNRSYVTTSTRTY	2.11E-07	3509.63	0.49
Vimentin	G3V8C3	RRMFGGSGTSSRPSSNRSYVTTSTRTYS	4.82E-11	3085.47	-0.86
Vimentin	G3V8C3	RQDVDNASLARLDLERKVESLQEEIA	3.02E-18	2996.55	0.48
Vimentin	G3V8C3	SVAAKNLQEAEEWYKSKFADLS	4.21E-12	2513.24	-1.74
Vimentin	G3V8C3	ANYIDKVRFLEQQNKILLA	9.29E-13	2275.27	-1.65
Vimentin	G3V8C3	MFGGSGTSSRPSSNRSYVTTST	3.65E-10	2266.03	-1.31
Vimentin	G3V8C3	MFGGSGTSSRPSSNRSYVTT	7.36E-20	2077.95	-2.05
Vimentin	G3V8C3	RKLLEGEESRISLPLPN	5.38E-14	1950.09	0.07
Vimentin	G3V8C3	SLARLDLERKVESL	1.91E-15	1627.93	0.08
Uncharacterized protein	D3ZCY4	MARTRRTARKPSGGKAPRKQLATKAALKSAPSTGRVKKLHPYRPGTV	4.44E-08	5080.96	3.45
Uncharacterized protein	F1LY12	NYRRRRPENPKPQDGKETKAADPPAENSSAPEAEQGGAE	2.23E-38	4247.03	-0.56
Uncharacterized protein	F1LY12	RRRRPENPKPQDGKETKAADPPAENSSAPEAEQGGAE	7.45E-49	3969.93	0.56
Uncharacterized protein	F1LTW2	LRSCSGLPSLSSQPGPVLSSVSSPPYPISAMRSTP	1.27E-12	3541.79	8
Uncharacterized protein	F1M4U4	AGKQLEDGRTLSDYNIQKESTLHLVLRLRGG	2.59E-18	3466.85	-2.21
Uncharacterized protein	F1LRB0	QTSEPCHSPRVMIHAKKVNTMSLTVLGLRL	1.89E-14	3345.77	-4.47
Uncharacterized protein	F1LYR1	SYMVKGRRLCQPKQKVQTEAEVEAPPAP	3.32E-08	3139.62	-2.76
Uncharacterized protein	F1LU72	TATQKLKLAHEYRPETAGEEAKAAGHGD	6.46E-06	2978.46	-6.3
Uncharacterized protein	F1LP73	KVLKQVHPDTGISSKAMGIMNSFV	6.63E-09	2586.37	-1.03
Uncharacterized protein	F1LZV7	FVKLISWYDNEYGYSNRVVDL	1.72E-10	2579.27	-1.3
Uncharacterized Protein	D3ZFK7	AIIKFPLTTESAMKKIEDNNTLV	1.85E-06	2575.39	-1.77
Uncharacterized protein	D3ZL16	EVFSILASSAGLLGCIFFQKCY	7.47E-12	2395.19	-5.29
Uncharacterized Protein	D3ZFK7	AIIKFPLTTESAMKKIEDNNT	1.15E-10	2363.24	1.92
Uncharacterized protein	F1M4U4	SDYNIQKESTLHLVLRLRGG	3.29E-18	2298.24	0.41
Uncharacterized protein	F1LP73	YKVLKQVHPDTGISSKAMG	1.62E-12	2058.09	0.6
Uncharacterized protein	D4A160	EKKAAKLKEKYEKDIAA	7.99E-16	1962.12	-0.29
Uncharacterized protein	F1LUF0	MKLACTDTHISSAYGLFV	7.08E-09	1955.95	-1.46
Uncharacterized protein	F1M4U4	NIQKESTLHLVLRLRGG	1.32E-24	1933.12	-0.55

Uncharacterized protein	F1M6B2	SEYRPKIKGEHPGLS	2.92E-12	1696.89	-0.69
Uncharacterized protein	D4A1X0	GFGFVTFSSMAEVDVA	5.75E-12	1662.77	3.51
Uncharacterized protein	D4A2A0	EKERKKGEGKEGER	4.75E-09	1658.86	-5.22
Uncharacterized protein	F1LUK3	EADIAAGKFIEHGEF	3.87E-11	1632.79	3.94
Uncharacterized protein	F1LXY2	EYTDGGILDPDDVLA	2.09E-06	1591.73	1.59
Uncharacterized protein	F1M2X2	GHLPKVQMPSLK	4.2E-28	1333.75	-0.8
Uncharacterized protein	E9PTR0	KSGVEVRLPNDL	2.71E-10	1325.73	5.08
Uncharacterized protein	F1LU95	GKAFRFPGSLPL	1.13E-09	1288.73	0.26
Uncharacterized protein	F1LX34	VHIYMCIFVL	1.45E-11	1236.64	3.91
Uncharacterized protein	F1LT80	EFQSPLENL	4.05E-11	1075.52	2.73
Uncharacterized protein	F1M3N2	GARKASNIVL	2.01E-08	1027.62	6.46
Uncharacterized protein	F1LZV9	FEDKHGSN	2.32E-10	932.399	5.08
Ubiquitin-60S ribosomal protein L40	P62986	MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGG	9.16E-25	8559.6	-2.47
Tubulin polymerization-promoting protein family member 3	Q5PPN5	IAGKEPANIGVTKAKTGGAVDRLTDTSK	2.62E-19	2797.53	-1.6
Tubulin beta-5 chain	P69897	VFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKEAESCD	1.04E-07	4036.89	-0.07
Tubulin beta-5 chain	P69897	VFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKE	5.41E-17	3531.74	-0.16
Tubulin beta-5 chain	P69897	NEATGGKYVPRAILVDLEPGTMDSVR	1.13E-25	2787.41	-1.92
Tubulin beta-5 chain	P69897	YTEGAELVDSVLDVVRKEAESCD	3.7E-16	2526.18	-0.38
Tubulin beta-5 chain	P69897	IREEYPDRIMNTF	3.66E-12	1682.81	-1.23
Tubulin beta-2A chain	P85108	AAGNKYVPRAILVDLEPGTMDSVR	9.12E-10	2571.35	0.17
Tubulin alpha-4A chain	Q5XIF6	GGGTGSGFTSLLMERL	3.77E-21	1581.78	-0.74
Tubulin alpha-3 chain	Q68FR8	IERPTYTNLNRLIGQIVS	4.15E-10	2086.15	-0.94
Tubulin alpha-1C chain	Q6AYZ1	FSETGAGKHVPRAVF	5.3E-34	1601.83	-2.23
Troponin T, fast skeletal muscle	F1LPQ5	AERRKPLNIDHLSDDKLRDKAKELWDT	5.98E-22	3261.72	-2.32
Triosephosphate isomerase	P48500	ASQPDVDGFLVGGASLKPEFVDIINAKQ	1.03E-06	2914.51	-0.71
Triosephosphate isomerase	P48500	APSRKFFVGGNWKMNGRKK	4.67E-24	2207.19	-0.66
Transmembrane emp24 domain-containing protein 9	Q5I0E7	ATPGLGMFVEVKDPEDKVILARQYGSEGRFTFTSHTPGEHQICLHSNSTK	1.03E-08	5514.72	2.33
Transitional endoplasmic reticulum ATPase	P46462	QANFISIKGPELLTM	6.7E-16	1660.89	-1.18
Kynurenine--oxoglutarate transaminase 1, mitochondrial	Q08415	VHLMWPLW	1.22E-11	1080.56	-2.1
3-hydroxyisobutyrate dehydrogenase, mitochondrial	P29266	ASLGFRGAASGLRYWSGRRRPVG	4.09E-07	2476.34	4.9
Transgelin	P31232	MGSNRGASQAGMTGYGRPRQIIS	9.41E-19	2394.16	-0.53
Transgelin	P31232	GSNRGASQAGMTGYGRPRQIIS	3.47E-26	2263.12	-0.51
Transferrin receptor protein 1	G3V679	SEKLNSIE	9.52E-15	918.466	-0.18
Thioredoxin	P11232	AAAGDKLVVVDF	7.36E-10	1203.65	0.78

Succinyl-CoA ligase subunit alpha, mitochondrial	P13086	DVFLKDPATEGIVL	2.26E-31	1515.82	-0.5
Stress-70 protein, mitochondrial	F1M953	IGIPPAPRGVPQIEVTF	8E-18	1790.01	-0.82
Serine/arginine-rich splicing factor 2	Q6PDU1	HDKRDAEDAMDAMDGAVLDGRELRV	2.66E-21	2784.29	-0.42
Scg2 protein	Q6P7R4	VPSPGSSEDDLQEEEQLEQAIKEHLGQGSSQEMEKLAKVS	8.05E-26	4366.08	0.33
Sarcolemmal membrane-associated protein	D3ZQC9	KTLKECSSLGIQVDDFLPKINGSTEKEKLMV	5.41E-11	3465.81	4615.06
Reticulon-4	D4AEM9	FALPAASEPVIPSSAEKIMDL	2.17E-18	2201.12	7264.94
Ras-related protein R-Ras	D3Z8L7	EDSYTKICTVDGIPARLDILDTAGQEEFGAMREQYMRAGNGFLLVFAINDRQSFIEVSKL	1.08E-05	6740.4	9.22
RanBP-type and C3HC4-type zinc finger-containing protein 1	D3ZGV7	LDLGVSIAENRSTLSYHCKTPDCRGW	5.6E-13	2920.42	5.35
Putative L-aspartate dehydrogenase	G3V9Z4	ELVFVWNRDPGRMAGSVPPALQLEDL	1.18E-15	2908.49	-3.87
Protein Zfp64	D3ZA54	FSRKDKLKTHMRCHTGVKPYKCKTCDYAAADSSSLNKHLRIHS	3.19E-08	4960.49	-1.5
Protein Zfp398	D3ZGH2	TFTHPSRLTYHLRVHNSTERPF	2.93E-07	2695.37	-4.92
Protein Wwc1	F1M6U0	VDAVSALLEQTAVEL	6.59E-09	1556.83	-0.81
Protein Wdr33	D3Z8Y4	QPIKFWDPKTGQSLA	6.76E-08	1714.9	1.94
Protein Ubqln2	D4AA63	GSPPQPPNPEVRFQQQLEQLNAMGFLNREANLQALIATGGDINAAIERLLGSQPS	4.87E-27	5895.01	0.29
Protein Tmem80	Q5XID3	ATLLMIVYKSTQGNLTEAEVPLAASLAFTA	7.24E-09	3122.66	-4.89
Protein Tmem80	Q5XID3	ATLLMIVYKSTQGNLTEAEVPLAASLAFT	1.17E-09	3051.62	-5.17
Protein Tbx19	D3Z977	FKEVTNEMIVTKNGRRMFPVLKISVTG	4.37E-08	3093.66	-7.46
Protein Tacc1	D3ZNW7	LTMEKEQALADLN	7.02E-12	1474.73	-0.04
Protein Stag1	D4A3Q2	LQCSHYSILWQLVKITD	3.22E-10	2046.05	-4.23
Protein Srrd	F1LTK4	CSSALETITECLRKQLEQLQSLTEALGRL	2E-19	3232.68	0.54
Protein Spint2	Q6P796	LASLLLSGAQAASRDLDVHENTIDGLARS	3.34E-08	2992.56	-4.6
Protein Spg20	E9PT90	ESPQRESQGGATSTEGTRDVERKM	1.39E-09	2635.23	10.45
Protein Spag6l	D3ZD28	QQTAALALGRLANYNDDLAEAWEMGVVGRHTPEHARAVAITNTLP	2.69E-12	4840.45	3.19
Protein Slc43a2	D3ZSK2	WMACTAVLENL	2.33E-10	1249.58	1.71
Protein Sf3b2	D3ZJX7	PMAHPPNLGPPPPLRVGEPVALSEEERLKLAQQQA	9.69E-19	3766	-0.57
Protein Serpinb11	D3ZJI7	LSSSNVGENI	1.07E-21	1018.5	6.51
Protein Sema6d	D3ZDA2	NTVDYHYSRQYPVFR	4.81E-13	1943.93	0.38
Protein RGD1565025	D4A806	IGLGDLL	1.79E-14	699.417	-0.66
Protein RGD1564745	F1M523	HDDPEIIKQA	1.6E-11	1164.58	5.87
Protein RGD1564626	F1LTP3	QAGASKLLRDARSLPVERLSH	1.28E-09	2303.28	10.26
Protein RGD1563996	F1M6R6	ERSHTAVYAVCGVAALLVLVGIGA	4.72E-08	2368.32	12.01
Protein RGD1562404	D3ZII2	LNTNIDGRWKI	5.37E-07	1328.71	-6.6
Protein RGD1561826	D3ZEM3	LNAKSKMQDLPVPI	9.33E-08	1552.86	-0.11

Protein RGD1559921	F1LTZ6	LTQQLAQGTGKPARFI	4.86E-07	1727.99	9.97
Protein RGD1310945	F1M6P5	FLIAKREMKN	2.35E-12	1248.71	9.48
Protein RGD1308134	D3ZY53	VSDSSPAGAQIKTTVKRKVYEDSGIPLPA	1.23E-08	3013.63	7.31
Protein Rfesd	D3ZF58	KYKITLATGEGLYQSIDPKDPSAKPKWCSK	1.01E-11	3351.76	2.79
Protein Prmt6	D4A307	EAGVGGRFRCSCYGSAPLH	8.33E-08	1965.89	7.29
Protein Olr633	D3ZMD0	SVEGRRKALSTCTSHFIV	1.91E-11	1990.04	-2.09
Protein Olr463	D4A338	EVTEFILLGLSDNPDLQCILFALFLVIYMVTLVGNLGMMALIKIDRSLHTPMYFFLSSLS	2.24E-07	6764.59	6.44
Protein Olr144	D3ZLN8	SWTESGILLAMSFDRYVAICN	1.2E-10	2375.13	-0.24
Protein Olr1347	G3V9E6	LACADTTLNEL	2.4E-14	1162.55	-0.49
Protein Olr1149	D3ZYP6	YISSCIFAGIPLS	3E-13	1369.7	-5.52
Protein Olr1096	D4ACL1	ILVSLFSRSGSPELLFSLVAAMFIIGLLGNTILLLLIQIDSKLHTPMYFLLSQLSLL	4.25E-08	6271.61	4.34
Protein Msl1	F1LTE3	IQESEPEVTSFFPEPDDVESLMITPFLPVVAFGRPLPKLTPQN	3.23E-10	4810.44	-1.2
Protein Mobkl2b	D3ZCN1	FVTEMNLIDRKELEPLKEMTTR	1.01E-08	2692.38	-3.96
Protein Mapkapk2	F1M244	KSIGEAIQYLHSINI	1.44E-08	1684.91	-2
Protein Mapk1ip1l	D3ZNX9	NPYQVPSGPAGAPPMPGGPHSYH	2.05E-14	2314.06	0.19
Protein LOC680353	D3ZZH2	TLVITDKEKAEKLKQSLPPGLAVKELK	2.63E-10	2975.76	-1.03
Protein LOC679739	D3ZCZ9	GVRVSRSGEKITHTGQVYDEKDYRRIR	5.12E-17	3204.69	0.64
Protein LOC500164	D3ZGH3	SPKRLIYLVSKLDSGIPDRFS	4.02E-09	2390.31	-7.06
Protein LOC100364909	D3ZFA8	GRVRTKTVKKAARVIIEKY	4.01E-16	2215.36	0.24
Protein LOC100364909	D3ZFA8	LDFGSLSNL	1.83E-09	964.487	-1.1
Protein LOC100362909	D4A8V1	LPAAKPGIPP	2.38E-08	959.591	7.23
Protein LOC100362458	D3ZP95	LPLDTTTPGPSLEQL	2.87E-12	1580.83	0.72
Protein Ints4	D4A649	ENQATQVRLVDVACKHLTDTSHGVR	3.75E-07	2776.4	0.26
Protein Fhdc1	D4ACI6	SSRGAGPWKRPELTSRATPRETPSSTDTQLSRRSS	1.74E-11	3841.95	-1.29
Protein Fbxw17	D3Z9G1	WNKENTSPILK	9.47E-09	1328.71	2.28
Protein Dzip3	D3ZY61	ALTAEVYFLQCRRDFGLLHLEQTEKECLNQLARVTHMAASNLE	1.05E-10	4960.49	1.6
Protein Dntt	E9PT58	KDIEGIPCLGD	1.89E-12	1158.57	5.73
Protein Dmrta2	D4A0L2	ESFSGSPLARASKEAGGSCPGSAG	1.76E-12	2209.01	1.83
Protein Birc6	F1LY70	MGRQGSLATCQLSEPLLWFILRVLDTSDALKAFHDMGGVQLICNN	8.47E-10	4960.49	0.09
Protein Arhgef5	E9PT59	DQQEAVTQSLQD	5.85E-10	1360.65	28.98
Protein Ank2	F1LZM2	EDGFTPLAVALQQGHNQAVAILLEND	3.82E-13	2762.39	-7.88
Protein AF1q	Q5M971	PIPELDLSELEGLGL	1.14E-23	1593.85	0.52
Protein AF1q	Q5M971	PIASIRSIDLDLL	6.1E-10	1424.82	-0.54
Procollagen isoform CRA_a	D4A111	VIVVLTDGQSEEDGFALPSAELKSADVNVFAVGVEDADERTLREIAS	9.33E-13	4960.48	-0.84
Prefoldin subunit 2	B0BN18	SAEQVIAGFNRLRQEQRGLASKAAELEMELNEHSLVIDTLKEVDETRKCYRMVGGVL	3.96E-07	6429.32	2.35
Thymosin beta-4	P62329	PSKETIEQEKQAGES	1.4E-07	1659.83	20.2

Phosphatidylethanolamine-binding protein 1	P31044	KGNDISSGTVLSEYVGSGPPKDTGLHRYVWLVY	4.39E-07	3593.82	0.4
Polymerase I and transcript release factor	P85125	KENLEKTRHTLEKR	3.61E-10	1780.99	-0.26
Polymerase (RNA) II polypeptide D	D4A259	LNSEVHMLL	1.96E-09	1054.55	-0.54
Pleckstrin homology domain-containing family A member 8	D3ZY60	NTSFSDIELLEDSGIPTEAFLA	1.68E-10	2368.15	9.94
Phosphatidylethanolamine-binding protein 1	P31044	AGPLSLQEVDEPPQHALRV	7.88E-12	2055.08	0.07
Peripherin	P21807	TTVPEVEPPQDSHSRKMVLIRTIETRDGEKVVTESQKEQHSELDKSSIHSY	3.27E-12	5859.93	-0.76
Peripherin	P21807	IRTIETRDGEKVVTESQKEQHSELDKSSIHSY	6.02E-33	3728.86	-0.18
Peripherin	P21807	RTIETRDGEKVVTESQKEQHSELDKSSIHSY	8.3E-15	3615.78	-0.68
Peripherin	P21807	IRTIETRDGEKVVTESQKEQHSELDKSSIHS	5.83E-14	3565.8	-0.02
Peripherin	P21807	RTIETRDGEKVVTESQKEQHSELDKSSIHS	4.38E-24	3452.71	0.07
Peripherin	P21807	RTIETRDGEKVVTESQKEQH	1.21E-24	2369.19	-1.46
Periaxin	D3ZWG4	AIAGQLKIPEVELVTPGAQETEKVTSGVKPSGLQVSTTRQVVAEGQEGAQRVSSLG	9.76E-24	5714.05	-0.48
Periaxin	D3ZWG4	ISLPQVELASFGEAGPEIAAPSAEGTVGSRIQVPQVM	2.87E-22	3734.92	0.3
Periaxin	D3ZWG4	PKVPDIKLPEIKLPKVPEMAVPDVPLPELQL	1.82E-10	3441.99	0.39
Periaxin	Q63425	TFGLSLLESRPSGPEVAAESKLKLPTLK	1.28E-11	2967.66	-0.36
Periaxin	D3ZWG4	ASFGEAGPEIAAPSAEGTVGSRIQVPQVM	2.9E-26	2855.41	-1.6
Periaxin	D3ZWG4	DTQEGAAVVKVPTLDVAAPSVEVD	1.78E-69	2409.22	-2.19
Periaxin	D3ZWG4	EVKLPKIPDMAVPDVRLPEL	5.96E-10	2258.27	-0.78
Periaxin	D3ZWG4	DTQEGAAVVKVPTLDVAAPSVE	4.91E-20	2195.13	-1.35
Periaxin	D3ZWG4	LGAPAAPAVEPPTTGIQVPQVE	5.44E-47	2141.13	-3.25
Periaxin	D3ZWG4	KLPKIPDMAVPDVRL	1.68E-16	1690.98	0.26
Periaxin	D3ZWG4	LELPGTQVAGGDLL	6.48E-26	1381.75	-1.28
Peptidyl-prolyl cis-trans isomerase A	P10111	KTEWLDGKHVVFGKVKEGMSIVEAMERFGSRNGKTSKKITISDCGQL	5.25E-08	5223.7	-0.09
Acyl-CoA-binding protein	P11030	SHFKQATVGDVNTDRPGLLDL	9.49E-15	2282.17	-1.52
Osteogenic growth peptide	P62804	KRQGRTLYGFGG	5.61E-10	1338.72	-0.65
Osteogenic growth peptide	P62804	QGRTLYGFGG	8.44E-12	1054.52	0.03
Pro-neuropeptide Y	P07808	YPSKPDNPGEDAPAEDMARYYSALRHYINLITRQRY	6.62E-17	4269.09	-230.39
Fibrinogen beta chain	P14480	TTDSDKVDLSIAR	3.82E-18	1419.72	-2.16
Pro-neuropeptide Y	P07808	SSPETLISDLLMRESTENAPRTRLEDPSMW	9.11E-18	3460.66	-0.63
Osteoglycin (Predicted)	D3ZVB7	SLLEELTLAENQLLRLPVLPPKLT	1.51E-08	2699.58	-0.39
Nuclear receptor corepressor 1	D3ZN55	TAADALAALVDAAASA	4.64E-15	1400.71	0.17
Non-muscle caldesmon	Q62736	TNAIEGTKASKPMKPAASDLPVPAEGVRNIKSMWEKGSV	8.54E-08	4094.13	0.08
Neurofilament light polypeptide	P19527	SGYSQSSQVFGRSAYSGLQSSSYLMSARAFPAYYTSHVQEEQSEVEETIEATKAEEAK	1.99E-29	6385.95	0.07
Neurofilament light polypeptide	P19527	SAPVSSSLSVRRSYSSSSGSLMPSLENLDLSQVAAISNDLK	3.6E-12	4239.13	-0.09

Neurofilament light polypeptide	P19527	SAAKNTDAVRAAKDEVSESRRLLK	1.36E-21	2614.41	-0.18
Neurofilament light polypeptide	P19527	EEQSEVEETIEATKAEEAK	4.62E-12	2148.99	-0.08
Neurofilament light polypeptide	P19527	LDLSQVAAISNDLK	2.18E-17	1485.8	0.36
Neurofilament light polypeptide	P19527	EETIEATKAEEAK	2.96E-09	1447.67	-22.08
Neurofilament light polypeptide	P19527	SLMPSLENL	8.8E-11	1002.51	-1.86
Neurofilament light polypeptide	P19527	FSYEPY	3.2E-07	804.333	-0.95
Neurofilament heavy polypeptide	F1M9Y4	GLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPEDKAAKGDK	1.29E-13	4381.18	-1.5
Neurofilament heavy polypeptide	F1M9Y4	LDRLSEAAKVNTDAMRSAQEEITEYRRQLQ	4.11E-10	3520.77	0.78
Neurofilament heavy polypeptide	F1M9Y4	AAQAQAQAEARDALK	3.32E-15	1540.8	0.09
Neurofilament 3, medium	G3V7S2	QHKFVEEIIEETKVEDEK	3.06E-13	2229.12	-0.3
Neurofilament 3, medium	G3V7S2	PSAYRRVTETRSSFSRVS	7.74E-12	2085.07	-0.32
Neurofilament 3, medium	G3V7S2	KTKVEAPKLKVQ	9.2E-10	1367.85	-0.78
NEDD8	Q71UE8	MLIKVKTLTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDEKTAADYKILGGSVLHLVLALRGG	5.65E-17	8554.66	-0.59
NADH-ubiquinone oxidoreductase chain 2	P11662	STLTLPLSSQLIT	1.3E-12	1372.78	0.39
NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Q66HF1	EVFVDGQSVMVEPGTTVLQAC	5.16E-14	2208.04	-2.97
NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 8	D4A311	PGIVELPTLEELKVEEVKVSSAVLKAA	2.44E-25	2847.61	-1.95
Myosin regulatory light chain 2, skeletal muscle isoform	P04466	KVLDPEGKGTIKKQFLEELLTTQCDR	1.25E-09	2988.6	0.58
Myeloblastosis oncogene-like 1 (Predicted)	D3ZF01	HLQTQNQFYIPIPGYQYVSPDGNCVEHVQT	2.63E-10	3474.62	-2.72
Myelin protein P0	P06907	KFHKSSKDSSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	4.56E-15	5402.91	-0.6
Myelin protein P0	F1MAN9	PVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	2.86E-26	3544.91	-1.06
MKI67 FHA domain-interacting nucleolar phosphoprotein	Q5RJM0	KEEKLNSGVVYLGHL	1.48E-13	1684.91	0.14
Midline-1	F1M2J9	YLTAPNPPTIREELCTASYDTITVHW	1.85E-05	2990.45	-1.46
Microtubule-associated protein 1B	P15205	KSTPLSDTKKPAALKPKVAKKEEPTKKEPIAAGKLKDKGKVKVIKKEGKTTE	3.3E-12	5624.33	-0.17
Microtubule-associated protein	D3ZHY7	SKANIKHKPGGGDVKIESQKLN	1.25E-34	2347.3	0.31
Mevalonate kinase	P17256	ETSIGAPGVSMHSATSIEDPVRQALGL	2.94E-13	2722.36	-0.17
Metabotropic glutamate receptor 1	D3ZSM4	WTYVSAVHTEGNYGESGMDAF	9.13E-11	2319.99	7.9
Matrix metalloproteinase 19	C0M4B0	PMKLNRVEPNLDAALYWPVNQKVFLFKGSGYWQW	1.89E-07	4094.1	6.97
Matrin-3	P43244	VEPFGVISNHLILNKINEAF	2.8E-10	2253.21	-2.47
Mammary cancer associated protein RMT-1	Q8VBT7	AARICPSEGATGRQAGLRSGLSEAAAAVPCV	6.89E-10	2968.5	1.49

Malate dehydrogenase, mitochondrial	P04636	AKVAVLGASGGIGQPLSLL	1.05E-21	1750.04	-0.27
Macrophage migration inhibitory factor	P30904	IVNTNVPRASVPEGFLSEL	4.01E-22	2041.08	0.85
L-lactate dehydrogenase C chain	P19629	SGCNLDSARFRYLIGEKLGVNPSSC	5.31E-12	2685.3	1.58
Lactoylglutathione lyase	Q6P7Q4	IEILNPNKMATII	1.98E-09	1468.83	-0.93
Krueppel-like factor 6	O35819	SDSSEELSPTTKFTSDPIGEVLVNSGNLS	2.28E-08	3009.41	-7.6
Insulin-like growth factor 2 mRNA-binding protein 1	Q8CGX0	DTKTADEVPLKI	1.86E-08	1328.71	-5.17
Importin subunit alpha-6	Q56R16	SSTVPIPEEDMITADMIQMIFSNNAEQ	1.72E-10	3010.34	-5.8
Hypothetical LOC294883	Q569A4	GKGVFSMKGGSRSSVGGSSSSGSKLKSDELQTI	5.41E-09	3244.65	4.36
HtrA serine peptidase 2		DVRQGEFVVAMGSPFALQNTIT	1.19E-12	2379.2	2.96
Hsc70-interacting protein	P50503	KERIERVKKAREEHEKAQREEEARRQSGSQ	6.32E-21	3676.92	-0.13
Histone H3.3	P84245	RFQSAAIGALQEASEAYL	9.24E-47	1923.97	-0.76
Histone H3.1	Q6LED0	RFQSSAVMALQEACEAYL	2.68E-08	2015.96	7.85
Histone H3	D3ZJ08	ARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVAL	1.29E-06	5052.92	0.05
Histone H3	D3ZJ08	RFQSSAVMALQEASEAY	2.44E-30	1886.88	-0.88
Histone H2B	G3V8B3	VYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK	1.38E-23	9341.99	0.28
Histone H2B	G3V8B3	VNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK	2.3E-10	6610.58	1.73
Histone H2B	G3V8B3	ERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK	4.3E-47	6022.28	0.09
Histone H2B	G3V9C7	NDIFERIAGEASRLAHYNKRSTITSREIQTA	9.6E-18	3546.83	0.38
Histone H2B	G3V9C7	NDIFERIAGEASRLAHYNKRSTITSREIQT	8.85E-10	3475.79	-0.71
Histone H2B	G3V8B3	LLPGELAKHAVSEGTKAVTKYTSSK	1.94E-38	2614.43	-0.22
Histone H2B	G3V8B3	PGELAKHAVSEGTKAVTKYTSSK	2.83E-19	2388.27	0.31
Histone H2B	G3V9C7	AGEASRLAHYNKR	4.96E-20	1471.76	-1.4
Histone H2A.J	A9UMV8	VGAGAPVYLAAVLEYLTAEILELAGNAAR	1.31E-64	2914.58	-1.22
Histone H2A type 1	P02262	QLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK	9.46E-19	4996.88	2.13
Histone H2A type 1	P02262	PNIQAVLLPKKTESHHKAKGK	7.16E-15	2323.34	-2.61
Histone H2A type 1	P02262	IQAVLLPKKTESHHKAKGK	1.14E-32	2112.25	-0.6
Histone H2A	D4ACV3	ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHKAKSK	3.3E-10	7370.25	-1.23
Histone H2A	D4ACV3	VGAGAPVYMAAVLEYLTAEILELAGNAAR	6.91E-41	2932.54	-0.94
Histone H2A	D4ACV3	AGNAARDNKKTRIIPRHLQL	3.67E-18	2271.3	-0.91
Histone H2A	D4ACV3	KSRSSRAGLQFPVGRVHR	2.8E-12	2037.15	0.7
Histone H1.4	P15865	KASGPPVSELITKAVAASKERSGVSLAAL	2.21E-13	2836.6	0.01
Histone H1.4	P15865	ASGPPVSELITKAVAASKERSGVSLAAL	1.15E-14	2708.51	-1.5
Histone H1.4	P15865	KKALAAAGYDVEKNNSRIKLG	3.66E-10	2245.25	-0.56

High mobility group nucleosomal binding domain 2	Q4KLJ0	PKRKAEGDAKGDKAKVKDEPQRRSARLSA	4.11E-43	3191.76	-1.12
Heterogeneous nuclear ribonucleoprotein C	P17132	IFVGGLSPDTPEEKIREYFGGFGEVESIEL	2.08E-16	3313.64	-0.14
Heterogeneous nuclear ribonucleoprotein C	P61980	TGTQDQIQNAQYLLQNSVKQYSGKFF	2.7E-19	3005.49	1.64
Hemoglobin subunit beta-1	P02091	GDLSSASAIMGNPKVKAHGKKVINAFNDGLKHLDNLKGTF	4.99E-12	4192.22	0.53
Hemoglobin subunit beta-1	P02091	FDSFGDLSSASAIMGNPKVKAHGKK	6.42E-13	2591.32	-0.22
Hemoglobin subunit beta-1	P02091	LVVYPWTQRYFDSF	4.06E-38	1819.89	-1.08
Hemoglobin subunit beta-1	P02091	GKVNPDDVGGEALGRLL	6.8E-34	1708.91	-0.92
Hemoglobin subunit beta-1	P02091	GKVNPDDVGGEALGRL	1.23E-42	1595.83	-0.54
Hemoglobin subunit beta-1	P02091	KVNPDDVGGEALGRL	7.03E-13	1538.81	0.09
Hemoglobin subunit beta-1	P02091	VNPDDVGGEALGRLL	3.12E-10	1523.79	1.34
Hemoglobin subunit beta-1	P02091	NPDDVGGEALGRLL	6.79E-20	1424.73	-1.03
Hemoglobin subunit beta-1	P02091	LVVYPWTQRY	4.72E-31	1323.7	-1.11
Hemoglobin subunit beta-1	P02091	NPDDVGGEALGRL	4.28E-33	1311.64	-0.51
Hemoglobin subunit beta-1	P02091	DDVGGEALGRLL	8.27E-28	1213.63	-1.21
Hemoglobin subunit beta-1	P02091	VVYPWTQRY	1.87E-28	1210.61	-1.38
Hemoglobin subunit beta-1	P02091	PDDVGGEALGRL	1.87E-27	1197.6	0.03
Hemoglobin subunit beta-1	P02091	DDVGGEALGRL	3.95E-36	1100.55	-0.51
Hemoglobin subunit beta-1	P02091	DVGGEALGRLL	2.03E-27	1098.6	-0.61
Hemoglobin subunit beta-1	P02091	DVGGEALGRL	5.89E-30	985.519	-0.47
Hemoglobin subunit beta-1	P02091	VGGEALGRLL	2.05E-18	983.577	-0.88
Hemoglobin subunit beta-1	P02091	VGGEALGRL	2.83E-21	870.492	-0.53
Hemoglobin subunit beta-1	P02091	PWTQRY	7.11E-14	849.413	-2.08
Hemoglobin subunit alpha-1/2	P01946	SHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGALST	1.71E-11	3890.03	0.24
Hemoglobin subunit alpha-1/2	P01946	AADHVEDLPGALSTLSDLHAHKL	1.13E-15	2409.23	-1.06
Hemoglobin subunit alpha-1/2	P01946	YFSHIDVSPGSAQVKAHGKKV	1.5E-07	2254.19	-0.61
Hemoglobin subunit alpha-1/2	P01946	EDLPGALSTLSDLHAHKL	3.28E-11	1916	-0.14
Hemoglobin subunit alpha-1/2	P01946	HHPGDFTPAMHASLDK	5.89E-19	1759.81	-0.21
Hemoglobin subunit alpha-1/2	P01946	KFLSHCLLVT	2.32E-08	1159.64	0.03
Heat shock protein beta-1	D3ZNT4	PFSLLRSPSWEPFRDWYPAHSRLFDQA	1.98E-16	3304.62	0.46
Heat shock protein beta-1	D3ZNT4	FGVPRFPDEWSQWFSSAGWPGYVR	1.58E-07	2857.34	-1.39
Heat shock protein beta-1	D3ZNT4	PFSLLRSPSWEPFRDWYPAHSRL	1.97E-27	2843.43	0.58
Heat shock protein beta-1	D3ZNT4	AAPAFSRALNRQLSSGVSEIRQT	1.47E-12	2458.3	0.42
Heat shock protein beta-1	D3ZNT4	SSGVSEIRQTADRWRVSL	6.17E-12	2046.06	0.21
Heat shock protein beta-1	D3ZNT4	RSPSWEPFRDWYPAHS	1.09E-06	2016.92	1.26
Heat shock 27kDa protein 1	G3V913	PRFPDEWSQWFSSAGWPGYVRPLPAATAEGPAAVTL	8.74E-13	3913.91	-3.62

Heat Schock Protein 70	F1LZI1	VVTVPAYFNDSQRQATKDAGTIAGLNVL	4.63E-22	2947.55	2.45
H2-K region expressed gene 2, rat orthologue	Q6MGC4	ESQLRDLERQSEQQRETLAQLQQEFQRAQNAKAPGKA	6.84E-14	4309.19	0.24
Guanine nucleotide-binding protein G(q) subunit alpha	D4AE68	VDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTI	1.25E-09	3957.96	1.75
Gamma-synuclein	D4ACB0	YVGTKTKENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	5.59E-23	9001.48	-0.26
Gamma-synuclein	D4ACB0	VGTKTKENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	6.72E-20	8838.41	-0.57
Gamma-synuclein	D4ACB0	TKTKENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	5.85E-08	8682.32	-1.32
Gamma-synuclein	D4ACB0	KENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	1.25E-12	8352.14	0.48
Gamma-synuclein	F1LQ96	SVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	9.52E-58	7367.61	-0.1
Gamma-synuclein	F1LQ96	KTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRKEDLEPPAQDQEAKEQEEGEEAKSGGD	5.21E-39	6981.43	0.25
Gamma-synuclein	F1LQ96	LEPPAQDQEAKEQEEGEEAKSGGD	4.65E-07	2570.13	-0.49
Gamma-enolase	P07323	AGNSDLILPVPAFNVINGGSHAGNKLAMQEF	7.52E-14	3180.6	-0.68
Gamma-enolase	P07323	AGNSDLILPVPAFNVINGGSHAGNKL	7.56E-15	2574.36	0.83
Galectin-1	P11762	NLKPGECLKVRGELAPDAKSFVLNLGKDSNNL	1.55E-21	3438.83	1.2
Galectin-1	P11762	NLKPGECLKVRGELAPDAKSFVL	5.59E-24	2483.36	0.34
Galectin-1	P11762	PDGHEFKFPNRLNMEAI	2.52E-07	2013.97	0.91
Galectin-1	P11762	AADGDFKIKCVAFE	1.75E-09	1512.73	-0.17
Galectin-1	P11762	LAPDAKSFVLNL	2.22E-10	1286.72	0.11
Fructose-bisphosphate aldolase A	P05065	PHPYPALTPEQKKELADIAHRIVAPGKGILA	3.26E-24	3329.86	-0.11
Fructose-bisphosphate aldolase A	P05065	SYGRALQASALKAWGGKKENLKAAQEE	8.37E-14	2903.53	0.49
Fructose-bisphosphate aldolase A	P05065	IKRALANSLACQGKYTPSGQSGAAASES	8.29E-30	2765.38	0.81
Fructose-bisphosphate aldolase A	P05065	SNEEIAMATVTALRRTVPPAVPGVT	1.99E-15	2579.37	-0.37
Far upstream element-binding protein 1	Q32PX7	NFIVPTGKTGLIIGKGGETIKSISQQSGARIEL	2.41E-11	3411.91	0.24
Ezrin	P31977	FEQKTKRAEKELSEQIEKALQLEE	4.55E-12	2903.52	-0.61
Exocyst complex component 2	F1LMB9	GEASVFQQPKTQEEVCQL	4.04E-11	2019.95	-5.13
Eukaryotic translation initiation factor 4H	F8WG14	QVANPNSAIFGGARPREEVVQKEQE	7.82E-14	2752.38	-2.35
Eukaryotic translation initiation factor 4H	F8WG14	AIFGGARPREEVVQKEQE	8.38E-14	2042.05	0.6
Eukaryotic translation initiation factor 4B	Q5RKG9	LGNLPYDVTEDSIKDFFRGLNISAV	2.8E-10	2782.42	-0.74
Eukaryotic translation initiation factor 4B	Q5RKG9	GNLPYDVTEDSIKDFFRGLNISAV	5.31E-14	2669.33	0.31

Eukaryotic translation initiation factor 1A, Y-linked	B5DF60	NADEARSLKAYGELPEHAK	3.25E-07	2098.04	0.16
Eukaryotic translation initiation factor 1	B0K008	IGLAKDDQLKVHGF	2.31E-09	1539.84	-0.3
Estradiol 17-beta-dehydrogenase 2	Q62730	VNVSSMGAMIPFQMVA	7.39E-07	1680.8	-1.76
Erythrocyte protein band 4.1-like 3	A3E0T0	QTRRASALIDRPAPYFE	7.5E-15	1990.04	-0.33
ELKS/Rab6-interacting/CAST family member 1	D3ZC47	EAEMHVHHLESLLEQKE	3E-13	2057.97	-2.75
Ecotropic viral integration site 2A	Q5HZW9	LFLICTFLFLSTVVL	1.21E-08	1727.98	-6.06
E3 ubiquitin-protein ligase TRIM9	D3ZP18	PHQLSLHSSLQSLNAPGCNFETQSASYSQLVDIKKLLAVAWFAFD	2.32E-10	4960.49	0.19
Dynein heavy chain 1, axonemal	Q63164	LQEDLKLFSGIVSDL	6.04E-15	1675.9	-2.31
DNA primase	Q5M832	KTGRISVPIDFQKVDQFDPFVVPTISAICRELDVVSTTEKEKE	1.62E-08	4863.6	11.42
Dihydropyrimidinase-related protein 2	P47942	SAKTSPAKQQAPPVRNLHQSGFSLSGAQIDDNIPRRTTQRIVAPPGGRANITSLG	1.61E-24	5761.06	-0.5
Dihydropyrimidinase-related protein 2	P47942	QSGFSLSGAQIDDNIPRRTTQRIV	2.84E-23	2658.37	-2.28
Desumoylating isopeptidase 1	F1M410	AGCPRAIVAAATGP	4.48E-13	1253.67	4.81
Deoxyribonuclease	D3ZF29	EVRDPDLSAVSLLMEQINSVSKHE	6.89E-07	2695.36	3.54
DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted)	D4A9D6	LDAVIEAEHTLRELDALDANDELTPLGRIL	3.13E-13	3314.73	-2.8
D(1A) dopamine receptor	P18901	KAVAEIAGFWPLGPFCNIWVA	3.39E-13	2288.18	3.42
Cytochrome c, somatic	P62898	SYTDANKNKGITWGEDTLMEYLENPKKYIPGTKM	6.83E-13	3934.9	-1.47
Cytochrome c oxidase subunit 7C, mitochondrial	P80432	SHYEEGPGKNLPFSVENKWRLLLMMTVYFGSGFAAPFFIVRHQLLKK	1.29E-28	5481.85	-4.55
Cytochrome c oxidase subunit 7C, mitochondrial	P80432	TVYFGSGFAAPFFIVRHQLLKK	1.66E-12	2525.39	-0.94
Cytochrome c oxidase subunit 7A2, mitochondrial	P35171	FENKVPEKQKLFQEDNGMPVHLKGGTSDALLYRATMLLTVGGTAYAIYMLAMAAFPKKQN	1.67E-16	6644.41	-0.13
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	ELRPTLNELGISTPEELGLDKV	4.57E-34	2422.3	-1.6
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	ELRPTLNELGISTPEELGL	1.11E-18	2080.11	1.6
Cytochrome b-c1 complex subunit 7	B2RYS2	LKEVIRERKEREEWAKK	1.18E-20	2226.26	-0.43
Cysteine-rich protein 1	P63255	SAMFGPKGFGRGGAESHTFK	1.58E-14	2068	-0.37
Crystallin, zeta (Quinone reductase)-like 1	Q5XI39	KEFFPVGREVAGIVLDVGKKVSFFQPDD	2.98E-10	3122.64	1.45
Creatine kinase M-type	P00564	MVEMEKKLEKGQSIDDMIPAQK	1.12E-15	2547.27	-0.34
Copper transport protein ATOX1	Q9WUC4	IESEHSSDILLATLNKTGKAVSYLGPK	1.56E-27	2870.54	-0.93
Contactin-5	P97527	FYRQEGHSKGQVIETQKPQAVVPLPEAGVYIIEVRAYSEGGDGTAS	2.68E-08	4960.49	-1.95
Collagen alpha-1(II) chain	P05539	GGPGFLGAPGAKGEAGPTGARGPEG	1.99E-13	2164.07	2.93
Coagulation factor II, isoform CRA_a	G3V843	FEKKSLTDKTEKELLDSYIDGR	5.55E-26	2614.35	0.43

Clathrin coat assembly protein AP180	D3ZJG9	SPSPTPATQSPKKPPAKDPLADLNIKDFL	5.3E-13	3072.65	-1.36
Chromatin modifying protein 2A	B2RZB5	SLTDELSNLPSTGGSLSVAAGGKKAEATASALADADADLEERL	6.37E-10	4201.11	3.89
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	RPTLNELGISTPEELGLDKV	1.45E-10	2180.17	0.43
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	VGYDLVPEPKIIDA	5.57E-16	1527.82	-0.3
Actin, gamma-enteric smooth muscle	P63269	PLNPKANREKMTQIMFETF	2.13E-12	2294.16	-1.99
Serine protease inhibitor A3N	P09006	SAKLDPLIIAFDRPFLMIISDTETAIAPFLAKIFNPK	6.27E-09	4116.27	-0.09
Myelin protein P0	P06907	DSSKRGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	5.39E-24	4560.43	-2.29
Myelin protein P0	P06907	RGRQTPVLYAMLDHSRSTKAASEKKSKGLGESRKDKK	2.85E-15	4143.24	0.13
Lipoprotein lipase	Q06000	ISLYGTVAESENIPFTLP	1.49E-09	1949.99	-7.37
Cytochrome c oxidase subunit 6A1, mitochondrial	P10818	PFPWGDGNHTLFHNPHMNPLPTGYEDE	8.04E-15	3118.37	-0.5
Hereditary hemochromatosis protein homolog	O35799	SLKGWDYMFIVDFWTIMGN	1.48E-08	2322.09	-2.96
ATPase inhibitor, mitochondrial	Q03344	REKTREQLAALKKHHEDEIDHHSKEIER	9.64E-19	3461.78	-2.13
Alpha-1-antiproteinase	P17475	LPPQVKFDHPFIFMIVESETQSPLFVGKVIDPTR	6.75E-14	3911.07	-1.12
Heparin cofactor 2	Q64268	STQVRFTVDRPFLFLVYEHRTSCLLFMGRVANPAKS	5.65E-09	4185.18	-0.4
Inhibin beta C chain	Q9WUK5	VAGMPGISASFHTAVLNLLKANTDAGTARRGSCCVPT	3.51E-07	3685.85	-0.1
Prolargin	Q9EQP5	LDSNKIETIPSGYFKDFPNLA	1.62E-10	2368.19	-2.18
Chymase	P50339	AGIAQGIASYVHPNAKPPAVFT	8.59E-17	2208.17	0.42
Chymase	P50339	RISHYRPWINKILREN	3.74E-11	2094.16	0.06
Mast cell protease 1	P09650	TRISPYVPW	1.66E-10	1117.59	-0.33
Mast cell protease 2	P09650	VCAGVAHGIVS	9.97E-09	1011.52	-0.26
Midkine	Q9R1S9	STGTKARQGTLKKARYNAQCQETIRVTKPC	5.08E-09	3336.75	1.12
Alpha-2-HS-glycoprotein	P24090	SVESASGEVLHSPKVGQPGDAGAAGPVAPLCPGRVRYFKI	7.02E-22	4003.07	0.41
Lumican	P51886	YLDNNKITNIPDEYFNRFTGLQYL	3.67E-14	2950.45	-0.33
Lumican	P51886	IYLQHNQLKEEAVSASLKGLKSLE	2.75E-20	2697.47	-0.21
Fibroblast growth factor 1	P61149	SNGGHFLRILPDGTVDGTRDRSDQHIQL	3.78E-18	3103.55	0.01
Fibroblast growth factor 1	P61149	ILFLPLPV	1.39E-14	910.589	-0.18
Mast cell carboxypeptidase A	P21961	IRSHLNSIKA	1.33E-19	1137.66	1.26
Mast cell protease 1-like 4	Q6IE57	SNIHDIMLLK	4.9E-14	1182.64	-0.31
Cathepsin L1	P07154	AVATVGPISV	4.2E-15	912.528	0.81
Cathepsin B	P00787	SYSVSDSEKEIMAEIYKNGPVE	1.49E-17	2474.15	-1.97
Ubiquitin-60S ribosomal protein L40	P62986	IIEPSLRQL	1.34E-09	1067.63	0.13
Centrosomal protein of 63 kDa	D3ZLK6	EAQRKALAEQSEIIQA	1.29E-11	1783.94	0.52
Centromere protein Q	F1LQ20	EIDKIVETTESMTENIESLKTKIEILTNEVE	1.17E-07	3577.89	19.55

CD248 antigen, endosialin (Predicted)	D3ZN06	CQAGRGTSLLCVKQPSGGVGWS	9.54E-14	2190.09	7.37
CArG-binding factor A	Q9QX80	PIDPKLNKRRGFVFITF	2.9E-11	2047.17	-0.37
Cappuccino homolog (Mouse)	G3V6R9	EAFVRMIG	2.1E-06	921.484	6.66
Calpastatin	E9PT27	STLNKLSDKSGVNAALDDLIDTLGECEDTNKDDPPYTGPVVLDPMDSTYLEALGI	3.3E-09	5837.79	-0.37
Beta-soluble NSF attachment protein	P85969	HDSATSFVDAGNAYKKADPQEAINCLNAAI	4.62E-07	3133.47	-1.74
Beta-2 adrenergic receptor		HWYRATHKQAIDCYAKET	5.77E-09	2220.04	-3.36
ATP synthase-coupling factor 6, mitochondrial	P21571	NKELDPVQKLFLDKIREYKAKRLASGGPVDTGPEYQQEVDRELFKLKQMYGKGEMDKFPTFNFEDPKFEVLDKPQS	2.37E-09	8921.55	-0.24
ATP synthase-coupling factor 6, mitochondrial	P21571	ASGGPVDTGPEYQQEVDRELFKLKQMYGKGEMDKFPTFNFEDPKFEVLDKPQS	6.65E-11	6095.91	-1.45
ATP synthase subunit e, mitochondrial	P29419	VPPVQVSPLIKFGRYSALILGMAYGAKRYSYLKPRAEEERRIAAEEKKRLDELKRIERELAEAEDVSIFK	2.24E-20	8118.44	-0.12
ATP synthase subunit e, mitochondrial	P29419	VPPVQVSPLIKFGRYSALIL	9.14E-25	2196.3	-0.53
ATP synthase subunit beta, mitochondrial	P10719	DEGLPPILNA	1.58E-12	1037.54	0.13
AT rich interactive domain 4A (Rbp1 like) (Predicted), isoform CRA_b	D4ADE4	QFRTIHHHEPKVKEEK	1.74E-11	2042.05	-13.94
Argininosuccinate lyase	Q4QRB8	IRWSHWILSHAVALTRDLERLKEVQKRINVLPLGSGAIAGNPLGVDREFLCAELNFGA	5.56E-09	6448.49	11.12
Apoptosis regulator BAX	Q9JKL3	MKTGAFLLQGFIQDRAERMAGETPEL	6.05E-10	2908.48	6.72
Antisense paternally expressed gene 3	Q810D7	HSLKAKTLRFTGKSFRFHEFTIKRTMSWLENKNPTLKNTSNVTIFCMKTT	1.49E-07	5918.11	0.6
AN1-type zinc finger protein 6	Q6DGF4	PGPVSNQSLLSESVAPSQVDSTSVDK	1.71E-10	2627.3	2.64
Histone H4	P62804-2	DVVYALKRQGRTLYGFGG	8.22E-27	1999.06	-0.38
Histone H4	P62804-2	YALKRQGRTLYGFGG	2.41E-19	1685.9	-0.69
Microtubule-associated protein 2	P15146-2	DEELEVLMAAEAQAEPKDGSPDAPATPE	4.56E-12	2909.33	5.37
Alt Splice Form D3 dopamine receptor	P19020-2	LRERALQTTTNYL	5.16E-08	1577.86	5.98
cAMP-regulated phosphoprotein 19	Q712U5-2	MKNKQLPAAAPDKTEVTGDHIPTPQDLPQRKPSLVASKLAG	5.44E-09	4347.34	0.1
Myelin basic protein S	P02688-5	AEGQKPGFGYGGRASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	2.73E-13	5705.88	-0.06
Myelin basic protein S	P02688-5	RASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR	1.22E-07	4557.35	-0.12
Myelin basic protein S	P02688-4	GKGRGLSLSRFSWGGRDSRSGSPMARR	1.13E-06	2920.51	0.39
Myelin basic protein S	P02688-4	KGRGLSLSRFSWGGRDSRSGSPMARR	2.9E-10	2863.48	-1.38
Myelin basic protein S	P02688-4	GRGLSLSRFSWGGRDSRSGSPMARR	1.74E-11	2735.39	0.27
Myelin basic protein S	P02688-4	RGLSLSRFSWGGRDSRSGSPMARR	9.09E-16	2678.37	0.27
Myelin basic protein S	P02688-4	LSLSRFSWGGRDSRSGSPMARR	3.11E-10	2465.25	0.14
Myelin basic protein S	P02688-4	SLSRFSWGGRDSRSGSPMARR	1.47E-09	2352.16	-0.75
E3 ubiquitin-protein ligase	Q9JK66-5	FAGKELQNHLTVQNCDLE	1.31E-15	2057.98	-1.93
Myelin basic protein S	P02688-4	FKNIVTPRTPPPSQGKGRGLSLSRFSWGGRDSRSGSPMARR	2.89E-21	4483.36	-0.62
Myelin basic protein S	P02688-4	SGDRGAPKRGSGKDSHTRTTHYGSLPQKS	1.9E-35	4371.16	-0.31

		QRTQDENPVVH			
Myelin basic protein S	P02688-4	KNIVTPRTPPPSQGKGRGLSLSRFSWGGRDSRSGSPMARR	2.84E-15	4336.3	0.05
Myelin basic protein S	P02688-4	GAPKRGSGKDSHTRTTHYGSLPQKSQRTQDENPVVH	2.17E-13	3955.98	0.44
Myelin basic protein S	P02688-4	TPRTPPPSQGKGRGLSLSRFSWGGRDSRSGSPMARR	3.51E-17	3882	-0.09
Myelin basic protein S	P02688-4	STMDHARHGFLPRHRDTGILDSIGRFFSGDR	6.92E-07	3553.74	-1.82
Myelin basic protein S	P02688-4	TPPPSQGKGRGLSLSRFSWGGRDSRSGSPMARR	1.27E-12	3527.8	-0.59
Myelin basic protein S	P02688-4	SIGRFFSGDRGAPKRGSGKDSHTRTTHYG	7.15E-12	3134.54	-2.64
Myelin basic protein S	P02688-4	GAPKRGSGKDSHTRTTHYGSLP	7.53E-12	2309.16	0.41
Myelin basic protein S	P02688-4	RFSWGGRDSRSGSPMARR	1.55E-10	2065.01	-0.08
Myelin basic protein S	P02688-4	TPRTPPPSQGKGRGLSLSR	5.18E-13	1991.1	-0.13
Myelin basic protein S	P02688-4	TPPPSQGKGRGLSLSRF	2.29E-11	1783.97	-1.05
Myelin basic protein S	P02688-4	TPPPSQGKGRGLSLSR	3.06E-11	1636.9	0.14
Myelin basic protein S	P02688-4	SWGGRDSRSGSPMAR	2.85E-10	1605.74	-0.29
Serine protease HTRA3	D3ZA76-2	GEFVVAIGSPFALQNTVTTGIVSTAQRDG	4.12E-08	2934.53	5.16
Rho GTPase-activating protein 20	Q6REY9-2	QGSKDSASPSQLQEPFLMEQLPREMQCQFILKPTRLATAQQLSDSSHKT	3.15E-10	5514.72	-2.37
Protein Hikeshi	Q5M808-2	MNIVRTPSVAQIGISVELLDSLAQQTPVGS	1.45E-08	3122.71	16.44
Microtubule-associated protein 6	Q63560-2	RTEGHEEKPLPPAQSQTQEGGPAAGKASGADQRDTRRKAGPA	4.89E-22	4337.15	-2.27
Microtubule-associated protein 7	Q63560-2	SADARDPEGAGGAGVPAAGKASGADQRDTRRKAGPA	5.02E-13	3390.67	-0.17
Microtubule-associated protein 4	Q5M7W5-2	ADPFNVHHDDGLADLLFVSSGPTNA	7.59E-10	2608.21	-3.36
Hormone-sensitive lipase	P15304-2	DNMAFFSSQGPGETARRLSNVFAGVREQAL	1.12E-11	3254.58	-3.58
Fibrinogen alpha chain	P06399-2	KQVTKSYKMADEAASEAHQEGDTRTTK	3.27E-10	3009.45	-0.42
Breast carcinoma-amplified sequence 1 homolog	Q3ZB98-2	GNPHGVSAGKDIVDSEERKQEVDTL	5.55E-15	2679.32	5.42
Alpha-internexin		SAGLSLKKEEEEEEEEEEGASKEVTKKTSKVGESFEETLEETVVSTKK	4.56E-11	5330.63	1.17
Alpha-crystallin B chain	P23928	TSSLSSDGVLTVNGPRKQASGPERTIPITREEKPAVTAAPKK	2.29E-11	4373.37	0.35
Alpha-crystallin B chain	P23928	PFFPFHSPSRLFDQFFGEHLL	7.62E-20	2564.26	-0.96
Alpha-2B adrenergic receptor	P19328	GVPTSAKVPTLVSPLSS	4.67E-10	1638.93	6.12
Alpha-1-macroglobulin	Q63041	SFSYKPRAPSAEVEMTAYVLLAYLTSASSRPT	4.68E-12	3492.76	0.47
Aldose reductase	P07943	IRFPIQRNLVVIPKSVTPARIAENFKVFDF	3.24E-15	3514	0.84
Alanine--tRNA ligase, cytoplasmic	P50475	FANAGMNQFKPIFL	1.25E-13	1596.81	-1.29
ADP-ribosylation factor-like protein 3	P37996	ILIYVIDSADRKRFEETGQELTELLEEEKL	1.58E-10	3578.89	6.05
Actin, cytoplasmic 2	F2Z3T1	ALDFEQEMATAASSSSLEKSYELPDGQVITI	5.94E-13	3329.59	2.05
Ab2-427	Q7TP39	HPPIRSPSASSVGSRGSSGSSSKPA	1.32E-12	2379.19	2.03
Ab1-334	Q7TP85	VAHIFAIYVAQGTQVT	6.91E-07	1716.92	-15.12

60S ribosomal protein L41	P62948	MRAKWRKKRMRRLKRKRRKMRQRSK	2.36E-07	3454.1	1.37
60S ribosomal protein L39	P62893	SSHKTFRIKRFLAKKQKQNRPIPQWIRMKTGNKIRYNSKRRHWRRTKLGL	2.15E-15	6271.61	-0.17
60S ribosomal protein L34	B2RZD4	RRRLSYNTASNKTRLSRTPGNRIV	4.19E-17	2815.57	-2.05
60S acidic ribosomal protein P2	P02401	AALGGNSNPSAKDIKKILDSVGIEADDERLNKVISEL	1.88E-08	3879.07	1.5
60S acidic ribosomal protein P1	P19944	ALILHDDEVTVTEDKINALIKA	1.05E-13	2420.32	-0.98
40S ribosomal protein S30	P62864	VNVVPTFGKKKGPNANS	6.65E-09	1755.96	-0.83
40S ribosomal protein S28	P62859	DDTSRSIIRNVKGPVREGDVLTLLESEREARRLR	3.52E-15	3935.14	-0.19
40S ribosomal protein S28	P62859	SIIRNVKGPVREGDVLTLLESEREARRLR	1.2E-15	3360.91	-0.32
40S ribosomal protein S19	P17074	PGVTVKDVNQQEFVRALAAFLKKSGKLKVPEWVDTVKLAKHKELAPYDENW	7.01E-07	5819.16	-0.8
40S ribosomal protein S19	P17074	PGVTVKDVNQQEFVRALAAFL	6.18E-09	2301.25	0.32
40S ribosomal protein S19	P17074	PGVTVKDVNQQEFVRALAA	1.83E-14	2041.1	-0.03
40S ribosomal protein S16	P62250	PSKGPLQSVQVF	6.8E-12	1285.7	-0.75
3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	G3V6R7	LNYVPLEAQEWKTEGRCIGLTN	6.19E-08	2533.27	1.99
28 kDa heat- and acid-stable phosphoprotein	Q62785	AIIRKQREEAARKKEEERKAKDDATLSGKR	3.28E-15	3509.95	0.18
10 kDa heat shock protein, mitochondrial	P26772	KVGDKVLLPEYGGTKVVLDDKDYFLFRDGDILGKYVD	5.29E-10	4189.2	-0.59

Table S3. Details on the mass spectral calibrations using internal standards for the MALDI MS regional release profiling experiments.

1) Calibration for DR region release mass spectra

Algorithm: ReferenceMassAssignment

Mode: Tof Cubic Enhanced

Result: OK

Calibration Quality : 175.914

Assigned Calibrants: 9

Calibrant 1:

- Calibrant Name: Na+
- Calibrant Mass: 22.990 Da
- Mass After Calibration: 22.996 Da
- Mass Error: 271.180 ppm

Calibrant 2:

- Calibrant Name: K+
- Calibrant Mass: 38.964 Da
- Mass After Calibration: 38.949 Da
- Mass Error: 390.232 ppm

Calibrant 3:

- Calibrant Name: DHB_[M+H]+_mono
- Calibrant Mass: 155.034 Da
- Mass After Calibration: 155.047 Da
- Mass Error: 82.129 ppm

Calibrant 4:

- Calibrant Name: DHB + Na
- Calibrant Mass: 177.016 Da
- Mass After Calibration: 177.020 Da
- Mass Error: 22.481 ppm

Calibrant 5:

- Calibrant Name: DHB + K
- Calibrant Mass: 192.990 Da
- Mass After Calibration: 193.007 Da
- Mass Error: 86.861 ppm

Calibrant 6:

- Calibrant Name: DHB ion +
- Calibrant Mass: 439.200 Da
- Mass After Calibration: 439.165 Da
- Mass Error: 80.467 ppm

Calibrant 7:

- Calibrant Name: Neurofilament 3, medium Acyl (SYTLDSLGNPSAYRRVTETR)
- Calibrant Mass: 2328.158 Da
- Mass After Calibration: 2328.201 Da
- Mass Error: 18.289 ppm

Calibrant 8:

Calibrant Name: Neurofilament 3, medium (VEAPKLKVQHKFVEEIIEETKVEDEK).
Calibrant Mass: 3094.667 Da
Mass After Calibration: 3094.630 Da
Mass Error: 11.839 ppm
Calibrant 9:
Calibrant Name: Thymosin beta 4 acetate + [Mono]
Calibrant Mass: 4961.486 Da
Mass After Calibration: 4961.491 Da
Mass Error: 0.987 ppm

2) Calibration for DRG region release mass spectra

Algorithm: ReferenceMassAssignment
Mode: Tof Cubic Enhanced
Result: OK
Calibration Quality : 140.633
Assigned Calibrants: 9
Calibrant 1:
Calibrant Name: Na+
Calibrant Mass: 22.990 Da
Mass After Calibration: 22.995 Da
Mass Error: 210.057 ppm
Calibrant 2:
Calibrant Name: K+
Calibrant Mass: 38.964 Da
Mass After Calibration: 38.952 Da
Mass Error: 309.635 ppm
Calibrant 3:
Calibrant Name: DHB_[M+H]+_mono
Calibrant Mass: 155.034 Da
Mass After Calibration: 155.051 Da
Mass Error: 105.786 ppm
Calibrant 4:
Calibrant Name: DHB + Na
Calibrant Mass: 177.016 Da
Mass After Calibration: 177.025 Da
Mass Error: 49.812 ppm
Calibrant 5:
Calibrant Name: DHB ion +
Calibrant Mass: 439.200 Da
Mass After Calibration: 439.172 Da
Mass Error: 63.931 ppm
Calibrant 6:
Calibrant Name: Neurofilament 3, medium Acyl (SYTLDSLGNPSAYRRVTETR)
Calibrant Mass: 2328.158 Da
Mass After Calibration: 2328.176 Da

Mass Error: 7.604 ppm

Calibrant 7:

Calibrant Name: Vimentin

Calibrant Mass: 2335.160 Da

Mass After Calibration: 2335.191 Da

Mass Error: 13.326 ppm

Calibrant 8:

Calibrant Name: Neurofilament 3, medium (VEAPKLKVQHKFVEEIIEETKVEDEK).

Calibrant Mass: 3094.667 Da

Mass After Calibration: 3094.620 Da

Mass Error: 15.030 ppm

Calibrant 9:

Calibrant Name: Thymosin beta 4 acetate + [Mono]

Calibrant Mass: 4961.486 Da

Mass After Calibration: 4961.494 Da

Mass Error: 1.570 ppm

3) Calibration for spinal nerve region release mass spectra

Algorithm: ReferenceMassAssignement

Mode: Tof Cubic Enhanced

Quality After Calibration: 138.039

Assigned Calibrants: 12

Calibrant 1:

Calibrant Name: Na+

Calibrant Mass: 22.990 Da

Mass After Calibration: 22.995 Da

Mass Error: 234.919 ppm

Calibrant 2:

Calibrant Name: K+

Calibrant Mass: 38.964 Da

Mass After Calibration: 38.950 Da

Mass Error: 342.179 ppm

Calibrant 3:

Calibrant Name: DHB_[M+H]+_mono

Calibrant Mass: 155.034 Da

Mass After Calibration: 155.051 Da

Mass Error: 103.993 ppm

Calibrant 4:

Calibrant Name: DHB + Na

Calibrant Mass: 177.016 Da

Mass After Calibration: 177.013 Da

Mass Error: 16.599 ppm

Calibrant 5:

Calibrant Name: DHB + K

Calibrant Mass: 192.990 Da

```
  Mass After Calibration: 193.008 Da
  Mass Error: 94.648 ppm
Calibrant 6:
  Calibrant Name: 9-AA [M+H]+
  Calibrant Mass: 195.092 Da
  Mass After Calibration: 195.105 Da
  Mass Error: 70.810 ppm
Calibrant 7:
  Calibrant Name: DHB -H + 2Na
  Calibrant Mass: 198.998 Da
  Mass After Calibration: 198.982 Da
  Mass Error: 81.612 ppm
Calibrant 8:
  Calibrant Name: DHB ion +
  Calibrant Mass: 439.200 Da
  Mass After Calibration: 439.168 Da
  Mass Error: 72.100 ppm
Calibrant 9:
  Calibrant Name: Neurofilament 3, medium Acyl (SYTLDSLGNPSAYRRVTETR)
  Calibrant Mass: 2328.158 Da
  Mass After Calibration: 2328.185 Da
  Mass Error: 11.455 ppm
Calibrant 10:
  Calibrant Name: Vimentin
  Calibrant Mass: 2335.160 Da
  Mass After Calibration: 2335.181 Da
  Mass Error: 8.825 ppm
Calibrant 11:
  Calibrant Name: Neurofilament 3, medium (VEAPKLKVQHKFVEEIIEETKVEDEK).
  Calibrant Mass: 3094.667 Da
  Mass After Calibration: 3094.623 Da
  Mass Error: 14.056 ppm
Calibrant 12:
  Calibrant Name: Thymosin beta 4 acetate + [Mono]
  Calibrant Mass: 4961.486 Da
  Mass After Calibration: 4961.493 Da
  Mass Error: 1.370 ppm
```

4) Calibration for VR region release mass spectra

```
Algorithm: ReferenceMassAssignement
Mode: Tof Cubic Enhanced
Result: OK
Calibration Quality : 48.924
Assigned Calibrants: 10
Calibrant 1:
  Calibrant Name: Na+
```

```
  Calibrant Mass: 22.990 Da
  Mass After Calibration: 22.991 Da
  Mass Error: 56.875 ppm
Calibrant 2:
  Calibrant Name: K+
  Calibrant Mass: 38.964 Da
  Mass After Calibration: 38.960 Da
  Mass Error: 86.371 ppm
Calibrant 3:
  Calibrant Name: DHB_[M+H]+_mono
  Calibrant Mass: 155.034 Da
  Mass After Calibration: 155.046 Da
  Mass Error: 75.865 ppm
Calibrant 4:
  Calibrant Name: DHB + Na
  Calibrant Mass: 177.016 Da
  Mass After Calibration: 177.005 Da
  Mass Error: 61.098 ppm
Calibrant 5:
  Calibrant Name: DHB + K
  Calibrant Mass: 192.990 Da
  Mass After Calibration: 192.996 Da
  Mass Error: 30.433 ppm
Calibrant 6:
  Calibrant Name: DHB ion +
  Calibrant Mass: 439.200 Da
  Mass After Calibration: 439.192 Da
  Mass Error: 18.346 ppm
Calibrant 7:
  Calibrant Name: Neurofilament 3, medium Acyl (SYTLDSLGNPSAYRRVTETR)
  Calibrant Mass: 2328.158 Da
  Mass After Calibration: 2328.177 Da
  Mass Error: 7.789 ppm
Calibrant 8:
  Calibrant Name: Vimentin
  Calibrant Mass: 2335.160 Da
  Mass After Calibration: 2335.160 Da
  Mass Error: 0.017 ppm
Calibrant 9:
  Calibrant Name: Neurofilament 3, medium (VEAPKLKVQHKFVEEIIEETKVEDEK).
  Calibrant Mass: 3094.667 Da
  Mass After Calibration: 3094.649 Da
  Mass Error: 5.901 ppm
Calibrant 10:
  Calibrant Name: Thymosin beta 4 acetate + [Mono]
```

Calibrant Mass: 4961.486 Da
Mass After Calibration: 4961.490 Da
Mass Error: 0.683 ppm

Table S4. Peaks detected in releasates from different regions, with their identities assigned via matching the MALDI MS and FT MS data sets and information on their protein of origin. For several cases, an ~1 and 2 Da difference between the molecular mass of the analyte and predicted molecule appears because the intensity was low and only the most intense monoisotopic peaks were observed (e.g., *m/z* 4977.5 for thymosin beta 4 related peptide). Shading is used to alternate between groups of peaks of the same nominal mass values.

Origin of data or information	**Protein**	**[M+H]+ (calculated or observed)**	**Protein Name**
Dorsal root		616.30	
Spinal nerve		616.30	
DRG		616.31	
Ventral root		624.28	
Ventral root		626.29	
Ventral root		642.30	
Dorsal root		643.17	
Ventral root		643.30	
Dorsal root		709.33	
Ventral root		732.30	
Spinal nerve		733.19	
Dorsal root		733.20	
Spinal nerve		734.20	
Dorsal root		734.20	
Ventral root		778.34	
Ventral root		796.28	
Spinal nerve		815.62	
Spinal nerve		869.18	
DRG		869.19	
Dorsal root		869.21	
Ventral root		871.29	
ProSight	P02091 - HBB1_RAT	871.49	Hemoglobin subunit beta-1
Spinal nerve		875.21	
Dorsal root		881.39	
Ventral root		887.30	
Spinal nerve		891.18	
Dorsal root		907.35	
Spinal nerve		907.36	
PEAKS	sp|P31000|VIME_RAT	907.46	Vimentin
Ventral root		912.36	
PEAKS	sp|P02091|HBB1_RAT	912.47	Hemoglobin subunit beta-1
Ventral root		962.34	
Spinal nerve		1053.21	
Ventral root		1053.37	

DRG		1066.24	
PEAKS	sp|P19527|NFL_RAT	1085.53	Neurofilament light polypeptide
Dorsal root		1085.70	
PEAKS	sp|P02688|MBP_RAT	1098.57	Myelin basic protein
Dorsal root		1098.73	
DRG		1103.69	
Dorsal root		1108.74	
PEAKS	sp|P07150|ANXA1_RAT	1165.58	Annexin A1
DRG		1165.82	
DR		1165.85	
Ventral root		1231.47	
PEAKS	sp|P31000|VIME_RAT	1231.67	Vimentin
Dorsal root		1349.48	
PEAKS	sp|P19527|NFL_RAT	1370.68	Neurofilament light polypeptide
Dorsal root		1370.83	
PEAKS	sp|P19527|NFL_RAT	1379.77	Neurofilament light polypeptide
PEAKS	sp|P31000|VIME_RAT	1379.79	Vimentin
Dorsal root		1379.87	
Ventral root		1397.54	
PEAKS	tr|B1H216|B1H216_RAT	1450.81	Hemoglobin alpha, adult chain 2
Dorsal root		1450.87	
PEAKS	sp|P62329|TYB4_RAT	1451.66	Thymosin beta-4
Ventral root		1488.57	
Dorsal root		1508.92	
PEAKS	sp|P02770|ALBU_RAT	1556.74	Serum albumin
PEAKS	sp|P62859|RS28_RAT	1556.85	40S ribosomal protein S28
Dorsal root		1556.90	
PEAKS	sp|P20788|UCRI_RAT	1655.94	Cytochrome b-c1 complex subunit Rieske, mitochondrial
Dorsal root		1655.98	
Ventral root		1671.83	
PEAKS	sp|P02688|MBP_RAT	1671.86	Myelin basic protein
DRG		1671.95	
Dorsal root		1671.97	
ProSight	P12839 - NFM_RAT	1700.99	Neurofilament 3, medium
DRG		1701.01	
Dorsal root		1701.07	
PEAKS	sp|P19527|NFL_RAT	1701.81	Neurofilament light polypeptide
Spinal nerve		1701.97	
Ventral root		1703.85	
ProSight	P12839 - NFM_RAT	1703.91	Neurofilament 3, medium
PEAKS	tr|G3V7S2|G3V7S2_RAT	1703.91	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Dorsal root		1704.00	

ProSight	P12839 - NFM_RAT	1741.84	Neurofilament 3, medium
PEAKS	tr|G3V7S2|G3V7S2_RAT	1741.84	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
DRG		1741.94	
Spinal nerve		1741.95	
PEAKS	sp|P0CC09|H2A2A_RAT	1741.97	Histone H2A type 2-A
Dorsal root		1741.98	
PEAKS	sp|P02688|MBP_RAT	1762.88	Myelin basic protein
DRG		1762.94	
PEAKS	sp|P19527|NFL_RAT	1763.85	Neurofilament light polypeptide
PEAKS	sp|P31000|VIME_RAT	1763.94	Vimentin
Dorsal root		1763.98	
Ventral root		1784.93	
ProSight	P02688 - MBP_RAT	1784.94	Myelin basic protein S (Alt Splice Form 3)
ProSight	P02688 - MBP_RAT	1784.97	Myelin basic protein S (Alt Splice Form 4)
ProSight	Q9QXU9 - PCSK1_RAT	1784.97	Peptide (Little SAAS) [42-59] in ProSAAS
Spinal nerve		1784.99	
DRG		1785.00	
Dorsal root		1785.04	
PEAKS	sp|Q5M7W5|MAP4_RAT	1794.82	Microtubule-associated protein 4
Dorsal root		1795.00	
Spinal nerve		1812.98	
Dorsal root		1813.01	
ProSight	P12839 - NFM_RAT	1836.90	Neurofilament 3, medium
DRG		1836.99	
Spinal nerve		1836.99	
Dorsal root		1837.02	
PEAKS	sp|P19527|NFL_RAT	1848.86	Neurofilament light polypeptide
DRG		1848.99	
PEAKS	sp|P02688|MBP_RAT	1853.01	Myelin basic protein
DRG		1853.04	
Spinal nerve		1853.05	
Dorsal root		1853.08	
PEAKS	sp|P02688|MBP_RAT	1855.98	Myelin basic protein
Dorsal root		1856.07	
Ventral root		1911.95	
PEAKS	sp|P02688|MBP_RAT	1911.96	Myelin basic protein
Ventral root		1913.96	
PEAKS	tr|D4A115|D4A115_RAT	1913.96	Protein Col6a3
Ventral root		1939.05	
Spinal nerve		1939.09	
PEAKS	tr|G3V7S2|G3V7S2_RAT	1939.10	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
DRG		1939.12	

Dorsal root		1939.15	
Ventral root		1957.00	
PEAKS	sp|P02688|MBP_RAT	1957.03	Myelin basic protein
PEAKS	sp|P13668|STMN1_RAT	1959.01	Stathmin
DRG		1959.05	
Spinal nerve		1959.05	
Dorsal root		1959.09	
PEAKS	sp|P02688|MBP_RAT	1962.99	Myelin basic protein
Spinal nerve		1963.04	
DRG		1963.05	
Dorsal root		1963.05	
PEAKS	sp|P19527|NFL_RAT	1985.92	Neurofilament light polypeptide
DRG		1986.03	
Dorsal root		1986.07	
PEAKS	sp|P19527|NFL_RAT	1993.94	Neurofilament light polypeptide
Ventral root		1993.97	
PEAKS	sp|P02688|MBP_RAT	1994.04	Myelin basic protein
PEAKS	sp|P19527|NFL_RAT	2008.93	Neurofilament light polypeptide
PEAKS	sp|P31000|VIME_RAT	2008.93	Vimentin
Ventral root		2008.94	
DRG		2009.01	
Spinal nerve		2009.02	
Dorsal root		2009.05	
PEAKS	sp|P02688|MBP_RAT	2020.01	Myelin basic protein
Spinal nerve		2020.07	
DRG		2020.08	
Dorsal root		2020.10	
PEAKS	sp|P02688|MBP_RAT	2028.07	Myelin basic protein
Ventral root		2028.08	
Spinal nerve		2028.08	
Dorsal root		2028.12	
DRG		2062.09	
PEAKS	sp|P19527|NFL_RAT	2102.10	Neurofilament light polypeptide
Dorsal root		2102.14	
PEAKS	sp|P02688|MBP_RAT	2108.03	Myelin basic protein
Ventral root		2108.06	
PEAKS	sp|P02688|MBP_RAT	2110.06	Myelin basic protein
DRG		2110.11	
Spinal nerve		2110.11	
Dorsal root		2110.13	
PEAKS	tr|G3V7S2|G3V7S2_RAT	2140.99	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Ventral root		2141.01	
DRG		2141.10	

Spinal nerve		2141.11	
Dorsal root		2141.14	
ProSight	P19527	2149.99	Neurofilament light polypeptide
PEAKS	sp|P10111|PPIA_RAT	2150.05	Peptidyl-prolyl cis-trans isomerase A
DRG		2150.10	
Dorsal root		2150.14	
Ventral root		2158.07	
PEAKS	sp|P19527|NFL_RAT	2158.10	Neurofilament light polypeptide
PEAKS	sp|P69897|TBB5_RAT	2158.11	Tubulin beta-5 chain
DRG		2158.12	
Dorsal root		2158.16	
PEAKS	sp|P02688|MBP_RAT	2167.08	Myelin basic protein
Spinal nerve		2167.13	
DRG		2167.13	
Dorsal root		2167.15	
PEAKS	sp|P02091|HBB1_RAT	2167.17	Hemoglobin subunit beta-1
PEAKS	sp|P19527|NFL_RAT	2174.00	Neurofilament light polypeptide
DRG		2174.05	
Dorsal root		2174.11	
PEAKS	sp|P19527|NFL_RAT	2189.13	Neurofilament light polypeptide
Dorsal root		2190.16	
Ventral root		2202.15	
PEAKS	sp|P06907|MYP0_RAT	2202.16	Myelin protein P0
ProSight	P01946 - HBA_RAT	2202.16	Hemoglobin subunit alpha-1/2
Dorsal root		2202.18	
Ventral root		2210.04	
PEAKS	sp|P61972|NTF2_RAT	2210.05	Nuclear transport factor 2
DRG		2210.08	
Spinal nerve		2210.09	
Dorsal root		2210.12	
PEAKS	sp|P05942|S10A4_RAT	2217.15	Protein S100-A4
Dorsal root		2217.22	
PEAKS	sp|P31000|VIME_RAT	2257.11	Vimentin
PEAKS	sp|P02688|MBP_RAT	2257.13	Myelin basic protein
DRG		2257.16	
Spinal nerve		2257.16	
Dorsal root		2263.25	
PEAKS	sp|P06907|MYP0_RAT	2263.27	Myelin protein P0
PEAKS	sp|P19527|NFL_RAT	2310.09	Neurofilament light polypeptide
Ventral root		2310.10	
DRG		2310.15	
ProSight	P02688 - MBP_RAT	2310.16	Myelin basic protein S (Alt Splice Form 3)
Ventral root		2313.15	

PEAKS	sp|P11762|LEG1_RAT	2313.20	Galectin-1
ProSight	P12839 - NFM_RAT	2328.15	Neurofilament 3, medium
PEAKS	tr|G3V7S2|G3V7S2_RAT	2328.15	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
DRG		2328.18	
Ventral root		2328.18	
Spinal nerve		2328.19	
DR		2328.20	
PEAKS	tr|G3V7S2|G3V7S2_RAT	2329.18	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
DRG		2329.19	
ProSight	P12839 - NFM_RAT	2329.19	Neurofilament 3, medium
PEAKS	sp|P31000|VIME_RAT	2335.15	Vimentin
Ventral root		2335.16	
Spinal nerve		2335.18	
DRG		2335.19	
Dorsal root		2335.21	
DRG		2336.14	
ProSight	sp|P19527|NFL_RAT	2337.07	Neurofilament light polypeptide
Dorsal root		2337.17	
PEAKS	sp|Q03344|ATIF1_RAT	2351.18	ATPase inhibitor, mitochondrial
DRG		2351.18	
Spinal nerve		2358.21	
PEAKS	sp|P19527|NFL_RAT	2358.21	Neurofilament light polypeptide
Ventral root		2358.23	
DRG		2358.23	
Dorsal root		2358.24	
Spinal nerve		2373.20	
PEAKS	sp|P19527|NFL_RAT	2374.21	Neurofilament light polypeptide
DRG		2374.22	
Dorsal root		2374.24	
PEAKS	sp|P19527|NFL_RAT	2377.12	Neurofilament light polypeptide
DRG		2377.18	
Dorsal root		2377.21	
PEAKS	sp|P31000|VIME_RAT	2391.15	Vimentin
Spinal nerve		2391.19	
Ventral root		2406.24	
PEAKS	sp|P06907|MYP0_RAT	2406.29	Myelin protein P0
PEAKS	tr|G3V7S2|G3V7S2_RAT	2415.18	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Ventral root		2415.20	
DRG		2415.22	
PEAKS	sp|P19527|NFL_RAT	2415.24	Neurofilament light polypeptide
PEAKS	tr|F1LRZ7|F1LRZ7_RAT	2425.19	Neurofilament heavy polypeptide
Ventral root		2425.19	

PEAKS	sp|P19527|NFL_RAT	2438.12	Neurofilament light polypeptide
Ventral root		2438.17	
Spinal nerve		2438.21	
DRG		2447.27	
Spinal nerve		2447.27	
Dorsal root		2447.32	
PEAKS	sp|P68370|TBA1A_RAT	2447.33	Tubulin alpha-1A chain
Ventral root		2448.28	
PEAKS	sp|P62902|RL31_RAT	2448.36	60S ribosomal protein L31
Dorsal root		2457.26	
PEAKS	tr|G3V7S2|G3V7S2_RAT	2457.28	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
ProSight	P12839 - NFM_RAT	2457.28	Neurofilament 3, medium
PEAKS	sp|P04631|S100B_RAT	2464.21	Protein S100-B
Spinal nerve		2464.29	
Ventral root		2470.29	
PEAKS	sp|P02688|MBP_RAT	2470.37	Myelin basic protein
Dorsal root		2480.35	
PEAKS	tr|G3V8L9|G3V8L9_RAT	2480.48	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
PEAKS	sp|Q6PDU1|SRSF2_RAT	2481.19	Serine/arginine-rich splicing factor 2
Ventral root		2481.25	
DRG		2499.25	
Ventral root		2499.26	
Dorsal root		2499.26	
Spinal nerve		2499.26	
DRG		2501.25	
Dorsal root		2501.27	
DRG		2512.27	
Spinal nerve		2512.28	
PEAKS	sp|P02688|MBP_RAT	2512.30	Myelin basic protein
Ventral root		2513.25	
Dorsal root		2513.30	
Ventral root		2515.25	
Ventral root		2534.28	
Dorsal root		2534.36	
Ventral root		2539.22	
Ventral root		2570.32	
Spinal nerve		2570.33	
DRG		2570.33	
Dorsal root		2570.35	
ProSight	P12839 - NFM_RAT	2570.36	Neurofilament 3, medium
Dorsal root		2594.38	
PEAKS	sp|P02688|MBP_RAT	2599.27	Myelin basic protein

Ventral root		2599.29	
ProSight	P12839 - NFM_RAT	2606.22	Neurofilament 3, medium
Ventral root		2606.27	
PEAKS	tr|F1LRZ7|F1LRZ7_RAT	2606.36	Neurofilament heavy polypeptide
DRG		2618.30	
Dorsal root		2618.33	
Ventral root		2618.33	
PEAKS	tr|G3V7S2|G3V7S2_RAT	2618.35	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
ProSight	P12839 - NFM_RAT	2618.35	Neurofilament 3, medium
PEAKS	tr|F1M7P4|F1M7P4_RAT	2628.30	Peripherin
Ventral root		2629.30	
Ventral root		2643.38	
PEAKS	sp|P06907|MYP0_RAT	2643.46	Myelin protein P0
DRG		2663.32	
PEAKS	sp|Q6JE36|NDRG1_RAT	2663.38	Protein NDRG1
PEAKS	sp|P31000|VIME_RAT	2664.28	Vimentin
Dorsal root		2664.33	
DRG		2665.31	
Ventral root		2667.35	
PEAKS	sp|P02688|MBP_RAT	2670.31	Myelin basic protein
Ventral root		2670.35	
Ventral root		2675.34	
PEAKS	sp|P02688|MBP_RAT	2686.30	Myelin basic protein
Ventral root		2687.33	
DRG		2702.25	
PEAKS	sp|P19527|NFL_RAT	2702.26	Neurofilament light polypeptide
Spinal nerve		2702.27	
Dorsal root		2702.28	
Ventral root		2702.31	
Dorsal root		2711.36	
DRG		2711.37	
Ventral root		2711.38	
PEAKS	sp|P02688|MBP_RAT	2711.42	Myelin basic protein
PEAKS	tr|F1LRZ7|F1LRZ7_RAT	2721.35	Neurofilament heavy polypeptide
Ventral root		2723.38	
PEAKS	sp|P06907|MYP0_RAT	2723.42	Myelin protein P0
PEAKS	sp|P31000|VIME_RAT	2723.46	Vimentin
DRG		2724.31	
PEAKS	tr|Q8R4A2|Q8R4A2_RAT	2724.32	Caveolin 1
Dorsal root		2724.36	
Ventral root		2742.34	
DRG		2746.37	
Dorsal root		2746.41	

ProSight	P12839 - NFM_RAT	2746.44	Neurofilament 3, medium
PEAKS	tr|G3V7S2|G3V7S2_RAT	2746.44	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Spinal nerve		2763.34	
Dorsal root		2763.35	
DRG		2763.35	
PEAKS	sp|P19527|NFL_RAT	2763.36	Neurofilament light polypeptide
PEAKS	sp|P31000|VIME_RAT	2763.41	Vimentin
Ventral root		2764.37	
DRG		2777.34	
Dorsal root		2777.35	
Spinal nerve		2777.35	
PEAKS	sp|P31000|VIME_RAT	2777.36	Vimentin
Ventral root		2777.39	
Ventral root		2780.40	
PEAKS	sp|P62630|EF1A1_RAT	2780.68	Elongation factor 1-alpha 1
PEAKS	sp|P19527|NFL_RAT	2792.32	Neurofilament light polypeptide
DRG		2798.36	
Spinal nerve		2798.37	
Dorsal root		2799.38	
PEAKS	sp|P02688|MBP_RAT	2826.41	Myelin basic protein
Ventral root		2826.43	
PEAKS	sp|P62329|TYB4_RAT	2829.40	Thymosin beta-4
Dorsal root		2830.39	
DRG		2865.32	
PEAKS	sp|P19527|NFL_RAT	2865.32	Neurofilament light polypeptide
Spinal nerve		2865.35	
Dorsal root		2865.36	
Ventral root		2865.38	
Spinal nerve		2886.32	
PEAKS	sp|P19527|NFL_RAT	2886.32	Neurofilament light polypeptide
Dorsal root		2886.34	
DRG		2886.35	
Ventral root		2887.38	
DRG		2964.42	
Dorsal root		2964.44	
PEAKS	sp|P63312|TYB10_RAT	2964.49	Thymosin beta-10
Ventral root		2964.50	
PEAKS	sp|P02688|MBP_RAT	2986.34	Myelin basic protein
Ventral root		2987.48	
Ventral root		3005.48	
Dorsal root		3014.55	
PEAKS	tr|G3V7S2|G3V7S2_RAT	3014.63	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.

ProSight	P12839 - NFM_RAT	3014.63	Neurofilament 3, medium
Ventral root		3015.53	
Ventral root		3020.47	
PEAKS	sp|P02688|MBP_RAT	3020.49	Myelin basic protein
ProSight	P12839 - NFM_RAT	3033.47	Neurofilament 3, medium
PEAKS	tr|G3V7S2|G3V7S2_RAT	3033.47	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Dorsal root		3034.47	
Ventral root		3034.49	
PEAKS	sp|P19527|NFL_RAT	3042.43	Neurofilament light polypeptide
DRG		3042.44	
Spinal nerve		3042.45	
Dorsal root		3042.46	
Ventral root		3042.46	
Ventral root		3052.54	
PEAKS	sp|Q63544|SYUG_RAT	3052.61	Gamma-synuclein
DRG		3065.48	
Spinal nerve		3065.54	
Dorsal root		3065.54	
Ventral root		3065.60	
PEAKS	sp|P02688|MBP_RAT	3065.62	Myelin basic protein
Dorsal root		3073.57	
PEAKS	sp|P06907|MYP0_RAT	3073.65	Myelin protein P0
Ventral root		3073.68	
DRG		3074.56	
PEAKS	tr|G3V7S2|G3V7S2_RAT	3074.62	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
PEAKS	tr|G3V7S2|G3V7S2_RAT	3078.52	Neurofilament, medium. Uncharacterized protein. Gene - Nefm.
Ventral root		3078.58	
DRG		3079.47	
PEAKS	sp|P02091|HBB1_RAT	3088.57	Hemoglobin subunit beta-1
Ventral root		3089.55	
Dorsal root		3089.56	
PEAKS	sp|P06907|MYP0_RAT	3089.64	Myelin protein P0
DRG		3094.62	
Spinal nerve		3094.62	
Dorsal root		3094.63	
Ventral root		3094.65	
ProSight	P12839 - NFM_RAT	3094.66	Neurofilament 3, medium
DRG		3108.54	
Spinal nerve		3108.55	
Dorsal root		3108.61	
DRG		3116.65	
Spinal nerve		3117.53	

Dorsal root		3117.55	
PEAKS	sp|P69897|TBB5_RAT	3119.50	Tubulin beta-5 chain
Dorsal root		3119.53	
Dorsal root		3132.51	
Ventral root		3132.55	
PEAKS	tr|Q8R4A2|Q8R4A2_RAT	3177.55	Caveolin 1
Ventral root		3177.55	
PEAKS	sp|P19527|NFL_RAT	3200.49	Neurofilament light polypeptide
Dorsal root		3200.51	
Spinal nerve		3200.51	
DRG		3200.53	
Ventral root		3200.59	
ProSight	|P69897 |TBB5_RAT	3200.59	Tubulin beta-5 chain
DRG		3200.76	
DRG		3211.56	
Dorsal root		3211.56	
Spinal nerve		3211.58	
Dorsal root		3231.58	
Dorsal root		3297.52	
PEAKS	sp|Q63544|SYUG_RAT	3297.53	Gamma-synuclein
DRG		3297.53	
Spinal nerve		3297.53	
Ventral root		3299.62	
Spinal nerve		3332.60	
Dorsal root		3397.58	
PEAKS	tr|D3ZAY2|D3ZAY2_RAT	3397.69	Protein Epb41l2
DRG		3414.55	
Dorsal root		3414.55	
Dorsal root		3414.56	
PEAKS	sp|P19527|NFL_RAT	3414.58	Neurofilament light polypeptide
Spinal nerve		3414.58	
Ventral root		3415.63	
Dorsal root		3471.81	
Ventral root		3499.70	
Ventral root		3516.77	
Dorsal root		3528.70	
ProSight	P02688 - MBP_RAT	3528.80	Myelin basic protein S (Alt Splice Form 4)
PEAKS	sp|P19527|NFL_RAT	3569.70	Neurofilament light polypeptide
Dorsal root		3570.68	
PEAKS	sp|P19527|NFL_RAT	3570.68	Neurofilament light polypeptide
DRG		3570.71	
PEAKS	sp|P19527|NFL_RAT	3570.77	Neurofilament light polypeptide
Ventral root		3570.77	

Spinal nerve		3571.68	
Dorsal root		3572.66	
Dorsal root		3668.72	
Spinal nerve		3668.75	
Dorsal root		3703.83	
ProSight	P12839 - NFM_RAT	3704.84	Neurofilament 3, medium
Dorsal root		3704.87	
Dorsal root		3728.72	
DRG		3728.76	
Spinal nerve		3729.76	
Ventral root		3836.73	
ProSight	P60711 - ACTB_RAT	3836.97	Actin, cytoplasmic 2
Dorsal root		3857.81	
Dorsal root		4112.90	
DRG		4113.04	
Spinal nerve		4114.01	
Dorsal root		4211.95	
Spinal nerve		4225.05	
Dorsal root		4225.09	
ProSight	|P31000 |VIME_RAT	4225.18	Vimentin
Ventral root		4225.19	
DRG		4226.16	
DRG		4227.09	
Spinal nerve		4227.13	
Dorsal root		4281.12	
Spinal nerve		4282.23	
DRG		4282.48	
ProSight	P12839 - NFM_RAT	4342.08	Neurofilament 3, medium
Dorsal root		4342.11	
ProSight	P19527 - NFL_RAT	4397.03	Neurofilament light polypeptide
Dorsal root		4398.03	
Spinal nerve		4467.19	
Spinal nerve		4469.12	
Dorsal root		4557.95	
Dorsal root		4669.36	
DRG		4669.38	
Spinal nerve		4669.39	
ProSight	P12839 - NFM_RAT	4669.40	Neurofilament 3, medium
Ventral root		4669.42	
DRG		4672.38	
Spinal nerve		4818.67	
PEAKS	sp|P63312|TYB10_RAT	4934.52	Thymosin beta-10
Dorsal root		4935.40	

Spinal nerve		4935.49	
DRG		4935.50	
Ventral root		4936.69	
ProSight	sp|P62329|TYB4_RAT	4961.49	Thymosin beta-4
Ventral root		4961.49	
Dorsal root		4961.49	
Spinal nerve		4961.49	
DRG		4961.49	
PEAKS	sp|P63312|TYB10_RAT	4975.55	Thymosin beta-10
DRG		4976.43	
Dorsal root		4977.43	
PEAKS	sp|P62329|TYB4_RAT	4977.48	Thymosin beta-4
DRG		4978.54	
Spinal nerve		4979.44	
Dorsal root		4979.48	

Table S5. Peak statistics data from ClinProTools including the averages, standard deviations, and covariance for selected peaks from the DRG cell cultures measured using MALDI-TOF MS.

m/z (MALDI)	Identification	P Value of Kruskal-Wallis Test	Ave1 (Control)	Ave2 (Pre-Stim)	Ave3 (Stim)	Ave4 (Post-stim)	Ave5 (Blank)	StdDev (Control)	StdDev (Pre-Stim)	StdDev (Stim)	StdDev (Post-stim)	StdDev (Blank)
601.17	Unassigned Peak	0.000432	1.44	2.46	4.02	4.04	2.28	0.83	1.43	2.38	2.85	0.97
616.27	Unassigned Peak	0.0348	1.27	2.39	2.16	2.09	2.48	1.08	2.22	1.27	0.98	1.51
650.86	Unassigned Peak	0.234	2.05	3.76	3.73	3.53	2.21	1.16	2.78	2.75	2.23	0.72
739.43	Unassigned Peak	0.00000148	1.28	2.1	3.02	3.01	2.18	0.78	0.82	1.18	0.93	0.77
768.71	Hemoglobin subunit beta-1	0.00103	4.1	2.68	2.13	1.78	1.84	2.29	1.32	0.87	0.68	0.76
770.68	Unassigned Peak	0.0856	4.14	5.4	4.02	3.61	2.61	2.88	10.95	4.58	4.35	1.29
916.69	Myelin protein P0	< 0.000001	1.04	4.23	7.39	7.54	2.8	0.48	2.14	3.98	3.65	2.94
1180.79	Histone H2B	0.00337	1.5	2.15	1.7	3.08	2.1	0.53	0.67	1.02	1.69	0.95
1204.85	Peptidyl-prolyl cis-trans isomerase FKBP1A	0.0000023	2.6	2.51	1.86	1.82	1.26	1.36	1.75	1.05	0.66	0.24
1213.86	Histone H2B/Gamma-synuclein	0.0000151	3.92	3.52	2.32	2.52	5.63	0.87	0.98	0.61	0.97	6.26
1253.72	Mast cell protease 1	< 0.000001	2.26	8.13	11.01	13.25	3.94	0.75	5.58	6.01	9.11	1.77
1268.75	Unassigned Peak	< 0.000001	1.62	3.73	4.66	5.37	2.35	0.57	1.98	1.92	2.69	0.84
1332.81	Neurofilament light polypeptide/Neurofilament medium polypeptide/Myelin protein P0	0.0000059	8.5	7.16	5.47	4.54	2.15	7.48	7.38	3.38	1.55	0.71
1354.68	Vimentin	0.0000226	2.65	2	1.53	1.33	1.26	1.59	1.07	0.57	0.23	0.16
1573.59	Lumican/Ubiquitin carboxyl-terminal hydrolase isozyme L1	< 0.000001	2.98	2.23	1.38	1.37	0.85	1.42	1.04	0.51	0.42	0.22
1575.87	Mast cell protease 1/Vimentin/Serum albumin	< 0.000001	2.8	1.9	1.24	1.19	0.82	1.65	0.48	0.43	0.31	0.15
1820.61	Actin cytoplasmic 2/Hemoglobin subunit beta-1	< 0.000001	6.88	3.74	1.75	1.16	0.83	9.67	4.64	1.79	0.75	0.14
1857.81	Unassigned Peak	< 0.000001	3.65	1.9	1.02	0.87	0.65	3.13	1.53	0.38	0.19	0.15
1872.86	Unassigned Peak	< 0.000001	3.59	2.33	1.33	0.91	0.61	2.93	2.32	1.11	0.33	0.16

1898.02	Histone H2B/Cytochrome c oxidase subunit 6A1 mitochondrial	< 0.000001	4.74	2.54	1.26	1.22	0.69	3.26	1.02	0.58	0.53	0.15
1969.98	Nucleoside diphosphate kinase alpha isoform	< 0.000001	4.83	3.03	1.4	1.08	0.6	2.97	2.32	1.14	0.46	0.2
2010.07	High mobility group protein B1/Protein Hmg1l1	< 0.000001	4.87	3.28	1.48	1.06	0.68	5.95	5.13	1.13	0.29	0.33
2060.9	Histone H2B	< 0.000001	3.3	2.06	1.15	0.81	1.02	2.86	2.35	1.32	0.4	0.53
2099.2	Histone H2B	< 0.000001	5.89	3.35	1.53	1.06	0.55	4.83	2.77	1.69	0.67	0.19
2211.15	Unassigned Peak	< 0.000001	5.02	2.22	0.98	0.85	0.51	6.96	0.89	0.43	0.28	0.14
2246.86	Unassigned Peak	< 0.000001	6.16	3.39	1.57	0.9	0.51	6.48	4.43	2.34	0.61	0.15
2272.3	Periaxin	< 0.000001	7.91	4.32	2.07	1.5	0.49	10.69	3.67	2.75	1.26	0.14
2359.82	Unassigned Peak	< 0.000001	4.83	2.57	1.58	1.1	0.87	3.68	1.72	1.37	0.41	0.27
2440.19	Unassigned Peak	< 0.000001	3.05	1.83	0.96	0.79	0.56	1.46	0.84	0.43	0.28	0.13
2482.21	Unassigned Peak	< 0.000001	2.84	1.84	1.21	1.16	1.33	1.24	0.59	0.48	0.39	0.68
2498.08	Unassigned Peak	< 0.000001	3.4	2.05	1.16	0.92	0.61	2.88	0.86	0.65	0.35	0.11
2559.41	Unassigned Peak	< 0.000001	8.97	5.29	2.13	1.12	0.6	5.99	5.46	3.32	0.77	0.09
2595.24	Unassigned Peak	< 0.000001	2.43	1.92	1.04	0.95	0.73	1.13	1.01	0.38	0.38	0.23
2616.13	Neurofilament heavy polypeptide	< 0.000001	2.87	1.82	0.93	0.75	0.5	0.93	0.82	0.38	0.29	0.13
2629.5	Unassigned Peak	< 0.000001	4.69	3.72	1.71	1.3	0.48	2.46	2.31	1.65	0.8	0.14
2722.51	Unassigned Peak	< 0.000001	3.73	1.97	1.02	0.73	0.48	2.6	0.9	0.64	0.25	0.12
2748.43	Heat shock 27kDa protein 1	< 0.000001	3.47	2.35	1.04	0.9	0.47	1.85	1.42	0.45	0.45	0.13
2807.86	Unassigned Peak	< 0.000001	4.83	12.02	7.42	8.13	0.6	6.34	22.65	8.72	11.32	0.26
3502.77	Unassigned Peak	0.00188	1.03	1.11	1.83	2.15	0.68	0.6	0.47	2.14	3.54	0.46
3516.78	Unassigned Peak	< 0.000001	2.01	20.86	36.97	47.14	10.46	2.45	27.54	36.5	40.94	16.13
3807.51	Unassigned Peak	< 0.000001	3.93	1.94	0.75	0.61	0.35	3.1	1.52	0.46	0.36	0.09

Table S6. Fold changes between sample classes for DRG cell culture MALDI-TOF MS.

Theoretical Mass	m/z (MALDI)	Protein ID	Peptide Sequence	Identification	Stim/ Pre	Post/ Pre	Pre/ Control
600.17	601.17	Unassigned			0.47	0.31	0.54
615.27	616.27	Unassigned			0.47	0.31	0.54
649.86	650.86	Unassigned			0.50	0.48	0.54
738.43	739.43	Unassigned			0.66	0.72	0.90
767.71	768.71	sp|P02091|HBB1_RAT	A.LAHKYH	Hemoglobin subunit beta-1	0.44	0.38	0.68
769.68	770.68	Unassigned			0.79	0.66	0.65
915.69	916.69	sp|P06907|MYP0_RAT	Y.AMLDHSRS.T	Myelin protein P0	0.45	0.32	0.67
1179.79	1180.79	tr|G3V8B3|G3V8B3_RAT	E.RIAGEASRLAH.Y	Histone H2B	0.46	0.32	0.57
1203.85	1204.85	sp|Q62658|FKB1A_RAT	L.VFDVELLKLE	Peptidyl-prolyl cis-trans isomerase FKBP1A	0.50	0.48	0.54
1212.86	1213.86	tr|F1LQ96|F1LQ96_RAT	M(+42.01)DVFKKGFSI.A	Gamma-synuclein	0.56	0.39	0.62
1212.86	1213.86	tr|G3V8B3|G3V8B3_RAT	G.TKAVTKYTSSK	Histone H2B	0.66	0.72	0.90
1252.72	1253.72	sp|P09650|MCPT1_RAT	Y.NFYSNLHDIM.L	Mast cell protease 1	0.56	0.39	0.62
1267.75	1268.75	Unassigned			0.50	0.48	0.54
1331.81	1332.81	sp|P06907|MYP0_RAT	K.SKGLGESRKDKK	Myelin protein P0	0.56	0.39	0.62
1331.81	1332.81	sp|P19527|NFL_RAT	Y.SAPVSSSLSVRRS.Y	Neurofilament light polypeptide	0.79	1.43	1.43
1331.81	1332.81	tr|G3V7S2|G3V7S2_RAT	E.IIEETKVEDEK.S	Neurofilament medium polypeptide	0.62	0.61	0.75
1353.68	1354.68	sp|P31000|VIME_RAT	L.NDRFANYIDKV.R	Vimentin	1.35	1.63	3.60
1572.59	1573.59	sp|P51886|LUM_RAT	M.SKLPAGLPTSLLTLY.L	Lumican	0.65	0.63	0.68
1572.59	1573.59	sp|Q00981|UCHL1_RAT	MQLKPMEINPEML.N	Ubiquitin carboxyl-terminal hydrolase isozyme L1	1.75	1.78	4.07
1574.87	1575.87	sp|P09650|MCPT1_RAT	R.AAGWGQTGVTKPTSNT.L	Mast cell protease 1	0.76	0.63	0.84
1574.87	1575.87	sp|P31000|VIME_RAT	T.VETRDGQVINETSQ.H	Vimentin	0.51	0.41	0.63
1819.61	1820.61	sp|P02091|HBB1_RAT	L.LVVYPWTQRYFDSF.G	Hemoglobin subunit beta-1	0.76	0.63	0.84
1819.61	1820.61	sp|P63259|ACTG_RAT	M.E(+42.01)EEIAALVIDNGSGMCK.A	Actin cytoplasmic 2	0.76	0.63	0.84
1856.81	1857.81	Unassigned			0.46	0.36	0.63
1871.86	1872.86	Unassigned			0.74	0.73	0.97
1897.02	1898.02	sp|P10818|CX6A1_RAT	L.FHNPHMNPLPTGYEDE	Cytochrome c oxidase subunit 6A1 mitochondrial	0.48	0.35	0.55
1897.02	1898.02	tr|D3ZWM5|D3ZWM5_RAT		Histone H2B	0.45	0.32	0.67
1897.02	1898.02	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRLAH.Y	Histone H2B	0.62	0.61	0.75
1968.98	1969.98	tr|Q9QWQ4|Q9QWQ4_RAT	M.A(+42.01)NLERTFIAIKPDGVQR.G	Nucleoside diphosphate kinase alpha isoform	0.77	0.67	0.75

2009.07	2010.07	sp|P63159|HMGB1_RAT	M.SAKEKGKFEDMAKADKAR.Y	High mobility group protein B1	0.65	0.63	0.68
2009.07	2010.07	tr|D3ZCR3|D3ZCR3_RAT		Protein Hmg1l1	1.63	1.64	1.71
2059.9	2060.9	tr|D4A817|D4A817_RAT		Histone H2B	0.90	0.87	1.88
2059.9	2060.9	tr|G3V8B3|G3V8B3_RAT	F.VNDIFERIAGEASRLAHY.N	Histone H2B	0.99	0.94	1.83
2059.9	2060.9	tr|D3ZWM5|D3ZWM5_RAT		Histone H2B	1.44	1.43	1.64
2098.2	2099.2	tr|D3ZWM5|D3ZWM5_RAT	L.LPGELAKHAVSEGTKAVTKY.T	Histone H2B	0.74	0.67	1.30
2210.15	2211.15	Unassigned			1.25	1.44	2.30
2245.86	2246.86	Unassigned			0.54	0.46	0.52
2271.3	2272.3	sp|Q63425|PRAX_RAT	V.KLPKIPDMAVPDVRLPELQL.P	Periaxin	0.57	0.39	0.65
2358.82	2359.82	Unassigned			0.44	0.38	0.44
2439.19	2440.19	Unassigned			0.46	0.27	0.55
2481.21	2482.21	Unassigned			0.61	0.43	0.53
2497.08	2498.08	Unassigned			0.52	0.43	0.60
2558.41	2559.41	Unassigned			0.66	0.63	0.65
2594.24	2595.24	Unassigned			0.57	0.45	0.60
2615.13	2616.13	tr|F1LRZ7|F1LRZ7_RAT	M(+42.01)MSFGGADALLGAPFAPLHGGGSLHY.A	Neurofilament heavy polypeptide	0.40	0.21	0.59
2628.5	2629.5	Unassigned			0.54	0.49	0.79
2721.51	2722.51	Unassigned			0.46	0.35	0.79
2747.43	2748.43	tr|G3V913|G3V913_RAT	L.RSPSWEPFRDWYPAHSRLFDQA.F	Heat shock 27kDa protein 1	0.52	0.37	0.53
2806.86	2807.86	Unassigned			0.62	0.68	2.49
3501.77	3502.77	Unassigned			1.65	1.94	1.08
3515.78	3516.78	Unassigned			1.77	2.26	10.38
3806.51	3807.51	Unassigned			0.39	0.31	0.49

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