Supplemental Table 1. Neuropeptides and other secretory pathway peptides found in peptidomics analyses

Precursor	Peptide name	Peptide sequence	z	Theor. Mass	Times found	Comments
7B2	167-176	(LLYEKMKGGQ)	3	1165.600	22	
7B2	200-212	SVPHFSEEEKEAE	3	1516.668	7	
7B2	200-212 + phosphate	(SVPHFpSEEEKEAE)	3	1596.626	16	
Calcitonin gene-related peptide 1 precursor	63-82	ELEQEEEQEAEGSSVTAQKR	3	2276.040	1	Only in Cpe<fat/fat>
Cerebellin 1 precursor protein	Cerebellin 2-15	GSAKVAFSAIRSTN	3	1407.747	49	
Cerebellin 1 precursor protein	Cerebellin 1-15	SGSAKVAFSAIRSTN	3	1494.779	104	
Cerebellin 1 precursor protein	Cerebellin 2-16	GSAKVAFSAIRSTNH	4	1544.806	42	
Cerebellin 1 precursor protein	Cerebellin	SGSAKVAFSAIRSTNH	4	1631.838	124	
Cerebellin 2	89-102	GSAKVAFSATRSTN	3	1395.711	22	
Cerebellin 2	88-102	(SGSAKVAFSATRSTN)	3	1482.743	14	
Cerebellin 2	89-103	(GSAKVAFSATRSTNH)	4	1532.770	10	
Cerebellin 2	88-103	(SGSAKVAFSATRSTNH)	4	1619.802	29	
Cerebellin 4	66-77	SKVAFSAVRSTN	3	1265.673	102	
Cerebellin 4	65-77	(NSKVAFSAVRSTN)	3	1379.716	2	
Cerebellin 4	64-77	ANSKVAFSAVRSTN	3	1450.753	28	
Cerebellin 4	63-77	AANSKVAFSAVRSTN	3	1521.790	22	
Chromogranin A	392-402	AYGFRDPGPQL	2	1219.600	52	
Chromogranin A	392-404	AYGFRDPGPQLRR	4	1531.800	4	Only in Cpe<fat/fat>
Chromogranin A	358-371	WSRMDQLAKELTAE	3	1676.820	59	
Chromogranin A	374-388	LEGEDDPDRSMKLSF	3	1737.788	3	
Chromogranin A	374-389	LEGEDDPDRSMKLSFR	3	1893.889	2	Only in Cpe<fat/fat>
Chromogranin A	358-371	WSRMDQLAKELTAEKR	5	1961.015	7	Only in Cpe<fat/fat>
Chromogranin A	374-390	LEGEDDPDRSMKLSFRT	4	1994.937	59	
Chromogranin A	374-391	LEGEDDPDRSMKLSFRTR	3	2151.038	7	Only in Cpe<fat/fat>
Chromogranin A	392-410	(AYGFRDPGPQLRRGWRPSS)	3	2202.119	17	
Chromogranin A	405-432	(GWRPSSREDSVEARSDFEEKKEEEGSAN)	3	3210.450	1	
Chromogranin B	592-597	(APQLDL)	1	655.35	5	
Chromogranin B	438-446	LLDEGHYPV	2	1041.521	95	
Chromogranin B	588-597	SFARAPQLDL	2	1116.590	108	
Chromogranin B	438-446	(LLDEGHYPVR)	3	1197.620	1	Only in Cpe<fat/fat>
Chromogranin B	602-613	GVAELDQLLHY	2	1256.640	4	
Chromogranin B	364-374	GSEEDRAPRPR	2	1268.622	6	
Chromogranin B	457-466	YPQSKWQEQE	2	1321.594	16	
Chromogranin B	602-613	DGVAELDQLLHY	2	1371.667	1	
Chromogranin B	588-599	SFARAPQLDLKR	4	1400.780	13	Only in Cpe<fat/fat>
Chromogranin B	503-513	pE-YEPYPITEKR	2	1405.714	1	Only in Cpe<fat/fat>
Chromogranin B	375-385	SEESQEREYKR	2	1439.664	2	Only in Cpe<fat/fat>
Chromogranin B	202-215	SEASAKKKDESVAR	2	1504.785	1	Only in Cpe<fat/fat>
Chromogranin B	186-199	(HIEDSGEKPNTFSN)	4	1573.701	1	
Chromogranin B	600-613	(pE-YDGVAELDQLLHY)	2	1645.789	2	
Chromogranin B	186-199 + phosphate	HIEDpSGEKPNTFSN	3	1653.670	6	
Chromogranin B	600-613	QYDGVAELDQLLHY	2	1662.789	48	
Chromogranin B	341-355	(ASEEEPEYGEESRSY)	2	1760.701	1	
Chromogranin B	438-453	LLDEGHYPVRESPIDT	3	1839.900	46	
Chromogranin B	186-201	HIEDSGEKPNTFSNKR	3	1857.897	2	Only in Cpe<fat/fat>
Chromogranin B	438-454	LLDEGHYPVRESPIDTA	3	1910.930	105	
Chromogranin B	313-330	PSPKESKEADVATVRLGE	4	1911.990	54	
Chromogranin B	341-356	ASEEEPEYGEESRSYR	3	1916.802	1	Only in Cpe<fat/fat>

Chromogranin B	186-201 + phosphate	HIEDpSGEKPNTFSNKR	3	1937.863	1	Only in Cpe<fat/fat>
Chromogranin B	499-513	FPDRQYEPYPITEKR	3	1937.964	1	Only in Cpe<fat/fat>
Chromogranin B	357-373	(GLQYRGRGSEEDRAPRP)	5	1942.97	20	
Chromogranin B	357-373 + phosphate	GLQYRGRGpSEEDRAPRP	4	2022.97	38	
Chromogranin B	600-616	(QYDGVAELDQLLHYRKK)	5	2075.070	1	Only in Cpe<fat/fat>
Chromogranin B	357-374	GLQYRGRGSEEDRAPRPR	4	2099.073	60	
Chromogranin B	357-374 + phosphate	GLQYRGRGpSEEDRAPRPR	5	2179.073	65	
Chromogranin B	438-456	LLDEGHYPVRESPIDTAKR	5	2195.133	7	Only in Cpe<fat/fat>
Chromogranin B	313-332	PSPKESKEADVATVRLGEKR	3	2196.186	1	Only in Cpe<fat/fat>
Chromogranin B	64-83	(SGKEVKGEEKGENQNSKFEV)	7	2222.081	13	
Chromogranin B	517-535	GALFNPYFDPLQWKNSDFE	3	2287.059	1	
Chromogranin B	64-84	SGKEVKGEEKGENQNSKFEVR	3	2378.183	2	Only in Cpe<fat/fat>
Chromogranin B	516-535	LGALFNPYFDPLQWKNSDFE	2	2400.151	104	
Chromogranin B	309-330	(EERRPSPKESKEADVATVRLGE)	6	2482.278	7	
Chromogranin B	386-407	NHPDSELESTANRHGEETEEER	4	2565.096	2	Only in Cpe<fat/fat>
Chromogranin B	333-353 + phosphate	SHHLAHYRApSEEEPEYGEESR	4	2592.066	1	Only in Cpe<fat/fat>
Chromogranin B	64-86	SGKEVKGEEKGENQNSKFEVRLL	6	2604.351	104	
Chromogranin B	516-537	LGALFNPYFDPLQWKNSDFEKR	4	2684.339	10	Only in Cpe<fat/fat>
Chromogranin B	516-537 +54 Da on Lys	LGALFNPYFDPLQW-(K+54)-NSDFEKR	4	2738.349	1	Only in Cpe<fat/fat>
Chromogranin B	287-310	(RPRHHHGRSGSNKSSYEGHPLSEE)	6	2740.293	6	
Chromogranin B	64-87	SGKEVKGEEKGENQNSKFEVRLLR	4	2760.452	2	Only in Cpe<fat/fat>
Chromogranin B	333-356	SHHLAHYRASEEEPEYGEESRSYR	4	2918.297	1	Only in Cpe<fat/fat>
Chromogranin B	588-614	(SFARAPQLDLKRQYDGVAELDQLLHY)	5	3045.567	1	
Chromogranin B	386-417	NHPDSELESTANRHGEETEEERSYEGANGRQH	7	3664.576	3	
Chromogranin B	386-437	NHPDSELESTANRHGEETEEERSYEGANGRQH RGRGREPGAHSALDTREEKR	6	5923.745	4	Only in Cpe<fat/fat>
Chromogranin B	458-513	(PQSKWQEQEKNYLNYGEEGDQGRWWQQEEQ LGPEESREEVRFPDRQYEPYPITEKRKR)	11	7282.458	5	Only in Cpe<fat/fat>
Cocaine- and amphetamine-regulated transcript	82-86	(IPIYE)	1	633.337	5	
Cocaine- and amphetamine-regulated transcript	82-88	IPIYEKK	2	889.527	1	Only in Cpe<fat/fat>
Cocaine- and amphetamine-regulated transcript	33-50	APGAMLQIEALQEVLKKL	3	1951.120	31	
Cocaine- and amphetamine-regulated transcript	37-55	ALDIYSAVDDASHEKELPR	3	2128.044	1	Only in Cpe<fat/fat>
Cocaine- and amphetamine-regulated transcript	33-52	APGAMLQIEALQEVLKKLKS	4	2166.245	22	
Cocaine- and amphetamine-regulated transcript	33-52	(APGAMLQIEALQEVLKKLKSKR)	6	2450.440	1	Only in Cpe<fat/fat>
Cocaine- and amphetamine-regulated transcript	N-terminus after signal peptide cleavage	(AQEDAELQPRALDIYSAVDDASHEKELPR)	5	3265.585	6	
Cystatin C precursor	29-45	MLGAPEEADANEEGVRR	3	1842.853	1	Only in Cpe<fat/fat>
Cystatin C precursor	N-terminus after signal peptide cleavage	ATPKQGPRMLGAPEEADANEEGV	3	2366.110	21	
Cystatin C precursor	N-terminus after signal peptide cleavage	ATPKQGPRMLGAPEEADANEEGVRR	4	2678.319	2	Only in Cpe<fat/fat>
HMW Kininogen	Des-Arg9 Bradykinin	RPPGFSPF	2	903.460	4	
Mast cell protease 3 or 4	N-terminus after pro peptide cleavage	IIGGVESRPHSRPY	4	1566.827	38	

Mast cell protease 4	158-167	SDILREVKLR	3	1227.730	2	
Mast cell protease 4	121-132	ETPSVNVIPLPR	2	1320.740	1	
Mast cell protease 4	91-102	KVEKQIVHPKYN	5	1481.835	25	
Procholecystokinin	56-63	ARLGALLA	2	783.497	25	
Procholecystokinin	Cholecystokinin-8 (without sulfate)	(DYMGWMDF-amide)	1	1062.378	1	
Procholecystokinin	36-44	(AQEAPRRQL)	3	1067.584	7	
Procholecystokinin	46-55	AVLRTDGEPR	3	1112.594	1	
Procholecystokinin	52-62	(GEPRARLGALL)	3	1151.677	43	
Procholecystokinin	65-74	(YIQQVRKAPS-amide)	3	1187.677	1	
Procholecystokinin	46-57	AVLRTDGEPRAR	3	1339.732	1	
Procholecystokinin	116-126	DYMGWMDFGRR	2	1432.602	1	Only in Cpe<fat/fat>
Procholecystokinin	46-58	(AVLRTDGEPRARL-amide)	4	1451.818	26	
Procholecystokinin	43-55	(QLRAVLRTDGEPR)	4	1509.838	25	
Procholecystokinin	46-60	AVLRTDGEPRARLGA	4	1580.875	42	
Procholecystokinin	21-35	pE-PVVPAEATDPVEQR	2	1617.826	1	Only in Cpe<fat/fat>
Procholecystokinin	46-61	AVLRTDGEPRARLGAL	4	1693.959	46	
Procholecystokinin	46-62	AVLRTDGEPRARLGALL	4	1807.040	83	
Procholecystokinin	46-63	AVLRTDGEPRARLGALLA	4	1878.080	85	
Procholecystokinin	43-60	(QLRAVLRTDGEPRARLGA)	5	1978.118	68	
Procholecystokinin	46-64	AVLRTDGEPRARLGALLAR	4	2034.180	12	Only in Cpe<fat/fat>
Procholecystokinin	77-94	(MSVLKNLQSLDPSHRISD)	4	2039.047	3	
Procholecystokinin	77-95	(MSVLKNLQSLDPSHRISDR)	5	2195.150	2	Only in Cpe<fat/fat>
Procholecystokinin	21-42	pE-PVVPAEATDPVEQRAEEAPR	3	2270.130	1	Only in Cpe<fat/fat>
Procholecystokinin	72-93	(APSGRMSVLKNLQSLDPSHRIS)	5	2392.264	18	
Procholecystokinin	72-94	APSGRMSVLKNLQSLDPSHRISD	5	2507.291	76	
Procholecystokinin	71-94	KAPSGRMSVLKNLQSLDPSHRISD	6	2635.386	107	
Procholecystokinin	72-95	(APSGRMSVLKNLQSLDPSHRISDR)	6	2663.390	1	Only in Cpe<fat/fat>
Procholecystokinin	46-69	(AVLRTDGEPRARLGALLARYIQQV)	4	2665.514	42	
Procholecystokinin	21-44	pE-PVVPAEATDPVEQRAQEAPRRQL	3	2667.390	5	
Procholecystokinin	N-terminus after signal peptide cleavage	pE-PVVPAEATDPVEQRAQEAPRRQLR	4	2823.484	3	Only in Cpe<fat/fat>
Procholecystokinin	65-94	(YIQQVRKAPSGRMSVLKNLQSLDPSHRISD)	6	3422.820	11	
Procorticotropin Releasing Factor	127-142	GAEDALGGHQGALERE	3	1608.749	2	
Prodynorphin	Dynorphin A8	YGGFLRRI	3	980.556	72	
Prodynorphin	Dynorphin A (10-17)	PKLKWDNQ	3	1027.545	42	
Prodynorphin	β-neoendorphin	YGGFLRKYP	3	1099.581	22	
Prodynorphin	Dynorphin A8	(YGGFLRRIR)	4	1136.660	2	Only in Cpe<fat/fat>
Prodynorphin	α-neoendorphin	YGGFLRKYPK	4	1227.676	144	
Prodynorphin	α-neoendorphin-Arg	(YGGFLRKYPKR)	5	1383.780	1	Only in Cpe<fat/fat>
Prodynorphin	Dynorphin B13	(YGGFLRRQFKVVT)	4	1569.878	56	
Prodynorphin	Dynorphin B (15-28)	SQENPNTYSEDLDV	2	1609.674	5	
Prodynorphin	183-199	DEDGGQDGDQVGHEDLY	2	1847.708	5	
Prodynorphin	183-201	DEDGGQDGDQVGHEDLYKR	3	2131.904	2	Only in Cpe<fat/fat>
Prodynorphin	Dynorphin A17	(YGGFLRRIRPKLKWDNQ)	6	2146.191	8	
Prodynorphin	177-199	SSEMARDEDGGQDGDQVGHEDLY	3	2508.994	10	
Prodynorphin	177-201	SSEMARDEDGGQDGDQVGHEDLYKR	4	2793.190	4	Only in Cpe<fat/fat>
Proenkephalin	Leu-enkephalin	YGGFL	1	555.269	24	
Proenkephalin	Met-enkephalin	YGGFM	1	573.226	44	
Proenkephalin	Des-Tyr Leu-enkephalin-Lys-Arg	GGFLKR	2	676.402	3	Only in Cpe<fat/fat>
Proenkephalin	Des-Tyr Met-enkephalin-Lys-Arg	GGFMKR	2	694.358	3	Only in Cpe<fat/fat>

Proenkephalin	Octapeptide (3-8)	GFMRSL	2	709.358	1	
Proenkephalin	Leu-enkephalin-Arg	YGGFLR	2	711.370	2	Only in Cpe<fat/fat>
Proenkephalin	Des-Tyr heptapeptide	GGFMRF	2	713.332	26	
Proenkephalin	Met-enkephalin-Arg	YGGFMR	2	729.327	13	
Proenkephalin	Des-Tyr octapeptide	GGFMRSL	2	766.380	8	
Proenkephalin	Met-enkephalin-Lys-Lys	(YGGFMKK)	3	829.410	2	Only in Cpe<fat/fat>
Proenkephalin	Leu-enkephalin-Lys-Arg	(YGGFLKR)	3	839.460	2	Only in Cpe<fat/fat>
Proenkephalin	Leu-enkephalin-Lys-Arg	YGGFLKR	2	839.465	4	Only in Cpe<fat/fat>
Proenkephalin	Met-enkephalin-Lys-Arg	YGGFMKR	2	857.422	5	Only in Cpe<fat/fat>
Proenkephalin	Heptapeptide	YGGFMRF	2	876.395	117	
Proenkephalin	Met-Enkephalin-Arg-Arg	YGGFMRR	2	885.428	5	Only in Cpe<fat/fat>
Proenkephalin	Octapeptide	YGGFMRSL	2	929.443	90	
Proenkephalin	Metorphamide	YGGFMRRV-amide	3	983.496	18	
Proenkephalin	221-228	PEWWMDYQ	1	1153.454	7	
Proenkephalin	Metorphamide-Gly-Arg	YGGFMRRVGR	4	1197.619	14	
Proenkephalin	Octapeptide-Lys-Arg	YGGFMRSLKR	4	1213.639	16	Only in Cpe<fat/fat>
Proenkephalin	201-210	EDEAKELQKR	2	1244.636	1	Only in Cpe<fat/fat>
Proenkephalin	197-207	SPQLEDEAKEL	2	1257.609	9	
Proenkephalin	220-228	RPEWWMDYQ	2	1309.555	4	
Proenkephalin	200-210	LEDEAKELQKR	2	1357.720	1	Only in Cpe<fat/fat>
Proenkephalin	219-228	GRPEWWMDYQ	2	1366.576	4	
Proenkephalin	197-208	SPQLEDEAKELQ	2	1385.667	83	
Proenkephalin	221-230	PEWWMDYQKR	2	1437.650	2	Only in Cpe<fat/fat>
Proenkephalin	218-228	VGRPEWWMDYQ	2	1465.645	88	
Proenkephalin	199-210	pE-LEDEAKELQKR	3	1468.759	3	Only in Cpe<fat/fat>
Proenkephalin	199-210	QLEDEAKELQKR	4	1485.779	3	Only in Cpe<fat/fat>
Proenkephalin	197-210	SPQLEDEAKELQKR	3	1669.833	10	Only in Cpe<fat/fat>
Proenkephalin	218-230	VGRPEWWMDYQKR	3	1749.841	5	Only in Cpe<fat/fat>
Proenkephalin	196-210	RSPQLEDEAKELQKR	3	1825.965	3	Only in Cpe<fat/fat>
Proenkephalin	217-230	RVGRPEWWMDYQKR	3	1905.942	1	Only in Cpe<fat/fat>
Proenkephalin	114-133	MDELYPMEPEEEANGGEILA	2	2235.955	13	
Proenkephalin	114-133	MDELYPMEPEEEANGGEILA	2	2235.955	14	
Proenkephalin	116-135	ELYPMEPEEEANGGEILAKR	3	2274.084	1	Only in Cpe<fat/fat>
Proenkephalin	211-228 (BAM18)	(YGGFMRRVGRPEWWMDYQ)	4	2333.062	6	
Proenkephalin	197-216	SPQLEDEAKELQKRYGGFMR	4	2381.180	1	Only in Cpe<fat/fat>
Proenkephalin	115-135	DELYPMEPEEEANGGEILAKR	3	2389.111	2	Only in Cpe<fat/fat>
Proenkephalin	238-261	FAESLPSDEEGENYSKEVPEIE	3	2497.100	42	
Proenkephalin	241-261 + phosphate	SLPpSDEEGENYSKEVPEIEKR	3	2514.116	1	Only in Cpe<fat/fat>
Proenkephalin	114-135	MDELYPMEPEEEANGGEILAKR	3	2520.151	5	Only in Cpe<fat/fat>
Proenkephalin	240-263	ESLPSDEEGENYSKEVPEIEKR	4	2563.193	1	Only in Cpe<fat/fat>
Proenkephalin	238-261 + phosphate	FAESLPpSDEEGENYSKEVPEIE	3	2577.060	49	
Proenkephalin	211-230	YGGFMRRVGRPEWWMDYQKR	4	2617.258	2	Only in Cpe<fat/fat>
Proenkephalin	143-167	DADEGDTLANSSDLLKELLGTGDNR	3	2618.231	1	
Proenkephalin	113-135	KMDELYPMEPEEEANGGEILAKR	4	2648.246	2	Only in Cpe<fat/fat>
Proenkephalin	238-263	FAESLPSDEEGENYSKEVPEIEKR	4	2781.298	8	Only in Cpe<fat/fat>
Proenkephalin	239-264 + phosphate	(FAESLPpSDEEGENYSKEVPEIEKR)	4	2861.250	1	Only in Cpe<fat/fat>
Proenkephalin	143-170	DADEGDTLANSSDLLKELLGTGDNRAKD	4	2932.390	1	
Proenkephalin	107-135	YGGFMKKMDELYPMEPEEEANGGEILAKR	4	3331.556	3	Only in Cpe<fat/fat>

Proenkephalin	143-186	(DADEGDTLANSSDLLKELLGTGDNRAKDSHQQESTNNDEDMS)	5	4534.980	6	
Proenkephalin	143-186	(DADEGDTLANSSDLLKELLGTGDNRAKDSHQQESTNNDEDMSKR)	7	4819.170	1	Only in Cpe<fat/fat>
Proenkephalin	143-196	DADEGDTLANSSDLLKELLGTGDNRAKDSHQQESTNNDEDMSKRYGGFMRSLKR	7	6014.799	9	Only in Cpe<fat/fat>
Progalanin	65-72	(ELQLEVEE)	1	987.476	6	
Progalanin	33-61	(GWTLNSAGYLLGPHAIDNHRSFSDKHGLT-amide)	6	3162.575	7	
Progastrin releasing peptide	43-52	(GSHWAVGHLM-amide)	3	1092.514	17	
Prohormone convertase 1	619-628	GVEKMVNVVE	2	1102.569	30	
Prohormone convertase 1	619-630	GVEKMVNVVEKR	3	1386.765	6	Only in Cpe<fat/fat>
Prohormone convertase 1	90-104	(LSDDDRVTWAEQQYE)	2	1853.807	5	
Prohormone convertase 1	90-108	LSDDDRVTWAEQQYEKERS	4	2354.070	10	
Prohormone convertase 1	90-110	LSDDDRVTWAEQQYEKERSKR	4	2638.274	5	Only in Cpe<fat/fat>
Prohormone convertase 2	C-terminus	SLQSILRKN	3	1057.620	70	
Prohormone convertase 2	94-104	IKMALQQEGFD	2	1278.64	58	
Prohormone convertase 2	616-627	(QELEEELDEAVE)	2	1431.625	3	
Prohormone convertase 2	616-628	QELEEELDEAVER	2	1587.726	1	Only in Cpe<fat/fat>
Prohormone convertase 2	C-terminus	pE-ELEEELDEAVERSLQSILRKN	3	2610.314	25	
Promelanin concentrating hormone	Neuropeptide EI (2-13)	IGDEENSAKFPI-amide	2	1317.640	2	
Promelanin concentrating hormone	Neuropeptide EI	EIGDEENSAKFPI-amide	2	1446.683	88	
Promelanin concentrating hormone	Neuropeptide EI-Gly-Arg	EIGDEENSAKFPIGR	2	1660.806	1	Only in Cpe<fat/fat>
Promelanin concentrating hormone	22-37	IGDEENSAKFPIGRR	3	1687.864	2	Only in Cpe<fat/fat>
Promelanin concentrating hormone	Neuropeptide EI-Gly-Arg-Arg	EIGDEENSAKFPIGRR	3	1816.907	8	Only in Cpe<fat/fat>
Promelanin concentrating hormone	Melanin concentrating hormone	(DFDMLRCMLGRVYRPCWQV)	3	2387.116	3	
Promelanin concentrating hormone variant (Ile to Thr)	Neuropeptide EI variant (2-13)	TGDEENSAKFPI-amide	2	1305.604	1	
Promelanin concentrating hormone variant (Ile to Thr)	Neuropeptide EI with Ile to Thr variant	ETGDEENSAKFPI-amide	2	1434.647	8	
Proneuromedin B	114-120	LLEPLLQ	2	824.501	6	
Proneuromedin B	97-113	ALGMNFSGPAPPIQYRR	3	1873.962	2	Only in Cpe<fat/fat>
Proneuropeptide Y	68-88	SSPETLISDLLMKESTENAPR	3	2317.147	1	Only in Cpe<fat/fat>
Proneuropeptide Y	68-90	SSPETLISDLLMKESTENAPRTR	4	2574.296	1	Only in Cpe<fat/fat>
Proneuropeptide Y	C-terminus	SSPETLISDLLMKESTENAPRTRLEDPSMW	4	3432.650	103	
Proneuropeptide Y	Neuropeptide Y	(YPSKPDNPGEDAPAEDMARYYSALRHYINLITRQRY-amide)	7	4269.065	14	
Proneuropeptide Y	Neuropeptide Y - Gly-Lys-Arg	(YPSKPDNPGEDAPAEDMARYYSALRHYINLITRQRYGKR)	8	4611.280	4	Only in Cpe<fat/fat>
Proneurotensin	Neuromedin N	KIPYIL	2	745.474	86	
Proneurotensin	Neuromedin N - Lys-Arg	KIPYILKR	4	1029.660	6	Only in Cpe<fat/fat>
Proneurotensin	Neurotensin	pE-LYENKPRRPYIL	3	1671.900	97	
Proneurotensin	Neurotensin-Lys-Arg	(pE-LYENKPRRPYILKR)	4	1956.100	5	Only in Cpe<fat/fat>
Pronociceptin/orphanin FQ	103-108	SLVQVR	2	700.460	1	Only in Cpe<fat/fat>
Pronociceptin/orphanin FQ	101-107	(VRSLVQV)	2	799.492	6	
Pronociceptin/orphanin	Nociceptin	FGGFTGARKSARKLANQ	5	1807.981	69	

FQ						
Pronociceptin/orphanin FQ	109-138	(DAEPGADAEPGADAEPGADDAEEVEQKQLQ)	3	3051.306	4	
Pronociceptin/orphanin FQ	109-140	DAEPGADAEPGADAEPGADDAEEVEQKQLQKR	4	3335.502	3	Only in Cpe<fat/fat>
Pronociceptin/orphanin FQ	103-140	SLVQVRDAEPGADAEPGADAEPGADDAEEVEQKQLQKR	5	4017.915	1	Only in Cpe<fat/fat>
Pronociceptin/orphanin FQ	101-140	(VRSLVQVRDAEPGADAEPGADAEPGADDAEEVEQKQLQKR)	6	4273.085	2	Only in Cpe<fat/fat>
Proopiomelanocortin	α-MSH 9-13	(WGKPV-amide)	2	584.343	4	
Proopiomelanocortin	γ-1-MSH 1-7	(KYVMGHF)	3	880.427	3	
Proopiomelanocortin	CLIP 1-8	RPVKVYPN	3	971.555	1	
Proopiomelanocortin	β-endorphin 18-27	(FKNAIIKNAH)	4	1154.656	3	
Proopiomelanocortin	γ-1-MSH	KYVMGHFRWD	3	1337.640	13	
Proopiomelanocortin	α-MSH 1-10	Ac-SYSMEHFRWG	2	1340.561	1	
Proopiomelanocortin	J-peptide 6-18	(VWGDGSPEPSPRE-amide)	2	1410.637	1	
Proopiomelanocortin	Acetyl-α-MSH 3-13-amide	Ac-SMEHFRWGKPV-amide	3	1413.700	5	
Proopiomelanocortin	Di-acetyl-α-MSH 1-11	DiAc-SMEHFRWGKPV-amide	3	1455.716	2	
Proopiomelanocortin	J-peptide 5-18	(AVWGDGSPEPSPRE-amide)	2	1481.690	7	
Proopiomelanocortin	Des-acetyl-MSH	SYSMEHFRWGKPV-amide	3	1621.782	22	
Proopiomelanocortin	Dehydro α-MSH	Ac-dehydroS-YSMEHFRWGKPV-amide	3	1645.790	7	
Proopiomelanocortin	α-MSH	Ac-SYSMEHFRWGKPV-amide	3	1663.793	58	
Proopiomelanocortin	Diacetyl-α-MSH	(DiAc-SYSMEHFRWGKPV-amide)	3	1705.810	4	
Proopiomelanocortin	J-peptide 1-17	AEEEAVWGDGSPEPSPR	2	1811.796	1	Only in Cpe<fat/fat>
Proopiomelanocortin	J-peptide 2-18	EEEAVWGDGSPEPSPRE-amide	2	1868.802	6	
Proopiomelanocortin	127-144	GAEDALGGHQGALERERR	3	1920.951	1	Only in Cpe<fat/fat>
Proopiomelanocortin	J-peptide, dehydro	AEEEAVWGDGSPEPSPRE-amide -18	3	1921.940	1	
Proopiomelanocortin	J-peptide	AEEEAVWGDGSPEPSPRE-amide	2	1939.855	53	
Proopiomelanocortin	γ-LPH 23-38	GPYRVEHFRWSNPPKD	4	1983.970	1	
Proopiomelanocortin	J-peptide + N-terminal Arg	(RAEEEAVWGDGSPEPSPRE-amide)	2	2095.940	7	
Proopiomelanocortin	103-122	AEEEAVWGDGSPEPSPREGK	3	2125.955	1	Only in Cpe<fat/fat>
Proopiomelanocortin	103-123	AEEEAVWGDGSPEPSPREGKR	3	2282.056	4	Only in Cpe<fat/fat>
Proopiomelanocortin	Ac-β-endorphin 1-21	Ac-YGGFMTSEKSQTPLVTLFKNA	3	2360.172	2	
Proopiomelanocortin	CLIP	RPVKVYPNVAENESAEAFPLEF	3	2505.260	48	
Proopiomelanocortin	121-144	AEPAERGAEDALGGHQGALERERR	4	2574.265	2	Only in Cpe<fat/fat>
Proopiomelanocortin	CLIP + phosphate	RPVKVYPNVAENEpSAEAFPLEF	4	2585.230	31	
Proopiomelanocortin	γ-lipotropin 1-25	(ELEGERPLGLEQVLESDAEKDDGPY)	2	2787.309	12	
Proopiomelanocortin	CLIP -Lys-Arg	RPVKVYPNVAENESAEAFPLEFKR	4	2789.450	3	Only in Cpe<fat/fat>
Proopiomelanocortin	CLIP-Lys-Arg +phosphate	RPVKVYPNVAENEpSAEAFPLEFKR	4	2869.426	1	Only in Cpe<fat/fat>
Proopiomelanocortin	Ac-β-endorphin 1-26	(Ac-YGGFMTSEKSQTPLVTLFKNAIIKNA)	4	2899.515	5	
Proopiomelanocortin	CLIP -Lys-Arg +134 Da	RPVKVYPNVAENESAEAFPLEFKR +134 Da	4	2923.250	1	Only in Cpe<fat/fat>
Proopiomelanocortin	Ac-β-endorphin 1-27	(Ac-YGGFMTSEKSQTPLVTLFKNAIIKNAH)	5	3036.574	1	
Proopiomelanocortin	β-endorphin 1-31	YGGFMTSEKSQTPLVTLFKNAIIKNAHKKGQ	7	3435.834	3	
Proopiomelanocortin	γ-lipotropin 1-30	(ELEGERPLGLEQVLESDAEKDDGPYRVEHF)	5	3455.648	3	
Proopiomelanocortin	γ-lipotropin	ELEGERPLGLEQVLESDAEKDDGPYRVEHFRWSNPPKD	7	4436.130	4	
Proopiomelanocortin	γ-lipotropin-Lys-Arg	ELEGERPLGLEQVLESDAEKDDGPYRVEHFRWSNPPKDKR	7	4720.327	4	Only in Cpe<fat/fat>
Prooxytocin	Oxytocin	CYIQNCPLG-amide	1	1006.440	25	
Prooxytocin	Oxytocin-Lys-Arg	(CYIQNCPLGGKR)	3	1348.650	1	Only in Cpe<fat/fat>
ProPACAP	111-128	GAGENLGGSAVDDPAPLT	1	1639.769	19	
ProPACAP	111-130	GAGENLGGSAVDDPAPLTKR	3	1923.965	5	Only in Cpe<fat/fat>
ProPACAP	81-110	DVAHEILNEAYRKVLDQLSARKYLQSVVAR	5	3483.895	1	Only in Cpe<fat/fat>

Propeptidyl-amidating-monooxygenase	Pro peptide (2-8)	RSPLSVF	2	804.46	6	
Propeptidyl-amidating-monooxygenase	Pro peptide	FRSPLSVF	2	951.527	104	
Propeptidyl-amidating-monooxygenase	Pro peptide -Lys-Arg	FRSPLSVFKR	3	1235.714	11	Only in Cpe<fat/fat>
Propeptidyl-amidating-monooxygenase	438-460	DLGRSDAREGAEHEEGGNAILVR	4	2450.190	2	Only in Cpe<fat/fat>
ProSAAS	KEP 3-8	PVKEPR	2	724.423	4	
ProSAAS	KEP	(ARPVKEP)	3	795.460	7	
ProSAAS	KEP 2-8	RPVKEPR	1	880.524	6	
ProSAAS	144-152	RLDPAALAA	3	896.5079	4	
ProSAAS	KEP	ARPVKEPR	3	951.561	23	
ProSAAS	Little LEN	LENPSPQAPA	2	1022.503	24	
ProSAAS	Little SAAS 5-16	ASAPLVETSTPL	1	1184.629	31	
ProSAAS	Little SAAS 7-18	APLVETSTPLRL	2	1295.745	5	
ProSAAS	Little SAAS 1-14, di-dehydro	SLSAASAPLVETST - 36	2	1296.677	4	
ProSAAS	Little SAAS 1-14, dehydro	(SLSAASAPLVETST) -18	1	1314.677	10	
ProSAAS	Little LEN-Arg-Arg	LENPSPQAPARR	3	1334.705	4	
ProSAAS	Little SAAS 5-17	(ASAPLVETSTPLR)	3	1340.730	1	Only in Cpe<fat/fat>
ProSAAS	GAV 1-14	AVPRGEAAGAVQEL	2	1366.720	8	
ProSAAS	GAV 2-15	VPRGEAAGAVQELA	2	1366.720	1	
ProSAAS	GAV 1-15	AVPRGEAAGAVQELA	2	1437.758	4	
ProSAAS	Little SAAS 5-18	ASAPLVETSTPLRL	2	1453.814	47	
ProSAAS	200-214	ILTGSSEPEAAPAPR	2	1494.768	1	Only in Cpe<fat/fat>
ProSAAS	Little SAAS 4-18	AASAPLVETSTPLRL	2	1524.850	1	
ProSAAS	129-143	PDAPAAQLARALLRA	3	1532.897	3	
ProSAAS	Little SAAS 1-16	SLSAASAPLVETSTPL	2	1542.814	132	
ProSAAS	Little SAAS 1-16 +17 Da	SLSAASAPLVETSTPL +17	2	1559.810	19	
ProSAAS	Little SAAS 3-18	SAASAPLVETSTPLRL	2	1611.883	2	
ProSAAS	Big LEN 1-15	(LENPSPQAPARRLLP)	3	1657.926	17	
ProSAAS	Little SAAS 1-17 +17 Da	(SLSAASAPLVETSTPLR) +17	3	1715.910	1	Only in Cpe<fat/fat>
ProSAAS	Big LEN	LENPSPQAPARRLLPP	3	1754.979	150	
ProSAAS	200-216	ILTGSSEPEAAPAPRRL	3	1763.953	1	
ProSAAS	Little SAAS 5-17 -Arg-Arg	(ASAPLVETSTPLRLRR)	4	1766.010	2	Only in Cpe<fat/fat>
ProSAAS	GAV 1-18	AVPRGEAAGAVQELARAL	3	1777.980	9	
ProSAAS	Little SAAS	SLSAASAPLVETSTPLRL	2	1812.01	246	
ProSAAS	PEN-18	(SVDQDLGPEVPPENVLGA)	2	1834.895	14	
ProSAAS	Little SAAS 4-18 -Arg-Arg	AASAPLVETSTPLRLRR	3	1837.053	2	Only in Cpe<fat/fat>
ProSAAS	Little SAAS 3-18 -Arg-Arg	SAASAPLVETSTPLRLRR	3	1924.085	2	Only in Cpe<fat/fat>
ProSAAS	PEN-19	(SVDQDLGPEVPPENVLGAL)	2	1947.979	16	
ProSAAS	Little SAAS -Arg	SLSAASAPLVETSTPLRLR	3	1968.100	2	Only in Cpe<fat/fat>
ProSAAS	198-216	GRILTGSSEPEAAPAPRRL	4	1977.076	14	
ProSAAS	PEN-20	SVDQDLGPEVPPENVLGALL	3	2061.063	56	
ProSAAS	Little SAAS -Arg-Arg	SLSAASAPLVETSTPLRLRR	3	2124.201	15	Only in Cpe<fat/fat>
ProSAAS	GAV 1-22	AVPRGEAAGAVQELARALAHLL	4	2212.244	2	
ProSAAS	PEN	SVDQDLGPEVPPENVLGALLRV	2	2316.232	147	
ProSAAS	GAV 1-23	AVPRGEAAGAVQELARALAHLLE	4	2341.287	1	
ProSAAS	121-143	PPLAPDDDPDAPAAQLARALLRA	3	2353.239	7	
ProSAAS	Big SAAS 1-24	ARPVKEPRSLSAASAPLVETSTPL	4	2476.365	32	
ProSAAS	GAV 5-28	GEAAGAVQELARALAHLLEAERQE	4	2531.310	40	
ProSAAS	PEN-Lys-Arg	SVDQDLGPEVPPENVLGALLRVKR	3	2600.320	12	Only in Cpe<fat/fat>
ProSAAS	Big SAAS 1-25	ARPVKEPRSLSAASAPLVETSTPLR	4	2632.466	2	Only in Cpe<fat/fat>

ProSAAS	PEN-Lys-Arg +54 Da	SVDQDLGPEVPPENVLGALLRVKR +54	4	2654.320	1	Only in Cpe<fat/fat>
ProSAAS	GAV 5-28 -Arg	GEAAGAVQELARALAHLLEAERQER	4	2687.410	2	Only in Cpe<fat/fat>
ProSAAS	Big SAAS	ARPVKEPRSLSAASAPLVETSTPLRL	5	2745.550	66	
ProSAAS	Big SAAS-Arg	ARPVKEPRSLSAASAPLVETSTPLRLR	4	2901.651	1	Only in Cpe<fat/fat>
ProSAAS	GAV	AVPRGEAAGAVQELARALAHLLEAERQE	5	2954.576	147	
ProSAAS	Big SAAS 2-26 -Arg-Arg	RPVKEPRSLSAASAPLVETSTPLRLRR	5	2986.715	5	Only in Cpe<fat/fat>
ProSAAS	Big SAAS-Arg-Arg	ARPVKEPRSLSAASAPLVETSTPLRLRR	6	3057.750	11	Only in Cpe<fat/fat>
ProSAAS	GAV -Arg	AVPRGEAAGAVQELARALAHLLEAERQER	4	3110.680	6	Only in Cpe<fat/fat>
ProSAAS	Big SAAS-Arg-Arg +54 Da	ARPVKEPRSLSAASAPLVETSTPLRLRR +54	5	3111.750	1	Only in Cpe<fat/fat>
ProSAAS	Big GAV	(AVPRGEAAGAVQELARALAHLLEAERQERA)	6	3181.707	14	
Prosomatostatin	Somatostatin 28-14	SANSNPAMAPRE	2	1243.562	19	
Prosomatostatin	Somatostatin 28-14 -Arg	SANSNPAMAPRER	2	1399.663	1	Only in Cpe<fat/fat>
Prosomatostatin	73-88	LPQAAEQDEMRLELQR	3	1925.963	2	Only in Cpe<fat/fat>
Prosomatostatin	N-terminus after signal peptide cleavage	(APSDPRLRQFLQKSLAAATGKQELAKYFLAELL SEPNQTENDALEPEDLPQAAEQDEMRLELQRS ANSNPAMAPRE)	8	*8480.413*	4	
Prosomatostatin	N-terminus after signal peptide cleavage	APSDPRLRQFLQKSLAAATGKQELAKYFLAELL SEPNQTENDALEPEDLPQAAEQDEMRLELQR SANSNPAMAPRERK	12	*8764.776*	6	Only in Cpe<fat/fat>
Protachykinin A	Neurokinin A 2-10	KTDSFVGLM-amide	2	995.495	1	
Protachykinin A	87-95	LYGHGQISH	3	1010.493	3	
Protachykinin A	61-69	ALNSVAYER	2	1021.519	3	
Protachykinin A	Substance P 3-11	KPQQFFGLM-amide	2	1093.558	6	
Protachykinin A	Neurokinin A	HKTDSFVGLM-amide	3	1132.554	71	
Protachykinin A	Substance P 2-11	PKPQQFFGLM-amide	2	1190.611	5	
Protachykinin A	Substance P	RPKPQQFFGLM-amide	3	1346.736	159	
Protachykinin A	Neurokinin A -Gly-Lys-Arg	HKTDSFVGLMGKR	2	1474.772	6	Only in Cpe<fat/fat>
Protachykinin A	Substance P -Gly-Lys-Arg	RPKPQQFFGLMGKR	4	1688.930	13	Only in Cpe<fat/fat>
Protachykinin A	C-terminal flanking peptide	ALNSVAYERSAMQNYE	2	1844.840	91	
Protachykinin A	72-94	(DADSSVEKQVALLKALYGHGQIS)	3	2428.260	10	
Protachykinin A	72-95	DADSSVEKQVALLKALYGHGQISH	5	2565.319	28	
Protachykinin A	37-60	DAGHGQISHKRHKTDSFVGLMGKR	4	2661.367	1	Only in Cpe<fat/fat>
Protachykinin A, isoform CRA_a	Neuropeptide gamma	(DAGHGQISHKRHKTDSFVGLM-amide)	5	2319.17	41	
Protachykinin B	Neurokinin B	DMHDFFVGLM-amide	2	1209.515	66	
Protachykinin B	Neurokinin B -Gly-Lys-Arg	DMHDFFVGLMGKR	2	1551.733	9	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	53-59	(FLRKDLQ)	3	918.529	4	
Prothyrotropin Releasing Hormone	161-169	FPWMESDVT	1	1110.469	3	
Prothyrotropin Releasing Hormone	53-61	(FLRKDLQRV)	4	1173.698	10	
Prothyrotropin Releasing Hormone	160-169	SFPWMESDVT	1	1197.500	37	
Prothyrotropin Releasing Hormone	63-74	GDLGAALDSWIT	1	1217.593	13	
Prothyrotropin Releasing Hormone	95-106	GDLGEVGAWRPH	3	1292.626	14	
Prothyrotropin Releasing Hormone	160-171	SFPWMESDVTKR	3	1481.690	8	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	95-108	(GDLGEVGAWRPHKR)	5	1576.820	2	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	57-74	DLQRVRGDLGAALDSWIT	2	1985.033	14	

Prothyrotropin Releasing Hormone	154-171	pE-HPGRRSFPWMESDVTKR	3	2196.073	1	Only in Cpe<fat/fat>
Prothyrotropin releasing hormone	133-151	(PSWLPDFFLDSWFSDAPQV)	2	2253.042	5	
Prothyrotropin Releasing Hormone	53-74	(FLRKDLQRVRGDLGAALDSWIT)	4	2529.382	7	
Prothyrotropin releasing hormone	178-200	FIDPELQRSWEETEGEEGGLMPE	2	2677.185	27	
Prothyrotropin Releasing Hormone	83-106	EEKEEDVEAEERGDLGEVGAWRPH	5	2765.253	37	
Prothyrotropin Releasing Hormone	N-terminus after signal peptide cleavage	LLEAAQEEGAVTPDLPGLEKVQVRPE	3	2787.480	109	
Prothyrotropin Releasing Hormone	53-76	FLRKDLQRVRGDLGAALDSWITKR	4	2813.578	1	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	178-202	FIDPELQRSWEETEGEEGGLMPEKR	4	2961.381	2	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	83-107	EEKEEDVEAEERGDLGEVGAWRPHKR	5	3049.449	1	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	N-terminus after signal peptide cleavage	LLEAAQEEGAVTPDLPGLEKVQVRPERR	5	3099.668	2	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone	154-202	pE-HPGRRSFPWMESDVTKRQHPGRRFIDPELQRSWEETEGEEGGLMPEKR	5	3675.775	1	Only in Cpe<fat/fat>
Prothyrotropin Releasing Hormone variant	83-105 of variant	(EEKLEDEAEERGDLGEVGAWRPH)	5	2650.226	7	
Prothyrotropin Releasing Hormone variant	83-107 of variant	EEKLEDEAEERGDLGEVGAWRPHKR	4	2934.422	2	Only in Cpe<fat/fat>
Prourotensin 2B	63-75	(GDLPSKLEELRQV)	3	1482.804	4	
Provasoactive intestinal peptide	146-152	(YLNSILN-amide)	2	834.46	3	
ProVasoactive Intestinal Peptide	111-122	ISSSISEDPVPI	2	1242.634	26	
ProVasoactive Intestinal Peptide	111-124	ISSSISEDPVPIKR	2	1526.830	2	Only in Cpe<fat/fat>
Provasoactive intestinal peptide	125-138	HSDAVFTDNYTRLR	2	1693.817	1	Only in Cpe<fat/fat>
Provasoactive intestinal peptide	82-111	HADGVFTSDYSRLLGQISAKKYLESLIGKR	5	3351.794	1	Only in Cpe<fat/fat>
Provasopressin	151-165	VQLAGTRESVDSAKP	3	1556.820	13	
Provasopressin	C-terminus	GTRESVDSAKPRVY	4	1563.800	3	
Provasopressin	C-terminus	AGTRESVDSAKPRVY	4	1634.84	29	
Provasopressin	150-165	(LVQLAGTRESVDSAKP)	3	1669.900	1	
Provasopressin	C-terminus	VQLAGTRESVDSAKPRVY	4	1975.049	110	
Secretogranin II	516-524	(PELLNTNQL)	1	1040.550	7	
Secretogranin II	569-578	IPVGSLKNED	2	1070.560	11	
Secretogranin II	287-297	SGQLGLPDEEN	2	1157.520	2	
Secretogranin II	Secretoneurin 22-33	QELGKLTGPSNQ	2	1270.652	1	
Secretogranin II	516-526	PELLNTNQLKR	2	1324.746	3	Only in Cpe<fat/fat>
Secretogranin II	569-581	IPVGSLKNEDTPN	2	1382.704	2	
Secretogranin II	430-442	PDGLSVEDILNVL	2	1382.729	2	
Secretogranin II	287-299	SGQLGLPDEENRR	2	1469.722	3	Only in Cpe<fat/fat>
Secretogranin II	429-442	LPDGLSVEDILNVL	2	1495.813	1	
Secretogranin II	274-286	TEKNEQINEEMKR	2	1647.789	1	Only in Cpe<fat/fat>
Secretogranin II	300-316	ESKDQLSEDASKVITYL	3	1924.960	94	
Secretogranin II	Secretoneurin 15-33	ATLESVFQELGKLTGPSNQ	3	2018.032	10	
Secretogranin II	269-286	DSKENTEKNEQINEEMKR	3	2221.028	1	Only in Cpe<fat/fat>
Secretogranin II	300-318	ESKDQLSEDASKVITYLRR	3	2237.165	3	Only in Cpe<fat/fat>
Secretogranin II	287-316	(SGQLGLPDEENRRESKDQLSEDASKVITYL)	5	3376.675	2	
Secretogranin II	Secretoneurin	TNEIVEEQYTPQSLATLESVFQELGKLTGPSNQ	4	3649.800	42	
Secretogranin II	Secretoneurin - Lys-Arg	TNEIVEEQYTPQSLATLESVFQELGKLTGPSNQKR	4	3933.996	1	Only in Cpe<fat/fat>

Secretogranin II	527-566	VPSPVSSEDDLQEEEQLEQAIKEHLGPGSSQEME RLAKVS	5	4405.123	9	
Secretogranin II	527-566 +phosphate	(VPSPVSSEDDLQEEEQLEQAIKEHLGPGSSQEME RLAKVS) +1 phosphate (site not identified)	5	4485.097	6	
Secretogranin II	Peptide + 2 phosphates	VPSPVpSSEDDLQEEEQLEQAIKEHLGPGSpSQEME RLAKVS	5	4565.063	1	
Secretogranin II	527-568	VPSPVSSEDDLQEEEQLEQAIKEHLGPGSSQEME RLAKVSKR	5	4689.319	5	Only in Cpe<fat/fat>
Secretogranin II	569-610	IPVGSLKNEDTPNRQYLDEDMLLKVLEYLNQEQA EQGREHLA	6	4895.440	34	
Secretogranin II	569-612	IPVGSLKNEDTPNRQYLDEDMLLKVLEYLNQEQA EQGREHLAKR	6	5179.644	8	Only in Cpe<fat/fat>
Secretogranin II isoform	527-566 with Pro27Gln	VPSPVSSEDDLQEEEQLEQAIKEHLGQGSSQEME RLAKVS	5	4436.129	4	
Secretogranin II isoform	527-568 with Pro27Gln	VPSPVSSEDDLQEEEQLEQAIKEHLGQGSSQEME RLAKVSKR	7	4720.325	3	Only in Cpe<fat/fat>
Secretogranin III	N-terminus after signal peptide cleavage	FPKPEGSQDKSLHN	4	1582.774	125	
Secretogranin III	38-55	(ELSAERPLNEQIAEAEAD)	2	1983.938	5	
VGF	211-218	(ASWGEFQA)	2	894.387	4	
VGF	220-236	VPERAPLPPPVPSQFQA	3	1828.980	13	
VGF	491-507	(PPEPVPPPRAAPAPTHVR)	4	1885.030	1	Only in Cpe<fat/fat>
VGF	489-507	NAPPEPVPPPRAAPAPTHV	3	1914.010	120	
VGF	180-197 w/ pE	pE-QETAAAETETRTHTLTR	3	2025.998	1	Only in Cpe<fat/fat>
VGF	489-507	(NAPPEPVPPPRAAPAPTHVR)	4	2070.110	1	Only in Cpe<fat/fat>
VGF	487-507	KKNAPPEPVPPPRAAPAPTHV	5	2170.201	60	
VGF	NERP-1 (285-310)	LEGSFLGGSEAGERLLQQGLAQVEA-amide	3	2557.321	24	
VGF	348-372	(DLGGRELQETQQERENEREEEAEQE)	4	3030.340	12	
VGF	180-209	pE-QETAAAETETRTHTLTRVNLESPGPERVW	4	3389.687	3	
VGF	180-209	(QQETAAAETETRTHTLTRVNLESPGPERVW)	5	3406.69	6	
VGF	TLQP-30	(TLQPPASSRRRHFHHALPPARHHPDLEAQA)	5	3429.778	3	
VGF	181-210	pE-QETAAAETETRTHTLTRVNLESPGPERVWR	5	3545.762	1	Only in Cpe<fat/fat>
VGF	588-617	(AQEEADAEERRLQEQEELENYIEHVLLHRP)	6	3672.777	25	
VGF	N-terminus after signal peptide cleavage	(APPGRPDVFPPPLSSEHNGQVAEDAVSRPKD DGVPEV)	5	3861.980	18	
VGF	N-terminus after signal peptide cleavage	APPGRPDVFPPPLSSEHNGQVAEDAVSRPKD DGVPEVR	6	4017.993	4	Only in Cpe<fat/fat>

Abbreviations: CLIP, corticotrophin-like intermediate lobe peptide; Mox = methionine oxide; MSH, melanocyte stimulating hormone; PACAP, pituitary adenylate cyclase activating peptide; pE = pyroGlu; pS = phosphoSer; pT = phosphoThr; Theor. mass, theoretical mass; z, charge state. Note that proSAAS, the names of proSAAS-derived peptides (SAAS, PEN, LEN, GAV, KEP), and VGF are names, not abbreviations. For most peptides, the monoisotopic mass of the unprotonated peptide is indicated; for larger peptides the average mass is shown (this is indicated in italics). The comment "only in Cpe<fat/fat>" means that the peptide was detected in $Cpe^{fat/fat}$ mouse brain after affinity chromatography and not detected in wild-type mice. Peptide sequences in parentheses are tentative matches to peptides that are either known to exist in brain, or predicted based on the presence of a known cleavage site on one or both sides of the peptide and the expression of the peptide precursor in the appropriate brain region. These tentative matches did not have high-quality MS/MS spectra that allowed for unequivocal assignment, and were based on the precursor mass (within 40 parts per million of the theoretical mass), the correct number of trimethylammoniumbutyrate tags incorporated (which reflects the number of free amines on the peptide) and a theoretical charge state consistent with the observed charge. All other sequences (i.e. those not in parentheses) were identified by MS/MS sequencing and also the above criteria.

Supplemental Table 2. Peptides derived from intracellular proteins

Precursor	Sub. Loc.	Peptide name	USF	Peptide sequence	DSF	z	Theor. Mass	Times found	Notes
Actin (beta or gamma)	Cyto	170-177 of beta	A	LPHAILRL	D	3	931.605	13	
Actin (beta or gamma)	Cyto	169-177 of beta	Y	ALPHAILRL	D	3	1002.641	54	
Actin (beta or gamma)	Cyto	95-108	L	RVAPEEHPVLLTEA	P	3	1559.831	15	
Actin (beta or gamma)	Cyto	357-371	W	ISKQEYDESGPSIVH	R	3	1687.794	2	
Actin (beta or gamma)	Cyto	356-371	M	WISKQEYDESGPSIVH	R	3	1873.885	1	
Actin, gamma	Cyto	N-terminus	M	Ac-EEEIAALVIDNGSGM	C	2	1588.729	1	
AF1q (ALL1-fused gene from chromosome 1q)	Cyto	C-terminus	A	PIASIHSVDLDLL	*	2	1391.766	5	
Aldolase A	Mito	46-57	Q	SIGTENTEENRR	F	2	1404.659	1	c
Aspartate aminotransferase, cytoplasmic	Cyto	N-terminus	M	APPSVFAQVPQAPPVLV	F	3	1715.961	1	
Aspartate aminotransferase, mitochondrial	Mito	N-terminus		SSWWTHVEMGPPD	P	2	1527.645	18	a
ATP synthase subunit alpha	Mito	C-terminus	D	AKLKEIVTNFLAGFEP	*	3	1775.982	19	
ATP synthase subunit d	Mito	46-59	L	SEKPPAIDWAYYRA	V	3	1665.815	2	
ATP synthase subunit e	Mito	N-terminus	M	VPPVQVSPLIKFGRYS	A	3	1786.014	15	
ATP synthase subunit g	Mito	C-terminus	F	YIGEIIGKRGIVGYDV	*	2	1750.962	1	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	C-terminus	D	PKFEVIDKPQS	*	3	1286.695	56	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	C-terminus	D	DPKFEVIDKPQS	*	2	1401.722	18	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	97-109	Y	GKGEMDTFPTFKF	D	3	1503.707	4	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	C-terminus	F	DDPKFEVIDKPQS	*	3	1516.748	19	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	C-terminus	F	KFDDPKFEVIDKPQS	*	4	1791.904	5	
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mito	C-terminus	F	PTFKFDDPKFEVIDKPQS	*	4	2137.062	8	
ATP synthase, H+ transporting, mitochondrial F1 complex, subunit O	Mito	24-40	P	FAKLVRPPVQVYGIEGR	Y	3	1928.100	1	c
ATP/ADP translocase 1 (Solute carrier family 25, member 4)	Mito	C-terminus	L	VLYDEIKKYV	*	3	1268.702	2	
ATPase inhibitor	Mito	84-94	K	EIERLQKQIER	H	2	1440.805	1	c
ATPase inhibitor	Mito	30-50	S	SDSMDTGAGSIREAGGAFGKR	E	3	2068.960	1	c
ATPase inhibitor	Mito	29-50	D	SSDSMDTGAGSIREAGGAFGKR	E	3	2155.992	1	c
Calmodulin	Cyto	C-terminus	N	YEEFVQMMTAK	*	2	1375.615	2	c
Calmodulin	Cyto	C-terminus	D	GQVNYEEFVQMMTAK	*	2	1773.807	29	
Calmodulin	Cyto	69-86	F	DKDGDGTITTKELGTVMR	S	3	1935.957	1	
Calmodulin	Cyto	C-terminus	D	GDGQVNYEEFVQMMTAK	*	2	1945.863	42	

Calmodulin	Cyto	66-86	F	SLFDKDGDGTITTKELGTVMR	S	3	2283.142	2	c
Calmodulin	Cyto	N-terminus	M	Ac-ADQLTEEQIAEFKEAFSLFD	K	3	2372.106	28	
Calmodulin	Cyto	N-terminus	M	Ac-ADQLTEEQIAEFKEAFSLFD +54 on internal region 6-16	K	3	2426.106	3	
Calmodulin	Cyto	N-terminus	M	Ac-ADQLTEEQIAEFKEAFSLFDKD	G	2	2615.231	43	
Calmodulin	Cyto	Entire protein	M	Ac-ADQLTEEQIAEFKEAFSLFDKDGDGTITTK ELGTVMRSLGQNPTEAELQDMINEVDADGN GTIDFPEFLTMMARKMKDTDSEEEIREAFRV FDKDGNGYISAAELRHVMTNLGEKLTDEEVD EMIREADIDGDGQVNYEEFVQMMTAK +42 on internal site (could be trimethyl Lys in position 115)	*	14	*16790.538*	43	
Calmodulin-like protein	Cyto	C-terminus	D	IDGDGQVNYEESVQMMTAK	*	2	2113.930	1	c
Cathepsin B precursor	Lyso	8-18	G	IESEIVAGIPR	T	2	1182.661	1	c
Cathepsin B precursor	Lyso	320-331	C	GIESEIVAGIPR	T	2	1239.682	2	c
Cathepsin D	Lyso	65-72	T	EPVSELLK	N	2	913.519	2	
Cathepsin D	Lyso	C-terminus	Y	YTVFDRDNNRVGFANAVV	L	3	2056.013	29	
Clathrin light chain A	Cyto	C-terminus	L	KQAPLVH	*	3	791.465	13	
Clathrin light chain A	Cyto	C-terminus	I	SLKQAPLVH	*	3	991.589	66	
Clathrin light chain A	Cyto	C-terminus	R	SVLISLKQAPLVH	*	3	1403.850	26	
Clathrin light chain A	Cyto	189-205	C	DFNPKSSKQAKDVSRMR	S	3	1993.016	2	c
Clathrin light chain A	Cyto	164-187	A	AEEAFVNDIDESSPGTEWERVARL	C	3	2719.272	2	
Clathrin light chain B	Cyto	C-terminus	R	SVLMSLKQTPLSR	*	3	1458.823	10	
Cofilin, non-muscle isoform (Cofilin-1)	Cyto	C-terminus	L	GGSAVISLEGKPL	*	2	1226.687	2	
Cofilin, non-muscle isoform (Cofilin-1)	Cyto	N-terminus	M	Ac-ASGVAVSDGVIKV	F	2	1242.682	6	
Cold-inducible RNA-binding protein	Cyto	N-terminus	M	Ac-ASDEGKLFVGGLSF	D	2	1467.725	1	
Cytochrome c oxidase subunit 2	Mito	C-terminus	L	KYFENWSASMI	*	2	1374.628	4	
Cytochrome c oxidase subunit 5a	Mito	126-132	L	RPTLNEL	G	2	841.466	6	
Cytochrome c oxidase subunit 5a	Mito	79-87	L	VPEPKIIDA	A	2	980.554	6	
Cytochrome c oxidase subunit 5a	Mito	56-64	Y	FNKPDIDAW	E	2	1104.524	1	
Cytochrome c oxidase subunit 5a	Mito	57-66	F	NKPDIDAWEL	R	2	1199.582	6	
Cytochrome c oxidase subunit 5a	Mito	77-87	Y	DLVPEPKIIDA	A	2	1208.673	6	
Cytochrome c oxidase subunit 5a	Mito	96-107	L	NDFASAVRILEV	V	2	1332.704	8	
Cytochrome c oxidase subunit 5a	Mito	56-66	Y	FNKPDIDAWEL	R	2	1346.651	4	
Cytochrome c oxidase subunit 5a	Mito	C-terminus	L	GISTPEELGLDKV	*	2	1356.714	31	
Cytochrome c oxidase subunit 5a	Mito	95-107	R	LNDFASAVRILEV	V	2	1445.788	1	
Cytochrome c oxidase subunit 5a	Mito	C-terminus	L	RPTLNELGISTPEELGLDKV	*	3	2180.169	18	
Cytochrome c oxidase subunit 5a	Mito	108-126	V	VKDKAGPHKEIYPYVIQEL	R	4	2226.205	1	

Cytochrome c oxidase subunit 5a	Mito	C-terminus	E	LRPTLNELGISTPEELGLDKV	*	3	2293.253	5	
Cytochrome c oxidase subunit 5b	Mito	32-49	M	ASGGGVPTDEEQATGLER	E	2	1772.818	2	c
Cytochrome c oxidase subunit 6a	Mito	49-57	A	LPGVGVSML	N	2	871.484	3	
Cytochrome C oxidase subunit 6a	Mito	47-57	F	VALPGVGVSML	N	2	1041.589	5	
Cytochrome c oxidase subunit 6a	Mito	46-57	Y	FVALPGVGVSML	N	2	1188.658	7	
Cytochrome c oxidase subunit 6a	Mito	98-111	H	NPHVNPLPTGYEDE	*	2	1580.711	4	
Cytochrome c oxidase subunit 6a	Mito	96-111	L	FHNPHVNPLPTGYEDE	*	3	1864.827	8	
Cytochrome c oxidase subunit 6b	Mito	N-terminus	M	(Ac-AEDIKTKIKN)	Y	3	1200.671	3	
Cytochrome c oxidase subunit 6b	Mito	N-terminus	M	Ac-AEDIKTKIKNY	K	3	1363.735	30	
Cytochrome c oxidase subunit 6b	Mito	C-terminus	W	DDRIAEGTFPGKI	*	3	1417.720	7	
Cytochrome c oxidase subunit 6b	Mito	N-terminus	M	Ac-AEDIKTKIKNYKT	A	4	1592.877	19	
Cytochrome c oxidase subunit 6b	Mito	N-terminus	M	(Ac-AEDIKTKIKNYKTA)	P	4	1663.914	10	
Cytochrome c oxidase subunit 6b	Mito	C-terminus	S	AWDDRIAEGTFPGKI	*	3	1674.837	27	
Cytochrome c oxidase subunit 6b	Mito	13-27	Y	KTAPFDSRFPNQNQT	K	3	1749.843	4	
Cytochrome c oxidase subunit 6b	Mito	C-terminus	W	VSAWDDRIAEGTFPGKI	*	3	1860.926	10	
Cytochrome c oxidase subunit 6c	Mito	56-75	N	DSMKDFEEMRKAGIFQSAK	*	3	2380.119	1	c
Cytochrome c oxidase subunit 6c	Mito	55-75	R	NYDSMKDFEEMRKAGIFQSAK	*	4	2494.162	1	c
Cytochrome c oxidase subunit 6c	Mito	53-75	F	YRNYDSMKDFEEMRKAGIFQSAK	*	4	2813.327	1	c
Cytochrome c oxidase subunit 7b	Mito	67-78	M	SPVGRVTPKEWR	D	2	1410.773	2	c
Cytochrome c oxidase subunit 7b	Mito	N-terminus		SHQKRAPSFHDKYGNAILA	G	4	2139.105	65	a
Cytochrome c oxidase subunit 7c	Mito	C-terminus	F	IVRHQLLKK	*	5	1133.740	1	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	27-32	L	FIYSHF	K	2	812.386	1	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	C-terminus	Y	VEKVDELKKKYGI	*	5	1547.892	15	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	36-50	A	TVGDVNTDRPGLLDL	K	2	1583.815	10	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKR	I	3	1648.805	2	c
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	35-50	Q	(ATVGDVNTDRPGLLDL)	K	2	1654.853	3	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLK	T	4	1889.984	5	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	33-50	F	KQATVGDVNTDRPGLLDL	K	3	1911.006	18	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	58-74	A	AEEVKRLKTQPTDEEML	F	4	2016.020	2	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	58-77	A	AEEVKRLKTQPTDEEMLFIY	S	3	2439.236	6	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEML	F	4	2934.428	5	

Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	58-83	A	AEEVKRLKTQPTDEEMLFIYSHFKQA	T	5	3137.586	4	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEMLFI	Y	4	3194.580	5	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEMLFIY	S	4	3357.644	7	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEMLFIYS	H	4	3444.676	5	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEMLFIYSHF	K	4	3728.793	11	
Diazepam binding inhibitor (Acyl-CoA-binding protein)	Cyto	N-terminus	M	Ac-SQAEFDKAAEEVKRLKTQPTDEEMLFIYSHFKQA	T	6	4055.980	11	
Dihydrolipoamide S-succinyltransferase	Mito	C-terminus	D	PRVLLLDL	*	2	937.596	21	
Dipeptidyl-peptidase 2	Lyso	462-472	N	SEDPPSVVEVR	K	2	1212.599	1	
Dynein light chain 2	Cyto	N-terminus	M	Ac-SDRKAVIKNADMSEDMQQDAVD	C	5	2507.135	34	
Elongation factor 1 beta 2	Cyto	N-terminus	M	GFGDLKTPAGL	Q	2	1074.571	1	
Elongation factor 1 beta 2	Cyto	N-terminus	M	GFGDLKTPAGLQV	L	2	1301.698	6	
Elongation factor 1 beta 2	Cyto	N-terminus	M	GFGDLKTPAGLQVL	N	2	1414.782	17	
Elongation factor 1 beta 2	Cyto	N-terminus	M	GFGDLKTPAGLQVLNDYL	A	3	1919.999	11	
ES1 protein homolog	Mito	C-terminus	D	GIGAMVKNVLELTGK	*	3	1528.860	21	
Eukaryotic translation initiation factor 3, subunit F	Cyto	269-282	G	LSSDLQQVGGASAR	I	2	1387.706	1	c
Eukaryotic translation initiation factor 4E-binding protein 2	Cyto	N-terminus	M	Ac-SASAGGSHQPSQSRAIPTRTV	A	3	2136.067	4	
Eukaryotic translation initiation factor 5A	Cyto	C-terminus	I	SAMTEEAAVAIKAMAK	*	3	1620.821	2	
Excitatory amino acid transporter 1 (Solute carrier family 1, member 3)	Memb	174-184	L	IRNMFPPNLVE	A	2	1328.691	1	
Excitatory amino acid transporter 1 (Solute carrier family 1, member 3)	Memb	C-terminus	D	NEPEKPVADSETKM	*	3	1573.729	7	
Excitatory amino acid transporter 2 (Solute carrier family 1, member 2)	Memb	78-85	L	IAFPGDIL	M	2	844.469	1	
Ferritin light chain 1	Cyto	C-terminus	G	APQGSLGEYLFERLTLKHD	*	4	2173.117	1	
FK506-binding protein 1A (FKBP12)	Cyto	C-terminus	F	DVELLKLE	*	2	957.538	1	
FK506-binding protein 1A (FKBP12)	Cyto	C-terminus	L	VFDVELLKLE	*	2	1203.675	7	
FK506-binding protein 1A (FKBP12)	Cyto	56-67	E	VIRGWEEGVAQM	S	2	1373.676	2	
FK506-binding protein 1A (FKBP12)	Cyto	N-terminus	M	GVQVETISPGDGRTFPKRGQT	C	4	2229.150	45	
G2 isoform of V-ATPase subunit	Mito	32-48	R	RLKQAKEEAQMEVEQYR	R	3	2135.079	1	c
GTP-binding regulatory protein gamma-4 chain	Memb	N-terminus	*	MKEGMSNNSTTSISQAR	K	3	1840.841	1	c
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	(Ac-AGQAFRKFL)	A	2	1078.592	11	
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	Ac-AGQAFRKFLPL	F	2	1288.729	4	
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	(Ac-AGQAFRKFLPLFDR)	V	3	1706.926	4	
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	Ac-AGQAFRKFLPLFDRV	L	3	1805.983	20	

Heat shock protein 1 (chaperonin 10)	Mito	45-65	A	(TVVAVGSGGKGKSGEIEPVSV)	K	3	1956.053	5	
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	(Ac-AGQAFRKFLPLFDRVLVE)	R	3	2147.189	1	
Heat shock protein 1 (chaperonin 10)	Mito	N-terminus	M	Ac-AGQAFRKFLPLFDRVLVER	S	4	2303.290	8	
Heat shock protein J2	Cyto	N-terminus	M	VDYYEVLGVQR	H	2	1339.677	1	c
Heat shock protein J2	Cyto	N-terminus	M	VDYYEVLGVQR	Y	2	1339.677	1	c
Hemoglobin alpha	Cyto	93-99	L	RVDPVNF	K	2	845.447	2	
Hemoglobin alpha	Cyto	C-terminus	S	TVLTSKYR	*	3	966.550	1	c
Hemoglobin alpha	Cyto	26-34	Y	GAEALERMF	A	2	1022.493	2	
Hemoglobin alpha	Cyto	84-92	A	LSDLHAHKL	R	4	1032.572	20	
Hemoglobin alpha	Cyto	α-Hemopressin (VD-Hp9-α)	R	VDPVNFKLL	S	2	1043.602	1	
Hemoglobin alpha	Cyto	α-Hemopressin (RVD-Hp10-α)	L	RVDPVNFKLL	S	3	1199.703	1	
Hemoglobin alpha	Cyto	71-83	A	AGHLDDLPGALSA	L	2	1235.615	3	
Hemoglobin alpha	Cyto	C-terminus	A	SVSTVLTSKYR	*	2	1239.682	5	
Hemoglobin alpha	Cyto	N-terminus	M	VLSGEDKSNIKA	A	3	1259.672	4	
Hemoglobin alpha	Cyto	α-Hemopressin (VD-Hp11-α)	R	VDPVNFKLLSH	C	3	1267.692	6	
Hemoglobin alpha	Cyto	C-terminus	L	ASVSTVLTSKYR	*	2	1310.719	2	c
Hemoglobin alpha	Cyto	N-terminus	M	VLSGEDKSNIKAA	W	3	1330.709	20	
Hemoglobin alpha	Cyto	124-136	H	ASLDKFLASVSTV	L	3	1336.724	1	
Hemoglobin alpha	Cyto	71-84	A	AGHLDDLPGALSAL	S	2	1348.699	4	
Hemoglobin alpha	Cyto	α-Hemopressin (RVD-Hp12-α)	L	RVDPVNFKLLSH	C	4	1423.794	51	
Hemoglobin alpha	Cyto	130-142	F	LASVSTVLTSKYR	*	2	1423.804	1	c
Hemoglobin alpha	Cyto	111-124	L	ASHHPADFTPAVHA	S	3	1456.685	3	
Hemoglobin alpha	Cyto	68-83	L	ANAAGHLDDLPGALSA	L	2	1491.732	1	
Hemoglobin alpha	Cyto	82-95	L	SALSDLHAHKLRVD	P	3	1560.837	2	
Hemoglobin alpha	Cyto	68-84	L	ANAAGHLDDLPGALSAL	S	2	1604.816	4	
Hemoglobin alpha	Cyto	117-130	A	DFpTPAVHASLDKFL	A	3	1639.798	1	
Hemoglobin alpha	Cyto	35-48	F	ASFPTTKTYFPHFD	V	4	1657.778	1	
Hemoglobin alpha	Cyto	14-30	A	AWGKIGGHGAEYGAEAL	E	3	1685.816	1	
Hemoglobin alpha	Cyto	C-terminus	D	KFLASVSTVLTSKYR	*	4	1698.967	24	
Hemoglobin alpha	Cyto	64-83	V	ADALANAAGHLDDLPGALSA	L	2	1861.917	1	
Hemoglobin alpha	Cyto	110-127	T	LASHHPADFTPAVHASLD	K	4	1884.912	1	
Hemoglobin alpha	Cyto	64-84	V	ADALANAAGHLDDLPGALSAL	S	3	1975.001	1	
Hemoglobin alpha	Cyto	17-35	G	KIGGHGAEYGAEALERMFA	S	3	2005.968	1	

Hemoglobin alpha	Cyto	77-95	D	LPGALSALSDLHAHKLRVD	P	4	2012.117	14	
Hemoglobin alpha	Cyto	110-128	T	LASHHPADFTPAVHASLDK	F	5	2013.007	1	
Hemoglobin alpha	Cyto	45-63	F	PHFDVSHGSAQVKGHGKKV	A	5	2014.050	1	
Hemoglobin alpha	Cyto	C-terminus	A	SLDKFLASVSTVLTSKYR	*	4	2014.110	6	
Hemoglobin alpha	Cyto	13-32	K	AAWGKIGGHGAEYGAEALER	M	3	2041.997	2	
Hemoglobin alpha	Cyto	111-129	L	ASHHPADFTPAVHASLDKF	L	5	2046.991	2	
Hemoglobin alpha	Cyto	76-95	D	DLPGALSALSDLHAHKLRVD	P	4	2127.144	4	
Hemoglobin alpha	Cyto	111-130	L	ASHHPADFTPAVHASLDKFL	A	5	2160.075	1	
Hemoglobin alpha	Cyto	110-129	T	LASHHPADFTPAVHASLDKF	L	5	2160.075	1	
Hemoglobin alpha	Cyto	108-128	L	VTLASHHPADFTPAVHASLDK	F	5	2213.123	1	
Hemoglobin alpha	Cyto	71-92	A	AGHLDDLPGALSALSDLHAHKL	R	5	2250.176	3	
Hemoglobin alpha	Cyto	110-130	T	LASHHPADFTPAVHASLDKFL	A	5	2273.159	1	
Hemoglobin alpha	Cyto	107-128	L	LVTLASHHPADFTPAVHASLDK	F	5	2326.207	1	
Hemoglobin alpha	Cyto	108-129	L	VTLASHHPADFTPAVHASLDKF	L	5	2360.191	1	
Hemoglobin alpha	Cyto	68-92	L	ANAAGHLDDLPGALSALSDLHAHKL	R	4	2506.293	4	
Hemoglobin alpha	Cyto	111-136	L	ASHHPADFTPAVHASLDKFLASVSTV	L	5	2704.361	1	
Hemoglobin alpha	Cyto	C-terminus	D	(FTPAVHASLDKFLASVSTVLTSKYR)	*	4	2737.490	10	
Hemoglobin alpha	Cyto	64-92	V	ADALANAAGHLDDLPGALSALSDLHAHKL	R	5	2876.478	9	
Hemoglobin alpha	Cyto	N-terminus	M	VLSGEDKSNIKAAWGKIGGHGAEYGAEAL	E	5	2927.478	9	
Hemoglobin alpha	Cyto	N-terminus	M	VLSGEDKSNIKAAWGKIGGHGAEYGAEALER	M	4	3212.621	5	
Hemoglobin alpha	Cyto	C-terminus	L	ASHHPADFTPAVHASLDKFLASVSTVLTSKYR	*	5	3452.784	1	c
Hemoglobin beta	Cyto	50-58	L	(SSASAIMGN)	A	1	836.370	1	
Hemoglobin beta	Cyto	β-Hemopressin (VD-Hp7-β)	H	VDPENFR	L	2	875.414	1	
Hemoglobin beta	Cyto	6-17	T	DAEKAAVSGLWG	K	2	1202.593	1	
Hemoglobin beta	Cyto	VV-Hemorphin-7	L	VVYPWTQRY	F	3	1210.650	5	
Hemoglobin beta	Cyto	N-terminus	M	VHLTDAEKAAVS	G	2	1239.646	11	
Hemoglobin beta	Cyto	β-Hemopressin (VD-Hp12-β)	H	VDPENFRLLGNM	I	2	1403.687	12	
Hemoglobin beta	Cyto	C-terminus	K	VVAGVAAALAHKYH	*	3	1405.783	1	
Hemoglobin beta	Cyto	C-terminus	Q	KVVAGVAAALAHKYH	*	5	1533.878	1	
Hemoglobin beta	Cyto	18-33	G	KVNADEVGGEALGRLL	V	4	1639.889	1	
Hemoglobin beta	Cyto	β-Hemopressin (KLHVD-Hp17-β)	D	KLHVDPENFRLLGNMIV	I	3	1994.077	4	
Hemoglobin beta	Cyto	C-terminus	A	AQAAFQKVVAGVAAALAHKYH	*	5	2150.175	1	
Histone H2A type 1-F	Nuc	100-113	G	RVTIAQGGVLPNIQ	A	3	1464.841	1	

Histone H2A type 2-A	Nuc	53-59	M	AAVLEYL	T	2	777.427	1	
Histone H2A type 2-A	Nuc	46-59	G	AGAPVYMAAVLEYL	T	2	1466.748	1	
Lysosomal alpha-glucosidase	Lyso	517-527	W	LDMNEPSNFVR	G	2	1320.613	2	c
Macrophage migration inhibitory factor	Cyto	N-terminus	M	PMFIVNTNV	P	2	1033.527	7	
Macrophage migration inhibitory factor	Cyto	C-terminus	M	NAANVGWNGSTFA	*	2	1307.589	1	
Macrophage migration inhibitory factor	Cyto	C-terminus	D	MNAANVGWNGSTFA	*	2	1438.630	1	
Macrophage migration inhibitory factor	Cyto	C-terminus	Y	DMNAANVGWNGSTFA	*	2	1553.657	3	
Macrophage migration inhibitory factor	Cyto	11-27	V	PRASVPEGFLSELTQQL	A	2	1870.979	14	
Macrophage migration inhibitory factor	Cyto	28-47	L	AQATGKPAQYIAVHVVPDQL	M	3	2105.127	48	
Macrophage migration inhibitory factor	Cyto	N-terminus	M	PMFIVNTNVPRASVPEGFLSEL	T	3	2416.246	8	
Macrophage migration inhibitory factor	Cyto	28-50	L	AQATGKPAQYIAVHVVPDQLMTF	S	3	2484.283	14	
Macrophage migration inhibitory factor	Cyto	5-27	F	IVNTNVPRASVPEGFLSELTQQL	A	3	2511.333	3	
Macrophage migration inhibitory factor	Cyto	N-terminus	M	PMFIVNTNVPRASVPEGFLSELTQQL	A	3	2886.495	28	
Malate dehydrogenase, mitochondrial	Mito	27-43	K	VAVLGASGGIGQPLSLL	L	3	1550.903	3	
MEF2-activating SAP transcriptional regulator	Nuc	360-372	S	SLPSPTSSLSPSP	R	2	1255.630	1	
Microtubule-associated protein 1B	Cyto	2196-2214	D	PPPAPMQDRSPSPRHPDVS	M	4	2066.996	19	
Microtubule-associated protein 2	Cyto	1444-1459	R	KVAKKEPSTVSRDEVR	R	3	1828.017	1	c
Microtubule-associated protein 2	Cyto	687-699	R	SLGLGGRSAIEQR	S	2	1342.732	1	c
Microtubule-associated protein 2	Cyto	C-terminus	L	TLAEDVTAALAKQGL	*	2	1499.819	2	
Microtubule-associated protein 2	Cyto	C-terminus	L	LESPQLATLAEDVTAALAKQGL	*	3	2238.211	1	
Microtubule-associated protein 6	Cyto	23-33	A	DIAVPLVFTKY	S	2	1264.707	1	
Microtubule-associated protein tau	Cyto	C-terminus	L	ADEVSASLAKQGL	*	2	1287.667	7	
Microtubule-associated protein tau	Cyto	C-terminus	A	TLADEVSASLAKQGL	*	2	1501.799	1	
Microtubule-associated protein tau	Cyto	C-terminus	D	SPQLATLADEVSASLAKQGL	*	3	1998.071	24	
Myelin basic protein	Cyto	132-137	R	GLSLSR	F	2	631.365	1	
Myelin basic protein	Cyto	138-143	R	FSWGGR	D	2	708.334	2	c
Myelin basic protein	Cyto	158-163	R	HGFLPR	H	2	725.397	2	c
Myelin basic protein	Cyto	132-138	R	GLSLSRF	S	2	778.434	1	
Myelin basic protein	Cyto	132-139	R	GLSLSRFS	W	2	865.466	1	
Myelin basic protein	Cyto	43-52	R	FFSGDRGAPK	R	3	1080.535	1	c
Myelin basic protein	Cyto	89-98	R	TTHYGSLPQK	S	3	1130.572	1	c
Myelin basic protein	Cyto	13-24	K	YLATASTMDHAR	H	2	1335.624	4	c
Myelin basic protein	Cyto	164-175	R	HRDTGILDSIGR	F	2	1338.700	1	c

Myelin basic protein	Cyto	250-262	N	IVTPRTPPPSQGK	G	3	1376.778	2	c
Myelin basic protein	Cyto	249-262	K	NIVTPRTPPPSQGK	G	3	1490.821	2	c
Myelin basic protein	Cyto	11-24	R	SKYLATASTMDHAR	H	2	1550.751	3	c
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYL	A	4	1589.864	28	
Myelin basic protein	Cyto	255-270	R	TPPPSQGKGRGLSLSR	F	4	1636.901	1	c
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLA	T	4	1660.910	67	
Myelin basic protein	Cyto	N-terminus, from second ATG	M	Ac-MDHARHGFLPRHR	D	5	1670.822	2	
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLAT	A	4	1761.958	122	
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLATA	S	4	1832.995	137	
Myelin basic protein	Cyto	C-terminus	R	FSWGGRDSRSGSPMARR	*	3	1908.913	1	c
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLATAS	T	4	1920.025	83	
Myelin basic protein	Cyto	N-terminus	M	(Ac-ASQKRPSQRSKYLATAST)	M	4	2021.075	18	
Myelin basic protein	Cyto	13-30	K	YLATASTMDHARHGFLPR	H	3	2043.011	1	c
Myelin basic protein	Cyto	158-175	R	HGFLPRHRDTGILDSIGR	F	4	2046.087	1	c
Myelin basic protein	Cyto	33-52	R	DTGILDSIGRFFSGDRGAPK	R	3	2108.065	1	c
Myelin basic protein	Cyto	211-228	R	TQDENPVVHFFKNIVTPR	T	3	2140.107	1	c
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLATASTM	D	4	2152.115	29	
Myelin basic protein	Cyto	11-30	R	SKYLATASTMDHARHGFLPR	H	3	2258.138	1	c
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLATASTMD	H	4	2267.142	48	
Myelin basic protein	Cyto	N-terminus	M	(Ac-ASQKRPSQRSKYLATASTMDHAR)	H	5	2631.319	49	
Myelin basic protein	Cyto	N-terminus	M	Ac-ASQKRPSQRSKYLATASTMDHARHGFLPR	H	7	3338.706	30	
Myelin basic protein	Cyto	196-228	R	TTHYGSLPQKSQHGRTQDENPVVHFFKNIVTPR	T	5	3817.940	1	c
Myelin basic protein - isoform 4 or 6	Cyto	C-terminus	L	SLSRFSWGGRDSRSGSPMARR	*	5	2352.162	1	c
Na and Cl-dependent GABA transporter	Memb	C-terminus	D	GTISAITEKETHF	*	3	1432.720	24	
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 3	Mito	C-terminus	D	PLGPSLDWLKNL	*	2	1351.750	9	
NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 8	Mito	C-terminus	D	PTKEPEPVVHYDI	*	3	1522.770	20	
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Mito	C-terminus	K	SYGANFSWNKRTRVSTK	*	5	2001.018	1	
NADH dehydrogenase (ubiquinone) Fe-S protein 6	Mito	N-terminus	F	AIDLIAQQPVNEVEHR	I	3	1830.959	1	c
NADH dehydrogenase (ubiquinone) Fe-S protein 6	Mito	21-41	F	GVQVSPSGEKITHTGQVYDEK	D	3	2258.118	1	c
NADH dehydrogenase (ubiquinone) Fe-S protein 6	Mito	22-44	G	VQVSPSGEKITHTGQVYDEKDYR	R	4	2635.288	1	c
NADH dehydrogenase (ubiquinone) Fe-S protein 6	Mito	21-44	F	GVQVSPSGEKITHTGQVYDEKDYR	R	4	2692.309	2	c
NADH dehydrogenase (ubiquinone) Fe-S protein	Mito	21-47	F	GVQVSPSGEKITHTGQVYDEKDYRRVR	F	5	3103.580	2	c

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NaDH dehydrogenase (ubiquinone) flavo-protein 1	Mito	17-28	V	SVRFSSGTTAPK	K	3	1236.646	3	
Neurogranin	Cyto	C-terminus	R	KGPGPGGPGGAGGARGGAGGGPSGD	*	3	1903.888	32	
Neurogranin	Cyto	24-43	D	PGANAAAAKIQASFRGHMAR	K	3	2024.049	1	c
Neurogranin	Cyto	20-43	I	PLDDPGANAAAAKIQASFRGHMAR	K	4	2464.240	2	c
Neurogranin	Cyto	19-43	D	IPLDDPGANAAAAKIQASFRGHMAR	K	4	2577.323	1	c
Nucleoporin-like protein 1	Nuc	526-537	P	SGSLSAGFGSSS	T	1	1042.457	2	
PC4 and SFRS1-interacting protein (Lens epithelium-derived growth factor)	Nuc	N-terminus	M	Ac-TRDFKPGDLIFA	K	2	1420.735	5	
Peptidylprolyl isomerase A	Cyto	92-100	K	HTGPGILSM	A	2	911.453	4	
Peptidylprolyl isomerase A	Cyto	91-100	L	KHTGPGILSM	A	3	1039.548	46	
Peptidylprolyl isomerase A	Cyto	84-92	F	EDENFILKH	H	3	1143.556	6	
Peptidylprolyl isomerase A	Cyto	30-39	V	PKTAENFRAL	S	3	1145.619	10	
Peptidylprolyl isomerase A	Cyto	N-terminus	M	VNPTVFFDIT	A	2	1151.586	9	
Peptidylprolyl isomerase A	Cyto	26-36	F	ADKVPKTAENF	R	3	1218.624	19	
Peptidylprolyl isomerase A	Cyto	136-145	G	MNIVEAMERF	G	2	1238.579	1	
Peptidylprolyl isomerase A	Cyto	89-100	F	ILKHTGPGILSM	A	3	1265.717	2	
Peptidylprolyl isomerase A	Cyto	72-83	N	GTGGRSIYGEKF	E	3	1270.631	2	
Peptidylprolyl isomerase A	Cyto	130-141	F	GKVKEGMNIVEA	M	3	1273.670	14	
Peptidylprolyl isomerase A	Cyto	15-25	D	EPLGRVSFELF	A	2	1292.676	1	
Peptidylprolyl isomerase A	Cyto	135-145	E	GMNIVEAMERF	G	2	1295.600	1	
Peptidylprolyl isomerase A	Cyto	119-129	K	TEWLDGKHVVF	G	3	1329.672	1	
Peptidylprolyl isomerase A	Cyto	8-19	F	FDITADDEPLGR	V	2	1347.631	1	c
Peptidylprolyl isomerase A	Cyto	26-37	F	ADKVPKTAENFR	A	4	1374.726	4	
Peptidylprolyl isomerase A	Cyto	40-53	L	STGEKGFGYKGSSF	H	3	1450.673	8	
Peptidylprolyl isomerase A	Cyto	118-129	A	KTEWLDGKHVVF	G	4	1457.767	59	
Peptidylprolyl isomerase A	Cyto	23-35	F	ELFADKVPKTAEN	R	3	1460.751	1	
Peptidylprolyl isomerase A	Cyto	27-39	A	DKVPKTAENFRAL	S	3	1487.810	2	
Peptidylprolyl isomerase A	Cyto	117-129	T	AKTEWLDGKHVVF	G	4	1528.804	4	
Peptidylprolyl isomerase A	Cyto	9-22	F	DITADDEPLGRVSF	E	2	1533.731	8	
Peptidylprolyl isomerase A	Cyto	26-39	F	ADKVPKTAENFRAL	S	4	1558.847	81	
Peptidylprolyl isomerase A	Cyto	12-25	T	ADDEPLGRVSFELF	A	2	1593.767	5	
Peptidylprolyl isomerase A	Cyto	23-36	F	ELFADKVPKTAENF	R	3	1607.819	5	
Peptidylprolyl isomerase A	Cyto	38-53	R	ALSTGEKGFGYKGSSF	H	3	1634.794	1	

Peptidylprolyl isomerase A	Cyto	8-22	F	FDITADDEPLGRVSF	E	2	1680.799	2	
Peptidylprolyl isomerase A	Cyto	84-100	F	EDENFILKHTGPGILSM	A	3	1899.940	71	
Peptidylprolyl isomerase A	Cyto	8-24	F	FDITADDEPLGRVSFEL	F	3	1922.926	1	
Peptidylprolyl isomerase A	Cyto	23-39	F	ELFADKVPKTAENFRAL	S	4	1948.042	37	
Peptidylprolyl isomerase A	Cyto	63-83	C	QGGDFTRHNGTGGRSIYGEKF	E	5	2283.078	11	
Peptidylprolyl isomerase A	Cyto	N-terminus	M	VNPTVFFDITADDEPLGRVSF	E	2	2338.148	41	
Peptidyl-prolyl isomerase A	Cyto	55-61	H	RIIPGFM	C	2	832.463	1	
Peptidyl-prolyl isomerase A	Cyto	37-48	F	RALSTGEKGFGY	K	3	1284.646	1	
Peroxiredoxin V	Mito	N-terminus of splice variant	M	APIKVGDAIPSVEVF	E	2	1540.850	22	
Phosphatidylethanolamine-binding protein 1	Cyto	59-66	L	DPGKLYTL	V	2	905.486	9	
Phosphatidylethanolamine-binding protein 1	Cyto	57-66	D	GLDPGKLYTL	V	2	1075.591	2	
Phosphatidylethanolamine-binding protein 1	Cyto	93-103	M	KGNDISSGTVL	S	2	1089.567	16	
Phosphatidylethanolamine-binding protein 1	Cyto	48-57	N	RPSSISWDGL	D	2	1116.556	2	
Phosphatidylethanolamine-binding protein 1	Cyto	39-48	G	KVLTPTQVMN	R	2	1129.617	1	
Phosphatidylethanolamine-binding protein 1	Cyto	Hippocampal cholinergic neurostimulating peptide	M	Ac-AADISQWAGPL	C	2	1169.561	1	
Phosphatidylethanolamine-binding protein 1	Cyto	56-66	W	DGLDPGKLYTL	V	2	1190.618	1	
Phosphatidylethanolamine-binding protein 1	Cyto	174-184	W	DDYVPKLYEQL	S	2	1381.677	1	
Phosphatidylethanolamine-binding protein 1	Cyto	106-119	D	YVGSGPPSGTGLHR	Y	3	1383.689	1	
Phosphatidylethanolamine-binding protein 1	Cyto	C-terminus	W	DDYVPKLYEQLSGK	*	3	1653.825	7	
Phosphatidylethanolamine-binding protein 1	Cyto	31-46	A	GVTVDELGKVLTPTQV	M	2	1654.914	1	
Phosphatidylethanolamine-binding protein 1	Cyto	172-184	A	EWDDYVPKLYEQL	S	2	1696.798	2	
Phosphatidylethanolamine-binding protein 1	Cyto	30-46	Y	AGVTVDELGKVLTPTQV	M	3	1725.951	17	
Phosphatidylethanolamine-binding protein 1	Cyto	104-120	L	SDYVGSGPPSGTGLHRY	V	3	1748.812	1	
Phosphatidylethanolamine-binding protein 1	Cyto	C-terminus	E	WDDYVPKLYEQLSGK	*	3	1839.904	14	
Phosphatidylethanolamine-binding protein 1	Cyto	50-66	R	PSSISWDGLDPGKLYTL	V	2	1847.930	1	
Phosphatidylethanolamine-binding protein 1	Cyto	C-terminus	A	EWDDYVPKLYEQLSGK	*	3	1968.947	31	
Phosphatidylethanolamine-binding protein 1	Cyto	48-65	N	RPSSISWDGLDPGKLYTL	V	3	2004.032	7	
Phosphatidylethanolamine-binding protein 1	Cyto	48-66	M	NRPSSISWDGLDPGKLYTL	V	3	2118.075	5	
Phosphatidylethanolamine-binding protein 1	Cyto	C-terminus	Y	QAEWDDYVPKLYEQLSGK	*	3	2168.043	24	
Phosphatidylethanolamine-binding protein 1	Cyto	47-66	V	MNRPSSISWDGLDPGKLYTL	V	3	2249.115	7	
Phosphatidylethanolamine-binding protein 1	Cyto	26-46	L	RVDYAGVTVDELGKVLTPTQV	M	3	2259.211	9	
Phosphatidylethanolamine-binding protein 1	Cyto	C-terminus	T	CYQAEWDDYVPKLYEQLSGK +25 on N-term (cyano?)	*	3	2459.115	12	

Phosphatidylethanolamine-binding protein 1	Cyto	30-65	Y	AGVTVDELGKVLTPTQVMNRPSSI SWDGLDPGKLYTL	V	4	3957.056	1	
Phospholipase D3	Memb (ER)	396-406	L	FVVPTDESQAR	I	2	1247.615	2	
Phospholipase D3	Memb (ER)	396-411	L	FVVPTDESQARIPYAR	V	3	1847.953	1	
Plasminogen activator inhibitor 1 RNA-binding protein	Cyto	N-terminus	M	PGHLQEGFG	C	2	940.440	8	
Prefoldin 1	Cyto	N-terminus	M	Ac-AASVDLELKKAFTEL	Q	2	1675.903	11	
Pre-rRNA-processing protein TSR2 homolog	Cyto	N-terminus	M	Ac-AGAAEDVRVLFGAAVRA	A	3	1713.916	1	
Proteasome subunit, beta type, 6	Cyto	34-41	F	(TTIMAVQF)	N	2	909.463	6	
Purkinje cell protein	Cyto	C-terminus	D	PAALSFRRNSSPQPQTQAP	*	3	2052.050	1	
Purkinje cell protein 4	Cyto	C-terminus	F	(RKFQKKKAGSQS)	*	5	1391.800	1	
Purkinje cell protein 4	Cyto	34-51	D	MDAPETERAAVAIQSQFR	K	3	2018.984	1	c
Purkinje cell protein 4	Cyto	Entire protein	M	Ac-SERQSAGATNGKDKTSGDND GQKKVQEEFDIDMDAPETERAAV AIQSQFRKFQKKKAGSQS	*	10	*6718.267*	39	
Purkinje cell protein 4-like protein	Cyto	Entire protein	M	(Ac-SELNTKTPPAANQASDPEEKG KPGSIKKAEEEEEIDIDLTAPETEKA ALAIQGKFRRFQKRKKDSSS)	*	10	*7413.196*	9	
Pyruvate kinase isozymes M1/M2	Cyto	110-120	A	VALDTKGPEIR	T	3	1197.672	1	c
Pyruvate kinase isozymes M1/M2	Cyto	C-terminus	P	FTNTMRVVPVP	*	2	1259.670	7	
Ribosomal protein S21	Cyto	C-terminus	A	KADGIVSKNF	*	3	1077.582	10	
Ribosomal protein S21	Cyto	C-terminus	L	AKADGIVSKNF	*	3	1148.619	11	
RNA binding motif protein 3	Cyto	N-terminus	M	Ac-SSEEGKLFVGGLNF	N	2	1524.746	10	
S100 calcium binding protein A11	Cyto	C-terminus	C	HDSFIQTSQKRI	*	4	1458.758	1	
Seryl tRNA synthetase	Cyto	N-terminus	M	VLDLDLFRVDKGGD	P	3	1560.815	18	
Sodium/potassium-transporting ATPase subunit beta-1	Memb	59-78	L	LTISELKPTYQDRVAPPGLT	Q	3	2198.195	1	
Splicing factor, arginine/serine-rich 1	Cyto	40-50	Y	(GAIRDIDLKNR)	R	3	1269.715	4	
Splicing factor, arginine/serine-rich 3	Cyto	43-53	A	RNPPGFAFVEF	E	2	1279.635	2	
Stathmin 1	Cyto	N-terminus	M	Ac-ASSDIQVKELEKR	S	2	1543.821	1	
Stathmin 1	Cyto	N-terminus	M	Ac-ASSDIQVKELEKRASGQAFELILSPR	S	4	2913.556	1	
Structural maintenance of chromosomes 1A	Nuc	737-747	K	LESELANFGPR	I	2	1231.620	1	
Synapsin (1, 2 or 3)	Cyto	C-terminus	R	KSFASLFSD	*	2	1000.494	2	
Synaptosomal-associated protein (Snap91)	Memb (cyto)	750-762	K	GLGSDLDSSLASL	V	2	1233.609	1	
Synaptosomal-associated protein (Snap91)	Memb (cyto)	C-terminus	D	PLADLNIKDFL	*	2	1257.697	26	
Synaptosomal-associated protein (Snap91)	Memb (cyto)	749-762	S	KGLGSDLDSSLASL	V	2	1361.704	3	
Synaptosomal-associated protein (Snap91)	Memb (cyto)	748-762	A	SKGLGSDLDSSLASL	V	2	1448.736	3	

Synaptosomal-associated protein (Snap91)	Memb (cyto)	747-762	A	ASKGLGSDLDSSLASL	V	2	1519.773	4	
Synaptosomal-associated protein (Snap91)	Memb (cyto)	C-terminus	L	SPSPTPATQSPKKPPAKDPLADLNIKDFL	*	4	3072.649	27	
Synuclein, alpha or beta	Cyto	N-terminus	M	Ac-MDVFMKGL	S	2	981.466	29	
Synuclein, beta	Cyto	N-terminus	M	Ac-MDVFMKGLSM	A	2	1199.539	7	
Thioredoxin 1	Cyto	18-27	A	AGDKLVVVDF	S	2	1061.576	5	
Thioredoxin 1	Cyto	17-27	A	AAGDKLVVVDF	S	2	1132.613	3	
Thioredoxin 1	Cyto	16-27	L	AAAGDKLVVVDF	S	2	1203.650	4	
Thioredoxin 1	Cyto	N-terminus	M	VKLIESKEAFQEAL	A	3	1603.882	53	
Thioredoxin 1	Cyto	N-terminus	M	VKLIESKEAFQEALAA	A	3	1745.956	8	
Thioredoxin 1	Cyto	N-terminus	M	VKLIESKEAFQEALAAAGDKLVVVDF	S	4	2789.521	2	
Thymosin beta-10	Cyto	25-39	E	KNTLPTKETIEQEKR	S	2	1813.990	1	c
Thymosin beta-10	Cyto	C-terminus	N	TLPTKETIEQEKRSEIS	*	3	1988.043	42	
Thymosin beta-10	Cyto	20-40	K	KTETQEKNTLPTKETIEQEKR	S	4	2530.324	2	
Thymosin beta-10	Cyto	N-terminus	M	Ac-ADKPDMGEIASFDKAKLKKTETQE KNTLPTKETIEQEKR	S	7	4517.322	10	
Thymosin beta-10	Cyto	Entire protein	M	Ac-ADKPDMGEIASFDKAKLKKTETQE KNTLPTKETIEQEKRSEIS	*	8	4933.523	109	
Thymosin beta-4	Cyto	C-terminus	N	PLPSKETIEQEKQAGES	*	3	1869.932	51	
Thymosin beta-4	Cyto	Entire protein	M	Ac-SDKPDMAEIEKFDKSKLKKTETQE KNPLPSKETIEQEKQAGES	*	8	4960.486	222	
Transcription factor BTF3 homolog 4	Nuc	6-22	K	LAKLQAQVRIGGKGTAR	R	3	1766.064	3	c
Triosephosphate isomerase	Cyto	56-63	K	LDPKIAVA	A	2	825.496	1	
Triosephosphate isomerase	Cyto	43-51	C	APPTAYIDF	A	2	993.481	1	
Triosephosphate isomerase	Cyto	56-66	K	LDPKIAVAAQN	C	2	1138.635	1	
Triosephosphate isomerase	Cyto	43-53	C	APPTAYIDFAR	Q	2	1220.619	2	c
Triosephosphate isomerase	Cyto	149-163	T	KVIADNVKDWSKVVL	A	4	1712.982	27	
Triosephosphate isomerase	Cyto	C-terminus	L	ASQPDVDGFLVGGASLKPEFVDIINAKQ	*	4	2914.508	19	
Tripeptidyl-peptidase I	Lyso	496-506	G	RPPLGFLNPRL	Y	3	1278.763	32	
Tubulin alpha	Cyto	142-157	F	GGGTGSGFTSLLMERL	S	2	1581.782	10	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	258-264	M	VPFPRLH	F	3	864.497	3	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	M	MREIVH(I/L)	Q	3	896.490	37	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	M	REIVH(I/L)QA	G	3	964.545	11	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	240-248	C	LRFPGQLNA	D	2	1014.561	5	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	*	MREIVH(I/L)QA	G	3	1095.586	50	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	*	MREIVH(I/L)QAG	Q	3	1152.607	1	

Tubulin beta (2, 3, 4, 5 or 6)	Cyto	254-264	L	AVNMVPFPRLH	F	3	1279.686	1	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	*	MREIVH(I/L)QAGQ	C	3	1280.670	75	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	220-231	T	PTYGDLNHLVSA	T	2	1285.630	1	
Tubulin beta (2, 3, 4, 5 or 6)	Cyto	N-terminus	*	MREIVH(I/L)QAGQC + Glutathione on Cys	G	4	1688.760	49	
Tubulin beta (2, 4 or 5)	Cyto	266-275	F	FMPGFAPLTS	R	2	1066.516	1	
Tubulin beta (2, 4 or 5)	Cyto	265-275	H	FFMPGFAPLTS	R	2	1213.584	1	
Tubulin beta (2, 4, 5 or 6)	Cyto	79-90	S	GPFGQ(I/L)FRPDNF	I	2	1393.678	5	
Tubulin beta (2, 4, 5 or 6)	Cyto	78-90	R	SGPFGQ(I/L)FRPDNF	V	2	1480.710	3	
Tubulin beta (2, 4, 5 or 6)	Cyto	218-231	L	TTPTYGDLNHLVSA	T	2	1487.726	7	
Tubulin beta (2, 4, 5 or 6)	Cyto	77-90	V	RSGPFGQ(I/L)FRPDNF	V	2	1636.811	8	
Tubulin beta (2, 4, 5 or 6)	Cyto	216-231	L	KLTTPTYGDLNHLVSA	T	3	1728.905	7	
Tubulin beta (3, 4, or 5)	Cyto	168-185	F	SVVPSPKVSDTVVEPYNA	T	2	1886.963	15	
Tubulin beta 2	Cyto	56-66	T	GNKYVPRAILV	D	3	1228.729	5	
Tubulin beta 2	Cyto	55-66	A	AGNKYVPRAILV	D	3	1299.766	2	
Tubulin beta 2	Cyto	55-76	A	AGNKYVPRAILVDLEPGTMDSV	R	3	2344.210	2	
Tubulin polymerization-promoting protein family member 3	Cyto	N-terminus	M	Ac-AASTDIAGLEESFRKF	A	2	1782.879	1	
Tubulin polymerization-promoting protein family member 3	Cyto	N-terminus	M	Ac-AASTDIAGLEESFRKFAIHGD	P	3	2276.115	8	
Ubiquinol-cytochrome c reductase complex 11 kDa protein	Mito	C-terminus	H	CVAHKLFKNLK +25 on N-term (cyano?)	*	4	1324.749	95	
Ubiquinol-cytochrome c reductase complex 11 kDa protein	Mito	N-terminus		GDPKEEEEEELVD	P	2	1516.642	15	a
Ubiquinol-cytochrome c reductase complex 11 kDa protein	Mito	N-terminus		GDPKEEEEEELVDPLTTVR	E	3	2184.043	1	a
Ubiquinol-cytochrome c reductase complex 11 kDa protein	Mito	N-terminus		GDPKEEEEEELVDPLTTVREH	C	4	2450.145	62	a
Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C	Mito	N-terminus	M	GREFGNLARI	R	3	1131.615	11	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	69-77	T	GLNVPASVR	F	2	911.519	1	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	69-78	V	GLNVPASVRF		2	1058.587	28	b
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	68-78	T	VGLNVPASVRF		2	1157.656	1	b
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	6-17	A	ARSGPFAPVLSA	T	2	1171.635	3	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	56-68	L	SGQAAARPLVATV	G	3	1239.694	13	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	56-68	L	SGQAAARPLVATV	G	2	1239.694	2	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	67-78	A	TVGLNVPASVRF	S	2	1258.703	4	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	6-18	A	ARSGPFAPVLSAT	S	2	1272.683	2	

Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	5-18	V	AARSGPFAPVLSAT	S	2	1343.720	1	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	N-terminus	M	Ac-MLSVAARSGPFAPVLSA	T	2	1714.908	1	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	52-68	C	RESLSGQAAARPLVATV	G	3	1724.953	6	
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	79-93	F	SHTDVKVPDFSDYRR	A	3	1820.881	2	c
Ubiquinol-cytochrome c reductase iron-sulfur subunit	Mito	56-78	L	SGQAAARPLVATVGLNVPASVRF		3	2280.270	1	b
Ubiquitin-activating enzyme E1	Cyto	1043-1058	D	ESGEDVEVPYVRYTIR	*	3	1910.937	1	c
Ubiquitin-activating enzyme E1	Cyto	1042-1058	N	DESGEDVEVPYVRYTIR	*	3	2025.964	1	c
Vacuolar proton pump subunit G 2	Lyso	C-terminus	V	RPQVHPNYRVTV	*	4	1464.795	1	
Vacuolar proton pump subunit G 2	Lyso	C-terminus	E	VRPQVHPNYRVTV	*	4	1563.863	4	
Vacuolar proton pump subunit G 2	Lyso	C-terminus	C	EVRPQVHPNYRVTV	*	4	1692.913	64	
Vacuolar proton pump subunit G 2	Lyso	N-terminus	M	Ac-ASQTQGIQQLLQAEKR	A	3	1839.980	1	
Vesicle-associated membrane protein-associated protein A (VAP-33)	Memb	N-terminus, from second ATG	M	Ac-AKHEQILVLD	P	2	1206.669	18	
Vesicle-associated membrane protein-associated protein A (VAP-33)	Memb	N-terminus, from upstream ATG	M	Ac-ASASGAMAKHEQILVLD	P	3	1781.910	40	
Voltage-dependent anion channel protein 1	Mito	C-terminus	N	AGGHKLGLGLEFQA	*	3	1396.746	42	
Voltage-dependent anion channel protein 1	Mito	N-terminus	M	Ac-AVPPTYADLGKSAR	D	2	1486.778	1	
Voltage-dependent anion channel protein 2	Mito	C-terminus	N	AGGHKLGLALELEA	*	3	1377.762	24	
Voltage-dependent anion channel protein 3	Mito	C-terminus	N	AGGHKVGLGFELEA	*	3	1383.715	15	
Zinc finger protein 53	Nuc	128-134	N	CALYIRR	D	2	893.491	2	c

Abbreviations: Sub. Loc., subcellular localization of protein (Cyto, cytosolic; Lyso, lysosomal; Memb, membrane; Mito, mitochondrial; Nuc, nuclear); USF, upstream flanking amino acid residue; DSF, downstream flanking amino acid residue; * termini; a, N-terminus of protein after removal of mitochondrial targeting peptide; b, C-terminus of protein after known cleavage; c, found when using anhydrotrypsin affinity columns to purify peptides with C-terminal Lys or Arg residues. Other abbreviations and annotations as in Supplementary Table 1.