

**Thimet oligopeptidase (EC 3.4.24.15) key functions suggested by knockout mice phenotype characterization**

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**Running Title:** THOP1 knockout mice

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Peptides individual MS identification and quantitation  
Pre frontal cortex

Protein name	Peptide sequence	Elution time Run1	Elution time Run2	Elution time Run 3	m/z Light	m/z Heavy	Z	diff	T	m/z 1	m/z 2	average m/z	SD	Observed mass	Theoretical mass	ppm	Peptide sequence	Ratio K01/W11	Ratio K02/W12	RATIO K03/W13	Average ratio	SE	n		
Acyl-CoA-binding protein	VEKVDLKKYGI	34.1	nd	40.5	845.0430	855.097	2	20	5.0	5	1547.8955	1548.028	1547.96175	0.03699	1547.9618	1.547.8996	40	VEKVDLKKYGI		0.40	nd	0.39	0.40	0.005	2
Acyl-CoA-binding protein	VEKVDLKKYGI	34.1	nd	40.5	563.6916	570.4003	3	20	5.0	5	1547.8943	1548.0289	1547.9606	0.03703	1547.9606	1.547.8996	39	VEKVDLKKYGI		0.50	nd	0.30	0.40	0.100	2
Acyl-CoA-binding protein	KQATVGDVNTDRPGLLDL	50.2	57.0	55.4	656.6995	659.3848	3	8	2.0	2	1911.0119	1911.0704	1911.04115	0.04137	1911.0412	1.911.0134	15	KQATVGDVNTDRPGLLDL		0.66	0.46	0.25	0.46	0.118	3
Acyl-CoA-binding protein	TVGDVNTDRPGLLDL	59.6	63.5	62.1	806.9342	808.9464	2	4	1.0	1	1583.8211	1583.8468	1583.83395	0.01817	1583.8228	1.583.8228	7	TVGDVNTDRPGLLDL		0.98	0.62	0.32	0.64	0.191	3
Cerebellin-4	AANSKVAFSAVRSTN	25.7	33.1	31.9	789.9358	793.9625	2	8	2.0	2	1521.7933	1521.849	1521.821	0.0396	1521.8210	1.521.7972	16	AANSKVAFSAVRSTN		1.1	1.33	1.02	1.12	0.107	3
Clathrin coat assembly protein AP180	ASKGLGSDLDSSLASL	61.1	63.5	63.5	788.9265	792.9523	2	8	2.0	2	1519.7744	1519.8296	1519.8015	0.03833	1519.8015	1.519.7802	14	ASKGLGSDLDSSLASL		0.75	0.42	0.42	0.53	0.110	3
Clathrin coat assembly protein AP180	SKGLGSDLDSSLASL	60.7	63.2	63.9	753.4092	757.4341	2	8	2.0	2	1448.7398	1448.7922	1448.766	0.03705	1448.7660	1.448.7431	16	SKGLGSDLDSSLASL		0.78	0.38	0.50	0.55	0.120	3
Clathrin coat assembly protein AP180	SPSPPTATQSPKKPPAKDPLADLNKDFL	65.2	69.1	67.3	643.5716	647.5959	4	16	4.0	4	2458.1292	2458.2316	3072.6568	0.07241	3072.6568	3.072.6568	0	SPSPPTATQSPKKPPAKDPLADLNKDFL		0.75	0.41	0.36	0.51	0.123	3
Clathrin coat assembly protein AP180	KGLGSDLDSSLASL	59.8	63.0	62.5	709.8629	713.9183	2	8	2.0	2	1361.7072	1361.7606	1361.7339	0.03776	1361.7339	1.361.7111	17	KGLGSDLDSSLASL		0.83	0.40	0.44	0.56	0.137	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	ARSGFPAPLVAT	47.4	54.4	53.1	651.3831	653.3387	2	4	1.0	1	1272.1189	1272.6274	1272.67315	0.0647	1272.6732	1.272.6899	-13	ARSGFPAPLVAT		0.95	1.05	0.44	0.81	0.189	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	SGQAAARPLVATV	33.0	40.3	39.5	634.8712	636.8837	2	4	1.0	1	1239.6951	1239.7214	1239.70825	0.0186	1239.7083	1.239.7008	6	SGQAAARPLVATV		0.88	0.91	0.46	0.75	0.144	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	GLNVPASVRF	51.8	56.3	57.1	544.3185	546.3308	2	4	1.0	1	1058.5897	1058.6156	1058.60265	0.01831	1058.6027	1.058.5946	8	GLNVPASVRF		0.88	1.33	0.63	0.94	0.206	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	TVGLNVPASVRF	58.6	61.2	60.6	644.3771	646.3301	2	4	1.0	1	1258.7089	1258.6142	1258.66055	0.06555	1258.6606	1.258.7106	-40	TVGLNVPASVRF		1.00	1.21	0.63	0.95	0.171	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	SGQAAARPLV	23.7	31.4	29.6	534.8123	536.8249	2	4	1.0	1	1039.5733	1039.6038	1039.59055	0.01874	1039.5906	1.039.5847	6	SGQAAARPLV		0.84	1.22	0.51	0.86	0.207	3
Cytochrome c oxidase subunit 5A, mitochondrial	NDFASAVRILEV	nd	75.0	72.0	681.3769	683.3907	2	4	1.0	1	1332.7065	1332.7354	1332.72095	0.02044	1332.7210	1.332.7110	7	NDFASAVRILEV	nd		0.47	0.24	0.36	0.115	2
Cytochrome c oxidase subunit 5A, mitochondrial	RPTLNELGISTPEELGLDKV	64.2	66.0	65.9	746.4207	749.1039	3	8	2.0	2	2180.1755	2180.2277	2180.2016	0.03691	2180.2016	2.180.1761	12	RPTLNELGISTPEELGLDKV		0.66	0.33	0.27	0.42	0.121	3
Cytochrome c oxidase subunit 5A, mitochondrial	GISTPEELGLDKV	53.9	67.0	57.6	707.3982	711.423	2	8	2.0	2	1356.7178	1356.77	1356.7439	0.03691	1356.7439	1.356.7209	17	GISTPEELGLDKV		0.54	0.55	0.38	0.49	0.055	3
Cytochrome c oxidase subunit 6A1, mitochondrial	HNPHVNPVPTGYEDE	32.1	38.6	37.7	873.9091	875.921	2	4	1.0	1	1717.7709	1717.796	1717.7845	0.01775	1717.7835	1.717.7769	4	HNPHVNPVPTGYEDE		1	0.97	0.61	0.86	0.127	3
LM zinc-binding domain-containing Nebulette	TOVVSDAAYKGVPHV	37.8	44.0	43.4	618.6789	621.3605	3	8	2.0	2	1796.9441	1796.9975	1796.9708	0.03776	1796.9708	1.797.0492	-44	TOVVSDAAYKGVPHV		0.67	0.64	0.48	0.59	0.059	3
Macrophage migration inhibitory factor	AQATGKPAQYIAVHVVPDQL	54.5	57.4	56.2	721.4068	724.0897	3	8	2.0	2	2105.1338	2105.1851	2105.15945	0.03627	2105.1595	2.105.1342	12	AQATGKPAQYIAVHVVPDQL		0.80	0.40	0.57	0.59	0.115	3
Macrophage migration inhibitory factor	AQATGKPAQYIAVHVVPDQL	54.5	57.4	56.2	1081.6061	1085.6301	2	8	2.0	2	2105.1336	2105.1842	2105.1589	0.03578	2105.1589	2.105.1342	12	AQATGKPAQYIAVHVVPDQL		0.71	0.61	0.62	0.65	0.032	3
Macrophage migration inhibitory factor	AQATGKPAQYIA	26.4	33.4	32.2	637.8604	641.8852	2	8	2.0	2	1217.6422	1217.6944	1217.6683	0.03691	1217.6683	1.217.6477	17	AQATGKPAQYIA		1.11	0.93	0.71	0.92	0.116	3
Microtubule-associated protein tau	ADEVSAASLAKGL	40.8	46.8	46.7	672.8729	676.8983	2	8	2.0	2	1287.6672	1287.7206	1287.6939	0.03776	1287.6939	1.287.6743	15	ADEVSAASLAKGL		1.245	0.59	0.50	0.78	0.235	3
Neurogranin	GRKPGPGGGAGGARGGAGGGPSPGD	16.3	22.9	21.3	725.3692	728.0518	3	8	2.0	2	2117.021	2117.0714	2117.0184	0.03564	2117.0184	2.117.0184	0	GRKPGPGGGAGGARGGAGGGPSPGD		0.79	0.56	0.45	0.60	0.100	3
Neurogranin	KGPGPGGGAGGARGGAGGGPSPGD	18.0	23.8	22.6	980.9863	985.0108	2	8	2.0	2	1903.894	1903.9456	1903.9196	0.03649	1903.9198	1.903.8958	13	KGPGPGGGAGGARGGAGGGPSPGD		0.90	0.53	0.22	0.55	0.197	3
Neurogranin	RKPGPGPGGGAGGARGGAGGGPSPGD	16.2	22.9	21.2	706.3615	709.0445	3	8	2.0	2	2059.9979	2060.0495	2060.0237	0.03649	2060.0237	2.059.9969	13	RKPGPGPGGGAGGARGGAGGGPSPGD		0.71	1.34	0.77	0.94	0.200	3
Peptidyl-prolyl cis-trans isomerase A	EDENFILKHTGPGLISM	63.6	66.5	64.8	979.0121	983.0385	2	8	2.0	2	1899.9456	1900.001	1899.9733	0.03917	1899.9733	1.899.9473	14	EDENFILKHTGPGLISM		0.73	1.00	0.66	0.80	0.104	3
Peptidyl-prolyl cis-trans isomerase A	ELFADKVPKTAENFRAL	51.9	55.2	55.2	678.3856	682.3981	3	12	3.0	3	1948.0389	1947.9603	1947.9996	0.05558	1947.9996	1.948.0491	-25	ELFADKVPKTAENFRAL		0.52	0.75	1.68	0.98	0.355	3
Peptidyl-prolyl cis-trans isomerase A	LFADKVPKTAENFRAL	44.3	50.9	49.3	635.3727	639.3986	3	12	3.0	3	1819.0002	1819.0818	1819.041	0.0577	1819.0410	1.819.0065	19	LFADKVPKTAENFRAL		1.16	0.98	0.65	0.93	0.149	3
Peptidyl-prolyl cis-trans isomerase A	ADKVPKTAENFRAL	31.3	39.0	38.4	548.6557	552.6805	3	12	3.0	3	1558.8492	1558.9275	1558.88835	0.05537	1558.8884	1.558.8540	22	ADKVPKTAENFRAL		0.90	0.77	0.63	0.77	0.079	3
Peptidyl-prolyl cis-trans isomerase A	ITADDEPLGRVSF	55.5	60.5	59.1	724.3787	726.3914	2	4	1.0	1	1418.7101	1418.7368	1418.72345	0.01888	1418.7235	1.418.7114	8	ITADDEPLGRVSF		0.98	0.50	0.50	0.66	0.160	3
Peptidyl-prolyl cis-trans isomerase A	ADKVPKTAENF	25.9	33.0	32.3	652.3679	658.4055	2	12	3.0	3	1218.6259	1218.705	1218.66545	0.05593	1218.6517	1.218.6317	28	ADKVPKTAENF		0.75	0.93	0.45	0.71	0.140	3
Peptidyl-prolyl cis-trans isomerase A	ADDEPLGRVSF	47.5	54.7	54.3	617.3111	619.3237	2	4	1.0	1	1204.5749	1204.6014	1204.58815	0.01874	1204.5882	1.204.5797	7	ADDEPLGRVSF		1	0.98	0.58	0.85	0.137	3
Peptidyl-prolyl cis-trans isomerase FKBP1A	VDVYELLKLE	71.0	72.2	72.4	630.8781	634.9038	2	8	2.0	2	1203.6776	1203.7316	1203.7046	0.03818	1203.7046	1.203.6824	18	VDVYELLKLE		0.77	1.10	0.65	0.84	0.135	3
Phosphatidylethanolamine-binding protein 1	DQYVPKLYEQLSGK	56.6	60.2	59.6	580.3149	584.3407	3	12	3.0	3	1653.8268	1653.9081	1653.86745	0.05749	1653.8675	1.653.8323	21	DQYVPKLYEQLSGK		0.59	0.83	0.60	0.67	0.078	3
ProSAA5	SLSAASAPLVETSTPLRL	64.7	66.4	65.9	921.0261	923.039	2	4	1.0	1	1812.0049	1812.032	1812.01845	0.01916	1812.0185	1.812.0066	7	SLSAASAPLVETSTPLRL		0.75	1.00	1.00	0.92	0.083	3
Somatostatin	SANSNPAMAPRE	20.8	26.8	26.1	636.8049	638.8176	2	4	1.0	1	1243.5625	1243.5892	1243.57585	0.01888	1243.5759	1.243.5688	6	SANSNPAMAPRE		1.48	1.90	1.60	1.65	0.130	3
Somatostatin	SANSNPAMAPRE (methionine oxidation)	nd	23.4	22.9	644.8035	646.816	2	4	1.0	1	1259.5597	1259.586	1259.57285	0.0186	1259.5729	1.259.5637	7	SANSNPAMAPRE (OXI)	nd		2.50	1.59	2.03	0.470	2
Tubulin beta-3 chain	DDEESEAGQPK	nd	21.9	21.2	630.7849	634.8098	2	8	2.0	2	1203.4912	1203.5436	1203.5174	0.03705	1203.5174	1.203.4964	17	DDEESEAGQPK	nd		2.80	1.66	2.23	0.570	2

Abbreviations: z=charge; m/z=mass charge ratio; T=number of tags; nd= not detected

Protein name	Peptide sequence	Elution time Run1	Elution time Run2	Elution time Run3	m/z Light	m/z Heavy	Z	diff	T	m/z 1	m/z 2	average m/z	SD	Observed mass	Theoretical mass	ppm	Peptide sequence	Ratio KO1/W1	Ratio KO2/W2	RATIO KO3/W3	Average ratio KO/W	SE	n	
Acyl-CoA-binding protein	ATVGDVNTDRPGLLDL	60.9	61.0	64.6	842.4515	844.4658	2	4	1.0	1	1654.8557	1654.8856	1654.87065	0.02114	1654.8707	1654.8599	6	ATVGDVNTDRPGLLDL	0.87	1.66	0.80	1.04	0.318	3
Acyl-CoA-binding protein	KQATVGDVNTDRPGLLDL	51.8	52.5	57.5	984.5448	988.5694	2	8	2.0	2	1911.0111	1911.0628	1911.0369	0.03663	1911.0369	1911.0134	12	KQATVGDVNTDRPGLLDL	1.00	1.60	0.72	1.11	0.260	3
Acyl-CoA-binding protein	KQATVGDVNTDRPGLLDL	51.8	52.3	57.5	656.6985	659.3814	3	8	2.0	2	1911.0089	1911.0602	1911.03465	0.03627	1911.0346	1911.0134	11	KQATVGDVNTDRPGLLDL	0.95	1.52	0.61	1.03	0.265	3
Acyl-CoA-binding protein	SHFKQATVGDVNTDRPGLLDL	50.9	51.1	56.5	1170.1259	1174.1481	2	8	2.0	2	2282.1732	2282.2202	2282.1967	0.03323	2282.1967	2282.1728	10	SHFKQATVGDVNTDRPGLLDL	0.94	2.15	1.00	1.36	0.394	3
Acyl-CoA-binding protein	TVGDVNTDRPGLLDL	59.7	60.0	63.8	806.9318	808.944	2	4	1.0	1	1583.8163	1583.842	1583.82915	0.01817	1583.8292	1583.8228	4	TVGDVNTDRPGLLDL	0.86	1.68	0.88	1.07	0.308	3
Acyl-CoA-binding protein	VEKYDELKKYQI	36.6	36.4	41.3	963.6907	970.3989	3	20	5.0	5	1547.8916	1548.0227	1547.95715	0.0927	1547.9572	1547.8996	37	VEKYDELKKYQI	1.16	0.90	0.66	0.91	0.144	3
Clahtin coat assembly protein AP180	ASKGLGSDLDSSLASL	61.0	61.0	64.2	788.9254	792.9509	2	8	2.0	2	1519.7222	1519.8258	1519.799	0.0379	1519.7990	1519.7802	12	ASKGLGSDLDSSLASL	1.10	1.28	0.87	1.08	0.119	3
Clahtin coat assembly protein AP180	SPSPPTATQSPKKPPAKDPLADLNKDFL	67.8	67.7	68.7	804.2106	809.2419	4	20	5.0	5	3072.6539	3072.7856	3072.71975	0.09313	3072.7198	3072.6568	20	SPSPPTATQSPKKPPAKDPLADLNKDFL	1.00	1.53	0.87	1.17	0.182	3
Cysteine and glycine-rich protein 1	GQGAGALVHSE	23.8	23.5	27.9	527.2706	529.2832	2	4	1.0	1	1024.4939	1024.5204	1024.50715	0.01874	1024.5072	1024.5010	6	GQGAGALVHSE	1.05	1.10	1.10	1.08	0.017	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	SGQAARPLVATV	35.8	35.7	40.2	634.8714	636.8636	2	4	1.0	1	1239.6955	1239.7212	1239.70835	0.01817	1239.7084	1239.7008	6	SGQAARPLVATV	1.00	1.10	1.85	1.25	0.202	3
Cytochrome b-c1 complex subunit Rieske, mitochondrial	TVGLNVPASVRF	58.8	59.2	60.7	644.3762	646.3892	2	4	1.0	1	1258.7051	1258.7324	1258.71875	0.0193	1258.7188	1258.7106	8	TVGLNVPASVRF	1.48	1.05	0.88	1.17	0.156	3
Cytochrome c oxidase subunit 5A, mitochondrial	GISTPEELGLDKV	54.5	54.8	58.2	707.3970	711.4219	2	8	2.0	2	1356.7154	1356.7678	1356.7416	0.03705	1356.7416	1356.7209	15	GISTPEELGLDKV	1.00	1.40	0.75	1.05	0.189	3
Cytochrome c oxidase subunit 5A, mitochondrial	RPTLNELGISTPEELGLDKV	64.9	65.2	66.0	746.4198	749.1033	3	8	2.0	2	2180.1728	2180.2259	2180.19935	0.03755	2180.1994	2180.1761	11	RPTLNELGISTPEELGLDKV	1.25	1.60	0.75	1.20	0.247	3
Cytochrome c oxidase subunit 6A1, mitochondrial	FHNPHVNLPTGYEDE	39.3	39.1	43.4	947.4431	949.4562	2	4	1.0	1	1864.8389	1864.8664	1864.85265	0.01945	1864.8527	1864.8453	4	FHNPHVNLPTGYEDE	1.06	1.33	0.87	1.09	0.133	3
Cytochrome c oxidase subunit 6A1, mitochondrial	HNPHVNLPTGYEDE	33.8	34.0	38.1	873.9086	875.921	2	4	1.0	1	1717.7699	1717.7986	1717.78295	0.01846	1717.7830	1717.7769	4	HNPHVNLPTGYEDE	1.14	1.75	0.50	1.13	0.361	3
Glyceroldehyde-3-phosphate dehydrogenase	AFRVPTPNVSVIDL	68.3	68.1	69.1	771.4396	773.4476	2	4	1.0	1	1512.8319	1512.8492	1512.84055	0.01223	1512.8406	1512.8373	2	AFRVPTPNVSVIDL	1.33	1.60	1.80	1.51	0.090	3
Macrophage migration inhibitory factor	AQATGKPAQYIAHVHVPDQL	54.3	54.6	57.1	721.4048	724.0881	3	8	2.0	2	2105.1278	2105.1803	2105.15405	0.03712	2105.1541	2105.1342	9	AQATGKPAQYIAHVHVPDQL	1.10	1.10	1.32	1.17	0.073	3
Microtubule-associated protein tau	ADEVASLAKQGL	42.3	42.4	47.5	672.8734	676.8988	2	8	2.0	2	1287.6682	1287.7216	1287.6949	0.03776	1287.6949	1287.6743	16	ADEVASLAKQGL	1.00	1.02	1.50	1.17	0.163	3
Neurogranin	GRKGPGGGPGGAGGARGAGGGPSPGD	17.8	17.1	21.9	544.2773	546.2896	4	8	2.0	2	2117.0146	2117.0664	2117.0405	0.03663	2117.0405	2117.0184	10	GRKGPGGGPGGAGGARGAGGGPSPGD	0.89	0.78	0.85	0.84	0.032	3
Neurogranin	KGPGPGGGAGGARGAGGGPSPGD	19.2	18.6	23.1	654.3266	657.0099	3	8	2.0	2	1903.8932	1903.9457	1903.91945	0.03712	1903.9195	1903.8958	12	KGPGPGGGAGGARGAGGGPSPGD	0.78	0.77	0.79	0.78	0.006	3
Neurogranin	KGPGPGGGAGGARGAGGGPSPGD	18.9	18.9	23.1	980.9834	985.008	2	8	2.0	2	1903.8882	1903.94	1903.9141	0.03663	1903.9141	1903.8958	10	KGPGPGGGAGGARGAGGGPSPGD	0.62	0.69	0.62	0.64	0.023	3
Neurogranin	RKGPFGPGGGAGGARGAGGGPSPGD	17.3	16.9	21.8	706.3609	709.044	3	8	2.0	2	2059.9961	2060.048	2060.02205	0.0367	2060.0221	2059.9969	12	RKGPFGPGGGAGGARGAGGGPSPGD	1.16	2.30	0.39	1.28	0.555	3
Peptidyl-prolyl cis-trans isomerase A	ADDEPLGRVSF	49.1	49.5	55.2	617.3094	619.3221	2	4	1.0	1	1204.5715	1204.5982	1204.58485	0.01888	1204.5849	1204.5797	4	ADDEPLGRVSF	1.08	1.08	1.15	1.10	0.023	3
Peptidyl-prolyl cis-trans isomerase A	ADKVPKTAENFRAL	33.7	33.5	38.2	822.4785	828.5163	2	12	3.0	3	1558.8471	1558.9266	1558.88685	0.05621	1558.8869	1558.8540	21	ADKVPKTAENFRAL	1.10	1.02	1.65	1.26	0.198	3
Peptidyl-prolyl cis-trans isomerase A	ADKVPKTAENFR	23.8	23.7	nd	487.2813	491.3062	3	12	3.0	3	1374.726	1374.8046	1374.7653	0.05558	1374.7653	1374.7328	24	ADKVPKTAENFR	1.06	1.66	nd	1.36	0.300	2
Peptidyl-prolyl cis-trans isomerase A	ELFADKVPKTAENF	48.3	48.7	nd	846.9666	853.0028	2	12	3.0	3	1607.8233	1607.8996	1607.86145	0.05396	1607.8615	1607.8268	22	ELFADKVPKTAENF	0.96	1.42	nd	1.19	0.230	2
Phosphatidylethanolamine-binding protein 1	KGNDISSGTVLSDYVSGSPPSGTGL	61.4	61.6	nd	1211.1600	1215.1393	2	8	2.0	2	2364.2414	2364.2026	2364.222	0.02744	2364.2220	2364.1518	30	KGNDISSGTVLSDYVSGSPPSGTGL	1.33	1.62	nd	1.38	0.045	2
Phosphatidylethanolamine-binding protein 1	AGVTVDLQKVL	60.5	60.9	nd	628.8796	632.9054	2	8	2.0	2	1199.6806	1199.7348	1199.7077	0.03833	1199.7077	1199.6834	20	AGVTVDLQKVL	0.87	1.35	nd	1.11	0.240	2
Phosphatidylethanolamine-binding protein 1	GVTVDLQKVLTPQTQV	64.5	64.9	66.4	856.5344	860.5231	2	8	2.0	2	1654.9902	1654.9702	1654.9802	0.01414	1654.9802	1654.9214	36	GVTVDLQKVLTPQTQV	0.83	1.50	1.33	1.22	0.201	3
Phosphatidylethanolamine-binding protein 1	DDYVPKLYEQLSGK	56.9	57.2	60.5	580.3149	584.3407	3	12	3.0	3	1653.8268	1653.9081	1653.86745	0.05749	1653.8675	1653.8323	21	DDYVPKLYEQLSGK	0.85	1.42	1.06	1.11	0.166	3
Phosphatidylethanolamine-binding protein 1	AGVTVDLQKVLTPQTQV	65.6	65.7	67.0	892.0162	896.0409	2	8	2.0	2	1725.9538	1726.0058	1725.9798	0.03677	1725.9798	1725.9595	12	AGVTVDLQKVLTPQTQV	1.33	1.40	1.46	1.40	0.038	3
Proenkephalin-A	SPQLEDEAKELQ	38.5	38.4	44.2	721.8737	725.8987	2	8	2.0	2	1385.6688	1385.7214	1385.6951	0.03719	1385.6951	1385.6747	15	SPQLEDEAKELQ	1.10	0.25	0.71	0.69	0.246	3
ProSAAS	ASAPLVETSTPLRL	57.8	58.5	nd	741.9335	743.9453	2	4	1.0	1	1453.8197	1453.8446	1453.83215	0.01761	1453.8322	1453.8213	7	ASAPLVETSTPLRL	1.42	0.99	nd	1.20	0.216	2
ProSAAS	SLSAASAPLVETSTPLRL	66.0	66.0	67.1	921.0241	923.0366	2	4	1.0	1	1812.0009	1812.0272	1812.01405	0.0186	1812.0141	1812.0068	4	SLSAASAPLVETSTPLRL	1.43	1.60	0.58	1.20	0.316	3
Secretogranin-1	SFARAPOLDL	51.6	52.5	57.2	573.3200	575.3326	2	4	1.0	1	1116.5927	1116.6192	1116.60595	0.01874	1116.6060	1116.6000	5	SFARAPOLDL	2.00	1.00	1.00	1.33	0.333	3
Secretogranin-1	LLEDGHPVRESPIDTA	41.6	41.5	46.2	970.4936	972.5067	2	4	1.0	1	1910.9399	1910.9714	1910.95565	0.02227	1910.9557	1910.9447	6	LLEDGHPVRESPIDTA	1.52	1.60	2.00	1.71	0.148	3
Somatostatin	SANSNPAMAPRE	21.8	21.4	25.7	638.8052	638.8178	2	4	1.0	1	1243.5631	1243.5896	1243.57635	0.01874	1243.5764	1243.5688	8	SANSNPAMAPRE	2.85	0.75	2.50	2.03	0.850	3
Somatostatin	SANSNPAMAPRE (methionine oxidation)	18.2	17.9	nd	644.8033	646.8157	2	4	1.0	1	1259.5593	1259.5854	1259.57235	0.01846	1259.5724	1259.5637	7	SANSNPAMAPRE (methionine oxidation)	2.66	0.87	2.00	1.84	0.523	3
Synapsin-1	AGGPPHPQLNKS	22.4	22.1	nd	629.8502	633.8749	2	8	2.0	2	1201.6218	1201.6738	1201.6478	0.03677	1201.6478	1201.6276	17	AGGPPHPQLNKS	1.25	0.68	nd	0.97	0.285	2
Tubulin beta-2A chain	SGPFGQIFRPDNF	67.5	67.4	69.7	755.3795	757.3921	2	4	1.0	1	1480.7117	1480.7382	1480.72495	0.01874	1480.7250	1480.7172	5	SGPFGQIFRPDNF	0.97	0.75	1.48	1.07	0.216	3

Protein name	Peptide sequence	Elution time Run1	Elution time Run2	Elution time Run 3	m/z	Light	m/z	Heavy	Z	diff	T	m/z 1	m/z 2	average m/z	SD	Observed mass	Theoretical mass	ppm	Peptide sequence	Ratio K01/W11	Ratio K02/W12	RATIO K03/W13	Average ratio	SE	n
Acyl-CoA-binding protein	ATVGDVNTRDPLLDL	60.3	57.6	64.2	842.4547	744.4669	2	4	1.0	1	1654.8621	1654.8878	1654.87495	0.01817264	1654.8750	1654.8599	9	ATVGDVNTRDPLLDL	0.72	1.66	3.00	1.79	0.662	3	
Acyl-CoA-binding protein	GDVNTDRPGLLDL	53.2	51.8	61.1	706.8754	708.8877	2	4	1.0	1	1383.7035	1383.7294	1383.71645	0.01831407	1383.7165	1383.7087	7	GDVNTDRPGLLDL	1.07	1.55	3.01	1.88	0.583	3	
Acyl-CoA-binding protein	KQATVGDVNTRDPLLDL	48.9	47.4	56.9	984.5476	986.5691	2	8	2.0	2	1911.0166	1911.0622	1911.0394	0.03224407	1911.0394	1911.0134	14	KQATVGDVNTRDPLLDL	0.77	2.00	4.72	2.49	1.168	3	
Acyl-CoA-binding protein	KQATVGDVNTRDPLLDL	48.9	47.4	56.9	656.6997	659.381	3	8	2.0	2	1911.0125	1911.0579	1911.03575	0.03288047	1911.0358	1911.0134	12	KQATVGDVNTRDPLLDL	0.75	1.76	4.00	2.17	0.961	3	
Acyl-CoA-binding protein	TVGVDNTRDPLLDL	58.8	56.4	63.7	806.9332	808.9454	2	4	1.0	1	1583.8191	1583.8448	1583.83195	0.01817264	1583.8320	1583.8228	6	TVGVDNTRDPLLDL	0.85	1.82	5.25	2.64	1.335	3	
Acyl-CoA-binding protein	VEKVDELKKYGI	34.4	34.4	41.6	563.6919	570.4003	3	20	5.0	5	1547.8952	1549.0269	1547.96105	0.00312596	1547.9611	1547.8996	40	VEKVDELKKYGI	1.00	1.75	4.00	2.25	0.901	3	
Acyl-CoA-binding protein	VEKVDELKKYGI	34.3	34.5	41.6	845.0334	855.0981	2	20	5.0	5	1547.8943	1548.0302	1547.96225	0.00605681	1547.9623	1547.8996	40	VEKVDELKKYGI	0.87	1.93	3.40	2.07	0.734	3	
ATP synthase-coupling factor 6, mitochondrial	KFDDPKFEVDKPS	38.0	37.5	nd	953.0285	961.0734	2	16	4.0	4	1791.9118	1792.0108	1791.9613	0.07000357	1791.9613	1791.9116	28	KFDDPKFEVDKPS	0.87	1.38	nd	1.12	0.255	2	
Cerebellin-4	SKVAFSAVRSTN	25.0	24.1	29.6	441.5750	444.2707	3	8	2.0	2	1265.6744	1265.7281	1265.70125	0.03797163	1265.7013	1265.6801	17	SKVAFSAVRSTN	1.33	0.65	0.70	0.89	0.216	3	
Citathrin coat assembly protein AP180	ASKGLGSLDSSLASL	60.8	58.5	64.2	788.9260	792.9506	2	8	2.0	2	1519.7734	1519.8252	1519.7993	0.03662813	1519.7993	1519.7802	13	ASKGLGSLDSSLASL	1.11	1.07	0.97	1.05	0.042	3	
Citathrin coat assembly protein AP180	SPSPPTATQSPKPKPAKDPLADLNKDFL	66.0	62.2	68.7	804.2125	809.244	4	20	5.0	5	3072.6615	3072.794	3072.7275	0.00369165	3072.7278	3.072.6568	23	SPSPPTATQSPKPKPAKDPLADLNKDFL	1.12	0.93	0.92	0.99	0.065	3	
Cysteine and glycine-rich protein 1	GQGAGALVHSE	23.2	22.6	27.9	527.2711	529.2838	2	4	1.0	1	1024.4949	1024.5216	1024.50825	0.01887975	1024.50825	1024.501	7	GQGAGALVHSE	0.90	3.00	2.60	2.17	0.644	3	
Cytochrome b-c1 complex subunit Rieske, mitochondrial	SGQAAARPLVA	24.8	24.5	29.1	534.8131	536.8254	2	4	1.0	1	1039.5789	1039.6048	1039.59185	0.01831407	1039.5919	1039.5847	7	SGQAAARPLVA	1.08	0.80	1.14	1.01	0.103	3	
Cytochrome b-c1 complex subunit Rieske, mitochondrial	SGQAAARPLVATV	33.6	33.4	40.2	634.8714	636.8836	2	4	1.0	1	1239.6955	1239.7212	1239.70835	0.01817264	1239.7084	1239.7004	8	SGQAAARPLVATV	0.99	0.78	1.05	0.94	0.083	3	
Cytochrome b-c1 complex subunit Rieske, mitochondrial	TVGLNVPASVRF	57.3	54.7	60.7	644.3773	646.3898	2	4	1.0	1	1258.7073	1258.7336	1258.72045	0.01859691	1258.7205	1258.7106	8	TVGLNVPASVRF	1.15	0.71	1.07	0.98	0.136	3	
Cytochrome c oxidase subunit 5A, mitochondrial	GISTPEELGLDKV	51.9	50.5	58.2	707.3984	711.4236	2	8	2.0	2	1356.7182	1356.7712	1356.7447	0.03747686	1356.7447	1356.7209	18	GISTPEELGLDKV	0.84	1.77	1.53	1.51	0.339	3	
Cytochrome c oxidase subunit 5A, mitochondrial	NDFASARVLEIV	69.8	69.2	72.5	681.3779	683.3907	2	4	1.0	1	1332.7085	1332.7354	1332.72195	0.01902117	1332.7220	1332.7110	8	NDFASARVLEIV	0.95	2.00	2.15	1.70	0.376	3	
Cytochrome c oxidase subunit 5A, mitochondrial	RPTLNELGISTPEELGLDKV	64.6	62.5	66.1	746.4225	749.1057	3	8	2.0	2	2180.1809	2180.2331	2180.207	0.03691097	2180.2070	2.180.1781	14	RPTLNELGISTPEELGLDKV	0.79	1.80	2.00	1.53	0.374	3	
Cytochrome c oxidase subunit 6A1, mitochondrial	HNPHVNLPTGYEDE	36.9	37.4	44.1	947.4456	949.4577	2	4	1.0	1	1864.8439	1864.8694	1864.85665	0.01803122	1864.8567	1864.8453	6	HNPHVNLPTGYEDE	1.00	0.96	1.40	1.12	0.139	3	
Cytochrome c oxidase subunit 6A1, mitochondrial	HNPHVNLPTGYEDE	37.2	32.6	37.4	873.9091	875.922	2	4	1.0	1	1717.7709	1717.798	1717.78445	0.01916259	1717.7845	1717.7769	4	HNPHVNLPTGYEDE	0.98	1.27	1.66	1.30	0.198	3	
Cytochrome c oxidase subunit 6A1, mitochondrial	NPHVNLPTGYEDE	37.2	36.9	43.4	805.3803	807.3929	2	4	1.0	1	1580.7133	1580.7398	1580.72655	0.01873833	1580.7266	1580.7180	5	NPHVNLPTGYEDE	1.11	0.74	1.36	1.07	0.180	3	
Gamma-enolase	AGNSDLPLVPFAFNVINGGSHAGNKL	71.7	69.5	72.8	877.8140	880.4963	3	8	2.0	2	2574.3554	2574.4049	2574.38015	0.03500179	2574.3802	2.574.3827	7	AGNSDLPLVPFAFNVINGGSHAGNKL	1.11	0.42	0.74	0.76	0.198	3	
Glyceraldehyde-3-phosphate dehydrogenase	AFRVPTPNVSVDDL	66.9	66.1	69.1	771.4396	773.4497	2	4	1.0	1	1512.8319	1512.8534	1512.84265	0.01520028	1512.8427	1.512.8373	4	AFRVPTPNVSVDDL	0.83	1.14	1.00	0.99	0.088	3	
LIM zinc-binding domain-containing Nebulette	TQVVSDAAYKGQVPHV	38.1	37.6	44.6	927.5132	931.5369	2	8	2.0	2	1796.9478	1796.9978	1796.9728	0.03535534	1796.9728	1.796.9494	13	TQVVSDAAYKGQVPHV	1.30	0.53	0.95	0.93	0.223	3	
Macrophage migration inhibitory factor	AQATGKPAQVIA	27.1	26.7	nd	637.8605	641.8856	2	8	2.0	2	1217.6424	1217.6952	1217.6688	0.03733524	1217.6688	1.217.6477	17	AQATGKPAQVIA	1.15	1.18	nd	1.17	0.017	2	
Macrophage migration inhibitory factor	AQATGKPAQYIAHHVPPDQL	50.9	49.3	57.3	1081.6071	1085.6313	2	8	2.0	2	2105.1386	2105.1866	2105.1611	0.03866245	2105.1611	2.105.1342	13	AQATGKPAQYIAHHVPPDQL	1.02	0.71	0.51	0.75	0.150	3	
Macrophage migration inhibitory factor	AQATGKPAQYIAHHVPPDQL	50.9	49.9	57.3	721.4066	724.0896	3	8	2.0	2	2105.1332	2105.1848	2105.159	0.03849671	2105.1590	2.105.1342	12	AQATGKPAQYIAHHVPPDQL	0.95	0.75	0.88	0.87	0.068	3	
Microtubule-associated protein 2	AEDVTAALAKQGL	48.1	47.4	54.4	671.8840	675.9103	2	8	2.0	2	1285.6894	1285.7446	1285.717	0.03903229	1285.7170	1.285.6951	17	AEDVTAALAKQGL	0.99	0.78	0.86	0.87	0.060	3	
Microtubule-associated protein tau	ADEVSAASLAKQGL	41.1	40.4	47.6	672.8743	676.8996	2	8	2.0	2	1287.67	1287.7232	1287.6966	0.03761808	1287.6966	1.287.6743	17	ADEVSAASLAKQGL	1.12	0.71	1.03	0.95	0.122	3	
Neurogranin	GRKPGPGGGPGGAGGARGAGGGPGSGD	16.4	16.1	21.4	725.3685	728.0512	3	8	2.0	2	2117.0189	2117.0696	2117.04425	0.03585031	2117.0443	2.117.0184	12	GRKPGPGGGPGGAGGARGAGGGPGSGD	0.85	1.68	0.71	1.08	0.301	3	
Neurogranin	KGPFGPGGGAGGARGAGGGPGSGD	18.7	18.0	22.9	980.9864	985.0126	2	8	2.0	2	1903.8942	1903.9492	1903.9217	0.03889087	1903.9217	1.903.8958	14	KGPFGPGGGAGGARGAGGGPGSGD	0.86	2.08	1.81	1.58	0.370	3	
Neurogranin	KGPFGPGGGAGGARGAGGGPGSGD	18.7	17.9	22.9	654.3271	657.0103	3	8	2.0	2	1903.8947	1903.9499	1903.9208	0.03891097	1903.9208	1.903.8958	13	KGPFGPGGGAGGARGAGGGPGSGD	0.97	2.27	1.66	1.63	0.374	3	
Neurogranin	RKPGPGGGPGGAGGARGAGGGPGSGD	17.0	16.1	21.7	706.3608	709.044	3	8	2.0	2	2059.9958	2060.0480	2060.0219	0.03691097	2060.0219	2.059.9969	12	RKPGPGGGPGGAGGARGAGGGPGSGD	1.23	1.16	2.33	1.57	0.379	3	
Peptidyl-prolyl cis-trans isomerase A	FDITADDEPLGRVSF	67.4	67.4	71.0	855.4278	857.4405	2	4	1.0	1	1680.8083	1680.835	1680.82165	0.01887975	1680.8217	1.680.8068	9	FDITADDEPLGRVSF	1.10	1.37	0.61	1.03	0.221	3	
Peptidyl-prolyl cis-trans isomerase A	ITADDEPLGRVSF	53.7	52.0	59.8	724.3763	726.3896	2	4	1.0	1	1418.7053	1418.7332	1418.71925	0.01972828	1418.7193	1.418.7114	6	ITADDEPLGRVSF	1.04	0.62	0.98	0.88	0.130	3	
Peptidyl-prolyl cis-trans isomerase A	LFADKVPKTAENF	40.4	39.4	47.1	521.9648	525.9901	3	12	3.0	3	1478.7785	1478.8563	1478.8164	0.05642712	1478.8164	1.478.7842	22	LFADKVPKTAENF	1.36	0.59	0.92	0.96	0.223	3	
Peptidyl-prolyl cis-trans isomerase FKBP1A	VFDVLLKLE	70.3	68.5	nd	630.8798	634.905	2	8	2.0	2	1203.681	1203.7338	1203.7074	0.03733524	1203.7074	1.203.6824	21	VFDVLLKLE	0.82	1.25	nd	1.01	0.216	2	
Phosphatidylethanolamine-binding protein 1	KGNDISSGTVL	31.3	31.3	37.5	573.8236	577.8486	2	8	2.0	2	1089.5686	1089.6122	1089.5949	0.03719382	1089.5949	1.089.5739	19	KGNDISSGTVL	1.14	0.87	1.28	1.10	0.120	3	
Phosphatidylethanolamine-binding protein 1	GLDPGKLYTL	53.8	52.0	60.6	566.8395	570.8616	2	8	2.0	2	1075.5944	1075.6472	1075.6208	0.03733524	1075.6208	1.075.5986	21	GLDPGKLYTL	1.00	0.50	0.80	0.77	0.145	3	
Phosphatidylethanolamine-binding protein 1	GLDPGKLYTL	59.3	57.3	63.5	624.3498	628.3755	2	8	2.0	2	1190.621	1190.675	1190.648	0.03818377	1190.6480	1.190.6256	19	GLDPGKLYTL	0.75	1.00	1.42	1.06	0.195	3	
Phosphatidylethanolamine-binding protein 1	DDYVPKLYEQLSGK	53.5	53.6	60.5	580.3162	584.3405	3	12	3.0	3	1653.8307	1653.9075	1653.8691	0.0543058	1653.8691	1.653.8253	22	DDYVPKLYEQLSGK	0.85	0.68	0.85	0.79	0.057	3	
Phosphatidylethanolamine-binding protein 1	AGVTVDELGKLTPTQV	64.9	63.6	67.0	892.0186	896.0447	2	8	2.0	2	1725.9586	1726.0134	1725.986	0.03874945	1725.9860	1.725.9585	16	AGVTVDELGKLTPTQV	0.95	0.60	0.88	0.81	0.107	3	
Proenkephalin-A	SPOLEDEAKELQ	36.9	36.8	44.2	721.8748	725.8996	2	8	2.0	2	1385.671	1385.7232	1385.6971	0.03691097	1385.6971	1.385.6747	16	SPOLEDEAKELQ	1.04	0.43	1.00	0.83	0.196	3	
ProSAAS	SLSAASAPLVETSTPLRL	64.7	62.4	nd	921.0273	923.039	2	4	1.0	1	1812.0073	1812.032	1812.01965	0.01746554	1812.0197	1.812.0066	7	SLSAASAPLVETSTPLRL	1.00	0.68	nd	0.84	0.161	2	
Secretogranin-1	SFARAPQLDL	48.4	47.6	57.2	573.3215	575.3341	2	4	1.0	1	1116.5957	1116.6222	1116.60895	0.01873833	1116.6090	1.116.6000	8	SFAR							