Supplemental Table 1:

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
14-3-3 protein beta/alpha	Q9CQV8	28,086	A	1	6	2	15/18	3.5095	DSTLIM*QLLR
			B	2	6	3	23/64	2.563	EAFSLFDKDGDGTITTK
						2	17/22	2.256	DGNGYISAAELR
14-3-3 protein eta	P68510	28,212	A	1	5	2	21/26	4.2086	AVTEQGAELSNEER
			B	1	5	2	16/20	2.006	FDEETTNGEGR
14-3-3 sigma	O70456	27,713	B	1	4	2	20/26	3.687	AVTEQGAELSNEER
			C	1	4	2	22/26	4.332	AVTEQGAELSNEER
Adenylyl cyclase-associated protein 2	Q9CYT6	52,862	A	1	4	2	39/44	2.1131	SALFAQLNQGEAITK
			B	1	4	2	18/24	2.648	LEQLSAGLDGPPR
			C	1	4	2	19/24	3.866	LEQLSAGLDGPPR
Aldehyde dehydrogenase, mitochondrial	P47738	56,538	A	2	4	2	19/32	4.0426	VAEQTPLTALYVANLIK
						2	22/32	3.7335	VAEQTPLTALYVANLIK
			C	1	4	2	13/16	2.141	VVGNPFDSR
Alpha-catenin 2	Q61301	105,286	B	1	1	2	16/20	2.962	NATNEQDLANR
			C	1	1	2	16/20	3.342	NATNEQDLANR
Ankyrin 2	Q6PCN2	117,436	A	4	1	2	15/22	3.1207	ATFSPIVTLEPR
						2	20/24	3.9321	TLEQQENFSEVAR
						2	17/22	3.691	ATFSPIVTLEPR
						2	17/22	3.3016	ATFSPIVTLEPR
	Q6PCN2	117,436	B	3	1	2	20/24	3.977	TLEQQENFSEVAR
						2	20/24	3.877	TLEQQENFSEVAR
						2	20/24	3.934	TLEQQENFSEVAR
	Q6PCN2	117,436	C	1	1	2	14/16	2.187	GAAVDFTAR
Ankyrin 2	Q8C8R3	131,202	A	2	1	2	16/20	3.0633	GIIDSTVSEQR
						2	18/26	3.7184	LIEVGPSGAQFLGK
	Q8C8R3	131,202	B	2	1	2	15/26	2.755	LIEVGPSGAQFLGK
						3	19/56	2.624	GNANMVKLLLDRGAK
	Q8C8R3	131,202	C	1	1	2	11/14	2.216	VALLLLEK
AP-2 complex subunit beta-1	Q9DBG3	104,583	B	2	1	3	24/40	3.204	CAIKVEQSAER
						2	14/20	2.364	LQNNNVYTIAK
			C	1	1	2	10/18	2.061	YISQCIDEIK
AP-3 complex subunit beta-2	Q9JME5	119,193	A	1	1	2	14/20	2.5323	LLTQYVLSLAK
			B	1	1	2	13/14	2.324	YNDPIYVK
Brain acid soluble protein 1; BASP1, NAP-22	Q91XV3	22,087	A	7	4	3	33/144	3.3787	AEPEKSEGAAEEQPEPAPAPEQEAAAPGPAAGGEAPK
						2	16/44	2.5587	AGEASAESTGAADGAAPEEGEAK
						3	37/120	4.6222	APAPAAPAAAEPQAEAPAAAASSEQSVAVKE
						2	20/26	3.46	ESEPQAAADATEVK
						2	19/24	3.802	AEGAGTEEEGTPK
						2	18/26	3.1044	ESEPQAAADATEVK
						2	20/26	3.224	ETPAASEAPSSAAK
			B	2	4	2	18/26	2.267	ESEPQAAADATEVK
						2	20/26	3.224	ETPAASEAPSSAAK
Calmodulin	P62204	16,838	A	1	6	2	22/28	3.5436	IAAAQYSVTGSAVAR
			B	1	6	2	19/28	3.012	IAAAQYSVTGSAVAR
			C	2	6	2	20/28	4.071	IAAAQYSVTGSAVAR
						2	13/14	2.958	FIQYLASR
cAMP-dependent protein kinase, PKA	P68181	40,708	A	1	3	2	16/22	3.6969	ILQAVNFPFLVK

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
			B	1	3	2	11/20	2.031	FLALGCSSLGR
Clathrin coat assembly protein AP180	Q61548	91,851	A	1	2	2	18/22	3.5174	NTLFNLSNFLDK
			C	2	2	2	20/28	4.071	IAAAQYSVTGSAVAR
						2	13/14	2.958	FIQYLASR
Contactin-1	P12960	113,388	A	1	1	2	16/20	2.5144	VQVTSQEYSAR
			B	3	1	2	16/20	3.181	VQVTSQEYSAR
						3	28/88	4.128	IKTDGAAPNVAPSDVGGGGGTNR
						2	20/26	3.656	NDGGIYTCFAENNR
Endophilin-1	Q62420	39,877	A	2	4	2	17/22	4.1497	TIEYLQPNPASR
						2	18/22	3.7452	TIEYLQPNPASR
			C	1	4	2	17/22	3.011	QAVQILQQVTVR
Endophilin-2	Q62419	41,518	A	1	3	2	39/43	2.3245	TIEYLQPNPASR
			C	1	3	2	13/24	2.254	QTEVLLQPNPSAR
						2	16/20	2.245	LASDAGIFFTR
Fascin	Q61553	54,508	A	2	3	2	15/24	3.0781	LSCFAQSVSPAEK
						3	31/60	5.2301	LVARPEPATGFTLEFR
			B	5	3	2	15/18	2.182	FLVVAHDDGR
						2	18/24	3.499	LSCFAQSVSPAEK
						2	18/32	3.326	YWTLTATGGVQSTASTK
						3	26/60	3.291	LVARPEPATGFTLEFR
						2	16/24	3.152	LSCFAQSVSPAEK
Gamma-soluble NSF attachment protein	Q9CWZ7	34,732	A	1	4	2	16/24	2.6851	LGLSLVVPGGGIK
			B	1	4	2	14/18	2.187	LPEAVQLIEK
Gelsolin	P13020	85,942	A	1	2	2	13/24	2.6262	SGALNSNDAFVLK
			B	3	2	3	34/56	4.297	DSQEEEKTEALTSAK
						2	16/32	2.592	QTQVSVLPEGGETPLFK
						3	31/56	3.555	DSQEEEKTEALTSAK
Glutathione S-transferase Mu 1	P10649	25,970	A	1	5	2	39432	2.4096	ITQSNAILR
			C	1	5	2	15/22	2.719	ADIVENQVMDTR
Guanine nucleotide-binding protein alpha-12	P27600	44,095	A	2	4	2	18/22	3.2104	TTGIVETHFTFK
						2	19/28	3.5463	IAQSDYIPTQQDVLR
			C	2	4	2	13/20	2.052	ILLLGAGESGK
						2	18/20	3.35	ILLLGAGESGK
Guanine nucleotide-binding protein G(i), alpha-2	P08752	40,471	A	1	4	2	17/20	3.094	LLLLGAGESGK
			B	2	4	2	11/14	2.157	LFDVGGQR
						2	10/22	2.083	QFEDLNRNKETK
Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta 3	Q61011	37,240	A	1	4	2	16/18	3.0221	LLVSASQDGK
			C	1	4	2	11/14	2.188	LFDVGGQR
Guanine nucleotide-binding protein G(o) alpha 1	P18872	40,085	A	7	4	2	13/14	2.4097	YYLDSLDR
						2	18/28	3.9429	IGAGDYQPTEQDILR
						2	19/28	4.1886	IGAGDYQPTEQDILR
						3	27/52	3.8682	AM*DTLGVEYGDKER
						2	20/28	4.2066	IGAGDYQPTEQDILR
						2	20/32	4.3227	M*EDTEPFSAELLSAM*M*R
						2	17/24	2.8351	IIHEDGFSGEDVK
			B	2	4	2	17/28	3.757	IGAGDYQPTEQDILR
						2	19/28	4.507	IGAGDYQPTEQDILR
			C	6	4	2	13/14	2.532	MVCDVVSR
						3	24/48	2.796	IIHEDGFSGEDVK

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
						2	19/24	2.938	IIHEDGFSGEDVK
						1	9/14	1.745	YYLDSLDR
						2	14/20	2.975	SREYQLNDSAK
						2	16/20	3.418	SREYQLNDSAK
Guanine nucleotide-binding protein G(q) alpha	P21279	41,483	A	1	4	2	19/36	4.2588	VPTTGIIEYPFDLQSVIFR
			B	1	4	2	13/18	2.559	LINQPLPDLK
Heat shock protein HSP 90-beta	P11499	83,325	A	2	2	2	39/43	2.5783	IDILPNPQER
						2	21/24	4.1016	TLTLVDTGIGM*TK
			B	2	2	2	10/16	2.199	APFDLFENK
						2	15/18	2.718	SIYYITGESK
Homer protein homolog 1	Q9Z2Y3	41,413	A	1	4	2	18/28	4.5292	TELNQTVQELEETLK
			B	1	4	3	18/68	2.664	CGASSGQTSGCGSGQSTR
Kinesin-like protein KIF2	P28740	79,756	B	1	2	2	11/16	2.063	SLASLVEIK
			C	1	2	2	13/20	2.236	FSLIDLAGNER
L-lactate dehydrogenase A chain	P06151	36,499	A	2	4	2	39434	2.4377	VTLTPEEEAR
						2	19/22	2.8313	VIGSGCNLDSAR
			B	1	4	2	18/22	2.909	VIGSGCNLDSAR
Microtubule-associated protein tau	P10637	76,243	A	2	4	2	13/20	2.5948	SPVVSGDTSPR
						2	13/22	2.881	LQTAPVPM*PDLK
			B	1	4	2	14/16	2.451	IAENVEEVK
			C	5	4	2	11/24	2.227	GTKEASLQEPPGK
						2	17/20	3.16	SPVVSGDTSPR
						2	17/28	3.328	SGYSSPGSPGTPGSR
						2	15/28	3.023	SGYSSPGSPGTPGSR
						2	18/20	3.1	SPVVSGDTSPR
Mitsugumin-23	Q3UBX0	26,306	B	1	6	2	14/20	2.665	NNNQQLAQLQK
			C	1	6	2	14/20	2.784	NNNQQLAQLQK
Myosin-VI	Q64331	146,409	A	1	1	2	22/28	4.4478	IVEANPLLEAFGNAK
			B	3	1	2	16/20	2.462	IQAEVEAQLAR
						2	22/28	3.662	YLTESYGTGQDIDDR
						2	20/28	3.546	IVEANPLLEAFGNAK
Myristoylated alanine-rich C-kinase substrate	P26645	29,661	B	3	2	3	30/68	3.682	KESGEGAEAEGATAEGAK
						2	23/32	3.964	ESGEGAEAEGATAEGAK
						2	17/28	3.194	AEDGAAPSPSSETPK
			A	1	2	2	14/28	2.453	AEDGAAPSPSSETPK
Nck-associated protein 1	P28660	128,784	A	1	1	2	14/18	2.6849	AAEDLFVNIR
			B	1	2	2	16/18	2.657	AAEDLFVNIR
Neuromodulin (GAP-43)	P06837	23,632	A	3	5	2	16/20	2.8689	AGSAETESAAK
						2	20/46	3.4089	QADVPAAVTDAAATTPAAEDAATK
						2	18/22	2.5513	KGDAPAAEAEAK
			C	1	5	2	16/22	2.167	KGDAPAAEAEAK
Phosphatase 2A inhibitor, TAF-1, SET	Q9EQU5	33,378	B	1	4	2	20/26	4.166	AIEQSIEQEEGLNR
			C	2	4	2	16/20	3.585	LNEQASEEILK
						2	15/18	2.716	VEVTEFEDIK
Probable oxidoreductase KIAA1576	Q80TB8	45,817	A	1	4	2	17/22	3.5346	AVVLAGFGGLNK
			B	1	4	2	15/16	2.248	LAIFTDDIK
Protein disulfide-isomerase A3	P27773	56,678	A	3	4	2	18/28	3.6569	M*DATANDVPSPYEVK2
						2	12/20	2.1983	ELNDFISYLQR
						2	15/20	2.4851	LAPEYEAAATR

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
			C	1	4	2	14/18	2.643	YGVSGYPTLK
Protein kinase C gamma type	P63318	78,358	A	1	2	2	16/20	2.5913	SGENFDKFFTR
			C	1	2	2	17/20	2.451	SGENFDKFFTR
Protein phosphatase 1 regulatory subunit 7	Q3UM45	41,262	A	2	4	2	22/34	4.6823	AIENIDTLTNLESLFLGK
						2	21/34	5.1646	AIENIDTLTNLESLFLGK
			C	1	3	2	20/34	2.787	AIENIDTLTNLESLFLGK
Ras-related protein Rab-2A	P53994	23,548	B	1	5	3	18/56	2.66	LVEALPHNTSLVELK
			C	1	5	2	17/20	2.556	LLIIGNSSVGK
Serine/threonine-protein phosphatase 2B	P63328	58,644	A	2	3	2	17/22	2.8446	LFEVGGSPANTR
						2	16/18	2.1796	IITEGASILR
			C	1	3	2	12/16	2.53	YENNVMNIR
Serine/threonine-protein phosphatase PP1-alpha	P62137	37,540	A	2	4	2	14/16	2.6103	LNLDSIIGR
						2	13/16	2.6992	YPENFFLLR
			B	1	4	2	16/20	2.775	FDEETTNGEGR
Spectrin beta chain	P15508	245,250	A	1	1	3	25/36	3.3898	HRPDLIDFDK
			B	2	1	3	32/56	5.113	KFEEFQTDLAAHEER
						3	26/52	3.373	FEEFQTDLAAHEER
Synaptogyrin-1	O55100	25,653	A	1	5	2	17/22	3.2587	AGGAFDPYTLVR
			B	1	5	2	16/20	2.505	YLSEVASGENK
Synaptojanin-1	Q8CHC4	172,617	A	1	1	2	19/22	2.6371	VLDAYGLLGVLR
			B	1	1	2	18/22	2.354	VLDAYGLLGVLR
Syntaxin-1A	O35526	33,054	A	1	6	2	17/26	3.0398	SIEQSIEQEEGLNR
			B	1	4	2	18/22	3.056	NSVVEASEAAYK
Syntaxin-1B	O35525	33,079	A	1	4	3	25/52	3.9199	TKQELEDLTADIKK
			B	1	4	2	18/26	3.204	TASNVEEAFINTAK
						2	17/22	3	AGAAFDPVSFAR
Tenascin-R	Q8BYI9	149,563	A	1	1	2	18/24	3.1806	SSLTSTVFTTGGR
			C	1	1	2	20/24	2.674	SSLTSTVFTTGGR
Transgelin-3	Q9R1Q8	22,471	A	4	5	2	39430	2.5451	AAEVYGVR
						2	39369	1.6532	YDADLENK
						2	39400	1.8075	GFSEEQLR
						2	15/22	2.4667	TLM*ALGSVAVTK
			B	3	5	2	15/20	2.972	YLSEVASGENK
						2	20/22	2.935	YLILNATQAESK
						2	12/16	2.838	DTDSEEEIR
Tropomodulin-2	Q9JKK7	39,511	A	1	4	2	17/26	3.665	SNDPVALAFAEM*LK
				1	4	2	16/20	2.775	FDEETTNGEGR
Ubiquitin-activating enzyme E1	Q02053	117,809	A	2	1	2	30/68	2.562	NEEDATELVGLAQAVNAR
						2	20/26	4.251	QPAENVNQYLTDSK
			B	2	1	2	14/20	2.311	AENYDISPADR
						2	12/26	2.2	QPAENVNQYLTDSK
			C	3	1	2	20/34	3.122	NEEDATELVGLAQAVNAR
						3	27/68	3.405	NEEDATELVGLAQAVNAR
						2	11/26	2.305	QPAENVNQYLTDSK
Ubiquitin carboxyl-terminal hydrolase 5	P56399	95,833	B	1	1	2	15/24	2.215	EEDTSAGTGDPPR
			C	2	2	2	13/18	2.626	SSENPNEVFR
						2	12/20	2.312	DGLGGLPDIVR
Vacuolar proton translocating ATPase A1	Q9Z1G4	96,501	A	1	1	2	13/20	2.7782	DLNPDVNVFQR
			B	2	2	2	16/18	3.092	TSATWFALSR

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
						2	17/20	2.612	LNIPVNQVNPR
			C	2	2	2	15/30	2.383	ADIGIAMGITGSDVSK

Supplemental Table 1: **Proteins and peptides identified by LC-ESI-MS/MS that are exclusive to wild-type mouse brain tissue samples and appear in at least two of three data sets.** The columns indicate the SWISS-PROT accession number (acc. no), protein mass in Daltons (Da), whether the peptide was identified in data set A, B, or C (data set), the number of matched peptides, the gel slice from which the peptide originated, the charge state of the ion, the number of ions identified/the maximum number of ions, the Xcorr value, and the assigned amino acid sequence. M*, oxidized methionine residue. Table 1 lists proteins that were identified in at least two of the three data sets from α-bgtx isolations of different mouse brain preparations.

Supplemental Table 2:

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
14-3-3 protein theta	P68254	27,778	A	1	6	2	21/26	4.2086	AVTEQGAELSNEER
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	Q8K3R3	92,694	B	1	1	2	12/16	2.33	TVQMIMETR
2,4-dienoyl-CoA reductase	Q9LTV6	31,796	C	1	6	2	19/24	3.142	VAFITGGGTGLGK
26S proteasome subunit p45	P62196	45,626	B	1	4	2	20/24	3.522	LEGGSGGDSEVQR
3-hydroxybutyrate dehydrogenase	Q3UL45	38,299	A	1	4	2	14/20	2.6697	FGIEAFSDCLR
4F2 heavy chain (AA 1-526)	P10852	58,337	B	2	2	2	15/20	2.621	VAEDETEAGVK
						2	17/18	3.189	IGDLQAFVGR
6-phosphofructokinase	P47857	85,269	C	1	3	2	16/20	3.431	NLEQISANITK
ACF7 neural isoform 1	Q9QXZ0	607,977	C	1	2	3	20/72	2.734	NTQGTTTSSHTSASADIEK
Actin related protein 2	Q8BMA4	37,322	A	2	4	2	18/22	2.5906	DLM*VGDEASELR
						2	16/22	3.0164	ILLTEPPM*NPTK
Actin-binding LIM protein 2	Q8BL65	68,107	B	1	3	2	12/16	2.302	DCFTCSNCK
Aczonin	Q9QYX7	547,570	C	1	1	2	11/16	2.101	APVADVEPK
ADP-ribosylation GTPase-activating protein 1	Q9EPJ9	45,288	C	1	4	1	8/16	1.581	DVTTFFSGK
Alpha glucosidase II, beta subunit	O08795	58,793	B	2	4	2	11/18	2.153	SLEDQVETLR
						2	11/20	2.06	ESLQQLAEVTR
Alpha-internexin	P46660	55,742	A	1	3	2	15/18	2.4596	ALEAELAALR
Alpha-S1	P19228	35,602	C	1	6	2	11/24	2.176	QADYVPSDQDLLR
Aminopeptidase	P97449	109,651	C	1	2	2	13/16	2.475	SPVYLTVLK
						2	11/24	2.341	VLGATLSPELIQK
Apolipoprotein E	P08226	35,867	C			2	13/16	2.71	LGPLVEQGR
Apoprotein A-I	Q00623	30,587	C	1	5	2	18/24	3.203	VAPLGAELQESAR
Beta-enolase	P21550	47,025	A	2	4	2	20/28	3.9976	VNQIGSVTESIQACK
						2	17/28	3.9896	VNQIGSVTESIQACK
BIT	P97797	56,425	C	1	5	3	25/64	2.554	DGQELHPLETTVNPSGK
BTB/POZ domain-containing protein KCTD12	Q6WVG3	35,892	A	1	4	2	13/22	2.9174	EAEYFELPELVR
Calcium-binding protein 1	Q9JLK7	25,943	C	1	5	2	13/20	2.3	GESPVDYDGGR
Calcium-bindingcarrier protein Aralar1	Q8BH59	74,570	C	2	3	2	14/18	2.303	SPSVAVAQPK
Calcium-dependent secretion activator 1	Q80TJ1	153,044	A	1	1	2	18/20	3.3277	FVTILEGVLAK
Capping protein alpha 1 subunit	P47753	32,940	B	2	4	3	23/56	2.541	SKQEALKNDLVEALK
						3	23/52	2.84	KLEVEANNAFDQYR
						2	20/24	3.446	LEVEANNAFDQYR
Casein kinase II subunit alpha	Q60737	45,162	A	1	4	3	23/56	3.0749	TPALVFEHVNNTDFK
Cation-transporting ATPase	Q8K314	101,683	A	1	1	2	16/20	3.0633	GIIDSTVSEQR
Coiled-coil protein	Q9ESK9	182,365	B	1	3	2	8/16	2.098	LVKNHEQDK
COP9 signalosome complex subunit 1	Q99LD4	53,442	C	2	4	2	16/22	2.216	ATTADGSSILDR
						2	19/22	2.876	ATTADGSSILDR
Coronin-3	Q9WUM4	53,121	B	2	3	2	15/18	2.022	NADPILISLK
						3	23/48	2.799	KPTDTASVQNEAK
Cytochrome C	P62897	11,605	B	3	7	2	16/26	3.549	TGQAAGFSYTDANK
						2	13/14	2.233	ADLIAYLK
						3	23/56	3.069	KTGQAAGFSYTDANK
Dihydrolipoyllysine-residue succinyltransferase	Q9D2G2	48,995	A	4	4	2	19/40	3.0799	NDVITVQTPAFAESVTEGDVR
						2	15/20	2.3649	VEGGTPLFTLR
						2	18/22	3.582	NVETM*NYADIER
						2	29/40	5.8293	ASAFALQEQPVVNAVIDDATK
Dihydropyrimidinase-related protein 4	O35098	61,962	B	1	2	2	16/18	3.223	SAADIIALAR

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
Drebrin A	Q9QXS6	77,287	B	1	1	2	20/34	4.44	SPSDSSTASTPIAEQIER
				1	2	2	22/34	4.292	SPSDSSTASTPIAEQIER
Dynamin-like 120 kDa protein	P58281	111,339	C	2	1	2	12/18	2.15	GVEVDPSLIK
						2	14/22	2.947	EVLEDFAEDGEK
Electron transferring flavoprotein, alpha polypeptide	Q99LC5	35,009	B	1	4	2	25/34	4.755	GTSFEAAATSGGSASSEK
Elongation factor 1-alpha	Q3TII3	50,104	A	1	4	3	32/92	4.8238	VETGVLKPGM*VVTFAPVNVTTEVK
Elongation factor 2	O89069	28,657	B	1	5	2	16/18	2.774	GEGQLSAAER
Endophilin-B2	Q8R3V5	44,503	C	1	5	2	21/24	4.233	QTEVLLQPNPSAR
Endoplasmin	P08113	92,476	A	2	1	2	39434	2.5856	EAESSPFVER
						2	20/26	4.2036	GVVDSDDLPLNVSR
Eukaryotic translation elongation factor 1-delta	P57776	31,293	B	1	4	2	15/22	2.148	GVVQDLQQAISK
Excitatory amino acid transporter 1, Slc1a3	P56564	59,622	A	2	4	3	29/76	3.6442	TTTNVLGDSLGAGIVEHLSR
						3	33/56	4.6479	IVQVTAADAFLDLIR
Ezrin-radixin-moesin-binding phosphoprotein 50	P70441	38,600	A	1	4	2	19/26	2.7348	AVDPDSPAEASGLR
F-actin-capping protein subunit alpha-2	Q2QL88	33,023	A	2	4	3	23/68	3.1948	EATDPRPYEAENAIESWR
						2	39430	1.8006	TSVETALR
F-box only protein 2	Q80UW2	33,676	A	2	4	2	19/22	4.089	TDAGSLYELTVR
						2	21/28	4.7231	VLAELPATELVQACR
Fumarate hydratase, mitochondrial precursor	P97807	54,371	A	5	4	2	15/20	3.0676	KPVHPNDHVNK
						2	17/22	3.2091	AIEM*LGGELGSK
						2	13/16	2.4526	AADEVAEGK
						2	18/22	3.3324	AIEM*LGGELGSK
						2	21/40	3.5006	SGLGELILPENEPGSSIM*PGK
G protein-coupled receptor, family C2A	Q8K4Z6	104,213	C	1	1	2	13/22	2.237	GQFNSLYQMAPK
Gamma-1 adducin	Q9QYB5	78,763	B	1	2	2	20/26	3.405	GLSFSEATASTLVK
Gamma-aminobutyric acid transporter 4, GAT4	P31650	69,889	B	1	2	2	20/30	2.865	GSETLGGGGGGAAGTR
Gamma-amino-N-butyrate transaminase	P61922	56,452	A	2	4	2	18/24	3.2707	VDIEFDYDGPLM*K
						2	16/28	3.0847	IDIPSFDWPIAPFPR
Glucose-6-phosphate isomerase	P06745	62,767	A	2	4	2	21/28	4.7525	ILLANFLAQTEALM*K
						2	20/28	4.6326	TFTTQETITNAETAK
Glutamate receptor 2	P23819	98,662	B	2	1	2	12/18	2.485	GADQEYSAFR
						2	19/28	3.814	QTEIAYGTLDSGSTK
GS2NA	Q9ERG2	87,150	C	1	2	2	17/24	2.548	AYIASAGADALAK
GTP-binding protein G25K	P60766	21,311	C	1	6	2	13/18	2.77	YVECSALTQR
GTP-binding protein S10	P97950	26,541	C	1	6	2	14/20	2.306	IIVIGDSNVGK
Guanine nucleotide-binding protein G(s) subunit alpha	P63094	45,664	C	1	3	2	17/24	2.548	AYIASAGADALAK
Guanine nucleotide-binding protein G(t) subunit alpha-1	P20612	39,967	C	1	4	2	11/16	2.299	KGEFQEVLR
Heat shock protein 105 kda	Q61699	96,407	A	1	1	2	14/24	2.9056	VLGTAFDPFLGGK
Histone H2B type 1-B	Q64475	13,952	A	1	2	2	16/28	3.2927	AM*GIM*NSFVNDIFER
Immunoglobulin superfamily receptor PGRL	Q8R366	65,011	B	1	2	2	14/22	2.906	DSQFSYAVFGPR
Impact	O55091	36,276	C	1	4	2	12/20	2.08	NFTNTPDESTK
Inositol 1,4,5-trisphosphate receptor	P11881	313,197	C	3	1	3	21/48	2.811	TATPQQAQEVHEK
						2	15/24	3.172	TATPQQAQEVHEK
						3	20/40	2.656	LDEREAGITEK
Inositol monophosphatase	O55023	30,436	A	1	6	2	17/20	2.8252	SLLVTELGSSR
Isocitrate dehydrogenase 3 (NAD+) beta	Q91VA7	42,195	A	2	4	2	17/18	2.7757	HNNLDLVIIR
						2	18/32	4.2496	NIANPTAM*LLSATNM*LR
Kinesin heavy chain	Q61768	109,549	B	1	1	3	20/40	2.803	FRPLNEAEILR
Leucine-rich acidic nuclear protein, Anp32, Lanp	O35381	28,538	A	1	6	2	18/20	3.1226	ISGDLEVLAEK

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
Leukocyte surface antigen CD47	Q61735	33,098	A	1	4	2	15/26	3.3352	ISVSDLINGIASLK
						2	18/24	3.8705	NVEAQSTEEM*FVK
Manganese superoxide dismutase	P09671	24,603	B	2	5	2	20/26	3.831	GDVTTQVALQPALK
						3	28/56	3.359	HHAAYVNNLNATEEK
MAP kinase kinase 2	Q01986	43,465	C	1	4	1	7/12	1.587	EVELTWR
MAPB1	Q00659	76,071	C	2	2	2	19/26	3.128	TPQASTYSYETSDR
						2	15/20	2.879	TPEVSGYTYEK
Methylglutaconyl-coa hydratase	Q9JLZ3	33,395	A	1	6	2	39/43	2.4334	GIVVLGINR
MKIAA0302 protein	Q6A087	222,918	A	9	1	2	17/20	3.484	NQEAVQQLLGR
						2	39/40	1.532	AAELQAQWER
						2	39/69	1.8409	DLEAISAR
						2	17/20	2.94	DQADPQCLFLR
						3	27/100	3.2893	EKEVEAIQAQAQALAQEDQSAGEVER
						2	17/20	3.089	IIGTQEQLNQR
						3	19/44	2.5008	LAQAHGFQGFLR
						2	39400	1.8547	LEALAEER
						3	33/96	4.5451	VGELTQEANALAAGHPAQAPAINTR
MKIAA0968 protein;Ser/Thr protein kinase family.	Q80TN1	55,014	A	1	3	2	16/18	2.8679	VLAGQEYAAK
Myosin containing PDZ domain	Q9JMH9	232,755	B	3	1	2	19/28	3.292	QDQSIVLLGSSGSGK
						2	20/32	3.71	NTGESASQLLDAETAER
						2	13/18	3.051	DLDIAGFTQK
Myosin-10	Q61879	228,996	A	20	5	2	34/38	2.7649	EQADFAVEALAK
						2	33/39	1.5997	LVWIPSER
						2	15/24	3.146	QVLALQSQLADTK
						2	13/22	2.175	SDLLLEGFNNYR
						2	23/34	5.8477	SLEAEILQLQEELASSER
						3	22/60	2.2803	TTLQVDTLNTELAAER
						2	14/18	2.4513	ALELDPNLYR
						2	14/26	1.7609	DELADEIANSASGK
						2	22/26	4.6021	ELDDATEANEGLSR
						2	39/40	2.231	ELEAELEDER
						2	13/18	2.3801	GGPISFSSSR
						3	18/64	2.1993	HATALEELSEQLEQAKR
						3	22/44	2.2626	HGFEAASIKEER
						2	39/98	2.2665	IVFQEFR
						3	24/60	2.4711	LQQELDDLTVDLDHQR
						2	39/77	1.627	NTNPNFVR
						2	39/40	2.729	QLEEAEEEATR
						3	24/60	2.4373	QLEEAEEEATRANASR
						2	39/43	2.0989	TGLEDPER
						2	33/35	1.9596	YLFVDR
Myosin-9	Q8VDD5	226,357	A	1	1	2	16/18	3.2707	ALELDSNLYR
Myosin-Va	Q99104	215,595	A	3	1	2	16/26	3.2603	SAPEVTAPGAPAYR
						2	3346	1.8662	VSVSFIR
						2	39/40	1.7581	YQNLLNEFSR
Myosin-XVIIIa	Q9JMH9	232,755	A	2	1	2	39/43	2.2253	TALEEQLSR
						2	13/14	1.9425	TFLQELER
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	Q9CQH3	21,710	B	1	6	2	13/20	2.363	TLAILQIESEK
Neural cell adhesion molecule 1	P13595	119,351	A	1	1	2	18/20	2.8538	FFLCQVAGDAK

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
Neuronal growth regulator 1, Neurotractin	Q80Z24	37,900	A	1	3	2	18/24	3.3601	VIVNFAPTIQEIK
Neuroplastin precursor	P97300	31,277	C			2	14/16	2.78	NGVELTATR
N-tropomodulin	P70566	39,492	B	2	3	2	18/22	3.572	DREDFVPFTGEK
				1	4	2	21/28	4.373	ANDPSLQEVNLNNIK
						2	20/28	4.401	ANDPSLQEVNLNNIK
Nucleosome assembly protein 1-like 1	P28656	45,345	A	1	4	2	16/18	2.5161	IVTSEEVIIR
			B	2	3	2	14/20	2.679	EAATVEELNPK
			B			3	26/64	3.255	LDNVSHTPSSYIETLPK
p23	P63028	19,462	C	1	7	2	12/14	2.027	DVNVNFEK
P400 protein	P11881	313,197	C	3	1	3	27/76	4.006	EADPDDHYQSGEGTQATTDK
						2	15/18	2.85	DPQEQVTPVK
						2	12/18	2.368	DLDFANDASK
Paladin	P70261	96,740	C	1	2	2	11/22	2.041	RVLQKLQTDGLK
Paralemmin	Q9Z0P4	41,614	A	1	4	2	18/30	3.9605	EIDVLEFGESAPAASK
Parathymosin	Q9D0J8	11,430	A	1	6	2	13/20	2.1221	SVEAAAELSAK
Peroxin-5-related protein	Q8C437	63,135	C	1	3	2	13/22	2.192	SPVDSSVLEGVK
Peroxiredoxin-5, mitochondrial	P99029	21,897	A	3	6	2	15/30	2.033	GVLFGVPGAFTPGCSK
						2	17/32	2.7377	VGDAIPSVEVFEGEPGK
						2	15/20	2.5227	LLADPTGAFGK
Phosphoglycerate kinase 1	P09411	44,550	A	5	4	2	20/34	4.2138	VLNNM*EIGTSLYDEEGAK
						2	15/20	2.9922	VLPGVDALSNV
						2	17/34	3.707	ITLPVDFVTADKFDENAK
						3	26/100	3.6482	DCVGPEVENACANPAAGTVILLENLR
						2	14/34	2.7853	ITLPVDFVTADKFDENAK
Physophilin	P51863	40,301	A	2	4	2	22/24	3.6623	LLFEGAGSNPGDK
						2	16/20	3.0475	LYPEGLAQLAR
Potassium-transporting ATPase alpha chain 2	Q9Z1W8	114,726	A	4	1	2	13/16	2.7069	LIIVEGCQR
						2	34/36	2.0147	VAEIPFNSTNK
						2	16/24	2.8933	VIM*VTGDHPITAK
						3	36/68	4.4437	SAGIKVIM*VTGDHPITAK
ProSAAS	Q9QXV0	27,270	B	2	6	3	29/52	4.126	ARAEAQEAEDQQAR
						2	17/28	3.748	ILTGSSEPEAAPAPR
						2	19/22	3.534	GEAAGAVQELAR
Proteasome 26S subunit ATPase 2	P46471	48,648	C	1	3	2	17/24	2.651	FDDGAGGDNEVQR
						2	15/20	2.41	ALDEGDIALLK
Protein 4.1B	Q9WV92	103,338	B	1	4	2	16/28	3.035	VESTSVGSISPGGAK
Protein KIAA1045	Q80TL4	45,223	A	1	3	2	17/22	4.0336	ALTDEQEEQAAR
						3	16/68	2.523	VLADLGVTPDKITNSGQR
Protein kinase C inhibitor	P70349	13,777	B	2	7	2	16/26	2.462	AQVAQPGGDTIFGK
Protein NDRG2	Q9QYG0	40,789	A	1	4	2	22/26	3.5967	TASLTSAASIDGSR
Put. Eif-4A (aa 1-390)	P60843	46,154	B	1	3	2	19/26	2.72	GYDVIAQAQSGTGK
Putative adenosylhomocysteinase 3	Q68FL4	66,899	A	1	2	2	39/40	2.2829	TPELTWER
Putative tyrosine-protein phosphatase auxilin	Q80TZ3	102,299	A	1	1	2	15/22	2.2432	AITVSPVPFFNK
Pyridoxal kinase	Q8K183	35,015	A	2	4	2	24/40	4.2156	VVPVADIITPNQFEAELLSGR
						2	15/18	2.5652	VLSIQSHVVR
Pyrroline-5-carboxylate reductase	P54904	28,624	B	1	6	2	15/20	2.625	LGAQALLGAAK
Pyruvate dehydrogenase E1 component alpha subunit	P35486	43,232	A	7	4	2	12/16	1.9717	YGM*GTSVER
						3	20/52	3.0767	YHGHSM*SDPGVSYR
						3	38/132	5.2073	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
						3	36/132	4.8175	EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR
						2	15/20	3.1778	GPILM*ELQTYR
						2	15/16	2.3394	AILAELTGR
						2	15/18	2.9167	VDGM*DILCVR
Rab GDP dissociation inhibitor alpha	P50396	50,522	A	2	4	2	23/36	4.3087	SPYLYPLYGLGELPQGFAR
						2	18/36	3.7278	NPYYGGESSSITPLEELYK
						2	18/28	3.7636	TDDYLDQPCLETINR
Rab GDP dissociation inhibitor beta	Q61598	50,537	A	1	3	2	39/40	2.4656	FVSISDLFVPK
Rab3 GDP/GTP exchange protein	Q80U28	175,180	C	1	1	2	15/22	2.22	SSNSSENQQFLK
Rab5c protein	P35278	23,413	B	2	5	2	17/22	2.328	NEPQNAAGAPGR
						2	14/22	2.826	GVDLQESNPASR
Ras association domain protein 1	Q99MK9	38,789	C	1	5	2	10/16	2.014	KFMVVDDPR
Ras homolog (Rheb)	Q9ESR1	20,393	C	1	5	2	10/18	2.045	ENQTAVDVFK
Ras-related protein Rab-10	P61027	22,541	C	2	5	3	20/44	2.709	NIDEHANEDVER
						2	18/22	3.332	NIDEHANEDVER
Ras-related protein Rab-3	P63011	24,970	C	1	5	2	15/22	2.22	SSNSSENQQFLK
Ras-related protein Rab-31	Q921E2	21,331	C	1	5	2	14/18	2.811	LGNQSLQASR
Ras-related protein Rab-3A	P63011	24,970	A	1	5	2	19/30	4.585	M*SESLDTADPAVTGAK
Ras-related protein Rab-5C	P35278	23,413	C	2	5	2	17/22	3.584	GVDLQESNPASR
						2	14/22	2.1	GVDLQESNPASR
Ras-related protein Rap-1A	P62835	20,987	B	1	5	2	12/18	2.084	YDPTIEDSYR
Regulator of G-protein signaling 7	O54829	54,723	B	1	3	2	16/20	2.514	SSAYQELLQAK
Rho GDP-dissociation inhibitor 1	Q99PT1	23,407	B	1	4	2	20/30	3.856	VAVSADPNVPNVIVTR
RTN1-C	Q7M6W1	23,558	A	1	6	2	39/43	2.3302	SQAIDLLYWR
S-adenosyl homocysteine hydrolase	P50247	47,688	C	1	5	2	13/14	2.135	TPELTWER
SCG10-related protein hiat3, Stathmin-3	O70166	20,954	B	1	5	2	13/18	2.631	ALEENNNFSR
Sec23	Q01405	86,162	C	1	3	2	13/22	2.822	GPQVQQPPPSNR
Septin-10	Q8C650	52,422	A	1	3	2	39/42	2.4827	VNIIPLIAK
Serine/threonine protein phosphatase	Q3U7K1	37,033	A	1	4	2	14/18	2.7041	NVQLQENEIR
Serine/threonine protein phosphatase	Q9DBY2	37,217	A	2	4	3	22/40	3.3456	IKYPENFFLLR
						2	14/18	2.4469	IVQM*TEAEVR
Serine/threonine-protein kinase 2	Q60592	190,534	C	1	1	2	14/20	2.1	NIGALPVDMVR
Serum deprivation-response protein	Q63918	46,764	C	1	4	2	14/16	2.78	NGVELTATR
						2	13/18	2.005	IVTSEEVIIR
Sideroflexin 3	Q91V61	35,406	B	1	4	2	15/24	2.695	NLLLSGEQLEASR
SLIT-ROBO Rho GTPase-activating protein 1	Q91Z69	121,430	B	1	1	2	14/20	2.319	GMADIDIQDDK
Sm D3	P62320	13,916	C	1	7	2	15/18	2.862	VAQLEQVYIR
Sodium/potassium-transporting ATPase subunit alpha-4	Q9WV27	114,816	C	2	1	2	16/20	3.121	LNIPVNQVNPR
						2	14/18	2.115	TSATWFALSR
Sodium-dependent glutamate/aspartate transporter 2	P43006	62,030	A	2	4	2	21/28	4.2933	NDEVSSLDAFLDLIR
						2	16/20	3.14	SELDTIDSQHR
Spnb3 protein	Q68FM2	96,032	A	4	1	2	13/12	1.5391	QQQLPDGTGR
						2	13/14	2.0953	SAVAWEER
						2	16/18	3.3276	DLNAAEALQR
						2	39/40	1.538	DVSSADLVIK
STOP protein	O55129	96,464	B	1	2	2	16/28	2.892	DPEGAGGAGVLAAGK
Succinate semialdehyde dehydrogenase, mitochondrial	Q8BWF0	55,968	A	2	4	3	29/116	4.089	VSM*ELGGLAPFIVFDSANVDQAVAGAM*ASK
						2	12/26	2.8028	EVGEVLCTDPLVSK
Succinyl-coa:3-ketoacid-coenzyme A transferase 1	Q9D0K2	55,989	A	4	4	2	17/24	3.5353	GM*GGAM*DLVSSSK

Protein	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides	slice no.	charge state	ions	Xcorr	assigned sequence
						2	24/52	4.3724	AGGAGVPAFYTSTGYGTLVQEGGSPIK
						2	26/40	4.9338	DLTAVSNNAGVDNFGLGLLLR
						2	19/24	3.6097	GM*GGAM*DLVSSSK
Synaptic vesicle glycoprotein 2A	Q9JIS5	82,647	A	1	1	2	14/18	2.2599	HLQAVDYAAR
Synaptophysin, Major synaptic vesicle protein p38	Q62277	34,025	A	1	4	3	24/48	3.4501	LHQVYFDAPSCVK
T-complex protein 1 subunit delta	P80315	58,066	A	1	4	2	23/30	3.5078	ALIAGGGAPEIELALR
T-complex protein 1 subunit epsilon	P80316	59,624	C	1	3	2	17/18	3.853	IADGYEQAAR
T-complex protein 1 subunit zeta	P80317	58,004	C	1	3	2	15/16	2.354	SETDTSLIR
Thioesterase superfamily member 2; PNAS-27	Q9CQR4	15,183	B	1	1	2	19/22	3.074	TLAFASVDLTNK
Thy-1 membrane glycoprotein	P01831	18,080	A	2	6	2	17/26	3.0398	VTSLTACLVNQNLR
						2	13/18	3.1013	VTLSNQPYIK
Trypsinogen 7	Q9CPN9	26,422	B	1	3	2	13/22	2.137	YVNWIQQTIAAN
TSC22-related inducible leucine zipper 2	Q9EQN3	39,988	B	1	5	2	17/22	2.708	NAALEQENGLLR
Tyrosine 3-monooxygenase/try. 5-monooxygenase activator	Q8BPH1	29,189	A	2	6	2	13/20	2.4338	EAAENSLVAYK
						2	16/20	2.7155	YLAEFATGNDR
Ubiquinol-cytochrome-c reductase complex core protein 1	Q9CZ13	52,769	A	4	4	2	18/40	3.7366	VVELLADIVQNSSLEDSQIEK
						2	17/18	2.965	IQEVDAQM*LR
						2	24/40	5.3877	VVELLADIVQNSSLEDSQIEK
						3	29/152	3.2915	EM*QENDASM*QNVVFDYLHATAFQGTPLAQAVEGPSENVR
Vesicle trafficking protein sec22b	O08547	24,741	B	1	5	2	15/18	2.897	DLQQYQSQAK
Vimentin	P20152	53,688	C	1	5	2	17/18	3.141	FADLSEAANR
Voltage dependent anion channel 3	Q60931	30,753	B	1	4	2	16/20	2.477	LSQNNFALGYK
Wrd43 protein	Q68FC6	66,324	B	1	4	2	13/18	2.019	VFASLPQVER

Supplemental Table 2: Proteins identified by LC-ESI-MS/MS and exclusive to wild-type mouse brain tissue samples, but appearing in only one data set. This table lists proteins that were isolated by α-bgtx beads of wild-type mouse brain tissue that are not present in knockout mouse samples. The columns indicate the SWISS-PROT accession number (acc. no), protein mass in Daltons (Da), whether the peptide was identified in data set A, B, or C (data set), the number of matched peptides, the gel slice from which the peptide originated, the charge state of the ion, the number of ions identified/the maximum number of ions, the Xcorr value, and the assigned amino acid sequence. Table 1 lists proteins that were identified in at least twice out of three data sets from α-bgtx isolations of different mice. M*, oxidized methionine residue.

Supplementary Table 3:

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
14-3-3 protein epsilon	P62259	29,174	B	1	1	4	ko	2	13/20	2.42	YLAEFATGNDR
							wt	2	17/22	2.513	HLIPAANTGESK
			C	3	1	4	ko	1	12/20	2.325	EALQDVEDENQ
							ko	2	15/20	2.611	YLAEFATGNDR
							ko	2	16/20	3.074	EALQDVEDENQ
							wt	2	17/22	3.839	TIEYLQPNPASR
14-3-3 protein zeta	P63101	27,771	A	2	1	4	ko	2	14/22	2.5122	FLIPNASQPESK
							ko	2	21/26	4.7006	SVTEQGAELSNEER
							wt	2	18/22	3.3398	FLIPNASQPESK
			B	4	6	4	ko	2	21/26	3.912	SVTEQGAELSNEER
							ko	2	21/26	4.875	SVTEQGAELSNEER
							ko	2	23/34	4.618	GIVDQSQQAYQEAFEISK
							wt	2	15/20	2.055	YLAEVAAGDDK
							wt	2	21/26	4.532	SVTEQGAELSNEER
							wt	2	22/26	4.275	SVTEQGAELSNEER
							wt	3	28/44	3.116	YLAEVAAGDDKK
							wt	3	24/68	2.895	GIVDQSQQAYQEAFEISK
							wt	2	17/22	2.172	FLIPNASQPESK
							ko	2	16/22	2.263	FLIPNASQPESK
			C	5	3	4	ko	1	10/26	2.208	SVTEQGAELSNEER
							ko	2	19/22	3.542	YLAEVAAGDDKK
							ko	2	21/26	4.773	SVTEQGAELSNEER
							ko	2	20/26	4.046	SVTEQGAELSNEER
							ko	2	18/22	2.244	FLIPNASQPESK
							wt	2	21/26	4.759	SVTEQGAELSNEER
							wt	3	28/52	3.858	SVTEQGAELSNEER
							wt	2	18/22	2.4	FLIPNASQPESK
2',3'-cyclic-nucleotide 3'-phosphodiesterase	P16330	47,123	A	1	1	3	ko	2	14/20	2.7096	LSISALFVTPK
				0	8	4	wt	2	12/16	1.9337	AIFTGYYGK
							wt	2	12/16	2.5024	HFISGDEPK
							wt	2	16/20	3.1856	VLVLDDTNHER
							wt	2	14/20	3.0872	LSISALFVTPK
							wt	2	17/24	2.8431	GGSQGEAVGELPR
							wt	2	17/24	2.8431	GGSQGEAVGELPR
							wt	2	19/24	4.4537	GGSQGEAVGELPR
							wt	2	19/26	4.2986	AAGAEEYAQQEVVK
							wt	2	16/20	2.5144	VQVTSQEYSAR
			B	1	0	4	wt	2	13/24	2.501	GGSQGEAVGELPR
			C	6	7	4	ko	1	10/16	1.808	AIFTGYYGK
				6	4	3	ko	1	9/14	1.637	ADFSEAYK
							ko	2	14/24	2.795	GGSQGEAVGELPR
							ko	2	19/24	3.612	GGSQGEAVGELPR
							ko	2	13/14	2.02	ADFSEAYK
							ko	2	18/24	3.99	GGSQGEAVGELPR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	13/16	2.598	HFISGDEPK
							ko	2	14/16	2.889	LELVSYFGK
							ko	2	13/16	2.271	ADFSEAYKR
							ko	2	20/28	4.215	AAGAEEYAQQEVVKR
							ko	2	20/26	4.303	AAGAEEYAQQEVVK
							ko	1	9/14	1.565	MVSADAYK
							wt	2	15/20	2.995	VLVLDDTNHER
							wt	1	9/16	1.525	AIFTGYYGK
							wt	2	16/20	3.299	NQWQLSADDLK
							wt	1	9/14	1.562	ADFSEAYK
							wt	2	9/16	2.143	HFISGDEPK
							wt	2	19/24	3.589	GGSQGEAVGELPR
							wt	2	18/24	3.665	GGSQGEAVGELPR
							wt	2	18/24	3.429	GGSQGEAVGELPR
							wt	2	13/16	2.541	HFISGDEPK
							wt	2	12/16	2.069	ADFSEAYKR
							wt	2	20/26	4.397	AAGAEEYAQQEVVK
2410014A08Rik protein	Q6ZQI3	32,342	B	2	1	3	ko	2	17/22	2.544	FAEVYFAQSQQK
							ko	2	17/24	3.182	STPEDQILYQTER
							wt	2	18/24	3.484	STPEDQILYQTER
3-methylcrotonyl-coa carboxylase alpha subunit	Q99MR8	79,344	C	4	4	2	ko	2	13/28	3.123	IIEEAPAPGINPEVR
							ko	2	16/20	2.595	VFFSEGAQANR
							ko	2	16/20	3.394	DGSYDMQIDNK
							ko	3	27/52	4.332	HAPLVEFEEEESDK
							wt	2	16/20	2.935	VFFSEGAQANR
							wt	2	16/20	3.091	DGSYDMQIDNK
							wt	2	21/28	3.473	IIEEAPAPGINPEVR
							wt	3	27/56	3.888	IIEEAPAPGINPEVR
6-phosphofructokinase type C	Q9WUA3	85,455	A	1	1	1	ko	2	16/20	2.6005	DLLFQPVAELK
							wt	2	16/20	3.1776	
Acetyl-CoA acetyltransferase	Q8QZT1	44,816	A	1	1	3	ko	2	23/28	4.3949	TIAIIAEGIPEALTR
							wt	2	22/28	4.5177	TIAIIAEGIPEALTR
			B	0	1	3	wt	2	18/32	3.255	TPIGSFLGSLASQPATK
			C	1	3	3	ko	2	19/24	3.184	QEQDTYALSSYTR
							wt	2	14/24	2.734	FASEITPITISVK
							wt	2	20/22	2.993	LGTAAIQGAIEK
							wt	2	20/24	3.217	QEQDTYALSSYTR
Aconitate hydratase	Q99KI0	85,464	A	2	2	1	ko	2	17/28	3.5825	NAVTQEFGPVPDTAR
							ko	3	24/48	3.1416	ATIERDGYAQILR
							wt	2	16/24	2.8919	ATIERDGYAQILR
							wt	2	22/28	3.7066	NAVTQEFGPVPDTAR
			C	3	4	1	ko	2	20/28	3.835	WVVIGDENYGEGSSR
							ko	2	19/24	3.41	SQFTITPGSEQIR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	3	28/60	4.257	IVYGHLDDPANQEIER
							wt	2	12/16	2.254	NTIVTSYNR
							wt	2	24/28	4.352	NAVTQEFGPVPDTAR
							wt	2	20/24	3.379	SQFTITPGSEQIR
							wt	3	27/60	4.06	IVYGHLDDPANQEIER
Alpha actinin 4	P57780	104,977	B	1	1	1	ko	2	20/30	3.267	ETTDTDTADQVIASFK
							wt	2	18/30	3.274	ETTDTDTADQVIASFK
Alpha-actin-2	P62737	42,009	B	2	3	4	ko	2	18/22	3.676	TINEVENQILTR
							ko	2	19/22	2.893	TINEVENQILTR
							wt	2	22/26	3.617	FAIQDISVEETSAK
							wt	2	19/22	2.893	TINEVENQILTR
							wt	2	22/26	3.617	FAIQDISVEETSAK
Alpha-actinin-1	Q7TPR4	103,068	A	1	1	3	ko	2	18/22	4.3998	VGWEQLLTTIAR
							wt	2	18/22	3.6671	TINEVENQILTR
Annexin II	P07356	38,676	B	5	7	4	ko	2	13/18	3.032	TNQELQEINR
							ko	2	16/20	2.56	SLYYYIQQDTK
							ko	2	17/20	3.001	TPAQYDASELK
							ko	2	16/20	3.267	TPAQYDASELK
							ko	2	20/32	4.32	AEDGSVIDYELIDQDAR
							wt	2	14/18	3.009	TNQELQEINR
							wt	2	15/18	3.287	TNQELQEINR
							wt	2	16/20	2.852	SLYYYIQQDTK
							wt	2	15/20	2.59	TPAQYDASELK
							wt	2	18/20	2.717	TPAQYDASELK
							wt	2	14/20	2.673	TPAQYDASELK
							wt	2	15/20	2.864	TPAQYDASELK
			C	1	1	4	ko	2	16/20	3.188	TPAQYDASELK
							wt	2	12/20	2.598	TPAQYDASELK
AP-2 complex subunit alpha-1	P17426	107,664	A	1	2	1	ko	2	15/18	2.3493	GLAVFISDIR
							wt	2	16/18	3.3595	GLAVFISDIR
							wt	2	16/18	3.3595	GLAVFISDIR
			B	2	6	1	ko	2	16/20	2.896	LVECLETVLNK
							ko	2	16/18	3.714	GLAVFISDIR
							wt	2	25/36	4.665	QGAIVAVTGDGVNDSPALK
							wt	2	24/34	4.066	NLEAVETLGSTSTICSDK
							wt	2	14/16	2.421	ALLLSTYIK
							wt	2	16/22	2.34	GPGAASALDDSR
							wt	2	15/16	2.021	DDVQGYAAK
							wt	2	16/20	2.608	QLSLPLQEAQK
Aspartate aminotransferase	P05202	47,411	C	2	4	4	ko	2	14/22	2.078	IAATILTSPDLR
				4	5	3	ko	2	15/22	2.767	PLYSNPPLNGAR
							ko	2	14/16	2.63	MNLGVGAYR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	16/26	3.783	FVTVQTISGTGALR
							ko	2	16/18	3.709	DAGMQLQGYR
							ko	2	17/22	3.48	IAATILTSPDLR
							wt	2	13/14	2.147	NMGLYGER
							wt	2	21/28	4.25	ASAELALGENNEVLK
							wt	2	19/26	3.881	FVTVQTISGTGALR
							wt	2	15/16	2.596	MNLGVGAYR
							wt	2	13/22	2.196	IAATILTSPDLR
							wt	2	16/18	3.271	DAGMQLQGYR
							wt	2	19/22	3.559	IAATILTSPDLR
							wt	2	12/24	2.354	IVAATLSDPELFK
							wt	2	15/16	3.229	VGNLTVVGK
							wt	2	17/20	2.942	LVLGDNSPAIR
ATP synthase subunit alpha	Q03265	59,753	A	3	2	3	ko	2	20/30	3.714	TGAIVDVPVGEELLGR
				2	3	4	ko	2	14/18	2.4023	VLSIGDGIAR
							ko	2	15/18	3.0483	AVDSLVPIGR
							ko	2	17/34	3.1043	VVDALGNAIDGKGPIGSK
							ko	2	17/28	3.6017	ILGADTSVDLEETGR
							wt	2	17/22	3.1634	TSIAIDTIINQK
							wt	2	15/30	2.2425	TGAIVDVPVGEELLGR
							wt	2	22/30	4.1809	TGAIVDVPVGEELLGR
							wt	2	14/18	3.2646	AVDSLVPIGR
							wt	3	26/68	3.1879	VVDALGNAIDGKGPIGSK
			B	3	5	3	ko	2	17/20	2.943	HALIIYDDLSK
							ko	2	20/22	3.085	VVDALGNAIDGK
							ko	2	23/28	4.119	ILGADTSVDLEETGR
							wt	2	17/22	2.466	VVDALGNAIDGK
							wt	2	14/20	2.27	HALIIYDDLSK
							wt	2	13/18	2.404	AVDSLVPIGR
							wt	2	18/20	2.824	HALIIYDDLSK
							wt	2	15/20	2.626	HALIIYDDLSK
			C	16	20	3	ko	2	13/20	2.161	IVEIPFNSTNK
							ko	2	14/20	2.055	NMVPQQALVIR
							ko	2	13/16	2.349	NSVFQQGMK
							ko	2	14/16	2.573	NSVFQQGMK
							ko	2	19/24	2.693	AVAGDASESALLK
							ko	2	15/20	2.438	NMVPQQALVIR
							ko	2	16/20	2.989	LNIPVSQVNPR
							ko	2	18/24	2.47	AVAGDASESALLK
							ko	2	23/28	4.161	VDNSSLTGESEPQTR
							ko	2	21/28	4.459	VDNSSLTGESEPQTR
							ko	2	16/24	3.311	SPDFTNENPLETR
							ko	2	18/24	4.203	SPDFTNENPLETR
							ko	2	13/34	2.445	GVGIISEGNETVEDIAAR
							ko	2	20/28	4.359	VDNSSLTGESEPQTR
							ko	2	23/34	4.424	GVGIISEGNETVEDIAAR
							ko	3	23/40	3.564	LNIPVSQVNPR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	14/16	2.505	NSVFQQGMK
							wt	2	14/16	2.411	NSVFQQGMK
							wt	2	20/28	4.082	VDNSSLTGESEPQTR
							wt	2	16/20	2.987	LNIPVSQVNPR
							wt	2	22/28	4.411	VDNSSLTGESEPQTR
							wt	2	21/28	3.679	VDNSSLTGESEPQTR
							wt	2	20/24	2.968	AVAGDASESALLK
							wt	2	18/24	3.154	SPDFTNENPLETR
							wt	2	19/24	3.325	SPDFTNENPLETR
							wt	2	18/24	3.537	SPDFTNENPLETR
							wt	2	22/34	4.527	GVGIISEGNETVEDIAAR
							wt	2	24/34	4.157	GVGIISEGNETVEDIAAR
							wt	2	16/24	3.32	SPDFTNENPLETR
							wt	2	21/34	4.226	GVGIISEGNETVEDIAAR
							wt	2	19/24	3.53	AVAGDASESALLK
							wt	2	26/34	5.195	GVGIISEGNETVEDIAAR
							wt	3	23/40	3.709	LNIPVSQVNPR
							wt	3	29/68	3.196	GVGIISEGNETVEDIAAR
							wt	3	26/56	3.866	VDNSSLTGESEPQTR
							wt	3	29/68	4.124	GVGIISEGNETVEDIAAR
ATP synthase subunit beta	P56480	56,300	A	3	2	3	ko	2	12/20	2.17	IGLFGGAGVGK
				3	3	4	ko	2	11/28	1.8327	VALVYGQM*NEPPGAR
							ko	2	17/24	2.796	TVLIM*ELINNVAK
							ko	2	17/24	2.796	TVLIM*ELINNVAK
							ko	2	18/36	4.0956	AIAELGIYPAVDPLDSTSR
							ko	2	18/26	4.0098	FTQAGSEVSALLGR
							wt	2	16/20	3.0315	IGLFGGAGVGK
							wt	2	19/24	3.4203	TVLIM*ELINNVAK
							wt	2	21/28	3.8064	VALVYGQM*NEPPGAR
							wt	2	20/26	4.1493	FTQAGSEVSALLGR
							wt	3	35/72	4.5639	VLDSGAPIKIPVGPETLGR
Beta actin	P60710	41,737	B	0	1	3	ko	3	21/48	2.7	QEYDESGPSIVHR
				1	3	4	wt	3	20/48	2.685	QEYDESGPSIVHR
							wt	3	24/52	3.035	QEYDESGPSIVHRK
							wt	3	25/48	3.487	QEYDESGPSIVHR
							wt	3	22/48	2.694	QEYDESGPSIVHR
			C	5	4	4	ko	2	16/24	2.458	QEYDESGPSIVHR
							ko	2	14/24	2.344	QEYDESGPSIVHR
							ko	3	25/48	2.968	QEYDESGPSIVHR
							ko	3	26/48	3.113	QEYDESGPSIVHR
							ko	3	24/48	3.606	QEYDESGPSIVHR
							wt	3	22/48	2.704	QEYDESGPSIVHR
							wt	3	24/48	3.135	QEYDESGPSIVHR
							wt	3	26/48	3.246	QEYDESGPSIVHR
							wt	3	26/48	3.396	QEYDESGPSIVHR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
Beta-1-globin	P02089	15,878	B	0	2	6	ko	2	17/22	2.51	DFTPAAQAAFQK
				2	3	7	ko	2	18/22	2.586	DFTPAAQAAFQK
							wt	2	17/20	2.734	LIIWDSYTTNK
							wt	2	15/24	2.64	VNPDEVGGEALGR
							wt	2	18/24	3.36	VNPDEVGGEALGR
							wt	2	13/24	2.749	GTFASLSELHCDK
							wt	2	17/22	2.863	DFTPAAQAAFQK
			C	3	1	6	ko	1	12/22	2.53	DFTPAAQAAFQK
				7	5	7	ko	1	14/22	2.948	DFTPAAQAAFQK
							ko	2	12/16	2.137	AAVSGLWGK
							ko	2	17/22	2.802	DFTPAAQAAFQK
							ko	2	15/24	2.91	VNPDEVGGEALGR
							ko	2	15/22	2.466	DFTPAAQAAFQK
							ko	2	18/24	4.262	VNPDEVGGEALGR
							ko	2	16/24	3.067	VNVEEVGGEALGR
							ko	2	13/24	2.62	VNVEEVGGEALGR
							ko	2	16/24	3.176	VNVEEVGGEALGR
							wt	2	13/24	2.783	VNPDEVGGEALGR
							wt	2	15/24	3.447	VNPDEVGGEALGR
							wt	2	18/22	3.116	DFTPAAQAAFQK
							wt	2	18/22	3.239	DFTPAAQAAFQK
							wt	2	15/24	3.548	VNVEEVGGEALGR
							wt	2	18/24	3.614	VNVEEVGGEALGR
Beta-synuclein	Q91ZZ3	14,052	C	1	1	6	ko	2	20/26	4.068	TSGVVQGVASVAEK
							wt	2	20/26	4.174	TSGVVQGVASVAEK
Calcium/calmodulin-dependent protein kinase II alpha	P11798	54,115	A	3	4	3	ko	2	15/20	2.9109	GAILTTM*LATR
							ko	2	20/22	3.9948	ITQYLDAGGIPR
							ko	2	16/22	2.9143	DLKPENLLLASK
							wt	2	10/16	1.5614	FYFENLWSR
							wt	2	16/20	3.4709	GAILTTM*LATR
							wt	2	20/22	4.5047	ITQYLDAGGIPR
							wt	3	24/44	3.4717	DLKPENLLLASK
Cell cycle exit and neuronal differentiation protein 1	Q9JKC6	14,987	C	2	4	5	ko	2	18/30	3.603	GPGDGAEEDESNTGGR
							ko	3	26/72	3.385	DTQAEKQEQAAAPGPAATK
							wt	2	16/36	3.452	DTQAEKQEQAAAPGPAATK
							wt	2	17/30	4.01	GPGDGAEEDESNTGGR
							wt	3	29/72	3.789	DTQAEKQEQAAAPGPAATK
							wt	3	29/72	3.494	DTQAEKQEQAAAPGPAATK
Cofilin	P18760	18,560	C	2	2	6	ko	2	15/20	2.096	YALYDATYETK
							ko	2	18/20	3.411	YALYDATYETK
							wt	2	18/20	3.598	YALYDATYETK
							wt	2	17/20	2.938	YALYDATYETK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
Creatine kinase	P30275	47,004	A	5	1	3	ko	2	17/24	2.9903	FCTGLTQIETLFK
							wt	2	13/14	2.2973	LLIEM*EQR
							wt	2	22/40	3.9948	GTGGVDTAAVGGVFDVSNADR
							wt	2	17/30	2.5256	LAVEALSSLDGDLSGR
							wt	2	15/18	2.9963	DLFDPIIEER
							wt	2	19/24	3.8179	FCTGLTQIETLFK
			B	3	3	3	ko	2	11/12	2.161	SGYFDER
			B	1	0	4	ko	2	17/18	2.263	VVVDALSGLK
							ko	2	23/40	4.869	GTGGVDTAATGSVFDISNLDR
							ko	3	25/44	3.347	AGVHIKLPLLSK
							wt	2	16/18	2.143	VVVDALSGLK
							wt	2	29/40	5.565	GTGGVDTAATGSVFDISNLDR
							wt	3	27/84	3.389	RGTGGVDTAATGSVFDISNLDR
			C	0	2	3	ko	2	16/18	2.674	DLFDPIIEER
							ko	2	16/18	2.255	VVVDALSGLK
CtBP1 protein	O88712	47,745	B	1	1	4	wt	2	14/20	2.489	IGSGFDNIDIK
							wt	2	15/20	2.404	GETLGIIGLGR
			C	0	1	4	ko	2	17/18	2.549	QGAFLVNTAR
Cyclophilin CyP-S1	P24369	22,713	B	1	0	1	ko	2	17/24	3.074	DTNGSQFFITTVK
							ko	2	13/24	2.317	TVDNFVALATGEK
							wt	2	13/24	2.197	TVDNFVALATGEK
							wt	2	11/22	2.092	VVFGLFGKTVPK
							wt	2	13/24	2.197	TVDNFVALATGEK
Dihydropyrimidinase-related protein 1; Crmp1	P97427	62,168	A	2	2	3	ko	2	16/18	3.9025	SAADIIALAR
							ko	2	17/24	2.8257	QIGENLIVPGGVK
							wt	2	17/18	3.9171	SAADIIALAR
							wt	2	14/22	2.5511	IVFEDGNISVSK
			B	1	2	3	ko	2	13/20	2.311	ADGSTQVIDTK
							wt	2	20/26	4.026	TASGVTQLADIYEK
							wt	2	16/18	3.223	SAADIIALAR
Dihydropyrimidinase-related protein 2; DRP-2	O08553	62,278	A	4	4	3	ko	2	17/18	4.0816	SAAEVIAQAR
							ko	2	17/30	3.0798	SITIANQTNCPLYVTK
							ko	2	18/30	3.3373	IVLEDGTLHVTEGSGR
							ko	2	16/28	2.4512	GLYDGPVCEVSVTPK
							wt	2	17/30	3.8635	SITIANQTNCPLYVTK
							wt	2	16/30	2.4127	IVLEDGTLHVTEGSGR
							wt	2	17/28	2.48	GLYDGPVCEVSVTPK
							wt	2	17/18	3.8308	SAAEVIAQAR
			B	2	5	3	ko	2	11/12	2.197	VFNLYPR
							ko	2	16/30	2.996	SITIANQTNCPLYVTK
							wt	2	16/20	2.599	GSPLVVISQGK
							wt	2	13/16	2.216	KPFPDFVYK
							wt	2	18/28	3.075	GLYDGPVCEVSVTPK
							wt	2	14/30	3.16	IVLEDGTLHVTEGSGR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	3	29/60	3.798	SITIANQTNCPLYVTK
Dynamin-1	P39053	97,803	A	6	4	1	ko	2	10/18	1.8464	SSVLENFVGR
							ko	2	12/14	1.9811	GYIGVVNR
							ko	2	16/22	3.5012	NLVDSYM*AIVNK
							ko	2	16/22	3.7414	TSGNQDEILVIR
							ko	2	22/34	4.4245	IEGSGDQIDTYELSGGAR
							ko	3	28/80	3.9026	GPPPSGIATLVSGIAGEEPQR
							wt	2	20/34	3.6684	IEGSGDQIDTYELSGGAR
							wt	2	12/14	2.1858	GYIGVVNR
							wt	2	16/22	3.9378	TSGNQDEILVIR
							wt	2	15/22	3.1307	NLVDSYM*AIVNK
			C	1	1	1	ko	2	16/20	3.833	LDLMDEGTDAR
							wt	2	18/20	3.546	LDLMDEGTDAR
Elongation factor 1 A-2	P62631	50,454	A	0	1	3	wt	2	16/20	3.755	IGGIGTVPVGR
			B	1	2	3	ko	2	11/22	2.462	EGIPALDNFLDK
				0	1	4	wt	2	15/20	2.55	IGGIGTVPVGR
							wt	2	18/26	3.218	ETVSEESNVLCLSK
							wt	2	13/18	2.636	STTTGHLIYK
			C	2	4	3	ko	2	19/20	3.032	IGGIGTVPVGR
				1	1	4	ko	2	13/20	2.379	MDSTEPPYSQK
							ko	2	16/20	3.162	IGGIGTVPVGR
							wt	2	17/20	2.718	IGGIGTVPVGR
							wt	2	17/20	2.461	IGGIGTVPVGR
							wt	2	19/20	3.338	IGGIGTVPVGR
							wt	2	19/20	3.631	IGGIGTVPVGR
							wt	2	14/20	2.311	MDSTEPAYSEK
Elongation factor 1-gamma	Q9D8N0	50,061	A	2	1	3	ko	2	15/18	2.7858	STFVLDEFKR
							ko	2	19/24	4.1199	ALIAAQYSGAQVR
							wt	2	19/24	3.8545	ALIAAQYSGAQVR
Elongation factor Tu	Q8BFR5	49,508	B	2	1	4	ko	2	16/22	2.89	AEAGDNLGALVR
							wt	2	20/22	2.818	AEAGDNLGALVR
			C	1	1	4	ko	2	19/22	3.912	AEAGDNLGALVR
							ko	2	19/22	4.016	AEAGDNLGALVR
							wt	2	17/22	3.563	AEAGDNLGALVR
Enolase, alpha	P17182	47,141	B	1	2	4	ko	2	24/36	4.714	DATNVGDEGGFAPNILENK
							wt	2	23/36	3.758	DATNVGDEGGFAPNILENK
							wt	2	24/34	4.031	AAVPSGASTGIYEALELR
F-actin-capping protein subunit beta	P47757	31,345	A	1	1	6	ko	2	14/18	2.2053	STLNEIYFGK
							wt	2	15/18	2.8966	STLNEIYFGK
Fructose-bisphosphate aldolase A	P05064	39,356	A	0	3	3	wt	2	18/28	3.1246	FSNEEIAM*ATVTALR
							wt	2	11/16	2.2915	AAQEEYIKR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	20/26	4.375	GILAADESTGSIAK
			B	3	4	3	ko	3	24/76	3.673	IGEHTPSALAIMENANVLAR
							ko	2	16/26	2.805	GILAADESTGSIAK
							ko	2	19/26	3.128	GILAADESTGSIAK
							wt	2	15/20	2.136	ALANSLACQGK
							wt	3	29/88	4.617	GVVPLAGTNGETTTQGLDGLSER
							wt	2	20/26	3.102	GILAADESTGSIAK
							wt	2	19/26	3.589	GILAADESTGSIAK
			C	6	6	4	ko	2	14/20	2.645	ALANSLACQGK
							ko	2	15/20	2.799	ALANSLACQGK
							ko	2	12/16	2.759	AAQEEYIKR
							ko	2	21/24	3.144	LQSIGTENTEENR
							ko	2	20/26	4.039	GILAADESTGSIAK
							ko	2	20/26	4.152	GILAADESTGSIAK
							wt	2	15/20	2.81	ALANSLACQGK
							wt	2	15/20	3.088	ALANSLACQGK
							wt	2	17/24	3.098	LQSIGTENTEENR
							wt	2	18/24	2.924	LQSIGTENTEENR
							wt	2	20/26	4.046	GILAADESTGSIAK
							wt	2	20/26	4.046	GILAADESTGSIAK
Fructose-bisphosphate aldolase C	P05063	39,395	A	1	0	3	ko	2	23/30	5.2307	TPSALAILENANVLAR
				0	1	4	wt	2	9/16	1.8301	QVLFSADDR
							wt	2	24/30	5.2625	TPSALAILENANVLAR
			B	1	1	4	wt	2	23/30	4.38	TPSALAILENANVLAR
							wt	2	17/22	3.4	EANELQQWITEK
			C	3	3	4	ko	2	13/16	2.14	QVLFSADDR
							ko	2	18/24	3.228	LSQIGVENTEENR
							ko	2	18/22	3.286	DNAGAATEEFIK
							wt	2	12/16	2.074	QVLFSADDR
							wt	2	20/26	3.744	GILAADESVGSMAK
							wt	2	20/26	4.108	GILAADESVGSMAK
GABA transporter 4	P31650	69,889	B	0	1	2	wt	2	20/30	2.865	GSETLGGGGGGAAGTR
			C	3	2	2	ko	2	20/30	3.492	GSETLGGGGGGAAGTR
							ko	2	23/30	3.968	GSETLGGGGGGAAGTR
							ko	2	20/30	3.492	GSETLGGGGGGAAGTR
							wt	2	20/30	3.452	GSETLGGGGGGAAGTR
							wt	2	22/30	4.127	GSETLGGGGGGAAGTR
Gamma-enolase	P17183	47,297	C	1	1	3	ko	3	26/72	3	DATNVGDEGGFAPNILENK
							wt	2	22/36	2.891	DATNVGDEGGFAPNILENK
Glial fibrillary acidic protein	P03995	49,900	C	4	4	3	ko	2	14/18	2.072	QEADEATLAR
							ko	2	17/18	3.2	FADLTDAASR
							ko	2	16/18	3.013	ALAAELNQLR
							ko	2	17/20	3.418	LEAENNLAAYR
							wt	2	12/18	2.096	QEADEATLAR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	16/18	3.461	ALAAELNQLR
							wt	2	15/20	3.105	ESASYQEALAR
							wt	2	16/18	3.383	LADVYQAELR
Glutamate dehydrogenase 1	P26443	61,337	A	2	6	4	ko	2	12/18	2.5035	TAAYVNAIEK
							ko	2	15/20	2.5651	YSTDVSVDEVK
							wt	2	10/14	1.9866	YNLGLDLR
							wt	2	12/18	2.5035	TAAYVNAIEK
							wt	2	15/20	2.5651	YSTDVSVDEVK
							wt	3	31/80	3.1909	IIAEGANGPTTPEADKIFLER
			B	0	2	4	wt	2	11/20	2.427	YSTDVSVDEVK
							wt	2	15/18	2.64	TAAYVNAIEK
Glyceraldehyde-3-phosphate dehydrogenase	P16858	35,810	A	2	4	4	ko	2	15/28	3.0403	GAAQNIIPASTGAAK
							ko	2	16/22	3.2041	VVDLM*AYM*ASKE
							wt	2	16/26	2.5086	LVINGKPITIFQER
							wt	2	20/28	3.9067	GAAQNIIPASTGAAK
							wt	2	16/20	3.4336	VVDLM*AYM*ASK
							wt	2	18/26	4.2166	LISWYDNEYGYSNR
			C	3	5	4	ko	2	21/32	4.179	IVSNASCTTNCLAPLAK
							ko	2	24/34	4.492	DGRGAAQNIIPASTGAAK
							ko	2	15/16	2.857	LISEVIGER
							wt	2	22/32	4.27	IVSNASCTTNCLAPLAK
							wt	2	20/34	4.41	DGRGAAQNIIPASTGAAK
							wt	2	15/26	3.061	VPTPNVSVVDLTCR
							wt	2	15/16	2.765	LISEVIGER
							wt	2	15/18	2.591	NYLSSDVEVR
Glycogen phosphorylase	Q8CI94	96,730	A	3	1	1	ko	2	13/14	2.3106	VIFLENYR
							ko	2	12/22	1.8403	VLYPNDNFFEGK
							ko	2	17/22	3.3379	GIAGLGDVAEVR
							wt	2	14/22	2.1458	GIAGLGDVAEVR
			B	2	1	1	ko	2	16/26	2.766	VPTPNVSVVDLTCR
							ko	2	17/22	2.382	GIAGLGDVAEVR
							wt	2	18/22	2.528	GIAGLGDVAEVR
			C	2	1	1	ko	2	15/22	2.425	GIAGLGDVAEVR
							ko	2	15/26	2.651	QAVDQISSGFFSPK
							wt	2	13/16	2.074	YEFGIFNQK
GTP-binding protein Di-Ras2	Q5PR73	22,498	C	1	2	6	ko	2	18/22	2.625	EVQSSEAEALAR
							wt	2	15/22	2.865	EVQSSEAEALAR
							wt	2	18/22	3.69	EVQSSEAEALAR
Guanine deaminase	Q9R111	51,013	A	1	2	3	ko	2	15/16	2.5089	TPPLALVFR
							wt	2	14/16	2.6572	TPPLALVFR
							wt	2	17/20	3.4153	STDVAEEVYTR
			C	2	1	3	ko	2	17/20	3.446	STDVAEEVYTR
			C				ko	2	16/18	2.919	NIEEVYVGGK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
			C				wt	2	17/20	3.67	STDVAEEVYTR
Guanine nucleotide-binding protein subunit beta 4	P29387	37,379	A	1	1	4	ko	2	14/20	2.2952	LIIWDSYTTNK
							wt	2	17/20	3.8901	LIIWDSYTTNK
Heat shock 70 kDa protein 12A	Q8K0U4	74,871	A	4	4	2	ko	2	13/20	2.1729	TPTTILLTPER
							ko	2	16/24	3.0246	GAVLFGLDPAVIK
							ko	2	19/22	3.1228	SPLTYGVGVLNR
							ko	2	19/24	3.1138	TTPSYVAFTDTER
							wt	2	14/20	2.5637	TPTTILLTPER
							wt	2	17/24	3.0038	GAVLFGLDPAVIK
							wt	2	17/22	3.3315	SPLTYGVGVLNR
							wt	2	19/24	3.3328	TTPSYVAFTDTER
			C	4	4	3	ko	2	15/22	3.004	WEGGDPGVSNQK
							ko	2	14/22	2.691	WEGGDPGVSNQK
							ko	2	14/24	2.952	ETAPTSTYSSPAR
							ko	2	16/24	2.435	ETAPTSTYSSPAR
							wt	2	13/20	2.184	TPTTILLTPER
							wt	2	23/26	3.827	LDLTGSGGTAVPAR
							wt	2	15/22	3.173	WEGGDPGVSNQK
							wt	2	14/24	3.096	ETAPTSTYSSPAR
Heat shock 70 kDa protein 4L	P48722	94,382	B	2	2	1	ko	2	16/26	3.289	ELSTTLNADEAVTR
							ko	2	18/24	3.422	VLATAFDTTLGGR
							wt	2	14/26	2.628	AGGIETIANEYSDR
							wt	2	20/24	3.436	VLATAFDTTLGGR
Heat shock 70 kDa protein 5: BiP	P20029	72,422	A	3	6	2	ko	2	15/20	2.861	VEIIANDQGNR
							ko	2	24/30	4.1517	IINEPTAAAIAYGLDK
							ko	2	23/32	3.8788	SQIFSTASDNQPTVTIK
							wt	2	11/16	2.1115	ITITNDQNR
							wt	2	19/20	3.1396	VEIIANDQGNR
							wt	2	15/22	2.4472	DAGTIAGLNVM*R
							wt	2	20/30	3.0335	IINEPTAAAIAYGLDK
							wt	2	17/26	3.0739	ITPSYVAFTPEGER
							wt	2	25/32	4.749	SQIFSTASDNQPTVTIK
			B	2	2	2	ko	2	13/20	2.064	VEIIANDQGNR
							wt	2	18/22	3.264	ADLINNLGTIAK
			C	1	1	2	ko	2	18/20	2.887	VEIIANDQGNR
							wt	2	18/20	3.024	VEIIANDQGNR
Heat shock 70 kDa protein 8	P63017	70,871	A	10	6	2	ko	2	11/14	1.58	GTLDPVEK
							ko	2	13/20	2.4332	NSLESYAFNM*K
							ko	2	20/22	3.6719	DAGTIAGLNVLR
							ko	2	16/26	1.9315	SQIHDIVLVGGSTR
							ko	2	18/20	2.9645	M*KEIAEAYLGK
							ko	2	20/30	3.7155	QATKDAGTIAGLNVLR
							ko	2	14/18	2.7305	VQVEYKGETK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	19/26	3.9681	SFYPEEVSSM*VLTK
							ko	3	30/64	3.5655	LDKSQIHDIVLVGGSTR
							ko	3	34/68	4.7799	TVTNAVVTVPAYFNDSQR
							wt	2	17/22	3.8039	DAGTIAGLNVLR
							wt	2	13/18	2.4063	VQVEYKGETK
							wt	2	17/34	3.163	TVTNAVVTVPAYFNDSQR
							wt	2	15/20	3.213	NSLESYAFNM*K
							wt	2	19/26	3.5906	SQIHDIVLVGGSTR
							wt	3	21/40	3.073	M*KEIAEAYLGK
Heat shock 70 kDa protein 9	P38647	73,528	A	2	3	2	ko	2	14/28	1.6422	NAVITVPAYFNDSQR
							ko	2	17/20	2.9903	VQQTVQDLFGR
							wt	2	17/22	2.8142	AQFEGIVTDLIK
							wt	2	16/22	3.2057	DAGQISGLNVLR
							wt	2	15/20	2.9732	VQQTVQDLFGR
			B	3	3	2	ko	2	15/20	2.634	VQQTVQDLFGR
							ko	2	17/22	3.132	DAGQISGLNVLR
							ko	2	17/26	3.189	TTPSVVAFTADGER
							wt	2	18/22	3.239	DAGQISGLNVLR
							wt	2	14/20	2.748	VQQTVQDLFGR
							wt	2	17/20	3.278	VQQTVQDLFGR
							wt	2	19/26	3.283	TTPSVVAFTADGER
Heat shock cognate 71 kDa	P63017	70,871	B	10	7	2	ko	2	18/22	2.978	DAGTIAGLNVLR
							ko	2	18/22	3.508	DAGTIAGLNVLR
							ko	2	14/16	2.021	LLQDFFNGK
							ko	2	12/20	2.811	NSLESYAFNMK
							ko	2	10/24	2.012	TTPSYVAFTDTER
							ko	2	14/18	2.639	FEELNADLFR
							ko	2	17/24	2.588	TTPSYVAFTDTER
							ko	2	20/26	3.315	SFYPEEVSSMVLTK
							ko	2	22/28	4.061	NQVAMNPTNTVFDAK
							ko	2	18/24	3.241	TTPSYVAFTDTER
							wt	2	18/20	3.316	VAEDETEAGVK
							wt	2	14/18	2.474	FSEDDPEYLR
							wt	2	19/22	3.546	DAGTIAGLNVLR
							wt	2	14/18	3.273	FEELNADLFR
							wt	2	16/24	2.698	TTPSYVAFTDTER
							wt	2	17/24	3.001	TTPSYVAFTDTER
							wt	3	26/68	3.66	TVTNAVVTVPAYFNDSQR
			C	14	15	2	ko	1	10/24	1.829	TTPSYVAFTDTER
							ko	1	10/24	2.31	TTPSYVAFTDTER
							ko	2	14/18	2.769	FEELNADLFR
							ko	2	19/22	4.148	DAGTIAGLNVLR
							ko	2	19/22	3.705	DAGTIAGLNVLR
							ko	2	18/20	3.377	FDDAVVQSDMK
							ko	2	14/18	2.488	VQVEYKGETK
							ko	2	20/22	3.86	DAGTIAGLNVLR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	19/24	3.006	TTPSYVAFTDTER
							ko	2	20/30	4.486	STAGDTHLGGEDFDNR
							ko	2	19/24	2.946	TTPSYVAFTDTER
							ko	2	23/28	4.466	NQVAMNPTNTVFDAK
							ko	3	19/60	2.7	STAGDTHLGGEDFDNR
							ko	3	24/60	2.856	STAGDTHLGGEDFDNR
							wt	2	17/22	3.124	DAGTIAGLNVLR
							wt	2	17/20	2.916	FDDAVVQSDMK
							wt	2	20/22	3.974	DAGTIAGLNVLR
							wt	2	16/22	2.915	DAGTIAGLNVLR
							wt	2	20/22	3.79	DAGTIAGLNVLR
							wt	2	17/22	3.145	DAGTIAGLNVLR
							wt	2	10/16	2.352	EIAEAYLGK
							wt	2	14/18	2.858	FEELNADLFR
							wt	2	16/20	3.653	NSLESYAFNMK
							wt	2	14/18	3.055	VQVEYKGETK
							wt	2	19/30	4.147	STAGDTHLGGEDFDNR
							wt	2	19/24	3.258	TTPSYVAFTDTER
							wt	2	23/28	4.394	NQVAMNPTNTVFDAK
							wt	2	19/24	2.843	TTPSYVAFTDTER
							wt	3	22/60	2.647	STAGDTHLGGEDFDNR
Heat shock protein 60 kDa	P63038	60,955	C	7	9	3	ko	2	13/14	2.697	VGEVIVTK
							ko	2	15/16	2.915	VGLQVVAVK
							ko	2	18/22	2.818	NAGVEGSLIVEK
							ko	2	15/16	2.954	LSDGVAVLK
							ko	2	17/22	3.016	TVIIEQSWGSPK
							ko	2	15/16	3.398	VTDALNATR
							ko	2	18/22	3.008	GYISPYFINTSK
							wt	2	13/14	2.445	VGEVIVTK
							wt	2	15/16	2.725	LSDGVAVLK
							wt	2	15/16	3.377	VTDALNATR
							wt	2	16/22	2.806	TVIIEQSWGSPK
							wt	2	19/22	3.597	NAGVEGSLIVEK
							wt	2	15/16	3.329	VTDALNATR
							wt	2	16/22	2.876	GYISPYFINTSK
							wt	2	16/22	3.585	VGGTSDVEVNEK
							wt	3	27/96	4.266	LVQDVANNTNEEAGDGTTTATVLAR
Heat shock protein HSP 90-alpha	P07901	84,788	A	4	9	2	ko	2	17/22	3.0091	ADLINNLGTIAK
							ko	2	10/18	1.9647	RAPFDLFENR
							ko	2	11/20	2.0275	DQVANSAFVER
							ko	2	20/26	4.0091	GVVDSEDLPLNISR
							wt	2	10/12	2.0585	ALLFVPR
							wt	2	7/12	1.5659	FYEQFSK
							wt	2	13/16	2.9177	YIDQEELNK
							wt	2	13/18	2.8267	RAPFDLFENR
							wt	2	20/26	4.0296	GVVDSEDLPLNISR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	14/20	2.5452	DQVANSAFVER
							wt	2	15/16	2.8428	APFDLFENR
							wt	2	19/28	3.6018	NPDDITNEEYGEFYK
							wt	2	21/24	4.1016	TLTIVDTGIGM*TK
			B	4	3	2	ko	2	15/20	2.548	QLVEADINGLR
							ko	2	12/22	2.389	ELISNSSDALDK
							ko	2	18/22	2.963	ADLINNLGTIAK
							ko	2	18/22	2.973	ADLINNLGTIAK
							wt	2	10/16	2.199	APFDLFENK
							wt	2	15/18	2.718	SIYYITGESK
							wt	2	16/20	2.067	QLVEADINGLR
			C	9	2	2	ko	2	11/12	2.05	FYEAFSK
							ko	2	12/16	2.397	APFDLFENK
							ko	2	18/28	3.986	NPDDITQEEYGEFYK
							ko	2	14/16	3.602	YIDQEELNK
							ko	2	14/22	2.373	ADLINNLGTIAK
							ko	2	16/22	2.996	ELISNSSDALDK
							ko	2	18/22	2.917	ADLINNLGTIAK
							ko	2	19/22	3.054	ADLINNLGTIAK
							ko	2	14/18	3.272	EDQTEYLEER
							wt	2	16/22	3.066	ELISNSSDALDK
							wt	2	15/18	3.068	EDQTEYLEER
Heat shock-related 70 kDa protein 2	P17156	69,741	A	3	3	2	ko	2	22/32	4.4568	IINEPTAAAIAYGLDKK
							ko	2	14/18	2.7005	FEELNADLFR
							ko	3	23/44	3.5482	ARFEELNADLFR
							wt	2	14/22	2.4516	ARFEELNADLFR
							wt	2	14/18	2.7297	FEELNADLFR
							wt	2	17/30	3.7083	STAGDTHLGGEDFDNR
Hemoglobin subunit epsilon-Y2	P02104	16,137	C	2	2	6	ko	2	20/24	2.942	VNSDEVGGEALGR
							ko	2	22/24	3.681	VNSDEVGGEALGR
							wt	2	22/24	3.209	VNSDEVGGEALGR
							wt	2	22/24	3.578	VNSDEVGGEALGR
Hexokinase-1	P17710	108,302	A	1	2	1	ko	2	13/20	2.7394	GAAM*VTAVAYR
							wt	2	12/18	2.6518	FLLSESGSGK
							wt	2	15/20	2.6365	GAAM*VTAVAYR
			C	3	2	1	ko	2	12/14	2.024	ITPELLTR
							ko	2	17/20	2.743	GAALITAVGVR
							ko	2	16/20	2.732	GAAMVTAVAYR
							wt	2	17/20	2.727	GAALITAVGVR
							wt	2	17/20	2.633	GAAMVTAVAYR
Histone protein	P62806	11,367	B	7	4	6	ko	1	8/12	1.549	TLYGFGG
							ko	2	12/18	2.351	ISGLIYEETR
							ko	2	15/18	3.219	ISGLIYEETR
							ko	2	18/22	2.165	TVTAMDVVYALK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	15/18	2.742	ISGLIYEETR
							ko	2	17/18	3.555	ISGLIYEETR
							ko	2	17/18	3.688	ISGLIYEETR
							wt	2	12/18	2.522	ISGLIYEETR
							wt	2	16/18	3.119	ISGLIYEETR
							wt	2	17/18	3.686	ISGLIYEETR
							wt	2	16/18	3.042	ISGLIYEETR
Hydroxysteroid 17-beta dehydrogenase 6	Q9R092	36,103	B	1	2	5	ko	2	19/24	3.051	AVANYDSVEAGEK
							wt	2	18/24	3.097	AVANYDSVEAGEK
							wt	2	15/22	2.483	SGSGEVYQGPAK
Isocitrate dehydrogenase [NAD] subunit alpha	Q9D6R2	39,639	A	2	1	4	ko	2	16/22	2.4234	TPYTDVNIVTIR
							ko	2	17/18	3.4927	IAEFAFEYAR
							wt	2	17/22	3.0472	TPYTDVNIVTIR
LanC-like protein 1	O89112	45,341	C	1	1	4	ko	2	16/22	3.337	SLAENYFDSTGR
							wt	2	15/22	3.136	SLAENYFDSTGR
Large GTP binding protein	P58281	111,339	B	1	2	1	ko	2	15/20	2.841	ALGYFAVVTGK
							wt	2	15/20	2.58	ESVEQQADSFK
							wt	2	15/20	2.37	ALGYFAVVTGK
L-lactate dehydrogenase B chain	P16125	36,572	C	2	1	4	ko	2	16/18	2.302	VTLTPEEEAR
							ko	2	16/18	2.525	VTLTPEEEAR
							wt	2	16/18	2.282	VTLTPEEEAR
Malate dehydrogenase, cytoplasmic	P14152	36,511	A	1	3	4	ko	2	15/22	3.06	FVEGLPINDFSR
							wt	2	13/24	2.7244	DLDVAVLVGSM*PR
							wt	2	14/18	2.4772	GEFITTVQQR
							wt	2	19/22	3.3033	FVEGLPINDFSR
Malate dehydrogenase, mitochondrial	P08249	35,611	A	2	8	4	ko	2	17/20	3.1346	IFGVTTLDIVR
							ko	2	16/30	2.7589	AGAGSATLSM*AYAGAR
							wt	2	14/18	2.7118	M*IAEAIPELK
							wt	2	12/24	2.4636	GYLGPEQLPDCLK
							wt	2	13/16	2.7116	ANTFVAELK
							wt	2	12/18	2.8467	IQEAGTEVVK
							wt	2	17/20	3.516	IFGVTTLDIVR
							wt	2	19/24	4.0899	GCDVVVIPAGVPR
							wt	2	19/22	3.4715	TIIPLISQCTPK
							wt	2	20/26	3.9754	VDFPQDQLATLTGR
Mapsin	P70124	42,111	B	2	1	5	ko	2	23/28	4.033	DVPFGFQTVTSDVNK
							ko	2	16/22	3.018	ILVVNAAYFVGK
							wt	2	17/20	2.365	DVEDESTGLEK
Microtubule-associated protein 1B	P14873	270,411	A	1	1	1	ko	2	16/18	3.0446	AVLDALLEGK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
				1	0	2	ko	2	16/26	3.2631	SVGNTIEPVILFQK
							wt	2	15/26	3.2223	SVGNTIEPVILFQK
Mitochondrial stress-70 protein	P38647	73,528	C	5	6	2	ko	2	15/22	3.217	DAGQISGLNVLR
							ko	2	14/20	2.275	VQQTVQDLFGR
							ko	2	16/20	3.304	VQQTVQDLFGR
							ko	2	20/26	3.51	QAVTNPNNTFYATK
							ko	2	19/26	3.6	TTPSVVAFTADGER
							wt	2	13/20	2.4	VQQTVQDLFGR
							wt	2	16/22	3.767	DAGQISGLNVLR
							wt	2	14/20	3.135	VQQTVQDLFGR
							wt	2	17/20	3.038	VQQTVQDLFGR
							wt	2	16/26	3.373	QAVTNPNNTFYATK
							wt	2	21/26	3.596	TTPSVVAFTADGER
Mu-crystallin	O54983	33,523	B	0	1	4	wt	2	10/16	2.099	QAVLYVDSR
				2	0	2	ko	2	17/18	2.199	FASTVQGDVR
							ko	2	13/16	2.307	QAVLYVDSR
Myelin basic protein	Q62079	26,567	A	3	4	5	ko	1	10/18	1.5529	DTGILDSIGR
				1	5	6	ko	2	12/18	2.3426	DTGILDSIGR
							ko	2	17/22	3.183	TQDENPVVHFFK
							ko	2	14/18	2.6532	DTGILDSIGR
							wt	2	13/18	2.1749	TTHYGSLPQK
							wt	2	11/18	1.9057	FFSGDRGAPK
							wt	2	13/18	2.4625	DTGILDSIGR
							wt	2	16/18	3.4852	DTGILDSIGR
							wt	2	17/18	3.9204	DTGILDSIGR
							wt	3	18/44	2.1562	TQDENPVVHFFK
							wt	3	19/44	3.0369	HRDTGILDSIGR
							wt	3	20/44	3.3997	HRDTGILDSIGR
							wt	3	25/44	3.3762	TQDENPVVHFFK
			B	4	4	4	ko	2	16/18	3.056	DTGILDSIGR
				3	8	5	ko	2	16/18	2.534	DTGILDSIGR
							ko	2	16/18	2.905	DTGILDSIGR
							ko	2	16/20	2.893	GAYDAQGTLSK
							ko	2	15/20	2.834	GAYDAQGTLSK
							ko	2	16/20	2.919	GAYDAQGTLSK
							ko	2	10/18	2.144	TTHYGSLPQK
							wt	2	16/18	2.947	DTGILDSIGR
							wt	2	13/18	2.657	DTGILDSIGR
							wt	2	16/18	2.568	DTGILDSIGR
							wt	2	17/18	3.049	DTGILDSIGR
							wt	2	17/18	2.917	DTGILDSIGR
							wt	2	16/18	2.429	DTGILDSIGR
							wt	2	16/20	3.075	GAYDAQGTLSK
							wt	2	16/20	3.233	GAYDAQGTLSK
							wt	2	16/20	3.24	GAYDAQGTLSK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	16/20	3.147	GAYDAQGTLSK
							wt	2	12/18	2.442	TTHYGSLPQK
							wt	2	12/18	2.392	TTHYGSLPQK
			C	5	3	4	ko	2	12/18	2.538	TTHYGSLPQK
				1	3	5	ko	2	13/18	2.531	DTGILDSIGR
							ko	2	16/18	3.114	DTGILDSIGR
							ko	2	15/18	2.871	DTGILDSIGR
							ko	2	17/18	3.082	DTGILDSIGR
							wt	2	15/18	2.381	DTGILDSIGR
							wt	2	15/18	2.648	DTGILDSIGR
							wt	2	17/18	2.891	DTGILDSIGR
							wt	2	16/18	3.048	DTGILDSIGR
							wt	2	16/18	3.388	DTGILDSIGR
							wt	2	15/18	3.299	DTGILDSIGR
Myelin proteolipid protein	P60202	26,274	C	7	7	6	ko	2	13/20	2.72	LAPEYEAAATR
							ko	1	11/20	1.843	GLSATVTGGQK
							ko	2	17/20	2.681	GLSATVTGGQK
							ko	2	17/20	2.65	GLSATVTGGQK
							ko	2	14/20	2.178	GLSATVTGGQK
							ko	2	18/20	2.97	GLSATVTGGQK
							ko	2	17/20	3.266	GLSATVTGGQK
							wt	1	10/20	1.7	GLSATVTGGQK
							wt	2	17/20	2.278	GLSATVTGGQK
							wt	2	16/20	3.122	GLSATVTGGQK
							wt	2	17/20	2.596	GLSATVTGGQK
							wt	2	17/20	3.028	GLSATVTGGQK
							wt	2	16/20	3.129	GLSATVTGGQK
							wt	2	18/24	3.532	TSASIGSLCADAR
NAD-dependent deacetylase sirtuin-2	Q8VDQ8	43,256	C	1	3	4	ko	2	20/22	3.435	SPSTGLYANLEK
							wt	2	16/24	2.267	NLFTQTLGLGSQK
							wt	2	19/22	3.122	SPSTGLYANLEK
							wt	3	38/92	4.67	EHANIDAQSGSQAPNPSTTISPGK
N-ethylmaleimide sensitive fusion protein	P46460	82,613	B	8	14	2	ko	2	15/18	2.462	YVGESEANIR
							ko	2	16/20	2.973	AENSSLNLIGK
							ko	2	12/20	2.389	NIDSNPYDTDK
							ko	2	17/24	3.179	SQLSCVVVDDIER
							ko	2	17/24	3.492	VLDDGELLVQQTK
							ko	2	19/24	3.718	VLDDGELLVQQTK
							ko	2	15/18	2.32	LLDYVPIGPR
							ko	2	15/20	2.727	NIDSNPYDTDK
							wt	1	10/18	1.612	EEGASPLDFD
							wt	2	16/18	2.932	LFADAEEEQR
							wt	2	16/18	2.54	YVGESEANIR
							wt	2	15/20	2.85	AENSSLNLIGK
							wt	2	17/20	3.264	AENSSLNLIGK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	15/22	2.689	GILLYGPPGCGK
							wt	2	14/18	2.388	LLDYVPIGPR
							wt	2	14/20	2.833	NIDSNPYDTDK
							wt	2	14/18	2.405	LLDYVPIGPR
							wt	2	15/20	2.268	NIDSNPYDTDK
							wt	2	17/24	3.425	VLDDGELLVQQTK
							wt	2	20/24	3.795	SQLSCVVVDDIER
							wt	2	19/24	3.602	VLDDGELLVQQTK
							wt	2	21/24	4.097	SQLSCVVVDDIER
			C	19	20	2	ko	1	8/18	2.03	EEGASPLDFD
							ko	2	12/20	2.855	IAEESNFPFIK
							ko	2	13/20	2.404	DIEAMDPSILK
							ko	2	13/16	2.053	MIGFSETAK
							ko	2	12/20	2.404	IAEESNFPFIK
							ko	2	13/18	2.597	LLDYVPIGPR
							ko	2	16/22	2.802	NFSGAELEGLVR
							ko	2	16/20	2.678	AENSSLNLIGK
							ko	2	16/20	2.509	AENSSLNLIGK
							ko	2	17/20	3.293	AENSSLNLIGK
							ko	2	15/24	2.271	VLDDGELLVQQTK
							ko	2	20/24	3.903	VLDDGELLVQQTK
							ko	2	13/20	2.279	NIDSNPYDTDK
							ko	2	15/20	2.742	NIDSNPYDTDK
							ko	2	18/24	3.68	VLDDGELLVQQTK
							ko	2	14/18	2.928	VVNGPEILNK
							ko	2	14/18	2.387	VVNGPEILNK
							ko	2	15/20	3.101	NIDSNPYDTDK
							ko	2	15/20	2.916	NIDSNPYDTDK
							wt	1	12/24	1.723	VLDDGELLVQQTK
							wt	1	9/18	1.984	EEGASPLDFD
							wt	1	10/18	2.023	EEGASPLDFD
							wt	2	15/18	2.566	LLDYVPIGPR
							wt	2	12/18	2.46	LLDYVPIGPR
							wt	2	16/18	3.183	LFADAEEEQR
							wt	2	18/22	3.6	NFSGAELEGLVR
							wt	2	13/24	2.409	VLDDGELLVQQTK
							wt	2	16/22	2.954	NFSGAELEGLVR
							wt	2	13/20	2.901	IAEESNFPFIK
							wt	2	11/18	2.025	LLDYVPIGPR
							wt	2	15/20	3.221	NIDSNPYDTDK
							wt	2	13/18	2.725	VVNGPEILNK
							wt	2	16/18	2.81	LLDYVPIGPR
							wt	2	15/18	2.665	VVNGPEILNK
							wt	2	17/24	3.68	VLDDGELLVQQTK
							wt	2	21/24	3.619	VLDDGELLVQQTK
							wt	2	18/24	3.841	VLDDGELLVQQTK
							wt	2	15/20	2.824	NIDSNPYDTDK
							wt	2	14/20	3.29	NIDSNPYDTDK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
Neurofascin	Q810U3	137,975	A	1	1	1	ko	2	13/28	2.9524	YVVGQTPVYVPYEIR
							wt	2	16/18	3.2833	DLELTDLAER
Neurofilament protein NF-L	P08551	61,508	B	1	1	3	ko	2	13/18	2.271	LAAEDATNEK
							wt	2	14/18	2.468	LAAEDATNEK
Neuroglycan C	Q71M36	60,419	C	1	1	3	ko	2	18/24	3.028	ETGSAIEAEELVR
							wt	2	19/24	3.355	ETGSAIEAEELVR
Neuroplastin precursor	P97300	31,277	C	1	1	3	ko	2	14/16	2.581	NGVELTATR
							wt	2	14/16	2.78	NGVELTATR
NIPSNAP1 protein	O55125	33,363	C	1	1	4	ko	2	14/16	2.556	AGPNIYELR
							wt	2	14/16	3.098	AGPNIYELR
Nonselenium glutathione peroxidase	O08709	24,871	C	1	1	5	ko	2	17/24	3.581	DINAYNGETPTEK
							wt	2	17/24	4.302	DINAYNGETPTEK
Nucleolin	P09405	76,723	C	3	2	2	ko	2	14/26	2.518	GFGFVDFNSEEDAK
							ko	2	15/16	2.894	NDLAVVDVR
							ko	2	20/24	3.352	TLVLSNLSYSATK
							wt	2	15/16	3.001	NDLAVVDVR
							wt	2	20/24	3.705	TLVLSNLSYSATK
PACSIN	Q61644	50,575	B	0	1	3	wt	2	11/16	2.408	GPQYGSLER
			C	3	1	3	ko	2	12/16	2.468	GPQYGSLER
							ko	3	28/88	3.641	KAEGATLSNATGAVESTSQAGDR
							ko	2	15/18	2.788	NSLLNEDLEK
							wt	2	12/16	2.343	GPQYGSLER
PEA-15	Q62048	15,054	B	0	1	6	wt	2	13/18	2.532	ISEEEELDTK
			C	1	1	6	ko	2	15/18	2.958	ISEEEELDTK
							wt	2	15/18	3.007	ISEEEELDTK
Peanut	Q9Z2Q6	42,748	C	1	1	4	ko	2	18/22	3.896	DVTNNVHYENYR
							wt	2	17/22	3.568	DVTNNVHYENYR
Peroxisomal multifunctional enzyme type 2	P51660	79,482	B	1	1	3	ko	2	20/24	3.305	VVLVTGAGGGLGR
							wt	2	21/24	3.384	VVLVTGAGGGLGR
Plakoglobin	Q02257	81,801	B	9	5	2	ko	2	11/20	2.126	VSVELTNSLFK
							ko	2	14/22	2.185	HPEAEMAQNSVR
							ko	2	17/22	2.651	LLNDEDPVVVTK
							ko	2	15/26	2.558	NEGTATYAAAVLFR
							ko	2	17/20	2.599	VSVELTNSLFK
							ko	2	18/22	3.136	TMQNTSDLDTAR
							ko	2	20/26	3.626	ALMGSPQLVAAVVR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	15/22	2.667	LLNDEDPVVVTK
							ko	2	18/22	3.071	TMQNTSDLDTAR
							wt	2	17/22	2.207	LLNDEDPVVVTK
							wt	2	15/22	2.198	LLNDEDPVVVTK
							wt	2	16/22	2.335	LLNDEDPVVVTK
							wt	2	16/22	2.834	TMQNTSDLDTAR
							wt	2	16/20	2.19	VSVELTNSLFK
Plakophilin-1	P97350	80,896	B	1	1	4	ko	2	15/20	2.486	ELLIIGGVAAR
				0	2	5	wt	2	20/26	3.993	AQSELSGAADEAAR
							wt	2	16/18	2.69	GIVDSITGQR
							wt	2	13/18	2.107	GIVDSITGQR
Plasma membrane calcium-transporting ATPase 2	Q9R0K7	132,588	C	9	11	1	ko	2	22/26	4.213	IDESSLTGESDQVR
							ko	2	19/20	3.388	MVTGDNINTAR
							ko	2	19/20	3.511	MVTGDNINTAR
							ko	2	23/30	4.052	TSPNEGLSGNPADLER
							ko	2	22/32	4.008	QVVAVTGDGTNDGPALK
							ko	2	23/32	4.203	QVVAVTGDGTNDGPALK
							ko	2	18/32	3.518	EASDIILTDDNFSSIVK
							ko	2	20/30	2.746	TSPVEGLPGTAPDLEK
							ko	2	18/26	3.613	IDESSLTGESDQVR
							wt	2	21/30	3.659	TSPNEGLSGNPADLER
							wt	2	18/20	3.036	MVTGDNINTAR
							wt	2	12/14	2.09	FFDIDSGR
							wt	2	23/30	3.575	TSPNEGLSGNPADLER
							wt	2	23/32	4.528	QVVAVTGDGTNDGPALK
							wt	2	23/32	3.771	QVVAVTGDGTNDGPALK
							wt	2	15/20	2.362	GIIDSTHTEQR
							wt	2	18/30	2.857	TSPVEGLPGTAPDLEK
							wt	2	17/30	2.808	TSPVEGLPGTAPDLEK
							wt	2	20/26	2.963	IDESSLTGESDQVR
							wt	2	23/26	3.454	IDESSLTGESDQVR
Profilin II	Q9JJV2	15,032	B	2	3		ko	2	18/26	2.117	SQGGEPTYNVAVGR
							ko	2	17/26	3.015	SQGGEPTYNVAVGR
							wt	2	18/26	2.749	SQGGEPTYNVAVGR
							wt	2	17/26	3.468	SQGGEPTYNVAVGR
							wt	2	19/26	3.638	SQGGEPTYNVAVGR
Proliferation associated gene (pag)	Q60848	95,126	B	3	6	5	ko	2	14/20	2.286	QITVNDLPVGR
							ko	2	12/14	2.189	ADEGISFR
							ko	2	16/18	3.1	LVQAFQFTDK
							wt	2	11/14	2.119	ADEGISFR
							wt	2	12/20	2.285	QITVNDLPVGR
							wt	2	11/14	2.372	GLFIIDDK
							wt	2	15/18	2.7	LVQAFQFTDK
							wt	2	13/20	2.163	QITVNDLPVGR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	12/14	2.17	ADEGISFR
			C	2	3	5	ko	2	14/20	2.434	QITVNDLPVGR
							ko	2	12/14	2.872	ADEGISFR
							wt	2	14/20	2.421	ATAVMPDGQFK
							wt	2	13/20	2.463	QITVNDLPVGR
							wt	2	13/14	2.626	ADEGISFR
Propionyl Coenzyme A carboxylase, alpha	Q91ZA3	79,922	C	8	8	2	ko	2	15/18	2.312	HIEIQVLGDK
							ko	2	11/14	2.056	VYAEDPYK
							ko	2	12/14	2.203	VYAEDPYK
							ko	2	15/28	2.671	VVEEAPSIFLDPETR
							ko	2	15/18	2.31	HIEIQVLGDK
							ko	2	16/28	2.968	AGDTVGEGDLLVELE
							ko	2	19/26	3.069	FSSQEAASSFGDDR
							ko	2	20/28	3.866	VVEEAPSIFLDPETR
							wt	2	11/20	2.048	FLSDVYPDGFK
							wt	2	11/20	2.172	FLSDVYPDGFK
							wt	2	12/14	2.2	VYAEDPYK
							wt	2	13/28	2.545	VVEEAPSIFLDPETR
							wt	2	18/28	3.756	YSSAGTVEFLVDSQK
							wt	2	18/28	2.895	VVEEAPSIFLDPETR
							wt	2	23/26	3.707	FSSQEAASSFGDDR
							wt	2	21/26	3.905	FSSQEAASSFGDDR
Propionyl Coenzyme A carboxylase, beta	Q8CFZ3	58,376	C	4	5	2	ko	2	24/28	5.205	GHQDVEAAQAEYVEK
				4	3	3	ko	3	27/56	3.777	GHQDVEAAQAEYVEK
							ko	2	21/26	4.492	FSSQEAASSFGDDR
							ko	2	15/24	3.506	GFVDDIIQPSSTR
							ko	2	18/24	4.53	GFVDDIIQPSSTR
							ko	2	19/22	2.867	AYGGAYDVMSSK
							ko	2	20/30	5.112	SVTNEDVTQEQLGGAK
							ko	2	18/28	2.516	LVPELDTVVPLESSK
							wt	2	24/28	5.239	GHQDVEAAQAEYVEK
							wt	2	17/26	3.915	DTSYLFITGPEVVK
							wt	2	16/24	3.376	GFVDDIIQPSSTR
							wt	2	16/24	3.902	GFVDDIIQPSSTR
							wt	2	19/22	3.808	AYGGAYDVMSSK
							wt	2	15/28	2.522	LVPELDTVVPLESSK
							wt	2	20/28	2.153	LVPELDTVVPLESSK
							wt	2	21/30	5.273	SVTNEDVTQEQLGGAK
Protein-L-isoaspartate(D-aspartate) O-methyltransferase	P23506	24,634	B	0	1	6	wt	2	14/20	2.305	ELVDDSITNVK
			C	8	15	5	ko	2	14/20	2.067	ELVDDSITNVK
							ko	2	16/20	2.888	ELVDDSITNVK
							ko	2	16/20	2.719	ELVDDSITNVK
							ko	2	16/20	2.888	ELVDDSITNVK
							ko	2	16/20	2.719	ELVDDSITNVK
							ko	2	15/18	2.265	DDPMLLSSGR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	14/20	2.067	ELVDDSITNVK
							ko	3	27/52	3.606	SGGASHSELIHNLR
							wt	1	12/20	1.881	ELVDDSITNVK
							wt	1	11/20	2.344	ELVDDSITNVK
							wt	2	14/20	3.098	ELVDDSITNVK
							wt	2	14/18	2.325	DDPMLLSSGR
							wt	2	16/18	2.345	DDPMLLSSGR
							wt	2	16/20	2.658	ELVDDSITNVK
							wt	2	16/20	2.692	ELVDDSITNVK
							wt	2	16/20	2.692	ELVDDSITNVK
							wt	2	14/18	2.325	DDPMLLSSGR
							wt	2	14/20	3.098	ELVDDSITNVK
							wt	1	12/20	1.881	ELVDDSITNVK
							wt	1	11/20	2.344	ELVDDSITNVK
							wt	2	16/20	2.658	ELVDDSITNVK
							wt	2	16/18	2.345	DDPMLLSSGR
							wt	3	24/52	2.84	SGGASHSELIHNLR
Pyruvate carboxylase	Q05920	129,685	A	2	2	1	ko	2	17/26	3.2876	AEAEAQAEELSFPR
							ko	2	17/28	3.9881	DFTATFGPLDSLNTR
							wt	2	14/22	2.2171	GTPLDTEVPLER
							wt	2	16/28	2.8289	DFTATFGPLDSLNTR
Pyruvate carboxylase			C	17	17	1	ko	1	12/22	1.543	GTPLDTEVPLER
							ko	1	12/22	2.248	GTPLDTEVPLER
							ko	2	12/20	3.066	IAPYVAHNFNK
							ko	2	14/16	2.114	HYFIEVNSR
							ko	2	15/22	2.787	SSSAPVASPNVR
							ko	2	14/16	2.374	ALAVSDLNR
							ko	2	14/20	2.535	PGASLPPLNLK
							ko	2	14/20	2.046	QKADEAYLIGR
							ko	2	17/22	3.055	GTPLDTEVPLER
							ko	2	15/18	2.595	GQIGAPMPGK
							ko	2	14/16	2.764	HYFIEVNSR
							ko	2	15/16	3.345	ADEAYLIGR
							ko	2	19/24	4.187	ADFAQACQDAGVR
							ko	2	16/28	3.392	DFTATFGPLDSLNTR
							ko	2	21/26	4.522	AEAEAQAEELSFPR
							ko	2	19/28	4.272	DFTATFGPLDSLNTR
							ko	2	21/26	4.468	AEAEAQAEELSFPR
							wt	2	13/22	2.192	SPVDSSVLEGVK
							wt	1	14/26	2.775	AEAEAQAEELSFPR
							wt	2	14/16	2.518	ALAVSDLNR
							wt	2	14/22	2.22	SSSAPVASPNVR
							wt	2	14/16	2.585	ALAVSDLNR
							wt	2	11/16	2.565	HYFIEVNSR
							wt	2	15/22	2.594	SSSAPVASPNVR
							wt	2	17/22	2.762	GTPLDTEVPLER
							wt	2	14/16	2.222	HYFIEVNSR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	15/16	3.33	ADEAYLIGR
							wt	2	15/16	3.317	ADEAYLIGR
							wt	2	19/24	4.075	ADFAQACQDAGVR
							wt	2	17/26	3.696	AEAEAQAEELSFPR
							wt	2	18/22	2.781	GTPLDTEVPLER
							wt	2	18/28	3.336	DFTATFGPLDSLNTR
							wt	2	20/28	4.368	DFTATFGPLDSLNTR
							wt	2	21/26	3.718	AEAEAQAEELSFPR
Pyruvate kinase isozymes M1/M2	P52480	57,845	A	2	8	2	ko	2	19/24	3.7415	NTGIICTIGPASR
							ko	2	19/24	3.7415	NTGIICTIGPASR
							wt	2	10/16	1.9551	GDYPLEAVR
							wt	2	10/16	1.9551	GDYPLEAVR
							wt	2	16/20	3.5239	LDIDSAPITAR
							wt	2	16/20	3.5239	LDIDSAPITAR
							wt	2	23/34	4.4042	GADFLVTEVENGGSLGSK
							wt	2	23/34	4.4042	GADFLVTEVENGGSLGSK
							wt	2	19/24	4.1784	NTGIICTIGPASR
							wt	2	19/24	4.1784	NTGIICTIGPASR
			B	1	4	2	ko	2	25/34	4.888	GADFLVTEVENGGSLGSK
							wt	2	13/16	2.599	GDYPLEAVR
							wt	2	18/24	3.397	IYVDDGLISLQVK
							wt	2	20/32	2.923	GVNLPGAAVDLPAVSEK
							wt	2	25/34	4.726	GADFLVTEVENGGSLGSK
			C	3	6	2	ko	2	16/20	2.811	GDLGIEIPAEK
							ko	2	14/16	2.616	GDYPLEAVR
							ko	2	20/32	3.998	GVNLPGAAVDLPAVSEK
							wt	2	20/32	4.079	GVNLPGAAVDLPAVSEK
							wt	2	13/14	2.628	APIIAVTR
							wt	2	19/34	3.933	GADFLVTEVENGGSLGSK
							wt	2	19/24	3.732	NTGIICTIGPASR
							wt	2	15/18	3.009	ITLDNAYMEK
							wt	2	20/34	3.486	GADFLVTEVENGGSLGSK
RNA-binding protein FUS	P56959	52,673	B	1	1	2	ko	2	19/26	2.681	GEATVSFDDPPSAK
							wt	2	19/26	3.085	GEATVSFDDPPSAK
Septin 3	Q9Z1S5	40,038	C	1	1	4	ko	2	11/16	2.346	ADTMTLEEK
							wt	2	12/16	2.453	STLVNTLFK
Septin-11	Q8C1B7	49,695	A	2	2	4	ko	2	15/18	2.9347	SYELQESNVR
							ko	2	16/20	2.2835	STLM*DTLFNTK
							wt	2	11/16	2.4827	VNIIPIIAK
							wt	2	15/18	2.9148	SYELQESNVR
			B	2	1	3	ko	2	15/22	2.526	TIISYIDEQFER
							ko	2	12/20	2.474	ELEEEVSNFQK
							wt	2	16/20	2.843	ELEEEVSNFQK
			C	1	1	3	ko	2	14/16	2.357	VNNFPPLPK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	15/20	3.562	ELEEEVSNFQK
Signal recognition particle 19 kDa protein	Q9D7A6	16,191	C	1	2	7	ko	2	17/20	3.365	ALSQLAEVEEK
							wt	2	15/28	2.469	SGGADPSLQQGEGSK
							wt	2	20/28	3.661	SGGADPSLQQGEGSK
Sodium/potassium-transporting ATPase alpha-1	Q8VDN2	112,982	A	8	17	1	ko	2	18/36	3.126	QGAIVAVTGDGVNDSPALK
							ko	2	14/20	2.367	LNIPVNQVNPR
							ko	2	13/16	2.1066	GIVVYTGDR
							ko	2	39436	2.0983	NM*VPQQALVIR
							ko	2	17/28	2.7441	VDNSSLTGESEPQTR
							ko	2	17/24	3.6451	SPDFTNENPLETR
							ko	2	25/34	5.2473	GVGIISEGNETVEDIAAR
							ko	3	26/76	3.0212	QGAIVAVTGDGVNDSPALKK
							wt	2	10/16	1.9882	GIVVYTGDR
							wt	2	16/20	2.4641	NM*VPQQALVIR
							wt	2	17/20	2.6458	LNIPVNQVNPR
							wt	2	21/28	3.6507	VDNSSLTGESEPQTR
							wt	2	18/24	3.7059	SPDFTNENPLETR
							wt	2	18/34	3.4201	GVGIISEGNETVEDIAAR
							wt	2	14/28	2.5238	VDNSSLTGESEPQTR
							wt	2	18/28	3.448	AVFQANQENLPILKR
							wt	2	24/34	4.6395	GVGIISEGNETVEDIAAR
							wt	2	22/36	3.6632	QGAIVAVTGDGVNDSPALK
							wt	2	21/30	3.9961	ADIGVAM*GIVGSDVSK
							wt	2	25/34	5.4003	GVGIISEGNETVEDIAAR
							wt	2	16/24	3.5296	SPDFTNENPLETR
							wt	2	24/36	4.96	QGAIVAVTGDGVNDSPALK
							wt	2	23/34	4.6915	GVGIISEGNETVEDIAAR
							wt	3	25/64	3.3948	IM*ESFKNM*VPQQALVIR
							wt	2	16/30	2.2659	ADIGVAM*GIAGSDVSK
			C	3	4	1	ko	2	15/18	2.674	TSATWFALSR
							ko	2	16/20	2.553	LNIPVNQVNPR
							ko	3	24/56	2.946	DKYEPAAVSEHGDKK
							wt	2	14/18	2.115	TSATWFALSR
							wt	2	15/18	3.092	TSATWFALSR
							wt	2	14/20	2.648	LNIPVNQVNPR
							wt	2	16/20	3.121	LNIPVNQVNPR
Sodium/potassium-transporting ATPase alpha-2	Q6PIE5	112,217	A	4	0	1	wt	2	14/20	2.233	LNIPVSQVNPR
							wt	2	14/20	2.8992	LNIPVSQVNPR
							wt	2	21/24	3.1833	DTAGDASESALLK
							wt	2	17/24	2.8563	SPEFTHENPLETR
			B	5	1	1	ko	2	14/16	2.428	GIVVYTGDR
							ko	2	14/20	2.318	LNIPVSQVNPR
							ko	2	21/28	4.035	VDNSSLTGESEPQTR
							ko	2	20/24	3.256	AVAGDASESALLK
							ko	2	19/24	3.446	SPDFTNENPLETR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	22/28	3.897	VDNSSLTGESEPQTR
							wt	2	13/16	2.209	GIVVYTGDR
							wt	2	16/26	2.684	AVFQANQENLPILK
							wt	2	19/24	2.942	AVAGDASESALLK
							wt	2	17/24	3.908	SPDFTNENPLETR
							wt	2	19/28	3.637	VDNSSLTGESEPQTR
							wt	2	18/24	3.751	SPDFTNENPLETR
							wt	2	21/34	4.063	GVGIISEGNETVEDIAAR
							wt	2	26/34	4.996	GVGIISEGNETVEDIAAR
							wt	2	16/18	3.092	TSATWFALSR
Sodium/potassium-transporting ATPase alpha-3	Q6PIC6	111,692	A	4	7	1	ko	2	20/24	3.9868	DVAGDASESALLK
							ko	2	24/30	4.8551	ADIGVAM*GIAGSDVSK
							ko	2	13/22	2.0735	IATLASGLEVGK
							ko	2	22/24	4.3393	DVAGDASESALLK
							wt	2	20/28	3.2183	AVFKGGQDNIPVLKR
							wt	2	18/22	3.1739	IATLASGLEVGK
							wt	2	21/24	4.3137	DVAGDASESALLK
							wt	2	21/24	3.9721	DVAGDASESALLK
							wt	2	16/30	2.2659	ADIGVAM*GIAGSDVSK
							wt	2	18/22	3.0323	IATLASGLEVGK
							wt	2	20/28	3.2183	AVFKGGQDNIPVLKR
Sodium/potassium-transporting ATPase beta-2	P14231	33,344	B	1	0	4	ko	2	24/34	4.147	GVGIISEGNETVEDIAAR
			C	3	2	4	ko	2	18/20	3.621	AYGENIGYSEK
							ko	2	15/24	2.332	YNPNVLPVQCTGK
							ko	2	19/26	2.36	VAPPGLTQIPQIQK
							wt	2	19/22	3.444	TIAMDGTEGLVR
							wt	2	17/24	2.278	YNPNVLPVQCTGK
Spectrin alpha chain	Q3URW8	97,906	A	18	43	1	ko	2	15/22	2.2285	GVIDM*GNSLIER
							ko	2	15/20	2.321	WTQLLANSATR
							ko	2	15/16	2.0028	DLTGVQNLR
							ko	2	14/22	2.197	GVIDM*GNSLIER
							ko	2	14/22	2.7512	DVDEIEAWISEK
							ko	2	13/16	2.985	SLQQLAEER
							ko	2	16/28	3.0783	LSDDNTIGQEEIQQR
							ko	2	16/18	2.7469	SSEEIESAFR
							ko	2	17/20	3.3418	DLSSVQTLLTK
							ko	2	11/18	2.0581	LLVSSEDYGR
							ko	2	17/22	3.6582	LGESQTLQQFSR
							ko	2	19/26	3.6159	LAALADQWQFLVQK
							ko	2	15/18	2.6074	SSEEIESAFR
							ko	2	18/20	3.9248	KVEDLFLTFAK
							ko	2	17/20	3.2684	DVTGAEALLER
							ko	2	16/22	3.9518	LGESQTLQQFSR
							ko	2	16/24	3.9312	ENLLEEQGSIALR
							ko	3	27/68	4.6257	DLAALGDKVNSLGETAQR
							wt	1	5/8	1.2098	SLFVN

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	14/16	2.6797	DLTGVQNLR
							wt	2	10/16	1.8054	LLEAQSHFR
							wt	2	10/10	1.4686	FLSDFR
							wt	2	12/16	2.5176	SLQQLAEER
							wt	2	10/16	2.0386	GLVSSDELAK
							wt	2	11/20	1.896	KVEDLFLTFAK
							wt	2	12/16	2.4075	EELYQNLTR
							wt	2	13/18	2.4053	VEDLFLTFAK
							wt	2	17/20	3.1172	DVTGAEALLER
							wt	2	20/28	4.1323	LSDDNTIGQEEIQQR
							wt	2	11/24	1.7879	ELPTAFDYVEFTR
							wt	2	17/20	3.1617	WTQLLANSATR
							wt	2	15/20	2.9424	WTQLLANSATR
							wt	2	13/18	2.3595	LLVSSEDYGR
							wt	2	14/16	2.4723	DLTGVQNLR
							wt	2	16/18	3.2466	SSEEIESAFR
							wt	2	12/16	2.2428	EELYQNLTR
							wt	2	16/22	2.9225	SQLLGSAHEVQR
							wt	2	17/22	3.0152	DVDEIEAWISEK
							wt	2	20/24	3.892	ENLLEEQGSIALR
							wt	2	21/28	4.1995	LSDDNTIGQEEIQQR
							wt	2	16/22	2.8645	GVIDM*GNSLIER
							wt	2	21/34	4.409	SSLSSAQADFNQLAELDR
							wt	2	17/20	3.029	DLSSVQTLLTK
							wt	2	18/20	3.4622	DVTGAEALLER
							wt	2	18/20	4.2942	KVEDLFLTFAK
							wt	2	19/22	4.1663	LGESQTLQQFSR
							wt	2	16/22	3.4896	SQLLGSAHEVQR
							wt	2	16/18	3.3094	SSEEIESAFR
							wt	2	17/22	4.321	LGESQTLQQFSR
							wt	2	21/26	4.2872	LAALADQWQFLVQK
							wt	2	13/24	2.0682	ELPTAFDYVEFTR
							wt	2	27/34	5.41	SSLSSAQADFNQLAELDR
							wt	3	17/32	2.1288	RQEENDKLR
							wt	3	22/44	3.555	M*QHNLEQQIQAR
							wt	3	19/52	2.2745	HQLLEADISAHEDR
							wt	3	23/72	2.4834	LLVSSEDYGRDLTGVQNLR
							wt	3	32/80	2.8097	EAALTNEEVGADLEQVEVLQK
							wt	3	30/80	2.4839	NQALNTDNYGHDLASVQALQR
							wt	3	33/56	4.1482	GRELPTAFDYVEFTR
							wt	3	30/80	3.5836	NQALNTDNYGHDLASVQALQR
							wt	3	30/56	3.1955	GRELPTAFDYVEFTR
							wt	3	34/68	5.0206	DLAALGDKVNSLGETAQR
							wt	3	34/68	4.8697	DLAALGDKVNSLGETAQR
			B	1	16	1	ko	2	17/20	2.924	DLSSVQTLLTK
							wt	2	13/20	2.475	KLLVSSEDYGR
							wt	2	13/20	2.434	DLSSVQTLLTK
							wt	2	20/24	3.838	VNDVCTNGQDLIK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	15/20	2.849	DLSSVQTLLTK
							wt	2	17/20	3.142	ADVVESWIGEK
							wt	2	17/20	2.706	DLSSVQTLLTK
							wt	2	25/34	4.881	SSLSSAQADFNQLAELDR
							wt	2	16/18	2.787	LLVSSEDYGR
							wt	2	17/20	3.216	DLSSVQTLLTK
							wt	2	16/20	2.99	KVEDLFLTFAK
							wt	2	16/22	2.847	LGESQTLQQFSR
							wt	2	16/18	2.45	VEDLFLTFAK
							wt	2	14/18	2.033	GLVSSDELAK
							wt	2	19/24	3.41	CTELNQAWTSLGK
							wt	2	17/20	2.612	LNIPVNQVNPR
							wt	2	13/18	2.166	DLDYYATLLK
Spectrin beta chain	Q62261	274,223	A	16	37	1	ko	2	8/10	1.7446	FREFAR
							ko	2	15/18	3.0842	DQNTVETLQR
							ko	2	8/16	1.8583	DTGNIGQER
							ko	2	13/16	2.1407	VQAVVAVAR
							ko	2	12/10	1.9004	EIGQSVDEVEK
							ko	2	8/16	1.6607	ENEVLEAWK
							ko	2	7/14	1.5124	QLQEDAAR
							ko	2	13/18	2.2823	VLDNAIETEK
							ko	2	14/16	2.3061	LLEVLSGER
							ko	2	13/16	2.2175	VAVVNQIAR
							ko	2	11/18	2.459	VLLLSQDYGK
							ko	2	16/28	2.2402	TLETPAAQM*EGFLNR
							ko	2	21/32	3.3763	SQNIITDSSSLNAEAIR
							ko	2	15/20	2.2581	LVSDGNINSDR
							ko	2	22/26	3.6266	SALPAQSAATLPAR
							ko	3	22/60	2.2802	LQAAYAGDKADDIQKR
							wt	2	9/16	1.6284	ENEVLEAWK
							wt	2	8/16	1.7093	ETWLSENQR
							wt	2	12/18	2.3932	ELALRNELIR
							wt	2	8/12	1.5906	LPEELGR
							wt	2	13/20	2.1581	FM*ELLEPLSER
							wt	2	12/16	1.9684	SLLDACEGR
							wt	2	10/10	1.8844	FREFAR
							wt	2	15/18	2.8985	VLLLSQDYGK
							wt	2	16/18	3.6429	DQNTVETLQR
							wt	2	11/16	1.8009	EAASELLM*R
							wt	2	12/14	2.4923	SAATWDER
							wt	2	12/20	2.4674	QALQDTLALYK
							wt	2	13/16	2.6012	DTGNIGQER
							wt	2	10/12	2.0539	LAGIEER
							wt	2	13/20	2.0102	EIGQSVDEVEK
							wt	2	15/16	3.118	LLEVLSGER
							wt	2	17/36	3.1322	LVSQDNFGFDLPAVEAATK
							wt	2	16/18	3.0496	LTTLELLEVR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	13/20	2.3319	HLLGVEDLLQK
							wt	2	13/16	2.7399	VAVVNQIAR
							wt	2	14/22	2.8062	LSDGNEYLFQAK
							wt	2	16/20	3.5634	DLDDFQSWLSR
							wt	2	11/18	2.5784	VLDNAIETEK
							wt	2	16/20	3.3717	DLM*LWM*EDVIR
							wt	2	19/24	4.1971	EQWANLEQLSAIR
							wt	2	21/26	3.7409	SALPAQSAATLPAR
							wt	2	26/32	5.9811	SQNIITDSSSLNAEAIR
							wt	2	17/20	3.1737	LVSDGNINSDR
							wt	2	23/28	3.9276	TLETPAAQM*EGFLNR
							wt	3	22/72	2.9701	DASVAEAWLLGQEPYLSSR
							wt	3	19/56	2.3199	KHEAIETDIAAYEER
							wt	3	20/72	2.3141	EAEKLESEHPDQAQAILSR
							wt	3	19/44	2.5879	TQILAASYELHK
							wt	3	25/64	3.186	M*HTTFEHDIQALGTQVR
							wt	3	25/76	3.1145	VIESTQDLGNDLAGVM*ALQR
							wt	3	20/76	2.4686	AQTLPTSVVTITSESSPGKR
							wt	3	26/64	3.7389	LPEELGRDQNTVETLQR
			B	4	13	1	ko	2	17/18	3.028	LTTLELLEVR
							ko	2	12/16	2.576	ITDLYTDLR
							ko	2	18/20	2.364	LVSDGNINSDR
							ko	2	17/20	2.559	HLLGVEDLLQK
							wt	2	19/22	3.76	LGESQTLQQFSR
							wt	2	14/16	2.897	LLEVLSGER
							wt	2	16/18	2.865	LTTLELLEVR
							wt	2	15/16	2.713	ITDLYTDLR
							wt	2	15/16	2.769	LLEVLSGER
							wt	2	15/16	3.093	LLEVLSGER
							wt	2	13/18	2.527	VLDNAIETEK
							wt	2	15/18	2.68	DQNTVETLQR
							wt	2	13/16	2.125	VAVVNQIAR
							wt	2	19/26	2.924	FQIQDISVETEDNK
							wt	2	15/16	3.208	ITDLYTDLR
							wt	2	15/20	2.447	HLLGVEDLLQK
							wt	3	29/52	4.445	HQAFEAELHANADR
			C	8	10	1	ko	2	16/20	2.996	DLSSVQTLLTK
							ko	2	18/20	3.383	DVTGAEALLER
							ko	2	17/20	2.905	DVTGAEALLER
							ko	2	14/22	2.372	GVIDMGNSLIER
							ko	2	17/22	3.735	LGESQTLQQFSR
							ko	2	16/18	2.954	DQNTVETLQR
							ko	2	19/20	3.106	LVSDGNINSDR
							ko	2	16/18	3.172	VLDNAIETEK
							wt	2	15/18	2.337	LLVSSEDYGR
							wt	2	16/20	2.918	DLSSVQTLLTK
							wt	2	17/20	3.748	DLSSVQTLLTK
							wt	2	15/18	2.138	GLVSSDELAK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	18/28	2.651	LSDDNTIGQEEIQQR
							wt	2	18/20	2.699	WTQLLANSATR
							wt	2	18/20	2.989	DVTGAEALLER
							wt	2	18/22	3.659	LGESQTLQQFSR
							wt	2	17/18	3.364	DQNTVETLQR
							wt	2	19/20	3.381	LVSDGNINSDR
Synapsin-1	O88935	74,097	A	1	1	2	ko	2	15/22	2.9796	TYATAEPFIDAK
				0	1	3	wt	2	16/22	2.9085	TYATAEPFIDAK
							wt	2	18/22	3.7652	TYATAEPFIDAK
			B	2	2	2	ko	2	16/22	2.25	TYATAEPFIDAK
							ko	2	15/22	2.856	TYATAEPFIDAK
							wt	2	16/22	2.656	TYATAEPFIDAK
							wt	2	18/22	2.472	TYATAEPFIDAK
			C	3	4	2	ko	1	9/14	1.516	SFASLFSD
				3	5	3	ko	2	12/24	2.112	EMLSSTTYPVVVK
							ko	2	17/22	3.311	TYATAEPFIDAK
							ko	2	18/22	3.079	TYATAEPFIDAK
							ko	2	16/22	2.999	TYATAEPFIDAK
							ko	2	17/22	3.723	TYATAEPFIDAK
							wt	1	11/22	1.772	TYATAEPFIDAK
							wt	2	11/12	2.149	MTQALPR
							wt	2	11/12	2.016	MTQALPR
							wt	2	16/22	3.024	TYATAEPFIDAK
							wt	2	15/22	2.685	TYATAEPFIDAK
							wt	2	16/22	2.93	TYATAEPFIDAK
							wt	2	18/24	3.34	EMLSSTTYPVVVK
							wt	2	18/22	3.418	TYATAEPFIDAK
							wt	2	16/22	3.341	TYATAEPFIDAK
Synapsin-2	Q64332	63,373	C	2	1	4	ko	2	22/30	4.488	GSHSQSSSPGALTLGR
							ko	2	24/36	5.149	QTAASAGLVDAPAPSAASR
							wt	2	27/36	4.973	QTAASAGLVDAPAPSAASR
Synaptobrevin 2	P63044	12,691	B	1	4	6	ko	2	19/32	3.736	ADALQAGASQFETSAAK
							wt	2	25/32	4.551	ADALQAGASQFETSAAK
							wt	2	23/32	4.019	ADALQAGASQFETSAAK
							wt	2	22/32	4.225	ADALQAGASQFETSAAK
							wt	3	22/64	2.995	ADALQAGASQFETSAAK
			C	2	1	7	ko	2	21/32	5.067	ADALQAGASQFETSAAK
							ko	3	31/64	4.785	ADALQAGASQFETSAAK
							wt	2	24/32	4.938	ADALQAGASQFETSAAK
Synaptogyrin-3	Q8R191	24,561	A	1	2	5	ko	2	16/22	2.8712	AGAAFDPVSFAR
							wt	1	7/12	1.2603	GYQVPAY
							wt	2	15/22	2.5058	AGAAFDPVSFAR
			B	1	1	5	ko	2	17/22	3.246	AGAAFDPVSFAR
							wt	2	17/22	3	AGAAFDPVSFAR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
Syntaxin-binding protein 1	O08599	67,569	B	2	4	2	ko	2	18/24	2.334	SSASFSTTAVSAR
							ko	2	15/18	2.671	NGITEENLNK
							wt	2	16/18	3.742	ISEQTYQLSR
							wt	2	16/20	2.377	HIAEVSQEVTR
							wt	2	15/24	2.404	LAEQIATLCATLK
							wt	2	19/24	2.25	SSASFSTTAVSAR
T-complex protein 1 subunit alpha A	P11984	60,341	A	1	1	3	ko	2	12/18	2.0931	EQLAIAEFAR
							wt	2	11/18	2.5156	EQLAIAEFAR
T-complex protein 1 subunit beta	P80314	57,477	B	1	1	3	ko	2	17/22	3.53	GATQQILDEAER
							wt	2	17/22	3.297	GATQQILDEAER
T-complex protein 1 subunit delta	Q3TII0	58,084	A	0	2	3	wt	2	23/30	3.5078	ALIAGGGAPEIELALR
							wt	2	23/30	3.5078	ALIAGGGAPEIELALR
			B	1	1	3	ko	2	17/24	2.716	VIDPATATSVDLR
							wt	2	16/24	2.761	VIDPATATSVDLR
T-complex protein 1 subunit gamma; Matricin	P80318	60,630	A	2	2	3	ko	2	16/20	3.1875	AVAQALEVIPR
			A				ko	2	18/20	3.5709	TAVETAVLLLR
			A				wt	2	13/20	2.362	IVLLDSSLEYK
			A				wt	2	14/20	2.7166	AVAQALEVIPR
T-complex protein 1 subunit theta	P42932	59,555	A	5	0	3	ko	2	13/18	2.2412	DVDEVSSLLR
							ko	2	17/18	3.0753	FAEAFEAIPR
							ko	2	17/22	2.9259	LFVTNDAATILR
							ko	2	17/26	1.9555	LVPGGGATEIELAK
							ko	2	21/28	3.7141	AIAGTGANVIVTGGK
			B	2	1	4	ko	2	13/20	2.605	LATNAAVTVLR
							ko	2	16/28	2.945	AIAGTGANVIVTGGK
							wt	2	13/22	2.364	LFVTNDAATILR
			C	1	2	3	ko	2	16/22	2.528	GIDPFSLDALAK
							wt	2	15/18	3.076	FAEAFEAIPR
							wt	2	14/18	3.437	DVDEVSSLLR
Tetraspan TM4SF; Tspan-2	Q922J6	24,181	C	1	1	1	ko	2	13/22	2.473	ESSEQVQPTCPK
							wt	2	14/22	3.503	ESSEQVQPTCPK
Transitional endoplasmic reticulum ATPase	Q01853	89,322	A	3	1	1	ko	2	11/22	1.9688	GVLFYGPPGCGK
							ko	2	39432	2.0566	DVDLEFLAK
							ko	2	18/22	2.992	GILLYGPPGTGK
							wt	2	17/22	3.0965	GILLYGPPGTGK
Triosephosphate isomerase	P17751	26,713	B	1	2	5	ko	2	18/22	2.951	SNVNDGVAQSTR
							wt	2	12/24	2.965	TATPQQAQEVHEK
							wt	2	17/22	2.749	SNVNDGVAQSTR
Triosephosphate isomerase			C	2	2	4	ko	2	14/24	2.928	TATPQQAQEVHEK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	19/24	3.894	IIYGGSVTGATCK
							wt	2	12/20	2.054	LVVVGGGGVGK
							wt	2	15/24	3.172	TATPQQAQEVHEK
Tropomyosin alpha-1 chain	P58771	32,681	A	1	0	3	ko	2	12/18	2.4441	IQLVEEELDR
				5	2	4	ko	2	14/26	2.8698	IQLVEEELDRAQER
							ko	2	15/30	2.9805	AISEELDHALNDM*TSI
							ko	2	17/18	2.8333	IQLVEEELDR
							ko	3	28/56	3.3811	RIQLVEEELDRAQER
							wt	2	17/18	3.2632	IQLVEEELDR
							wt	3	24/56	3.0186	RIQLVEEELDRAQER
Tropomyosin-3	P21107	32,863	A	1	1	6	ko	2	19/24	4.0921	TIDDLEDELYAQK
							wt	2	15/24	2.8846	AADAEAEVASLNR
			B	0	3	6	wt	2	20/24	4.351	LEEAEKAADESER
							wt	3	24/48	3.656	LEEAEKAADESER
							wt	3	23/76	4.415	LATALQKLEEAEKAADESER
Tubulin alpha-1A chain	P68362	50,136	B	10	11	2	ko	2	15/18	2.787	DVNAAIATIK
							ko	2	16/18	2.894	DVNAAIATIK
							ko	2	15/18	2.881	DVNAAIATIK
							ko	2	16/18	3.009	DVNAAIATIK
							ko	2	12/18	2.28	DVNAAIATIK
							ko	2	12/28	2.189	AVFVDLEPTVIDEVR
							ko	2	18/34	2.392	VGINYQPPTVVPGGDLAK
							ko	2	16/18	3.094	DVNAAIATIK
							ko	2	17/34	2.65	VGINYQPPTVVPGGDLAK
							ko	2	22/38	5.027	TIGGGDDSFNTFFSETGAGK
							wt	2	17/18	2.627	DVNAAIAAIK
							wt	2	16/18	2.633	DVNAAIAAIK
							wt	2	17/18	2.763	DVNAAIAAIK
							wt	2	15/18	2.879	DVNAAIATIK
							wt	2	17/18	2.785	DVNAAIATIK
							wt	2	15/18	3.06	DVNAAIATIK
							wt	2	16/18	3.286	DVNAAIATIK
							wt	2	14/18	2.747	DVNAAIATIK
							wt	2	15/18	2.757	DVNAAIATIK
							wt	2	16/18	3.279	DVNAAIATIK
							wt	2	18/34	2.803	VGINYQPPTVVPGGDLAK
			C	22	33	3	ko	1	11/18	2.135	DVNAAIAAIK
							ko	1	11/18	1.731	DVNAAIATIK
							ko	1	11/18	1.778	DVNAAIATIK
							ko	1	11/18	1.806	DVNAAIATIK
							ko	1	12/18	2.538	DVNAAIATIK
							ko	2	15/34	2.054	VGINYQPPTVVPGGDLAK
							ko	2	17/18	2.922	DVNAAIAAIK
							ko	2	12/18	2.186	DVNAAIATIK
							ko	2	15/18	3.121	DVNAAIATIK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	16/18	3.049	DVNAAIAAIK
							ko	2	13/14	2.395	PTYTNLNR
							ko	2	16/18	3.128	DVNAAIATIK
							ko	2	11/14	2.206	PTYTNLNR
							ko	2	14/18	2.957	DVNAAIATIK
							ko	2	13/18	2.618	DVNAAIATIK
							ko	2	16/18	3.159	DVNAAIATIK
							ko	2	16/18	3.107	DVNAAIATIK
							ko	2	16/18	3.437	DVNAAIATIK
							ko	2	16/18	3.104	DVNAAIATIK
							ko	2	16/18	3.336	DVNAAIATIK
							ko	2	14/34	2.647	VGINYQPPTVVPGGDLAK
							ko	3	19/56	2.613	AVFVDLEPTVIDEVR
							wt	1	12/18	2.373	DVNAAIAAIK
							wt	1	7/12	1.503	LSVDYGK
							wt	1	11/18	1.656	DVNAAIATIK
							wt	1	11/18	2.125	DVNAAIATIK
							wt	1	12/18	1.648	DVNAAIATIK
							wt	1	11/18	2.058	DVNAAIAAIK
							wt	1	12/18	2.055	DVNAAIATIK
							wt	1	14/18	1.996	DVNAAIATIK
							wt	1	12/18	2.141	DVNAAIATIK
							wt	2	14/18	2.479	DVNAAIAAIK
							wt	2	13/16	2.477	EIIDPVLDR
							wt	2	15/18	2.505	DVNAAIATIK
							wt	2	16/18	3.039	DVNAAIAAIK
							wt	2	11/14	2.318	PTYTNLNR
							wt	2	16/18	3.01	DVNAAIATIK
							wt	2	16/18	3.179	DVNAAIAAIK
							wt	2	16/18	3.224	DVNAAIAAIK
							wt	2	16/18	3.653	DVNAAIAAIK
							wt	2	17/18	3.351	DVNAAIAAIK
							wt	2	16/38	2.005	TIGGGDDSFNTFFSETGAGK
							wt	2	16/18	3.504	DVNAAIATIK
							wt	2	16/18	2.696	DVNAAIAAIK
							wt	2	16/18	3.172	DVNAAIATIK
							wt	2	17/18	3.308	DVNAAIATIK
							wt	2	16/18	2.968	DVNAAIATIK
							wt	2	15/34	2.314	VGINYQPPTVVPGGDLAK
							wt	2	16/18	3.006	DVNAAIATIK
							wt	2	15/34	2.704	VGINYQPPTVVPGGDLAK
							wt	2	18/34	3.457	VGINYQPPTVVPGGDLAK
							wt	2	20/34	3.041	VGINYQPPTVVPGGDLAK
							wt	2	15/38	3.268	TIGGGDDSFNTFFSETGAGK
							wt	2	20/34	3.268	VGINYQPPTVVPGGDLAK
Tubulin beta 1	Q80ZV2	21,454	A	15	32	4	ko	2	12/38	2.387	TIGGGDDSFNTFFSETGAGK
							ko	2	15/26	2.8395	NLDIERPTYTNLNR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	14/24	2.4897	TIQFVDWCPTGFK
							ko	2	12/16	2.105	EIIDLVLDR
							ko	2	18/28	3.2759	AVFVDLEPTVIDEVR
							ko	2	12/16	2.1616	EIIDLVLDR
							ko	2	13/16	2.1089	EIIDLVLDR
							ko	2	15/18	3.388	DVNAAIATIK
							ko	2	18/30	3.3521	IHFPLATYAPVISAEK
							ko	2	22/28	4.8433	AVFVDLEPTVIDEVR
							ko	2	19/34	3.393	VGINYQPPTVVPGGDLAK
							ko	2	20/28	4.0869	AVFVDLEPTVIDEVR
							ko	2	20/38	3.6376	TIGGGDDSFNTFFSETGAGK
							ko	2	22/32	4.26	AVCM*LSNTTAIAEAWAR
							ko	3	23/56	3.237	AVFVDLEPTVIDEVR
							wt	2	11/14	2.0673	LSVDYGKK
							wt	2	10/30	1.8348	IHFPLATYAPVISAEK
							wt	2	11/20	2.0673	LSVDYGKK
							wt	2	9/12	1.6622	FDLM*YAK
							wt	2	15/16	2.9669	EIIDLVLDR
							wt	2	15/26	2.8325	NLDIERPTYTNLNR
							wt	2	16/34	2.7893	VGINYQPPTVVPGGDLAK
							wt	2	15/18	2.5065	DVNAAIATIK
							wt	2	16/28	2.9232	AVFVDLEPTVIDEVR
							wt	2	13/18	2.2407	DVNAAIATIK
							wt	2	18/34	2.6652	VGINYQPPTVVPGGDLAK
							wt	2	21/28	4.205	AVFVDLEPTVIDEVR
							wt	2	15/34	2.5749	VGINYQPPTVVPGGDLAK
							wt	2	15/18	2.8072	DVNAAIATIK
							wt	2	12/16	2.6196	EIIDLVLDR
							wt	2	18/28	3.2887	AVFVDLEPTVIDEVR
							wt	2	15/16	2.8187	EIIDLVLDR
							wt	2	15/18	3.0306	DVNAAIATIK
							wt	2	16/18	2.5734	DVNAAIATIK
							wt	2	21/28	4.1293	AVFVDLEPTVIDEVR
							wt	2	18/24	3.1688	TIQFVDWCPTGFK
							wt	2	17/18	3.9988	DVNAAIATIK
							wt	2	17/38	3.4816	TIGGGDDSFNTFFSETGAGK
							wt	2	21/34	3.5442	VGINYQPPTVVPGGDLAK
							wt	2	19/38	3.8348	TIGGGDDSFNTFFSETGAGK
							wt	2	15/22	2.1822	QLFHPEQLITGK
							wt	2	24/32	5.2467	AVCM*LSNTTAIAEAWAR
							wt	2	22/38	4.754	TIGGGDDSFNTFFSETGAGK
							wt	3	27/60	3.4395	IHFPLATYAPVISAEK
							wt	3	29/80	3.9176	QLFHPEQLITGKEDAANNYAR
							wt	3	27/60	3.8346	GDVVPKDVNAAIATIK
Tubulin beta-2A chain	Q99J49	34,001	C	1	2	2	ko	2	13/16	2.06	YLTVATVFR
							wt	2	14/16	2.324	YLTVATVFR
							wt	2	14/16	2.351	YLTVATVFR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
Tubulin beta-3 chain	Q9ERD7	50,419	A	0	1	1	ko	2	14/20	2.1141	KLAVNM*VPFPR
							ko	2	13/16	2.2097	YLTVATVFR
							ko	2	20/28	3.4975	ALTVPELTQQM*FDAK
							ko	2	18/26	3.3407	NSSYFVEWIPNNVK
							ko	2	16/18	3.2406	LAVNM*VPFPR
							ko	2	16/18	3.0089	LAVNMVPFPR
							ko	2	21/28	3.9593	AILVDLEPGTM*DSVR
							wt	2	14/28	3.1871	AILVDLEPGTMDSVR
							wt	2	16/20	2.5093	FPGQLNADLRK
							wt	2	14/26	2.53	NSSYFVEWIPNNVK
							wt	2	18/28	2.9169	ALTVPELTQQM*FDAK
							wt	2	12/20	2.3568	KLAVNM*VPFPR
							wt	2	14/28	2.6584	ALTVPELTQQM*FDAK
							wt	2	14/16	2.98	VAVCDIPPR
							wt	2	15/18	2.8445	FPGQLNADLR
							wt	2	20/28	3.3845	ALTVPELTQQM*FDAK
							wt	2	16/18	3.2323	LAVNM*VPFPR
							wt	2	14/16	3.1715	YLTVATVFR
							wt	2	13/18	2.8337	LAVNM*VPFPR
							wt	2	15/26	3.0388	NSSYFVEWIPNNVK
							wt	2	20/26	4.1605	NSSYFVEWIPNNVK
							wt	2	15/18	3.3951	LAVNMVPFPR
							wt	2	20/28	4.139	AILVDLEPGTM*DSVR
							wt	2	15/18	2.9675	LAVNM*VPFPR
							wt	2	18/22	3.7962	IM*NTFSVVPSPK
Tubulin beta-4 chain	Q9D6F9	49,586	A	8	10	4	ko	2	13/16	2.0644	TAVCDIPPR
							ko	2	13/16	2.0644	TAVCDIPPR
							ko	2	15/16	2.629	YLTVAAVFR
							ko	2	15/16	2.629	YLTVAAVFR
							ko	2	19/30	3.2862	INVYYNEATGGNYVPR
							ko	2	19/30	3.2862	INVYYNEATGGNYVPR
							ko	2	18/28	3.7216	AVLVDLEPGTM*DSVR
							ko	2	18/28	3.7216	AVLVDLEPGTM*DSVR
							wt	2	15/16	2.73	TAVCDIPPR
							wt	2	15/16	2.73	TAVCDIPPR
							wt	2	15/16	3.3898	YLTVAAVFR
							wt	2	15/16	3.3898	YLTVAAVFR
							wt	2	23/30	4.2184	INVYYNEATGGNYVPR
							wt	2	23/30	4.2184	INVYYNEATGGNYVPR
							wt	2	20/28	3.9356	AVLVDLEPGTM*DSVR
							wt	2	20/28	3.9356	AVLVDLEPGTM*DSVR
							wt	2	20/28	4.0911	AVLVDLEPGTMDSVR
							wt	2	20/28	4.0911	AVLVDLEPGTMDSVR
Tubulin beta-5 chain	P99024	49,671	B	2	4	3	ko	2	15/16	2.154	TAVCDIPPR
							ko	2	17/18	3.22	LAVNMVPFPR

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							wt	2	14/18	2.706	FPGQLNADLR
							wt	2	14/16	2.18	YLTVAAVFR
							wt	3	24/40	2.818	FPGQLNADLRK
							wt	2	18/28	2.89	AVLVDLEPGTMDSVR
			C	10	14	4	ko	2	12/22	2.288	IMNTFSVVPSPK
							ko	2	14/16	2.77	TAVCDIPPR
							ko	2	13/18	2.556	FPGQLNADLR
							ko	2	17/18	3.082	FPGQLNADLR
							ko	2	17/18	2.939	FPGQLNADLR
							ko	2	15/22	3.373	IMNTFSVVPSPK
							ko	2	17/18	3.583	LAVNMVPFPR
							ko	2	15/16	2.578	NMMAACDPR
							ko	2	17/18	3.199	LAVNMVPFPR
							ko	2	19/22	3.81	EVDEQMLSVQSK
							wt	2	17/22	3.148	IMNTFSVVPSPK
							wt	2	16/18	3.029	FPGQLNADLR
							wt	2	16/18	2.993	FPGQLNADLR
							wt	2	14/18	2.636	LAVNMVPFPR
							wt	2	19/22	3.78	IMNTFSVVPSPK
							wt	2	15/16	2.515	TAVCDIPPR
							wt	2	18/22	4.204	IMNTFSVVPSPK
							wt	2	16/28	3.043	AVLVDLEPGTMDSVR
							wt	2	15/18	2.718	LAVNMVPFPR
							wt	2	17/18	3.107	LAVNMVPFPR
							wt	2	13/16	2.15	NMMAACDPR
							wt	2	15/18	2.566	LAVNMVPFPR
							wt	2	19/22	3.909	EVDEQMLSVQSK
							wt	2	19/22	3.482	EVDEQMLSVQSK
Vacuolar ATP synthase subunit A	P50516	68,326	A	3	3	3	ko	2	11/16	2.24	GVNVSALSR
							ko	2	13/28	2.439	TALVANTSNM*PVAAR
							ko	2	18/32	4.2164	LAEM*PADSGYPAYLGAR
							wt	2	14/16	2.6456	GVNVSALSR
							wt	2	14/32	2.2053	LAEM*PADSGYPAYLGAR
							wt	3	24/64	4.2541	IKADYAQLLEDM*QNAFR
Vacuolar ATP synthase subunit B	P62814	56,551	A	4	3	4	ko	2	13/20	2.1076	SGQVLEVSGSK
							ko	2	13/18	1.9866	TPVSEDM*LGR
							ko	2	14/22	2.5875	IPQSTLSEFYPR
							ko	2	16/22	2.8117	IPQSTLSEFYPR
							wt	2	14/20	3.0022	NFITQGPYENR
							wt	2	14/22	2.5967	IPQSTLSEFYPR
							wt	2	22/28	4.4745	AVVQVFEGTSGIDAK
			B	1	2		ko	2	18/28	3.049	AVVQVFEGTSGIDAK
							wt	2	19/28	3.036	AVVQVFEGTSGIDAK
							wt	2	21/28	3.694	AVVQVFEGTSGIDAK
Vesicle-fusing ATPase	P46460	82,613	A	6	10	3	ko	2	15/20	2.6393	IAEESNFPFIK

protein name	Swiss-Prot acc. no.	protein mass (Da)	data set	matched peptides		slice no.	sample	charge state	ions	Xcorr	assigned sequence
				ko	wt						
							ko	2	17/24	3.3908	VLDDGELLVQQTK
							ko	2	18/24	4.0325	VLDDGELLVQQTK
							ko	2	17/22	3.018	NFSGAELEGLVR
							ko	2	13/24	2.8628	SQLSCVVVDDIER
							ko	2	14/20	2.9104	IAEESNFPFIK
							wt	2	15/20	2.5738	IAEESNFPFIK
							wt	2	16/18	2.8322	LLDYVPIGPR
							wt	2	14/18	3.1046	KLLIIGTTSR
							wt	2	14/20	2.6587	IAEESNFPFIK
							wt	2	18/22	3.1195	NFSGAELEGLVR
							wt	2	17/24	2.9614	VLDDGELLVQQTK
							wt	2	20/24	4.3509	VLDDGELLVQQTK
							wt	2	19/22	3.7818	NFSGAELEGLVR
							wt	2	20/24	3.5765	SQLSCVVVDDIER
							wt	3	24/60	3.725	TPLVSVLLEGPPHSGK

Supplementary Table 3: Proteins identified by LC-ESI-MS/MS in samples originating from both wild-type and α7 nAChR knockout mice. The columns indicate the Swiss-Prot accession number (acc. no), protein mass in Daltons (Da), whether the peptide was identified in data set A, B, or C (data set), the number of matched peptides in either wild type (wt) or α7 nAChR knockout (ko) mouse brain samples, the gel slice from which the peptide originated, whether the peptide was identified originated in the wild-type (wt) or knockout (ko) sample, the charge state of the ion, the number of ions identified/the maximum number of ions (ions), the Xcorr value, and the assigned amino acid sequence. M*, oxidized methionine residue.

Supplementary Table 4:

Protein	Swiss-Prot acc. no	Sub-cellular locations	Function
Basic metabolic proteins			
Adenylyl cyclase-associated protein 2	Q9CYT6	Membrane, multi-pass	Member of CAP family, Binds actin.
Aldehyde dehydrogenase, mitochondrial	P47738	Mitochondrion matrix	Conversion of retinaldehyde to retinoic acid.
Glutathione S-transferase Mu 1	P10649	Cytoplasm	Conjugation of reduced glutathione to exogenous and endogenous hydrophobic electrophiles
L-lactate dehydrogenase A chain	P06151	Cytoplasm	Fermentation of pyruvate to lactate.
Myristoylated alanine-rich C-kinase substrate (MARCKS)	P26645	Membrane, lipid-anchor; Cytoplasm, cytoskeleton	Cellular substrate for protein kinase C. Binds calmodulin, actin, and synapsin.
Protein disulfide-isomerase A3	P27773	Endoplasmic reticulum	Catalyzes the rearrangement of -S-S- bonds in proteins.
Probable oxidoreductase KIAA1576	Q80TB8	Cytoplasm	Oxidoreductase.
Vacuolar proton translocating ATPase A isoform 1	Q9Z1G4	Cytoplasmic vesicle membrane	Required for assembly and activity of the vacuolar ATPase.
Cell structure and protein trafficking			
Alpha-catenin 2	Q61301	Cytoplasm, cytoskeleton	Cell-cell adhesion protein.
Ankyrin 2, isoform 1	Q6PCN2	Cytoplasm	Regulation of apoptosis.
Ankyrin 2, isoform 2	Q8C8R3	Cytoplasm	Regulation of apoptosis.
AP-2 complex subunit beta-1	Q9DBG3	Cell membrane.	Component of the adaptor complexes which link clathrin to receptors in coated vesicles.
AP-3 complex subunit beta-2	Q9JME5	Golgi; Cytoplasmic vesicle	Plays a role in protein sorting in the late-Golgi/trans-Golgi network.
Brain acid soluble protein 1; BASP1, NAP-22	Q91XV3	Membrane protein	Involved in cell projection and neuronal growth cones.
Endophilin-1	Q62420	Cytoplasm; Peripheral membrane protein	Implicated in synaptic vesicle endocytosis.
Endophilin-2	Q62419	Cytoplasm; Peripheral membrane protein	Implicated in endocytosis.
Fascin	Q61553	Cytoplasm	Organizes filamentous actin into bundles, associates with beta-catenin.
Gamma-soluble NSF attachment protein	Q9CWZ7	Peripheral membrane protein	Vesicular transport between the endoplasmic reticulum and the Golgi apparatus.
Homer protein homolog 1	Q9Z2Y3	Cytoplasm, synapse; Postsynaptic cell membrane	Postsynaptic density scaffolding protein, involved in neuronal plasticity, Ca++ channel regulator.
Kinesin-like protein KIF2	P28740	Cytoplasm	Plus end-directed microtubule-dependent motor, regulate microtubule dynamics during axonal growth.
Microtubule-associated protein tau	P10637	Cytoplasm; Peripheral membrane protein	Promotes axonal microtubule assembly and stability.
Myosin-VI	Q64331	Golgi; Cytoplasm; Peripheral membrane protein	Vesicular membrane trafficking and cell migration.
Nck-associated protein 1	P28660	Cell membrane, cell projection	Member of the lamellipodial complex that controls Rac-dependent actin remodeling.
Spectrin beta chain	P15508	Cytoplasm, cytoskeleton	The major constituent of the cytoskeletal network.
Synaptogyrin-1	O55100	Membrane protein, multi-pass	Associated with presynaptic vesicles and signal transmission.
Synaptojanin-1	Q8CHC4	Cytoplasm	Lipid phosphatase involved in lipid uncoating of vesicles in neurons.
Syntaxin-1A	O35526	Membrane	Involved in docking of synaptic vesicles at presynaptic active zones, neurotransmitter exocytosis.
Syntaxin-1B	O35525	Membrane	Involved in docking of synaptic vesicles at presynaptic active zones, neurotransmitter exocytosis.
Tropomodulin-2	Q9JKK7	Cytoplasm	Binds to the N-terminus of tropomyosin and to actin.
Chaperones			
14-3-3 protein beta/alpha	Q9CQV8	Cytoplasm	Adapter protein implicated in the regulation of general and specialized signaling pathway.
14-3-3 protein eta	P68510	Cytoplasm	Adapter protein implicated in the regulation of general and specialized signaling pathway.
14-3-3 sigma	O70456	Cytoplasm	Adapter protein implicated in the regulation of general and specialized signaling pathway.
Gelsolin Actin-depolymerizing factor Brevin	P13020	Cytoplasm, cytoskeleton	Calcium-regulated, actin-modulating protein that binds to the plus ends of actin.
Heat shock protein HSP 90-beta	P11499	Cytoplasm	Molecular chaperone. Has ATPase activity.
Proteolytic pathway proteins			
Ubiquitin carboxyl-terminal hydrolase 5	P56399	Cytoplasm	Cleaves linear and branched multiubiquitin polymers
Ubiquitin-activating enzyme E1	Q02053	Cytoplasm	Activator in ubiquitin protein degradation pathway.
Signal transduction			
Calmodulin	P62204	Cytoplasm	Mediates the control of a large number of enzymes and other proteins by Ca++ binding.
cAMP-dependent protein kinase, PKA	P68181	Cytoplasm	Mediates cAMP-dependent signaling triggered by receptor binding to GPCRs.
Clathrin coat assembly protein AP180 (SNAP91)	Q61548	Membrane	Believed to interact with the cytoplasmic tails of membrane proteins
Contactin-1	P12960	Membrane, lipid-anchor	Mediates cell surface interactions during nervous system development.

Protein	Swiss-Prot acc. no	Sub-cellular locations	Function
Guanine nucleotide-binding protein alpha-12 subunit	P27600	Membrane, lipid-anchor	Modulators or transducers in various transmembrane signaling systems.
Guanine nucleotide-binding protein G(i), alpha-2 subunit	P08752	Membrane, lipid-anchor	Involved in hormonal regulation of adenylate cyclase.
Guanine nucleotide-binding protein G(q) subunit alpha	P21279	Membrane, lipid-anchor	Modulator or transducer in various transmembrane signaling systems.
Mitsugumin-23	Q3UBX0	Endoplasmic reticulum membrane	Widely distributed protein may play a role in mediating protein-protein interactions.
Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta 3	Q61011	Membrane, lipid-anchor	Modulator or transducer in various transmembrane signaling systems.
Guanine nucleotide-binding protein G(o) subunit alpha 1	P18872	Membrane, lipid-anchor	Modulator or transducer in various transmembrane signaling systems.
Neuromodulin (GAP-43)	P06837	Peripheral membrane protein, axononal	Located in growth cone, bind calmodulin with greater affinity in absence of Ca++.
Phosphatase 2A inhibitor, TAF-1, SET	Q9EQU5	Cytoplasm; Endoplasmic reticulum	Multitasking protein, involved in apoptosis, transcription, nucleosome assembly and histone binding.
Protein kinase C gamma type	P63318	Cytoplasm	Calcium-activated, phospholipid-dependent, serine- and threonine-specific enzyme.
Protein phosphatase 1 regulatory subunit 7	Q3UM45	Nucleus	Regulatory subunit of protein phosphatase 1.
Ras-related protein Rab-2A	P53994	Endoplasmic reticulum; Golgi	Required for protein transport from the endoplasmic reticulum to the Golgi complex.
Serine/threonine-protein phosphatase 2B catalytic	P63328	Nucleus	Calcium-dependent, calmodulin-stimulated protein phosphatase.
Serine/threonine-protein phosphatase PP1-alpha	P62137	Cytoplasm	Regulation of glycogen metabolism, muscle contractility and protein synthesis.
Tenascin-R	Q8BYI9	Neural extracellular matrix (ECM) protein	Evokes a stable adhesion and differentiation, or repulsion and inhibition of neurite growth.
Transgelin-3	Q9R1Q8	Cytoplasm	Actin cross linker, binds calcium.

Supplementary Table 4: Sub-cellular location and function of proteins listed in Table 1. Information on sub-cellular location and function was obtained from the Swiss-Prot (http://ca.expasy.org/sprot/) and NCBI databases (http://www.ncbi.nlm.nih.gov/).