Table S1. Ratios of phosphopeptides identified by MS2 from p1 or p45 cortex over a common internal standard (N15 labeled rat brain). Peptides were identified from MS2 spectra.

Peptide	Protein Index	Protein Name	p1/N15	p45/N15	p
R.EMDESLANLS(p)EDEYYS(p)EEER.N	IPI00187694.2	PREDICTED: similar to AOF2 protein	1.43	0.93	
K.MES(p)EAGADDS(p)AEEGDLLDDDDNEDR.G	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	2.57	1.37	
K.SEEEQSSAS(p)VKKDETNVK.M	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	2.02	0.91	
R.SAAEMYGSVPEHPSPS(p)PLLSSSFDLDYDFQR.D	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	1.11	X	
K.MESEAGADDS(p)AEEGDLLDDDDNEDR.G	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	1.68	0.68	
K.MESEAGADDS(p)AEEGDLLDDDDNEDRGDDQLELK.D	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	1.22	0.9	
K.SEEEQS(p)SAS(p)VKKDETNVK.M	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	3.08	X	
R.SAAEMYGSVPEHPSPSPLLSS(p)SFDLDYDFQR.D	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	0.34	X	
K.MES(p)EAGADDS(p)AEEGDLLDDDDNEDR.G	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	X	0.98	
K.SEEEQSS(p)AS(p)VKKDETNVK.M	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	X	1.39	
K.MESEAGADDS(p)AEEGDLLDDDDNEDR.G	IPI00187860.3	Heterogeneous nuclear ribonucleoprotein C	X	1.02	
R.NAS(p)VPNLR.G	IPI00188468.2	Hypothetical protein RGD1305453	X	1.06	
K.SPASVKS(p)PSEAK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.66	
K.SPAS(p)VKSPSEAKS(p)PAGAK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.47	
K.SPAEAKS(p)PAEVKS(p)PAEVK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.39	
K.S(p)PASVKS(p)PSEAK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.59	
K.SPSEAKS(p)PAGAKS(p)PAEAK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.43	
K.SPAGAKS(p)PAEAK.S	IPI00188524.2	Neurofilament triplet H protein	X	0.54	
K.TTSTS(p)NPSSPAPDWY(p)KDFVTDADAEVLEHSGK.M	IPI00188882.3	PREDICTED: similar to ATRX protein	1.52	X	
K.TTS(p)TSNPSS(p)PAPDWYKDFVTDADAEVLEHSGK.M	IPI00188882.3	PREDICTED: similar to ATRX protein	1.54	X	
K.YVES(p)DDEKPTDENVNEK.A	IPI00188882.3	PREDICTED: similar to ATRX protein	1.8	0.78	
R.EESS(p)DNEHSVEHDVTILLEDSDLR.R	IPI00188882.3	PREDICTED: similar to ATRX protein	1.19	X	
K.TTSTS(p)NPSS(p)PAPDWYKDFVTDADAEVLEHSGK.M	IPI00188882.3	PREDICTED: similar to ATRX protein	1.53	X	
R.QNYSESSNY(p)DSELER.E	IPI00188882.3	PREDICTED: similar to ATRX protein	1.19	1.07	
K.T(p)TSTSNPSSPAPDWY(p)KDFVTDADAEVLEHSGK.M	IPI00188882.3	PREDICTED: similar to ATRX protein	1.38	X	
K.TTSTSNPS(p)S(p)PAPDWYKDFVTDADAEVLEHSGK.M	IPI00188882.3	PREDICTED: similar to ATRX protein	1.64	0.69	
R.QNYSES(p)SNYDSELER.E	IPI00188882.3	PREDICTED: similar to ATRX protein	1.19	X	
R.QNYS(p)ESSNYDS(p)ELER.E	IPI00188882.3	PREDICTED: similar to ATRX protein	X	1.2	
R.QTESNPAVSNS(p)DEEGNETIK.E	IPI00188882.3	PREDICTED: similar to ATRX protein	X	0.8	
K.Y(p)VESDDEKPTDENVNEK.A	IPI00188882.3	PREDICTED: similar to ATRX protein	X	0.69	
K.SVSDKEEHDFS(p)EDEK.Q	IPI00188882.3	PREDICTED: similar to ATRX protein	X	0.58	
K.DSGSDEDFLMEDDDDS(p)DYGSSK.K	IPI00189138.1	Nuclear ubiquitous casein and cyclin-dependent kinases substrate	X	0.5	
K.VVDYSQFQES(p)DDADEDYGR.D	IPI00189138.1	Nuclear ubiquitous casein and cyclin-dependent kinases substrate	X	0.66	
R.NIDQSEFEGFS(p)FVNSEFLKPEVK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	0.05	1.66	
K.ENIWDGVTTKT(p)FCGTPDYIAPEIIAYQPYGK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.28	
K.ENIWDGVT(p)TKTFCGTPDYIAPEIIAYQPYGK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.59	
K.ENIWDGVTT(p)KTFCGTPDYIAPEIIAYQPYGK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.72	
R.NIDQSEFEGFSFVNS(p)EFLKPEVK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.91	
K.T(p)FCGTPDYIAPEIIAYQPYGK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.16	
R.NIDQSEFEGFS(p)FVNSEFLKPEVK.S	IPI00189278.4	Splice Isoform Beta-II of Protein kinase C beta type	X	1.48	
R.DSLGDFIEHYAQLGPSS(p)PEQLAAGAEEGGGPR.R	IPI00189358.2	Transcriptional activator protein Pur-beta	0.29	0.94	
R.DSLGDFIEHYAQLGPS(p)SPEQLAAGAEEGGGPR.R	IPI00189358.2	Transcriptional activator protein Pur-beta	X	0.72	
R.KFS(p)LAATR.S	IPI00189722.1	Tropomodulin-2	X	1.13	
R.TTQSLQDFPVADS(p)EEEAEEEFQK.E	IPI00190035.1	Tuftelin interacting protein 11	0.57	0.98	
R.TTQSLQDFPVADS(p)EEEAEEEFQK.E	IPI00190035.1	Tuftelin interacting protein 11	1.11	1.15	
K.GAEEEEEEEDDDS(p)EEEIK.A	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	0.09	1.23	
R.HLS(p)AEDFSR.V	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	1.47	
K.ST(p)SPPPS(p)PEVWAESR.T	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	3.83	
R.DSSVPGS(p)PSNIVAK.M	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	4.06	

K.STS(p)PPPS(p)PEVWAESR.T	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	3.52
K.STS(p)PPPSPEVWAESR.T	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	1.48
R.KGAEEEEEEEDDDS(p)EEEIKAIR.E	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	0.61
R.KGAEEEEEEEDDDS(p)EEEIK.A	IPI00190488.3	PREDICTED: similar to dematin 48 kDa subunit	X	1.22
K.WLEEADSSSGS(p)PTSIDK.I	IPI00190631.1	POU domain, class 3, transcription factor 2	0.78	X
R.DSDS(p)DADEATPTTTPR.V	IPI00191460.4	H/ACA ribonucleoprotein complex subunit 4	X	0.73
R.DS(p)DSDADEATPTTTPR.V	IPI00191460.4	H/ACA ribonucleoprotein complex subunit 4	X	0.93
R.GLYDGPVCEVSVT(p)PK.T	IPI00192034.1	Dihydropyrimidinase-related protein 2	X	0.76
K.NDGVKES(p)SES(p)TNTTIEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	0.98
K.ESS(p)ESTNTTIEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	1.13
K.ESSES(p)TNT(p)TIEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	0.94
K.ESS(p)ESTNTT(p)IEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	1.28
K.ESSESTNTT(p)IEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	1.02
K.NDGVKES(p)S(p)ESTNTTIEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	1.01
K.ESSES(p)TNTTIEDEDTK.V	IPI00192337.1	Calcium/calmodulin-dependent protein kinase type II alpha chain	X	1.13
K.ILEGDNGLDS(p)DMEEEADR.G	IPI00192552.1	Hypothetical protein MGC125002	0.36	1.33
K.LEQEQEGEKDAATEEPGS(p)PVKST(p)PAS(p)PVQSPTR.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.7
K.DAATEEPGS(p)PVKS(p)TPAS(p)PVQSPTR.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.8
R.KKLEQEQEGEKDAATEEPGS(p)PVK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.16
R.KKLEQEQEGEKDAATEEPGS(p)PVK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.05
K.TESVTSGPLSPEGS(p)PSKS(p)PSK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.3
R.VTMILQSPS(p)FREELEGLIQEQMK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.74
K.TESVTSGPLS(p)PEGS(p)PSKSPSK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.42
K.TESVTSGPLS(p)PEGS(p)PSK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.31
K.STPAS(p)PVQSPTR.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.16
K.TESVTSGPLSPEGSPSKS(p)PSK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.83
R.AGTKS(p)PAVSPS(p)KASEDAK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.67
K.TESVTSGPLS(p)PEGSPSKS(p)PSK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.33
K.TESVTSGPLS(p)PEGSPSKS(p)PSK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.38
K.LEQEQEGEKDAATEEPGS(p)PVKS(p)TPAS(p)PVQSPTR.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.29
K.STPAS(p)PVQS(p)PTR.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	0.91
K.SRSPS(p)TESQLASK.G	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.61
K.KLEQEQEGEKDAATEEPGS(p)PVK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.11
R.AGTKS(p)PAVS(p)PSKASEDAK.K	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.7
K.LEQEQEGEKDAATEEPGS(p)PVK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	0.91
K.LEQEQEGEKDAATEEPGS(p)PVK.S	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	1.16
K.STPASPVQSPT(p)R.A	IPI00192626.2	Splice Isoform 1 of Beta-adducin	X	0.72
K.EAAS(p)PVVQEAS(p)PELSPEER.R	IPI00192778.2	Hypothetical protein LOC498154	0.89	X
R.S(p)LDGAPIGVVDQSLMK.D	IPI00192909.2	78 kDa protein	X	0.61
K.ELEDLLS(p)PLEESVK.E	IPI00192973.1	Nuclear pore glycoprotein p62	X	0.42
R.GLVAAYSGDS(p)DNEEELVER.L	IPI00193008.3	PREDICTED: similar to RNA binding motif protein 5	X	0.69
K.SAS(p)PAPADVAPAQEDLR.T	IPI00193648.1	PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	0.36	X
K.S(p)ASPAPADVAPAQEDLR.T	IPI00193648.1	PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	X	1.71
R.YQDEVFGGFVTEPQEES(p)EEEVEEPEER.Q	IPI00193648.1	PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	X	1.64
R.YS(p)PESQSQTVLHPR.P	IPI00194183.3	PREDICTED: nuclear receptor co-repressor 1	X	0.72
R.Y(p)SPESQSQTVLHPR.P	IPI00194183.3	PREDICTED: nuclear receptor co-repressor 1	X	0.69
R.SRS(p)GEGEVSGLMR.K	IPI00194567.3	PREDICTED: tripartite motif protein 28	2.83	0.82
R.S(p)GEGEVSGLMR.K	IPI00194567.3	PREDICTED: tripartite motif protein 28	X	0.61
R.LAS(p)PSGSTSS(p)GLEVVAPEVTSAPVSGPGILDDSATICR.V	IPI00194567.3	PREDICTED: tripartite motif protein 28	X	1

K.LDT(p)FCGSPPYAAPELFQGK.K	IPI00194773.1	Serine/threonine-protein kinase MARK2	0.55	1.24
R.DYDDMS(p)PR.R	IPI00194974.2	Hnrpk protein	X	1.65
K.IIPTLEEGLQLPSPT(p)ATSQLPLESDAVECLNYQHYK.G	IPI00194974.2	Hnrpk protein	X	1.39
K.IIPTLEEGLQLPS(p)PTATSQLPLESDAVECLNYQHYK.G	IPI00194974.2	Hnrpk protein	X	1.83
R.KLS(p)LTSSLNSR.I	IPI00195067.1	Guanine nucleotide release/exchange factor	X	4.98
R.RAS(p)TIEMPQQAR.Q	IPI00195376.1	Cardiac phospholamban	X	1.59
R.SY(p)EDLTELEDR.E	IPI00195732.1	PREDICTED: similar to RIKEN cDNA 2810468K17	0.61	1.2
K.AAQAS(p)LSALNDPSAVEQALQEK.K	IPI00195904.3	Rattus norvegicus utrophin	X	0.99
R.ANSFVGT(p)AQYVSPELLTEK.S	IPI00195987.1	3-phosphoinositide-dependent protein kinase 1	X	1.57
R.ANS(p)FVGTAQYVSPELLTEK.S	IPI00195987.1	3-phosphoinositide-dependent protein kinase 1	X	1.39
K.S(p)LVGTPYWMAPEVISR.L	IPI00196161.3	53 kDa protein	X	1.01
K.S(p)LVGTPYWMAPEVISR.S	IPI00196161.3	53 kDa protein	X	1.32
K.AALPAGEGES(p)PEGAK.I	IPI00196508.1	Amphiphysin	0.03	1.57
K.AALPAGEGES(p)PEGAKIDVESTELASSES(p)PQAAELE AGAPQEK.V	IPI00196508.1	Amphiphysin	X	1.66
K.DGQDAIAQS(p)PEK.E	IPI00196639.3	39 kDa protein	3.46	2.46
K.DGQDAIAQS(p)PEKEAK.G	IPI00196639.3	39 kDa protein	X	1.48
K.REDS(p)PGPEVQPMDK.Q	IPI00196677.1	Tripartite motif protein 3	0.53	0.94
K.AGAYDFPS(p)PEWDTVTPEAK.N	IPI00196730.1	Splice Isoform A of Calcium/calmodulin-dependent protein kinase type II gamma chain	X	1.29
R.QS(p)SAPASPAASAAGLAGQAAK.S	IPI00196730.1	Splice Isoform A of Calcium/calmodulin-dependent protein kinase type II gamma chain	X	0.63
R.PLDTFRVLS(p)QPY(p)PRPELLCAFRHPPLYPGPAHGLG ASAGGPCSCLACHSGPSNGLAPR.A	IPI00196850.1	PREDICTED: similar to Evx1	0.82	X
K.EFGISPSDIPFSQGSGSRPDLSPS(p)YDYDDFSPSITR.V	IPI00198168.4	Kinesin-like protein KIF2	0.72	X
R.ARPSQLPEQSSSAQQNGSVSDIS(p)PVQAAK.K	IPI00198168.4	Kinesin-like protein KIF2	0.28	1.15
K.EFGISPSDIPFSQGSGSRPDLSPSY(p)DYDDFSPSITR.V	IPI00198168.4	Kinesin-like protein KIF2	0.84	0.6
K.EFGISPSDIPFSQGSGSRPDLS(p)PSYDYDDFSPSITR.V	IPI00198168.4	Kinesin-like protein KIF2	0.75	0.68
R.AGS(p)PLCNSNLQDSEEDVEPPSYHLFR.E	IPI00198211.2	Glucocorticoid receptor DNA-binding factor 1	2.04	X
R.TSFSVGS(p)DDELGPIR.K	IPI00198211.2	Glucocorticoid receptor DNA-binding factor 1	X	0.94
R.HSSLPTES(p)DEDIAPAQR.V	IPI00198486.3	PREDICTED: similar to mBLVR	0.25	0.32
R.VDIITEEMPENALPS(p)DEDDKDPNDPYR.A	IPI00198486.3	PREDICTED: similar to mBLVR	X	0.49
R.LSS(p)LRAS(p)TSK.S	IPI00199355.3	27 kDa protein	X	3.36
R.LSS(p)LRAS(p)TSKSESSQK.-	IPI00199355.3	27 kDa protein	X	2.06
R.LSS(p)LRAST(p)SK.S	IPI00199355.3	27 kDa protein	X	2.92
R.TEATQGLDYVPSAGTIS(p)PTSSLEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	0.21	X
R.TEATQGLDYVPSAGTIS(p)PTSS(p)LEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	0.12	1.98
R.FTDQSLSPEDAES(p)LSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	0.13	X
K.ADS(p)VEQQDGAALEK.T	IPI00199693.2	Microtubule associated protein 1A (Fragment)	0.25	X
R.KVAELEEEQSQGS(p)SSYSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.47
K.QLS(p)PESLGTLQFGELNLGKEER.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.24
R.FT(p)DQSLSPEDAESLSVLSVVSPDT(p)TK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	4.27
R.TEATQGLDYVPSAGTIS(p)PTS(p)SLEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.09
R.FTDQSLS(p)PEDAESLSVLSVVSPDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.57
R.TEATQGLDYVPSAGTIS(p)PT(p)SSLEEDKGFK.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.13
R.TEATQGLDYVPSAGTIS(p)PT(p)SSLEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.51
R.CLS(p)PDDSTVK.M	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	4.07
R.TEATQGLDYVPSAGTIS(p)PTSSLEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.94
K.EPVPAWEGKS(p)PEQEVR.Y	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	5.91
R.FTDQSLSPEDAES(p)LSVLSVVS(p)PDTTKQEATPR.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	4.28
R.KVAELEEEQS(p)QGSSSYSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.53
R.TEATQGLDYVPSAGTISPTS(p)S(p)LEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.58
K.GFKS(p)PPCEDFSVTGESEK.K	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.74
R.EAELGPENTAAREESEAEVKEDVIEKAELEEMEETHPS(p)DEEGEETKAESFYQK.H	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.87
R.TEATQGLDYVPSAGTIS(p)PTSSLEEDKGFKS(p)PPCED FSVTGESEK.K	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.83
R.FTDQSLS(p)PEDAESLSVLSVVS(p)PDTTKQEATPR.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.94

K.VAELEEEQSQGSSS(p)YSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.4
R.ALGLEES(p)PAEGSK.A	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.26
K.VAELEEEQSQGSSSY(p)SDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.52
R.TEATQGLDYVPSAGTISPT(p)S(p)SLEEDKGFKS(p)PPCEDFSVTGESEK.K	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.35
K.VAELEEEQSQGSS(p)SYSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.65
R.DFQEDS(p)WGETK.H	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.81
K.VAELEEEQS(p)QGSSSYSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.54
R.TEATQGLDYVPSAGTISPTS(p)SLEEDKGFKSPPCEDFSVTGESEK.K	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.26
K.VAELEEEQSQGS(p)SSYSDWVK.N	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.5
R.ELALS(p)S(p)PEDLTQDFEELK.R	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.65
R.AKPAS(p)PAR.R	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.83
K.AELEEMEETHPS(p)DEEGEETK.A	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.65
K.HTQEALKAS(p)PK.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.46
R.EKEVVPDS(p)PGDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.65
R.TEATQGLDYVPSAGTIS(p)PTSS(p)LEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.49
R.TEATQGLDYVPSAGTISPTSS(p)LEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.77
R.ELALS(p)S(p)PEDLTQDFEELKR.E	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.61
R.ELALS(p)S(p)PEDLTQDFEELKR.E	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.61
R.S(p)PTPGKGPVDR.T	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.71
R.FTDQSLS(p)PEDAESLSVLSVVSPDTT(p)K.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.64
R.EESEAEVKEDVIEKAELEEMEETHPS(p)DEEGEETKAESFYQK.H	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.69
R.FTDQS(p)LSPEDAESLSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.36
R.TEATQGLDYVPSAGTIS(p)PTSS(p)LEEDKGFKS(p)PPCEDFSVTGESEK.K	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.71
R.EKEVVPDS(p)PGDKGSTNR.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.87
R.ELALS(p)S(p)PEDLTQDFEELKREER.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.5
R.FTDQSLS(p)PEDAESLSVLSVVSPDTTKQEATPR.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.93
R.TEATQGLDYVPSAGTIS(p)PTSSLEEDKGFK.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.02
K.EVVPDS(p)PGDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.73
K.QLSPES(p)LGTLQFGELNLGK.E	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.43
R.TEATQGLDYVPSAGTISPT(p)S(p)SLEEDK.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.3
R.FT(p)DQSLSPEDAESLSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	4.23
R.FT(p)DQSLSPEDAESLSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.25
K.EVVPDS(p)PGDKGSTNR.G	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	0.91
R.ADS(p)KES(p)LKAAPK.T	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.59
R.FTDQSLS(p)PEDAESLSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.44
R.FTDQSLS(p)PEDAESLSVLSVVS(p)PDTTK.Q	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.36
R.TEATQGLDYVPSAGTIS(p)PTSS(p)LEEDKGFK.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	2.09
R.DFQEDSWGETKHS(p)PGVSK.E	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	3.94
R.TEATQGLDYVPSAGTISPT(p)SSLEEDKGFK.S	IPI00199693.2	Microtubule associated protein 1A (Fragment)	X	1.24
R.TWT(p)LCGTPEYLAPEIILSK.G	IPI00200013.3	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha	0.26	1.65
R.T(p)WTLCGTPEYLAPEIILSK.G	IPI00200013.3	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha	0.26	1.71
R.T(p)WTLCGTPEYLAPEIILSK.G	IPI00200013.3	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha	X	1.65
R.TWT(p)LCGTPEYLAPEIILSK.G	IPI00200013.3	PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha	X	1.69
R.TRLS(p)PPR.A	IPI00200047.3	Coactivator activator	1.11	1.11
K.AETSESSGS(p)APAVPEASAS(p)PK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	0.08	0.35
K.MPFQAS(p)PGGK.G	IPI00200221.1	Methyl-CpG-binding protein 2	0.85	1.34
K.AETS(p)ESSGSAPAVPEASAS(p)PK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	0.08	0.76
R.AGS(p)LESDGCPKEPAK.T	IPI00200221.1	Methyl-CpG-binding protein 2	1.28	X
K.AETSESSGSAPAVPEAS(p)ASPK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	0.51	X
K.AETS(p)ESSGS(p)APAVPEASAS(p)PK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	X	1.02
K.AETSES(p)SGSAPAVPEASAS(p)PK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	X	0.35
K.AETSESSGSAPAVPEAS(p)ASPK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	X	0.95
K.AETSESSGSAPAVPEASAS(p)PK.Q	IPI00200221.1	Methyl-CpG-binding protein 2	X	0.97

K.EVDYSDS(p)LTEK.Q	IPI00200390.2	PREDICTED: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	8.72	1.28
K.AQAVS(p)EEEEEEEGESSSPK.K	IPI00200634.1	DEAD box polypeptide 24	0.44	0.71
K.IGAGPQTVETGSET(p)EDEAIFESLIWAAK.K	IPI00200876.3	Per1 interacting protein of the suprachiamatic nucleus	X	0.92
R.SAS(p)SDTSEELNAQDSPK.R	IPI00200898.2	Ezrin-radixin-moesin-binding phosphoprotein 50	0.02	0.22
K.VQIS(p)PDSGGLPER.S	IPI00200920.1	Far upstream element-binding protein 2	X	0.78
R.LSTTPS(p)PT(p)NSLHEDGVDDFRR.Q	IPI00201166.3	Epidermal Langerhans cell protein LCP1	X	2.69
R.ATEEPSGTGS(p)DELIK.S	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	0.13	2.01
R.ATEEPS(p)GT(p)GSDELIK.S	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	X	2.36
K.EGDELGEGERPEEDAAAIELS(p)S(p)DEAVEVEEVIEESR.A	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	X	0.86
K.ESEALPEKEGDELGEGERPEEDAAAIELS(p)S(p)DEAVEVEEVIEESR.A	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	X	1.98
R.ATEEPS(p)GTGS(p)DELIK.S	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	X	2.28
K.SLKESEALPEKEGDELGEGERPEEDAAAIELS(p)S(p)DEAVEVEEVIEESR.A	IPI00201300.1	PREDICTED: similar to polymerase I-transcript release factor; PTRF	X	1.11
R.SYT(p)PEYR.R	IPI00201580.4	PREDICTED: similar to RIKEN cDNA G430041M01	0.43	X
R.RS(p)PS(p)PYYSR.Y	IPI00201580.4	PREDICTED: similar to RIKEN cDNA G430041M01	X	0.94
R.AHT(p)PTPGIYMGR.P	IPI00201580.4	PREDICTED: similar to RIKEN cDNA G430041M01	X	0.86
R.TFCGT(p)PDYIAPEIIAYQPYGK.S	IPI00201797.1	Protein kinase C gamma type	X	1.09
R.LVLASIDQADFQGFTY(p)VNPDFVHPDAR.S	IPI00201797.1	Protein kinase C gamma type	X	0.69
R.T(p)FCGTPDYIAPEIIAYQPYGK.S	IPI00201797.1	Protein kinase C gamma type	X	1.18
K.NSPVDESEVQTAADS(p)PSVKPSEVEEETTSNIGT(p)EPSVHQEELGKEEPK.Q	IPI00202201.3	PREDICTED: similar to nuclear protein, NP220	1.42	X
K.NSPVDESEVQTAADS(p)PSVKPSEVEEETTSNIGTEPSVHQEELGKEEPK.Q	IPI00202201.3	PREDICTED: similar to nuclear protein, NP220	0.98	X
R.LDQIPAANLDADDPLT(p)DEEDEDFEEES(p)DDDDTAALLAELEK.I	IPI00202933.1	Hypothetical protein RGD1310669	0.69	1.15
K.HTGPNS(p)PDTANDGFVR.L	IPI00203088.4	51 kDa protein	1.45	X
K.HTGPNS(p)PDTANDGFVR.L	IPI00203088.4	51 kDa protein	1.17	0.9
R.ATENDIYNFFS(p)PLNPVR.V	IPI00203088.4	51 kDa protein	1.08	0.67
K.HTGPNSPDT(p)ANDGFVR.L	IPI00203088.4	51 kDa protein	X	0.85
K.AQPAPPELNSESEDYS(p)PSSSETVR.S	IPI00203195.3	Serine/threonine-protein kinase DCAMKL1	0.95	2.52
R.DKS(p)DSETEGLVFAR.D	IPI00203239.1	Rat brain 4.1(L)	X	0.77
K.GPSSQEDESGGIEDS(p)PDR.G	IPI00203239.1	Rat brain 4.1(L)	X	1.11
K.ELKPEQETT(p)PR.H	IPI00203239.1	Rat brain 4.1(L)	X	2.35
R.LLS(p)SNEDDASILSS(p)PTDR.S	IPI00203892.2	thyroid hormone receptor associated protein 4	0.98	X
K.LVEDEET(p)DQGYKYPDK.Y	IPI00204024.1	P80 coilin	X	0.65
K.LVEDEET(p)DQGYK.Y	IPI00204024.1	P80 coilin	X	0.5
R.TATDENEDDLGS(p)PPSPGDSSYYQDQVDEFHEAR.S	IPI00204100.1	Something about silencing protein 10	X	0.72
K.FTGYQTIQQQSSSETEGEGGNTADAS(p)SEEEGDRVEDGK.G	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	0.44	0.3
K.FTGYQTIQQQSSSETEGEGGNT(p)ADAS(p)SEEEGDRVEDGK.G	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	1.34	0.58
K.FTGYQTIQQQSSSETEGEGGNTADASS(p)EEEGDRVEDGK.G	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	0.44	0.26
K.FTGYQTIQQQSSSETEGEGGNT(p)ADASSEEEGDRVEDGK.G	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	0.26	X
K.FTGYQTIQQQSSSETEGEGGNTADAS(p)S(p)EEEGDRVEDGK.G	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	1.37	0.68
R.KSPGDEDDKDCKEEENKS(p)SSEGGDAGNDTR.N	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	1.12	0.57
K.FTGYQTIQQQSSSETEGEGGNT(p)ADASS(p)EEEGDRVEDGKGK.R	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	X	0.59
K.FTGYQTIQQQSSSETEGEGGNTADAS(p)S(p)EEEGDRVEDGKGK.R	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	X	0.65
R.KSPGDEDDKDCKEEENKS(p)S(p)SEGGDAGNDTR.N	IPI00204130.1	Hepatoma-derived growth factor-related protein 3	X	0.61

R.VPS(p)PDHR.R	IPI00204724.2	PREDICTED: similar to hypothetical protein FLJ14936	1.58	0.94
R.ADSEGDLS(p)ENDDGAGDLR.S	IPI00204776.1	A-kinase anchor protein 8	0.83	0.42
R.ADS(p)EGDLS(p)ENDDGAGDLR.S	IPI00204776.1	A-kinase anchor protein 8	1	0.61
K.S(p)PLAQMEEER.R	IPI00204899.1	Septin-7	X	0.74
K.IYEFPET(p)DDEEENKLVK.K	IPI00204899.1	Septin-7	X	0.9
K.IYEFPET(p)DDEEENK.L	IPI00204899.1	Septin-7	X	1.15
R.AQS(p)PTPS(p)LPASWK.Y	IPI00205262.3	PREDICTED: similar to Synaptopodin-2	X	2.42
R.AQS(p)PTPSLPASWK.Y	IPI00205262.3	PREDICTED: similar to Synaptopodin-2	X	2.93
R.KTS(p)LVIVESTDDQPQVFEK.L	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	1
R.SY(p)IETETESR.E	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	4.01
K.TEGDS(p)PAAALS(p)PQMHQESVQQDFSGK.M	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	0.45
R.KT(p)SLVIVESTDDQPQVFEK.L	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	1.09
K.ARS(p)YIETETESR.E	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	4.46
K.LNVPETMTEVLDVS(p)DEEGDDTVTGDGGEYLRPEDLK.E	IPI00205634.3	PREDICTED: similar to ankyrin 2 isoform 2	X	0.99
R.NLAS(p)PEGTLATLGLK.T	IPI00205721.3	187 kDa protein	0.2	0.71
R.YRS(p)PEPDPYLSYR.W	IPI00205776.5	Dual specificity protein kinase CLK3	X	1.2
K.DQALKDDDAETGLT(p)DGEEKEEPKEEEK.L	IPI00206170.6	Synaptotagmin-1	X	1.69
K.DQALKDDDAETGLT(p)DGEEKEEPKEEEK.L	IPI00206170.6	Synaptotagmin-1	X	1.37
R.IPESSHPPLESSSSS(p)FESQK.M	IPI00206312.1	Splice Isoform 2 of Regulating synaptic membrane exocytosis protein 1	0.54	X
K.S(p)SDSDVSDVSAISR.A	IPI00206312.1	Splice Isoform 2 of Regulating synaptic membrane exocytosis protein 1	0.33	X
K.SSDS(p)DVSDVSAISR.A	IPI00206312.1	Splice Isoform 2 of Regulating synaptic membrane exocytosis protein 1	X	0.85
K.SS(p)DSDVSDVSAISR.A	IPI00206312.1	Splice Isoform 2 of Regulating synaptic membrane exocytosis protein 1	X	0.85
K.WLEEADSSTGS(p)PTSIDK.I	IPI00206981.1	POU domain, class 3, transcription factor 3	5.4	1.68
R.VSS(p)FSMPSSSR.Y	IPI00206986.1	Inositol 1,4,5-trisphosphate receptor type 3	X	3.32
R.LRS(p)EDGVEGDLGETQSR.T	IPI00207087.3	PREDICTED: similar to AHNAK	X	4.22
R.SGPTSS(p)PFSSPASSR.S	IPI00207273.1	Nuclear envelope pore membrane protein POM 121	0.44	X
R.TSS(p)VSSLTSTCTGGIPSSSR.N	IPI00207273.1	Nuclear envelope pore membrane protein POM 121	X	1.13
K.TPVDYIDLPYSSS(p)PSR.S	IPI00207322.2	81 kDa protein	X	2.94
R.YS(p)FSEDTK.S	IPI00207322.2	81 kDa protein	X	2.75
R.DIS(p)PEEIDLK.N	IPI00207322.2	81 kDa protein	X	0.48
R.AYT(p)HQVVTR.W	IPI00207330.2	PREDICTED: cyclin-dependent kinase 7	X	1.83
K.T(p)EPRGPGGPLRS(p)ASPHR.S	IPI00207370.1	Neurabin-2	X	5.04
R.AYLQSITPQGYS(p)DSEER.E	IPI00207675.4	Zfhx1b zinc finger homeobox 1b	1.36	0.85
K.TGSS(p)PNSVSSSPT(p)NSAITQLR.N	IPI00207675.4	Zfhx1b zinc finger homeobox 1b	X	0.77
K.TGSSPNS(p)VSSS(p)PTNSAITQLR.N	IPI00207675.4	Zfhx1b zinc finger homeobox 1b	X	0.87
K.QLS(p)PESLGTLQFGELNLGK.E	IPI00207903.1	Microtubule associated protein 1A (Fragment)	0.17	0.53
K.AELEEMEETHPS(p)DEEGEETKAESFYQK.H	IPI00207903.1	Microtubule associated protein 1A (Fragment)	0.09	0.82
K.ELVSSSSSGSDSDS(p)EVEK.K	IPI00208123.3	Activated RNA polymerase II transcriptional coactivator p15 precursor	X	0.69
K.ELVS(p)SSSSGSDSDS(p)EVEK.K	IPI00208123.3	Activated RNA polymerase II transcriptional coactivator p15 precursor	X	0.69
K.SLDSDES(p)EDEDDDYQQK.R	IPI00208277.1	28 kDa heat- and acid-stable phosphoprotein	0.62	1.35
K.S(p)LDSDESEDEDDDYQQK.R	IPI00208277.1	28 kDa heat- and acid-stable phosphoprotein	0.49	1.5
K.S(p)LDSDES(p)EDEDDDYQQK.R	IPI00208277.1	28 kDa heat- and acid-stable phosphoprotein	1.04	1.77
K.SLDS(p)DESEDEDDDYQQK.R	IPI00208277.1	28 kDa heat- and acid-stable phosphoprotein	X	1.48
K.SLDS(p)DES(p)EDEDDDYQQK.R	IPI00208277.1	28 kDa heat- and acid-stable phosphoprotein	X	2.24
K.IYHLPDAES(p)DEDEDFKEQTR.L	IPI00208304.1	Vascular endothelial cell specific protein 11	0.59	1.09
K.IYHLPDAES(p)DEDEDFKEQTR.L	IPI00208304.1	Vascular endothelial cell specific protein 11	X	0.73
K.GTGDCS(p)DEEVDGK.A	IPI00209113.2	Myosin-9	X	1.18
R.KGTGDCS(p)DEEVDGKADGADAK.A	IPI00209113.2	Myosin-9	X	0.73
R.KGTGDCS(p)DEEVDGKADGADAK.A	IPI00209113.2	Myosin-9	X	0.62
R.NQSDLDDQHDYDSVAS(p)DEDTDQEPLPSAGATR.N	IPI00209293.1	ARF GTPase-activating protein GIT1	X	0.46
K.SLSS(p)PTDNLELSAR.N	IPI00209293.1	ARF GTPase-activating protein GIT1	X	0.81
R.TLS(p)DESIYSSQR.E	IPI00209335.1	Signal-induced proliferation-associated 1-like	X	1.93

		protein 1		
R.LTPSPDIIVLSDNEASS(p)PR.S	IPI00209340.1	Similar to transcription repressor p66	X	1.18
R.EDS(p)S(p)EEEEEEIDDEEIER.R	IPI00209527.3	PREDICTED: similar to microfibrillar-associated protein 1	0.75	0.83
R.SLAALDALNT(p)DDENDEEEYEAWK.V	IPI00209527.3	PREDICTED: similar to microfibrillar-associated protein 1	0.72	0.72
K.EAINNVDTSSS(p)DFTILQEMEEASLEPENEK.I	IPI00209618.2	PREDICTED: similar to Safb2 protein	2.86	X
R.SVVS(p)FDKVK.E	IPI00209618.2	PREDICTED: similar to Safb2 protein	3.07	1.57
K.EAINNVDTSS(p)SDFTILQEMEEASLEPENEK.I	IPI00209618.2	PREDICTED: similar to Safb2 protein	2.68	X
K.SEPVKEEGS(p)ELEQPFAQATSSVGPDRK.L	IPI00209618.2	PREDICTED: similar to Safb2 protein	X	1.54
K.TNTGS(p)AMLEQIAMSDR.Y	IPI00209653.3	59 kDa protein	X	0.81
K.TNT(p)GSAMLEQIAMSDR.Y	IPI00209653.3	59 kDa protein	X	0.81
R.RWS(p)APETR.K	IPI00210059.1	Ataxin-1	X	1.24
R.WS(p)APETR.K	IPI00210059.1	Ataxin-1	X	1.06
R.S(p)YASSETMVR.G	IPI00210211.2	Splice Isoform 2 of Glial fibrillary acidic protein, astrocyte	X	0.24
R.DNLTQDLGT(p)LR.Q	IPI00210211.2	Splice Isoform 2 of Glial fibrillary acidic protein, astrocyte	X	0.4
R.RS(p)YASSETMVR.G	IPI00210211.2	Splice Isoform 2 of Glial fibrillary acidic protein, astrocyte	X	0.26
R.MT(p)PPLPAR.V	IPI00210211.2	Splice Isoform 2 of Glial fibrillary acidic protein, astrocyte	X	0.46
R.SY(p)ASSETMVR.G	IPI00210211.2	Splice Isoform 2 of Glial fibrillary acidic protein, astrocyte	X	0.24
K.TESVTSGPLSPEGSPS(p)KSPSK.K	IPI00210489.1	52 kDa protein	0.17	X
R.AGTKS(p)PAVS(p)PSK.A	IPI00210489.1	52 kDa protein	0.24	1.75
K.TESVTSGPLSPEGSPSKSPS(p)K.K	IPI00210489.1	52 kDa protein	0.14	X
K.TESVTSGPLS(p)PEGSPS(p)KSPSK.K	IPI00210489.1	52 kDa protein	0.25	X
R.AGT(p)KSPAVSPS(p)KASEDAK.K	IPI00210489.1	52 kDa protein	0.26	1.62
R.S(p)LSTSGESLYHVLGLDK.N	IPI00210881.1	DnaJ homolog subfamily C member 5	0.08	1.19
R.SLS(p)TSGESLYHVLGLDK.N	IPI00210881.1	DnaJ homolog subfamily C member 5	X	0.98
K.ETVQTTQS(p)PAAVEK.E	IPI00211007.3	RA8	1.09	X
R.SGDPAPPDS(p)PTWEAK.K	IPI00211008.2	RA1	0.41	X
K.GTEETSWS(p)GEER.T	IPI00211008.2	RA1	2.32	1.57
R.FDIYDPFHPTDEAYS(p)PPPAPEQK.Y	IPI00211008.2	RA1	2.05	2.37
R.EVLYDS(p)EGLS(p)ADER.G	IPI00211008.2	RA1	X	1.79
R.FDIYDPFHPTDEAYS(p)PPPAPEQK.Y	IPI00211008.2	RA1	X	0.73
R.APS(p)PAPAVS(p)PK.R	IPI00211008.2	RA1	X	2.8
R.S(p)GDPAPPDS(p)PTWEAK.K	IPI00211008.2	RA1	X	2.53
R.APSPAPAVS(p)PK.R	IPI00211008.2	RA1	X	1.11
K.ES(p)SDSTNTTIEDEDAK.A	IPI00211185.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	X	0.8
K.ESS(p)DSTNTT(p)IEDEDAK.A	IPI00211185.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	X	0.83
K.ESS(p)DSTNTTIEDEDAK.A	IPI00211185.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	X	0.83
K.ESSDSTNTT(p)IEDEDAK.A	IPI00211185.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	X	0.73
K.ESSDS(p)TNTT(p)IEDEDAK.A	IPI00211185.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	X	0.62
R.SQS(p)PVHLR.R	IPI00211298.2	PREDICTED: similar to Msx-2 interacting nuclear target protein	X	0.8
R.GPDEAIEDGEEGS(p)EDDAEWVVTK.D	IPI00211448.2	Hypothetical protein MGEPS	X	0.8
K.KVPEPEEEIEEVEVS(p)EEEGEDPALDSLSQAIAFQQAK.I	IPI00211761.3	Hypothetical protein RGD1309851	X	0.74
K.VGES(p)FEETLEETVVSTK.K	IPI00211936.2	Alpha-internexin	0.56	2.4
K.VGES(p)FEETLEETVVSTK.K	IPI00211936.2	Alpha-internexin	0.58	2.33
K.VGES(p)FEETLEETVVSTKK.T	IPI00211936.2	Alpha-internexin	X	2.39
R.LSGPGGSGS(p)FR.S	IPI00211936.2	Alpha-internexin	X	2.07
R.LAIQGPEDS(p)PSR.Q	IPI00212141.1	PREDICTED: similar to Myeloid leukemia factor 2 homolog	0.46	0.96
K.DFQDYIEPEEGCQGS(p)PQR.R	IPI00212221.6	Dncli2 protein	0.52	0.83
K.EGDGSATTDAAPATS(p)PK.A	IPI00212320.1	Neuromodulin	0.51	1.34
K.EGDGSATTDAAPATS(p)PKAEEPSK.A	IPI00212320.1	Neuromodulin	X	1.61

R.DAPFFRES(p)PVGR.K	IPI00212580.3	PREDICTED: similar to Hypothetical protein 1600022A19Rik, isoform 1	X	1.28
K.DEILPT(p)TPISEQK.G	IPI00212776.1	40S ribosomal protein S3	X	0.86
R.LDQIPAANLDADDPLT(p)DEEDEDFEAES(p)DDDDT(p)AALLAELEK.I	IPI00212938.3	PREDICTED: similar to RIKEN cDNA 0610040D20	0.82	X
R.DLTGGGDLTS(p)PDASASSCGK.E	IPI00213246.1	Neurabin-1	X	0.89
R.GIS(p)PIVFDR.S	IPI00213467.1	Splice Isoform 1 of YTH domain-containing protein 1	X	0.9
R.AKS(p)PT(p)PDGSER.I	IPI00213467.1	Splice Isoform 1 of YTH domain-containing protein 1	X	1.69
R.DFQEYVEPGEDFPAS(p)PQRR.A	IPI00213552.1	Cytoplasmic dynein 1 light intermediate chain 1	0.25	X
K.ESTESSNTT(p)IEDEDVK.A	IPI00213583.2	Splice Isoform Delta 6 of Calcium/calmodulin-dependent protein kinase type II delta chain	X	0.54
R.RGS(p)DELTVPR.Y	IPI00213633.1	Splice Isoform 1 of p130Cas-associated protein	X	2.01
R.KDS(p)GSSSVFAES(p)PGGK.A	IPI00213633.1	Splice Isoform 1 of p130Cas-associated protein	X	2.5
R.KDS(p)GSSSVFAESPGGK.A	IPI00213633.1	Splice Isoform 1 of p130Cas-associated protein	X	2.14
K.DSGSSSVFAES(p)PGGK.A	IPI00213633.1	Splice Isoform 1 of p130Cas-associated protein	X	1.94
R.DTDAYSDLS(p)DGEK.E	IPI00213940.3	Hypothetical protein LOC500102	X	0.55
R.AS(p)SLGEIDDSSELR.V	IPI00214079.4	PREDICTED: protein kinase C-like 2	X	1.23
R.SDDGLSAAS(p)S(p)PEPGTSELPGDLK.A	IPI00214153.2	87 kDa protein	X	0.97
K.VLDKGS(p)PPPSSR.S	IPI00214153.2	87 kDa protein	X	1.44
R.FST(p)PPGDLLDGGLSGR.S	IPI00214153.2	87 kDa protein	X	1
R.ATTEEPETDEVDQVS(p)ESNS(p)IEELER.L	IPI00214210.2	141 kDa protein	0.37	0.47
K.YNLDAS(p)EEEDSNK.K	IPI00214258.1	Zinc finger protein 265	0.68	0.89
R.EES(p)DGEYDEFGR.K	IPI00214258.1	Zinc finger protein 265	0.83	0.88
K.EEPLS(p)EEEPCTSTAVPS(p)PEK.K	IPI00214536.1	Nucleolar protein NOP5	1.2	1.21
K.EEPLS(p)EEEPCTSTAVPSPEK.K	IPI00214536.1	Nucleolar protein NOP5	1.04	1.11
K.HIKEEPLS(p)EEEPCTSTAVPSPEK.K	IPI00214536.1	Nucleolar protein NOP5	0.79	1.14
K.EEPLS(p)EEEPCTSTAVPS(p)PEKK.K	IPI00214536.1	Nucleolar protein NOP5	1.81	X
K.HIKEEPLS(p)EEEPCTSTAVPS(p)PEK.K	IPI00214536.1	Nucleolar protein NOP5	X	1.28
K.NSDS(p)PDTGLDDSNTGFGK.L	IPI00214747.2	Hypothetical protein	X	0.86
K.RS(p)PTSTGDTELKEER.L	IPI00214839.1	Serine/threonine-protein kinase MARK2	X	2.52
R.TADSSSS(p)EDEEEYVVEK.V	IPI00214953.1	PREDICTED: similar to HP1 alpha protein	2.72	0.54
K.SS(p)FSNSADDIK.S	IPI00214953.1	PREDICTED: similar to HP1 alpha protein	1.7	0.6
K.S(p)SFSNSADDIK.S	IPI00214953.1	PREDICTED: similar to HP1 alpha protein	1.69	0.61
K.SSFS(p)NSADDIK.S	IPI00214953.1	PREDICTED: similar to HP1 alpha protein	X	0.6
R.KSS(p)FSNSADDIK.S	IPI00214953.1	PREDICTED: similar to HP1 alpha protein	X	0.56
K.TEETPSQLDQDTQVQDMDEGS(p)DDEEEGQK.V	IPI00215030.1	PREDICTED: similar to Splicing factor 3a, subunit 1	1.18	X
K.SDSNAS(p)FLR.A	IPI00215172.3	49 kDa protein	X	0.92
K.ALQEEAANS(p)ADDQSGGANTDSLDESVAPNK.I	IPI00215318.1	Double-stranded RNA-specific adenosine deaminase	X	1.37
K.LAS(p)PELER.L	IPI00215370.1	Transcription factor AP-1	X	1.5
R.S(p)SSVGSSSSYPISSAVPR.T	IPI00230793.1	Splice Isoform 3 of Plectin-1	0.07	0.86
R.SSSVGSS(p)SSYPISSAVPR.T	IPI00230793.1	Splice Isoform 3 of Plectin-1	0.07	X
K.GYY(p)SPYSVSGSGSTAGSR.T	IPI00230793.1	Splice Isoform 3 of Plectin-1	0.09	X
R.DTASLSTTPSES(p)PR.A	IPI00230795.2	Splice Isoform 1 of Gephyrin	X	0.8
R.RDS(p)VLAASR.D	IPI00230873.2	Splice Isoform 2 of Inositol 1,4,5-trisphosphate receptor type 1	X	0.59
R.SLYSSS(p)PGGAYVTR.S	IPI00230941.4	Vimentin	0.37	X
K.SPVVSGDTS(p)PR.H	IPI00230969.2	72 kDa protein	0.43	1.17
K.TDHGAEIVYKS(p)PVVSGDTS(p)PR.H	IPI00230969.2	72 kDa protein	3.27	2.96
K.TDHGAEIVYKS(p)PVVSGDTS(p)PR.H	IPI00230969.2	72 kDa protein	1.46	X
K.TDHGAEIVYKS(p)PVVS(p)GDTS(p)PR.H	IPI00230969.2	72 kDa protein	0.3	X
K.TDHGAEIVYKS(p)PVVS(p)GDTSPR.H	IPI00230969.2	72 kDa protein	3.25	2.96
K.SPVVS(p)GDT(p)SPR.H	IPI00230969.2	72 kDa protein	0.57	1.95
K.SPVVSGDT(p)SPR.H	IPI00230969.2	72 kDa protein	0.25	1.19
R.SGYSSPGS(p)PGTPGSR.S	IPI00230969.2	72 kDa protein	1.2	1.13
K.TDHGAEIVYKS(p)PVVSGDT(p)SPR.H	IPI00230969.2	72 kDa protein	2.22	2.89
K.TDHGAEIVYKS(p)PVVSGDT(p)SPR.H	IPI00230969.2	72 kDa protein	1.47	0.89
K.T(p)PPGSGEPPK.S	IPI00230969.2	72 kDa protein	0.84	X

K.SPVVS(p)GDTS(p)PR.H	IPI00230969.2	72 kDa protein	0.57	2.05
K.TDHGAEIVYKS(p)PVVSGDTSPR.H	IPI00230969.2	72 kDa protein	0.8	1.38
R.SGYS(p)S(p)PGSPGTPGSR.S	IPI00230969.2	72 kDa protein	2.54	X
K.TDHGAEIVY(p)KSPVVS(p)GDT(p)SPR.H	IPI00230969.2	72 kDa protein	0.28	X
R.HLSNVS(p)STGS(p)IDMVDSPQLATLADEVSASLAK.Q	IPI00230969.2	72 kDa protein	1.03	5.46
R.SGYSS(p)PGS(p)PGTPGSR.S	IPI00230969.2	72 kDa protein	1.94	0.94
R.SGYSS(p)PGSPGTPGSR.S	IPI00230973.2	39 kDa protein	X	1.13
K.ESPPQPPADDGSEEPGS(p)ET(p)SDAK.S	IPI00230973.2	39 kDa protein	X	1.47
K.TDHGAEIVYKSPVVS(p)GDTS(p)PR.H	IPI00230973.2	39 kDa protein	X	1.54
K.TDHGAEIVYKSPVVS(p)GDTS(p)PR.H	IPI00230973.2	39 kDa protein	X	0.87
K.TDHGAEIVYKSPVVSGDTS(p)PR.H	IPI00230973.2	39 kDa protein	X	1.24
K.AKTDHGAEIVYKS(p)PVVSGDTS(p)PR.H	IPI00230973.2	39 kDa protein	X	1.91
K.ESPPQPPADDGSEEPGSETSDAKS(p)TPTAEDVTAPLVEER.A	IPI00230973.2	39 kDa protein	X	1.2
K.SPVVS(p)GDTSPR.H	IPI00230973.2	39 kDa protein	X	1.98
K.STPT(p)AEDVTAPLVEER.A	IPI00230973.2	39 kDa protein	X	1.91
K.ESPPQPPADDGS(p)EEPGS(p)ETSDAK.S	IPI00230973.2	39 kDa protein	X	1.19
K.ST(p)PTAEDVTAPLVEER.A	IPI00230973.2	39 kDa protein	X	1.91
R.SGYS(p)SPGS(p)PGTPGSR.S	IPI00230973.2	39 kDa protein	X	1.59
K.S(p)TPTAEDVTAPLVEER.A	IPI00230973.2	39 kDa protein	X	1.76
R.HLSNVSST(p)GSIDMVDSPQLATLADEVSASLAK.Q	IPI00230973.2	39 kDa protein	X	3.24
K.AKTDHGAEIVYKS(p)PVVSGDTSPR.H	IPI00230973.2	39 kDa protein	X	2.44
K.ESPPQPPADDGSEEPGS(p)ETS(p)DAK.S	IPI00230973.2	39 kDa protein	X	1.46
R.HLSNVS(p)STGSIDMVDSPQLATLADEVSASLAK.Q	IPI00230973.2	39 kDa protein	X	1
K.VAVVRT(p)PPK.S	IPI00230973.2	39 kDa protein	X	1
K.TDHGAEIVYKS(p)PVVS(p)GDTS(p)PR.H	IPI00230973.2	39 kDa protein	X	2.03
K.TDHGAEIVYKSPVVS(p)GDTSPR.H	IPI00230973.2	39 kDa protein	X	1.08
K.ESPPQPPADDGSEEPGSET(p)SDAK.S	IPI00230973.2	39 kDa protein	X	0.48
K.TDHGAEIVYKSPVVSGDT(p)SPR.H	IPI00230973.2	39 kDa protein	X	1.41
K.TDHGAEIVYKS(p)PVVS(p)GDT(p)SPR.H	IPI00230973.2	39 kDa protein	X	2.01
K.AKTDHGAEIVYKS(p)PVVS(p)GDTSPR.H	IPI00230973.2	39 kDa protein	X	1.91
R.HLS(p)NVSS(p)TGSIDMVDSPQLATLADEVSASLAK.Q	IPI00230973.2	39 kDa protein	X	5.37
K.EEST(p)ETPDIPAIPSDVTQPQPEAVVSEPAEVR.G	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.77	2.65
K.DQPAALPLAAEETVNLPPS(p)PPPS(p)PASEQTAALEEATSGESAQAPSAFK.Q	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	2.38	X
K.ETS(p)PETSLIQDEVALK.L	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.56	3.69
K.DGS(p)PDAPATPEKEEVPFSEYK.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.16	0.64
K.DGS(p)PDAPATPEKEEVPFSEYK.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.15	0.65
R.IST(p)PERK.V	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	2.24	5.88
K.SGTSTPTTPGSTAITPGT(p)PPSYSSR.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	2.51	3.36
K.DGSPDAPAT(p)PEKEEVPFSEYK.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.14	0.66
K.VTDGITKS(p)PEKR.S	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.34	1.2
K.DKVTDGITKS(p)PEKR.S	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.05	1.44
K.DKVTDGITKS(p)PEKR.S	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.17	1.35
K.VTDGIT(p)KSPEKR.S	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.34	X
K.ET(p)SPETSLIQDEVALK.L	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.61	X
K.SEVQAHS(p)PSR.K	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.82	1.85
K.LEETSKVS(p)IEETVAKEEESLK.L	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.42	X
K.DGS(p)PDAPAT(p)PEKEEVPFSEYK.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.3	1.27

K.DGS(p)PDAPAT(p)PEKEEVPFSEYK.T	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	0.55	1.15
K.S(p)PASPFAQTFGTNLEDIK.Q	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.12	X
R.VDHGAEIITQS(p)PSR.S	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	5.44	6.57
K.KDDQS(p)PLDIK.V	IPI00231053.1	Splice Isoform MAP2d of Microtubule-associated protein 2	1.44	6.82
K.GS(p)YMEVEDNR.S	IPI00231089.1	Splice Isoform Short of Aquaporin-4	X	1.05
K.GSYMEVEDNRS(p)QVETEDLILKPGVVHVIDIDR.G	IPI00231089.1	Splice Isoform Short of Aquaporin-4	X	0.83
K.GSYMEVEDNRS(p)QVETEDLILKPGVVHVIDIDRGDEK.K	IPI00231089.1	Splice Isoform Short of Aquaporin-4	X	0.91
R.MS(p)GFIYQGK.L	IPI00231209.4	Rho guanine nucleotide exchange factor 7	X	0.55
R.TTHYGS(p)LPQK.S	IPI00231265.2	myelin basic protein isoform 4	X	1.67
R.TTHY(p)GSLPQK.S	IPI00231265.2	myelin basic protein isoform 4	X	1.61
R.S(p)YSSSSGSLMPSLENLDLSQVAAISNDLK.S	IPI00231302.4	Neurofilament triplet L protein	X	0.4
K.AEEAKDEPPS(p)EGEAEEEEK.E	IPI00231302.4	Neurofilament triplet L protein	X	0.58
R.AFPAYYTSHVQEEQSEVEETIEATKAEEAKDEPPS(p)EGEAEEEEK.E	IPI00231302.4	Neurofilament triplet L protein	X	0.63
K.AEEAKDEPPS(p)EGEAEEEEKEKEEGEEEEGAEEEEAAK.D	IPI00231302.4	Neurofilament triplet L protein	X	0.59
K.AEEAKDEPPS(p)EGEAEEEEKEKEEGEEEEGAEEEEAAK.D	IPI00231302.4	Neurofilament triplet L protein	X	0.61
K.AEEAKDEPPSEGEAEEEEKEKEEGEEEEGAEEEEAAKDES(p)EDAKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAK.K	IPI00231302.4	Neurofilament triplet L protein	X	0.64
K.AEEAKDEPPS(p)EGEAEEEEKEKEEGEEEEGAEEEEAAKDESEDAKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAK.K	IPI00231302.4	Neurofilament triplet L protein	X	0.64
K.AEEAKDEPPS(p)EGEAEEEEKEKEEGEEEEGAEEEEAAKDESEDAKEEEGGEGEEEDTKESEEEEKKEESAGEEQAAK.K	IPI00231302.4	Neurofilament triplet L protein	X	0.63
K.DEPPS(p)EGEAEEEEK.E	IPI00231302.4	Neurofilament triplet L protein	X	0.74
R.SYSSSSGS(p)LMPSLENLDLSQVAAISNDLK.S	IPI00231302.4	Neurofilament triplet L protein	X	0.4
R.SYSSSSGS(p)LMPSLENLDLSQVAAISNDLK.S	IPI00231302.4	Neurofilament triplet L protein	X	0.3
R.IYQY(p)IQSR.F	IPI00231347.1	Splice Isoform Short of Dual specificity tyrosine-phosphorylation-regulated kinase 1A	0.53	X
K.VLEIPDRDS(p)EEELEHVIEQIAYR.D	IPI00231379.2	solute carrier family 4, member 1	X	0.89
K.IDASKNEEDEGHSNS(p)SPR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	1.8	X
K.IDASKNEEDEGHSNS(p)SPR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	1.58	1.16
K.IDASKNEEDEGHS(p)NSSPR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	1.58	X
K.IDASKNEEDEGHSNSS(p)PR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	1.61	1.15
K.IDASKNEEDEGHS(p)NSSPR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	X	1.02
K.IFVGGLS(p)PDTPEEK.I	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	X	0.98
K.IDASKNEEDEGHS(p)NSS(p)PR.H	IPI00231384.1	Splice Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	X	1.13
K.S(p)PSPPPDGS(p)PAATPEIR.V	IPI00231388.2	Splice Isoform AMPH2-2 of Myc box-dependent-interacting protein 1	X	0.65
K.SPS(p)PPPDGSPAATPEIR.V	IPI00231388.2	Splice Isoform AMPH2-2 of Myc box-dependent-interacting protein 1	X	0.77
K.AASADST(p)TEGAPTDGFTVLSTK.S	IPI00231507.2	Splice Isoform 1 of Core histone macro-H2A.1	0.42	X
K.AASADS(p)TTEGAPTDGFTVLSTK.S	IPI00231507.2	Splice Isoform 1 of Core histone macro-H2A.1	X	0.77
-.S(p)ET(p)APAAPAAPAPAEK.T	IPI00231650.6	Histone H1.2	1.08	X
R.KAS(p)GPPVSELITK.A	IPI00231650.6	Histone H1.2	X	0.57
K.AEPEKS(p)EGAAEEQPEPAPAPEQEAAAPGPAAGGEAPK.A	IPI00231651.6	Brain acid soluble protein 1	X	1.64
K.GLS(p)EDTTEETLK.E	IPI00231827.6	Nucleolin	X	1.31
R.GYSYFTGS(p)SPPLSPSTPSESPTFSPSK.L	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	0.92
R.SQASEEESPVS(p)PLGRPR.P	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	0.8
R.SMS(p)DPKPLSPT(p)ADESSR.A	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	2.72
K.ISKFS(p)PIEEAK.D	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	2.49

R.SMS(p)DPKPLS(p)PTADESSR.A	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	2.35
K.DSFSQESSPSS(p)PSDLAK.L	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	1.13
K.TPPSNLS(p)PIEDAS(p)PTEELR.Q	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	1.21
K.DSFSQESSPS(p)SPSDLAK.L	IPI00231831.1	Splice Isoform 2 of Protein piccolo	X	1.13
K.NVTESPS(p)FSAGDNPHVLYSPEFR.I	IPI00231959.1	Splice Isoform S-MAG of Myelin-associated glycoprotein precursor	X	1.39
R.TEEVLSPDGSPS(p)KS(p)PSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	0.17	X
R.TEEVLSPDGS(p)PSKS(p)PSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	0.18	0.64
R.TEEVLS(p)PDGSPSK.S	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	0.14	X
R.TEEVLSPDGSPSKS(p)PSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	0.19	0.77
R.TEEVLSPDGSPSKSPS(p)K.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.8
K.SPDRTEEVLSPDGS(p)PSKSPS(p)K.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.63
K.SDVEIPATVTAFSFEDDSVPLS(p)PLK.Y	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.57
K.SPDRTEEVLSPDGS(p)PS(p)KSPSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.58
K.SPDRTEEVLSPDGS(p)PS(p)KSPSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.54
K.SPDRTEEVLSPDGSPSKS(p)PSK.K	IPI00231975.1	Splice Isoform 1 of Gamma-adducin	X	0.79
R.TSST(p)NEDEDLNPEQK.I	IPI00231979.1	Splice Isoform Beta of Transcription factor 12	1.69	X
R.DAEYTYDQQNQQGSLS(p)PTK.I	IPI00285687.1	Splice Isoform 3 of Mineralocorticoid receptor	X	0.49
R.DVEMGNS(p)VIEENEMK.K	IPI00324377.1	Splice Isoform GLAST-1 of Excitatory amino acid transporter 1	0.15	1.13
K.NSTLS(p)EEDYIER.R	IPI00324438.3	BCL2/adenovirus E1B 19 kDa-interacting protein 3	X	0.9
K.GSES(p)PNSFLDQEYR.K	IPI00324535.4	Splice Isoform 2 of Connector enhancer of kinase suppressor of ras 2	0.27	1.33
K.WLEETDSSS(p)GSPTNLDK.I	IPI00324954.1	POU domain, class 3, transcription factor 1	2.18	X
K.WLEETDSSSGS(p)PTNLDK.I	IPI00324954.1	POU domain, class 3, transcription factor 1	2.38	X
K.EVSADLS(p)EEENLLTDFK.L	IPI00325138.4	Splice Isoform 1 of Receptor-type tyrosine-protein phosphatase zeta precursor	0.14	1.08
K.EEKEEAEEKEEEPEVEKS(p)PVKS(p)PEAK.E	IPI00325609.3	Neurofilament triplet M protein	0.01	0.77
K.GVVTNGLDVS(p)PAEEK.K	IPI00325609.3	Neurofilament triplet M protein	0.06	0.61
K.EGS(p)SEKDEGEQEEEGET(p)EAEGEGEEAEAKEEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.63
K.AEEEGGS(p)EEEVGDKS(p)PQESKKEDIAINGEVEGK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.78
K.KEVAKES(p)PKEEK.V	IPI00325609.3	Neurofilament triplet M protein	X	0.87
K.EEKEEAEEKEEEPEVEKS(p)PVK.S	IPI00325609.3	Neurofilament triplet M protein	X	0.7
K.AEEEGGS(p)EEEVGDKSPQES(p)KKEDIAINGEVEGKEEEEQETQEK.G	IPI00325609.3	Neurofilament triplet M protein	X	0.72
K.S(p)PVEEVKPKPEAK.A	IPI00325609.3	Neurofilament triplet M protein	X	0.88
K.S(p)PVEEVKPKPEAK.A	IPI00325609.3	Neurofilament triplet M protein	X	0.84
K.EGSS(p)EKDEGEQEEEGETEAEGEGEEAEAKEEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.52
K.KAES(p)PVKEKAVEEMITITK.S	IPI00325609.3	Neurofilament triplet M protein	X	0.72
K.KAES(p)PVKEKAVEEMITITK.S	IPI00325609.3	Neurofilament triplet M protein	X	0.65
K.AEEEGGS(p)EEEVGDKSPQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.67
K.AEEEGGS(p)EEEVGDKSPQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.58
K.SDQAEEGGSEKEGS(p)S(p)EKDEGEQEEEGETEAEGEGEEAEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.45
K.AEEEGGSEEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.65
K.EGS(p)SEKDEGEQEEEGETEAEGEGEEAEAKEEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.48
K.EKAEEEGGS(p)EEEVGDKS(p)PQESKK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.82
K.AEEEGGSEEEVGDKS(p)PQES(p)KKEDIAINGEVEGKEEEEQETQEK.G	IPI00325609.3	Neurofilament triplet M protein	X	0.72
K.EKAEEEGGS(p)EEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.91
K.EKAEEEGGS(p)EEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.87
K.AEEEGGS(p)EEEVGDKS(p)PQESKK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.91
K.AEEEGGS(p)EEEVGDKS(p)PQESKK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.85
K.VKEKAEEEGGS(p)EEEVGDKSPQES(p)KKEDIAINGEVEGKEEEEQETQEK.G	IPI00325609.3	Neurofilament triplet M protein	X	0.61
K.S(p)IELESVR.G	IPI00325609.3	Neurofilament triplet M protein	X	0.83
R.VSGS(p)PSSGFR.S	IPI00325609.3	Neurofilament triplet M protein	X	0.55
K.VKEKAEEEGGS(p)EEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.86
K.EGS(p)SEKDEGEQEEEGETEAEGEGEEAEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.5
K.AEEEGGS(p)EEEVGDKS(p)PQESKKEDIAINGEVEGKEEEEQETQEK.G	IPI00325609.3	Neurofilament triplet M protein	X	0.73

K.KAES(p)PVKEK.A	IPI00325609.3	Neurofilament triplet M protein	X	0.65
K.EKAEEEGGS(p)EEEVGDKSPQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.76
K.VKEKAEEEGGS(p)EEEVGDKSPQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.8
K.VKEKAEEEGGS(p)EEEVGDKSPQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.65
K.EKAEEEGGSEEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.53
K.KEVAKES(p)PKEEKVEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.89
K.EEAEEKEEEPEVEKS(p)PVKSPEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.8
K.AEEEGGS(p)EEEVGDK.S	IPI00325609.3	Neurofilament triplet M protein	X	0.8
K.EGSS(p)EKDEGEQEEEGETEAEGEGEEAEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.51
K.DEGEQEEEGET(p)EAEGEGEEAEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.83
K.SPVKS(p)PEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.69
K.AKS(p)PVPK.S	IPI00325609.3	Neurofilament triplet M protein	X	0.53
K.EEAEEKEEEPEVEKS(p)PVKS(p)PEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.76
K.EEAEEKEEEPEVEKS(p)PVKS(p)PEAK.E	IPI00325609.3	Neurofilament triplet M protein	X	0.72
K.VKEKAEEEGGS(p)EEEVGDKS(p)PQESKKEDIAINGEVE GKEEEEQETQEK.G	IPI00325609.3	Neurofilament triplet M protein	X	0.69
K.AEEEGGS(p)EEEVGDKS(p)PQESK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.76
K.EKAEEEGGS(p)EEEVGDKSPQES(p)K.K	IPI00325609.3	Neurofilament triplet M protein	X	0.85
K.EVAKES(p)PKEEKVEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.97
K.EGS(p)S(p)EKDEGEQEEEGETEAEGEGEEAEAKEEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.91
K.GSGQEEEKGVVTNGLDVS(p)PAEEK.K	IPI00325609.3	Neurofilament triplet M protein	X	0.55
R.RTS(p)MGGTQQQFVEGVR.M	IPI00325912.1	Beta-catenin	X	1.2
R.QET(p)VECLK.K	IPI00326171.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	0.16	X
K.ESSDS(p)TNTTIEDEDAK.A	IPI00326171.1	Calcium/calmodulin-dependent protein kinase II, beta 3 isoform	0.08	0.83
K.DLS(p)LEEIQK.K	IPI00326596.2	Stathmin-2	1.09	X
K.SRS(p)PGT(p)PAGEGSGSPPK.W	IPI00327244.1	Splice Isoform 1 of Alpha-adducin	0.05	1.76
K.SPPDQSAVPNT(p)PPS(p)TPVK.L	IPI00327244.1	Splice Isoform 1 of Alpha-adducin	X	1.61
K.YSDVEVPASVTGHSFASDGDS(p)GTCS(p)PLR.H	IPI00327244.1	Splice Isoform 1 of Alpha-adducin	X	1.5
K.SPPDQSAVPNT(p)PPSTPVK.L	IPI00327244.1	Splice Isoform 1 of Alpha-adducin	X	1.35
K.EKS(p)PPDQSAVPNT(p)PPSTPVK.L	IPI00327244.1	Splice Isoform 1 of Alpha-adducin	X	1.32
R.TAS(p)PPVLPK.I	IPI00327589.3	PR domain zinc finger protein 2	1.07	X
K.DKVTDGITKS(p)PEKR.S	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	1.22
K.KSEVQAHS(p)PSR.K	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	0.96
K.KSEVQAHS(p)PSR.K	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	1.76
K.KETS(p)PETSLIQDEVALK.L	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	2.98
R.RLSNVSSS(p)GSINLLES(p)PQLATLAEDVTAALAK.Q	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	1.96
K.LSVEIPCPPPVSEADSS(p)IDEK.A	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	3.4
R.RLS(p)NVSSSGS(p)INLLESPQLATLAEDVTAALAK.Q	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	3.35
R.VKDEFTAEKEAS(p)PPSSADK.S	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	4.66
K.VTDGITKS(p)PEK.R	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	0.89
K.DGS(p)PDAPAT(p)PEKEEVPFSEYKTETYDDYKDETTID DSIMDADSLWVDTQDDDR.S	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	1.37
K.EES(p)TETPDIPAIPSDVTQPQPEAVVSEPAEVR.G	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	2.81
K.SPAS(p)PFAQTFGTNLEDIK.Q	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	8.08
K.DQPAALPLAAEETVNLPPS(p)PPPSPAS(p)EQTAALEED LLTASK.M	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	8.47
R.VKDEFTAEKEAS(p)PPSSADKSGLSR.E	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	4.09
K.DGS(p)PDAPATPEKEEVPFSEYKTETY(p)DDYKDETTID DSIMDADSLWVDTQDDDR.S	IPI00328017.4	Splice Isoform MAP2b of Microtubule-associated protein 2	X	1.17
K.S(p)ESPCESQYPNEK.D	IPI00357963.2	PREDICTED: similar to THO complex 2	2.24	X
R.AT(p)S(p)LSTLAEAGLQSVVPLDGSDTLKGRGER.A	IPI00357992.3	PREDICTED: similar to	1.96	X

		beta-1,4-galactosyltransferase V		
R.TYS(p)QDCSFK.N	IPI00358101.2	PREDICTED: similar to polybromo-1	1.81	0.91
R.YEEGESEAES(p)IT(p)SFMDVSNPFHQLYDTVR.S	IPI00358101.2	PREDICTED: similar to polybromo-1	1	X
R.SDS(p)PVADMEDSR.E	IPI00358110.2	PREDICTED: similar to mKIAA0333 protein	X	1.64
K.NSTKPETIPDMEDS(p)PPVS(p)DSEEQESVR.A	IPI00358110.2	PREDICTED: similar to mKIAA0333 protein	X	0.94
K.NSTKPETIPDMEDS(p)PPVSDS(p)EEQESVR.A	IPI00358110.2	PREDICTED: similar to mKIAA0333 protein	X	1.28
R.AADEDWDS(p)ELEDDLLGEDLLSGK.K	IPI00358126.2	PREDICTED: similar to hypothetical protein MGC20460	0.57	0.65
R.GFGDGYNGYGGGPGGGNFGGS(p)PGYGGGR.G	IPI00358211.2	PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1	1.1	1.45
R.GFGDGYNGYGGGPGGGNFGGS(p)PGYGGGR.G	IPI00358211.2	PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1	X	1.69
K.LFIGGLS(p)FETTEESLR.N	IPI00358211.2	PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1	X	1.64
R.NMGGPYGGGNYGPGGSGGS(p)GGYGGR.S	IPI00358211.2	PREDICTED: similar to Heterogeneous nuclear ribonucleoproteins A2/B1	X	1.43
R.TPEELDDS(p)DFETEDFDVR.S	IPI00358406.2	Catenin (Cadherin-associated protein), alpha 1, 102kDa	0.24	0.84
R.TPEELDDSDFET(p)EDFDVR.S	IPI00358406.2	Catenin (Cadherin-associated protein), alpha 1, 102kDa	X	0.76
R.TLS(p)PTPSAEGFQDGR.D	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	0.68	1.96
R.ST(p)SQGSINSPVYSR.H	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	X	1.68
R.STS(p)QGSINSPVYSR.H	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	X	1.57
R.STS(p)QGS(p)INSPVYSR.H	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	X	2.29
R.S(p)TSQGSINSPVYSR.H	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	X	1.52
R.STS(p)QGSINS(p)PVYSR.H	IPI00358533.3	PREDICTED: similar to actin-binding LIM protein 1 long isoform	X	0.72
R.ETAPTSAYSS(p)PAR.S	IPI00358537.2	PREDICTED: similar to mKIAA0417 protein	2.36	X
K.KKEPAIS(p)SQNSPEAR.E	IPI00358677.2	Transcription elongation factor A protein 1	X	0.65
R.ALS(p)PLSPVAIEQTSLK.M	IPI00358749.2	PREDICTED: similar to mFLJ00107 protein	0.23	X
R.SSTLEPEDEDDEDEDT(p)MTR.L	IPI00359020.1	PREDICTED: similar to 2610027C15Rik protein	X	1.39
K.AYS(p)PTCS(p)PTLGFK.E	IPI00359065.1	PREDICTED: similar to RIKEN cDNA D030015G18	0.74	X
K.AYSPTCS(p)PTLGFK.E	IPI00359065.1	PREDICTED: similar to RIKEN cDNA D030015G18	1.18	1.04
R.ANS(p)EASSSEGQSSLSSLEK.L	IPI00359065.1	PREDICTED: similar to RIKEN cDNA D030015G18	1.22	0.72
R.S(p)FDYNYR.R	IPI00359092.2	FUS interacting protein (Serine-arginine rich) 1	X	1.09
R.RES(p)GEGEEEVADSAR.L	IPI00359172.1	PREDICTED: similar to RIKEN cDNA 2900010D03	0.42	1.78
R.LS(p)PEPVAHR.R	IPI00359319.2	Hypothetical LOC313588	X	1.01
R.MDS(p)FDEDLAR.P	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.87	1.46
K.FSGEEGEIEDDES(p)GTENREEK.D	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.2	1.3
R.IDIS(p)PSTFR.K	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.23	0.78
K.EQTFSGGTS(p)QDIK.G	IPI00359323.1	Thyroid hormone receptor-associated protein 3	2.62	1.29
R.RIDIS(p)PSTFR.K	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.16	1.01
K.KS(p)PEIHR.R	IPI00359323.1	Thyroid hormone receptor-associated protein 3	0.11	0.87
R.ASVSDLS(p)PR.E	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.31	0.8
K.FSGEEGEIEDDES(p)GTENR.E	IPI00359323.1	Thyroid hormone receptor-associated protein 3	1.3	1.43
R.MDS(p)FDEDLARPSGLLAQER.K	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	1.53
K.WAHDKFS(p)GEEGEIEDDESGTENREEK.D	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	0.63
K.WAHDKFS(p)GEEGEIEDDES(p)GTENREEK.D	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	1.17
K.WAHDKFS(p)GEEGEIEDDESGTENR.E	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	0.83
K.FSGEEGEIEDDES(p)GTENREEK.D	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	1.2
K.FSGEEGEIEDDESGT(p)ENREEK.D	IPI00359323.1	Thyroid hormone receptor-associated protein 3	X	1.42
R.WQS(p)PVTK.S	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	1.22	X
R.RYS(p)PPIQR.R	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	1.02	0.7
K.EKS(p)PELPEPSVR.M	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear	0.97	0.69

		matrix protein		
K.RWQS(p)PVTK.S	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	X	1.19
R.KVELS(p)ESEEDKGSK.M	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	X	0.64
K.AAS(p)PSPQS(p)VR.R	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	X	0.56
K.AAS(p)PS(p)PQSVR.R	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	X	0.47
R.APQTSS(p)PPPVR.R	IPI00359359.3	PREDICTED: similar to Ser/Arg-related nuclear matrix protein	X	0.79
R.LS(p)PPPGDHDYIYNLDESEGVCDLFDVPVLK.L	IPI00359616.2	PREDICTED: similar to E2F transcription factor 4	0.69	X
K.EGS(p)LGDELLPLGYAEPEPQEGASAGAPSPTLDLASR.S	IPI00359734.2	PREDICTED: similar to predominantly fetal expressed T1 domain	X	0.76
R.LGAPENSGIST(p)LER.G	IPI00359762.2	PREDICTED: similar to FERM, RhoGEF, and pleckstrin domain protein 1 isoform 1	X	1.64
K.GSDYSWSYQT(p)PPSSPSSSSSR.K	IPI00359792.3	PREDICTED: similar to hypothetical protein BC002770	X	2.46
R.LEETS(p)ETEEDGGGDSDTLPR.G	IPI00359800.2	Hypothetical protein RGD1309387	1.38	0.83
K.DLFELDS(p)SEGEDSTDFFER.G	IPI00359800.2	Hypothetical protein RGD1309387	0.52	X
K.LPANISEDAEEGEVS(p)DEDS(p)ADEIEDDCK.L	IPI00359802.3	PREDICTED: similar to KIAA0450 protein	X	1.16
R.SLPS(p)LEDIDPDVLDSMHSLGCFR.D	IPI00360155.3	Brain serine/threonine kinase 2 (Fragment)	X	1.7
K.EKLTCKS(p)IGITK.R	IPI00360207.4	PREDICTED: similar to suppressor of variegation 3-9 homologue 2	0.92	X
R.SGDET(p)PGS(p)EAPGDKAVEEQGDDQDSEK.S	IPI00360386.2	76 kDa protein	X	0.69
R.S(p)GDETPGSEAPGDKAVEEQGDDQDSEK.S	IPI00360386.2	76 kDa protein	X	0.89
R.EGS(p)AFEDDDMLVSTSASNLLLEPEQSTSNLNEK.I	IPI00360494.3	Hypothetical protein MGC116373	1.25	X
R.GPAGEASAS(p)PPVR.R	IPI00360536.2	57 kDa protein	X	1.28
R.SEGFRAS(p)PR.H	IPI00360702.2	PREDICTED: similar to bullous pemphigoid antigen 1, 230\/240kDa	0.65	X
K.GSPVSEIGWETPPPES(p)PR.L	IPI00360767.2	PREDICTED: similar to beta1-syntrophin	X	0.5
R.RHS(p)TEGEEGDVSDVGSR.T	IPI00360804.3	PREDICTED: similar to mKIAA1940 protein	X	0.97
K.DCSYGAVTS(p)PTSTLESR.D	IPI00361275.2	PREDICTED: similar to KIAA1636 protein	X	1.46
R.YMAENPTAGVVQEEEEDNLEYDS(p)DGNPIAPSKK.I	IPI00361283.2	PREDICTED: similar to DEAD box polypeptide 42 protein	X	1.13
K.SGAPEDDDS(p)GVEVYYR.E	IPI00361560.3	PREDICTED: similar to RRP5 protein homolog	X	0.94
R.DHS(p)PTPSVFNSDEER.Y	IPI00361823.2	Pre-mRNA 3'-end-processing factor FIP1	1.56	1.09
R.ERDHSPT(p)PSVFNSDEER.Y	IPI00361823.2	Pre-mRNA 3'-end-processing factor FIP1	1.41	X
R.ERDHS(p)PTPSVFNSDEER.Y	IPI00361823.2	Pre-mRNA 3'-end-processing factor FIP1	1.41	1.02
R.DHS(p)PTPSVFNS(p)DEER.Y	IPI00361823.2	Pre-mRNA 3'-end-processing factor FIP1	X	0.92
R.SLVVS(p)DEEEAEEEAEK.R	IPI00361861.3	PREDICTED: similar to mKIAA0852 protein	1.63	0.74
K.AYT(p)PVVVTLWYR.A	IPI00361966.2	PREDICTED: similar to cell division cycle 2-like 1	0.24	X
R.GLEDSNISYGS(p)YEEPDPK.S	IPI00362018.2	PREDICTED: similar to CCG1	X	0.46
K.DFDDDS(p)DDEATFR.-	IPI00362037.1	PREDICTED: hypothetical protein XP_228576	X	0.94
R.SLS(p)GTLTELDEK.L	IPI00362153.2	PREDICTED: similar to bullous pemphigoid antigen 1-b	0.33	0.99
R.DKS(p)PSEGDVTPPKR.I	IPI00362186.3	PREDICTED: similar to 2010300C02Rik protein	X	3.92
R.DKS(p)PSEGDVAPPKR.I	IPI00362186.3	PREDICTED: similar to 2010300C02Rik protein	X	7.07
R.DKS(p)PSEGDVAPPK.R	IPI00362186.3	PREDICTED: similar to 2010300C02Rik protein	X	5.04
K.AFPKEELAS(p)DLEEMATSSISVPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	1.27	1.13
K.SLPKEEVAS(p)EPEEAAS(p)PITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	0.79	0.98
K.EEVAS(p)EPEEAASPITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	0.99	0.83
K.EELAS(p)DLEEMATSSISVPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	1.31	1.26
K.EELAS(p)DLEEMATSSISVPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	1.47	1.11
K.SLPKEEVAS(p)EPEEAASPITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	1.34	X
K.SLPKEEVAS(p)EPEEAASPITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	1.77	0.85
K.EEVAS(p)EPEEAASPIT(p)PK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted	X	1.11

		protein		
K.AFPKEELAS(p)DLEEMATSSISVPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	X	0.87
K.SLPKEEVAS(p)EPEEAASPIT(p)PK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	X	1.07
K.EEVAS(p)EPEEAAS(p)PITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	X	1.23
K.EEVAS(p)EPEEAAS(p)PITPK.K	IPI00362716.2	PREDICTED: similar to Nol5a_predicted protein	X	1.13
K.ETTSDT(p)SRTPEEEPLNLEGLVAHR.V	IPI00362755.2	PREDICTED: similar to tensin	X	1.3
R.RAAS(p)DGQYENQSPEATSPR.S	IPI00362755.2	PREDICTED: similar to tensin	X	2.05
R.AAS(p)DGQYENQS(p)PEATSPR.S	IPI00362755.2	PREDICTED: similar to tensin	X	2.02
K.ETTSDTS(p)RTPEEEPLNLEGLVAHR.V	IPI00362755.2	PREDICTED: similar to tensin	X	1.46
R.AAS(p)DGQYENQSPEATSPR.S	IPI00362755.2	PREDICTED: similar to tensin	X	1.61
R.SQS(p)LPTTLLSPVR.V	IPI00362824.2	PREDICTED: similar to KRAP	X	0.88
R.ASS(p)PPDRIDIFGR.T	IPI00362888.1	Hypothetical protein RGD1310061	1.3	1.2
R.ASS(p)PPDRIDIFGR.T	IPI00362888.1	Hypothetical protein RGD1310061	2.31	1.07
K.LGADSIS(p)EEADS(p)EPGSSALGK.N	IPI00362896.3	PREDICTED: similar to WDR protein, form B	X	0.39
R.SES(p)PPAELPSLR.R	IPI00362998.3	Gene trap locus 6	2.2	1.13
K.YS(p)PPRDDDKVDNQAK.S	IPI00362998.3	Gene trap locus 6	X	1.25
K.NKAGPS(p)EQSAS(p)EQLT(p)K.L	IPI00363119.3	Hypothetical protein LOC317498	1.01	X
K.ASVDS(p)ETESS(p)PGVNETAAASGQR.L	IPI00363201.1	RNA	X	1.39
R.S(p)VGGASPSEVS(p)PEDDGSFQK.V	IPI00363261.2	PREDICTED: similar to OTTHUMP00000028561	X	1.5
K.DRAS(p)PESLDLTR.D	IPI00363426.2	PREDICTED: similar to prospero-related homeobox 1	0.76	0.37
K.INENS(p)DKEAEVEESSEK.I	IPI00363433.3	PREDICTED: similar to formin binding protein 30	0.96	X
K.KHS(p)QTDLVSR.L	IPI00363438.1	PREDICTED: similar to hypothetical protein	X	1.9
K.TVAS(p)DS(p)EEEVGKEESSVK.K	IPI00363456.5	IWS1-like protein	1.36	X
R.VIS(p)DADDS(p)DSDVVSDK.S	IPI00363456.5	IWS1-like protein	X	0.82
K.T(p)VASDS(p)EEEVGKEESSVK.K	IPI00363456.5	IWS1-like protein	X	2.62
K.AAVLS(p)DS(p)EDEDKASAAK.K	IPI00363456.5	IWS1-like protein	X	1.39
K.T(p)VAS(p)DSEEEVGKEESSVK.K	IPI00363456.5	IWS1-like protein	X	0.79
R.LASTGSVDETKENGS(p)VEDK.S	IPI00363684.2	PREDICTED: similar to mKIAA1107 protein	X	1.76
R.LAST(p)GSVDETKENGSVEDK.S	IPI00363684.2	PREDICTED: similar to mKIAA1107 protein	X	15.73
K.VFVGGLS(p)PDTSEEQIK.E	IPI00363719.3	Heterogeneous nuclear ribonucleoprotein D-like	0.53	X
R.AKPAAQSEEETAAS(p)PAAS(p)PTPQSAQEPSAPGK.A	IPI00363771.3	Eukaryotic translation initiation factor 3 subunit 9	1.1	1.13
R.ALENGEADEPSFS(p)DPEDFVDDVSEEELLGDVLK.D	IPI00363771.3	Eukaryotic translation initiation factor 3 subunit 9	0.63	0.8
R.ALENGEADEPSFS(p)DPEDFVDDVS(p)EEELLGDVLK.D	IPI00363771.3	Eukaryotic translation initiation factor 3 subunit 9	0.75	1.09
R.AKPAAQSEEETAAS(p)PAASPTPQS(p)AQEPSAPGK.A	IPI00363771.3	Eukaryotic translation initiation factor 3 subunit 9	X	1.06
R.ALENGEADEPS(p)FSDPEDFVDDVS(p)EEELLGDVLK.D	IPI00363771.3	Eukaryotic translation initiation factor 3 subunit 9	X	0.92
K.SLS(p)DSESDDSK.S	IPI00364251.1	Chromobox homolog 3	1.43	0.69
R.GSS(p)DGRGSDSESDLPHR.K	IPI00364284.3	PREDICTED: similar to hypothetical protein	X	1.12
R.GSSDGRGS(p)DSESDLPHR.K	IPI00364284.3	PREDICTED: similar to hypothetical protein	X	1
K.VEATDPEACS(p)GEEVAVK.T	IPI00364359.2	PREDICTED: similar to mKIAA0211 protein	X	0.65
R.SS(p)GSPYGGGYGSGGGSGGYGSR.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	0.99	X
R.SSGSPYGGGY(p)GSGGGSGGYGSR.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	1.08	X
R.SSGSPYGGGYGSGGGSGGYGS(p)R.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	0.91	X
R.SSGS(p)PYGGGYGSGGGSGGYGSR.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	0.99	X
R.SSGSPYGGGYGS(p)GGGSGGYGSR.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	0.85	X
R.S(p)SGSPYGGGYGSGGGSGGYGSR.K	IPI00364363.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3	0.9	X
K.Y(p)TFDFSEEEEDDADDDDDNNDLEELK.V	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	0.44	1.09

K.KTSFDQDS(p)DVDIFPSDFTSEPPALPR.T	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	0.62	1.02
K.VKAS(p)PITNDGEDEFVPS(p)DGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.3	X
K.VKAS(p)PITNDGEDEFVPS(p)DGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	3.56	0.89
K.ASPITNDGEDEFVPSDGIDKDEYAFS(p)PGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.53	X
R.KAS(p)GS(p)ENEGDYNPGR.K	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.21	1.16
K.SEDDSAKFDS(p)NEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.75	1.06
K.VKASPIT(p)NDGEDEFVPSDGIDKDEY(p)AFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.3	X
K.VKAS(p)PITNDGEDEFVPSDGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.67	X
K.VKAS(p)PITNDGEDEFVPSDGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.49	0.61
K.VKAS(p)PITNDGEDEFVPSDGIDKDEYAFS(p)PGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	3.42	X
K.FDS(p)NEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.86	1.13
K.KT(p)SFDQDSDVDIFPSDFTSEPPALPR.T	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	0.29	1.13
K.SEDDS(p)AKFDSNEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	3.37	X
K.SEDDS(p)AKFDS(p)NEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.67	X
R.KAS(p)GSENEGDYNPGR.K	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.37	0.99
K.VKASPIT(p)NDGEDEFVPSDGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.06	X
K.YTFDFS(p)EEEEDDADDDDDNNDLEELK.V	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	0.45	1.08
K.YTFDFS(p)EEEEDDADDDDDNNDLEELK.V	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.9	1.17
K.ASPITNDGEDEFVPS(p)DGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.23	X
K.AS(p)PITNDGEDEFVPS(p)DGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	2.88	X
K.AS(p)PITNDGEDEFVPSDGIDKDEYAFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.23	0.76
K.KTS(p)FDQDSDVDIFPSDFTSEPPALPR.T	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	0.26	X
K.VKAS(p)PITNDGEDEFVPSDGIDKDEY(p)AFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	1.98	X
K.VKAS(p)PITNDGEDEFVPSDGIDKDEY(p)AFSPGK.S	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	3.63	X
K.VVEPANS(p)DS(p)DSELGNIPK.K	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	0.72
K.AS(p)GSENEGDYNPGR.K	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	1.25
K.SEDDSAKFDSNEEDT(p)TSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	0.97
K.S(p)EDDSAKFDS(p)NEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	1.17
K.ASGS(p)ENEGDYNPGR.K	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	1.37
K.S(p)EDDS(p)AKFDSNEEDTTSVFAPSFGLK.Q	IPI00364460.2	PREDICTED: similar to DNA topoisomerase	X	1.2
K.AAPS(p)PDVTVGASPVLDEIQFAALK.I	IPI00364626.3	PREDICTED: similar to Sfrs14 protein	0.59	0.96
K.AAPS(p)PDVTVGASPVLDEIQFAALK.I	IPI00364626.3	PREDICTED: similar to Sfrs14 protein	X	1.1
R.S(p)LNMADQEGTLIGK.G	IPI00364626.3	PREDICTED: similar to Sfrs14 protein	X	1.56
R.GRS(p)LNMADQEGTLIGK.G	IPI00364626.3	PREDICTED: similar to Sfrs14 protein	X	1.33
K.LEWAADDEEKKKS(p)PSEGTDEK.A	IPI00364637.3	PREDICTED: similar to D430018P08 protein	X	1.06
R.IGSTT(p)NPFLDIPHDPNAAVYK.S	IPI00364637.3	PREDICTED: similar to D430018P08 protein	X	3.61
K.VSS(p)PAPT(p)EEEEEEEHVDPK.L	IPI00364805.2	PREDICTED: similar to AT rich interactive domain 1A	0.51	0.99
K.VSS(p)PAPTEEEEEEEHVDPK.L	IPI00364805.2	PREDICTED: similar to AT rich interactive domain 1A	X	0.91
R.GPS(p)PSPVGSPASVAQSR.S	IPI00364805.2	PREDICTED: similar to AT rich interactive domain 1A	X	0.74
R.LIAS(p)SPTLISGITSPPLLDSIK.T	IPI00364807.2	42 kDa protein	0.81	X
R.LIASS(p)PTLISGITSPPLLDSIK.T	IPI00364807.2	42 kDa protein	0.28	X
R.VYYS(p)PPVAR.R	IPI00364818.2	PREDICTED: similar to FLJ44670 protein	1	X
R.TFQQIQEEEDDDYPGSYS(p)PQDPSAGPLLTEELIK.A	IPI00364827.3	PREDICTED: similar to Protein C20orf77 homolog	0.77	X
R.TFQQIQEEEDDDYPGS(p)YSPQDPSAGPLLTEELIK.A	IPI00364827.3	PREDICTED: similar to Protein C20orf77 homolog	X	0.77
K.RIS(p)GLIYEETR.G	IPI00364897.2	PREDICTED: similar to Histone H2B 291B	0.66	1.07
K.TVTAMDVVY(p)ALK.R	IPI00364897.2	PREDICTED: similar to Histone H2B 291B	X	0.48
R.KPS(p)VDNSASAPDYK.S	IPI00364908.3	PREDICTED: similar to archvillin	1.31	X
R.GIITDS(p)FGR.H	IPI00364987.3	PREDICTED: similar to Cerebral cavernous malformation 2 homolog	X	2.35
R.SNSSYLGSDETGS(p)GDELPCDIR.I	IPI00365036.2	PREDICTED: similar to mKIAA1415 protein	X	1.15
R.IGELGAPEVWGLS(p)PK.I	IPI00365073.3	Nuclear NF-kappaB activating protein	X	1.24
R.IYLESEHGS(p)PLTPR.V	IPI00365080.2	Bcl11a protein	6.16	1.34
K.RLS(p)LESEGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	0.02	3.7
K.AANKT(p)PPKS(p)PGDPAK.A	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	3.12

K.RLSLES(p)EGANEGAAAAPELSALEEAFRR.F	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	3.39
K.RLS(p)LESEGANEGAAAAPELSALEEAFRR.F	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	3.76
K.RLS(p)LES(p)EGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	1.41
R.LS(p)LESEGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	2.82
K.AANKT(p)PPKSPGDPAK.A	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	3.32
K.RLSLES(p)EGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	1.37
K.RLSLES(p)EGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	4.89
K.RLS(p)LESEGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	2.47
K.RLS(p)LESEGANEGAAAAPELSALEEAFR.R	IPI00365393.2	PREDICTED: similar to RIKEN cDNA 2900041A09	X	4.89
R.EGS(p)TPEDDFPSSSGNGNK.A	IPI00365410.2	PREDICTED: similar to Wilms tumor 1-associating protein	X	1.76
R.KTS(p)PASLDFPEPQK.S	IPI00365414.2	PREDICTED: similar to DNA segment, Chr 8, ERATO Doi 457, expressed	1.38	0.91
K.DS(p)QESSDAELSSSEFR.A	IPI00365414.2	PREDICTED: similar to DNA segment, Chr 8, ERATO Doi 457, expressed	2.44	X
K.DSQESS(p)DAELSSSEFR.A	IPI00365414.2	PREDICTED: similar to DNA segment, Chr 8, ERATO Doi 457, expressed	X	2.09
R.HAELSGS(p)PLK.S	IPI00365503.3	PREDICTED: similar to mKIAA1266 protein	X	1.23
R.RAS(p)VCAEAYNPDEEEDDAESR.I	IPI00365600.2	cAMP-dependent protein kinase type II-beta regulatory subunit	X	5.3
R.RAS(p)VCAEAYNPDEEEDDAESR.I	IPI00365600.2	cAMP-dependent protein kinase type II-beta regulatory subunit	X	4.98
K.VEEEQEADEEDVS(p)EEETENR.E	IPI00365626.3	Thioredoxin domain containing 1	0.66	0.44
R.S(p)PQPPAEEDEDDFDDTLVAIDTYNCDLHFK.V	IPI00365665.2	PREDICTED: similar to EIB-55kDa associated protein 5	0.32	X
R.GRS(p)PQPPAEEDEDDFDDTLVAIDTYNCDLHFK.V	IPI00365665.2	PREDICTED: similar to EIB-55kDa associated protein 5	0.7	0.39
R.SSSEDDDLDVES(p)DFDDASINSYSVSDGSTSR.S	IPI00365698.2	PREDICTED: chromodomain helicase DNA binding protein 4	X	1.57
R.ESGQDELLPVPGS(p)PSR.A	IPI00365711.2	PREDICTED: similar to mKIAA0947 protein	0.45	X
R.AAS(p)PQEVTAQADEK.T	IPI00365741.2	PREDICTED: similar to NSD1 protein	2.01	X
K.DWEDDS(p)DEDMSNFDR.F	IPI00365935.2	PREDICTED: similar to Sid3177p	X	0.32
R.DEYEYVS(p)DDGELK.I	IPI00365997.3	PREDICTED: similar to PHD finger protein 2	1.69	X
K.DSDYVYPSLES(p)DEDNPVFK.S	IPI00365997.3	PREDICTED: similar to PHD finger protein 2	1.62	1.37
K.DSDYVYPS(p)LESDEDNPVFK.S	IPI00365997.3	PREDICTED: similar to PHD finger protein 2	X	1.35
R.EES(p)EEEEEEDDDDEDEEEEK.E	IPI00365999.1	Protein DEK	0.86	0.48
K.EVDGLLTSDPMGS(p)PVSSK.A	IPI00366038.2	PREDICTED: similar to Ataxin 2-like	X	1.05
R.VDDDS(p)LGEFPVTNSR.A	IPI00366160.2	PREDICTED: similar to hypothetical protein	X	1.43
R.AGS(p)ATPLSPTR.L	IPI00366190.3	PREDICTED: similar to Lmnb2 protein	X	1.43
R.ELS(p)PDFYQPGPDYIK.Q	IPI00366345.2	PREDICTED: similar to junctophilin type 1	X	0.82
K.SVPTIDS(p)GNEDDDSSFK.I	IPI00366370.2	PREDICTED: similar to Eukaryotic translation initiation factor 5B	0.89	0.43
R.S(p)SGTASSVAFT(p)PLQGLEIVNPQAAEK.K	IPI00366375.3	PREDICTED: similar to PRP31	3.07	X
R.SSGTASS(p)VAFT(p)PLQGLEIVNPQAAEK.K	IPI00366375.3	PREDICTED: similar to PRP31	X	1.99
R.SSGTASS(p)VAFT(p)PLQGLEIVNPQAAEK.K	IPI00366375.3	PREDICTED: similar to PRP31	X	1.26
R.KLS(p)GDQITLPTTVDYSSVPK.Q	IPI00366400.1	Receptor-binding cancer antigen expressed on SiSo cells (Fragment)	0.47	0.77
R.ALS(p)PVIPIIPR.T	IPI00366472.2	PREDICTED: similar to Myeloid/lymphoid or mixed-lineage leukemia protein 2	1.6	1.09
K.LEGPAS(p)PDVELGKEETEESK.K	IPI00366472.2	PREDICTED: similar to Myeloid/lymphoid or mixed-lineage leukemia protein 2	1.28	X
R.DGSIS(p)PVSSECSAVER.T	IPI00366505.3	Hypothetical protein RGD1308984	0.59	X
K.NSTDLDSAPEDPTS(p)PK.R	IPI00366800.2	PREDICTED: similar to capicua protein	0.8	X
K.NSTDLDSAPEDPT(p)SPK.R	IPI00366800.2	PREDICTED: similar to capicua protein	X	1.38
R.SMSETGT(p)AAAPGVSSELLSAAAQTLLSSDTK.A	IPI00366800.2	PREDICTED: similar to capicua protein	X	1.72
R.SFLSEPS(p)SPGR.A	IPI00366816.2	PREDICTED: similar to mKIAA1429 protein	X	2.56
R.SFLSEPSS(p)PGR.A	IPI00366816.2	PREDICTED: similar to mKIAA1429 protein	X	2.38

R.TMIIS(p)PER.L	IPI00366952.2	PREDICTED: splicing factor 3b, subunit 1	2.93	1.87
R.DTPGHGSGWAET(p)PR.T	IPI00366952.2	PREDICTED: splicing factor 3b, subunit 1	1.71	1.32
R.MDGS(p)DFESTGSR.S	IPI00367147.2	PREDICTED: similar to inhibitor of growth family, member 5	X	0.68
K.YST(p)SPASSDYAWK.S	IPI00367376.2	PREDICTED: similar to mKIAA1980 protein	1.57	X
K.YSTS(p)PASSDYAWK.S	IPI00367376.2	PREDICTED: similar to mKIAA1980 protein	X	1.63
K.TAHNSEADLEESFNEHELEPSS(p)PK.T	IPI00367694.3	PREDICTED: similar to PHD finger protein 6	3.1	0.98
K.TAHNSEADLEESFNEHELEPS(p)SPK.T	IPI00367694.3	PREDICTED: similar to PHD finger protein 6	3.01	0.86
K.AADKS(p)PESQNLIDGTK.K	IPI00367824.3	PREDICTED: similar to zinc finger protein 532	1.01	X
K.VQIPVSHPDPDPVS(p)DNEDDSY(p)DEDVHDPR.S	IPI00367848.2	PREDICTED: similar to ZO-1	X	1.06
R.HTSDYEDTDTEGGAYTDQELDETLNDEVGT(p)PPESAITR.S	IPI00367848.2	PREDICTED: similar to ZO-1	X	1.35
R.DS(p)DGVDGFEAEGK.K	IPI00367952.3	PREDICTED: similar to zinc finger RNA binding protein	0.5	1.06
R.RDS(p)DGVDGFEAEGK.K	IPI00367952.3	PREDICTED: similar to zinc finger RNA binding protein	X	1.32
R.KAS(p)PEPPDSAESALK.L	IPI00368005.2	Polyglutamine-containing protein	2.42	0.76
K.ATIS(p)DEEIER.Q	IPI00368144.2	PREDICTED: similar to RIKEN cDNA 1190006E07	0.27	0.88
K.AFYGS(p)EEDEAKGPGSEEAATAALPAR.K	IPI00368200.1	PREDICTED: similar to AP-3 complex beta3B subunit	X	0.39
R.DVEDMELS(p)DVEDDGSK.I	IPI00368287.3	PREDICTED: similar to 4930535B03Rik protein	1.09	0.87
K.SFNYS(p)PNSSTSEVSSTSASK.A	IPI00368287.3	PREDICTED: similar to 4930535B03Rik protein	0.46	0.53
R.GPTSTSVDNIDGT(p)PVRDER.S	IPI00368287.3	PREDICTED: similar to 4930535B03Rik protein	X	1.31
R.IETDEES(p)CDS(p)AHGDADQPAR.E	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.71	X
R.GSSEGQSLENAS(p)PDILR.E	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.42	0.74
R.IES(p)DEEEDFENVGK.V	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	2.2	0.78
K.VGS(p)PLDYSLVDLPSTNGQS(p)PGK.A	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.15	0.91
K.DIQRLS(p)PIPEEVVR.G	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.62	0.86
K.NSSQQEDPS(p)RESPTLEDEETKKDEETPK.Q	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.74	X
K.TSVDKDIQRLS(p)PIPEEVVR.G	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	1.27	0.7
K.VGS(p)PLDYSLVDLPSTNGQSPGK.A	IPI00368441.1	PREDICTED: similar to remodeling and spacing factor 1	X	0.65
R.AAQLQGS(p)PAPEKGEVLGDALQLDTLKQEAAK.L	IPI00368473.2	PREDICTED: nuclear mitotic apparatus protein 1	1.83	0.87
R.AAQLQGS(p)PAPEKGEVLGDALQLDTLK.Q	IPI00368473.2	PREDICTED: nuclear mitotic apparatus protein 1	2.56	0.93
R.TQPDGTSVPGEPAS(p)PISQR.L	IPI00368473.2	PREDICTED: nuclear mitotic apparatus protein 1	0.5	X
K.QAAS(p)PQEPSELEELR.G	IPI00368473.2	PREDICTED: nuclear mitotic apparatus protein 1	2.53	0.99
K.NLNNSNLFSPVNHDSEDLAS(p)PSEYPENGER.F	IPI00368476.2	PREDICTED: nucleoporin 98	0.96	1.13
K.NLNNSNLFS(p)PVNHDSEDLAS(p)PSEYPENGER.F	IPI00368476.2	PREDICTED: nucleoporin 98	0.97	X
K.YGLQDS(p)DEEEEEHPPK.T	IPI00368476.2	PREDICTED: nucleoporin 98	1.21	1.46
R.STGEYS(p)EADEDEEEEGKPSR.K	IPI00368594.1	PREDICTED: similar to remodeling and spacing factor 1	2.53	0.91
R.LQDSSDPDTCSEEEVS(p)SRLSPPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	0.74	X
R.LQDSS(p)DPDTCSEEEVSSR.L	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	0.6	6.28
R.LQDSS(p)DPDTCSEEEVSSRLS(p)PPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	7.32
R.LQDS(p)SDPDTCSEEEVSSRLS(p)PPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	7.55
R.LQDSSDPDTCS(p)EEEVSSRLS(p)PPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	7.76
R.LQDSSDPDTCSEEEVSS(p)RLSPPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	4.56
R.LQDSSDPDTCSEEEVSSRLS(p)PPHSPR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	5.02
R.LQDSSDPDTCSEEEVS(p)SRLSPPHS(p)PR.D	IPI00368617.2	Rho/rac guanine nucleotide exchange factor	X	5.27
K.SLDAEPSVPSAAKPAS(p)PEK.T	IPI00368671.2	PREDICTED: similar to Pogo transposable element with ZNF domain	2.93	1.07
K.SLDAEPSVPS(p)AAKPASPEK.T	IPI00368671.2	PREDICTED: similar to Pogo transposable element with ZNF domain	X	0.98
R.SSS(p)PVTELTARS(p)PVK.Q	IPI00368692.4	PREDICTED: similar to serine/arginine	0.64	1.04

		repetitive matrix 2		
R.SGS(p)VTNMQAEECSTT(p)PQR.Q	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.74	1.04
R.SSS(p)PVTELTAR.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.99	1.05
K.SMLQT(p)PPDQNLSGSK.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.56	X
R.SRTS(p)PVTR.R	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.88	X
R.T(p)PPVALSSSR.M	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.25	0.87
R.TS(p)PLLLDR.A	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1.26	1.63
K.SEQPLSQVLPTLS(p)PEHK.E	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1.06	1.27
R.S(p)SSPVTELTARS(p)PVK.Q	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.78	X
K.ELSHS(p)PPRDNSFESLEFR.N	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.99	0.98
K.VGIFSSQSVS(p)SPLLETVQQR.T	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.76	0.94
R.DKFS(p)PTQDRPESSTVLK.D	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.57	1.17
R.DKFS(p)PTQDRPESSTVLK.D	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.73	1.11
R.S(p)SSPVTELTAR.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1	X
R.SGSS(p)QELDGKPSVSPQER.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.3	0.71
R.RSS(p)SELSPEIVEK.V	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1.56	1.22
R.NSGPVLEVNTDFS(p)PEVK.E	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.81	0.76
K.SAVRPS(p)PS(p)PER.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.67	X
R.S(p)GSVTNMQAEECSTTPQR.Q	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.43	X
K.VGIFSSQSVSS(p)PLLETVQQR.T	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1.37	0.9
K.VGIFSSQSVSS(p)PLLETVQQR.T	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.67	X
K.SEQPLSQVLPT(p)LSPEHK.E	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	1.13	X
R.SS(p)SPVTELTAR.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	0.92	1.06
R.SGS(p)SQELDGKPSVSPQER.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	1.02
R.S(p)RT(p)SPVTR.R	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.82
R.QMHLES(p)PSLQSK.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	1.65
R.SGS(p)VTNMQAEECS(p)TTPQR.Q	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	1.06
K.ELSHS(p)PPR.D	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.81
R.SSSELS(p)PEIVEK.V	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.76
R.SSS(p)PVTELTARS(p)PVKQDK.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.98
R.SSS(p)PVTELTARS(p)PVKQDK.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.97
R.DKFSPT(p)QDRPESSTVLK.D	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	1.07
R.RSS(p)SELS(p)PEIVEK.V	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	0.94
R.SSS(p)PVTELT(p)ARSPVKQDK.S	IPI00368692.4	PREDICTED: similar to serine/arginine repetitive matrix 2	X	1.03
K.DGATS(p)EEETELEK.Q	IPI00368799.1	ABT1-associated protein	0.99	0.68
K.EPTPSIAS(p)DIS(p)LPIATQELR.Q	IPI00368857.3	PREDICTED: similar to chr2 synaptotagmin	X	0.89

R.ES(p)PEGSYTDDANQEVR.G	IPI00369169.3	Cdc42 effector, long isoform	2.08	X
K.AAS(p)SPSNPAALPVASDSS(p)PMGSK.T	IPI00369530.2	PREDICTED: similar to retinoic acid induced 1	X	0.98
K.AASS(p)PSNPAALPVASDSS(p)PMGSK.T	IPI00369530.2	PREDICTED: similar to retinoic acid induced 1	X	0.75
K.LGASNS(p)PGQPNSVK.R	IPI00369616.2	PREDICTED: similar to RNA binding motif protein 25	X	1.69
R.SLAALDALNT(p)DDENDEEEYEAWK.V	IPI00369629.2	PREDICTED: similar to microfibrillar-associated protein 1	X	0.63
K.IVEPEVVGES(p)DSEVEGDAWR.L	IPI00369629.2	PREDICTED: similar to microfibrillar-associated protein 1	X	0.42
R.KNDMDEPPPLDY(p)GSGEDDGKSDK.R	IPI00369880.2	PREDICTED: similar to chromodomain helicase DNA binding protein 3	0.76	X
K.EIQGDGPPSS(p)PTNDPTVK.Y	IPI00369880.2	PREDICTED: similar to chromodomain helicase DNA binding protein 3	2.66	1.47
K.TSPTT(p)PEAS(p)TTNSPCT(p)SKPATPAPSEK.G	IPI00369880.2	PREDICTED: similar to chromodomain helicase DNA binding protein 3	X	1.27
-.MDTDLY(p)DEFGNYIGPELDS(p)DEDDDELGR.E	IPI00370117.2	PREDICTED: similar to 116 kDa U5 small nuclear ribonucleoprotein component	0.64	0.57
-.MDT(p)DLYDEFGNYIGPELDS(p)DEDDDELGR.E	IPI00370117.2	PREDICTED: similar to 116 kDa U5 small nuclear ribonucleoprotein component	1.17	0.57
R.TGAGMITQHSSTAS(p)PVNR.I	IPI00370164.2	Similar to modulator of estrogen induced transcription	X	4.14
R.SSSS(p)STTPTSATSLYK.F	IPI00370165.3	PREDICTED: similar to junction-associated coiled-coil protein	X	1.16
R.LST(p)SPATREEAAS(p)PGAK.D	IPI00370170.2	PREDICTED: similar to Transcription factor 20	1.41	1.31
K.SSQEDDPAASQRPPS(p)NSGVK.E	IPI00370170.2	PREDICTED: similar to Transcription factor 20	0.73	X
R.LS(p)TSPATREEAAS(p)PGAK.D	IPI00370170.2	PREDICTED: similar to Transcription factor 20	X	1.29
R.LSTS(p)PATREEAAS(p)PGAK.D	IPI00370170.2	PREDICTED: similar to Transcription factor 20	X	1.35
K.VSSLS(p)PEQEQGLWK.Q	IPI00370217.2	PREDICTED: similar to RIKEN cDNA 2810485I05	X	1.25
K.VDSSTNSSPS(p)PQQSESLSPAHTS(p)DFR.T	IPI00370332.2	PREDICTED: similar to Bcl7b protein	0.33	X
K.VDSSTNSSPS(p)PQQSESLS(p)PAHTSDFR.T	IPI00370332.2	PREDICTED: similar to Bcl7b protein	X	1.09
R.RQS(p)LELQK.C	IPI00370333.1	PREDICTED: similar to Williams-Beuren syndrome deletion transcript 9 homolog	0.92	1.17
R.LADDEGDSDSES(p)VGQSR.G	IPI00370333.1	PREDICTED: similar to Williams-Beuren syndrome deletion transcript 9 homolog	0.94	X
R.LADDEGDS(p)DSES(p)VGQSR.G	IPI00370333.1	PREDICTED: similar to Williams-Beuren syndrome deletion transcript 9 homolog	0.88	0.91
R.LADDEGDS(p)DSESVGQSR.G	IPI00370333.1	PREDICTED: similar to Williams-Beuren syndrome deletion transcript 9 homolog	X	0.79
R.TAFYNEDDS(p)EEEQR.Q	IPI00370452.2	PREDICTED: similar to WD repeat domain 11 protein	1.31	0.92
R.AQS(p)YDIQAWR.K	IPI00370452.2	PREDICTED: similar to WD repeat domain 11 protein	X	1.24
R.ALNAET(p)PKS(p)SPLPAK.G	IPI00370616.2	PREDICTED: similar to DNA segment, Chr 5, Wayne State University 46, expressed	0.14	1.21
R.ALNAET(p)PKSS(p)PLPAK.G	IPI00370616.2	PREDICTED: similar to DNA segment, Chr 5, Wayne State University 46, expressed	X	0.57
K.S(p)LSPGKENINSLEVEK.E	IPI00370658.1	PREDICTED: similar to pinin	1.47	1.01
K.SLS(p)PGKENINSLEVEKESEEKEEK.E	IPI00370658.1	PREDICTED: similar to pinin	0.91	X
K.EAGVVHS(p)DAEKDQEEEEQKQETEAR.M	IPI00370658.1	PREDICTED: similar to pinin	0.85	X
K.SLS(p)PGKENINSLEVEK.E	IPI00370658.1	PREDICTED: similar to pinin	1.47	0.99
R.GFS(p)DSGGGPPAK.Q	IPI00370658.1	PREDICTED: similar to pinin	1.55	0.92
R.YLSTT(p)PETTHCR.K	IPI00370727.2	PREDICTED: similar to Zbtb20 protein	X	0.9
R.YLST(p)TPETTHCR.K	IPI00370727.2	PREDICTED: similar to Zbtb20 protein	X	0.91
R.NES(p)EECTEDTDQAEGTESEPK.G	IPI00370727.2	PREDICTED: similar to Zbtb20 protein	X	0.87
R.EGQVEAAQPEQAAEAPAESSAQPNQLETGAS(p)SPER.S	IPI00370727.2	PREDICTED: similar to Zbtb20 protein	X	0.73
K.TSS(p)DDES(p)EEDEDDLLQR.T	IPI00370746.2	PREDICTED: similar to novel protein (6230425C22Rik) similar to Homo sapiens CGI-48 protein	X	0.8
K.SGPTS(p)DNEEEDDEEDGSYLHPSLFASK.K	IPI00370880.3	Splicing factor, arginine/serine-rich 8	1.29	1.31
R.RNS(p)LEGYSR.S	IPI00371042.2	PREDICTED: similar to RNA binding motif protein 15B	X	1.66
K.TEDGGWEWS(p)DDEFDEESEEGK.A	IPI00371139.2	PREDICTED: similar to Osr1 protein	0.67	X
R.GSDS(p)PAADVEIEYVTEEPEIYEPNFIFFK.R	IPI00371470.3	PREDICTED: similar to Splicing factor 3b, subunit 2	0.96	0.8

R.GS(p)DSPAADVEIEYVTEEPEIYEPNFIFFK.R	IPI00371470.3	PREDICTED: similar to Splicing factor 3b, subunit 2	0.68	0.79
K.FDGES(p)DKEQFDDDQK.V	IPI00371562.2	PREDICTED: similar to KIAA1078 protein	0.96	1.28
K.ELGS(p)TEDIYLASR.K	IPI00371725.3	PREDICTED: similar to dishevelled associated activator of morphogenesis 2	X	1.35
K.NNPAADTEDEES(p)DGEDR.G	IPI00371827.2	PREDICTED: similar to delangin	0.99	0.36
K.AITSLLGGGS(p)PK.N	IPI00371827.2	PREDICTED: similar to delangin	2.4	0.85
K.YSLS(p)PSK.S	IPI00371944.2	PREDICTED: similar to Ran-binding protein 2	1.3	X
R.EDALDDSVSSSSVHASPLASS(p)PVRK.N	IPI00371944.2	PREDICTED: similar to Ran-binding protein 2	0.6	X
K.TPGDFNYAYQKPES(p)TTESPDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.26	1.62
K.HS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.57	0.45
K.TLEVVS(p)PSQSVTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.63	1.14
K.TLEVVSPSQSVTGSAGHT(p)PYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.29	X
K.EVPSKEEQS(p)PVK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.33	X
K.GEAEQS(p)EEEGEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.21	X
K.GEAEQS(p)EEEGEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.32	X
K.QGFSDKES(p)PVSDLTSDLYQDK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.52	1.72
R.SQGSTSNS(p)DWMK.N	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.6	0.24
K.TLEVVS(p)PSQSVTGSAGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.76	1.51
K.TLEVVSPS(p)QSVTGS(p)AGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.64	X
K.FEDEGAGFEESS(p)EAGDYEEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.56	0.46
R.SS(p)ISPMDEPVPDSES(p)PIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.55	1.82
K.AETEEAEEPEEDGEDNVSGSAS(p)KHSPTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.19	0.35
R.SSIS(p)PMDEPVPDS(p)ESPIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.31	X
K.ESTAAYQTSSS(p)PPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.13	2.14
K.ESTAAYQTSSS(p)PPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.14	1.58
K.AETEEAEEPEEDGEDNVSGS(p)ASKHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.09	0.39
K.ETEVS(p)KGSAES(p)PDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.57	X
K.AETEEAEEPEEDGEDNVSGS(p)ASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.75	0.25
K.TTRT(p)PEEGGYSYEISEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.74	1.89
K.TTRT(p)PEEGGYSYEISEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.24	1.84
K.ESTAAY(p)QTSSSPPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1	X
R.ES(p)SPTYSPGFSDST(p)SGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.69	X
K.TLEVVSPSQS(p)VTGS(p)AGHTPYY(p)QSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.84	X
R.SSIS(p)PMDEPVPDSESPIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.52	1.58
R.ESS(p)PTYSPGFSDSTSGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.32	1.82
K.DVSDERLS(p)PAK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	4.8	1.32
R.SQGS(p)TSNSDWMK.N	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.44	0.31
K.TLEVVS(p)PSQSVTGS(p)AGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.85	1.37

K.SRT(p)PVQDHR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.5	X
R.ESS(p)PTYS(p)PGFSDSTSGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.65	2.5
K.VQSLEGEKLS(p)PK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.06	2.39
K.AET(p)EEAEEPEEDGEDNVS(p)GSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.84	0.58
K.TLEVVSPS(p)QSVTGSAGHTPYY(p)QSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.7	X
K.VLSPLRS(p)PPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.18	1.44
R.S(p)SISPMDEPVPDSESPIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.52	1.61
K.GSAES(p)PDEGITTTEGEGECEQT(p)PEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	3.14	0.45
K.EEQS(p)PVKAEVAEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.39	X
R.ESVAS(p)GDDRAEEDMDEALEK.G	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.13	X
R.KLGGDGSPT(p)QVDVSQFGSFKEDTK.M	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.49	X
K.AETEEAEEPEEDGEDNVS(p)GSASKHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.92	0.37
R.KES(p)KEEAPEATK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.65	X
R.ESVASGDDRAEEDMDEALEKGEAEQS(p)EEEGEEEEDKAEDAR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.76	0.38
K.SAGFIPIKEDFS(p)PEK.K	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.48	2.23
R.DYNASASTIS(p)PPSSMEEDKFSK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.82	1.43
R.S(p)LMS(p)SPEDLTKDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.1	X
R.SSIS(p)PMDEPVPDSES(p)PIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.55	1.85
R.S(p)PDTSAYCYETMEK.I	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.64	1.75
K.AETEEAEEPEEDGEDNVSGS(p)ASKHSPTEDEEIAKAEADVHIK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.86	X
K.TLEVVSPS(p)QSVTGSAGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.88	X
K.TLEVVSPSQSVTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.75	1.24
K.TLEVVS(p)PSQSVTGSAGHT(p)PYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.01	X
R.SLMS(p)S(p)PEDLTK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.99	0.3
R.SLMS(p)S(p)PEDLTKDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.13	0.35
R.SLMS(p)S(p)PEDLTKDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.89	0.28
K.GEAEQS(p)EEEGEEEEDKAEDAR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.04	X
K.GEAEQS(p)EEEGEEEEDKAEDAR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.19	X
K.QGFSDKES(p)PVSDLTSDLYQDKQEEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	3.13	X
K.EVPSKEEQS(p)PVKAEVAEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.29	0.41
R.TIKS(p)PCDSGYSYETIEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	4.76	1.94
K.QGVDDIEKFEDEGAGFEESS(p)EAGDYEEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.98	0.48
K.TTKT(p)PEDGGYSCEITEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.52	1.81
K.SDIS(p)PLT(p)PR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.76	1.53
K.ETEVSKGS(p)AESPDEGITT(p)TEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.57	X

R.S(p)LMSS(p)PEDLTKDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.87	0.34
K.AET(p)EEAEEPEEDGEDNVSGSASKHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.88	0.51
K.AETEEAEEPEEDGEDNVS(p)GSAS(p)KHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.12	X
R.SLMS(p)SPEDLT(p)KDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.1	0.34
K.ESTAAYQT(p)SSSPPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.43	2.04
K.ETEVSKGS(p)AES(p)PDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.5	0.33
R.DVMS(p)DETNNEETES(p)PSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.65	0.47
R.T(p)PEEGGYSYEISEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.4	0.93
K.VLS(p)PLRSPPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.11	X
K.TLEVVS(p)PSQS(p)VTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.54	X
R.S(p)LMSSPEDLT(p)KDFEELKAEEIDVAK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.36	0.32
R.S(p)PPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.13	1.87
K.TLEVVSPS(p)QSVTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.64	1.12
K.TLEVVSPS(p)QSVTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.7	X
K.TPGDFNYAYQKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.07	1.63
K.TPGDFNYAYQKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.19	1.62
R.DVMSDETNNEETES(p)PSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.58	0.6
R.DVMSDETNNEETES(p)PSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.7	0.59
R.KLGGDGS(p)PTQVDVSQFGSFK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.78	2.17
K.LGGDGS(p)PTQVDVSQFGSFK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.5	1.79
K.AETEEAEEPEEDGEDNVSGSASKHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.37	0.38
K.AETEEAEEPEEDGEDNVS(p)GSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.35	X
K.AETEEAEEPEEDGEDNVS(p)GSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.74	0.38
K.TTRS(p)PDTSAYCYETMEK.I	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.54	1.63
R.ES(p)SPTYS(p)PGFSDSTSGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.66	2.51
K.GSAESPDEGITTTEGEGECEQT(p)PEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.26	0.41
R.DYNASASTIS(p)PPSSMEEDK.F	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.25	1.02
K.TLEVVSPSQS(p)VTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.63	1.14
K.AET(p)EEAEEPEEDGEDNVSGSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.38	0.46
R.AEEDMDEALEKGEAEQS(p)EEEGEEEEDKAEDAR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.29	0.32
R.AEEDMDEALEKGEAEQS(p)EEEGEEEEDKAEDAR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	1.44	X
K.SDIS(p)PLTPR.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.76	1.81
K.ETEVSKGS(p)AESPDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.55	0.41
K.FEDEGAGFEES(p)SEAGDYEEKAETEEAEEPEEDGEDNVSGSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	2.04	X
K.TLEVVSPS(p)QSVTGSAGHTPY(p)YQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	0.64	1.12

K.QGFS(p)DKESPVSDLTSDLYQDK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.57
K.TLEVVSPSQS(p)VTGS(p)AGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.45
R.S(p)SISPMDEPVPDSES(p)PIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.01
K.ES(p)PVSDLTSDLYQDK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.54
K.EVPSKEEQS(p)PVKAEVAEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.38
R.DLTTSSVEKDNGGKTPGDFNYAYQKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.83
R.DLTTSSVEKDNGGKTPGDFNYAYQKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.55
R.ESSPT(p)YSPGFSDSTSGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.26
R.DVMSDETNNEET(p)ESPSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.61
K.TLEVVSPSQSVT(p)GSAGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.65
K.GSAESPDEGIT(p)TTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.37
K.SPSLS(p)PSPPS(p)PIEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.93
R.SPDT(p)SAYCYETMEK.I	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.76
K.AET(p)EEAEEPEEDGEDNVSGS(p)ASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.45
K.ES(p)TAAYQTSSSPPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.84
K.GSAES(p)PDEGITTT(p)EGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.6
K.AETEEAEEPEEDGEDNVSGSAS(p)KHS(p)PTEDEEIAK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.39
R.SLMSS(p)PEDLTK.D	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.2
K.TLEVVSPSQSVTGSAGHTPYYQSPT(p)DEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.21
K.TPGDFNYAYQKPES(p)TTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.3
R.DVMSDETNNEETESPS(p)QEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.56
R.DVMSDETNNEETESPS(p)QEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.59
R.DYNASASTIS(p)PPSSMEEDKFSK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.64
K.SPSLSPSPPS(p)PIEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.27
K.DNGGKTPGDFNYAYQKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.06
R.DLTTSSVEKDNGGKTPGDFNYAYQKPEST(p)TESPDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.17
K.TLEVVSPSQSVT(p)GS(p)AGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.46
K.TPGDFNYAY(p)QKPESTTES(p)PDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.87
K.QGFSDKESPVS(p)DLTSDLYQDKQEEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.01
K.TLEVVSPSQSVT(p)GSAGHT(p)PYY(p)QSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.24
R.T(p)IKSPCDSGYSYETIEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.79
K.GSAESPDEGITT(p)TEGEGECEQT(p)PEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.65
K.TLEVVSPS(p)QSVT(p)GSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.47
K.ASAEGEATAVVSPGVTQAVVEEHCAS(p)PEEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.54
K.ETEVSKGSAES(p)PDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.48

R.DLTTSSVEKDNGGKTPGDFNYAY(p)QKPESTTESPDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.32
R.ESVASGDDRAEEDMDEALEKGEAEQS(p)EEEGEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.39
K.EST(p)AAYQTSSSPPIDAAAAEPYGFR.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.62
R.DYNASASTISPPS(p)SMEEDKFSK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.29
K.TLEVVSPSQSVTGS(p)AGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.24
K.TLEVVSPSQSVTGS(p)AGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.92
K.FEDEGAGFEES(p)SEAGDYEEK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.45
R.DVMSDET(p)NNEETES(p)PSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.46
R.DLTTSSVEKDNGGKTPGDFNY(p)AYQKPESTTESPDEEDYDYESHEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.54
R.DVMS(p)DETNNEETES(p)PSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.46
K.VLS(p)PLRS(p)PPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.55
K.VLS(p)PLRS(p)PPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.51
K.GSAESPDEGITTT(p)EGEGECEQT(p)PEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.57
K.QGVDDIEKFEDEGAGFEES(p)SEAGDYEEKAETEEAEEPEEDGEDNVSGSASK.H	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.43
K.GSAES(p)PDEGITTT(p)EGEGECEQT(p)PEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.67
R.SSIS(p)PMDEPVPDSES(p)PIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.83
K.T(p)PEDGGYSCEITEK.T	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.8
K.TLEVVSPS(p)QS(p)VTGSAGHTPYYQS(p)PTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.45
K.IAELEEERS(p)QGSTSNSDWMK.N	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.35
R.SSISPMDEPVPDS(p)ESPIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.56
R.DVMS(p)DETNNEETESPSQEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.45
R.ESVAS(p)GDDRAEEDMDEALEK.G	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.39
K.DLTGQVST(p)PPVK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.41
R.KLGGDGS(p)PTQVDVSQFGSFKEDTK.M	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.99
R.SQGST(p)SNSDWMK.N	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.31
R.DVMS(p)DETNNEETESPS(p)QEFVNITK.Y	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.43
K.MSISEGTVS(p)DK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.21
K.VLSPLRS(p)PPLIGSESAYEDFLSADDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.69
R.SSISPMDEPVPDSES(p)PIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.31
R.AEEDMDEALEKGEAEQS(p)EEEGEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.28
K.SAGFIPIKEDFS(p)PEKK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.4
K.SAGFIPIKEDFS(p)PEKK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	2.39
K.TLEVVSPSQS(p)VTGS(p)AGHTPYYQSPTDEK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.14
K.SSS(p)PVKKGDGK.S	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.45
K.GSAES(p)PDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.4

K.GSAES(p)PDEGITTTEGEGECEQTPEELEPVEK.Q	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.31
R.SS(p)ISPMDEPVPDSESPIEK.V	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.4
R.KES(p)KEEAPEATK.A	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	0.4
R.ES(p)SPTYSPGFSDSTSGAK.E	IPI00372009.3	PREDICTED: microtubule-associated protein 1b	X	1.82
R.QNS(p)DPTSENPPLPTR.I	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	0.92	1.66
R.TTSIS(p)PALAR.K	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	0.49	X
K.S(p)EGSPVLPHEPSK.V	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	0.6	X
R.VYQTS(p)PTDEDEEDDESSAAALFTSELLR.Q	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	X	1.71
R.VYQT(p)SPTDEDEEDDESSAAALFTSELLR.Q	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	X	1.7
K.SEGS(p)PVLPHEPSK.V	IPI00372166.2	PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4	X	1.39
R.SSQPS(p)PTAVPASDS(p)PSAK.Q	IPI00372186.4	94 kDa protein	X	0.43
R.KLS(p)LSEGK.V	IPI00372319.1	Cytokine-like nuclear factor n-pac	1.51	X
R.KLSLS(p)EGK.V	IPI00372319.1	Cytokine-like nuclear factor n-pac	X	0.69
R.S(p)AEDLTEGSYDAILSAEQLEK.L	IPI00372341.2	PREDICTED: similar to RIKEN cDNA 2810037C14	0.7	X
R.HDTPDAS(p)PPR.R	IPI00372459.2	Hypothetical protein RGD1308076	0.98	0.68
R.HDT(p)PDPS(p)PPR.R	IPI00372459.2	Hypothetical protein RGD1308076	1.75	X
K.YEHDSDLS(p)PPR.K	IPI00372459.2	Hypothetical protein RGD1308076	1.12	0.72
R.HDS(p)PDLELPK.A	IPI00372459.2	Hypothetical protein RGD1308076	1.36	X
R.HGT(p)PEPS(p)PPR.R	IPI00372459.2	Hypothetical protein RGD1308076	1.16	0.87
R.HDTPDPS(p)PPR.R	IPI00372459.2	Hypothetical protein RGD1308076	X	0.57
R.APTAAPS(p)PEPR.D	IPI00372502.2	PREDICTED: similar to Safb2 protein	1.71	1.51
K.SEPVKEEGS(p)ELEQPFAQATSSVGPDR.K	IPI00372502.2	PREDICTED: similar to Safb2 protein	1.35	1.8
R.SAVS(p)PDLHITPIYEGR.T	IPI00372752.2	PREDICTED: similar to Plakophilin 4	X	1.01
R.VGS(p)PLTLTDAQTR.V	IPI00372752.2	PREDICTED: similar to Plakophilin 4	X	1.16
R.AQS(p)PSYVTSTGVS(p)PSR.G	IPI00372752.2	PREDICTED: similar to Plakophilin 4	X	0.85
K.SSDS(p)VDIEEQEEK.M	IPI00372755.3	PREDICTED: similar to Rap1-interacting factor 1	1.78	0.97
R.GVLSS(p)PSLAFTPPIR.T	IPI00372778.1	Nucleoporin NUP53	0.61	1.05
R.GVLSS(p)PSLAFT(p)PPIR.T	IPI00372778.1	Nucleoporin NUP53	X	1
R.WTKPSSFS(p)DSER.-	IPI00372818.3	LEM domain containing 2	0.67	X
K.AEEPS(p)EEEADAPKPK.K	IPI00372862.2	PREDICTED: similar to mKIAA1279 protein	2.75	X
K.YLQAVVSSMPRY(p)ADS(p)SGR.N	IPI00372980.2	PREDICTED: similar to mKIAA3020 protein	X	4.08
R.FS(p)PVLGR.A	IPI00373059.3	PREDICTED: similar to Achalasia, adrenocortical insufficiency, alacrimia	1.45	1.24
R.KAAVVAS(p)PLLDQQR.N	IPI00373079.3	PREDICTED: similar to KIAA0853 protein	X	1.5
R.T(p)PS(p)PPPPILEDIILGK.K	IPI00373079.3	PREDICTED: similar to KIAA0853 protein	X	1.16
K.AAVVAS(p)PLLDQQR.N	IPI00373079.3	PREDICTED: similar to KIAA0853 protein	X	0.78
K.NSVTEDS(p)PQPPLPSVR.D	IPI00373107.3	PREDICTED: similar to 53BP1 protein	0.82	X
K.LQDDEAVDIEKPLLPSQPAVS(p)PQASTPVSR.S	IPI00373107.3	PREDICTED: similar to 53BP1 protein	3.68	3.24
R.ASQGSLS(p)PQEEVMEADLLEGLGANQDRPSK.I	IPI00373107.3	PREDICTED: similar to 53BP1 protein	3.03	1.12
R.RSDS(p)PEIPFQAATGSSDGLDSSSSGNSFVGLR.V	IPI00373107.3	PREDICTED: similar to 53BP1 protein	2.88	1.06
R.STPFIVPSSPT(p)EQGQR.K	IPI00373107.3	PREDICTED: similar to 53BP1 protein	2.83	X
R.TEEVGENTQVEDTEPSS(p)PVTK.S	IPI00373107.3	PREDICTED: similar to 53BP1 protein	1.9	3.1
R.ASQGS(p)LS(p)PQEEVMEADLLEGLGANQDRPSK.I	IPI00373107.3	PREDICTED: similar to 53BP1 protein	1.93	1.05
R.S(p)DSPEIPFQAATGSSDGLDSSSSGNSFVGLR.V	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	1.02
R.STPFIVPSS(p)PTEQGQR.K	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	3.63
K.MESLGS(p)PR.T	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	3.92
R.RS(p)DSPEIPFQAATGSSDGLDSSSSGNSFVGLR.V	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	0.87
R.SDS(p)PEIPFQAATGSSDGLDSSSSGNSFVGLR.V	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	1.02
R.ETVVSGPLGIEDTS(p)PSMSPDDK.S	IPI00373107.3	PREDICTED: similar to 53BP1 protein	X	0.07
R.S(p)ADVSPTTEGVK.R	IPI00373220.3	PREDICTED: similar to KIAA0517 protein	0.34	X
R.SADVS(p)PTTEGVK.R	IPI00373220.3	PREDICTED: similar to KIAA0517 protein	0.42	0.83

R.S(p)ADVS(p)PTTEGVK.R	IPI00373220.3	PREDICTED: similar to KIAA0517 protein	0.48	0.85
R.SADVSPTT(p)EGVK.R	IPI00373220.3	PREDICTED: similar to KIAA0517 protein	0.42	X
K.QNS(p)LEYMDQNDDR.L	IPI00373257.3	PREDICTED: similar to 2900042E01Rik protein	X	0.99
R.S(p)PGLPIR.S	IPI00373257.3	PREDICTED: similar to 2900042E01Rik protein	X	1.69
K.EYAENIGDGRS(p)PEFR.E	IPI00373345.3	Beta catenin-like 1	X	1.41
K.S(p)NSPVGEKVDPAPAK.D	IPI00373365.2	PREDICTED: similar to protein kinase C binding protein 1	1.76	X
K.DKAS(p)PEPEKDFAEK.A	IPI00373365.2	PREDICTED: similar to protein kinase C binding protein 1	1.3	X
K.SNS(p)PVGEKVDPAPAK.D	IPI00373365.2	PREDICTED: similar to protein kinase C binding protein 1	X	1.02
K.DKAS(p)PEPEKDFAEK.A	IPI00373365.2	PREDICTED: similar to protein kinase C binding protein 1	X	0.43
K.LNFDMTAS(p)PK.I	IPI00373365.2	PREDICTED: similar to protein kinase C binding protein 1	X	1.76
K.TDPACLET(p)GQDSEDDSGEPEDWVPDPVDADPAK.S	IPI00373399.2	PREDICTED: similar to mKIAA1406 protein	X	0.93
K.TDPACLETGQDSEDDS(p)GEPEDWVPDPVDADPAK.S	IPI00373399.2	PREDICTED: similar to mKIAA1406 protein	X	0.93
K.TDPACLETGQDS(p)EDDSGEPEDWVPDPVDADPAK.S	IPI00373399.2	PREDICTED: similar to mKIAA1406 protein	X	0.89
K.KQQSAAAS(p)ADSK.P	IPI00373432.1	Small inducible cytokine subfamily E, member 1	X	0.46
R.GRS(p)YENLLGR.E	IPI00373471.1	PREDICTED: similar to Gene model 996	X	1.02
R.NLTANDPSQDYVAS(p)DGEEDPEVEFLK.S	IPI00373631.2	CBF1 interacting corepressor	X	0.16
K.SPDEATAADQES(p)EDDLSASR.T	IPI00373724.2	PREDICTED: similar to Farp1 protein	0.43	1.09
R.SETGSTISMSS(p)LER.R	IPI00373771.2	PREDICTED: similar to brain-specific angiogenesis inhibitor 3	X	1.2
K.SVEDEMDS(p)PGEEPFYTGQGR.S	IPI00382107.1	Nuclear factor I-A2	X	0.48
R.GYS(p)YDDSMESR.S	IPI00382207.3	PREDICTED: similar to mKIAA1604 protein	X	1.26
K.TNQAILSQLYQS(p)PNR.R	IPI00387625.2	38 kDa protein	1.83	1.33
K.AEYVFIVDS(p)DGEDEATCR.Q	IPI00387638.2	49 kDa protein	X	1.4
K.SS(p)PATTVTS(p)PNSTPAK.T	IPI00387852.2	94 kDa protein	0.75	X
K.S(p)SPATTVTSPNST(p)PAK.T	IPI00387852.2	94 kDa protein	X	0.67
R.NVPQEES(p)LEDSDVDADFK.A	IPI00388159.1	37 kDa protein	1.54	2.29
R.NVPQEESLEDS(p)DVDADFK.A	IPI00388159.1	37 kDa protein	X	2.3
R.S(p)NSVEKPVSSLLSR.V	IPI00388318.1	44 kDa protein	X	0.57
K.NTADHDES(p)PPRT(p)PTGNAPSSESDIDISSPNVSHDE SIAK.D	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	1.01	0.61
R.LSQSSQDSS(p)PVR.N	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	0.3	X
R.S(p)SGSETEQAVDFSDR.E	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	0.61	X
K.NT(p)ADHDESPPRT(p)PTGNAPSSESDIDISSPNVSHDE SIAK.D	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	0.75	X
R.SSGS(p)ETEQAVDFSDR.E	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	X	0.5
R.SS(p)GSETEQAVDFSDR.E	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	X	0.5
K.NTADHDES(p)PPRT(p)PTGNAPSSESDIDISSPNVSHDE SIAK.D	IPI00388481.1	Splice Isoform 2 of Histone acetyltransferase MYST2	X	0.6
R.EHYSDS(p)EEEDDGGDVASAR.Q	IPI00388697.2	34 kDa protein	1.98	1.55
R.GDSET(p)DLEALFNAVMNPK.T	IPI00388880.4	Neuron-specific YAPdeltaC insert61 isoform	0.41	X
K.YLLGNAPVS(p)PSSQK.L	IPI00389023.2	30 kDa protein	3.12	1.41
K.S(p)IDDSEMESPVDDVFYPGTGR.S	IPI00389049.2	PREDICTED: NF1-X1 protein	2.02	0.59
K.SIDDS(p)EMESPVDDVFYPGTGR.S	IPI00389049.2	PREDICTED: NF1-X1 protein	2.02	1.02
R.SITS(p)PPSTSTTK.R	IPI00389049.2	PREDICTED: NF1-X1 protein	X	1.09
K.SIDDSEMES(p)PVDDVFYPGTGR.S	IPI00389049.2	PREDICTED: NF1-X1 protein	X	1.02
R.SLS(p)PSHLTEDR.Q	IPI00389167.2	32 kDa protein	2.95	1.43
K.LDSPS(p)RS(p)PSKVEVTEK.M	IPI00389245.2	Transmembrane protein 24	X	2.24
K.DDEPSGWEEPS(p)PQSISR.K	IPI00389253.2	PREDICTED: androgen receptor-related apoptosis-associated protein CBL27	X	0.49
R.SQS(p)VEPESQEK.E	IPI00389442.1	Hypothetical protein LOC499691	2.09	1.13
K.QAEVADQQTTDLPAENGETENQS(p)PAS(p)EEEKEAK.S	IPI00389774.2	10 kDa protein	3.26	0.82
K.QAEVADQQTTDLPAENGET(p)ENQSPAS(p)EEEKEAK.S	IPI00389774.2	10 kDa protein	2.87	X
K.QAEVADQQTTDLPAENGETENQS(p)PASEEEKEAK.S	IPI00389774.2	10 kDa protein	3.22	X
K.QAEVADQQTTDLPAENGETENQSPAS(p)EEEK.E	IPI00389774.2	10 kDa protein	2.73	0.84

K.QAEVADQQTTDLPAENGETENQSPAS(p)EEEKEAK.S	IPI00389774.2	10 kDa protein	2.61	0.59
K.QAEVADQQTTDLPAENGETENQS(p)PASEEEK.E	IPI00389774.2	10 kDa protein	2.49	0.82
K.QAEVADQQTTDLPAENGET(p)ENQSPAS(p)EEEK.E	IPI00389774.2	10 kDa protein	X	0.56
K.QAEVADQQTTDLPAENGETENQS(p)PAS(p)EEEK.E	IPI00389774.2	10 kDa protein	X	0.56
R.SLSEDS(p)GEEMDSVDPVTLYSYK.V	IPI00389806.3	PREDICTED: similar to inter-alpha-inhibitor H2 chain	2.33	X
K.YREGS(p)PLKEESLAR.E	IPI00389828.2	Hypothetical protein RGD1308367	X	0.45
R.SSGSPYGGGYGS(p)GGGSGGYGSR.R	IPI00389838.2	Protein	X	1.02
R.SSGSPY(p)GGGYGSGGGSGGYGSR.R	IPI00389838.2	Protein	X	1.37
R.S(p)SGSPYGGGYGSGGGSGGYGSR.R	IPI00389838.2	Protein	X	0.96
R.S(p)SGSPYGGGYGSGGGSGGYGSR.R	IPI00389838.2	Protein	X	1.18
R.SSGS(p)PYGGGYGSGGGSGGYGSR.R	IPI00389838.2	Protein	X	1.09
R.SS(p)GSPYGGGYGSGGGSGGYGSR.R	IPI00389838.2	Protein	X	1.06
R.TAS(p)EGS(p)EAETPEAPKQPAK.K	IPI00389960.2	Hypothetical protein	X	0.59
R.T(p)ASEGS(p)EAETPEAPKQPAK.K	IPI00389960.2	Hypothetical protein	X	0.54
R.LS(p)PVPVPR.A	IPI00390053.2	PREDICTED: hnRNP-associated with lethal yellow	1.95	X
K.KGDSSSGGGGGSSSGGGGSGNVGSGGSGGSGSSSS RPPAPQEDTAS(p)EAGT(p)PQGEVQTR.D	IPI00390053.2	PREDICTED: hnRNP-associated with lethal yellow	X	1.12
K.AIS(p)PTSATSSGR.T	IPI00390377.2	214 kDa protein	0.21	0.78
K.LPVS(p)PVKEDTQK.T	IPI00390422.2	34 kDa protein	1.43	X
R.TLS(p)MIEEEIR.A	IPI00390678.2	A kinase	0.54	3.03
K.S(p)PGEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.45
K.SPVEVKS(p)PEKAK.S	IPI00390850.2	114 kDa protein	X	0.36
K.EEIKPPAEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.52
K.KEEVKS(p)PVEEVK.A	IPI00390850.2	114 kDa protein	X	0.34
K.KEEVKS(p)PVEEVK.A	IPI00390850.2	114 kDa protein	X	0.32
R.SPEQVKS(p)PAKEEAK.S	IPI00390850.2	114 kDa protein	X	0.47
K.TLDVKS(p)PEAKT(p)PAKEEAK.R	IPI00390850.2	114 kDa protein	X	0.43
K.TLDVKS(p)PEAKT(p)PAKEEAK.R	IPI00390850.2	114 kDa protein	X	0.4
K.SPAEVKS(p)PAEVKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.46
K.SPAEVKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.47
K.S(p)PAEVKS(p)PVEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.38
K.SPAEAKS(p)PVEVKSPEK.A	IPI00390850.2	114 kDa protein	X	0.7
K.S(p)PAEAKS(p)PAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.47
K.SPAEVKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.33
K.SLAEAKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.35
K.S(p)PMKEEAKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.36
K.AKS(p)PMKEEAKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.38
K.SPAEAKS(p)PVVAK.S	IPI00390850.2	114 kDa protein	X	0.53
K.SPVVAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.57
K.SLAEAKS(p)PEKAK.S	IPI00390850.2	114 kDa protein	X	0.5
K.S(p)PATVKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.5
K.SPAEAKS(p)PAEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.5
K.SPAEAKS(p)PAEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.57
K.SPAEVKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.41
R.T(p)SVSSVSASPSR.F	IPI00390850.2	114 kDa protein	X	0.43
K.SPAKEEAKS(p)PEKEETR.T	IPI00390850.2	114 kDa protein	X	0.49
K.SPAKEEAKS(p)PEKEETR.T	IPI00390850.2	114 kDa protein	X	0.51
K.S(p)PAEAKPPAEAK.S	IPI00390850.2	114 kDa protein	X	0.43
K.S(p)PVKEEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.48
K.EEVKS(p)PVEEVK.A	IPI00390850.2	114 kDa protein	X	0.33
K.S(p)PAEVKS(p)PATVK.S	IPI00390850.2	114 kDa protein	X	0.51
K.SPVEVKS(p)PASVK.S	IPI00390850.2	114 kDa protein	X	0.57
R.SPEQVKS(p)PAKEEAKS(p)PEKEETR.T	IPI00390850.2	114 kDa protein	X	0.46
K.SPVEAKS(p)PAEVKS(p)PVTVK.S	IPI00390850.2	114 kDa protein	X	0.45
K.S(p)PAEAKS(p)PVEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.55
K.S(p)PAEVKS(p)PVTVK.S	IPI00390850.2	114 kDa protein	X	0.46
R.IGFGPS(p)PFSLTEGLPK.I	IPI00390850.2	114 kDa protein	X	0.28
K.S(p)PAEVKS(p)PAVAK.S	IPI00390850.2	114 kDa protein	X	0.46

K.SPAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.47
K.SPVTVKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.55
K.SPAEAKS(p)PVEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.57
K.SPAEAKS(p)PVEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.52
K.AKS(p)PVKEGAK.S	IPI00390850.2	114 kDa protein	X	0.6
K.SPAEAKS(p)PAEVKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.39
K.S(p)PVEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.47
K.S(p)PAEAKS(p)PASVK.S	IPI00390850.2	114 kDa protein	X	0.53
R.S(p)LEGEAAALR.Q	IPI00390850.2	114 kDa protein	X	0.64
K.SPAEAKS(p)PVEVK.S	IPI00390850.2	114 kDa protein	X	0.57
K.SPAEAKS(p)PVVAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.46
K.TLDVKS(p)PEAK.T	IPI00390850.2	114 kDa protein	X	0.27
K.S(p)PAEVKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.64
K.SPVEVKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.46
K.AEEKEPLTEKPKDS(p)PGEAK.K	IPI00390850.2	114 kDa protein	X	0.34
K.S(p)PAEAKS(p)PVVAK.S	IPI00390850.2	114 kDa protein	X	0.49
K.S(p)PAEAKS(p)PAEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.51
K.SPAEVKS(p)PVEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.44
K.SPAEVKS(p)PVEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.4
K.S(p)PAEVKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.44
K.SPAEAKS(p)PVEVKSPAS(p)VK.S	IPI00390850.2	114 kDa protein	X	0.57
K.SPMKEEAKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.69
K.SPMKEEAKS(p)PEK.A	IPI00390850.2	114 kDa protein	X	0.61
K.VAPKKEEVKS(p)PVEEVK.A	IPI00390850.2	114 kDa protein	X	0.32
K.SPAEAKS(p)PAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.49
K.SPATVKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.5
K.S(p)PVEVKS(p)PASVK.S	IPI00390850.2	114 kDa protein	X	0.61
K.SPAEAKS(p)PAEAKS(p)PVEVK.S	IPI00390850.2	114 kDa protein	X	0.43
K.SPAEAKS(p)PAEAKS(p)PVEVK.S	IPI00390850.2	114 kDa protein	X	0.39
K.SPGEAKS(p)PAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.43
K.SPGEAKS(p)PAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.47
R.TSVSSVSAS(p)PSRFR.G	IPI00390850.2	114 kDa protein	X	0.29
K.SPAEVKS(p)PATVK.S	IPI00390850.2	114 kDa protein	X	0.49
K.SPASVKS(p)PGEAK.S	IPI00390850.2	114 kDa protein	X	0.52
K.S(p)PAEAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.51
K.S(p)PAEVKSPAT(p)VKS(p)PVEAK.S	IPI00390850.2	114 kDa protein	X	0.42
K.SPAEVKS(p)PAEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.39
K.SPAEVKS(p)PVTVK.S	IPI00390850.2	114 kDa protein	X	0.55
K.SPAEAKS(p)PAEAK.S	IPI00390850.2	114 kDa protein	X	0.58
K.SPAVAKS(p)PAEVK.S	IPI00390850.2	114 kDa protein	X	0.46
K.SPAEVKS(p)PAVAK.S	IPI00390850.2	114 kDa protein	X	0.36
K.S(p)PAEAKS(p)PVEVK.S	IPI00390850.2	114 kDa protein	X	0.65
K.LCDFGSASHVADNDITPY(p)LVSR.F	IPI00390893.2	Protein	1.09	0.93
R.NHS(p)LEEEFER.A	IPI00390898.1	68 kDa protein	X	0.88
R.GGS(p)SGEELEDEEPVK.K	IPI00391633.4	Hepatoma-derived growth factor-related protein 2	0.71	X
R.SSQSLHCLS(p)PR.Q	IPI00392023.2	64 kDa protein	X	0.87
R.ATLS(p)DSEIETNSATSTIFGK.A	IPI00392124.2	172 kDa protein	X	0.42
R.ATLSDS(p)EIETNSATSTIFGK.A	IPI00392124.2	172 kDa protein	X	0.36
K.VAS(p)VEEGDESLDSPGSQSR.G	IPI00392386.2	67 kDa protein	1.01	4.73
K.KVAS(p)VEEGDESLDSPGSQSR.G	IPI00392386.2	67 kDa protein	X	0.99
R.NSFLGS(p)PR.F	IPI00392525.2	PREDICTED: similar to Probable serine/threonine-protein kinase KIAA1811	0.56	11.31
R.SLPS(p)NGELDPDVLESMASLGCFR.D	IPI00392525.2	PREDICTED: similar to Probable serine/threonine-protein kinase KIAA1811	X	3.08
R.SLPS(p)NGELDPDVLESMASLGCFR.D	IPI00392525.2	PREDICTED: similar to Probable serine/threonine-protein kinase KIAA1811	X	3.36
R.S(p)PVFSFSPEPGVGDEAR.G	IPI00392525.2	PREDICTED: similar to Probable serine/threonine-protein kinase KIAA1811	X	12.76
K.TTSSDS(p)VEEDTVDS(p)DTPPVLEK.E	IPI00392552.2	PREDICTED: similar to mKIAA3013 protein	1.36	0.9
K.CLES(p)CDEQTEENEQTK.N	IPI00392552.2	PREDICTED: similar to mKIAA3013 protein	2.01	X

R.EDSQPSSAS(p)PEDPTVATDAFYGR.R	IPI00392630.2	PREDICTED: similar to OTTHUMP00000046255	0.27	1.27
R.EIHDVAGDGDSLGS(p)PGPTR.S	IPI00392697.2	PREDICTED: similar to mKIAA0284 protein	X	0.49
K.TLTDEVNS(p)PDADR.R	IPI00393081.2	121 kDa protein	1.71	X
K.TLTDEVNS(p)PDADRR.D	IPI00393081.2	121 kDa protein	2.01	1.25
K.DMDEPS(p)PVPNVEEVTLPK.T	IPI00393081.2	121 kDa protein	1.39	1.08
R.TAS(p)AGTVSDAEVR.S	IPI00393112.2	132 kDa protein	X	1.96
R.SLERPSS(p)SASMAGDFR.K	IPI00393489.1	128 kDa protein	X	3.87
R.FSIES(p)LLEEETQVR.H	IPI00393489.1	128 kDa protein	X	2.7
R.ADLPGSSSTFTTSFISSSPSS(p)PSR.A	IPI00393489.1	128 kDa protein	X	3.17
R.ADLPGSSSTFTTSFISSSPS(p)SPSR.A	IPI00393489.1	128 kDa protein	X	3.06
R.ADLPGSSSTFTTSFISSSPS(p)SPSR.A	IPI00393489.1	128 kDa protein	X	2.46
R.SLERPSSS(p)AS(p)MAGDFR.K	IPI00393489.1	128 kDa protein	X	6.83
R.ADLPGSSSTFTTSFISS(p)SPSS(p)PSR.A	IPI00393489.1	128 kDa protein	X	7.25
R.ADLPGSSSTFTTSFISSS(p)PS(p)SPSR.A	IPI00393489.1	128 kDa protein	X	5.02
R.ADLPGSSSTFTTSFISS(p)SPS(p)SPSR.A	IPI00393489.1	128 kDa protein	X	3.69
R.ADLPGSSSTFTTSFISS(p)SPS(p)SPSR.A	IPI00393489.1	128 kDa protein	X	5.2
K.SHS(p)DNGTDAFK.E	IPI00393489.1	128 kDa protein	X	1.68
R.ADLPGSSSTFTTSFISS(p)SPSSPS(p)R.A	IPI00393489.1	128 kDa protein	X	7.18
R.ADLPGSSSTFTTSFISS(p)SPSSPS(p)R.A	IPI00393489.1	128 kDa protein	X	4.09
R.LSAPDLS(p)PTGPPK.K	IPI00393489.1	128 kDa protein	X	2.92
K.GSEDYPDPPLPHSYS(p)SDR.I	IPI00393489.1	128 kDa protein	X	0.91
K.S(p)IEDGPSADIVNEVR.G	IPI00393676.1	PREDICTED: similar to transcription factor ELYS	0.34	1.26
R.LEFIQQS(p)PTR.S	IPI00393676.1	PREDICTED: similar to transcription factor ELYS	1.48	X
R.EREDS(p)VSGVTEEPK.L	IPI00393676.1	PREDICTED: similar to transcription factor ELYS	1.82	1.31
R.EDS(p)VSGVTEEPK.L	IPI00393676.1	PREDICTED: similar to transcription factor ELYS	X	0.92
R.NT(p)TPTGATPPAGMASTR.V	IPI00393975.2	Microtubule-associated protein 4	0.58	X
K.DVS(p)PSPETETAK.N	IPI00393975.2	Microtubule-associated protein 4	1.26	X
K.ESEGS(p)PDTDAAPGPDTDVTLTK.D	IPI00393975.2	Microtubule-associated protein 4	1.08	6.48
K.ATS(p)PSTLVSTGSSSR.S	IPI00393975.2	Microtubule-associated protein 4	X	0.94
K.AT(p)SPSTLVSTGSSSR.S	IPI00393975.2	Microtubule-associated protein 4	X	1.24
R.AAS(p)PEACEVDSK.G	IPI00394214.1	24 kDa protein	2.47	X
K.LY(p)SSAEFGR.R	IPI00394355.2	133 kDa protein	X	1.09
R.HSWDS(p)PAFNNDVVQR.R	IPI00394517.2	92 kDa protein	X	1.18
R.SS(p)LEDTYGAGDGLK.R	IPI00394517.2	92 kDa protein	X	1.45
K.LAEGEEEKPEPDGSS(p)EESIS(p)TVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	1.06	0.63
K.LAEGEEEKPEPDGSS(p)EESISTVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	1.07	X
K.LAEGEEEKPEPDGSSEESIST(p)VEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	0.85	X
K.LAEGEEEKPEPDGSSEESIS(p)TVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	0.99	0.57
K.LAEGEEEKPEPDGS(p)SEESIS(p)TVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	0.82	0.69
K.LAEGEEEKPEPDGS(p)SEESISTVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	0.99	0.52
K.LAEGEEEKPEPDGSS(p)EES(p)ISTVEEPENETPPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	X	0.65
K.LAEGEEEKPEPDGSSEESISTVEEPENET(p)PPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	X	0.42
K.LAEGEEEKPEPDGS(p)SEESISTVEEPENET(p)PPAPSR.E	IPI00400578.1	Heterochromatin protein 1, binding protein 3	X	0.69
K.VAS(p)EEEEVPLVVYLK.E	IPI00417226.1	Splice Isoform 2 of Synaptopodin	0.12	5.06
R.SS(p)PGLYNAPVQDSLQPTAVS(p)PTYSSDISPVSPSR.A	IPI00417226.1	Splice Isoform 2 of Synaptopodin	X	2.57
R.SSPGLYNAPVQDSLQPTAVS(p)PTYSSDISPVSPSR.A	IPI00417226.1	Splice Isoform 2 of Synaptopodin	X	2.76
R.S(p)SPGLYNAPVQDSLQPTAVS(p)PTYSSDISPVSPSR.A	IPI00417226.1	Splice Isoform 2 of Synaptopodin	X	2.49
R.SSPGLY(p)NAPVQDSLQPTAVSPT(p)YSSDISPVSPSR.A	IPI00417226.1	Splice Isoform 2 of Synaptopodin	X	2.18
R.SSPGLY(p)NAPVQDSLQPTAVS(p)PTYSSDISPVSPSR.A	IPI00417226.1	Splice Isoform 2 of Synaptopodin	X	2.57
R.ASS(p)LEDLVLK.E	IPI00417365.1	Superkiller viralicidic activity 2-like	0.43	0.87
R.SEGS(p)EYEEIPK.R	IPI00417730.2	Large proline-rich protein BAT2	0.83	0.54
R.S(p)EGSEYEEIPK.R	IPI00417730.2	Large proline-rich protein BAT2	X	0.68
K.TGEDEDEEDNDALLKENES(p)PDVR.Q	IPI00421329.1	LRRGT00070	1	X

K.SES(p)PKEPEQLR.K	IPI00421500.8	Heterogeneous nuclear ribonucleoprotein A1	2.92	1.41
K.SES(p)PKEPEQLR.K	IPI00421500.8	Heterogeneous nuclear ribonucleoprotein A1	2.45	1.26
K.SES(p)PKEPEQLRK.L	IPI00421500.8	Heterogeneous nuclear ribonucleoprotein A1	2.68	1.31
K.SES(p)PKEPEQLRK.L	IPI00421500.8	Heterogeneous nuclear ribonucleoprotein A1	2.29	1.24
K.S(p)ESPKEPEQLRK.L	IPI00421500.8	Heterogeneous nuclear ribonucleoprotein A1	2.29	1.2
R.YSS(p)NDNLETPSKR.T	IPI00421524.1	Occludin	X	1.78
R.RPPS(p)PEPSAK.V	IPI00421677.2	26 kDa protein	0.23	1.19
K.GDQVSQNGLPAEQGS(p)PR.V	IPI00421677.2	26 kDa protein	0.35	X
K.VSEEAESQQWDTSKGDQVSQNGLPAEQGS(p)PR.V	IPI00421677.2	26 kDa protein	0.24	X
R.TSS(p)ESIVSVPASSTSGSPS(p)R.V	IPI00421799.2	68 kDa protein	X	0.69
R.TSS(p)PSSAGSVSLGHYTPTSR.S	IPI00421799.2	68 kDa protein	X	0.65
R.TSS(p)ESIVSVPASST(p)SGSPS(p)R.V	IPI00421799.2	68 kDa protein	X	0.55
R.TSS(p)ESIVSVPASST(p)SGSPSR.V	IPI00421799.2	68 kDa protein	X	0.7
R.TSSPS(p)SAGSVSLGHYTPTSR.S	IPI00421799.2	68 kDa protein	X	0.56
R.T(p)SSPSSAGSVSLGHYTPTSR.S	IPI00421799.2	68 kDa protein	X	0.6
R.TSS(p)ESIVSVPASSTS(p)GSPSR.V	IPI00421799.2	68 kDa protein	X	0.49
R.TS(p)SESIVSVPASSTSGS(p)PSR.V	IPI00421799.2	68 kDa protein	X	0.6
R.TSSES(p)IVSVPASSTSGS(p)PSR.V	IPI00421799.2	68 kDa protein	X	0.65
K.QLSVPAS(p)DEEDEVPVPVPR.G	IPI00421969.1	ATP-binding cassette sub-family F member 1	X	1.47
K.S(p)QSIDEIDVGTYK.V	IPI00454351.1	Splice Isoform 2 of Leucine-rich repeat-containing protein 7	X	1.85
K.SQS(p)IDEIDVGTYK.V	IPI00454351.1	Splice Isoform 2 of Leucine-rich repeat-containing protein 7	X	1.99
K.DTTS(p)PMELAALEK.V	IPI00464427.1	Splice Isoform PACS-1b of Phosphofurin acidic cluster sorting protein 1	X	1.83
R.VIENTDGS(p)EEEMDAR.D	IPI00464465.2	Splice Isoform 2 of Myosin-11 (Fragment)	0.02	2.18
R.RPDPDS(p)DEDEDYER.E	IPI00464500.1	RNA binding motif protein 17	1.61	0.69
K.NS(p)PGAVGGLNNAPGTPR.D	IPI00464634.1	Hypothetical LOC364534	0.87	X
R.S(p)PS(p)PKPTK.V	IPI00464732.1	RNA-binding protein with serine-rich domain 1	0.72	0.95
K.GATPAEDDEDNDIDLFGS(p)DEEEEDKEAAR.L	IPI00471525.2	Eukaryotic translation elongation factor 1 delta	1.16	0.69
R.ATAPQTQHVS(p)PMR.Q	IPI00471525.2	Eukaryotic translation elongation factor 1 delta	X	0.58
K.IEDVGS(p)DEEDDSGK.D	IPI00471584.5	Heat shock protein HSP 90-beta	0.47	0.91
K.RKS(p)PENAEGK.D	IPI00471783.1	High mobility group nucleosome-binding domain-containing protein 3	X	0.89
R.KSS(p)TGSPT(p)SPINAEK.L	IPI00475534.2	110 kDa protein	X	2.31
K.S(p)SLTPVLGTESDATVK.K	IPI00475534.2	110 kDa protein	X	4.28
R.KSS(p)TGSPTSPINAEK.L	IPI00475534.2	110 kDa protein	X	3.69
K.EEALS(p)DDGDDFR.D	IPI00475584.1	101 kDa protein	2.02	X
K.SEAAAPHANAGGGLS(p)S(p)DEEEGTSSQAEAAR.V	IPI00475584.1	101 kDa protein	X	0.72
R.TPEELEDDS(p)DFEQEDYDVR.S	IPI00475656.2	52 kDa protein	0.11	0.92
R.TS(p)VQTEDDQLIAGQSAR.A	IPI00475656.2	52 kDa protein	X	0.9
R.SRTS(p)VQTEDDQLIAGQSAR.A	IPI00475656.2	52 kDa protein	X	0.87
R.AALLKAS(p)PK.K	IPI00475722.2	60S ribosomal protein L14	X	0.8
K.SPFNSPS(p)PQDSPR.L	IPI00475727.2	42 kDa protein	0.35	0.68
K.S(p)GSMEEDVDTSPGGDYYTSPNS(p)PTSSSR.N	IPI00475727.2	42 kDa protein	X	0.7
K.SGSMEEDVDTS(p)PGGDYYTS(p)PNSPTSSSR.N	IPI00475727.2	42 kDa protein	X	0.57
R.ATT(p)PPNQGRPDS(p)PVYANLQELK.I	IPI00475825.1	81 kDa protein	X	0.96
R.LLDAEDVDVPS(p)PDEK.S	IPI00475854.2	622 kDa protein	1.4	0.75
K.AFLAELEQNS(p)PK.I	IPI00475854.2	622 kDa protein	X	1.28
R.WRS(p)LQQLAEER.S	IPI00475874.2	167 kDa protein	0.18	1.42
R.S(p)LQQLAEER.S	IPI00475874.2	167 kDa protein	X	1.31
K.S(p)RSPGT(p)PAGEGSGSPPK.W	IPI00475951.1	70 kDa protein	X	1.36
K.YSDVEVPASVTGHSFAS(p)DGDSGTCS(p)PLR.H	IPI00475951.1	70 kDa protein	X	1.65
K.SPPDQSAVPNT(p)PPS(p)TPVKLEGAGDGCAK.E	IPI00475951.1	70 kDa protein	X	1.32
K.YSDVEVPASVTGHSFASDGDSGTCS(p)PLR.H	IPI00475951.1	70 kDa protein	X	2.05
K.SPPDQSAVPNT(p)PPST(p)PVK.L	IPI00475951.1	70 kDa protein	X	1.87
K.EKSPPDQSAVPNT(p)PPSTPVK.L	IPI00475951.1	70 kDa protein	X	1.27
K.AEEKS(p)PVSINVK.T	IPI00476006.2	60 kDa protein	0.26	0.69
R.VQSQEEIHS(p)DEEDQASEPK.S	IPI00476372.2	82 kDa protein	1.31	1.06
K.LGVSVS(p)PSR.A	IPI00476372.2	82 kDa protein	X	0.9

K.DAEYIYPSLES(p)DDDDPALK.S	IPI00476402.2	28 kDa protein	X	0.9
R.IACDEEFS(p)DSEDEGEGGRR.N	IPI00476698.2	PREDICTED: histone deacetylase 2	X	1
K.YGPVSVADTTGSGAADAKDDDDIDLFGS(p)DDEEESEDAKR.L	IPI00476899.1	PREDICTED: similar to Eukaryotic translation elongation factor 1 beta 2	1.16	X
K.YGPVSVADTTGSGAADAKDDDDIDLFGS(p)DDEEESEDAKR.L	IPI00476899.1	PREDICTED: similar to Eukaryotic translation elongation factor 1 beta 2	1.27	0.58
K.DDDDIDLFGS(p)DDEEESEDAK.R	IPI00476899.1	PREDICTED: similar to Eukaryotic translation elongation factor 1 beta 2	X	0.45
K.YGPVSVADTTGSGAADAKDDDDIDLFGS(p)DDEEESEDAK.R	IPI00476899.1	PREDICTED: similar to Eukaryotic translation elongation factor 1 beta 2	X	0.46
K.GEAAAERPGEAAVASS(p)PSK.A	IPI00480687.1	Myristoylated alanine-rich C-kinase substrate	1.3	0.72
K.EGEEPTVYS(p)DDEEPKDEAAR.K	IPI00480820.2	Membrane-associated progesterone receptor component 1	0.26	0.58
R.TPPPVELLTGDGS(p)PTR.A	IPI00480859.1	Phf1 protein	X	1.05
K.SQEPISNDQKDS(p)DDDKEKGEGALPTGK.S	IPI00515783.2	Splice Isoform 3 of Protein LYRIC	X	0.49
R.ALQS(p)PEHHIDPIYEDR.V	IPI00553941.2	Protein	X	1.31
R.ALQS(p)PEHHIDPIYEDR.V	IPI00553941.2	Protein	X	1.08
R.KNDMDEPPPFDYGS(p)GDEDGKSEK.R	IPI00553952.2	239 kDa protein	X	0.92
R.TVGTNTPPS(p)PGFGR.R	IPI00553992.2	Tensin	X	2.21
R.TVGTNT(p)PPS(p)PGFGR.R	IPI00553992.2	Tensin	X	4.65
R.QGS(p)PTPALPEK.R	IPI00553992.2	Tensin	X	2.87
R.ITFTPS(p)SGISSEVTVPR.D	IPI00554031.1	Splice Isoform 2 of Tenascin-R precursor	X	0.87
R.S(p)YIETETESR.E	IPI00554111.1	115 kDa protein	0.21	X
R.GSYGS(p)DPEEEEEYR.Q	IPI00554248.4	PREDICTED: similar to Tjp2 protein	X	1.61
R.DSSKGEDS(p)AEESDGKPAVVAPPPVVEAVSNPSSVFPSDATTEQGPILTK.H	IPI00555218.1	Splice Isoform 1 of Interleukin enhancer-binding factor 3	0.78	X
K.GYGHGQGSYSSYSNSYNS(p)PGGGGGSDYSYDSK.F	IPI00555218.1	Splice Isoform 1 of Interleukin enhancer-binding factor 3	0.54	1.11
R.DSSKGEDS(p)AEES(p)DGKPAVVAPPPVVEAVSNPSSVFPSDATTEQGPILTK.H	IPI00555218.1	Splice Isoform 1 of Interleukin enhancer-binding factor 3	X	0.91
K.RPMEEDGEEKS(p)PSK.K	IPI00555218.1	Splice Isoform 1 of Interleukin enhancer-binding factor 3	X	1.35
R.FYYSSGSS(p)SPTHAK.S	IPI00555227.1	Claudin 11	X	0.65
R.FYYSS(p)GSS(p)SPTHAK.S	IPI00555227.1	Claudin 11	X	1.37
R.FYYSSGS(p)SSPTHAK.S	IPI00555227.1	Claudin 11	X	0.68
R.FYYSS(p)GSSS(p)PTHAK.S	IPI00555227.1	Claudin 11	X	1.66
R.S(p)YSPDGKES(p)PSDKK.S	IPI00555259.4	Matrin-3	1.18	1.02
R.SYS(p)PDGKES(p)PSDKK.S	IPI00555259.4	Matrin-3	1.1	X
K.SFQQSS(p)LGR.D	IPI00555259.4	Matrin-3	2.95	X
K.VDKIEELDQENEAALENGIKNEENTEPGAESAENADDPNKDAS(p)DNS(p)DGQNDENKEDYTIPDEYR.I	IPI00555259.4	Matrin-3	0.67	X
R.SYS(p)PDGK.E	IPI00555259.4	Matrin-3	1.88	0.93
R.S(p)YSPDGKESPS(p)DKK.S	IPI00555259.4	Matrin-3	0.75	X
R.TSS(p)KESS(p)PVPS(p)PTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	0.43	1.17
R.TS(p)SKESS(p)PVPS(p)PTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	0.45	1.2
K.GDQVSQNGLPAEQGS(p)PR.M	IPI00555287.2	Non-erythroid spectrin beta	0.41	1.09
R.TSS(p)KES(p)SPVPS(p)PTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	0.45	1.16
R.TSS(p)KESS(p)PVPSPTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	0.13	1.01
R.TSS(p)KESS(p)PVPS(p)PTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	0.45	1.2
R.TSS(p)KES(p)SPVPSPTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.17
K.DDDEMNTWIQAITSAISSDKHDTSAS(p)TQS(p)TPASSR.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.83
R.T(p)S(p)SKESSPVPS(p)PTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.23
K.GDQVS(p)QNGLPAEQGS(p)PR.M	IPI00555287.2	Non-erythroid spectrin beta	X	1.05
R.TSS(p)KESSPVPS(p)PTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	X	0.68
R.TSS(p)KESS(p)PVPSPTS(p)DRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.21
R.TSS(p)KESS(p)PVPSPT(p)SDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.17
R.TSS(p)KES(p)SPVPSPTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	X	1.24
R.TSS(p)KESS(p)PVPSPTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.06
R.TSS(p)KES(p)SPVPSPT(p)SDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1.37
K.VSEEAESQQWDTSKGDQVSQNGLPAEQGS(p)PR.M	IPI00555287.2	Non-erythroid spectrin beta	X	1.01
R.AQTLPTSVVTITSESS(p)PGKR.E	IPI00555287.2	Non-erythroid spectrin beta	X	1.44

R.TS(p)SKESS(p)PVPSPTSDR.K	IPI00555287.2	Non-erythroid spectrin beta	X	1.01
K.VSEEAESQQWDTSKGDQVS(p)QNGLPAEQGSPR.M	IPI00555287.2	Non-erythroid spectrin beta	X	1.01
K.VSEEAESQQWDTSKGDQVS(p)QNGLPAEQGS(p)PR.M	IPI00555287.2	Non-erythroid spectrin beta	X	1.02
R.TSS(p)KESS(p)PVPSPTS(p)DR.K	IPI00555287.2	Non-erythroid spectrin beta	X	1.2
R.T(p)SSKESS(p)PVPSPTSDRK.A	IPI00555287.2	Non-erythroid spectrin beta	X	1
K.DKS(p)PVREPIDNLTPEER.D	IPI00555302.1	RNA-binding region	1.35	0.91
K.DKS(p)PVREPIDNLTPEER.D	IPI00555302.1	RNA-binding region	0.3	0.81
R.YRS(p)PYSGPK.F	IPI00555302.1	RNA-binding region	1.68	1.31
R.Y(p)SSVSNIYSDHR.Y	IPI00556925.1	406 kDa protein	X	1.05
R.TDTAADGETS(p)ATES(p)DQEEDAELK.A	IPI00556956.1	Type II brain 4.1	0.05	0.74
R.TDTAADGETSATES(p)DQEEDAELK.A	IPI00556956.1	Type II brain 4.1	X	0.28
R.TDTAADGETS(p)AT(p)ESDQEEDAELKAQELDKTQDELVK.H	IPI00556956.1	Type II brain 4.1	X	0.52
R.S(p)LDGEVGTGQYATTK.V	IPI00556956.1	Type II brain 4.1	X	0.72
R.TDTAADGET(p)SAT(p)ESDQEEDAELK.A	IPI00556956.1	Type II brain 4.1	X	0.73
K.QTLPSS(p)PTTTK.S	IPI00556974.1	PREDICTED: similar to neuro-oncological ventral antigen 1 isoform 1	0.53	X
R.TYS(p)DEASQLR.A	IPI00557056.1	Protein	X	3
R.NYQQNYQNS(p)ESGEKNEGSESAPEGQAQQR.R	IPI00557219.1	PREDICTED: nuclease sensitive element binding protein 1	7.39	X
R.NYQQNYQNSESGEKNEGSES(p)APEGQAQQR.R	IPI00557219.1	PREDICTED: nuclease sensitive element binding protein 1	6.67	X
R.NYQQNYQNSESGEKNEGS(p)ESAPEGQAQQR.R	IPI00557219.1	PREDICTED: nuclease sensitive element binding protein 1	X	0.7
R.MES(p)PERTDVYGEQK.L	IPI00557230.1	58 kDa protein	0.79	X
R.RSS(p)LDAEIDSLTSILADLECSSPYKPR.A	IPI00557330.1	53 kDa protein	X	2.67
R.YVLT(p)SPR.S	IPI00557335.2	PREDICTED: similar to Gene model 1568	0.54	X
K.TNS(p)PSASPSVLSNAEHK.R	IPI00557381.1	97 kDa protein	X	0.49
K.LASDDRPS(p)PPR.G	IPI00557539.1	102 kDa protein	1.39	0.72
R.SSLFPFEDAFLDDSHGDQALSSGLSSPT(p)R.C	IPI00557547.1	63 kDa protein	X	1.17
R.TQFEDLVPS(p)PTSEK.S	IPI00557677.1	77 kDa protein	X	0.7
K.LANHEEGS(p)DEEEEETPK.K	IPI00557925.1	96 kDa protein	X	1.2
R.T(p)GSPLTVATGNDQAATEAK.I	IPI00557932.1	92 kDa protein	X	1.27
R.TGS(p)PLTVATGNDQAATEAK.I	IPI00557932.1	92 kDa protein	X	1.77
K.LPS(p)ISDLDSIFGPVLS(p)PK.S	IPI00557932.1	92 kDa protein	X	1.17
K.AVPAT(p)PPRT(p)GSPLTVATGNDQAATEAK.I	IPI00557932.1	92 kDa protein	X	1.85
K.AVPAT(p)PPRTGS(p)PLTVATGNDQAATEAK.I	IPI00557932.1	92 kDa protein	X	1.1
R.RST(p)PT(p)PELTSK.K	IPI00557932.1	92 kDa protein	X	0.24
R.NLS(p)SEEVARPR.R	IPI00557932.1	92 kDa protein	X	3.06
K.TEVLLDQPEIWGSGQPINPSMES(p)PK.L	IPI00557932.1	92 kDa protein	X	1.21
K.LPSIS(p)DLDSIFGPVLS(p)PK.S	IPI00557932.1	92 kDa protein	X	1.35
K.AVPATPPRT(p)GS(p)PLTVATGNDQAATEAK.I	IPI00557932.1	92 kDa protein	X	1.85
K.LPSIS(p)DLDSIFGPVLSPK.S	IPI00557932.1	92 kDa protein	X	0.64
R.AS(p)PALGSGPDGSGDSLEMSSLDR.A	IPI00558147.1	69 kDa protein	0.25	1.09
R.AS(p)PALGSGPDGSGDSLEMSSLDR.A	IPI00558147.1	69 kDa protein	X	1.2
K.TGLEQEEQPLNLSDS(p)PR.S	IPI00558298.1	42 kDa protein	X	1.15
R.STPSHGSVSSLNSTGSLS(p)PK.H	IPI00558375.1	76 kDa protein	X	0.64
K.SPSPSPTS(p)PGSLR.K	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	2.23	X
K.AQPAPPELNS(p)ESEDYS(p)PSSSETVR.S	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	1.98
K.SPSPSPT(p)SPGSLR.K	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	2.14
R.ISQHGGS(p)STSLSSTK.V	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	1.56
K.AQPAPPELNSES(p)EDYSPS(p)SSETVR.S	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	1.7
K.GIVYAIS(p)PDRFR.S	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	2.17
K.AQPAPPELNSESEDYS(p)PSSSETVR.S	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	1.01
K.VCSS(p)MDENDGPGEEESDEGFQIPATITER.Y	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	5.34

K.AQPAPPELNSESEDYS(p)PSS(p)SETVR.S	IPI00558655.1	Activity and neurotransmitter-induced early gene protein 4	X	1.51
K.ASS(p)FSGISILTR.G	IPI00558866.1	RGD1310066 protein	X	0.8
R.VIENTDGS(p)EEEMDARDSDFNGTK.A	IPI00558912.1	227 kDa protein	X	2.5
R.VIENTDGS(p)EEEMDARDSDFNGTK.A	IPI00558912.1	227 kDa protein	X	2.41
R.RVIENTDGS(p)EEEMDAR.D	IPI00558912.1	227 kDa protein	X	2.83
K.GQLS(p)DDEKFLFVDK.N	IPI00558912.1	227 kDa protein	X	1.58
R.RVIENTDGS(p)EEEMDARDSDFNGTK.A	IPI00558912.1	227 kDa protein	X	1.96
R.VIENT(p)DGS(p)EEEMDAR.D	IPI00558912.1	227 kDa protein	X	3.82
R.KADS(p)DSEDKGEESKPK.K	IPI00558990.1	17 kDa protein	X	0.87
R.LEQNGS(p)PLGR.G	IPI00559021.1	PREDICTED: special AT-rich sequence binding protein 1	X	0.39
R.ALYLEPSDGVS(p)PTQETGEAQSQDDER.S	IPI00559158.1	Protein	0.24	1.12
K.VGSLT(p)PPSSPK.T	IPI00559288.1	43 kDa protein	X	0.98
K.VGSLT(p)PPSS(p)PK.T	IPI00559288.1	43 kDa protein	X	2.5
K.GTVAVGDS(p)EEDGEDVFEVER.I	IPI00559367.1	PREDICTED: similar to Ab2-008	1.33	0.94
R.SYS(p)PDGKESPS(p)DKK.S	IPI00559390.1	Matrin-3	1.1	0.98
R.SYS(p)PDGKES(p)PSDKK.S	IPI00559390.1	Matrin-3	1.37	1.07
K.IEELDQENEAALENGIKNEENTEPGAESAENADDPNKDAS(p)DNS(p)DGQNDENKEDYTIPDEYR.I	IPI00559390.1	Matrin-3	0.76	X
R.SY(p)SPDGKES(p)PSDKK.S	IPI00559390.1	Matrin-3	0.68	1.07
R.SYS(p)PDGKESPSDKK.S	IPI00559390.1	Matrin-3	1.78	1.06
K.NEENTEPGAESAENADDPNKDAS(p)DNS(p)DGQNDENKEDYTIPDEYR.I	IPI00559390.1	Matrin-3	1	X
K.IEELDQENEAALENGIKNEENTEPGAESAENADDPNKDAS(p)DNS(p)DGQNDENKEDYTIPDEYR.I	IPI00559390.1	Matrin-3	X	0.9
R.SY(p)SPDGKESPS(p)DKK.S	IPI00559390.1	Matrin-3	X	1.08
R.SY(p)SPDGKESPSDKK.S	IPI00559390.1	Matrin-3	X	1.05
K.NEENTEPGAESAENADDPNKDAS(p)DNSDGQNDENKEDY(p)TIPDEYR.I	IPI00559390.1	Matrin-3	X	0.8
R.SYS(p)PDGKES(p)PSDK.K	IPI00559390.1	Matrin-3	X	1.1
R.SYS(p)PDGKESPSDK.K	IPI00559390.1	Matrin-3	X	0.98
K.YSPTS(p)PTYSPTS(p)PK.Y	IPI00559554.1	214 kDa protein	4.25	1.6
K.YSPTS(p)PKYS(p)PTSPK.Y	IPI00559554.1	214 kDa protein	1.1	X
K.YSPTS(p)PTYS(p)PTSPK.Y	IPI00559554.1	214 kDa protein	1.48	X
K.YSPTS(p)PTYSPTSPVYTPTS(p)PK.Y	IPI00559554.1	214 kDa protein	1.72	1.15
K.YSPT(p)SPTYSPTSPVYTPTS(p)PK.Y	IPI00559554.1	214 kDa protein	X	1.29
K.YSPTS(p)PTYSPTTPK.Y	IPI00559554.1	214 kDa protein	X	1.33
K.YSPTS(p)PTYSPT(p)SPK.Y	IPI00559554.1	214 kDa protein	X	1.58
K.YSPTS(p)PTYSPTSPVYTPT(p)SPK.Y	IPI00559554.1	214 kDa protein	X	1.24
R.DVTNLTVGGFTPMS(p)PR.I	IPI00559810.1	121 kDa protein	1.82	0.85
K.TDNSVASS(p)PSSAISTATPS(p)PK.S	IPI00559822.1	Protein	X	0.85
R.DVYLS(p)PRDDGYSTK.D	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	1.59	1.3
R.DVYLS(p)PR.D	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	1.45	X
R.DYSHS(p)SSRDDYPSR.G	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	X	2.06
R.DSYSSSRS(p)DLYSSGR.D	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	X	2.46
R.DYSHSSS(p)RDDYPSR.G	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	X	2.65
R.DVYLS(p)PR.D	IPI00559910.1	Heterogeneous nuclear ribonucleoprotein G	X	1.31
R.TAS(p)EINFDK.L	IPI00560004.1	PREDICTED: similar to mitogen-activated protein kinase kinase kinase kinase 5 isoform 2	X	2.65
K.SSQALLSQLYQS(p)PNR.R	IPI00560167.1	ELAV-like protein 4	0.94	X
R.NCPS(p)PMQTGAATDDSK.T	IPI00560167.1	ELAV-like protein 4	X	0.58
R.T(p)HSDAS(p)DDEAFPTSK.T	IPI00560241.1	LRRGT00098	X	1.5
R.THS(p)DASDDEAFPTSK.T	IPI00560241.1	LRRGT00098	X	0.94
K.DDFES(p)EEEDDVR.T	IPI00560544.1	Rbbp6 protein	2.42	1.04
K.VAGTEGPSSTLVDYTSTSSTGGS(p)PVRK.S	IPI00560544.1	Rbbp6 protein	1.37	X
R.PSANREDFS(p)PER.L	IPI00560544.1	Rbbp6 protein	1.65	1.38
K.VEGTEIVKPS(p)PK.R	IPI00560544.1	Rbbp6 protein	X	1.27
K.WDKDDFES(p)EEEDDVR.T	IPI00560544.1	Rbbp6 protein	X	1.21
K.S(p)ATPPPTEPASLPQEPPK.P	IPI00560565.1	54 kDa protein	0.6	X
R.YEDEVFGDS(p)EPELDEES(p)EDEVEEEQEDR.Q	IPI00560565.1	54 kDa protein	0.65	0.79

K.SAT(p)PPPTEPASLPQEPPK.P	IPI00560565.1	54 kDa protein	X	0.57
R.ASAPAT(p)PLSPTR.L	IPI00560927.1	PREDICTED: hypothetical protein XP_579583	X	1.29
R.DIYLS(p)PDWTSSSFAK.S	IPI00561112.1	52 kDa protein	X	1.04
K.RPTEAVS(p)PK.A	IPI00561254.2	Similar to splicing factor p54	0.52	0.73
R.DYDEEEQGYDS(p)EKEK.K	IPI00561254.2	Similar to splicing factor p54	1.19	0.74
R.DYDEEEQGYDS(p)EK.E	IPI00561254.2	Similar to splicing factor p54	X	0.91
R.DYDEEEQGYDS(p)EKEKK.E	IPI00561254.2	Similar to splicing factor p54	X	0.91
R.DYDEEEQGY(p)DSEKEK.K	IPI00561254.2	Similar to splicing factor p54	X	0.67
R.ELGYPQEDDEEDEDEDEEEDEEEDS(p)QAEVLK.G	IPI00561470.1	22 kDa protein	X	1.02
R.AFS(p)EDEALAQQDSK.H	IPI00561583.1	PREDICTED: similar to Protein KIAA1688 homolog	0.7	2.34
R.FLSFSS(p)LESLSSELEQTK.E	IPI00561621.3	CPG2 protein	X	1.2
R.S(p)GDETPGSEAPGDK.A	IPI00561756.1	76 kDa protein	0.81	1.08
R.S(p)KSPPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D	IPI00561756.1	76 kDa protein	0.74	0.82
R.S(p)KSPPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D	IPI00561756.1	76 kDa protein	0.86	0.93
R.SGDET(p)PGSEAPGDK.A	IPI00561756.1	76 kDa protein	0.83	X
R.SKS(p)PPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D	IPI00561756.1	76 kDa protein	0.82	0.85
R.SKS(p)PPPPEEEAKDEEEDQTLVNLDTYTSDLHFQISK.D	IPI00561756.1	76 kDa protein	0.75	0.85
R.TGDLGIPPNPEDRS(p)PS(p)PEPIYNSEGK.R	IPI00561804.1	Protein	X	0.8
R.S(p)PS(p)PEPIYNSEGK.R	IPI00561804.1	Protein	X	1.02
R.SKLS(p)PVLDGVSELR.H	IPI00561875.1	74 kDa protein	4.46	1.92
K.AALGLQDS(p)DDEDAAVDIDEQIESMFNSK.K	IPI00561934.1	118 kDa protein	0.76	1.06
R.DSGLEDGGES(p)PSFDTPSQR.V	IPI00562216.1	120 kDa protein	X	0.44
K.S(p)FDHLISDTK.A	IPI00562277.1	317 kDa protein	X	1.39
R.AQRPS(p)PPDPWDDEDGVSCTPFFGSEER.T	IPI00562291.1	117 kDa protein	X	0.83
R.EVS(p)PAPAPQGEPR.Q	IPI00562291.1	117 kDa protein	X	1.22
K.SHSS(p)PSLNPDASPVTAK.V	IPI00562441.1	29 kDa protein	0.08	0.7
K.SHS(p)SPSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	0.16	1.46
K.SHSSPSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	0.12	0.63
K.S(p)HS(p)SPSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	0.11	1.71
K.SHSS(p)PSLNPDASPVT(p)AK.V	IPI00562441.1	29 kDa protein	0.2	X
K.SHSS(p)PSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	0.05	1.98
K.SHS(p)SPSLNPDASPVTAK.V	IPI00562441.1	29 kDa protein	0.08	1.19
K.S(p)HSS(p)PSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	X	1.65
K.SHS(p)S(p)PSLNPDASPVTAK.V	IPI00562441.1	29 kDa protein	X	0.92
K.SHS(p)SPS(p)LNPDASPVTAK.V	IPI00562441.1	29 kDa protein	X	0.83
K.S(p)HSSPSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	X	1.49
K.S(p)HSSPSLNPDASPVTAK.V	IPI00562441.1	29 kDa protein	X	1.13
K.S(p)HSS(p)PSLNPDASPVTAK.V	IPI00562441.1	29 kDa protein	X	1.06
K.SHSS(p)PS(p)LNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	X	1.1
K.SHS(p)S(p)PSLNPDAS(p)PVTAK.V	IPI00562441.1	29 kDa protein	X	1.66
K.S(p)HSSPS(p)LNPDASPVTAK.V	IPI00562441.1	29 kDa protein	X	0.86
R.SEDS(p)DEEEPCAISGK.W	IPI00562448.1	132 kDa protein	X	1.09
K.SST(p)SVDLESDGKDSVPASPGAS(p)AADVPAETEPSK PSSK.Q	IPI00562522.1	172 kDa protein	1.41	X
K.ADASS(p)TENILYK.V	IPI00562575.1	179 kDa protein	X	1.33
K.EGINPGYDDYADS(p)DEDQHDAYLER.M	IPI00562672.1	81 kDa protein	1.45	0.72
K.EGINPGYDDYADS(p)DEDQHDAYLER.M	IPI00562672.1	81 kDa protein	X	0.79
R.EEAS(p)DDDMEGDEAVVR.C	IPI00562876.1	LOC296126 protein	0.93	1
K.LADS(p)PSRS(p)PSKVEVTEK.M	IPI00563186.1	PREDICTED: transmembrane protein 24	X	1.93
R.GDLS(p)DVEEEEEEEMDVDEATGAPK.K	IPI00563226.1	146 kDa protein	1.29	0.91
R.FQSS(p)AVIALQEASEAYLVGLFEDTNLCAIHAK.R	IPI00563236.1	15 kDa protein	X	0.95
R.AKS(p)PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I	IPI00563348.1	Heterogeneous nuclear ribonucleoprotein U	1.4	X
R.AKS(p)PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I	IPI00563348.1	Heterogeneous nuclear ribonucleoprotein U	1.79	1.02
R.AKS(p)PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I	IPI00563348.1	Heterogeneous nuclear ribonucleoprotein U	2.16	1.06
K.S(p)PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I	IPI00563348.1	Heterogeneous nuclear ribonucleoprotein U	1.99	X
R.LQAALDNEAGGRPAMEPGNGS(p)LDLGGDAAGR.S	IPI00563348.1	Heterogeneous nuclear ribonucleoprotein U	X	1.17
R.STSFSEVPRS(p)PK.H	IPI00563362.1	31 kDa protein	X	1.17
R.SS(p)TPLPTVSSSAENTR.Q	IPI00563743.1	46 kDa protein	2.4	0.97
R.SS(p)T(p)PLPTVSSSAENTR.Q	IPI00563743.1	46 kDa protein	2.35	0.9

K.GPPDFSSDEEREPT(p)PVLGSGASVGR.G	IPI00563743.1	46 kDa protein	1.65	1.06
R.S(p)STPLPTVSSSAENTR.Q	IPI00563743.1	46 kDa protein	1.84	X
R.AST(p)FCGTPDYIAPEILQGLK.Y	IPI00563745.1	80 kDa protein	X	1
K.GFS(p)FVNPK.Y	IPI00563745.1	80 kDa protein	X	1.12
R.LGS(p)FGSITR.Q	IPI00563816.1	161 kDa protein	X	1.02
K.SELNEIKENQRS(p)PVR.V	IPI00564003.1	peptidylprolyl isomerase G	1.02	X
R.SET(p)PPHWR.Q	IPI00564003.1	peptidylprolyl isomerase G	1.6	2.21
K.KADIDQS(p)PVSK.T	IPI00564003.1	peptidylprolyl isomerase G	1.22	1.07
K.ADIDQS(p)PVSK.T	IPI00564003.1	peptidylprolyl isomerase G	0.82	X
K.GDKSELNEIKENQRS(p)PVR.V	IPI00564003.1	peptidylprolyl isomerase G	X	0.87
K.ENDSS(p)EEMDVLQASS(p)PVSDDTTQEGAEEEDISAGNVR.R	IPI00564076.1	60 kDa protein	0.86	0.56
R.AES(p)PETSAVESTQSTPQK.G	IPI00564076.1	60 kDa protein	0.97	X
R.AES(p)PETSAVESTQSTPQK.G	IPI00564076.1	60 kDa protein	1.04	0.71
K.ENDS(p)SEEMDVLQASS(p)PVSDDTTQEGAEEEDISAGNVR.R	IPI00564076.1	60 kDa protein	X	1.08
K.ENDS(p)SEEMDVLQASSPVS(p)DDTTQEGAEEEDISAGNVR.R	IPI00564076.1	60 kDa protein	X	0.66
R.ESEGIS(p)DPELEQTDYCADPLPEGR.K	IPI00564481.2	PREDICTED: similar to Parn protein	1.07	X
R.ESEGIS(p)DPELEQTDYCADPLPEGR.K	IPI00564481.2	PREDICTED: similar to Parn protein	X	0.44
R.NS(p)PGLLVSPGNLNK.N	IPI00564898.1	PREDICTED: similar to MADS box transcription enhancer factor 2, polypeptide C	2.17	0.69
R.DLVQPDKPAS(p)PK.F	IPI00564935.1	82 kDa protein	0.78	X
K.AAATEAPADS(p)GAEEEK.S	IPI00565180.1	129 kDa protein	2.44	X
R.S(p)LDGAAAAESTDR.S	IPI00565191.1	96 kDa protein	X	0.55
R.S(p)PDSDSVSPDSWGGPVLGPWDPTFTSDALPFLDR.L	IPI00565336.1	PREDICTED: similar to KIAA1086 protein	0.33	X
K.S(p)PLTGYVR.F	IPI00565616.1	44 kDa protein	X	1.01
R.RFS(p)EPDDAVER.D	IPI00565713.1	184 kDa protein	X	1.62
K.LDPYDSSEDDKEY(p)VGFATLPNQVHR.K	IPI00565773.1	PREDICTED: peanut-like 2	X	0.99
K.LDPYDSS(p)EDDKEYVGFATLPNQVHR.K	IPI00565773.1	PREDICTED: peanut-like 2	X	1.09
K.IYQFPDCDS(p)DEDEDFKLQDQALK.E	IPI00565773.1	PREDICTED: peanut-like 2	X	0.63
K.LDPYDS(p)SEDDKEYVGFATLPNQVHR.K	IPI00565773.1	PREDICTED: peanut-like 2	X	0.97
R.TSS(p)PTTLPPLAR.S	IPI00565904.1	173 kDa protein	X	1.3
K.SSSFSEEKGES(p)DDEKPR.K	IPI00566133.1	147 kDa protein	2.1	3.72
R.TAQVPS(p)PPR.G	IPI00566133.1	147 kDa protein	1.6	1
R.LQPEQES(p)PKKCEAEEAEPPAATQPQTSEPQLSQLPEAER.T	IPI00566133.1	147 kDa protein	1.51	X
K.SQS(p)PSLPPLPEDLEK.A	IPI00566133.1	147 kDa protein	2.15	3.25
R.IS(p)EDETER.N	IPI00566133.1	147 kDa protein	X	1.35
R.HMS(p)QPEPEQK.H	IPI00566133.1	147 kDa protein	X	1.85
R.GLS(p)PLSSTADTK.A	IPI00566133.1	147 kDa protein	X	2.43
R.GLS(p)PLSSTADTKAES(p)PAER.V	IPI00566133.1	147 kDa protein	X	2.52
K.AAENNSGVESSSGYGS(p)PGPTWDR.G	IPI00566160.1	150 kDa protein	X	1.56
K.AAENNSGVESSSGYGS(p)PGPTWDR.G	IPI00566160.1	150 kDa protein	X	1.15
R.NSADDEELT(p)NDS(p)LTLSQSK.S	IPI00566375.1	PREDICTED: similar to PHD finger protein 14 isoform 1	1.1	X
K.SNEDS(p)LILEK.S	IPI00566375.1	PREDICTED: similar to PHD finger protein 14 isoform 1	2.12	X
R.SQSSHS(p)YDDSTLPLIDR.N	IPI00566502.1	102 kDa protein	X	0.83
R.RYS(p)PVAK.D	IPI00566635.1	PREDICTED: hypothetical protein XP_579440	X	2.24
R.LEEQLS(p)PR.S	IPI00566637.1	127 kDa protein	X	1.64
K.ESDETVTVALS(p)PK.E	IPI00567407.1	53 kDa protein	0.97	X
K.DVEDSLPIKESDETVTVALS(p)PK.E	IPI00567407.1	53 kDa protein	1	X
R.SS(p)S(p)VGSSSSYPISSAVPR.T	IPI00567739.1	Plectin 7	X	0.99
K.AQLEPVAS(p)PAK.K	IPI00567739.1	Plectin 7	X	1.49
R.SSS(p)VGSSSSYPISSAVPR.T	IPI00567739.1	Plectin 7	X	0.86
R.SS(p)SVGSSSSYPISSAVPR.T	IPI00567739.1	Plectin 7	X	0.85
R.S(p)SSVGSS(p)SSYPISSAVPR.T	IPI00567739.1	Plectin 7	X	0.93
R.SSS(p)VGS(p)SSSYPISSAVPR.T	IPI00567739.1	Plectin 7	X	0.98
K.RAS(p)FAEK.T	IPI00567739.1	Plectin 7	X	0.95
K.GYYS(p)PYSVSGSGSTAGSR.T	IPI00567739.1	Plectin 7	X	1.05

K.GYYSPYSVSGSGSTAGS(p)R.T	IPI00567739.1	Plectin 7	X	0.8
R.SEVS(p)LDEEEQR.G	IPI00567833.1	138 kDa protein	1.32	1.13
K.T(p)GSPSPSNQLNDS(p)PTFK.K	IPI00567833.1	138 kDa protein	0.09	X
K.TGSPS(p)PSNQLNDS(p)PTFK.K	IPI00567833.1	138 kDa protein	X	0.2
R.TDGDWDDQEVLDYFS(p)DKESAK.Q	IPI00567915.1	161 kDa protein	1.32	X
R.TDGDWDDQEVLDYFS(p)DKESAK.Q	IPI00567915.1	161 kDa protein	1.01	1.27
K.KAEGEPQEES(p)PLK.S	IPI00567915.1	161 kDa protein	1.42	1.11
K.KAEGEPQEESPLKS(p)K.S	IPI00567915.1	161 kDa protein	0.91	1.16
K.FHDS(p)EGDDTEETEDYR.Q	IPI00567915.1	161 kDa protein	1.42	1.2
R.IDIS(p)PSALR.K	IPI00567915.1	161 kDa protein	1.34	0.91
K.KEVQS(p)PEQVK.S	IPI00567915.1	161 kDa protein	0.58	X
K.AEGEPQEES(p)PLK.S	IPI00567915.1	161 kDa protein	1.4	X
K.ELFDYS(p)PPLHK.S	IPI00567915.1	161 kDa protein	1.29	0.94
K.SLAPDLS(p)DDEHDPVDSISRPR.F	IPI00568245.1	Protein	X	0.69
R.TLPS(p)EDEEGEEDKEFYLR.G	IPI00568384.1	108 kDa protein	X	1.59
K.ESS(p)PPREEAPPPPPPTEDSCAK.K	IPI00568480.1	76 kDa protein	X	2.78
R.LVPSDKLS(p)PR.T	IPI00568481.1	PREDICTED: hypothetical protein XP_579639	3.79	X
R.AEEDSKS(p)IQS(p)DAPVYLR.R	IPI00568481.1	PREDICTED: hypothetical protein XP_579639	X	1.18
K.QASASYDS(p)EEEEEGLPMSYDEK.R	IPI00568613.1	79 kDa protein	2.78	0.82
R.SES(p)PPPLSEPK.Q	IPI00568613.1	79 kDa protein	4.4	1.11
R.GPASQFYITPNTSLS(p)PR.Q	IPI00569270.1	75 kDa protein	X	1.5
K.SGSSPKWT(p)HDKYQGDGIVEDEEETMENNEEKKDR.R	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	0.82
R.TDGDWDDQEVLDY(p)FSDKESAK.Q	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	1.14
K.GRTDGDWDDQEVLDYFSDKES(p)AK.Q	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	0.96
K.GRTDGDWDDQEVLDYFS(p)DKESAK.Q	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	0.98
K.KAEGEPQEES(p)PLKSK.S	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	1.14
K.KAEGEPQEES(p)PLKSK.S	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	1.12
K.GRTDGDWDDQEVLDY(p)FSDKESAK.Q	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	0.83
K.SIFREES(p)PLR.I	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	1.06
R.RIDIS(p)PSALR.K	IPI00569619.1	PREDICTED: similar to Bcl-2-associated transcription factor	X	0.95
R.LYNSEESRPYT(p)NK.V	IPI00569900.2	CDC2-related kinase 7 isoform 1	1.75	2.03
K.SSSPS(p)ASLTENELLWEPTSVK.L	IPI00569912.1	10 kDa protein	X	1.67
K.QSNASS(p)DVEAEEKETSVS(p)KEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.6	X
K.QSNASSDVEAEEKET(p)SVSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.28	X
K.ETSVSKEDT(p)DQEEKASNEDVT(p)K.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.95	X
K.QSNASSDVEAEEKETSVSKEDT(p)DQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.03	0.94
K.QSNAS(p)SDVEAEEKETSVSKEDT(p)DQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.82	1.21
K.QSNASS(p)DVEAEEKETSVSK.E	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.27	X
K.NLAKPGVTS(p)TSDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1	0.74
K.NLAKPGVTSTS(p)DS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1	0.76
K.QSNASSDVEAEEKETS(p)VSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.52	0.69
K.PGVTSTSDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.92	X
K.NLAKPGVTSTS(p)DSEEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.73	0.37
K.QSNASS(p)DVEAEEKETSVSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.08	0.69
K.QSNASS(p)DVEAEEKETSVSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting	1.59	X

		protein		
K.QSNASS(p)DVEAEEKET(p)SVSKEDT(p)DQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.13	X
K.QSNAS(p)SDVEAEEKETSVS(p)KEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.76	X
K.QVDTEEAGVVTAATASNVKAS(p)PK.R	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.37	1.17
K.QVDTEEAGVVTAATASNVKAS(p)PK.R	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.11	0.9
K.ETSVSKEDT(p)DQEEKAS(p)NEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.89	1.13
K.ETSVSKEDT(p)DQEEKAS(p)NEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.65	X
K.QS(p)NASSDVEAEEKETS(p)VSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.82	X
K.PGVTST(p)SDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.01	X
K.QS(p)NASSDVEAEEKET(p)SVSKEDTDQEEKASNEDVT(p)K.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.83	X
K.ETSVSKEDTDQEEKAS(p)NEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.74	0.51
K.ETSVSKEDTDQEEKAS(p)NEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.69	0.45
K.NLAKPGVTSTSDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.63	X
K.NLAKPGVTSTSDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	0.66	X
K.QSNAS(p)SDVEAEEKETSVSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	1.27	X
K.QSNASSDVEAEEKET(p)SVSKEDTDQEEKASNEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.64
K.NLAKPGVTSTS(p)DS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.76
K.QSNASSDVEAEEKETS(p)VSKEDT(p)DQEEKASNEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.84
K.NLAKPGVT(p)STSDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.71
K.QSNASSDVEAEEKETSVSKEDT(p)DQEEKASNEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.41
K.NLAKPGVTST(p)SDS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.73
K.NLAKPGVTS(p)T(p)SDSEEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.5
K.NLAKPGVTSTS(p)DSEEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.38
K.QSNAS(p)SDVEAEEKETS(p)VSKEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	1.21
K.NLAKPGVTS(p)T(p)SDSEEDDDQEGEKK.R	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.73
K.QS(p)NASSDVEAEEKETSVSKEDTDQEEKAS(p)NEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.66
K.QSNASSDVEAEEKETSVS(p)KEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.99
K.PGVTSTS(p)DSEEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.43
K.PGVTSTS(p)DS(p)EEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.57
K.QSNAS(p)SDVEAEEKETS(p)VS(p)KEDTDQEEK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	1.14
K.NLAKPGVTSTS(p)DS(p)EEDDDQEGEKK.R	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.75
K.NLAKPGVTS(p)TS(p)DSEEDDDQEGEK.K	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.81
K.ETSVSKEDT(p)DQEEKASNEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.54
K.QSNASSDVEAEEKETS(p)VSKEDTDQEEKASNEDVTK.A	IPI00608154.1	Splice Isoform 2 of PC4 and SFRS1-interacting protein	X	0.8
R.AIS(p)LEGEPR.K	IPI00650088.1	Splice Isoform 6 of Discs large homolog 2	X	2.31
R.HYS(p)PVECDK.S	IPI00650088.1	Splice Isoform 6 of Discs large homolog 2	X	2.53

K.LAT(p)PEDKQDIDK.Q	IPI00655290.2	Splice Isoform 1 of Septin-5	0.56	2.4
K.LVLPS(p)NSPNVR.R	IPI00734616.1	PREDICTED: centromere autoantigen C	X	0.57
K.AQS(p)PLLPEPLK.N	IPI00734617.1	PREDICTED: microtubule-associated protein 6	X	2.43
K.GQS(p)PTAPGPPK.D	IPI00734617.1	PREDICTED: microtubule-associated protein 6	X	1.88
K.EVLDASDKEGLS(p)PAK.R	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	0.92	X
K.LCDFGSASHVADNDITPYLVS(p)R.F	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	1.1	X
K.LCDFGSASHVADNDITPY(p)LVSR.F	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	0.95	0.9
R.KKS(p)PIVNER.S	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	0.9	1.11
K.EVLDASDKEGLS(p)PAKR.T	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	0.75	X
K.EVLDASDKEGLS(p)PAKR.T	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	0.5	X
K.EVLDAS(p)DKEGLS(p)PAK.R	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	X	1.02
R.EQPEMDDADNS(p)EKS(p)VNEENGEVSEDQSQNK.H	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	X	0.85
R.TLS(p)PGRR.A	IPI00734688.1	PREDICTED: PRP4 pre-mRNA processing factor 4 homolog B	X	1.11
K.EEES(p)EEES(p)NEEEEEEDEEES(p)EAEAK.S	IPI00734711.1	PREDICTED: hypothetical protein XP_579138	X	0.72
K.EEES(p)EEES(p)NEEEEEEDEEESEAEAK.S	IPI00734711.1	PREDICTED: hypothetical protein XP_579138	X	0.43
K.TSNSTEKT(p)PS(p)PPEPEPAGTAQK.N	IPI00758425.1	Splice Isoform 4 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	2.08
K.TSNSTEKT(p)PS(p)PPEPEPAGTAQK.N	IPI00758425.1	Splice Isoform 4 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.96
K.SVKEDSLSTGAEENTSNST(p)EKTPS(p)PPEPEPAGTAQK.N	IPI00758437.1	Splice Isoform 3 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.17
K.EDSLSTGAEENTSNS(p)TEKTPS(p)PPEPEPAGTAQK.N	IPI00758437.1	Splice Isoform 3 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.28
K.SVKEDSLSTGAEENTSNSTEKT(p)PS(p)PPEPEPAGTAQK.N	IPI00758437.1	Splice Isoform 3 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.2
K.EDSLSTGAEENTSNSTEKT(p)PS(p)PPEPEPAGTAQK.N	IPI00758437.1	Splice Isoform 3 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.24
K.DSSCQTSNSTEKT(p)PS(p)PPEPEPAGTAQK.N	IPI00758441.1	Splice Isoform 5 of Breast carcinoma amplified sequence 1 homolog (Fragment)	X	1.16
K.ETSLLAVPGALS(p)PLAIPNAAAAAAAAAAGR.V	IPI00758469.1	Splice Isoform 1 of Polypyrimidine tract-binding protein 2	1.71	1.21
K.ETSLLAVPGALS(p)PLAIPNAAAAAAAAAAGR.V	IPI00758469.1	Splice Isoform 1 of Polypyrimidine tract-binding protein 2	1.82	1.05