

Comparative mass spectrometric analysis of neural adaptations in rats repeatedly exposed to amphetamine

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Supporting Information, Tables S1–S6

Table S1. List of peptides that distinguish brain regions in the control group of samples.

Peptide	Protein	Accession	Mass*	P-value	Ave_dSTR± Std	Ave_NA±Std	Ave_mPFC±Std
SHYEEGPGKNLPFSVENKWRL	Cox7c protein	B2RYT3	2488.81	0.0015	14.38±0.95	42.86±6.26	52.02±6.38
VVYPWTQRY	Hemoglobin subunit beta-1	P02091	1211.95	0.0271	18.45±4.23	40.3±14.27	47.05±12.98
LVVYPWTQRY	Hemoglobin subunit beta-1	P02091	1325.14	0.0351	25.11±7.67	59.57±21.93	79.74±29.02
VLLPKKTESHHKAKGK	Histone H2A type 1	P02262	1801.47	0.0014	29.34±0.98	24.22±5.5	17.15±1.76
acASQKRPSQRHGSKY	Myelin basic protein S	P02688	1672.24	0.0017	24.63±2.66	12.58±2.14	8.57±0.76
acASQKRPSQRHGSKYL	Myelin basic protein S	P02688	1785.57	0.0027	112.35±20.02	27.8±7.09	10.29±2.63
acASQKRPSQRHGSKYLA	Myelin basic protein S	P02688	1857.12	0.0007	58±4.56	21.5±4.72	11.43±1.33
IVTPRTPPPSQGKGRGLSL	Myelin basic protein S	P02688	1962.44	0.0339 †	44.66±1.18	16.27±3.31	10.55±1.39
SLPQKSQRTQDENPVVHF	Myelin basic protein S	P02688	2110.91	0.0339 †	29.01±1.75	7.7±1.86	5.18±1.22
SLPQKSQRTQDENPVVHFFK	Myelin basic protein S	P02688	2386.5	0.0339 †	38.79±4.3	10.96±2.82	8.17±2.16
AacSQKRPSQRHGSKYLATASTM DHARHGFLPRHRDTGIL	Myelin basic protein S	P02688	4329.1	0.0142	14.95±5.31	6.14±1.94	1.9±1.13
APVADGVEKKEGD	Neuromodulin	P07938	1314.27	0.0017	7.81±0.55	16.71±2.1	20.91±2.48
FADKVPKTAENF	Peptidyl-prolyl cis-trans isomerase A	P10111	1367.85	0.0002	26.67±1.53	11±2.91	5.3±1.48
KSRHEEHERPE	Cytochrome c oxidase subunit 6A1, mitochondrial	P10818	1433.3	0.0039	20.89±0.8	11.44±2.89	9.21±2.82
acSQADFDKAAEEVKRLKTQPTD EEML	Acyl-CoA-binding protein	P11030	2923.18	0.0133	9.28±1.03	28.84±6.7	35.88±12.44
RVAPPGLTQIPQIQKTE	Na/K ATPase subunit beta-2	P13638	1877.02	0.0647	38.34±2.75	37.62±5.68	50.62±6.56
DRVAPPGLTQIPQIQKTE	Na/K ATPase subunit beta-2	P13638	1991.52	0.0047	19.67±0.41	12.06±1.81	14.5±2.01
acASSDIQVKELEKRASGQFEL	Stathmin	P13668	2349.42	0.0339 †	23.53±4.42	37.97±3.83	115.02±16.27
IRNMFPPNLVE	Excitatory amino acid transporter 1	P24942	1330.15	0.0011	17.32±2.7	51.18±6.04	61.05±8.08
VPPVQVSPLIKFGRYSALIL	ATP synthase subunit e, mitochondrial	P29419	2197.81	0.0089	10.86±1.95	35.53±14.63	57.86±12.44
IRNLFPENL	(1)	P31596	1115.86	0.0041	15.79±2.31	38.25±5.77	56.55±12.97
HAHKLRVDPVNF	Glutamate/aspartate transporter 2	P31596	1343.17	0.0039	28.08±3.08	46.01±4.98	64.83±10.73
acSGTNNVAQARKLVEQL	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-7	P43425	1770.75	0.0011	18.03±1.77	10.14±2.64	3.74±0.65
acSDKPDMAEIEKFDKSKLKKTTET QEKNLPSKETIEQEQAGES	Thymosin beta-4	P62329	4965.15	0.0014	22.78±8.24	129.39±23.7	148.52±23.98

acADEIAKAQVAQPGGDTIFGKIIR KEIPAKIIF	Histidine triad nucleotide-binding protein 1	P62959	3478.89	0.0302	14.02±6.78	99.57±66.88	176.52±71.49
MQLKPMINPEMLN	Neuron cytoplasmic protein 9.5	Q00981	1685.78	0.0193	19.47±0.87	15.77±1.27	16.59±2.37
ILDIPLDGPGANAAAAKIQA	Neurogranin	Q04940	1976.56	0.0339 †	28.89±2.26	9.71±2.01	5.89±1.48
LLKNSPLVSRRTL	Malate dehydrogenase	Q0QF43	1453.41	0.0083	32.81±5.32	20.75±5.72	13.05±2.43
PSQDSSMPYAPYVEPSAGSD	Synaptogyrin-1	Q62877	2083.27	0.0178	13.16±1.07	14.51±5.15	24.92±3.9
FRKFQKKKAG	PEP-19	Q8CHN7	1237.99	0.0277	10.85±3.05	5.77±0.94	4.27±0.85
FRKFQKKKAGSQS	PEP-19	Q8CHN7	1540.47	0.0002	74.69±4.05	43.83±10.85	14.16±2.91
IDMDAPETERAAVAIQSQ	PEP-19	Q8CHN7	1945.97	0.0339 †	39.19±4.21	10.36±1.7	7.62±1.27
DIDMDAPETERAAVAIQSQ	PEP-19	Q8CHN7	2061.14	0.0339 †	49.09±5.69	14.04±3	9.65±2.72
AAPIHPDVVML	Glutamate transporter GLT1b	Q8K5B5	1161.94	0.0347	4.01±0.39	7.2±1.56	6.22±1.6
YYSSGSSSPTHAKSAH	Claudin-11	Q99P82	1766.6	0.0149	12.12±2.32	16.99±6.18	5.67±1.32
RSSLGAKMVAI	Regulating synaptic membrane exocytosis protein 3 (RIM 3)	Q9JIR3	1135	0.0041	11.6±2.17	60.57±16.24	56.33±10.45
	unknown		915.61	0.0225	1.24±0.16	5±1.65	4.17±1.66
	unknown		918.54	0.0513	2.68±0.84	5.62±2.08	6.58±2.29
	unknown		931.54	0.0193	0.69±0.12	2.74±0.71	3.25±2.88
	unknown		1002.69	0.0142	5.7±0.72	12.71±3.79	16.85±3.86
	unknown		1150.82	0.0025	2.14±0.17	8.24±1.47	9.23±1.41
	unknown		1171.13	0.0142	6.49±0.45	13.19±2.12	10.41±2.82
	unknown		1200.97	0.0174	5.51±0.43	7.85±1.14	9.13±1.57
	unknown		1253.91	0.0141	16.43±2.57	13.67±3.06	8.23±1.79
	unknown		1422.36	0.0014	9.91±0.6	17.84±1.25	20.46±3.97
	unknown		1471.22	0.0011	42.14±2.83	18.39±4.85	12.64±4.91
	unknown		1524.39	0.0041	12.18±1.9	22.12±2.83	20.48±1.47
	unknown		1628.38	0.0012	10.27±1.01	18.61±0.29	17.7±1.74
	unknown		1668.29	0.0013	16.62±1.33	10.15±0.98	8.12±0.55
	unknown		1694.62	0.0013	16.5±2.29	30.81±3.43	52.5±6.5
	unknown		1717.39	0.0339 †	25.78±2.1	8.11±0.51	5.62±0.48
	unknown		1817.83	0.0174	16.33±1.73	10.82±2.44	8.46±3.14
	unknown		1889.5	0.0344 †	26.93±2.18	10.18±0.47	9.65±1.11
	unknown		1900.74	0.0039	9.3±1.06	14.12±0.92	16.11±2.04
	unknown		2021.04	0.0073	11.42±1.17	21.44±2.73	19.36±3.82
	unknown		2044.33	0.0127	17.89±1.04	19.81±1.83	27.75±3.13
	unknown		2048.9	0.0622	8.22±1.27	9.83±2.08	11.45±1.38
	unknown		2055.2	0.0174	7.58±0.47	10±1.2	10.34±1.17

unknown	2152.5	0.0054	21.4±1.97	16.32±2.68	12.76±1.41
unknown	2168.16	0.0091	20.38±1.46	60.58±13.81	79.45±20.03
unknown	2224.8	0.0344	10.61±1.55	12.74±2.3	25.01±6.72
unknown	2238.11	0.0014	42.58±3.78	23.86±3.87	15.28±4.56
unknown	2418.8	0.0162	57.36±8.45	86.99±9.66	99.38±22.37
unknown	2472.83	0.0142	6.1±0.6	14.33±3.39	18.71±5.04
unknown	2482.83	0.0174	3.35±0.44	10.05±3.86	12.04±3.27
unknown	2539.93	0.0111	6.86±0.33	17.57±3.99	24.36±6.13
unknown	2678.88	0.0581	7.32±0.54	12.15±2.72	12.41±4.63
unknown	2714.86	0.026	3.98±0.19	9.78±3.92	14.03±4.3
unknown	2810.1	0.0377	4.79±0.42	9.16±2.21	11.29±4.8
unknown	2969.04	0.0493	1.81±0.28	8.68±3.99	18.72±12.16
unknown	2985.44	0.0084	14.56±1.78	51.54±10.65	48.77±14.1
unknown	3050.1	0.0039	24.86±3.36	18.23±4.54	7.3±3.23
unknown	3056.46	0.0124	3.37±0.57	18.69±4.9	16.24±6.14
unknown	3156.08	0.0038	10.34±2.39	16.28±2.35	5.02±1.68
unknown	3203.59	0.0174	3.64±1.58	16.65±10.26	27.7±8.35
unknown	3434.9	0.0194	4.2±1.76	32.71±21.93	52.07±17.55
unknown	3924.75	0.0056	3.01±0.6	10.35±1.87	12.3±3.78
unknown	4180.12	0.0155	2.05±0.76	25.05±8.64	26.35±11.74
unknown	4748.69	0.013	78.62±20.92	80.44±13.51	39.66±6.2

* **Mass** is defined as a centroid of the average peak of protonated molecular ion found on cumulative processed group spectrum in ClinPro Tools.

^F p-value corrected for not normally distributed data.

ac = acetylation.

Table S2. List of peptides differentially detected in the NA of rats treated with 3 mg chronic AMPH.

Peptide	Protein	Accession	Mass	p-value	NA (saline±SD)	NA (AMPH±SD)	Ratio
acSDKPDMAEIEKFDKSKLKKTTETQ EKNPLPSKETIEQEKQAGES	Thymosin beta-4	P62329	4965.24	0.01	127.04±23.06	317.35±82.93	2.5
acADKPDMGEIASFDKAKLKKTTET QEKNTLPTKETIEQEKRSEIS	Thymosin beta-10	P63312	4938.23	0.016	8.78±1.74	23.24±7.37	2.6
acASSDIQVKELEKRASGQFEL	Stathmin	P13668	2349.47	0.045	37.4±3.63	51.7±9.31	1.4
	unknown		2483.03	0.045	9.92±3.8	21.43±6.38	2.2
	unknown		2985.55	0.05	50.47±10.25	77.5 13.76	1.5

Mass is the centroid of the average protonated molecular ion found on the cumulative processed group spectrum.

The **p-value** is corrected for non-normally distributed data.

Ratio is calculated from the maximum intensity for each peak on the average group spectrum, AMPH/saline.

ac = acetylation.

Table S3. List of peptides differentially detected in the dSTR of rats treated with 3 mg chronic AMPH.

Peptide	Protein	Accession	Mass	p-value	dSTR (saline \pm SD)	dSTR (AMPH \pm SD)	Ratio
acASQKRPSQRHGSKY	Myelin basic protein S	P02688	1672.44	0.061	23.92 \pm 2.65	18.06 \pm 3.51	0.8
RVAPPGLTQIPQIQKTE	Na/K ATPase subunit beta-2	P13638	1877.08	0.026	38.08 \pm 2.66	46.71 \pm 4.89	1.2
DIDMDAPETERAAVAIQSQ	PEP-19	Q8CHN7	2061.25	0.061	48.25 \pm 5.49	61.95 \pm 9.84	1.3
	unknown		1471.33	0.006	41.38 \pm 2.9	55.33 \pm 5.82	1.3
	unknown		1519.15	0.026	17.34 \pm 0.9	21.17 \pm 2.21	1.2
	unknown		1799.98	0.001	28.83 \pm 1.07	36.66 \pm 2.37	1.3
	unknown		2151.91	0.026	20.1 \pm 1.83	29.2 \pm 5.9	1.4
	unknown		2238.4	0.026	40.11 \pm 3.62	77.41 \pm 23.4	1.9
	unknown		3156.1	0.034	10.07 \pm 2.37	22.38 \pm 8.66	2.2

Mass is the centroid of the average protonated molecular ion found on the cumulative processed group spectrum.

The **p-value** is corrected for non-normally distributed data.

Ratio is calculated from the maximum intensity for each peak on the average group spectrum, AMPH/saline.

ac = acetylation.

Table S4. List of peptides differentially detected in the mPFC of rats treated with 3 mg chronic AMPH.

Peptide	Protein	Accession	Mass	p-value	mPFC (saline±SD)	mPFC (AMPH±SD)	Ratio
SHYEEGPGKNLPFSVENKWRL	Cox7c protein	B2RYT3	2488.72	0.05	50.84±6.11	34.76±11.86	0.7
KLGGDRSRGSPMAR	Myelin basic protein S	P02688	1575.24	0.06	16.66±1.41	13.34±2.6	0.8
APVADGVEKKEGD	Neuromodulin	P07936	1314.23	0.05	17.94±2.5	12.67±2.69	0.7
RVAPPGLTQIPQIQKTE	Na/K ATPase subunit beta-2	P13638	1877.05	0.04	49.98±6.66	33.4±8.62	0.7
acSDKPDMAEIEKFDKSKLKKTTETQ EKNPLPSKETIEQEKQAGES	Thymosin beta-4	P62329	4965.16	0.04	145.17±23.18	271.67±100.11	1.9
acADEIAKAQVAQPGGDTIFGKIIRK EIPAKIIF	Histidine triad nucleotide-binding protein 1	P62959	3478.95	0.04	172.74±69.47	346.37±79.36	2
acADKPDMGEIASFDKAKLKKTTET QEKNLPTKETIEQEKRSEIS	Thymosin beta-10	P63312	4938.08	0.06	10.55±2.35	19.64±8.04	1.9
PSQDSSMPYAPYVEPSAGSD	Synaptogyrin-1	Q62877	2083.33	0.06	25.16±3.64	17.94±4.19	0.7
	unknown		1518.69	0.04	21.3±0.96	17.51±2.88	0.8
	unknown		1604.66	0.03	20.31±1.93	14.52±2.86	0.7
	unknown		1619.46	0.02	11.73±0.74	8.96±1.32	0.8
	unknown		1694.69	0.04	52.04±6.47	36.22±6.14	0.7
	unknown		1748.84	0.05	9.43±1.04	6.9±1.71	0.7
	unknown		1779.96	0.04	31.24±4.74	20.34±5.29	0.7
	unknown		1900.81	0.04	16.06±1.97	11.17±1.49	0.7
	unknown		1936.86	0.03	11.88±0.98	8.88±1.47	0.7
	unknown		1991.98	0.02	14.41±1.87	8.03±1.9	0.6
	unknown		2044.46	0.03	27.61±2.87	19.75±2.96	0.7
	unknown		2048.84	0.02	10.64±1.4	5.42±1.27	0.5
	unknown		2055.16	0.02	10.3±1.09	5.93±0.85	0.6
	unknown		3056.61	0.05	16.15±5.91	33.8±13.95	2.1

	unknown		3203.65	0.02	27.05±8.03	54.14±12.91	2
	unknown		3219.76	0.02	6.44±1.93	13.82±3	2.1
	unknown		3316.87	0.03	10.37±3.89	21.67±4.9	2.1
	unknown		3434.95	0.02	50.83±16.91	112.93±31.13	2.2
	unknown		3582.74	0.02	6.19±1.45	11.35±2.6	1.8
	unknown		3626.18	0.04	9.51±4.5	20.95±5.96	2.2
	unknown		4180.21	0.04	25.7±11.34	55.86±16.46	2.2

Mass is the centroid of the average protonated molecular ion found on the cumulative processed group spectrum.

The **p-value** is corrected for non-normally distributed data.

Ratio is calculated from the maximum intensity for each peak on the average group spectrum, AMPH/saline.

ac = acetylation.

Table S5. List of peptides identified by capLC-ESI-IT-MS/MS from the AMPH treated samples by different bioinformatics algorithms.

Peptide	Protein	Accession	Mr (calc)	ΔM , Da	PEAKS	MASCOT
YEMPSEEGYQDYEPEA*	Alpha-synuclein 1	P37377-1	1935.736	0.250	Y	
PSSEAYEMPSEEGYQDYEPEA*	Alpha-synuclein 2	P37377-2	2406.932	0.047	Y	
*VPPVQVSPLIKF	ATPsynthase, e chain , mitochondrial	P29419	1322.796	0.309	Y	
YYSSGSSSPHAKSAH	Claudin 11	Q6IRG7	1764.807	0.314	Y	Y
acASGVAVSDGVKVFNDM	Cofilin, non-muscle isoform	P45592	1749.861	0.405	Y	Y
TVLKYLPGPLQDM	Complexin-2	P84087	1473.790	0.596	Y	
IEVGA(ssC)NSAG(ssC)GPSSDVIET	Contactin-1	Q63198	1905.824	0.202	Y	
SHLESSYKKR	Cytochrom C oxidase	P80433	1275.657	0.388	Y	
KSRHEEHERPE	Cytochrome c oxidase subunit 6A1, mitochondrial, P10818	P10818	1432.681	0.394	Y	Y
AGIKKKGERADLIA	Cytochrome C, rat,	P62898	1468.872	0.402	Y	Y
KANAECTSGTSIKTVKIKKE	H+-transporting two-sector ATPase, epsilon chain	P29418	2160.248	0.081	Y	Y
HVEDLPGALSTLSDL	Hemoglobin alpha	P01946	1565.794	0.462	Y	Y
FQKVAVAGVASALAHKYH	Hemoglobin beta-2	P11517	1825	0.417	Y	Y
VLLPKKTESHHKAKGK	Histone H2A1	P02262	1800.073	0.225	Y	Y
AVRLLLPGELAKHAVSEGTKAVTKYTSSK	Histone H2B	Q00715	3053.724	0.349	Y	Y
SEGTKAVTKYTSSK	Histone H2B	Q00715	1527.778	-0.126	Y	Y
KQVHPDTGISSKAMGIMNSF	Histone H2B type 1	Q00715	2147.050	0.155	Y	
KLNPPDESQPGCMSCCK	Hras protein	Q5RJJ8	1661.721	-0.274	Y	Y
AEKAAVNGL	II beta-globin	Q6LD44	871.476	0.214	Y	Y
AKVAVLGASGGIGQPLSL	Malate dehydrogenase, mitochondrial	p04636	1750.035	0.430	Y	
SPQLATLADEVASLAKQG.L*	Microtubule-associated protein tau	P19332	1884.979	0.352	Y	Y
RDTGILDSIGRF	Myelin basic protein	P02688-4	1348.710	0.736	Y	
IVTPRTPPPSQGKGRGL	Myelin basic protein	P02688	1760.006	0.380	Y	
IVTPRTPPPSQGKGRGLS	Myelin basic protein	P02688	1847.038	0.228	Y	
TGILDSIGRF	Myelin basic protein	P02688	1077.582	0.303	Y	Y
KLGGRDSRSGSPMAR	Myelin basic protein	P02688	1573.811	0.258	Y	Y
DAQGTLKIFKLGGRD	Myelin basic protein	P02688	1704.916	0.465	Y	Y
SRFSWGGDRSRSGSPM	Myelin basic protein	P02688	1768.806	0.305	Y	Y
acASQKRPSQRHGSKYL	Myelin basic protein	P02688	1783.944	0.201	Y	Y
KSQRTQDENPVVHFF	Myelin basic protein	P02688	1829.917	0.163	Y	Y
SRFSWGGDRSRSGSPMA	Myelin basic protein	P02688	1839.843	0.06	Y	Y

IVTPRTPPPSQGKGRGLSL	Myelin basic protein	P02688	1960.122	0.168	Y	Y
SLPQKSQRTQDENPVVHFF	Myelin basic protein	P02688	2256.129	0.158	Y	Y
ILDIPLDDPGANAAAAKIQASF	Neurogranin	Q04940	2210.158	0.157	Y	Y
APAAEAEAKEKD	Neuromodulin	P07936	1228.594	0.472	Y	
APVADGVEKKEGD	Neuromodulin	P07938	1313.646	0.519	Y	
APAAEAEAKEKDD	Neuromodulin	P07937	1343.621	0.445	Y	
*VDFPWAAVDNM	Neuronal growth regulator 1,	Q9Z0J8	1263.559	0.586	Y	
FRKFQKKKAG	PEP-19	P63055	1236.745	0.315	Y	Y
DIDMDAPETERA	PEP-19	P63055	1361.577	0.489	Y	
RKFQKKKAGSQS	PEP-19	P63055	1391.8	0.341	Y	Y
FRKFQKKKAGSQS	PEP-19	P63055	1538.868	0.291	Y	Y
TphPGYphSphSGGGGGSGYQDLGTS	ProSAPiP1	Q8K1Q4	2100.675	-0.296	Y	Y
VHLLHQLPRAD	Protein tweety homolog 1	POC5X8	1297.725	-0.081	Y	Y
	Protein whose mRNA is enriched in					
*acSFFKTLVSPKNTETKKD	synaptosomes 2	Q3ZB98	2011.063	0.283	Y	
EDSPGLKVGVPVPLVM	Sec61 beta subunit	B2RZD1	1506.848	0.478	Y	
DTVLKYLPGPLQDM	Synaphin-1	P84087	1588.817	0.459	Y	Y
VGITKAAPILF	Synaptic vesicle glycoprotein 2A	Q02563	1128.691	0.595	Y	
*acMEGGAYGAGKAGGAFD	Synaptogyrin-1	Q62876	1499.635	0.043	Y	
PSQDSSMPYAPYVEPSAGSD	Synaptogyrin-1	Q62877	2083.868	0.117	Y	
*acMDVVNQLVAGGQF	Synaptophysin	P07825	1418.686	0.539	Y	
FEYPFRRRLHQVY	Synaptophysin	P07825	1497.741	0.725	Y	
*VKLIESKEAFQEALAAAGDKL	Thioredoxin	P11232	2230.221	0.18	Y	Y
SLTREKKKHVL	Thy-1 membrane glycoprotein	P01830	1337.814	0.389	Y	Y
SLTREKKKHVLSGTLGVPEHTY	Thy-1 membrane glycoprotein	P01830	2479.355	0.455	Y	Y
56 peptides	35 proteins				56 peptides	32 peptides

Masses are defined as calculated monoisotopic masses of molecular ions.

* denotes the location of N-or C-termini of the proteins.

ac and **ph** = acetylation and phosphorylation, respectively.

PEAKS denotes peptides identified in the automatic database search using Peaks Studio 4.6 software.

MASCOT denotes peptides identified in the automatic database search using local MASCOT server.

ΔM indicates difference between calculated and experimental peptides mass.

Table S6. List of peptides identified by nanoLC-ESI-FTICR-MS/MS from the AMPH treated samples.

Sequence	Position	Protein Description	Accession Number	Mr (calc)	ΔM , ppm	E-value
acASATRVIQKLRNWSGQDLQAKLQLR	(2-27)	Ndufa7 protein	A9UMV9	2992.67	-0.5	8×10^{-21}
SHYEEGPGKNLPFSVENKWRL	(17-37)	Cox7c protein	B2RYT3	2486.23	-1.0	1×10^{-18}
KHESQVDSVVKDKKAKETADAIKSKVKKATVN	(147-180)	Receptor expression-enhancing protein 5	B2RZ37	3724.00	0.0	8×10^{-24}
SVVKDKKAKETADAIKSKVKKATVNL	(154-181)	Receptor expression-enhancing protein 5	B2RZ37	3013.70	-0.9	1×10^{-57}
EREASPQFPAAQKPLLSL	(333-350)	Ttyh1 protein	B4F773	1981.06	-0.4	4×10^{-45}
FYLPGQAEGRSSNTYTL	(283-300)	CD166 antigen	O35112	2016.00	-0.5	4×10^{-11}
FAAFPTTKTYFSHIDVSPGSAQVKAHGKKVADALAKA ADHVEDLPGALSTLSDL	(34-87)	Hemoglobin subunit alpha-1/2	P01946	5592.89	-0.4	1×10^{-22}
AAFPTTKTYFSHIDVSPGSAQVKAHGKKVADALAKAA DHVEDLPGALSTLSDL	(35-87)	Hemoglobin subunit alpha-1/2	P01946	5445.82	-0.6	5×10^{-35}
AAFPTTKTYFSHIDVSPGSAQVKAHGKKVADALAKAA DHVEDLPGALSTLSDLHAHKLKRV	(35-95)	Hemoglobin subunit alpha-1/2	P01946	6402.35	-1.2	4×10^{-14}
FSHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGA LSTLSDL	(44-87)	Hemoglobin subunit alpha-1/2	P01946	4465.32	-0.8	1×10^{-37}
FSHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGA LSTLSDLHAHKLKRV	(44-95)	Hemoglobin subunit alpha-1/2	P01946	5421.85	-1.4	2×10^{-102}
FSHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGA LSTLSDLHAHKLKRVDPVN	(44-98)	Hemoglobin subunit alpha-1/2	P01946	5732.02	1.8	2×10^{-34}
FSHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGA LSTLSDLHAHKLKRVDPVNFK	(44-100)	Hemoglobin subunit alpha-1/2	P01946	6007.18	-5.8	7×10^{-22}
SHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGAL STLSDLHAHKLKRV	(45-95)	Hemoglobin subunit alpha-1/2	P01946	5274.79	-1.8	1×10^{-58}
SHIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGAL STLSDLHAHKLKRVDPVN	(45-98)	Hemoglobin subunit alpha-1/2	P01946	5584.95	-1.0	3×10^{-10}
HIDVSPGSAQVKAHGKKVADALAKAADHVEDLPGALS TLSDLHAHKLKRV	(46-95)	Hemoglobin subunit alpha-1/2	P01946	5187.75	0.3	7×10^{-17}
VSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLS DLHAHKLKRV	(49-93)	Hemoglobin subunit alpha-1/2	P01946	4608.49	-0.2	4×10^{-13}
VSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLS DLHAHKLKRV	(49-95)	Hemoglobin subunit alpha-1/2	P01946	4822.58	0.5	2×10^{-63}
VSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLS DLHAHKLKRVDPVN	(49-98)	Hemoglobin subunit alpha-1/2	P01946	5132.75	-0.5	1×10^{-28}
VSPGSAQVKAHGKKVADALAKAADHVEDLPGALSTLS DLHAHKLKRVDPVNFK	(49-100)	Hemoglobin subunit alpha-1/2	P01946	5407.91	1.8	3×10^{-16}

VHLTDAEKA AVNGLW	(2-16)	Hemoglobin subunit beta-1	P02091	1622.84	-0.2	2×10^{-8}
VHLTDAEKA AVNGLWGKVNPPDDVGGEALG	(2-30)	Hemoglobin subunit beta-1	P02091	2931.47	-2.1	1×10^{-7}
GKVNPPDDVGGEALGRLL	(17-33)	Hemoglobin subunit beta-1	P02091	1708.91	-0.9	2×10^{-54}
LAALGGNSNPSAKDIKKILDSVIEADDERLNKVISELN GKNIE	(9-52)	60S acidic ribosomal protein P2	P02401	4647.47	0.2	5×10^{-8}
LAALGGNSNPSAKDIKKILDSVIEADDERLNKVISELN GKNIED	(9-53)	60S acidic ribosomal protein P2	P02401	4762.50	0.4	7×10^{-21}
SQRTQDENPVVHFF	(101-114)	Myelin basic protein S	P02688	1702.81	-0.7	8×10^{-26}
LTISELKPTYQDRVAPPGLTQIPQIQ	(59-84)	Sodium/potassium-transporting ATPase subunit beta-1	P07340	2905.59	-1.1	1×10^{-12}
FEYPPFRLHQVY	(65-75)	Synaptophysin (Major synaptic vesicle protein p38)	P07825	1497.74	-1.3	9×10^{-10}
LQRQP PPPPPSAASPGATPGSAAASAERASTAAPVA SPAAPSPGSSGGGGFFSSLSNAVKQTTAAAAATFSE QVGGGSGGAGRGGAAARVL	(25-116)	Synapsin-1	P09951	8306.15	-0.9	2.89E-09 3×10^{-9}
MTDLQRQP PPPPPSAASPGATPGSAAASAERASTA APVASPAAPSPGSSGGGGFFSSLSNAVKQTTAAAAAT FSEQVGGGSGGAGRGGAAARVL	(22-116)	Synapsin-1	P09951	8653.27	-0.8	9.06E-08 9×10^{-8}
HLPEQAFYMGPIEEAVAKADKLAEEHGS	(501-529*)	ATP synthase subunit beta, mitochondrial	P10719	3165.54	-0.9	4×10^{-12}
acSQADFDKAAEEVKRLKTQPTDEEML	(2-26)	Acyl-CoA-binding protein	P11030	2920.41	-0.6	4×10^{-40}
IYSHFKQATVGDVNTDRPGLLDL	(28-50)	Acyl-CoA-binding protein	P11030	2558.31	-1.7	3×10^{-60}
VKLIESKEAFQEALAAAGDKL	(2-22)	Thioredoxin.	P11232	2230.22	-0.8	9×10^{-42}
acASSDIQVKELEKRASGQAFEL	(2-22)	Stathmin	P13668	2347.20	-1.7	7×10^{-55}
ITKAVAASKERSGVSLAALKKALAAAGY	(44-71)	Histone H1.2	P15865	2744.59	-1.2	1×10^{-52}
ITKAVAASKERSGVSLAALKKALAAAGYD	(44-72)	Histone H1.2	P15865	2859.62	-1.0	5×10^{-66}
ITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIK LGL	(44-84)	Histone H1.2	P15865	4211.41	2.2	6×10^{-30}
ITKAVAASKERSGVSLAALKKALAAAGYDVEKNNSRIK LGLKSL	(44-87)	Histone H1.2	P15865	4539.62	0.3	6×10^{-78}
SLEPVAEELKSLGKDV	(77-94)	Phosphoglycerate kinase 1	P16617	1881.08	-1.0	6×10^{-12}
LEGKVLPGVDALS NV	(403-417*)	Phosphoglycerate kinase 1	P16617	1509.84	-0.9	8×10^{-20}
IRNMFPPNLVE	(174-184)	Excitatory amino acid transporter 1	P24942	1328.69	-0.6	2×10^{-16}
SIDMVDPQLATLADEV SASLAKQGL	(727-752*)	Microtubule-associated protein tau (Neurofibrillary tangle protein)	P19332	2658.34	-1.9	9×10^{-47}
MVDSPQLATLADEV SASLAKQGL	(730-752*)	Microtubule-associated protein tau (Neurofibrillary tangle protein)	P19332	2343.2	-0.8	2×10^{-65}
VDSPQLATLADEV SASLAKQGL	(731-752*)	Microtubule-associated protein tau (Neurofibrillary tangle protein)	P19332	2212.16	-1.1	1×10^{-12}

SPQLATLADEVASLAKQGL	(733-752*)	Microtubule-associated protein tau (Neurofibrillary tangle protein)	P19332	1998.06	-1.1	9 x 10 ⁻³⁶
M(ac)LS(ac)VAARSGPFAPVLSATSRGVAGALRPL (Acetylation is potentially located at either Methionie or Serine residue.)	(1-29)	Cytochrome b-c1 complex subunit Rieske, mitochondrial	P20788	2893.60	-0.8	6 x 10 ⁻²¹
VPPVQVSPLIKFGRYSALIL	(2-21)	ATP synthase subunit e, mitochondrial	P29419	2196.30	-1.0	5 x 10 ⁻¹⁰
IVNTNVPRASVPEGFLSELQQLAQATGKPAQY	(5-37)	Macrophage migration inhibitory factor	P30904	3526.84	-1.4	1 x 10 ⁻¹⁰
TCIIWLAFLPIF	(769-780)	Metabotropic glutamate receptor 2	P31421	1435.79	1.6	5 x 10 ⁻¹⁶
AEKTKAQVTNVGGAVVTGVTAVAQKTVEGAGNIAAAT GFVKKD	(56-98)	Alpha-synuclein	P37377	4214.25	-0.9	2.5E-76 3 x 10 ⁻⁷⁶
KTKAQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGF VKKD	(58-98)	Alpha-synuclein	P37377	4014.18	-0.2	1 x 10 ⁻³³
acSGTNNVAQARKLVEQL	(2-17)	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-7	P43425	1768.94	-1.2	2 x 10 ⁻³⁶
acSGTNNVAQARKLVEQLRIEAG	(2-22)	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-7	P43425	2295.23	-1.6	2 x 10 ⁻³⁷
FTAHIIPLK	(297-306*)	Palmitoyl-protein thioesterase 1	P45479	1185.69	-1.0	2 x 10 ⁻¹⁰
VEFGSRVNVGGKTVKLIWDTAGQ	(43-67)	Ras-related protein Rab-4B	P51146	2687.44	-1.7	1 x 10 ⁻⁸
PRLRQLQKSLAAATGKQELAKYF	(29-52)	Somatostatin	P60042	2763.56	-0.2	2 x 10 ⁻⁸
IEKFDKSKLKKTTETQEKNPLPSKETIEQEKQAG	(10-42)	Thymosin beta-4	P62329	3829.05	-1.7	7 x 10 ⁻²²
IEKFDKSKLKKTTETQEKNPLPSKETIEQEKQAGES	(10-44*)	Thymosin beta-4	P62329	4045.12	-0.1	8 x 10 ⁻⁹
acADEIAKAQVAQPGGDTIFGKIIRKEIPAKIIF	(2-33)	Histidine triad nucleotide-binding protein 1	P62959	3478.96	-0.5	2 x 10 ⁻⁴⁷
TIFGKIIRKEIPAKIIF	(17-33)	Histidine triad nucleotide-binding protein 1	P62959	1986.24	-0.7	5 x 10 ⁻⁹
MQIFVKLTGKTITLEVEPSDTIENVKAKIQDKEGIPPD QQRLIFAGKQLEDGRTLSDYNIQKESTLHLVL	(1-71)	Ubiquitin	P62989	8020.29	-0.8	4 x 10 ⁻¹⁴
MQIFVKLTGKTITLEVEPSDTIENVKAKIQDKEGIPPD QQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLR	(1-74)	Ubiquitin	P62989	8445.57	0.5	6 x 10 ⁻⁶²
MQIFVKLTGKTITLEVEPSDTIENVKAKIQDKEGIPPD QQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLR	(1-76)	Ubiquitin	P62989	8559.62	1.2	4 x 10 ⁻²⁹
PSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTL SDYNIQKESTLHLVLR	(19-74)	Ubiquitin	P62989	6413.45	-1.1	8 x 10 ⁻¹⁵
acMEFVMKQALGGATKDMGKMLGGDEEKD	(1-27)	Complexin-1	P63041	2957.36	-1.2	2 x 10 ⁻⁴⁵
DIDMDAPETERAAVAIQSQF	(31-50)	Purkinje cell protein 4 (Brain-specific polypeptide PEP-19)	P63055	2206.02	-0.5	5 x 10 ⁻¹⁸
acAAKFESIGKFLAL	(2-16)	Prohibitin	P67779	1591.90	-0.9	2 x 10 ⁻¹⁹
acMDFVMKQALGGATKDMGKMLGGEEEKD	(1-27)	Complexin-2	P84087	2957.36	0.2	4 x 10 ⁻¹⁷

acAGQAFRKFLPLF	(2-13)	Chaperonin 10	P97601	1435.80	-0.9	3 x 10 ⁻²⁴
KQVHPDTGISSKAMGIMNSF	(47-66)	Histone H2B type 1	Q00715	2147.05	-0.5	1 x 10 ⁻²⁵
MQLKPMEINPEMLN	(1-14)	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (Neuron cytoplasmic protein 9.5)	Q00981	1686.81	-0.9	4 x 10 ⁻¹¹
ILDIPDDPGANAAAAKIQ	(16-34)	Neurogranin	Q04940	1905.02	-0.5	1 x 10 ⁻⁵⁵
ILDIPDDPGANAAAAKIQA	(16-35)	Neurogranin	Q04940	1976.06	-0.7	6 x 10 ⁻⁹
ILDIPDDPGANAAAAKIQAS	(16-36)	Neurogranin	Q04940	2063.09	-1.1	1 x 10 ⁻¹⁷
DIPLDDPGANAAAAKIQASF	(18-37)	Neurogranin	Q04940	1983.99	-0.6	9 x 10 ⁻⁶⁰
IPLDDPGANAAAAKIQASF	(19-37)	Neurogranin	Q04940	1868.96	-1.5	3 x 10 ⁻³⁵
DIDTAAKFIGAGAATVGVAG	(62-81)	ATP synthase lipid-binding protein, mitochondrial	Q06645	1803.94	-0.9	3 x 10 ⁻²³
YSAASKQKRLDQVEKELLRVGQLLKD	(46-71)	ATP synthase subunit O, mitochondrial	Q06647	3014.69	-1.0	2 x 10 ⁻²⁶
MTTVHAITATQKTVDGSPGKLRDGRGAAQNIIPAST	(150-205)	Glyceraldehyde-3-phosphate dehydrogenase	Q0QEU1	5653.05	-3.7	4 x 10 ⁻³²
GAAKAVGKVIPELNGKLTG						
GPSGKLWRDGRGAAQNIIPASTGAAKAVGKVIPELNGKLTG	(165-205)	Glyceraldehyde-3-phosphate dehydrogenase	Q0QEU1	4055.24	-0.2	2 x 10 ⁻⁹
AKVAVLGASGGIGQPLSL	(4-21)	Malate dehydrogenase	Q0QF43	1636.95	-0.7	7 x 10 ⁻⁶¹
LLKNSPLVSRLL	(22-34)	Malate dehydrogenase	Q0QF43	1452.90	-0.6	8 x 10 ⁻²⁴
VKEGSEPPLKMTQESALIF	(266-284)	Cell adhesion molecule 3	Q1WIM3	2103.09	-0.8	5 x 10 ⁻²²
AALNGKGLGEISAATEF	(579-594)	Ncam1 protein	Q3T1H3	1647.85	-1.0	4 x 10 ⁻³⁸
KQMKIMMERREEEHAKLMKALKKCK	(57-81)	Clusterin-like protein 1	Q3ZRW7	3116.66	6.7	5 x 10 ⁻¹⁰
TSVPPNAAHPMPAAALTNASGLGL	(849-873)	Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila)	Q5PQL6	2344.18	-1.5	6 x 10 ⁻⁹
PYEIKKVFASLPQVERGVSKILGGD	(2-26)	WD repeat-containing protein 1	Q5RKI0	2729.51	0.1	4 x 10 ⁻⁶⁴
TPSAQAAFQKVAGVASALAHKYH	(124-147*)	0 beta-2 globin	Q62670	2451.30	-0.2	4 x 10 ⁻³²
PGPTAPDPLKSQGPRGPQLPTVSPSPVMIPTVPHAEYIEGSpHP	(910-952*)	Microtubule-associated protein 6	Q63560	4475.22	0.7	1 x 10 ⁻⁹
ARVVAFMSNIPLLL	(164-178)	Prosaposin	Q6P7A4	1639.95	-0.8	2 x 10 ⁻²⁶
SSLLEKGLDGAKKAVGGKLGKDAVEDLESVGKGA	(63-110*)	Dermcidin	Q71DI1	4815.62	-1.1	1 x 10 ⁻⁵⁹
VHDVKDVLDSVL						
IKAYMDSTLGPFILNVTSALLCSEALCSGRGRCVHRP	(351-389)	Hyaluronidase-1	Q76HN1	4136.08	4.9	8 x 10 ⁻¹¹
S						
AAPIHPDVVML	(67-77)	Glutamate transporter GLT1b	Q8K5B5	1161.62	-0.5	1 x 10 ⁻⁹
IRNLFPENL	(172-180)	Glutamate transporter GLT1b	Q8K5B5	1114.61	-0.7	3 x 10 ⁻¹⁰
TVEPNARQLVEIAARDIEKL	(69-89)	L-type calcium channel alpha2/delta subunit	Q8VHS9	2378.29	-0.3	4 x 10 ⁻¹⁴
APIKVGDTIPSVEVF	(53-67)	Peroxisome oxidin-5, mitochondrial	Q9R063	1570.86	-0.9	9 x 10 ⁻²⁷

ac AVPPTYADLGKSARDVF	(2-18)	Voltage-dependent anion-selective channel protein 1	Q9Z2L0	1847.94	-0.6	7×10^{-37}
ac ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRD TGIL	(2-39)	Myelin basic protein S	P02688	4325.22	-1.2	2×10^{-26}
99 peptides		58 proteins				

Masses are defined as calculated monoisotopic masses of molecular ions.

* denotes the location of the C-terminal of the proteins.

ac and **ph** = acetylation and phosphorylation, respectively.

ΔM = difference between calculated and experimental peptides mass.