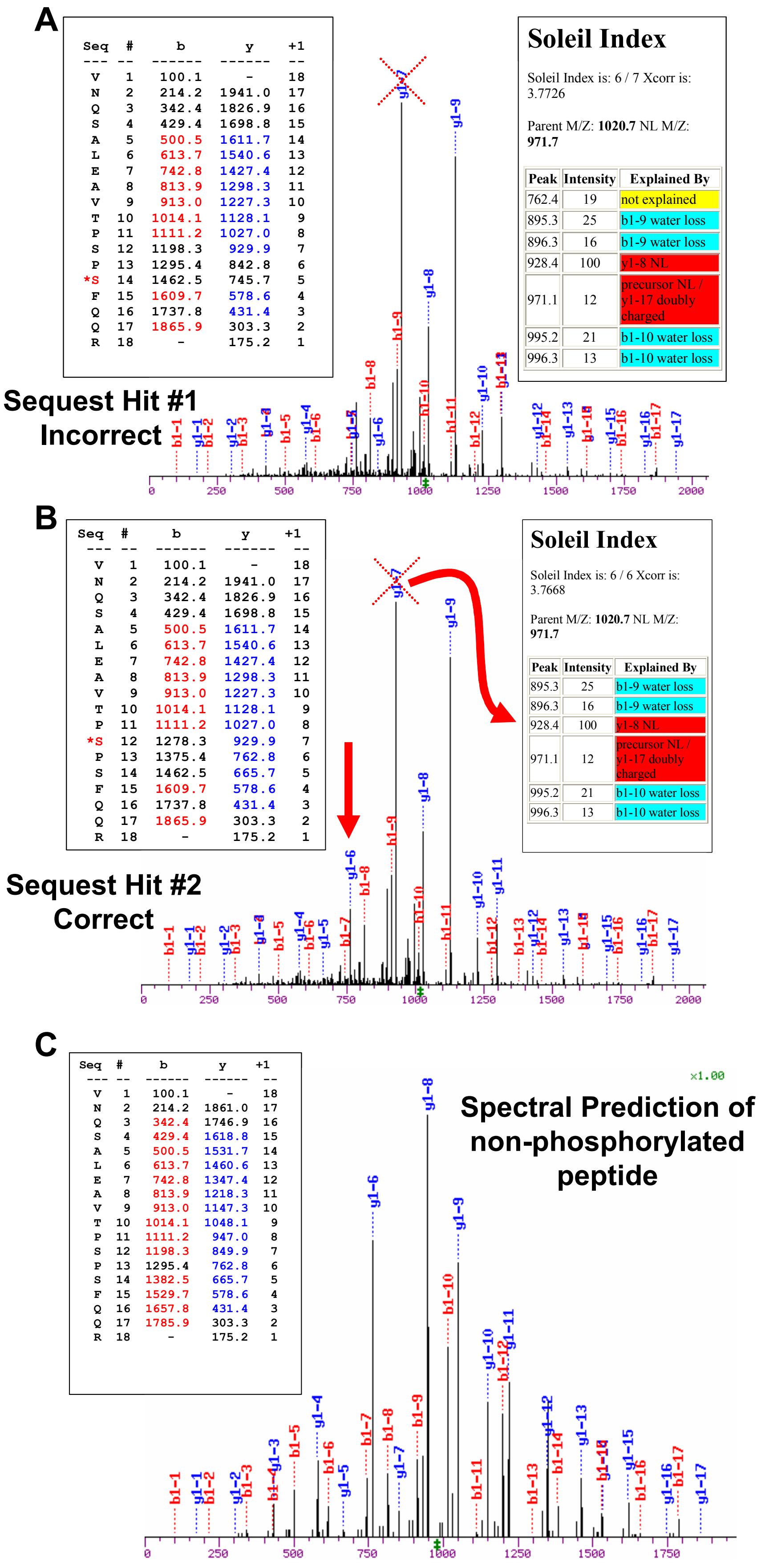
Supplementary Table 1.**Phosphoproteomic planning for studies involving mammalian cells.** Roughly 10-100fmol of most peptides is required for detection and fragmentation analysis in standard mass spectrometers. For a protein of 50kDa, 1fmol of protein is approximately 50pg. To achieve 10-100fmol (and thus 10-100fmol of an internal peptide) requires 0.5-5ng of the same 50kDa protein. Early studies have calculated the number and relative abundance of mRNA molecules in mammalian cells. The numbers reproduced here are averaged from values obtained from liver, kidney and brain mRNA (Hastie, N.D. and Bishop, J.O., 1976, *Cell* 9:761-764). Importantly, rare mRNAs represent as much as 95% of unique message expressed per cell. Whereas the relative abundance of any one protein is not always proportional to message levels, the wide range in protein expression levels appears to be consistent with that found at the mRNA level (Greenbaum D. et al, 2002, *Bioinformatics* 18:585-96; Greenbaum D. et al, 2003, *Genome Biology* 9:117). Thus, roughly defining proteins to be of equal size, and assuming no losses in yield and a relatively high phosphorylation stoichiometry of 10%, phosphoproteomic studies will be most successful as starting material approaches 1mg. However, phosphorylation stoichiometries may fall well below 10% and sample losses may be more or less anticipated, making high milligram amounts of starting material much more desirable.

mRNA Class	**#Unique mRNAs**	**Unique/ Total unique (%)**	**Copies unique**	**Copies unique (x) #Unique**	**Copies unique/ Total unique (%)**	**Unique protein/ 1mg extract**	**Unique Phosphoprotein at 10% Stoichiometry/ 1mg extract**
Abundant	6	0.05	12,296	73,776	2.700	27μg	2.7μg
Intermediate	595	4.94	276	164,220	0.061	0.61μg	0.061μg
Rare	**11,437**	**95.01**	**19**	**217,303**	**0.004**	**0.04μg**	**0.004μg**
Total	12,038	100		455,299			

Ballif *et al.* Supplementary Figure 1



A

Seq	#	b	y	+1
V	1	100.1	-	18
N	2	214.2	1941.0	17
Q	3	342.4	1826.9	16
S	4	429.4	1698.8	15
A	5	500.5	1611.7	14
L	6	613.7	1540.6	13
E	7	742.8	1427.4	12
A	8	813.9	1298.3	11
V	9	913.0	1227.3	10
T	10	1014.1	1128.1	9
P	11	1111.2	1027.0	8
S	12	1198.3	929.9	7
P	13	1295.4	842.8	6
*S	14	1462.5	745.7	5
F	15	1609.7	578.6	4
Q	16	1737.8	431.4	3
Q	17	1865.9	303.3	2
R	18	-	175.2	1

Soleil Index

Soleil Index is: 6 / 7 Xcorr is: 3.7726

Parent M/Z: **1020.7** NL M/Z: **971.7**

Peak	Intensity	Explained By
762.4	19	not explained
895.3	25	b1-9 water loss
896.3	16	b1-9 water loss
928.4	100	y1-8 NL
971.1	12	precursor NL / y1-17 doubly charged
995.2	21	b1-10 water loss
996.3	13	b1-10 water loss

B

Seq	#	b	y	+1
V	1	100.1	-	18
N	2	214.2	1941.0	17
Q	3	342.4	1826.9	16
S	4	429.4	1698.8	15
A	5	500.5	1611.7	14
L	6	613.7	1540.6	13
E	7	742.8	1427.4	12
A	8	813.9	1298.3	11
V	9	913.0	1227.3	10
T	10	1014.1	1128.1	9
P	11	1111.2	1027.0	8
*S	12	1278.3	929.9	7
P	13	1375.4	762.8	6
S	14	1462.5	665.7	5
F	15	1609.7	578.6	4
Q	16	1737.8	431.4	3
Q	17	1865.9	303.3	2
R	18	-	175.2	1

Soleil Index

Soleil Index is: 6 / 6 Xcorr is: 3.7668

Parent M/Z: **1020.7** NL M/Z: **971.7**

Peak	Intensity	Explained By
895.3	25	b1-9 water loss
896.3	16	b1-9 water loss
928.4	100	y1-8 NL
971.1	12	precursor NL / y1-17 doubly charged
995.2	21	b1-10 water loss
996.3	13	b1-10 water loss

C

Seq	#	b	y	+1
V	1	100.1	-	18
N	2	214.2	1861.0	17
Q	3	342.4	1746.9	16
S	4	429.4	1618.8	15
A	5	500.5	1531.7	14
L	6	613.7	1460.6	13
E	7	742.8	1347.4	12
A	8	813.9	1218.3	11
V	9	913.0	1147.3	10
T	10	1014.1	1048.1	9
P	11	1111.2	947.0	8
S	12	1198.3	849.9	7
P	13	1295.4	762.8	6
S	14	1382.5	665.7	5
F	15	1529.7	578.6	4
Q	16	1657.8	431.4	3
Q	17	1785.9	303.3	2
R	18	-	175.2	1

Supplementary Fig. 1. **Manual validation assists phosphorylation site identification**. A phosphopeptide is shown where manual validation finds the second Sequest hit correctly identifying the site of phosphorylation. In house software tools (Soleil Index) assisted in understanding peaks unassigned by Sequest. Further confidence of peptide identification may be obtained using a spectral prediction program (D. Schwartz, M. Chou and S. Gygi, manuscript in preparation) of the non-phosphorylated peptide. Note the prediction of the intense y9 and y6 peaks and the prediction of the weak y7 peak.

Comparisons of MS/MS data using a synthetic version of each phosphopeptide would provide an additional level of confidence. For large datasets this may become unwieldy. To be confident of the phosphorylation site assignment, we have therefore started with the very conservative Sequest Xcorr scores of 2.5 and 3.3 for doubly and triply charged phosphopeptide ions respectively. Further confidence of the assignments in this dataset is derived from the fact that the predicted solution charge states of the phosphopeptides are consistent with their observed elution from the SCX column (Fig. 3), and the predicted molecular weight range of their corresponding protein is in good agreement with the gel band from which they originated. We anticipate that instruments capable of increased mass accuracy will be important tools in future phosphoproteomic studies, permitting high confidence in phosphorylation site assignments, even when search algorithms give low scores.

Ballif *et al.* Supplementary Figure 2

Mode 1 (**R**XX**S**X**P**)

```
Hypothetical Protein RIKEN clone:B930032I08
Query: RAEPHSEDDSRDAsPPEPASPTIGLDKKTRRKF
Sbjct: RAEPHSEDDSRDASPPEPASPTIGLDKKTRRKF   gi|28557802|ref|NP_777580.1| [Homo sapiens]
Sbjct: RAEPHSEDDSRDASPPEPASPTIGLDKKTRRKF   gi|34873458|ref|XP_220885.2| [Rattus norvegicus]
Sbjct:      SKDDSRDASPPEPASPTIGLDKKTRRKF   gi|30911133|gb|AC136964.2|   [Sus scrofa]*

Hypothetical Protein mKIAA1761 protein
Query: EDSIKVIRNMRAAsPPASASDLIEQQQ---------KRG-RREHKALI
Sbjct: EDSIKVIRNMRAASPPASASDLIEQQQ---------KRG-RREHKALI gi|12698067|dbj|BAB21852.1|  [Homo sapiens]
Sbjct: EDSIKVIRNMRAASPPASASDLIEQQQ---------KRG-RREHKALI gi|34859791|ref|XP_342312.1| [Rattus norvegicus]
Sbjct: EDSIKVIRNMRAASPPASASDLIEQQQ---------KRG-RREHKALI gi|11041493|dbj|BAB17283.1|  [Macaca fascicularis]
Sbjct: EDSIRVIRSMRAASPPASASDLIEQQQ---------KRA-RREHKGLI gi|47229634|emb|CAG06830.1|  [Tetraodon nigroviridis]
Sbjct: EDSIRVVRSMRAASPPASASDLIEQQQ---------RRA-RREHKALI gi|47087247|ref|NP_998686.1| [Danio rerio]
Sbjct: EDTLEISKVMRASSPPITAPSNDDNQNA--------KRS-RPSRRSLI gi|31225507|ref|XP_317581.1| [Anopheles gambiae]
Sbjct: EDTLEVTKCMRASSPPATATDILENQYP--------KRNFKR---SLM gi|45550534|ref|NP_647806.2| [Drosophila melanogaster]
Sbjct: EDSIQVVKSMRAASPPSYTLDLGESQLAPPPSKLRGRRGSRR---QLL gi|6330197|dbj|BAA86484.1|   [Homo sapiens]
Sbjct: EDSIQVVKSMRAASPPSYTLDLGESQLAPPPSKLRGRRGSRR---QLL gi|26334907|dbj|BAC31154.1|  [Mus musculus]
Sbjct: EDSIQVVKSMRAASPPSYTLDLGESQLAPPPSKLRGRRGSRR-HK-YI gi|34855075|ref|XP_231564.2| [Rattus norvegicus]

Hypothetical Protein BC012010
Query: MDRNPsPPPPTCGSEDEEDLGG--GDRIGSTVYSKHWLFGV
Sbjct: MDRNPSPPPPPGRDKEEEEEVAG-GDCIGSTVYSKHWLFGV  ref|NP_612430.1|            [Homo sapiens]
Sbjct: MDRNPSPPPPSCDQEDEEDLGS--GDRIGNTVYSKHWLFGV  ref|XP_214948.2|            [Rattus norvegicus]
Sbjct: MDRNPSPP----SSDDESAPE---GDCIGDTIYSKHWFFST  ref|NP_998861.1|            [Xenopus tropicalis]
Sbjct: MDRNPSPP----SSDDEEAPEDD---SIGDTVYSKHWFFST  gi|46049582|dbj|BP701183.1| [Xenopus laevis]*
Sbjct: LDRNPSPPP----EEDETEATEE-ADAIGQTIYSKHWLFST  ref|NP_956429.1|            [Danio rerio]
Sbjct: SSASTTPPPAQEDAEEAELLERMRGDAVGNTMYSSRFILKT  ref|NP_611044.1|            [Drosophila melanogaster]

lunapark
Query: STNEAKSPVLRADsVPNLEPSEESLVTK
Sbjct: SVIETNSTVPGADSIPDPELSGESLTAE  gi|38176151|ref|NP_085153.1|  [Homo sapiens]
Sbjct: STNEAKSPVLRSDSVSNLELSEDSVVTK  gi|34855225|ref|XP_342451.1|  [Rattus norvegicus]

cordon-bleu (cobl)
Query: NLVSPHMNGSRTIsPPSAVVETDTPPIGKVKEFWRRNSME
Sbjct: NLVSPHATGIRIISLSSSVPEAESQPIGKVREFWRCNSVE  gi|28374332|gb|AAH45771.1|    [Homo sapiens]
Sbjct: NLMSPHMNGSRTISKPSAVAETEAPPIGKVKEFWRRNSME  gi|34879123|ref|XP_223597.2|  [Rattus norvegicus]
```

Mode 2 (**R**XXX**s**X**P**)

```
eIF-4B
Query: EPNIDRSRLPKsPPYTAFLGNLPYDVTEDSIKDFFRGLN
Sbjct: EPNIDRSRLPKSPPYTAFLGNLPYDVTEESIKEFFRGLN  gi|18146614|dbj|BAB82380.1|   [Homo sapiens]
Sbjct: EPNIDRSRLPKSPPYTAFLGNLPYDVTEDSIKDFFRGLN  gi|34868564|ref|XP_217058.2|  [Rattus norvegicus]
Sbjct: EPNIDRSRLPKSPPYTAFLGNLPYDVTEESIKDFFRGLN  gi|18000293|gb|AAL54908.1|    [Lapemis hardwickii]
Sbjct: EPNVDRSRLPRSPPYTAFLGNLPYDVTEDSIKNFFRGLS  gi|47682327|gb|AAH70016.1|    [Danio rerio]
Sbjct: EPNIDLSRLPRNPPYTAFLGNLPYDVTEDSIKDFFRGLA  gi|47212108|emb|CAF96690.1|   [Tetraodon nigroviridis]
Sbjct: IF-DDNS-IPHKAPFIAYINNLPFDANEDDLYEFFEGIN  gi|17946109|gb|AAL49096.1|    [Drosophila melanogaster]
Sbjct: ILNDD-S-IPTSPPFSVYVSNLPYDINENDLYDIFE-NV  gi|31203227|ref|XP_310562.1|  [Anopheles gambiae]
Sbjct: RKQKE---LPTEPPFTAYVGNLPFNTVQGDIDNIFKDLS  gi|38051913|gb|AAH60394.1|    [Xenopus laevis]

alveolar soft part sarcoma chromosome region, candidate 1 long isoform
Query: ADVLVARCMSRASGsPP-----LLPAPDPVSLESEPIAEDGALG
Sbjct: ADVLVARYMSRAAGSPS-----PLPAPDPAP-KSEPAAEEGALV  gi|13129078|ref|NP_076988.1|  [Homo sapiens]
Sbjct: ANESVSRCIL-GSPGPSCSSAEPPPSPETPADASTSTQEERA--  gi|47223847|emb|CAG06024.1|   [Tetraodon nigroviridis]
Sbjct: ADLLMARCLSKPLAPSASSSLESIVPALPEPEVGSDKKTERPEP  gi|41630381|emb|BX929853.1|   [Gallus gallus]*
```

Supplementary Fig. 2. **Conservation analysis of additional potential 14-3-3 binding motifs**. Alignments of additional potential 14-3-3 binding motifs generated from phosphopeptide data were performed as in Fig. 5. Motif residues are in bold with the identified phosphorylated serine residue in lower-case. *Indicates sequence was identified from the translated EST database.

Supplementary Table 2. Complete dataset of phosphopeptides identified in this study from murine embryonic brain extract. Phosphopeptides were sorted by accession number. The gel band from which the MS/MS spectrum originated, the charge state of the ion selected for MS/MS analysis, the Sequest Xcorr score, the accession numnber, the theoretical solution charge state and the SCX fraction containing the phosphopeptide are indicated. The sequence of the phosphopeptide is given with the position of the phosphate on serine, threonine or tyrosine followed by and asterisk (*). Under notes, "☺" indicates no ambiguity for at least one site on the phosphopeptide. Also denoted as notes are Sequest hit numbers if the top hit was not accepted, as well as the number of times (in Roman numerals) a given phosphopeptide was identified from distinct MS/MS spectra. If the same phosphopeptide was found in additional regions, tallies demarking such are indicated following a dash (e.g. (3-III)).The number of unique sites identified from each phosphopeptide follows. If the position of phosphate remained ambiguous, it was tabulated as such. The residues potentially phosphorylated were provided as notes with any preferred site (best fit of data) indicated by an asterisk (*). Additionally, the names and predicted molecular weights of the proteins harboring the tryptic phosphopeptides are indicated. This entire dataset is available on our lab website at the following link, http://gygi.med.harvard.edu/pubs/brain/PhosphoBrain.xls. Raw M

Gel Band	charge	Xcorr	Accession	Sol. charge	SCX Fraction	Sequence	Notes	# Unique Sites	# Ambig. Sites	Protein	Predicted MW
3	2	3.5596	SW:143Z_MOUSE	0	3,4	R.DNLTLWTSDT*QGDEAEAGEGGEN.-	Phosphorylation at S1 or T3		1	14-3-3 zeta/delta	28kDa
1	2	3.1138	SW:4ET_MOUSE	(+)1	14	R.IPS*PIGFPSGPQQLLGDPFQGMR.K	☺	1		eukaryotic translation initiation factor 4e transporter	108kDa
1	2	3.4159	SW:A180_MOUSE	(+)1	18	K.SSPATTVTS*PNSTPAK.T	☺Hit #3 (II)	1		Clatharin coat assembly protein 1p180	92kDa
2	2	3.746	SW:ACTA_HUMAN	(+)1	15	K.S*YELPDGQVITIGNER.F	Phosphorylation at S1* or Y1 (II)		1	alpha-actin 2	42kDa
1	2	3.6132	SW:ADDA_MOUSE	(+)1	19	K.SPPDQSAVPNT*PPSTPVK.L	☺(III)	1		alpha adducin	81kDa
1	2	2.8737	SW:ANS1_MOUSE	(+)1	16	K.SPS*FASEWDEIEK.I	☺Hit #2	1		ankyrin repeat and sam dom.containing protein 1	125kDa
1	2	3.2742	SW:APB2_MOUSE	(+)1	16	K.ESYQDYYPPETNGNTGGAS*PYR.M	☺	1		amyloid beta (A4) precursor pbp (mint-2)	83kDa
1	2	2.9397	SW:ARS2_MOUSE	(+)1	16	R.TQLWASEPGT*PPVPTSLPSQNPILK.N	☺	1		arsenite-resistance protein 2/acetylcholinesterase	100kDa
1	2	5.0027	SW:ARVC_MOUSE	(+)1	14	R.S*LAADDEGGPDLEPDYSTATR.R	☺(II)	1		armadillo repeat gene deleted in velo-cardio-facial syndrome	97-105kDa
2	2	3.8406	SW:AVEN_MOUSE	(+)1	19,20	R.VEEDS*DSETYGEENDEQGNFSR.R	☺(II)	1		cell death regulator aven	37kDa
1	2	2.6148	SW:BIN1_MOUSE	0	5,6	K.SPS*PPPDGS*PAATPEIR.V	☺Hit #2	2		bridging integrator 1 (amphiphysin-like protein) (amphiphysin ii)	65kDa
2	3	4.3935	SW:CC23_MOUSE	(+)1	15	R.NQGET*PTSDTPGTFFLPASLSANNTPTR.R	☺Hit #2 (II)	1		cell division cycle protein 23/anaphase promoting complex subunit 8	69kDa
2	3	4.4797	SW:CC23_MOUSE	(+)1	18	R.NQGETPTSDTPGTFFLPASLS*ANNTPTR.R	☺(III)	1		cell division cycle protein 23/anaphase promoting complex subunit 8	69kDa
4	2	2.6477	SW:CDN5_MOUSE	0	12	-.MLGGSSDAGLAT*AAAR.G	☺	1		cyclin-dependent kinase 4 inhibitor b (p14-ink4b) (p15-ink4b)	14kDa
4	2	2.6597	SW:CHR1_MOUSE	(+)1	19,20	K.REEEEDNEDDGS*DLGEALA.-	☺	1		chromatin accessibility complex protein 1 (chrac-1)	14kDa
2	2	3.4741	SW:CN1B_MOUSE	(+)1	15	R.QPS*LDVDVGDPNPDVVSFR.A	☺(VI)	1		calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1b	61kDa
2	2	3.4843	SW:CRK_MOUSE	(+)1	19,20	R.DSS*TSPGDYVLSVSENSR.V	☺	1		proto-oncogene c-crk	34kDa
3	2	3.4965	SW:CRKL_MOUSE	(+)1	13	R.YPS*PPVGSVSAPNLPTAEENLEYVR.T	☺(B-III)	1		crk-like (CrkL)	34kDa
3	3	4.2995	SW:CT77_MOUSE	(+)1	14	R.TFQQIQEEEDDDYPGSYS*PQDPSAGPLLTEELIK.A	☺(III)	1		protein c20orf77 homolog	37kDa
3	2	2.6757	SW:CTD2_MOUSE	(+)1	17	K.NSSLS*PGLNTSNGDGSETETTSAILASVK.E	☺	1		catenin delta-2	135kDa
1	2	2.7745	SW:CTN1_MOUSE	0	5,6	R.T*SVQT*EDDQLIAGQSAR.A	☺Phosphorylation at T2 and T1 or S1	1	1	alpha-1 catenin/alpha e-catenin	100kDa
1	2	4.1274	SW:CTN1_MOUSE	(+)1	16	R.TPEELDDS*DFETEDFDVR.S	☺(VI)	1		alpha-1 catenin/alpha e-catenin	100 kDa
1	2	4.2345	SW:CTN2_MOUSE	(+)1	16	K.QVQEAIAGISSAAQATS*PTDEAK.G	☺(II)	1		alpha-2 catenin/alpha n-catenin	105kDa
1	2	3.6034	SW:CTN2_MOUSE	(+)1	18	K.VYGTAAVNS*PVVSWK.M	☺	1		alpha-2 catenin/alpha n-catenin	105kDa
1	2	3.7751	SW:CTN2_MOUSE	(+)1	17	R.TPEELEDDS*DFEQEDYDVR.S	☺(V)	1		alpha-2 catenin/alpha n-catenin	105kDa
1	2	3.8399	SW:DBS_MOUSE	(+)1	16	R.TS*STGEEEESLAILR.R	Phosphorylation at T1, S1 or S2		1	guanine nucleotide exchange factor dbl's big sister	129kDa
1	2	2.6218	SW:DCK1_MOUSE	0	5,6	K.AQPAPPELNSES*EDYS*PSSSETVR.S	☺Phosphorylation at S3 and S1 or S2 (III)	1	1	doublecortin- like and cam kinase-like 1	84kDa
1	2	3.3267	SW:DCK1_MOUSE	(+)1	16	K.AQPAPPELNSESEDYS*PSSSETVR.S	☺(see doubly phosphorylated)			doublecortin- like and cam kinase-like 1	84kDa
2	2	3.212	SW:DCK1_MOUSE	(+)1	19,20	K.S*PASTSSVNGTPGSQLSTPR.S	Phosphorylation at S1, S2 or T1		1	doublecortin- like and cam kinase-like 1	84kDa
1	2	2.9378	SW:DCK1_MOUSE	(+)1	20	R.S*KS*PASTSSVNGTPGSQLSTPR.S	☺	2		doublecortin- like and cam kinase-like 1	84kDa
2	2	3.3428	SW:DCT2_MOUSE	(+)1	18	R.TGYES*GDYEMLGEGLGVK.E	☺(VI)	1		dynactin complex 50 kda subunit	44kDa
2	2	4.7463	SW:DCX_MOUSE	(+)1	16	K.S*PADSGNDQDANGTSSSQLSTPK.S	☺(IIII)	1		doublecortin	41kDa
2	2	3.0286	SW:DCX_MOUSE	0	9	R.S*KSPADSGNDQDANGTSSS*QLST*PK.S	☺Phosphorylation at S2 and S4, S5 or S6 and S7 or T2	1	2	doublecortin	41kDa
2	2	3.944	SW:DEMA_MOUSE	(+)1	16	R.LQS*TEFSPSGSEAGSPGLQNGEGQR.G	Phosphorylation at S1 or T1 (III)		1	dematin	45kDa
2	2	3.0687	SW:DMA1_MOUSE	(+)1	19,20	K.DTIIDVVGAPLT*PNSR.K	☺	1		dna methyltransferase 1-associated protein 1	53kDa
1	2	3.823	SW:DPY1_MOUSE	(+)1	17	R.GMYDGPVYEVPAT*PK.H	☺(IIII)(D-I)	1		dihydropyrimidinase related protein-2/ulip 3 protein	62 kDa
2	2	3.1496	SW:DPY2_MOUSE	(+)1	14	K.IVNDDQSFY*ADIYMEDGLIK.Q	Phosphorylation at S1* or Y1		1	dihydropyrimidinase related protein-2/ulip 2 protein	62kDa
1	2	3.3329	SW:DPY2_MOUSE	(+)1	17	R.GLYDGPVCEVSVT*PK.T	☺(II)(D-I)	1		dihydropyrimidinase related protein-2/ulip 2 protein	62kDa
2	2	4.2245	SW:DPY3_MOUSE	(+)1	21,22	R.GMYDGPVFDLTTT*PK.G	☺(XI)(D-II)	1		dihydropyrimidinase related protein-3/unc-33-like phosphoprotein	62kDa
1	2	3.7295	SW:DREB_MOUSE	0	7,8	R.SPSDSS*TAST*PIAEQIER.A	☺Hit #2 (IIII)	2		drebrin	77kDa
1	2	2.6082	SW:E4L1_MOUSE	(+)1	18	R.GACST*PEMPQFESVK.A	☺	1		neuronal protein 4.1/E4L1	98kDa
1	2	3.7793	SW:E4L3_MOUSE	(+)1	17	K.DSVS*AAEVGTGQYATTK.G	Phosphorylation at S1 or S2		1	band 4.1-like protein 3, dal-1	103kDa
1	2	2.7974	SW:E4L3_MOUSE	(+)1	19	K.GIS*QTNLITTVT*PEKK.A	☺	2		band 4.1-like protein 3, dal-1	103kDa
1	2	2.7644	SW:E4L3_MOUSE	(+)1	15	K.GIS*QTNLITTVTPEK.K	☺(see doubly phosphorylated)			band 4.1-like protein 3, dal-1	103kDa
1	2	2.7112	SW:E4L3_MOUSE	0	5,6	R.TDTAADGETS*ATES*DQEEDAEIK.A	☺ Hit #3	2		band 4.1-like protein 3, dal-1	103kDa
1	2	3.2996	SW:E4L3_MOUSE	(+)1	18	R.VESTSVGSIS*PGGAK.L	☺	1		band 4.1-like protein 3, dal-1	103kDa
3	3	3.9077	SW:ENAM_MOUSE	(+)1	7	R.KNQET*SPVHT*ES*SYIK.Y	☺Phosphorylation at T1, T2 and S2 or S3 (II)	2	1	enamelin precursor	141kDa
2	2	3.4222	SW:G3B2_MOUSE	(+)1	19,20	K.SAT*PPPAEPASLPQEPPK.A	☺(II)	1		ras-gtpase-activating protein bp2/g3bp-2	54kDa
1	2	4.1627	SW:G3BP_MOUSE	(+)1	16	K.STS*PAPADVAPAQEDLR.T	☺(IIII)(B-I)	1		ras-gtpase-activating protein bp1/g3bp-1	52 kDa
1	3	5.0823	SW:G3BP_MOUSE	(+)1	14	R.YQDEVFGGFVTEPQEES*EEEVEEPEER.Q	☺(B-I)(C-II)	1		ras-gtpase-activating protein bp1/g3bp-1	52 kDa
1	3	3.6975	SW:GRBA_MOUSE	(+)1	12	R.TASLPAIPNPFPELTGAAPGS*PPSVAPSSLPPPPSQPPAK.H	☺(II)	1		growth factor receptor-bound proreint 10 (grb10)	70kDa
1	3	5.9101	SW:H105_MOUSE	(+)1	15	K.NIQQDNSEAGTQPQVQTDGQQTSQSPPS*PELTSEESK.T	☺	1		heat-shock protein 105 kda	96kDa
4	2	3.3668	SW:HBB1_MOUSE	(+)1	17	R.YFDS*FGDLSSASAIMGNAK.V	☺	1		hemoglobin beta-1 chain (b1)	16kDa
2	3	4.4904	SW:HDGF_MOUSE	0	7,8	K.NS*TPS*EPDS*GQGPPAEEEEGEEEAAKEEAEAQGVR.D	☺Phosphorylation at S2 and S3 and S1 or T1	2	1	hepatoma-derived growth factor (hdgf)	26kDa
1	2	2.6856	SW:HS9B_MOUSE	(+)1	18	K.IEDVGS*DEEDDSGK.D	☺	1		Hsp90	83kDa
4	2	3.1168	SW:ICE3_MOUSE	(+)1	17	K.S*VDSGIYLDSSYK.M	☺(II)	1		caspase-3	31kDa
2	2	3.0027	SW:IF34_MOUSE	0	5,6	K.GIPLPTGDT*S*PEPELLPGDPLPPPK.E	☺	2		eukaryotic translation initiation factor 3, subunit 4	36kDa
3	2	3.9793	SW:IF34_MOUSE	(+)1	15	K.GIPLPTGDTS*PEPELLPGDPLPPPK.E	☺(VIIII)(B-I)(D-I)(see doubly phosphorylated)			eukaryotic translation initiation factor 3, subunit 4	36kDa
2	2	2.5054	SW:IF5_MOUSE	0	5,6	K.EAEEES*S*GGEEEDEDENIEVVYSK.T	☺	2		eukaryotic translation initiation factor 5	49kDa
2	2	4.4679	SW:IF5_MOUSE	(+)1	15	K.EAEEESS*GGEEEDEDENIEVVYSK.T	☺Hit #2 (see doubly phosphorylated)			eukaryotic translation initiation factor 5	49kDa
4	3	5.3903	SW:IPKG_MOUSE	(+)1	14	K.LAGDMGELALEGAEGQAEGSTPDKEAS*SQPESSDANTSS.-	☺Phosphorylation at S2 or S3		1	camp-dependent protein kinase inihibor, gamma form	8kDa
3	3	3.4744	SW:ITAB_MOUSE	(+)1	3,4	R.AS*CAWHS*LWLLQWTPLFLGPSAVPPVWALNLDSEK.F	☺	2		integrin alpha-iib precursor	113kDa

1	2	3.9896	SW:ITH2_MOUSE	(+)1	15	R.SLPEES*GEETDTVDPVTLYSYK.V	☺(V)(C-II)	1		inter-alpha-trypsin inhibitor heavy chain h2 precursor	106kDa
1	3	3.6741	SW:ITN1_MOUSE	(+)1	15	K.AQS*FDVASAPPAAEWAVPQSSR.L	Phosphorylation at S1* or S2		1	intersectin 1	194kDa
1	2	3.5069	SW:ITN1_MOUSE	(+)1	18	R.LPEEPSS*EDEQQPEK.K	☺	1		intersectin 1	194kDa
1	2	4.3181	SW:ITN1_MOUSE	0	7,8	R.SAFTPATATGSS*PS*PVLGQGEK.V	☺(II)	2		intersectin 1	194kDa
1	3	4.7426	SW:ITN1_MOUSE	(+)1	17	R.SAFTPATATGSSPS*PVLGQGEK.V	☺(see doubly phosphorylated)			intersectin 1	194kDa
1	2	3.0643	SW:ITN1_MOUSE	(+)1	17	R.SGS*GMSVISSSSVDQR.L	☺	1		intersectin 1	194kDa
1	2	3.0031	SW:K685_MOUSE	(+)1	18	R.NVPGLAAPSS*PTQK.E	☺(II)	1		kiaa0685 homolog	100kDa
1	2	3.6365	SW:K6A2_MOUSE	(+)1	14	R.GFS*FVASSLVQEPSQQDVPK.A	☺	1		ribosomal s6 kinase 3 pp90rsk3	83kDa
2	2	2.8924	SW:KAPA_MOUSE	(+)1	9	R.T*WTLCGTPEYLAPEIILSK.G	☺(II)	1		camp-dependent protein kinase alpha catalytic subunit	40kDa
1	2	3.6541	SW:KF3A_MOUSE	(+)1	15	R.S*AKPETVIDSLLQ.-	☺(II)	1		kinesin-like protein kif3a	80 kDa
2	2	2.5225	SW:KG3B_MOUSE	(+)1	21,22	R.IQAAAS*PPANATAASDTNAGDR.G	☺	1		glycogen synthase kinase-3 beta	47kDa
1	2	3.8883	SW:KG88_MOUSE	(+)1	17	R.AFS*EDEALAQQDSK.H	☺	1		kiaa1688 homolog (fragment).	>124kDa
1	3	5.0772	SW:KIF2_MOUSE	(+)1	16	K.EFGISPSDIPFSQGGGSRPDLSPS*YDYDDFS*PSITR.V	☺Phosphorylation at S7 and S5, S6*, Y1 or Y2	1	1	kinesin-like protein kif2	81kDa
1	3	5.0155	SW:KLC3_MOUSE	(+)1	16	R.AAS*LNYLNQPNAAPLQVSR.G	☺	1		probable kinesin light chain 3	69kDa
1	2	2.7595	SW:KPCE_MOUSE	(+)1	17	R.EEPILT*LVDEAIIK.Q	☺(D-I)	1		protein kinase c, epsilon type (npkc-epsilon)	84kDa
1	2	3.3358	SW:MACF_MOUSE	(+)1	17	R.LLDAEDVDVPS*PDEK.S	☺	1		microtubule-actin crosslinking factor 1 (macf1)	608kDa
1	2	2.5301	SW:MACS_MOUSE	(+)1	18	K.AEDGAAPSPSSET*PK.K	☺	1		myristoylated alanine-rich c-kinase substrate (marcks)	30kDa
1	2	3.9074	SW:MACS_MOUSE	0	3,4	K.EAAEAEPAEPSS*PAAEAEGASASSTSS*PK.A	☺Hit #2 (II)	2		myristoylated alanine-rich c-kinase substrate (marcks)	30kDa
1	2	3.1868	SW:MACS_MOUSE	(+)1	16	K.EAAEAEPAEPSS*PAAEAEGASASSTSSPK.A	☺Hit #2 (see doubly phosphorylated, V)			myristoylated alanine-rich c-kinase substrate (marcks)	30kDa
1	2	2.616	SW:MACS_MOUSE	(+)1	18	K.VNGDAS*PAAAEPGAK.E	☺	1		myristoylated alanine-rich c-kinase substrate (marcks)	30kDa
1	3	5.0937	SW:MACS_MOUSE	(+)1	14	R.EAEAAEPEQPEQPEQPAAEEPQAEEQS*EAAGEK.A	☺	1		myristoylated alanine-rich c-kinase substrate (marcks)	30kDa
1	3	4.1677	SW:MAP2_MOUSE	(+)1	16	K.ASQPS*PPAQEAGYSTLAQSYTPGHPSELPEEPSS*PQER.M	☺	2		microtubule-associated protein 2 (map 2)	199kDa
1	2	3.6104	SW:MAP2_MOUSE	(+)1	18	K.DGS*PDAPAT*PEKEEVAFSEYK.T	☺(III)	2		microtubule-associated protein 2 (map 2)	199kDa
1	2	2.5135	SW:MAP2_MOUSE	(-)1	1,2	K.SGTS*TPTTPGSTAIT*PGT*PPSYSSR.T	☺Phosphorylation at T6, T7 and S1, T1, S2 or T2	2	1	microtubule-associated protein 2 (map 2)	199kDa
2	2	2.6732	SW:MAP2_MOUSE	0	3,4	K.SGTS*TPTTPGSTAITPGT*PPSYSSR.T	☺Phosphorylation at T7 and S1, T1, S2 or T2 (see doubly and triply, II)			microtubule-associated protein 2 (map 2)	199kDa
1	2	2.802	SW:MAP2_MOUSE	0	3,4	K.SGTS*TPTTPGSTAITPGTPPSYSS*R.T	☺Phosphorylation at T7 and S1, T1, S2 or T2 (see triply phosphorylated, III)			microtubule-associated protein 2 (map 2)	199kDa
2	2	2.6788	SW:MAP2_MOUSE	(+)1	10	K.SGTSTPT*TPGSTAITPGTPPSYSSR.T	☺Hit #2	1		microtubule-associated protein 2 (map 2)	199kDa
1	3	3.7075	SW:MAP2_MOUSE	0	9	K.SGTSTPTTPGSTAITPGT*PPSY*SSR.T	☺Phosphorylation at T7 and S4*, S5 or S6		1	microtubule-associated protein 2 (map 2)	199kDa
1	3	4.0538	SW:MAP2_MOUSE	(+)1	18	K.SGTSTPTTPGSTAITPGT*PPSYSSR.T	☺(see doubly and triply phosphorylated, II)			microtubule-associated protein 2 (map 2)	199kDa
1	3	3.9249	SW:MAP2_MOUSE	(+)1	18	R.GHDLSPLAS*DILTNTS*GSMDEGDDYLPPTTPAVEK.M	☺Phosphorylation at S1 and T2 or S3	1	1	microtubule-associated protein 2 (map 2)	199kDa
1	2	2.5886	SW:MAP2_MOUSE	(+)1	19	R.GSAQESLDTIS*PK.N	☺	1		microtubule-associated protein 2 (map 2)	199kDa
1	2	2.7295	SW:MAP2_MOUSE	(+)1	18	R.LAS*VSADAEVAR.R	☺	1		microtubule-associated protein 2 (map 2)	199kDa
1	2	3.1564	SW:MAP4_MOUSE	(+)1	16	K.AAEQMSTLPIDAPS*PLENLEQK.E	☺(III)	1		microtubule-associated protein 4 (map 4)	118kDa
1	3	5.0229	SW:MAP4_MOUSE	(+)1	17	K.ALETMAEQTTDVVHS*PSTDTT*PGPDTEAALAK.D	☺	2		microtubule-associated protein 4 (map 4)	118kDa
1	2	3.1705	SW:MAP4_MOUSE	(+)1	18	K.AT*SPSTLVSTGPSSR.S	Phosphorylation at T1 or S1		1	microtubule-associated protein 4 (map 4)	118 kDa
1	2	3.1888	SW:MAP4_MOUSE	(+)1	16	K.DMS*PLPESEVTLGK.D	☺(IIII)	1		microtubule-associated protein 4 (map 4)	118kDa
1	2	2.6503	SW:MAP4_MOUSE	(+)1	17	K.DMS*PSAETEAPLAK.N	☺(II)	1		microtubule-associated protein 4 (map 4)	118 kDa
1	3	5.1929	SW:MAP4_MOUSE	(+)1	16	K.VAEFNNVTPLSEEEVT*SVKDMSPS*AETEAPLAK.N	☺Phosphorylation at S3 and T2 or S2 (II)	1	1	microtubule-associated protein 4 (map 4)	118kDa
1	2	3.5162	SW:MAPB_MOUSE	(+)1	16	K.FEDEGAGFEESS*ETGDYEEK.A	☺(III)	1		microtubule-associated protein 1b (map 1b)	270kDa
1	2	4.2823	SW:MAPB_MOUSE	(+)1	15	K.LGGDVS*PTQIDVSQFGSFK.E	☺(VI)	1		microtubule-associated protein 1b (map 1b)	270kDa
1	2	2.5069	SW:MAPB_MOUSE	0	7,8	K.SPSLS*PSPPS*PIEK.T	☺Hit #2 (II)	2		microtubule-associated protein 1b (map 1b)	270kDa
1	3	3.6084	SW:MAPB_MOUSE	0	5,6	K.TLEVVSPS*QSVTGSAGHTPYY*QS*PTDEK.S	☺(II Phosphorylation at S1, S5 and S2, S3, T1, T2*, Y1 or Y2	2	1	microtubule-associated protein 1b (map 1b)	270kDa
1	3	5.4597	SW:MAPB_MOUSE	(+)1	17	K.VLS*PLRS*PPLLGSESPYEDFLSADSK.V	☺	2		microtubule-associated protein 1b (map 1b)	270kDa
1	2	2.6979	SW:MAPB_MOUSE	0	5,6	R.ASLS*PMDEPVPDSES*PVEK.V	☺(XII)	2		microtubule-associated protein 1b (map 1b)	270kDa
2	2	2.7714	SW:MAPB_MOUSE	(+)1	18	R.ASLS*PMDEPVPDSESPVEK.V	☺(see doubly phosphorylated)			microtubule-associated protein 1b (map 1b)	270kDa
1	2	3.033	SW:MAPB_MOUSE	(+)1	16	R.ASLSPMDEPVPDSES*PVEK.V	☺(see doubly phosphorylated, III)			microtubule-associated protein 1b (map 1b)	212kDa
1	2	3.5409	SW:MAPB_MOUSE	(+)1	16	R.DVMSDETNNEETES*PSQEFVNITK.Y	☺(V)	1		microtubule-associated protein 1b (map 1b)	270kDa
1	2	2.5914	SW:MAPB_MOUSE	0	7,8	R.ESS*PLYS*PGFSDSTSAAK.E	☺(II)	2		microtubule-associated protein 1b (map 1b)	270kDa
1	2	3.4981	SW:MAPB_MOUSE	(+)1	16	R.SPPLLGSES*PYEDFLSADSK.V	☺Hit #2	1		microtubule-associated protein 1b (map 1b)	270kDa
1	2	2.789	SW:MAPB_MOUSE	(+)1	18	R.SVNFSLT*PNEIK.V	☺	1		microtubule-associated protein 1b (map 1b)	270kDa
1	2	2.5902	SW:MCM2_MOUSE	(+)1	20	R.GLLYDS*S*EEDEERPAR.K	☺	2		dna replication licensing factor mcm2	102kDa
1	2	2.8525	SW:MCM2_MOUSE	(+)1	19	R.ISDPLTSS*PGR.S	☺	1		dna replication licensing factor mcm2	102kDa
2	2	4.1577	SW:MCS1_MOUSE	(+)1	19,20	K.GDQVLNFS*DAEDLIDDSK.L	☺	1		microspherule protein 1	58kDa
2	2	2.9905	SW:MJD1_MOUSE	(+)1	17	R.VLEAADGS*GIFDEDEDDLQR.A	☺(II)	1		machado-joseph disease protein 1 (ataxin-3)	41kDa
2	2	2.8405	SW:MK08_MOUSE	0	5,6	R.GQPS*PLAQVQQ.-	☺	1		stress-activated protein kinase/c-jun n-terminal kinase 1 jnk1	44kDa
2	2	2.5573	SW:MK08_MOUSE	0	11	R.TAGTSFMMT*PY*VVTR.Y	☺	2		stress-activated protein kinase/c-jun n-terminal kinase 1 jnk1	44kDa
2	3	3.5578	SW:MPP2_MOUSE	(+)1	14	K.TYETPPPS*PGLDPTFSNQPVPPDAVR.M	Phosphorylation at T1, Y1, T2 or S1		1	maguk p55 subfamily member 2	62kDa
2	2	2.5605	SW:MRP_MOUSE	(+)1	21,22	K.AAAT*PESQEPQAK.G	☺Hit #2	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	4.1298	SW:MRP_MOUSE	(-)1	3,4	K.EGDTEEEAGPQAAEPST*PSGPESGPT*PASAEQNE.-	☺(see singly phosphorylated for first T*P)	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	5.8766	SW:MRP_MOUSE	0	5,6	K.EGDTEEEAGPQAAEPST*PSGPESGPTPASAEQNE.-	☺(XI)(D-II)(A-II)	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	4.5136	SW:MRP_MOUSE	0	3,4	K.EGDTEEEAGPQAAEPSTPS*GPESGPTPASAEQNE.-	☺(II)(D-III)(C-I)	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	6.0992	SW:MRP_MOUSE	(+)1	16	K.EGGGDSSASS*PTEEEQEQGEMSACSDEGTAQEGK.A	☺(II)	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	7.2476	SW:MRP_MOUSE	(+)1	19,20	K.EGGGDSSASSPTEEEQEQGEMSACS*DEGTAQEGK.A	☺	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	3.9697	SW:MRP_MOUSE	(-)1	3,4	K.GAEAS*AAS*KEGDTEEEAGPQAAEPST*PSGPESGPTPASAEQNE.-	☺Hit #2 (see singly phosphorylated for T*P)	2		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	4.5921	SW:MRP_MOUSE	(+)1	7,8	K.GAEASAASKEGDT*EEEAGPQAAEPSTPSGPESGPTPASAEQNE.-	☺	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	5.3622	SW:MRP_MOUSE	(+)1	10	K.GEGES*PPVNGTDEAAGATGDAIEPAPPSQEAEAK.G	☺Hit #2	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	3	5.0478	SW:MRP_MOUSE	(+)1	10	K.GEGESPPVNGTDEAAGATGDAIEPAPPS*QEAEAK.G	☺	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	2	3.1914	SW:MRP_MOUSE	(+)1	21,22	R.GDVTAEEAAGAS*PAK.A	☺	1		macrophage myristoylated alanine-rich c kinase substrate	20kDa
2	2	3.0931	SW:MY5A_MOUSE	(+)1	16	R.TSS*IADEGTYTLDSILR.Q	Phosphorylation at S1 or S2 (III)		1	dilute myosin heavy chain, non-muscle	216kDa
1	3	5.1736	SW:NCA1_MOUSE	(+)1	18	K.APPASKAS*PAPTPTPAGAAS*PLAAVAAPATDAPQAK.Q	☺(see overlapping phosphopeptides)	2		neural cell adhesion molecule 1/(n-cam 180)	120kDa

1	2	3.2298	SW:NCA1_MOUSE	0	5,6	K.AS*PAPT*PTPAGAASPLAAVAAPATDAPQAK.Q	☺Hit #2 (II, see overlapping phosphopeptides)			neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	3.9015	SW:NCA1_MOUSE	0	3,4	K.AS*PAPTPTPAGAAS*PLAAVAAPATDAPQAK.Q	☺(see overlapping phosphopeptides, V)			neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	4.0047	SW:NCA1_MOUSE	(+)1	12	K.AS*PAPTPTPAGAASPLAAVAAPATDAPQAK.Q	☺Hit #2 (see doubly phosphorylated, III)			neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	3.9084	SW:NCA1_MOUSE	(+)1	15	K.ASPAPTPTPAGAAS*PLAAVAAPATDAPQAK.Q	☺(see doubly phosphorylated, III)			neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	2.8262	SW:NCA1_MOUSE	(+)1	19	K.GVTASSSS*PASAPK.V	☺	1		neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	3.3661	SW:NCA1_MOUSE	(+)1	18	K.NPPEAATAPAS*PK.S	☺(IIII)	1		neural cell adhesion molecule 1/(n-cam 180)	120kDa
1	2	3.5082	SW:NEK1_MOUSE	(+)1	16	K.SSDVPLPLELLETGGS*PSK.Q	☺	1		nima-related protein kinase 1 (nek1)	88kDa
2	2	3.8467	SW:NEK3_MOUSE	(+)1	16	R.LDEEDT*DFEEDNENPDWVSELK.K	☺	1		nima-related protein kinase 3 (nek3)	57kDa
2	2	3.6416	SW:NEUM_MOUSE	(+)1	21,22	K.EGDGSATTDAAPATS*PK.A	☺	1		neuromodulin	24kDa
2	2	5.3865	SW:NEUM_MOUSE	(+)1	21,22	K.QADVPAAVTDAAATT*PAAEDAATK.A	☺(III)	1		neuromodulin	24kDa
1	2	2.8992	SW:NFIA_MOUSE	(+)1	17	K.SVEDEMDS*PGEEPFYTGQGR.S	☺	1		nuclear factor 1 a-type	59kDa
2	3	4.704	SW:NFIB_MOUSE	(+)1	16	K.TISIDENMEPSPTGDFYPSPNS*PAAGSR.T	☺(II)	1		nuclear factor 1 b-type	64kDa
2	2	4.128	SW:NFIX_MOUSE	(+)1	9	K.S*IDDSEMESPVDDVFYPGTGR.S	Phosphorylation at S1* or S2			nuclear factor 1 x-type	53kDa
2	2	2.5495	SW:NFIX_MOUSE	(+)1	19,20	K.SIDDSEMES*PVDDVFYPGTGR.S	Phosphorylation at S2 or S3*		1	nuclear factor 1 x-type	53kDa
1	2	3.9512	SW:NFM_MOUSE	(+)1	17	K.GVVTNGLDVS*PAEEK.K	☺(II)			neurofilament triplet m protein (NFM)	96kDa
2	2	3.5195	SW:NPL1_MOUSE	(+)1	19,20	R.LDGLVDT*PTGYIESLPK.V	☺(II)	1		nucleosome assembly protein 1-like 1 (nap-1 related protein)	45kDa
2	3	5.3126	SW:PA6A_MOUSE	(+)1	13	R.LTGPSSVGPGPTDPDS*DDDSSDLVIENR.H	☺	1		partitioning defective-6 homolog alpha (par-6 alpha)	37kDa
2	2	2.6753	SW:PAK1_MOUSE	0	5,6	R.DVATS*PIS*PTENNTTPPDALTR.N	☺(VI)	2		p21-activated kinase 1	61kDa
2	2	2.965	SW:PAK1_MOUSE	(+)1	18	R.DVATS*PISPTENNTTPPDALTR.N	☺(see doubly phosphorylated, II)			p21-activated kinase 1	61kDa
1	2	3.559	SW:PAK1_MOUSE	(+)1	16	R.DVATSPIS*PTENNTTPPDALTR.N	☺(see doubly phosphorylated, VI)			p21-activated kinase 1	61kDa
2	2	3.1201	SW:PALM_MOUSE	0	5,6	K.EENQTGPTTT*PS*DTQDLDMK.K	☺Hit #2	2		paralemmin	42kDa
1	2	3.5304	SW:PALM_MOUSE	0	9	K.SETLVNAQQT*PLGT*PK.E	☺	2		paralemmin	42kDa
1	2	2.6805	SW:PALM_MOUSE	(+)1	17	R.EPAPLNGS*AAELPATK.E	☺	1		paralemmin	42kDa
4	2	3.0456	SW:PCD5_MOUSE	(+)1	19,20	R.KVMDS*DEDDADY.-	☺	1		programmed cell death protein 5 (tfar19 protein)	15kDa
2	2	5.1174	SW:PDPK_MOUSE	(+)1	13	R.ANS*FVGTAQYVSPELLTEK.S	☺(IIII)(C-III)	1		3-phosphoinositide dependent protein kinase-1	64kDa
1	2	2.5439	SW:PIXB_MOUSE	(+)1	18	R.MS*GFIYQGK.L	☺	1		rho guanine nucleotide exchange factor 7/pak-interacting exchange factor beta	80kDa
1	2	3.5667	SW:PKL1_MOUSE	(+)1	16	R.TDVSNFDEEFTGEAPTLS*PPR.D	☺(III)	1		protein kinase c-like 1/(PRK-1)	104kDa
2	2	4.7797	SW:PSD4_MOUSE	(+)1	17	R.AAAASAAEAGIAT*PGTEDSDDALLK.M	☺	1		26s proteasome non-atpase regulatory subunit 4	41kDa
3	2	3.079	SW:PSN1_MOUSE	0	5,6	R.AAVQELSGS*ILT*SEDPEER.G	☺Hit #2	2		presenilin 1	53kDa
1	2	2.5239	SW:PTNC_MOUSE	(+)1	17	K.S*PAEVTDIGFGNR.C	☺	1		protein-tyrosine phosphatase p19	87kDa
2	2	2.8799	SW:RDP_MOUSE	(+)1	18	R.SLS*EQPVVDTATATEQAK.Q	☺(IIII)	1		rd protein	43kDa
1	3	4.703	SW:RGP1_MOUSE	(+)1	12	K.ILDPNSGEPAPVLSS*PTPTDLSTFLSFPSPEK.L	☺(II)	1		ran-gtpase activating protein 1	64kDa
3	2	3.0604	SW:RLA0_MOUSE	0	3,4	K.AEAKEES*EES*DEDMGFGLFD.-	☺(III)(B-I)	2		60s acidic ribosomal protein p0	34kDa
2	2	2.6356	SW:RLA0_MOUSE	(+)1	19,20	K.AEAKEES*EESDEDMGFGLFD.-	☺(see doubly phosphorylated)			60s acidic ribosomal protein p0	34kDa
4	2	3.5025	SW:RLA2_MOUSE	0	7	K.KEES*EES*DDDMGFGLFD.-	☺(XXVIII)	2		60s acidic ribosomal protein p2	12kDa
2	2	3.0891	SW:ROC_MOUSE	(+)1	16	K.MESEAGADDS*AEEGDLLDDDDNEDR.G	☺	1		heterogeneous nuclear ribonucleo proteins c1/c2	34kDa
2	2	2.5194	SW:RS10_MOUSE	(+)1	3,4	K.AEAGAGS*ATEFQFR.G	☺Hit #2	1		40s ribosomal protein s10	19kDa
4	2	3.3294	SW:RS17_MOUSE	(+)1	15	K.LLDFGS*LSNLQVTQPTVGMNFK.T	☺Hit #2	1		ribosomal protein S17	16kDa
1	2	3.5447	SW:RTN2_MOUSE	(+)1	15	R.EFS*EDEEEETTSQDWGTPR.E	☺	1		reticulon protein 2/nsp-like protein 1	51 kDa
1	2	3.023	SW:RU17_MOUSE	(+)1	19	R.GGGGS*GQDNGLEGLGSDGR.D	☺	1		u1 small nuclear ribonucleoprotein 70 kda	70kDa
1	2	2.7269	SW:SAL2_MOUSE	(+)1	16	R.GDSEEVS*GAEEEVATSVAAPTTVK.E	Phosphorylation at S1 or S2		1	sal-like protein 2 (msal-2)	105kDa
2	2	4.9825	SW:SEP5_MOUSE	(+)1	12	R.MES*PIPILPLPTPDAETEK.L	☺(II)(C-I)	1		spetin 5/cell division control related protein 1	40kDa
2	3	3.506	SW:SEP5_MOUSE	(+)1	19,20	R.MESPIPILPLPT*PDAETEK.L	☺	1		spetin 5/cell division control related protein 1	40kDa
2	2	3.6428	SW:SMN_MOUSE	(+)1	15	R.GTGQS*DDSDIWDDTALIK.A	☺(III)(C-I)	1		survival motor neuron protein	31kDa
4	2	2.7256	SW:SNN_MOUSE	(+)1	19,20	K.LMTANS*PEVHG.-	☺	1		stannin	10kDa
4	2	3.9475	SW:SNN_MOUSE	(+)1	19,20	R.ISQSEDEES*IVGDGETK.E	☺	1		stannin	10kDa
1	2	2.6062	SW:SPCO_MOUSE	0	5,6	K.GDQVS*QNGLPAEQGS*PR.M	☺	2		spectrin beta chain, brain 1	274kDa
1	2	3.4698	SW:SPCO_MOUSE	(+)1	19	K.GDQVSQNGLPAEQGS*PR.M	☺(see doubly phosphorylated)			spectrin beta chain, brain 1	274kDa
2	2	2.6167	SW:STN1_MOUSE	(+)1	7,8	K.ESVPDFPLS*PPK.K	☺(D-II)	1		stathmin (phosphoprotein p19)	17kDa
2	2	3.2228	SW:STN1_MOUSE	(+)1	9	R.ASGQAFELILS*PR.S	☺(II)(D-III)	1		stathmin (phosphoprotein p19)	17kDa
3	2	2.9072	SW:STN3_MOUSE	0	5,6	K.SPSDLS*PES*PVLSSPPK.R	☺(see additional doubly phosphorylated)	1		stathmin 3	21kDa
3	2	3.0011	SW:STN3_MOUSE	0	3,4	K.SPSDLSPES*PVLSS*PPK.R	☺(II)	2		stathmin 3	21kDa
2	2	2.7141	SW:STX7_MOUSE	(+)1	21,22	K.EFGSLPTT*PSEQR.Q	☺	1		syntaxin 7	30kDa
2	2	5.0792	SW:SX11_MOUSE	(+)1	15	K.VPAS*PTLSSAAESPEGASLYDEVR.A	☺(IIII)	1		transcription factor sox-11	43kDa
1	2	3.4941	SW:SYN1_MOUSE	(+)1	16	R.LPS*PTAAPQQSASQATPVTQGQGR.Q	☺(IIII)	1		synapsin i	70kDa
1	2	3.1791	SW:TABP_MOUSE	(+)1	17	K.SSGSLS*PGLETEDPLEAR.E	☺	1		182 kda tankyrase 1-binding protein	97kDa
1	2	2.9273	SW:TABP_MOUSE	0	5,6	R.VPS*S*DEEVVEEPQSR.R	☺(III)	2		182 kda tankyrase 1-binding protein	97kDa
2	2	2.9577	SW:TAU_MOUSE	(+)1	9	K.SPVVSGDTS*PR.H	☺(D-I)	1		microtubule-associated protein tau	76kDa
2	3	7.016	SW:TAU_MOUSE	0	7,8	R.HLS*NVSST*GS*IDMVDSPQLATLADEVSASLAK.Q	☺Phosphorylation at S4 and two of S1, S2, S3 and T1	1	2	microtubule-associated protein tau	76kDa
2	2	2.9551	SW:TBA1_HUMAN	(+)1	19,20	K.TIGGGDDS*FNTFFSETGAGK.H	☺Hit #2	1		tubulin alpha-1 chain	50kDa
2	2	2.9131	SW:TE2I_MOUSE	(+)1	21,22	K.YLLGNAPVS*PSSQK.L	☺	1		trf2- interacting telomeric protein rap1	43kDa
4	2	4.9637	SW:TEBP_MOUSE	(+)1	19,20	K.DWEDDS*DEDMSNFDR.F	☺(V)(B-II)	1		telomerase-binding protein p23	19kDa
1	2	2.8574	SW:TF1B_MOUSE	(+)1	17	R.S*GEGEVSGLLR.K	☺	1		tif1-beta/tripartite motif protein 28/krip-1	89kDa
1	2	2.8931	SW:TLE3_MOUSE	(+)1	19	R.ESSTNNSVS*PSESLR.A	☺Hit #2	1		transducin-like enhancer protein 3	83kDa
1	2	4.0527	SW:TP11_MOUSE	(+)1	15	R.TTQSLQDFPVADS*EEEAEEEFQK.E	☺	1		tuftelin-interacting protein 11	96kDa
	2 2	2.9737	SW:U33K_MOUSE	0	5,6	R.S*SPPATDPGPVPS*SPSQEPPTK.R	Phosphorylation at S1 or S2 and S3 or S4		2	uba/ubx	34kDa
2	2	4.5877	SW:U33K_MOUSE	(+)1	16	R.S*SPPATDPGPVPSSPSQEPPTK.R	Phosphorylation at S1 or S2 (see doubly phosphorylated)			uba/ubx	34kDa
1	2	3.9511	SW:UBP5_MOUSE	(+)1	15	R.GTGLQPGEEELPDIAPPLVT*PDEPK.G	☺(IIII)	1		deubiquitinating enzyme 5	96kDa
1	2	2.6277	SW:UBPA_MOUSE	(+)1	17	K.CS*PPVPSPLASEK.Q	☺	1		deubiquitinating enzyme 10	87kDa
1	2	3.0329	SW:UBPY_HUMAN	(+)1	16	R.SYS*SPDITQAIQEEEK.R	☺	1		deubiquitinating enzyme UBPY (mUBPY)	122kDa

1	2	2.606	SW:UTX_MOUSE	0	5,6	K.TDNSVASS*PSSAISTATPS*PK.S	☺Hit #3	2		ubiquitously transcribed tprp on X-chrom.	157kDa
4	2	5.7376	SW:VAM4_MOUSE	(+)1	17	R.NLLEDDS*DEEEDFFLR.G	☺(III)	1		vesicle-associated membrane protein 4 (vamp-4)	16kDa
2	2	3.6798	SW:VIME_MOUSE	(+)1	12	R.LLQDS*VDFSLADAINTEFK.N	☺(II)	1		vimentin	54kDa
2	2	3.8897	SW:VIME_MOUSE	(+)1	21,22	R.SLYSSS*PGGAYVTR.S	☺	1		vimentin	54kDa
2	2	3.1128	SW:XPA_MOUSE	(+)1	19,20	K.QTS*PEPVAADEPAQLPAAVR.A	☺Hit #2	1		dna-repair protein complementing xp-a cells homolog	31kDa
1	2	3.7619	SW:YAP1_MOUSE	(+)1	13	R.GDSET*DLEALFNAVMNPK.T	Phosphorylation at S1* or T1		1	65 kda yes-associated protein	51kDa
2	2	3.272	SW:YB1_MOUSE	0	3,4	K.AADPPAENSS*APEAEQGGAE.-	Phosphorylation at S1 or S2		1	Y box-binding protein 1	36kDa
1	2	3.9437	SW:ZIN_MOUSE	(+)1	15	R.S*LELNGAGEPVEGAPR.A	☺(II)(C-I)	1		striatin 4 (zinedin)	82kDa
1	2	4.2375	SWN:ALS2_MOUSE	(+)1	13	R.S*ESPEPGYVVTSSGLLLPVLLPR.L	Phosphorylation at S1 or S2 (II)		1	alsin	183kDa
1	2	2.8731	SWN:CN04_MOUSE	(+)1	21	R.NSSS*PVSPASVPGQR.R	☺Hit #2	1		protein c14orf4 homolog	81kDa
1	2	3.2332	SWN:CN31_MOUSE	(+)1	12	K.SVS*IIINVK.I	Phosphorylation at S1 or S2 (III)		1	protein c14orf31 homolog	72kDa
1	2	3.4802	SWN:I4G2_MOUSE	(+)1	17	R.TQT*PPLGQTPQLGLK.T	☺Hit #2	1		eukaryotic translation initiation factor 4 gamma 2 eif-4g 2	102kDa
1	2	3.123	SWN:M4K4_MOUSE	(+)1	18	R.AASS*PNLSNGETESVK.T	☺	1		mitogen-activated protein kinase kinase kinase kinase (mekkk 4)	141kDa
4	2	2.5717	SWN:MLRN_MOUSE	(+)1	17	R.ATS*NVFAMFDQSQIQEFK.E	☺	1		myosin regulatory light chain 2	20kDa
2	2	5.2862	SWN:NLFB_MOUSE	(+)1	11	R.KPS*PTQAAETPALDLPLPSVPAPATL.-	Phosphorylation at S1 or T1(C-II)		1	negative elongation factor b	66kDa
2	2	4.656	SWN:SIR2_MOUSE	(+)1	17	K.VQEAQDS*DSDTEGGATGGEAEMDFLR.N	Phosphorylation at S1 or S2 (V)		1	nad-dependent deacetylase sirtuin 2	43kDa
1	2	3.3862	SWN:SN3A_MOUSE	(+)1	13	R.GDLS*DVEEEEEEEMDVDEATGAPK.K	☺	1		paired amphipathic helix protein sin3a	146kDa
1	3	3.3675	SWN:TNIK_MOUSE	(+)1	12	R.VYQTSPT*DEDEEDDESSAAALFTSELLR.Q	☺	1		traf2 and nck interacting kinase	103kDa
1	3	3.2748	SWN:TNIK_MOUSE	(+)1	13	R.VYQTSPTDEDEEDDESS*AAALFTSELLR.Q	Phosphorylation at S2 or S3		1	traf2 and nck interacting kinase	103kDa
1	2	3.1659	SWN:UB4B_MOUSE	(+)1	18	R.LAGGQTSQPTTPLTS*PQR.E	☺	1		ubiquitin conjugation factor e4 b/ufd2a	133kDa
1	2	3.0408	SWN:UB4B_MOUSE	(+)1	17	R.SQS*MDIDGVSCEK.S	☺	1		ubiquitin conjugation factor e4 b/ufd2a	133kDa
1	3	3.79	SWN:UB4B_MOUSE	(+)1	17	R.SQSSEGVSSLSSS*PSNSLETQSQSLSR.S	Phosphorylation at S4, S5, S6, S7 or S8		1	ubiquitin conjugation factor e4 b/ufd2a	133kDa
1	3	4.4362	SWN:UB4B_MOUSE	(+)1	17	R.SQSSEGVSSLSSSPSNSLETQSQSLS*R.S	☺	1		ubiquitin conjugation factor e4 b/ufd2a	133kDa
2	2	3.2104	GP:AB015801	(+)1	21,22	R.IDST*EVIYQPR.R	Phosphorylation at S1 or T1		1	LKB1	49kDa
1	2	2.6949	GP:AB029291	(+)1	21	K.NVRS*DVS*DQEEDEESER.C	☺	2		pericentriolar material-1 (PCM-1)	229kDa
1	2	2.8792	GP:AB029291	(+)1	18	R.VTNAIS*PESSPGVGR.R	☺	1		pericentriolar material-1 (PCM-1)	229kDa
1	2	2.5438	GP:AB033615	(+)1	18	R.GAAGGALPTSPS*PALGAK.G	☺	1		phospholipase C-L2	126kDa
1	2	3.3506	GP:AB073672	0	5,6	K.ESETFS*DSS*PIEIIDEFPTFVSAK.D	☺(IIII)	2		nogo-A mRNA/RTN4	127kDa
1	2	2.5979	GP:AB073672	(+)1	13	K.ESETFS*DSSPIEIIDEFPTFVSAK.D	☺(see doubly phosphorylated)			nogo-A mRNA/RTN4	127kDa
1	3	4.6565	GP:AB073672	(+)1	13	K.ESETFSDSS*PIEIIDEFPTFVSAK.D	☺(see doubly phosphorylated)			nogo-A mRNA/RTN4	127kDa
1	2	2.8362	GP:AB082952	0	7,8	R.ILDTSSLTQS*APAS*PTNK.G	☺Hit #2 Phosphorylation at S4 and T2 or S3*	1	1	Raptor	150kDa
2	2	2.5544	GP:AB091121	(+)1	11	K.TMEPVAELPVPSAT*SSK.K	☺Hit #3 (II)	1		RNA polymerase I-associated factor PAF 49	44kDa
1	2	2.6949	GP:AB099288	0	5,6	R.TTNPFYNT*M.-	☺	1		slingshot-2L	158kDa
1	2	2.9905	GP:AF057285	(+)1	14	R.TALPTSGSST*GELELLAGEVPAR.S	Phosphorylation at S1, S2, or S3		1	epsin 1	63kDa
1	2	3.5878	GP:AF062655	0	5,6	R.S*PS*PAPPPPPPPPPR.R	☺(IIII)	2		plenty-of-prolines-101	101kDa
1	2	3.5491	GP:AF177346	(+)1	20	R.GPAAAPGAAS*PPAEPK.I	☺	1		PLIC-2/ubiquilin 2	67kDa
2	2	3.0492	GP:AF187731	0	5,6	R.AS*S*IDSASNTELQTHDMSS*DEK.K	☺Phosphorylation at S1, S2 and S5 or S6 (II)	2	1	LBA/LPS up-regulated	317kDa
1	2	3.2659	GP:AF202893	0	5,6	K.LQAENS*EET*DENEAEEEEEER.D	☺	2		kinesin-like protein kif21b	186kDa
1	2	3.0214	GP:AF307453	(+)1	17	K.SVQPEVELSGGSGS*GGDEGADESR.G	☺	1		neuron navigator 1	202kDa
1	2	2.9017	GP:AF326555	(+)1	16	R.DSLEETDIDIATEDKS*PIDT.-	☺Hit #2	1		phosphodiesterase 4B (Pde4b)	82kDa
1	2	3.0521	GP:AF338472	0	5,6	R.SSS*S*SSSGVGSPAVTPTEK.M	☺Phosphorylation at S4 and S1, S2 or S3 (III)	1	1	WRP/p140Rho-GAP	124kDa
2	2	3.852	GP:AF361882	(+)1	15	R.VDEPPPQAVSLTPGGVSSS*ALSR.M	Phosphorylation at S2, S3 or S4 (II)		1	endothelial cell-selective adhesion molecule (ESAM)	42kDa
2	2	3.3677	GP:AF374476	(+)1	15	R.TSSLDT*ITGPYLTGQWPR.D	Phosphorylation at T1, S1 or S2 (II)		1	GIG18/testhymin	47kDa
1	2	2.7111	GP:AF404774	0	5,6	R.TLS*PTPS*AEGYQDVR.D	☺	2		actin-binding LIM protein 1 long isoform	97kDa
1	2	2.8408	GP:AF404774	(+)1	17	R.TLS*PTPSAEGYQDVR.D	☺(see doubly phosphorylated, III)			actin-binding LIM protein 1 long isoform	97kDa
1	2	2.6508	GP:AF411837	(+)1	17	R.LQQQAALS*PTTAPAVSSVSK	☺Hit #3			transcription repressor p66	65kDa
1	2	3.0531	GP:AF424697	(+)1	14	K.SASS*SEELINTLNFLDEAQK.D	Phosphorylation at S1, S2 or S3		1	KIAA0903-like protein	136kDa
2	2	3.412	GP:AJ278891	(+)1	19,20	R.LEDNDSATS*EADAEIAAK.T	☺	1		testis specific protein a14	41kDa
2	2	2.5585	GP:AJ292467	(+)1	18	K.MKLTS*DAEDLSLESVCT*R.S	☺Phosphorylation at T2 and T1 or S1	1	1	WDR9 protein	259kDa
1	2	4.7113	GP:AK001486	(+)1	17	K.NWEDEDFYDS*DDDTFLDR.T	☺	1		similar to kanadaptin	89kDa
3	2	2.8361	GP:AK002671	0	3,4	R.EQES*S*GEEDNDLSPEER.E	☺(II)	2		protein phosphatase 1, regulatory (inhibitor) subunit 2	23kDa
2	2	5.2089	GP:AK003415	(+)1	18	R.SAS*PDDDLGSSNWEAADLGNEER.K	☺Hit #2 (D-III)(C-VIII)	1		small acidic protein	20kDa
2	2	2.594	GP:AK003638	0	7,8	R.TEARS*S*DEENGPPSS*PDLDR.I	☺	3		RIKEN clone:1110012J22	27kDa
2	2	3.9027	GP:AK003844	(+)1	13	R.SAPSS*APSTPLSTDAPEFLSIPK.D	☺	1		retinal degeneration B beta	39kDa
1	2	2.6348	GP:AK004073	0	9	R.ENPPS*PPTS*PAAPQPR.E	☺(II)	2		RIKEN clone:1110033L23 hypothetical protein	33kDa
4	2	2.6497	GP:AK004312	0	7	K.NSSLLSFDS*EDENE.-	☺(B-I)	1		RIKEN clone:C920004D01	17kDa
2	2	2.8191	GP:AK004332	(+)1	16	R.TAS*PVIALQNGLSEDEALQR.A	☺	1		RIKEN clone:1110060O18	28kDa
1	3	3.791	GP:AK004509	(+)1	9	R.ASGS*PPLLPAPDPVSLESEPIAEDGALGPPEPIQGTAQPVK.R	Phosphorylation at S1 or S2*		1	TUG	60kDa
1	2	3.4686	GP:AK004582	0	5,6	R.GPS*PAPVDTES*PVEMPEK.A	☺(IIII)	2		RIKEN clone:4732427P14	93kDa
1	2	2.5168	GP:AK004582	(+)1	16	R.GPS*PAPVDTESPVEMPEK.A	☺(see doubly phosphorylated)			RIKEN clone:4732427P14	93kDa
2	2	3.6661	GP:AK004678	(+)1	19,20	R.FDQLFDDES*DPFEVLK.A	☺	1		hypothetical RNA binding protein RDA288 homolog	45kDa
2	2	3.1042	GP:AK004762	(+)1	9	R.SGSPGT*PAYPLSDLLFQSYQER.E	☺	1		DNA segment, Chr 7, ERATO Doi 462	38kDa
1	2	3.1754	GP:AK005027	(+)1	16	R.AGSGEDPVLAPSGT*PPPSIPPDETFGGR.V	☺(II)	1		RIKEN clone:1300017A15	118kDa
2	2	3.3648	GP:AK005039	(+)1	15	R.GAIS*AEVYTEEDAASYVR.K	☺	1		protein kinase, cAMP dependent regulatory, type I, alpha	46kDa
2	2	4.2333	GP:AK005219	(+)1	13	K.VSTTTDSPVS*PAQAASPFIPVDELSSK.-	☺	1		RIKEN clone:1500011L08	30kDa
2	2	2.6592	GP:AK007793	0	7,8	R.SSGTAPAPAS*PS*PPEPGPGGEAESVR.V	☺	2		spastic paraplegia 4 homolog	61kDa
2	2	2.6253	GP:AK007896	(+)1	15	K.NAIS*LPQLNQATYDSLVMGK.L	☺	1		CDC42 effector protein (Rho GTPase binding) 1	43kDa
4	2	3.8346	GP:AK008805	(+)1	19,20	K.NWEDDS*DEDMSNFDR.F	☺(VIIII)(B-III)	1		telomerase binding protein, p23	19kDa
4	2	4.4944	GP:AK008915	0	7	R.YFQISQDEDGS*ESED.-	☺(V)	1		60S ribosomal protein L22	14kDa
2	2	2.6021	GP:AK009320	(+)1	3,4	K.LLLDPSST*PTK.A	☺(D-II)	1		RIKEN clone:2810468M23	18kDa

3	3	3.8139	GP:AK009414	(+)1	8,9	K.VTDALPEPEPAGAMAAS*EEGEEEEDEEDLEAMQSR.L	☺	1		Neuroendocrine Differentiation Factor homolog	25kDa
2	2	4.016	GP:AK009420	(+)1	18	R.YGVYEDENYEVES*DDEEIPFK.C	☺	1		RIKEN clone:2310020H19	39kDa
1	3	5.3675	GP:AK009972	(+)1	16	K.LQEEGGS*EEEEAGNPSEDGMQSGPTQAPPR.E	☺(II)	1		Periodic tryptophan protein 1 homolog	56kDa
2	2	3.2633	GP:AK010353	(+)1	12	K.EEENVDS*DDEGELQDLLSQDWR.V	☺	1		RIKEN clone:2410003C20	41kDa
2	2	3.0337	GP:AK010860	(+)1	19,20	R.TDKS*SASAPDVDDPEAFPALA.-	☺Hit #2	1		hypothetical RNA binding protein RDA288 homolog	43kDa
2	2	2.8111	GP:AK011253	(-)1	3,4	K.FVEWLQNAEEES*ES*EGEES.-	☺Hit #2	2		hypothetical eIF4-gamma/eIF5/eIF2-epsilon cont. protein	48kDa
3	2	3.4211	GP:AK011289	(+)1	12	R.ILGSLGALPT*EEEEEEEEEEEDK.Y	☺	1		similar to C-MYC TARGET JPO1	44kDa
2	2	2.7298	GP:AK011300	0	5,6	K.ASVAS*DPES*PPGGNEPAAASGQR.L	☺Hit #2	2		mRNA (Guanine-7-)Methyltransferase (fragment) homolog	53kDa
2	2	4.3294	GP:AK011300	(+)1	21-22	K.ASVASDPES*PPGGNEPAAASGQR.L	☺(see doubly phosphorylated, III)			mRNA (Guanine-7-)Methyltransferase (fragment) homolog	53kDa
2	2	4.4794	GP:AK011300	(+)1	17	K.EFGEDLVEQNSSYVQDS*PSK.K	☺	1		mRNA (Guanine-7-)Methyltransferase (fragment) homolog	53kDa
3	2	5.7276	GP:AK011303	(+)1	10,11	R.S*AEDLTDGSYDDILNAEQLK.K	☺(XIII)(D-II)	1		RIKEN clone:2610003C16	33kDa
1	2	3.4639	GP:AK011492	(+)1	16	R.IGELGAPEVWGLS*PK.N	☺(B-II)	1		RIKEN clone:2610020O08	47kDa
2	2	2.7972	GP:AK012309	(+)1	16	R.ANSTS*DSMFTETPSPVLK.N	☺Hit #3	1		CRIB-containing BORG2 protein homolog	27kDa
2	2	2.5629	GP:AK012804	(+)1	5,6	K.QLS*ETRISS*LLYTAPPLHS*K.Y	☺Hit #2	3		RIKEN clone:2810024N24	29kDa
2	2	3.6477	GP:AK012822	(+)1	16	K.LGSLTPEIVSTPSS*PEEEDK.S	☺(III)	1		RIKEN clone:2810026N18	37kDa
2	2	2.994	GP:AK013898	(+)2	21-22	R.DMQAWSAVGTKTQGWARPS*PR.R	☺(II)	1		RIKEN clone:3010024O21	15kDa
2	2	2.9442	GP:AK017713	(+)1	9	K.S*LVGTPYWMAPELISR.L	☺(II)	1		P21-activated kinase 4) (PAK-4) homolog	65kDa
4	2	4.0908	GP:AK017729	(+)1	17	R.LAS*TDDGYIDLQFK.K	☺	1		RIKEN clone:5730494N06	13kDa
2	2	2.6772	GP:AK018507	(+)1	19,20	R.YAGLDDTDS*EDELPPGWEER.T	☺	1		WW-domain oxidoreductase	46kDa
2	2	2.5473	GP:AK019878	0	5,6	R.NPS*PPPPTCGS*EDEEDLGGGDR.I	☺Hit #2	1		ARM repeat structure containing protein	53kDa
4	2	3.6731	GP:AK020110	(+)1	17	R.LPS*IVVEPTEGEVESGELR.W	☺(III)	1		limb bud and heart (Lbh)	12kDa
2	2	3.9595	GP:AK020775	(+)1	14	K.AATPVVVTAAAPAMEPGPSVS*PGPSR.S	☺Hit #2	1		NC8 tripartite motif-containing 35	59kDa
2	2	4.0439	GP:AK021409	(+)1	21,22	R.VAEPEES*EAEEPAAEGR.Q	☺	1		RIKEN clone:1810057P16	19kDa
4	3	4.1437	GP:AK028385	(+)1	16	R.LLTPNPGYGTQVGTSPAPTT*PTEEEDLR.R	☺	1		RIKEN clone:3830431	66kDa
2	2	4.3365	GP:AK028838	(+)1	19,20	R.EVDQDDEENS*EEDEMDSGTMVR.A	☺(A-I)	1		serine/threonine kinase 4	55kDa
2	2	3.6658	GP:AK030749	(+)1	12	R.ETFAS*DTNEALASLDEAQEGPGETK.L	Phosphorylation at T1 or S1		1	phosphorylated adaptor for RNA export	43kDa
2	2	3.767	GP:AK031203	(+)1	19,20	R.GPDEAIEDGEEGS*EDDAEWVVTK.D	☺	1		EH-domain containing protein 2	61kDa
2	2	3.5358	GP:AK031297	(+)1	19,20	R.LPATS*AESESAVISNGEH.-	Phosphorylation at T1 or S1		1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	58kDa
1	2	2.6302	GP:AK031472	0	5,6	R.SVAS*NQS*EMEYSSLQDMPK.E	☺(II)	2		IMAGE:3985250/P30 DBC PROTEIN homolog	103kDa
1	2	3.1461	GP:AK031472	(+)1	16	R.SVAS*NQSEMEYSSLQDMPK.E	☺(see doubly phosphorylated, II)			IMAGE:3985250/P30 DBC PROTEIN homolog	103kDa
2	3	3.6945	GP:AK031648	(+)1	19,20	K.VLSSTINNQVAEADEAAEEETPDS*PGVEK.H	☺	1		RIKEN clone:6030468D24	95kDa
2	2	3.9405	GP:AK031790	(+)1	18	K.TEDGGWEWS*DDEFDEESEEGR.A	☺	1		oxidative-stress responsive 1 homolog	52kDa
2	2	4.4526	GP:AK031877	(+)1	14	K.EPLS*DEDEEDNDDVEPISEFR.F	☺(II)(C-II)(D-I)	1		chloride channel, nucleotide-sensitive, 1A	27kDa
2	2	2.6842	GP:AK032027	0	7,8	R.MLQALS*PKQS*PVSSPT*R.S	☺Hit #2	3		phosphate cytidylyltransferase 1, choline, beta isoform	42kDa
2	2	4.1209	GP:AK032569	(+)1	13	R.VDSS*VEEDELMLTESK.S	☺Hit #2 (III)	1		hypothetical alpha/beta-Hydrolase	54kDa
1	2	3.0522	GP:AK032651	0	5,6	R.ASAVPDPSSVDPPS*DPS*ADR.I	☺	2		RIKEN clone:6530402L19	66kDa
2	2	2.6878	GP:AK034681	(+)1	12	R.T*WTLCGTPEYLAPEVIQSK.G	Phosphorylation at T1 or T2		1	PKA-related protein kinase	40kDa
3	2	3.5935	GP:AK034731	(+)1	12	R.S*PVSPLAAQGIPLPAQLTK.A	☺	1		hypothetical BTB/POZ domain containing protein	32kDa
2	2	3.244	GP:AK035227	(+)1	10	R.LS*QEKQNSDS*DSLGMNDSGSTLGR.R	☺(III)	2		similar to actin filament associated protein	52kDa
1	2	3.5073	GP:AK035236	(+)1	16	R.IQQFDDGGS*DEEDIWEEK.H	☺	2		Sporulation-induced transript 4-associated protein (SAPLB) homolog	95kDa
4	2	2.7022	GP:AK035238	(+)1	18	R.SFS*MQDLTTIR.G	☺	1		RIKEN clone:9530004E16	22kDa
1	2	2.6014	GP:AK036331	0	5,6	R.GSS*QPNLSTSYS*EQEYGK.A	☺ Hit #3	2		epsin 2	62kDa
2	2	2.7696	GP:AK036331	(+)1	19,20	R.GSS*QPNLSTSYSEQEYGK.A	☺(see doubly phosphorylated)			epsin 2	62kDa
2	2	2.5429	GP:AK044765	(+)1	19,20	R.DAS*PPEPASPTIGLDK.K	☺	1		RIKEN clone:A930041A10	45kDa
2	2	3.0969	GP:AK044889	(+)1	12	K.TTYLEDLPPLPEYELS*PSK.L	☺	1		RIKEN clone:B130010H02	53kDa
1	2	3.0783	GP:AK045250	0	3,4	K.YAALS*VDGEDEDEGDDCTE.-	☺	1		eukaryotic initiation factor 4B	69kDa
3	2	3.7293	GP:AK045977	0	5,6	R.KLDAES*DGST*EETDESET.-	☺Phosphorylation at S1 and S2 or T1	1	1	RIKEN clone:B230329H23	38kDa
2	2	3.9746	GP:AK046322	(+)1	13	K.AFT*FDDEDDELSQLK.E	☺(III)	1		hypothetical Aminoacyl-transfer RNA synthetases class-II protein	57kDa
1	2	3.6388	GP:AK047363	(+)1	16	R.NVTAS*DEEEGAGLFDSAGK.A	☺(III)	1		RIKEN clone:B930053E03	56kDa
1	3	4.1314	GP:AK048691	0	1,2	R.VDLAGS*PEQEASGLPDPQQQCPPGAS.-	☺	1		activator of G-protein signaling 3 homolog	74kDa
1	2	4.2366	GP:AK049495	(+)1	16	R.VFDDDS*DDIEEEEEADEK.E	☺	1		RIKEN clone:C430017F24	86 kDa
2	2	2.8369	GP:AK051665	0	5,6	R.DAS*PTPST*DAEYPANGSGADR.I	☺Phosphorylation at S1 and S2 or T2	1	1	SH2/SH3 adaptor protein (mNck-beta)	43kDa
2	2	3.3071	GP:AK051665	(+)1	19,20	R.DAS*PTPSTDAEYPANGSGADR.I	☺Hit #2 (see doubly phosphorylated, III)			SH2/SH3 adaptor protein (mNck-beta)	43kDa
2	2	3.8784	GP:AK051665	(+)1	18	R.DASPT*PSTDAEYPANGSGADR.I	☺Hit #2 (IIII)	1		SH2/SH3 adaptor protein (mNck-beta)	43kDa
3	2	2.8026	GP:AK053310	0	3,4	K.LGGS*PTNGNSAAPSPPESEP.-	☺(III)(D-I)	1		RIKEN clone:E130009D24	19kDa
4	2	3.2879	GP:AK053310	0	5,6	K.LGGSPT*NGNSAAPSPPESEP.-	☺	1		RIKEN clone:E130009D24	19kDa
1	3	3.4813	GP:AK053844	(+)1	16	R.SPEQPAES*DTPS*ELELSGHGPAAEASGAAGDPADADPATK.L	☺	2		A kinase (PRKA) anchor protein (gravin) 12	181kDa
3	3	3.5395	GP:AK054279	(+)1	10,11	R.TNS*EQVDEDADVDTAMASLDEQSREAQPPS*PR.S	☺Phosphorylation at S4 and T1 or S2	1	1	pVHL-interacting deubiquitinating enzyme 2 (Vdu2)	102kDa
2	2	2.6395	GP:AK077263	(+)1	12	R.DVS*PIVEIPDAAFIQAAR.R	☺	1		RIKEN clone:5031433E12	46kDa
3	2	3.3986	GP:AK078345	0	3,4	K.VENMSSNQDGNDS*DEFM.-	☺(IIII)	1		RIKEN clone:6530403I23	25kDa
2	2	4.1974	GP:AK078816	(+)1	17	K.VVDYSQFQES*DDADEDYGR.D	☺	1		nuclear ubiquitous casein and cyclin-dependnet kinases substrate	26kDa
4	2	2.7962	GP:AK080452	(+)1	18	K.GFGVENPVLPES*PPASMSSVMK.N	☺	1		RIKEN clone:A730017C20	17kDa
2	2	3.088	GP:AK082771	(+)1	11	K.AGS*PGSEVVTLQQFLEESNK.L	☺(III)(C-IIII)(A-I)	1		RIKEN cDNA A430106J12	82kDa
1	2	3.7235	GP:AK082771	(+)1	16	K.SSS*QENLLDEVMK.S	☺(II)	1		RIKEN cDNA A430106J12	82kDa
2	2	3.4872	GP:AK082775	(+)1	19,20	R.DLFSLDSEGPSPTS*PPLR.S	☺	1		RIKEN clone:C330013H05	28kDa
2	3	4.5802	GP:AK082912	(+)1	13	R.EDPGQVSSFFNSEEAES*GEDEDIVGPMPAK.G	☺	1		RIKEN clone:C430016O19: similar to Protein Phosphatase 4 regulatory subunit 2	39kDa
2	2	2.6425	GP:AK083747	(+)1	19,20	K.NS*DSNLLSLDGLDNEVK.V	☺	1		RIKEN clone:D030074E01	93kDa
2	3	4.1211	GP:AK087895	0	5,6	K.EGS*LGDELLPLGYAEPEPQEGASAGAPSPT*LELASR.S	☺Phosphorylation at S1 and S3* or T1	1	1	predominantly fetal expressed T1 domain (Pfet1)	36kDa
3	3	4.5096	GP:AK087895	(+)1	10,11	K.EGSLGDELLPLGYAEPEPQEGASAGAPSPT*LELASR.S	Phosphorylation at S3 or T1*(see doubly phosphoryated, B-I)			predominantly fetal expressed T1 domain (Pfet1)	36kDa
1	2	2.5636	GP:AK088527	(+)1	16	K.DTAATFQSVDGS*PQAEQSPLESTSK.E	☺(II)	1		RIKEN cDNA 1110054L24	55kDa

1	2	3.0226	GP:AK089105	0	5,6	R.GLVAAYSGES*DS*EEEQER.G	☺(II)	2		RNA-BINDING PROTEIN 10	95kDa
1	2	2.5137	GP:AK090123	0	5,6	R.SS*SELS*PEVVEK.V	☺ Phosphorylation at S4 and S1* or S2	1	1	RNA BINDING PROTEIN homolog	283kDa
1	2	2.5257	GP:AK122267	(+)1	18	R.SEGVQDAQEPQSLVGS*PSTR.G	☺	1		mKIAA0382	174 kDa
1	2	2.8873	GP:AK122314	0	5,6	K.LLEDS*ES*GEEAVGSNGSSLQK.K	☺(III)	2		DEAH (Asp-Glu-Ala-His) box polypeptide 16	119kDa
1	2	3.6153	GP:AK122330	(+)1	16	R.ST*SALSTAESVGQSDR.F	Phosphorylation at S1, T1 or S3*		1	mKIAA0622	88kDa
1	2	3.8898	GP:AK122330	(+)1	13	R.VLSTST*DLEAAVADALLLGDAR.S	Phosphorylation at T1, S2 or T2* (II)		1	mKIAA0622	88 kDa
1	2	3.186	GP:AK122399	(+)1	17	K.GSES*PNSFLDQEYR.K	☺Hit #2	1		mKIAA0902	120 kDa
2	2	2.6377	GP:AK122405	0	7,8	K.SHS*S*PSLNPDAS*PVTAK.V	☺Hit #2	3		mKIAA0942	31kDa
2	2	3.1585	GP:AK122405	0	7,8	K.SHSS*PS*LNPDAS*PVTAK.V	☺ Phosphorylation at S4, S5 and S2 or S3	1	1	mKIAA0942	31kDa
1	2	3.9714	GP:AK122475	(+)1	13	R.LPS*LSVQPVSNADWVWLVK.R	☺	1		mKIAA1244	185kDa
2	2	4.1649	GP:AK122494	(+)1	19,20	K.DYEIENQNPLAS*PTNTLLGSAK.E	☺(III)	1		mKIAA1321	78kDa
1	2	3.0543	GP:AK122505	(+)1	17	R.ASDT*PSGPPAADTVGVAMR.V	☺	1		mKIAA1403	159kDa
1	2	2.9534	GP:AK122574	(+)1	13	R.SASLS*SLFITPFPSPNSSLTR.S	Phosphorylation at S1, S2 or S3		1	mKIAA1961	132 kDa
2	2	3.7181	GP:AK129105	(+)1	16	K.VEEEDTGDPFGFDS*DDESLPVSSK.N	☺	1		mKIAA0261	143kDa
1	2	3.4849	GP:AK129310	(+)1	16	K.DTTS*FEDISPQGISDDSSTGSR.V	Phosphorylation at T1, T2 or S1		1	mKIAA1212	82kDa
2	2	2.814	GP:AK129375	(+)1	15	R.GPS*PETGAAAMAESIIIR.V	☺	1		mKIAA1499	74kDa
2	2	2.7495	GP:AY035997	(+)1	5,6	R.QPPDS*SEETPPTTQNFIIPK.K	Phosphorylation at S1or S2		1	phosphotyrosyl phosphatase activator	37kDa
1	2	2.9201	GP:AY098636	0	5,6	R.GPSPS*S*PTPPPAAAPAEQAPR.A	☺ Phosphorylation at S3 and S1 or S2	1	1	testhymin	58kDa
2	2	4.8304	GP:AY267461	(+)1	12	R.SPS*GGAAGPLLTPSQSLDGSR.R	☺(C-III)	1		predominantly fetal expressed T1 domain (Pfet1)	36kDa
1	2	2.5276	GP:AY337314	0	7,8	K.SQDSYPGS*PSLS*PR.H	☺ Hit #2	2		Ran-binding protein 10	70kDa
2	2	2.8067	GP:BC002150	0	5,6	K.NS*PGAVGGLSNAPGT*PR.D	☺	2		RIKEN cDNA 1210002E11	37kDa
1	3	7.1104	GP:BC005460	(+)1	18	K.KEDS*DEDEDEEDEEDS*DEDEDDEEEDEFEPPIVK.G	☺(V)	2		nucleolin	77kDa
2	3	4.7568	GP:BC010255	(+)1	10	K.ETSLLAVPGALS*PLAIPNAAAAAAAAAAGR.V	☺(A-I)	1		polypyrimidine tract binding protein 2	58kDa
2	3	3.5521	GP:BC010255	(+)1	18	R.GSDELLSGSVLSS*PNSNMSGMVVTANGNDSK.K	☺Hit #3 (III)	1		polypyrimidine tract binding protein 2	58kDa
1	2	3.0413	GP:BC017596	(+)1	16	R.TGS*PLTVATGNDQAATEAK.I	Phosphorylation at T1 or S1*		1	RIKEN cDNA 3110007P09	86kDa
1	2	4.0531	GP:BC017634	(+)1	15	K.AAAT*PEPAVAQPDSTALEGATGQAPPSSK.G	☺	1		IMAGE:4527857	55 kDa
1	2	4.0849	GP:BC019710	(+)1	13	R.S*FSLDEPPLFIPDNIATVK.K	☺	1		IMAGE:3992608	25 kDa
2	2	5.665	GP:BC023347	(+)1	19,20	R.DFQEYVEPGEDFPAS*PQR.R	☺	1		dynein, cytoplasmic, light intermediate chain 1	57kDa
2	2	2.8842	GP:BC023347	0	7,8	R.KPASVSPTT*PTS*PTEGEAS.-	☺(II)	2		dynein, cytoplasmic, light intermediate chain 1	57kDa
2	2	2.9689	GP:BC024115	(+)1	7,8	K.VS*PVNDVDVGVYQLMQSEQLLSR.K	☺(II)	1		RIKEN cDNA 6330407G04	51kDa
1	2	3.0591	GP:BC024817	(+)1	18	K.AALPAGEGGS*PEGAK.I	☺	1		amphiphysin	75kDa
2	2	3.3114	GP:BC024906	(+)1	17	R.YGVYEDENYEVGS*DDEEIPFK.C	☺	1		RIKEN cDNA 2810428C21	38kDa
2	2	2.6769	GP:BC025226	(+)1	10	K.IWDMTPVVGCSLATGFS*PH.-	☺	1		WD40 and FYVE domain containing 1, mRNA	35kDa
1	3	4.5282	GP:BC026519	(+)1	14	R.ATT*PQLTDVSEDLDQQSLPSEPEEALNR.E	Phosphorylation at T1 or T2		1	IMAGE:4913219	34kDa
2	2	3.8709	GP:BC029629	(+)1	14	K.S*MEDLVNEFDEK.L	☺(II)	1		fasciculation and elongation protein zeta 1 (zygin I)	45kDa
2	2	3.1759	GP:BC039951	(+)1	12	R.EMLLEDVGS*EEEPEEDDEAPFQEK.D	☺	1		RIKEN cDNA 8430423A01	26kDa
1	2	3.3179	GP:BC040465	0	5,6	K.VAS*VEEGDETLDS*PGSQSR.G	☺	2		IMAGE:6466491	68kDa
1	2	4.0366	GP:BC040465	(+)1	17	K.VAS*VEEGDETLDSPGSQSR.G	☺(see doubly phosphorylated)			IMAGE:6466491	68kDa
2	2	3.1488	GP:BC043658	(+)1	16	R.SCEEES*DPEPDPDPDTQAEAYVAR.V	☺	1		RIKEN cDNA 1110017H11	50kDa
1	2	2.9851	GP:BC046228	(+)1	19	R.SRS*PVDSPVPASMFAPEPSS*PGAAR.A	☺Phosphorylation at S1* or S2 and S5 or S6*		2	IMAGE:5708774, GTP binding protein 1	72kDa
1	2	2.9046	GP:BC049118	(+)1	17	R.SSLGQSASET*EEDTVSISK.K	Phosphorylation at S4 or T1		1	splicing factor 3b, subunit 2	98 kDa
1	2	3.266	GP:BC050855	(+)1	20	R.APTAALS*PEPQDSK.E	☺(II)	1		IMAGE:6333217	114kDa
2	2	4.0002	GP:BC052413	(+)1	15	K.AVGSMPTAGSAGS*VPENLNLFPEPGSK.S	☺	1		RIKEN cDNA 1810031K02	47kDa
2	3	5.0875	GP:BC056373	(+)2	21,22	K.LPEDDEPPARPPAPAGAS*PLAEPAAPPSTPAAPK.R	☺	1		nogo-A mRNA/RTN4	127kDa
1	2	3.6723	GP:BC056373	(+)1	16	K.LSTEPS*PEFSNYSEIAK.F	☺	1		nogo-A mRNA/RTN4	127kDa
2	2	3.4415	GP:BC056373	(+)1	9	R.GS*GSVDETLFALPAASEPVIPSSAEK.I	Phosphorylation at S1 or S2 (IIII)		1	nogo-A mRNA/RTN4	127kDa
2	2	3.4013	GP:BC057961	(+)1	14	R.ADS*VPNLEPSEESLVTK.-	☺(III)	1		lunapark (Lnp)	48kDa
2	3	5.1193	GP:BC058530	(+)1	19,20	K.GAEPS*PGGTPQPSRPGS*PTGPPEVITEDTQPPQLGQER.D	☺	2		B-cell CLL/lymphoma 7C	23kDa
1	2	2.7387	GP:BC058720	(+)1	16	K.DMDEPS*PVPNVEEVTLPK.T	☺(II)	1		RIKEN cDNA 5930405J04	121kDa
2	2	4.4551	GP:BC058948	(+)1	15	R.QNS*ATESADSIEIYVPEAQTR.L	☺(VIII)	1		mKIAA0964	106kDa
1	2	3.3016	GP:BC059883	(+)1	16	R.SAT*DADMVNSGWLVVGK.D	☺	1		IMAGE:6815625	92kDa
1	2	3.2957	GP:BC060061	(+)1	16	R.TIS*PPSAVVETDTPPIGK.V	☺	1		Mus musculus cordon-bleu (cobl)	144kDa
1	2	2.7545	GP:BC060632	0	7,8	K.GSDYSWSYQT*PPSS*PSSSNSR.K	☺	2		IMAGE:6848397	77kDa
2	2	4.4029	GP:BC062904	(+)1	14	R.S*ESLIDASEDSQLEAAIR.A	☺(III)	1		IMAGE:6812948	53kDa
1	2	2.615	GP:BC062904	0	5,6	R.SES*LIDASEDS*QLEAAIR.A	☺Phosphorylation at S4 and S1 or S2	1	1	IMAGE:6812948	53kDa
3	3	4.783	GP:D87660	(+)1	8,9	K.DST*LIIELLRDNLTLWTSDTQGDEAEAGEGGEN.-	Phosphorylation at S1 or T1 (II)		1	14-3-3 zeta	28kDa
4	2	2.6539	GP:M12313	(+)1	19,20	K.SIDPEEVES*RE.-	☺Hit #2	1		polytropic MLV-related provirus integrase	38-74kDa
1	2	2.5203	GP:U72520	(+)1	15	R.QNS*QLPAQVQNGPSQEELEIQR.R	☺	1		Mena (Mus musculus enabled protein homolog)	86kDa
2	2	3.2796	GP:U88588	(+)1	19,20	R.SSSET*ALSSLAGDDIVK.D	Phosphorylation at S1, S2, S3 or T1		1	cdr2, similar to human paraneoplastic cerebellar degeneration-associated antigen	52kDa
1	3	3.1345	GPN:AK004685	(+)1	17	K.AQSVS*PVQATPSGGSAQLLPGK.V	☺	1		capicua protein (Cic)	166kDa
1	2	2.9098	GPN:AK008111	(+)1	17	R.SNSPLPSIQLQPQS*PSASK.K	☺	1		RIKEN clone:2010005A06	13kDa
1	3	3.4125	GPN:AK009628	(+)1	17	R.QS*GTPPGMGAPGIPGASIVGGAGGR.E	Phosphorylation at S1 or T1 (II)		1	RIKEN clone:6030439E05 product:hypothetical ARM repeat containing protein	135kDa
1	2	2.9151	GPN:AK011521	(+)1	18	R.MGLAMGGAGGAS*FDR.A	☺(II)	1		heterogeneous nuclear ribonucleoprotein M	78kDa
3	2	2.8317	GPN:AK013188	(+)1	19	R.ENGSDNLPPS*PGSGDQTLPDHAPF.-	☺(IIII)	1		RIKEN clone:2810429C01 product:tumor protein D54 homolog	24kDa
1	2	3.2057	GPN:AK014020	(+)1	18	R.WAELLS*PLDESR.A	☺	1		RIKEN clone:3110007G05	11 kDa
1	3	3.922	GPN:AK014477	(+)1	14	K.SLSQS*FENLLDEPAYGLIQK.I	☺	1		RIKEN clone:4432405K22	77kDa
3	2	3.5854	GPN:AK027911	(+)1	19	K.DDDDIDLFGS*DDEEESEEAK.K	☺(IIII)	1		eukaryotic translation elongation factor 1 beta 2	28kDa
1	2	2.9383	GPN:AK028322	(+)1	18	K.ALGVISNFQSS*PK.Y	☺	1		RIKEN clone:3632431M01	36kDa
1	2	2.546	GPN:AK028542	(+)1	19	K.LNQSS*PDNLTDTK.G	☺	1		RIKEN clone:4632425I16 :hyothetical. Calponin-homology domain-cont. protein	133kDa
1	2	2.5179	GPN:AK029072	(+)1	18	R.SPNSAILLS*PVEIPFSK.G	☺	1		RIKEN clone:4732488L18	59kDa

1	2	2.6588	GPN:AK029763	(+)1	19	R.GDNAS*PSPSGTPLVR.A	☺	1		RIKEN clone:4930534J06: similar to superkiller viralicidic activity 2-like protein	138kDa
1	2	2.7946	GPN:AK029901	(+)1	17	R.DLS*PTLLDNSAAK.Q	☺	1		RIKEN clone:4931432P15	70kDa
1	2	2.6293	GPN:AK029945	(+)1	18	K.TASESISNLSEAGS*VK.K	☺	1		Riken clone:4932409G17:similar to RESTIN	93kDa
1	2	3.166	GPN:AK030909	(+)1	18	K.STETSDFENIES*PLNER.G	☺(II)	1		ubiquitin specific protease 47	79kDa
1	2	2.5354	GPN:AK031049	(+)1	17	R.AASAAGAS*PAATPAAPESGTIPK.K	☺	1		RIKEN clone:5832437L22 alkyl-dihydroxyacetonephosphate synthase homolog	72kDa
1	2	2.5781	GPN:AK031348	(+)1	18	K.LSQVNES*DADDEDNYGAR.L	☺	1		RIKEN clone:6030410K14 product:hypothetical ATP/GTP-binding motif A	49 kDa
1	3	3.4683	GPN:AK032060	(+)1	17	K.TQDQQEYYVTT*PGAEVEDPQK.A	☺(II)	1		ankyrin 2, neuronal long splice form	117kDa
1	3	3.3157	GPN:AK032300	(+)1	18	R.SQERPPETPPTSVSESLPTLSDSDPVPVADS*DDDAGS*ESAAR.D	☺Phosphorylation at S7 and S8 or S9	1	1	hypothetical metallo-hydrolase/oxidoreductase	103kDa
1	3	4.1738	GPN:AK033182	(+)1	13	K.GPENPQVEVLS*EEEGEEEEEEEDILSLAEEK.Y	☺	1		RIKEN clone:8030454G07	15kDa
1	2	3.2814	GPN:AK035833	(+)1	17	R.AAS*PPASASDLIEQQQK.R	☺(II)	1		AK035833_1 hypothetical proline-rich protein	45 kDa
1	2	4.6905	GPN:AK043551	(+)1	13	R.VLNTGS*DVEEAVADALLLGDIR.T	☺(III)	1		RIKEN clone:A830007J18	141 kDa
1	2	3.1996	GPN:AK045159	(+)1	17	R.AES*PETSAVESTQSTPQK.G	☺Hit #2	1		RIKEN clone:B130042B12 (AIPPSAP-2)	92 kDa
1	2	3.0518	GPN:AK045250	(+)1	12	K.S*PPYTAFLGNLPYDVTEDSIK.D	☺Hit #3	1		eukayotic initiation factor 4B	69kDa
1	2	3.7726	GPN:AK045438	(+)1	18	R.VNQSALEAVTPS*PSFQQR.H	☺Hit #2 (II)	1		adaptor protein APPL (signaling adaptor protein DIP13alpha) homolog	72 kDa
1	2	2.8414	GPN:AK046142	(+)1	18	K.TPT*PEPAEVETR.K	☺	1		RIKEN clone:B230344L17 (HLS7-IPK)	61 kDa
1	3	5.0031	GPN:AK049311	(+)1	15	R.YMAENPTAGVVQEEEEDNLEYDS*DGNPIAPSK.K	☺	1		RNA helicase-related protein homolog	89kDa
1	2	2.5022	GPN:AK049446	(+)1	20	K.AAPAIAT*FNNQPSGTPQCFVGEK.H	☺	1		RIKEN clone:C430013M08	30kDa
1	2	2.8785	GPN:AK051354	0	13	R.TSS*KESS*PVPS*PTLDR.K	☺	3		beta-spectrin 2	57kDa
1	2	2.5609	GPN:AK051354	(+)1	19	R.TSS*KESSPVPS*PTLDR.K	☺(see triply phosphorylated)			beta-spectrin 2	57kDa
1	2	2.9976	GPN:AK051735	(+)1	17	R.WLDES*DAEMELR.A	☺	1		B-IND1 protein similarity to eIF4GII	23-43 kDa
1	2	3.2763	GPN:AK053840	(+)1	17	R.TPSAATPAASSS*PSSALATPAK.H	☺	1		SRY-box containing gene 4-unamed	31 kDa
1	2	3.1124	GPN:AK053844	(+)1	17	K.GPSEAPQEAEAEEGATS*DGEK.K	☺	1		A kinase (PRKA) anchor protein (gravin) 12	181kDa
1	3	4.4074	GPN:AK075690	(+)2	18	R.GEIPEGLQDWEEGREDS*EADELGETLPDSTPLGLYLK.S	☺	1		intermediate filament protein nestin (Nes)	202kDa
1	3	4.9155	GPN:AK075999	(+)1	17	K.EGVILTNENAAS*PEQPGDEDAK.Q	☺(II)	1		hypothetical NOL1/NOP2/sun family containing protein	77kDa
1	2	3.2709	GPN:AK080419	(+)1	13	R.KPSPT*QAAETPALDLPLPSVPAPATL.-	Phosphorylation at S1 or T1		1	negative elongation factor b (nelf-b)	66 kDa
1	3	3.367	GPN:AK082771	(+)1	17	R.LPVSVDSS*PPTAGSSSTTASNVNK.V	☺	1		mKIAA1212 protein	82kDa
1	2	2.7427	GPN:AK083499	(+)1	17	R.LGSSGLGS*ASSIQAAVR.Q	☺	1		RIKEN clone:D030032D21	44kDa
1	2	4.0949	GPN:AK088465	(+)1	17	K.VAYIPDETAAQQNPS*PQLR.G	☺(II)	1		IGF-1 (mRNA)binding protein 3	64 kDa
1	2	3.1225	GPN:AK088766	(+)1	19	R.LEREDS*S*EEEEEEIDDEEIER.R	☺(II)	2		microfibrillar-associated protein 1	59kDa
1	2	3.4039	GPN:AK088774	(+)1	14	K.LENEGS*DEDIETDVLYSPQMALK.L	☺(II)	1		cytosolic beta-N-acetylglucosaminidase /meningioma expressed antigen 5	103 kDa
1	2	3.6116	GPN:AK090123	(+)1	18	K.VSS*PVLETVQQR.T	☺Hit #2	1		RNAbinding protein homolog--RCB-0545 OHTA	283 kDa
2	2	2.986	GPN:AY345342	(+)1	15	R.IES*PLETLSAQNHSASMTEVT.-	☺(II)	1		plasticity-related protein 3	36kDa
1	3	3.4257	GPN:BC037112	(+)1	14	R.NSPT*GLAPLPALS*PSALSPASTPHLPNLAAPSFPK.T	☺Phosphorylation at S2 and S1 or T1	1	1	IMAGE:5371896	104kDa
1	2	2.5965	GPN:BC040746	(+)1	17	K.SVPTVDS*GNEDDDSSFK.I	☺(VII)	1		IMAGE:3498498	46 kDa
1	2	2.7697	GPN:BC043939	(+)1	16	K.QAQSS*TEIPLQAESGQGTEEEAAK.D	Phosphorylation at S1* or S2		1	A kinase (PRKA) anchor protein (gravin) 12	181kDa
1	3	3.9291	GPN:BC049942	(+)2	17	R.LAEAPSPAPTPSPTPLEDFGLQTSASPGRLS*PDFVEELR.T	☺	1		scribble homolog 1	43kDa
1	3	3.3518	GPN:BC053918	(+)1	14	K.GQLISS*PTFTAPAALFGEAAPLVK.S	Phosphorylation at S1, S2, T1 or T2		1	Chr X, Immunex 50, expressed, mRNA	23kDa
1	2	2.7338	GPN:BC056373	(+)1	13	R.GSGS*VDETLFALPAASEPVIPSSAEK.I	Phosphorylation at S1, S2 or T1(II)		1	nogo-A mRNA/RTN4	127kDa
1	2	2.8785	GPN:BC057037	(+)1	15	R.DLS*PEGPAPLTEEELDLR.L	☺	1		IMAGE:5702855	108 kDa
1	2	3.3143	GPN:BC057044	(+)1	15	R.SVATGPMT*PQAAAPPAVPPVFPEVR.V	☺Phosphorylation at T1 or T2 (II)(B-I)		1	G protein-regulated inducer of neurite outgrowth 1	95 kDa
1	2	3.4266	GPN:BC057052	(+)1	17	K.GSNPFEDEDDEELAT*PEAEEEK.V	☺	1		IMAGE:6822067	81 kDa
1	2	3.0322	GPN:BC058672	(+)1	18	R.AAGALGSASSGS*MPNLAAR.S	☺	1		similar to NITZIN	115kDa
1	2	4.0077	GPN:BC060694	(+)1	16	K.AGPLGGSSY*EEEEEEEGGGGGER.K	Phosphorylation at S1* or S2		1	nectin-1	57kDa
1	2	2.5895	GPN:BC061473	0	3,4	K.SLAALS*RVS*GNVS*K.E	☺	3		expressed sequence AU067695	52kDa
1	2	3.2038	GPN:BC063094	(+)1	16	K.GGNVFEALIQDDS*EEEEEEEENR.V	☺(B-II)	1		ATP-binding cassette, sub-family F	212kDa
1	2	2.6795	GPN:BC063094	0	5,6	K.QLS*VPAS*DEEDEVPAPIPR.G	☺	2		ATP-binding cassette, sub-family F	212kDa
2	2	3.8173	GPN:BC063386	(+)1	13	R.ATLS*DSEIETNSATSAIFGK.A	Phosphorylation at T1 or S1		1	MAP-kinase activating death domain	173kDa
1	2	3.079	GPN:BC064442	(+)1	16	K.SAST*DLGTADVVLGR.V	Phosphorylation at S1*, S2 or T1		1	hypothetical R3H domain/Serine-rich region/Glutamine-rich region cont protein	107kDa
2	2	5.1823	GPN:BC064783	(+)1	19,20	R.DLYRPLS*SDDLDSVGDSV.-	☺Hit #2 (XXIII)(D-I)	1		double cortin and calcium/calmodulin-dependent protein kinase-like 1	40kDa
1	2	3.626	PIR2:A55817	(+)1	18	R.DLLSDLQDIS*DSER.K	☺	1		cyclin-dependent kinase p130-PITSLRE	91 kDa
2	3	4.1747	PIR2:A60670	0	3,4	R.LPPTEGEVYQTPGAGQGTPESSGPLT*P.-	☺(IIII)	1		beta-2 adducin	63kDa
1	3	4.7835	PIR2:JC4978	(+)1	14	K.EVDPSTGELQSLQMPESEGPS*SLDPSQEGPTGLK.E	Phosphorylation at S4 or S5--see below (B-I)		1	oxidative stress protein A170	48kDa
2	3	5.2586	PIR2:JC5630	(+)1	19,20	K.SAEPLANTVLASET*EEEGNAQALGPTAK.S	☺	1		Treacher Collins Franceschetti syndrome 1, homolog	135kDa
1	2	4.6023	PIR2:JC5662	0	5,6	R.GGS*S*GEELEDEEPVK.K	☺(VII)	2		hepatoma-derived growth factor-related protein 2	75kDa
1	2	3.7666	PIR2:JC5930	0	5,6	R.ADT*PS*GDEQEPNGALDSK.G	☺(II	2		serine/arginine-rich protein specific kinase 1 (SRPK1)	73kDa
1	3	6.1455	PIR2:JC7862	(+)1	14	R.QQPASESPPT*DEAAGSGGSEVGQTEDAEEDAEAGPEPEVR.A	☺	1		eukaryotic initiation factor 3 subunit, p116	91kDa
2	3	4.274	PIR2:T30827	(+)1	11	K.VQGEAVSNIQENTQTPT*VQEESEEEEVDETGVEVK.D	☺(II)	1		nascent polypeptide-associated complex alpha chain, non-muscle splice form	23kDa
3	3	7.0322	PIR2:T30827	(+)1	13	K.VQGEAVSNIQENTQTPTVQEES*EEEEVDETGVEVK.D	☺(XXXX)(B-XVIII)	1		nascent polypeptide-associated complex alpha chain, non-muscle splice form	23kDa
1	2	3.6587	PIR2:T34101	(+)1	13	K.LSYAS*AESLETMSEAELPLGFSR.M	Phosphorylation at S1 or S2		1	neural-specific protein (hyp)	131kDa
1	2	3.3949	PIR2:T34188	(+)1	18	K.SPAPSNPTLS*PSTPAK.T	Phosphorylation at S3 or T1		1	Myb-binding protein-160	152kDa
1	2	3.2879	PIR2:T42719	(+)1	17	K.GGEFDEFVNDDT*DDDLPVSK.K	☺	1		TPR-containing SH2-binding protein/cyclic gmp inhibited phosphodiesterase b	133kDa