Supplemental Table 1. Phosphorylated peptides and proteins by ING5 overexpression.

Protein accession	Position	Amino acid	Protein names	Gene names	Score	Modified sequence
A0FGR8	691	S	Extended synaptotagı	ESYT2	89.17	_SHMS(ph)GS(ph)PGF
A0FGR8	693	S	Extended synaptotagı	ESYT2	89.17	_SHMS(ph)GS(ph)PGF
A0FGR8	753	T	Extended synaptotagı	ESYT2	71.097	_EPT(ph)PS(ph)IAS(ph
A0FGR8	755	S	Extended synaptotagı	ESYT2	151.41	_EPTPS(ph)IAS(ph)DI
A0FGR8	758	S	Extended synaptotagı	ESYT2	180.34	_EPTPSIAS(ph)DIS(ph
A0FGR8	761	S	Extended synaptotagı	ESYT2	180.34	_EPTPSIAS(ph)DIS(ph
A0JLT2	226	S	Mediator of RNA poly	MED19	108.5	_NRHS(ph)PDHPGMG
A1L390	76	S	Pleckstrin homology (	PLEKHG3	110.08	_GPLS(ph)PFNSR_
A1L390	576	S	Pleckstrin homology (	PLEKHG3	127.97	_ALS(ph)S(ph)EEEEEI
A1L390	577	S	Pleckstrin homology (	PLEKHG3	127.97	_ALS(ph)S(ph)EEEEEI
A1L390	643	S	Pleckstrin homology (	PLEKHG3	65.652	_SSSVLS(ph)LEGSEK_
A1L390	827	S	Pleckstrin homology (	PLEKHG3	157.27	_IWEGMESSGGS(ph)I
A1L390	1037	S	Pleckstrin homology (	PLEKHG3	182.22	_S(ph)PLS(ph)PTETFS
A1L390	1040	S	Pleckstrin homology (	PLEKHG3	182.22	_S(ph)PLS(ph)PTETFS
A1L390	1154	S	Pleckstrin homology (	PLEKHG3	194.77	_GPLPS(ph)PTAGLEE
A1L390	1169	S	Pleckstrin homology (	PLEKHG3	194.37	_GPLPS(ph)PTAGLEE
A1X283	291	S	SH3 and PX domain-(	SH3PXD2B	55.779	_NSGEPLPPKPGPGS(
A2A2Y4	429	S	FERM domain-contai	FRMD3	88.427	_EYEDPPS(ph)EEEDK
A2AJT9	15	S	Uncharacterized prot	CXorf23	65.295	_HRS(ph)LS(ph)PVPR_
A2AJT9	17	S	Uncharacterized prot	CXorf23	65.295	_HRS(ph)LS(ph)PVPR_
A6NFI3	10	S	Zinc finger protein 31	ZNF316	134.29	_(ac)AALHTTPDS(ph)F
A8CG34	161	S	Nuclear envelope por	POM121C	47.302	_S(ph)TPPSPPTHR_
A8CG34	358	S	Nuclear envelope por	POM121C;POM12	127.18	_GLNSQSS(ph)DDHLN
C9JLW8	21	S	Protein FAM195B	FAM195B	204.31	_S(ph)PPSSSEIFTPAH
O00151	90	S	PDZ and LIM domain	PDLIM1	63.212	_VWS(ph)PLVTEEGK_
O00159	408	S	Unconventional myos	MYO1C	85.533	_DVES(ph)PSWR_
O00161	110	S	Synaptosomal-associ	SNAP23	52.849	_TTWGDGGENS(ph)P
O00193	17	S	Small acidic protein	SMAP	298.6	_SAS(ph)PDDDLGSSN
O00203	276	S	AP-3 complex subuni	AP3B1	137.73	_NFYES(ph)DDDQKEK
O00264	57	S	Membrane-associate(	PGRMC1	235.74	_GDQPAASGDS(ph)DI
O00264	181	S	Membrane-associate(	PGRMC1	317.85	_EGEEPTVYS(ph)DEE
O00267	32	S	Transcription elongati	SUPT5H	159.79	_S(ph)AAGS(ph)EKEE
O00267	36	S	Transcription elongati	SUPT5H	159.79	_S(ph)AAGS(ph)EKEE
O00267	666	S	Transcription elongati	SUPT5H	143.52	_DVTNFTVGGFAPMS(
O00429	616	S	Dynamin-1-like protei	DNM1L	80.508	_SKPIPIMPAS(ph)PQK
O00443	259	S	Phosphatidylinositol 4	PIK3C2A	71.879	_VSNLQVS(ph)PK_
O00499	296	S	Myc box-dependent-ir	BIN1	67.877	_GNKS(ph)PSPPDGSF
O00499	298	S	Myc box-dependent-ir	BIN1	77.554	_SPS(ph)PPDGSPAAT
O00505	60	S	Importin subunit alph	KPNA3	181.81	_NVPQEESLEDS(ph)D
O00512	278	S	B-cell CLL/lymphoma	BCL9	96.848	_PAAPPRPLDRES(ph)
O00559	36	S	Receptor-binding can	EBAG9	284.86	_KLS(ph)GDQITLPTTV
O00566	163	S	U3 small nucleolar rib	MPHOSPH10	252.77	_S(ph)PVFS(ph)DEDS(
O00566	167	S	U3 small nucleolar rib	MPHOSPH10	235.76	_S(ph)PVFS(ph)DEDS(
O00566	171	S	U3 small nucleolar rib	MPHOSPH10	252.77	_S(ph)PVFS(ph)DEDS(
O00566	242	S	U3 small nucleolar rib	MPHOSPH10	229.8	_KDDNDEEEEDIDFFE
O00567	468	T	Nucleolar protein 56	NOP56	82.581	_LAALALASSENSS(ph
O00567	519	S	Nucleolar protein 56	NOP56	152.47	_EELMS(ph)S(ph)DLEI
O00567	520	S	Nucleolar protein 56	NOP56	195.03	_EELMS(ph)S(ph)DLEI
O00567	569	S	Nucleolar protein 56	NOP56	131.4	_EEPVS(ph)S(ph)GPE
O00567	570	S	Nucleolar protein 56	NOP56	120.63	_EEPVS(ph)S(ph)GPE
O00712	328	S	Nuclear factor 1 B-typ	NFIB	61.963	_KPEKPLFSSAS(ph)P(
O00767	198	S	Acyl-CoA desaturase	SCD	99.881	_EKGS(ph)TLDLSDLE/

O00767	199	T	Acyl-CoA desaturase	SCD	110.57	_GST(ph)LDLSDLEAEI
O14497	363	S	AT-rich interactive do	ARID1A	92.565	_SHHAPMS(ph)PGSS(
O14497	696	S	AT-rich interactive do	ARID1A	138.05	_GPS(ph)PSPVGSPAS
O14497	1755	S	AT-rich interactive do	ARID1A	141.36	_VSS(ph)PAPMEGGEI
O14545	415	S	TRAF-type zinc finger	TRAFD1	127.97	_LDSQPQETS(ph)PEL
O14617	634	S	AP-3 complex subuni	AP3D1	56.903	_VPVPEGLDLDAWINE
O14617	636	S	AP-3 complex subuni	AP3D1	56.903	_KVPVPEGLDLDAWIN
O14617	829	S	AP-3 complex subuni	AP3D1	94.707	_NTETSKS(ph)PEKDV
O14639	431	S	Actin-binding LIM pro	ABLIM1	163.56	_TLS(ph)PTPSAEGYQ
O14639	435	S	Actin-binding LIM pro	ABLIM1	81.316	_TLS(ph)PTPS(ph)AEC
O14639	586	S	Actin-binding LIM pro	ABLIM1	124.29	_S(ph)SGREEDDEELL
O14639	587	S	Actin-binding LIM pro	ABLIM1	96.143	_RSS(ph)GREEDDEEL
O14639	655	S	Actin-binding LIM pro	ABLIM1	43.68	_TAS(ph)LPGYGR_
O14639	706	S	Actin-binding LIM pro	ABLIM1	36.114	_GVS(ph)MPNMLEPK_
O14646	215	S	Chromodomain-helica	CHD1	133.86	_QIDS(ph)S(ph)EEDDI
O14646	216	S	Chromodomain-helica	CHD1	133.86	_QIDS(ph)S(ph)EEDDI
O14646	1677	S	Chromodomain-helica	CHD1	79.317	_ASSSGPRS(ph)PLDC
O14646	1689	S	Chromodomain-helica	CHD1	147.33	_S(ph)PFEHSVEHK_
O14647	1373	S	Chromodomain-helica	CHD2	124.66	_HSDNPS(ph)EEGEVK
O14681	326	S	Etoposide-induced pr	EI24	74.853	_FPS(ph)PHPS(ph)PAI
O14681	330	S	Etoposide-induced pr	EI24	74.853	_FPS(ph)PHPS(ph)PAI
O14683	14	S	Tumor protein p53-in	TP53I11	97.957	_KHS(ph)QTDLVSR_
O14686	654	S	Histone-lysine N-meth	MLL2	69.864	_LS(ph)PLPVVSR_
O14686	1606	S	Histone-lysine N-meth	MLL2	78.903	_NLTMS(ph)PLHK_
O14686	1671	S	Histone-lysine N-meth	MLL2	182.43	_LEGPVS(ph)PDVEPG
O14686	2229	T	Histone-lysine N-meth	MLL2	84.166	_PGAGQPGEFHTT(ph
O14686	2274	S	Histone-lysine N-meth	MLL2	41.689	_ASEPLLS(ph)PPPFGI
O14686	3130	S	Histone-lysine N-meth	MLL2	55.546	_HPS(ph)PCQFTIATPK
O14686	4359	S	Histone-lysine N-meth	MLL2	131.54	_VS(ph)PAAAQLADTL
O14686	4682	T	Histone-lysine N-meth	MLL2	86.557	_SLDLLAALPT(ph)PPH
O14686	4738	S	Histone-lysine N-meth	MLL2	119.25	_ALS(ph)PVIPLIPR_
O14745	280	S	Na(+)/H(+) exchange	SLC9A3R1	82.609	_EALAEAALES(ph)PRI
O14745	290	S	Na(+)/H(+) exchange	SLC9A3R1	249.28	_SAS(ph)SDTSEELNS
O14828	76	S	Secretory carrier-ass	SCAMP3	104.82	_KLS(ph)PTEPK_
O14874	31	S	[3-methyl-2-oxobutan	BCKDK	176.49	_S(ph)TSATDTHHVEM
O14974	299	S	Protein phosphatase	PPP1R12A	85.498	_DKKS(ph)PLIESTANM
O14974	871	S	Protein phosphatase	PPP1R12A	173.6	_STGVSFWTQDSDEN
O14979	241	S	Heterogeneous nucle	HNRPDL	120.11	_VFVGGLS(ph)PDTSE
O15014	358	S	Zinc finger protein 60	ZNF609	93.478	_FCDS(ph)PTSDLEMR
O15014	467	S	Zinc finger protein 60	ZNF609	100.5	_TNS(ph)MGSATGPLF
O15014	491	S	Zinc finger protein 60	ZNF609	126.29	_NCPS(ph)PVLIDCPHI
O15014	576	S	Zinc finger protein 60	ZNF609	139.73	_LVEPHS(ph)PS(ph)PS
O15014	578	S	Zinc finger protein 60	ZNF609	97.095	_LVEPHS(ph)PS(ph)PS
O15014	746	T	Zinc finger protein 60	ZNF609	90.412	_ELESPLT(ph)PGK_
O15014	758	S	Zinc finger protein 60	ZNF609	76.165	_AEEGKS(ph)PFR_
O15027	891	S	Protein transport prot	SEC16A	40.616	_AQQELVPPQQQAS(p
O15027	1178	S	Protein transport prot	SEC16A	80.737	_S(ph)LHS(ph)AHSLAS
O15027	1181	S	Protein transport prot	SEC16A	80.737	_S(ph)LHS(ph)AHSLAS
O15042	485	S	U2 snRNP-associate	U2SURP	164.66	_LYSILQGDS(ph)PTK_
O15042	946	S	U2 snRNP-associate	U2SURP	61.48	_VKS(ph)PS(ph)PK_
O15042	948	S	U2 snRNP-associate	U2SURP	61.48	_VKS(ph)PS(ph)PK_
O15061	429	S	Synemin	SYNM	119.39	_TFS(ph)PTYGLLR_
O15061	653	S	Synemin	SYNM	79.177	_QFTQS(ph)PETEASA
O15061	1049	S	Synemin	SYNM	139.51	_SPAPGS(ph)PDEEG(

O15083	187	S	ERC protein 2;ELKS/I	ERC2;ERC1	62.466	_TFWS(ph)PELK_
O15085	556	S	Rho guanine nucleoti	ARHGEF11	46.145	_SSSQSTFHIPLS(ph)F
O15085	668	T	Rho guanine nucleoti	ARHGEF11	70.26	_SLENPT(ph)PPFTPK_
O15085	1413	S	Rho guanine nucleoti	ARHGEF11	47.894	_S(ph)PPSLALR_
O15155	50	S	BET1 homolog	BET1	98.253	_SLS(ph)IEIGHEVK_
O15164	811	S	Transcription interme	TRIM24	153.65	_SEWLDPSQKS(ph)PL
O15164	1028	S	Transcription interme	TRIM24	110.06	_NESEDNKFSDDS(ph)
O15164	1042	S	Transcription interme	TRIM24	77.192	_LKS(ph)IEER_
O15173	211	T	Membrane-associate	PGRMC2	230.66	_LLKPGEEPSEYT(ph)I
O15231	158	T	Zinc finger protein 18	ZNF185	106.88	_RSST(ph)SGDT(ph)EI
O15231	447	T	Zinc finger protein 18	ZNF185	146.67	_GGQGDPAVPAQQPA
O15231	453	S	Zinc finger protein 18	ZNF185	134.4	_QSS(ph)PSGSEQLVF
O15231	519	S	Zinc finger protein 18	ZNF185	56.914	_GGQGDPAVPTQQPA
O15258	95	S	Protein RER1	RER1	80.813	_VDPSLMEDS(ph)DDC
O15320	536	S	cTAGE family membe	CTAGE5	107.03	_AFLS(ph)PPTLLEGPL
O15320	594	S	cTAGE family membe	CTAGE5	121.21	_APSDTGS(ph)LS(ph)I
O15320	596	S	cTAGE family membe	CTAGE5	121.21	_APSDTGS(ph)LS(ph)I
O15320	635	S	cTAGE family membe	CTAGE5;CTAGE1	38.58	_LS(ph)GPAELR_
O15320	647	S	cTAGE family membe	CTAGE5;CTAGE1	67.997	_SFNMPS(ph)LDK_
O15374	279	S	Monocarboxylate tran	SLC16A4	75.686	_SDEES(ph)DKVISWS
O15417	1857	S	Trinucleotide repeat-c	TNRC18	130.77	_ALS(ph)PGLEESGLG
O15417	1989	S	Trinucleotide repeat-c	TNRC18	110.4	_EPGFEAGPEAS(ph)D
O15417	2716	S	Trinucleotide repeat-c	TNRC18	77.22	_ARPSAHS(ph)PGK_
O15438	911	S	Canalicular multispec	ABCC3	104.84	_QLSALS(ph)SDGEGC
O15439	646	T	Multidrug resistance-a	ABCC4	133.84	_DNEESEQPPVPGT(p
O15440	509	S	Multidrug resistance-a	ABCC5	118.24	_NATLAWDSSHSSIQN
O15446	285	S	DNA-directed RNA pc	CD3EAP	239.48	_QEQINTEPLEDTVLS(
O15446	490	S	DNA-directed RNA pc	CD3EAP	88.346	_MPETVPQEEMPGPP
O15541	84	S	RING finger protein 1	RNF113A	42.863	_AAYGDLS(ph)S(ph)EI
O15541	85	S	RING finger protein 1	RNF113A	42.863	_AAYGDLS(ph)S(ph)EI
O15550	769	S	Lysine-specific deme	KDM6A	118.51	_S(ph)PGLLSSDNPQL
O43150	701	S	Arf-GAP with SH3 do	ASAP2	183.07	_LLHEDLDES(ph)DDD
O43159	62	S	Ribosomal RNA-proc	RRP8	156.7	_ALEAASLSQHPPSLC
O43159	64	S	Ribosomal RNA-proc	RRP8	134.21	_ALEAASLSQHPPSLC
O43159	104	S	Ribosomal RNA-proc	RRP8	123.42	_QGPPCS(ph)DS(ph)E
O43159	106	S	Ribosomal RNA-proc	RRP8	123.42	_QGPPCS(ph)DS(ph)E
O43159	223	S	Ribosomal RNA-proc	RRP8	64.374	_TEVS(ph)PVPR_
O43166	1270	S	Signal-induced prolife	SIPA1L1	120.29	_QDPVVHLS(ph)PNK_
O43166	1433	S	Signal-induced prolife	SIPA1L1	113.43	_HSAS(ph)PVVFTSAR
O43166	1549	S	Signal-induced prolife	SIPA1L1	203.2	_LIDLES(ph)PTPESQK
O43166	1585	S	Signal-induced prolife	SIPA1L1	209.79	_TLS(ph)DESIYNSQR_
O43237	194	S	Cytoplasmic dynein 1	DYNC1LI2	221.83	_DFQDYMEPEEGCQG
O43290	448	S	U4/U6.U5 tri-snRNP-a	SART1	196.01	_RVS(ph)EVEEEKEPV
O43290	474	S	U4/U6.U5 tri-snRNP-a	SART1	47.864	_VENMDIS(ph)DEEEG
O43290	486	S	U4/U6.U5 tri-snRNP-a	SART1	47.864	_VENMDIS(ph)DEEEG
O43379	1228	S	WD repeat-containing	WDR62	88.976	_SIS(ph)LGDSEGPIVA
O43395	619	S	U4/U6 small nuclear r	PRPF3	168.17	_WDEQTSNTKGDDDE
O43399	12	S	Tumor protein D54	TPD52L2	146.18	_(ac)MDSAGQDINLNS
O43432	495	S	Eukaryotic translation	EIF4G3	103.45	_RS(ph)PVPAQIAITVP
O43463	391	S	Histone-lysine N-met	SUV39H1	116.46	_MDSNFGLAGLPGS(p
O43493	71	S	Trans-Golgi network i	TGOLN2	322.59	_DSPSKSS(ph)AEAQT
O43493	298	S	Trans-Golgi network i	TGOLN2	210.61	_TES(ph)GEETDLISPF
O43521	86	S	Bcl-2-like protein 11	BCL2L11	44.614	_RS(ph)S(ph)LLSR_
O43521	87	S	Bcl-2-like protein 11	BCL2L11	44.614	_RS(ph)S(ph)LLSR_

O43707	159	S	Alpha-actinin-4;Alpha	ACTN4;ACTN1;A(	137.45	_FAIQDIS(ph)VEETSA
O43719	452	S	HIV Tat-specific facto	HTATSF1	116.93	_TEDGGEFEEGASEN
O43719	453	S	HIV Tat-specific facto	HTATSF1	174.72	_TEDGGEFEEGASEN
O43719	498	S	HIV Tat-specific facto	HTATSF1	56.087	_GSEEDS(ph)PKK_
O43719	529	S	HIV Tat-specific facto	HTATSF1	271.2	_ESEDDLNKES(ph)EE
O43719	579	S	HIV Tat-specific facto	HTATSF1	174.99	_DLDEEGS(ph)EKELH
O43719	616	S	HIV Tat-specific facto	HTATSF1	131.83	_VLDEEGS(ph)EREFD
O43719	624	S	HIV Tat-specific facto	HTATSF1	295.35	_VLDEEGS(ph)EREFD
O43719	642	S	HIV Tat-specific facto	HTATSF1	362.31	_VFDDES(ph)DEKEDE
O43719	676	S	HIV Tat-specific facto	HTATSF1	283.01	_LFEES(ph)DDKEDED
O43719	702	S	HIV Tat-specific facto	HTATSF1	209.62	_LFEDDDS(ph)NEKLF
O43719	713	S	HIV Tat-specific facto	HTATSF1	124.07	_LFDEEEDS(ph)S(ph)E
O43719	714	S	HIV Tat-specific facto	HTATSF1	124.07	_LFDEEEDS(ph)S(ph)E
O43752	2	S	Syntaxin-6	STX6	84.605	_(ac)S(ph)MEDPFFVVI
O43818	50	S	U3 small nucleolar RN	RRP9	130.83	_MNEEIS(ph)S(ph)DS(
O43818	51	S	U3 small nucleolar RN	RRP9	130.83	_MNEEIS(ph)S(ph)DS(
O43818	53	S	U3 small nucleolar RN	RRP9	165.1	_MNEEIS(ph)S(ph)DS(
O43823	323	S	A-kinase anchor prote	AKAP8	129.32	_VDS(ph)EGDFS(ph)E
O43823	328	S	A-kinase anchor prote	AKAP8	129.32	_VDS(ph)EGDFS(ph)E
O43823	339	S	A-kinase anchor prote	AKAP8	125.45	_S(ph)GDEEFKGEDEL
O43852	44	S	Calumenin	CALU	94.96	_VHNDAQS(ph)FDYDH
O60231	103	S	Putative pre-mRNA-s	DHX16	119.38	_LLEDS(ph)EES(ph)SE
O60231	106	S	Putative pre-mRNA-s	DHX16	119.38	_LLEDS(ph)EES(ph)SE
O60231	160	S	Putative pre-mRNA-s	DHX16	160.43	_QQTEKPES(ph)EDEV
O60264	66	S	SWI/SNF-related mat	SMARCA5	181.87	_GGPEGVAAQAVASA
O60264	116	S	SWI/SNF-related mat	SMARCA5	93.098	_TPTS(ph)PLK_
O60271	730	S	C-Jun-amino-terminal	SPAG9	81.949	_SAS(ph)QSS(ph)LDK
O60271	733	S	C-Jun-amino-terminal	SPAG9	172.52	_SASQSS(ph)LDKLDQ
O60292	172	S	Signal-induced prolife	SIPA1L3	175.28	_SSS(ph)EITLSECDAE
O60292	1175	S	Signal-induced prolife	SIPA1L3	73.233	_YKPS(ph)PER_
O60292	1364	S	Signal-induced prolife	SIPA1L3	117.84	_REVS(ph)PAPAVAGC
O60292	1544	S	Signal-induced prolife	SIPA1L3	143.25	_TLS(ph)DESLCSGR_
O60292	1703	T	Signal-induced prolife	SIPA1L3	128.72	_TT(ph)PTMSEEPPLD
O60293	949	S	Zinc finger C3H1 dom	ZFC3H1	58.32	_LDSS(ph)PVSSPR_
O60293	1303	S	Zinc finger C3H1 dom	ZFC3H1	124.85	_KPISDNSFS(ph)S(ph)
O60293	1304	S	Zinc finger C3H1 dom	ZFC3H1	124.85	_KPISDNSFS(ph)S(ph)
O60318	527	S	80 kDa MCM3-associ	MCM3AP	65.766	_KPGDGEVS(ph)PSTE
O60341	131	S	Lysine-specific histon	KDM1A	151.12	_EMDESLANLS(ph)ED
O60341	137	S	Lysine-specific histon	KDM1A	151.12	_EMDESLANLS(ph)ED
O60341	166	S	Lysine-specific histon	KDM1A	75.46	_KLPPPPPQAPPEEEN
O60504	544	S	Vinexin	SORBS3	100.69	_HPS(ph)SPSALR_
O60508	16	S	Pre-mRNA-processin	CDC40	233.93	_(ac)SAAIAALAASYGS
O60508	22	S	Pre-mRNA-processin	CDC40	301.96	_(ac)SAAIAALAASYGS
O60508	43	S	Pre-mRNA-processin	CDC40	201.95	_S(ph)PSSKPSLAVAV
O60524	417	S	Nuclear export media	NEMF	140.9	_NPYLLS(ph)EEEDDD
O60658	457	S	High affinity cAMP-sp	PDE8A	96.153	_RLS(ph)GNEYVLSTK
O60671	252	S	Cell cycle checkpoint	RAD1	54.982	_GFLS(ph)LQY(ph)MIF
O60671	255	Y	Cell cycle checkpoint	RAD1	54.982	_GFLS(ph)LQY(ph)MIF
O60675	25	S	Transcription factor M	MAFK	106.11	_EAGENAPVLS(ph)DD
O60678	25	S	Protein arginine N-me	PRMT3	115.77	_GAVENEEDLPELS(pl
O60678	27	S	Protein arginine N-me	PRMT3	115.77	_GAVENEEDLPELS(pl
O60716	346	S	Catenin delta-1	CTNND1	89.507	_GS(ph)LAS(ph)LDSLF
O60716	349	S	Catenin delta-1	CTNND1	114.54	_GS(ph)LAS(ph)LDSLF
O60716	864	S	Catenin delta-1	CTNND1	59.005	_SQSSHS(ph)YDDSTL

O60762	9	S	Dolichol-phosphate m	DPM1	72.681	_(ac)ASLEVSRS(ph)PI
O60763	942	S	General vesicular trar	USO1	132.49	_DLGHPVEEEDELES(
O60825	493	S	6-phosphofructo-2-kir	PFKFB2	78.864	_PLKPLS(ph)PLR_
O60832	21	S	H/ACA ribonucleoprot	DKC1	91.594	_KS(ph)LPEEDVAEIQI
O60832	451	S	H/ACA ribonucleoprot	DKC1	227.04	_KRES(ph)ES(ph)ES(p
O60832	453	S	H/ACA ribonucleoprot	DKC1	227.04	_KRES(ph)ES(ph)ES(p
O60832	455	S	H/ACA ribonucleoprot	DKC1	211.43	_KRES(ph)ES(ph)ES(p
O60832	494	S	H/ACA ribonucleoprot	DKC1	208.64	_AGLESGAEPGDGDS
O60832	513	S	H/ACA ribonucleoprot	DKC1	139.31	_AKEVELVS(ph)E_
O60841	113	S	Eukaryotic translation	EIF5B	335.55	_QSFDDNDS(ph)EELE
O60841	135	S	Eukaryotic translation	EIF5B	155.17	_VEMYS(ph)GS(ph)DD
O60841	137	S	Eukaryotic translation	EIF5B	155.17	_VEMYS(ph)GS(ph)DD
O60841	182	S	Eukaryotic translation	EIF5B	202.47	_INS(ph)SGESGDES(p
O60841	190	S	Eukaryotic translation	EIF5B	202.47	_INS(ph)SGESGDES(p
O60841	214	S	Eukaryotic translation	EIF5B	217.5	_NKPGPNIES(ph)GNE
O60885	601	S	Bromodomain-contair	BRD4	109.67	_SKPPPTYES(ph)EEE
O60885	1083	S	Bromodomain-contair	BRD4	26.817	_EAPSPLMIHSPQMSC
O60885	1117	S	Bromodomain-contair	BRD4	47.603	_IHS(ph)PIIR_
O60930	76	S	Ribonuclease H1	RNASEH1	81.315	_KSAS(ph)PEVSEGHE
O60934	432	S	Nibrin	NBN	162.38	_IPNYQLS(ph)PTK_
O75054	1177	S	Immunoglobulin supe	IGSF3	70.718	_EPHLNYS(ph)PTCLE
O75143	361	S	Autophagy-related pr	ATG13	71.354	_AS(ph)PHDVLETIFVF
O75151	474	S	Lysine-specific deme	PHF2	59.005	_EKEEPPS(ph)PIEATF
O75151	539	S	Lysine-specific deme	PHF2	154.6	_ESAS(ph)PTIPNLDLL
O75151	625	S	Lysine-specific deme	PHF2	101.38	_LEKS(ph)PLAGNK_
O75151	882	S	Lysine-specific deme	PHF2	133.74	_DSDYVYPSLES(ph)D
O75151	1059	S	Lysine-specific deme	PHF2	98.572	_RPSASS(ph)PNNNTA
O75152	108	S	Zinc finger CCCH dor	ZC3H11A	52.185	_TVLPTVPES(ph)PEEI
O75152	171	S	Zinc finger CCCH dor	ZC3H11A	145.16	_VESSENVPSPTHPP\
O75179	2067	S	Ankyrin repeat domai	ANKRD17	69.289	_NSPLDCGSAS(ph)PN
O75190	277	S	DnaJ homolog subfar	DNAJB6	64.5	_HAPHCLS(ph)EEEGE
O75367	129	T	Core histone macro-H	H2AFY	148.44	_LEAIIT(ph)PPPAK_
O75369	983	S	Filamin-B	FLNB	86.944	_LDVTILS(ph)PSR_
O75369	2107	S	Filamin-B	FLNB	77.08	_APS(ph)VATVGSICDI
O75369	2478	S	Filamin-B	FLNB	115.58	_LVS(ph)PGSANETSS
O75376	999	S	Nuclear receptor core	NCOR1	54.425	_S(ph)PNREWEVLQP/
O75376	2120	S	Nuclear receptor core	NCOR1	47.815	_VS(ph)PENLVDK_
O75376	2151	S	Nuclear receptor core	NCOR1	143.32	_SHVSSEPYEPIS(ph)I
O75376	2184	S	Nuclear receptor core	NCOR1	158.45	_S(ph)PGSISYLPSFFT
O75376	2438	S	Nuclear receptor core	NCOR1	82.482	_EPAPLLSAQYETLSD
O75379	30	S	Vesicle-associated m	VAMP4	177.4	_NLLEDDS(ph)DEEED
O75381	232	S	Peroxisomal membra	PEX14	49.298	_QFPPS(ph)PSAPK_
O75381	275	S	Peroxisomal membra	PEX14	67.906	_SPSPSSPAAVNHHS
O75385	623	S	Serine/threonine-prot	ULK1	73.834	_NPLPPILGS(ph)PTK_
O75400	373	T	Pre-mRNA-processin	PRPF40A	110.25	_QETVADFT(ph)PK_
O75400	787	S	Pre-mRNA-processin	PRPF40A	48.288	_EPAFEDITLES(ph)EF
O75400	883	S	Pre-mRNA-processin	PRPF40A	75.611	_HKS(ph)DSPES(ph)D
O75400	888	S	Pre-mRNA-processin	PRPF40A	75.611	_HKS(ph)DSPES(ph)D
O75400	932	T	Pre-mRNA-processin	PRPF40A	176.7	_DSGNWDT(ph)S(ph)(
O75400	933	S	Pre-mRNA-processin	PRPF40A	162.26	_DSGNWDT(ph)S(ph)(
O75400	938	S	Pre-mRNA-processin	PRPF40A	263.95	_DSGNWDTSGSELS(p
O75427	25	S	Leucine-rich repeat a	LRCH4	57.573	_(ac)AAAVAAPLAAGG
O75448	873	S	Mediator of RNA poly	MED24	193.77	_LLSSNEDDANILSS(p
O75475	106	S	PC4 and SFRS1-inter	PSIP1	156	_QSNASS(ph)DVEVEE

O75475	118	S	PC4 and SFRS1-inter	PSIP1	146.67	_ETSVS(ph)KEDTDHE
O75475	122	T	PC4 and SFRS1-inter	PSIP1	125.59	_ETSVSKEDT(ph)DHE
O75475	129	S	PC4 and SFRS1-inter	PSIP1	239.49	_ETSVSKEDTDHEEK/
O75475	206	S	PC4 and SFRS1-inter	PSIP1	81.854	_QPCPS(ph)ESDIITEE
O75475	273	S	PC4 and SFRS1-inter	PSIP1	237.71	_TGVTSTS(ph)DS(ph)I
O75475	275	S	PC4 and SFRS1-inter	PSIP1	237.71	_TGVTSTS(ph)DS(ph)I
O75494	129	S	Serine/arginine-rich s	SRSF10	96.489	_S(ph)RS(ph)RS(ph)FI
O75494	131	S	Serine/arginine-rich s	SRSF10	165.54	_S(ph)RS(ph)FDYNYR_
O75494	133	S	Serine/arginine-rich s	SRSF10	165.54	_S(ph)RS(ph)FDYNYR_
O75509	541	S	Tumor necrosis factor	TNFRSF21	53.625	_LENSALLTVEPS(ph)I
O75533	129	S	Splicing factor 3B sub	SF3B1	145.99	_TMIIS(ph)PER_
O75533	142	T	Splicing factor 3B sub	SF3B1	69.181	_LDPFADGGKT(ph)PI
O75533	227	T	Splicing factor 3B sub	SF3B1	40.137	_LSSWDQAETPGHT(p
O75533	273	T	Splicing factor 3B sub	SF3B1	90.545	_GDT(ph)PGHATPGH(
O75533	303	T	Splicing factor 3B sub	SF3B1	75.764	_DT(ph)PGHGSGWAE
O75533	434	T	Splicing factor 3B sub	SF3B1	51.463	_LTAT(ph)PT(ph)PLG(
O75533	436	T	Splicing factor 3B sub	SF3B1	51.463	_LTAT(ph)PT(ph)PLG(
O75569	18	S	Interferon-inducible d	PRKRA	62.088	_EDS(ph)GTFSLGK_
O75626	750	S	PR domain zinc finge	PRDM1	25.978	_LEDVEDDIS(ph)VISV
O75643	225	S	U5 small nuclear ribo	SNRNP200	235.74	_EEAS(ph)DDDM(ox)E
O75665	774	S	Oral-facial-digital syn	OFD1	49.732	_MPLPS(ph)PTESR_
O75683	138	S	Surfeit locus protein 6	SURF6	105.2	_ELS(ph)PAALEK_
O75691	2601	S	Small subunit proces	UTP20	175.59	_AES(ph)DGEEKEEVK
O75821	42	S	Eukaryotic translation	EIF3G	157.75	_GIPLATGDTS(ph)PEI
O75822	11	S	Eukaryotic translation	EIF3J	176.78	_(ac)AAAAAAAGDS(ph
O75909	329	S	Cyclin-K	CCNK	103.2	_KPSPQPSS(ph)PR_
O75909	340	S	Cyclin-K	CCNK	153.81	_AVVVS(ph)PKEENK_
O75925	503	S	E3 SUMO-protein liga	PIAS1	65.949	_GILSLPHQAS(ph)PVS
O75970	230	S	Multiple PDZ domain	MPDZ	54.764	_GSLPQLVS(ph)PIVSI
O75976	1368	T	Carboxypeptidase D	CPD	238.86	_SLLSHEFQDET(ph)D
O75976	1370	T	Carboxypeptidase D	CPD	238.86	_SLLSHEFQDET(ph)D
O76021	361	S	Ribosomal L1 domain	RSL1D1	222.62	_ATNES(ph)EDEIPQLV
O76021	392	S	Ribosomal L1 domain	RSL1D1	89.467	_KS(ph)PAKS(ph)PNP
O76021	396	S	Ribosomal L1 domain	RSL1D1	89.467	_KS(ph)PAKS(ph)PNP
O76080	48	S	AN1-type zinc finger p	ZFAND5	133.58	_MS(ph)PMGTASGSN
O76094	621	S	Signal recognition par	SRP72	72.214	_TVSS(ph)PPTSPR_
O94762	815	S	ATP-dependent DNA	RECQL5	90.964	_YTGEEDGAGGHS(ph
O94769	304	S	Extracellular matrix pr	ECM2	58.955	_S(ph)PLPAPPR_
O94776	435	S	Metastasis-associate	MTA2	58.272	_GHLSRPEAQSLS(ph)
O94826	91	S	Mitochondrial import r	TOMM70A	219.3	_AS(ph)PAPGSGHPE(
O94842	178	S	TOX high mobility gro	TOX4	78.758	_LSTTPS(ph)PTSSLHI
O94864	108	S	STAGA complex 65 s	SUPT7L	146.94	_TEESEPLPSCPGS(pI
O94876	382	S	Transmembrane and	TMCC1	106.58	_FGS(ph)ADNIPNLK_
O94876	413	S	Transmembrane and	TMCC1	130.72	_ALGVISNFQS(ph)SPI
O94880	208	S	PHD finger protein 14	PHF14	67.253	_NRPLLDFVSMEELNI
O94880	287	T	PHD finger protein 14	PHF14	172.2	_NSADDEELT(ph)NDS
O94880	290	S	PHD finger protein 14	PHF14	172.2	_NSADDEELT(ph)NDS
O94880	781	S	PHD finger protein 14	PHF14	79.731	_NSYWQCSECDQAGS
O94880	782	S	PHD finger protein 14	PHF14	79.731	_NSYWQCSECDQAGS
O94880	835	S	PHD finger protein 14	PHF14	73.834	_S(ph)FVPEEEKHEER
O94913	489	S	Pre-mRNA cleavage	PCF11	113.11	_SRS(ph)PIIHS(ph)PK_
O94913	494	S	Pre-mRNA cleavage	PCF11	113.11	_SRS(ph)PIIHS(ph)PK_
O94913	1493	S	Pre-mRNA cleavage	PCF11	88.688	_IYHPSCYEDYQNTSS
O94916	561	S	Nuclear factor of activ	NFAT5	147.49	_EISS(ph)PARPCSFEI

O94923	73	S	D-glucuronyl C5-epim	GLCE	64.476	_QQS(ph)EEAFPQEQ(
O94979	527	S	Protein transport prot	SEC31A	84.741	_DSDQVAQS(ph)DGEI
O94979	799	S	Protein transport prot	SEC31A	136.71	_AQGEPVAGHES(ph)I
O94979	1163	S	Protein transport prot	SEC31A	100.39	_EQTLS(ph)PTITSGLH
O94992	237	S	Protein HEXIM1	HEXIM1	77.438	_SDDT(ph)S(ph)DDDF
O94992	252	S	Protein HEXIM1	HEXIM1	80.136	_SDDT(ph)S(ph)DDDF
O95071	1549	S	E3 ubiquitin-protein li	UBR5	106.67	_RIS(ph)QSQPVR_
O95104	154	S	Splicing factor, arginir	SCAF4	122.71	_IEIIQPLLDMAAGTSN
O95171	68	S	Sciellin	SCEL	61.235	_HNS(ph)HDALDR_
O95197	30	S	Reticulon-3	RTN3	62.253	_(ac)AEPSAATQSHSI
O95218	120	S	Zinc finger Ran-bindir	ZRANB2	306.69	_ENVEYIEREES(ph)D(
O95218	153	S	Zinc finger Ran-bindir	ZRANB2	400.69	_EVEDKES(ph)EGEEE
O95218	188	S	Zinc finger Ran-bindir	ZRANB2	223.76	_YNLDAS(ph)EEEDSN
O95232	3	S	Luc7-like protein 3	LUC7L3	138.66	_(ac)MIS(ph)AAQLLDE
O95239	1225	S	Chromosome-associa	KIF4A;KIF4B	92.098	_ALASNTSFFSGCS(ph
O95251	162	S	Histone acetyltransfe	KAT7	82.635	_DMSLKDS(ph)GS(ph)
O95251	164	S	Histone acetyltransfe	KAT7	82.635	_DMSLKDS(ph)GS(ph)
O95297	219	S	Myelin protein zero-lik	MPZL1	62.813	_KS(ph)PSDTEGLVK_
O95359	2317	S	Transforming acidic c	TACC2	121.09	_LDNTPAS(ph)PPRS(p
O95359	2321	S	Transforming acidic c	TACC2	121.09	_LDNTPAS(ph)PPRS(p
O95365	526	S	Zinc finger and BTB c	ZBTB7A	189.38	_GGAPDPSPGATATP(
O95365	549	S	Zinc finger and BTB c	ZBTB7A	53.186	_HFKDEDEDEDVAS(p
O95391	235	S	Pre-mRNA-splicing fa	SLU7	122.65	_DHNS(ph)EDEDEDK
O95400	49	S	CD2 antigen cytoplas	CD2BP2	249.51	_HSLDS(ph)DEEEDDD
O95425	221	S	Supervillin	SVIL	203.33	_QAHDLS(ph)PAAESS
O95425	245	S	Supervillin	SVIL	229.68	_DSSFTEVPRS(ph)PK
O95425	261	S	Supervillin	SVIL	198.05	_S(ph)PSFGDPQLS(ph
O95425	263	S	Supervillin	SVIL	171.85	_SPS(ph)FGDPQLS(ph
O95425	270	S	Supervillin	SVIL	198.05	_S(ph)PSFGDPQLS(ph
O95425	968	S	Supervillin	SVIL	144.68	_YGS(ph)FEEAEASYP
O95425	1322	S	Supervillin	SVIL	90.308	_S(ph)PVEMDEDFDVI
O95453	619	S	Poly(A)-specific ribon	PARN	92.703	_ELS(ph)PAGSISK_
O95453	628	S	Poly(A)-specific ribon	PARN	150.76	_NS(ph)PATLFEVPDT
O95466	1031	S	Formin-like protein 1	FMNL1	121.19	_GEPPAPKS(ph)PPK_
O95674	21	S	Phosphatidate cytidyl	CDS2	167.1	_VAHEPVAPPEDKES(
O95674	33	S	Phosphatidate cytidyl	CDS2	67.646	_VDGETAS(ph)DSESF
O95684	156	S	FGFR1 oncogene par	FGFR1OP	87.357	_EKGPTTGEGALDLSD
O95684	160	S	FGFR1 oncogene par	FGFR1OP	87.357	_EKGPTTGEGALDLSD
O95696	18	S	Bromodomain-contair	BRD1	43.501	_HPSS(ph)PCSVK_
O95696	128	S	Bromodomain-contair	BRD1	119.88	_IVEYS(ph)PPSAPR_
O95696	1052	S	Bromodomain-contair	BRD1	119	_VHGEPTS(ph)DLS(ph
O95696	1055	S	Bromodomain-contair	BRD1	119	_VHGEPTS(ph)DLS(ph
O95747	339	S	Serine/threonine-prot	OXSR1	158.94	_TEDGGWEWS(ph)DD
O95772	15	S	MLN64 N-terminal do	STARD3NL	87.111	_(ac)MNHLPEDMENAL
O95772	18	S	MLN64 N-terminal do	STARD3NL	87.111	_(ac)MNHLPEDMENAL
O95772	21	S	MLN64 N-terminal do	STARD3NL	87.111	_(ac)MNHLPEDMENAL
O95772	210	S	MLN64 N-terminal do	STARD3NL	62.554	_AALIPGGLSDGQFYS
O95772	214	S	MLN64 N-terminal do	STARD3NL	71.267	_AALIPGGLSDGQFY(p
O95772	218	S	MLN64 N-terminal do	STARD3NL	71.267	_AALIPGGLSDGQFY(p
O95785	983	S	Protein Wiz	WIZ	54.09	_GLGHPPSS(ph)PLLK
O95785	1012	S	Protein Wiz	WIZ	52.132	_SPQLSLS(ph)PR_
O95810	203	S	Serum deprivation-res	SDPR	93.339	_SLEETLHTVDLS(ph)S
O95810	204	S	Serum deprivation-res	SDPR	93.339	_SLEETLHTVDLS(ph)S
O95810	218	S	Serum deprivation-res	SDPR	90.935	_SLEETLHTVDLS(ph)S

O95810	293	S	Serum deprivation-re	SDPR	91.518	_VS(ph)PLTFGR_
O95810	366	S	Serum deprivation-re	SDPR	215.49	_GSNS(ph)GMDSNIDL
O95817	377	S	BAG family molecular	BAG3	99.7	_VPPAPVPCPPPS(ph)
O95817	385	S	BAG family molecular	BAG3	99.423	_VPPAPVPCPPPS(ph)
O95817	386	S	BAG family molecular	BAG3	139.67	_VPPAPVPCPPPSPGI
O95831	116	S	Apoptosis-inducing fa	AIFM1	58.848	_AALS(ph)ASEGEEVP
O95831	268	S	Apoptosis-inducing fa	AIFM1	69.915	_SLS(ph)AIDR_
O96013	181	S	Serine/threonine-prot	PAK4	77.469	_DKRPLS(ph)GPDVGT
O96013	474	S	Serine/threonine-prot	PAK4	154.46	_S(ph)LVGTPYWMAPI
P00352	6	T	Retinal dehydrogenas	ALDH1A1	168.66	_(ac)S(ph)SSGT(ph)PI
P00533	693	T	Epidermal growth fac	EGFR	228.01	_ELVEPLT(ph)PSGEA
P00533	991	S	Epidermal growth fac	EGFR	89.911	_MHLPS(ph)PTDSNFY
P00533	1026	S	Epidermal growth fac	EGFR	123.62	_ALMDEEDMDDVVDA
P00533	1166	S	Epidermal growth fac	EGFR	63.979	_GSHQIS(ph)LDNPDY
P00558	203	S	Phosphoglycerate kin	PGK1	128.38	_ALES(ph)PERPFLAIL
P01106	64	S	Myc proto-oncogene	MYC;MYCN	78.95	_KFELLPTPPLSPS(ph
P02545	22	S	Prelamin-A/C;Lamin-/	LMNA	149.52	_SGAQASSTPLS(ph)P
P02545	24	T	Prelamin-A/C;Lamin-/	LMNA	109.87	_SGAQASSTPLSPT(pI
P02545	301	S	Prelamin-A/C;Lamin-/	LMNA	115.58	_IDS(ph)LSAQLSQLQI
P02545	390	S	Prelamin-A/C;Lamin-/	LMNA	143.25	_LRLS(ph)PS(ph)PTSC
P02545	392	S	Prelamin-A/C;Lamin-/	LMNA	122.12	_LRLS(ph)PS(ph)PTSC
P02545	404	S	Prelamin-A/C;Lamin-/	LMNA	124.73	_ASS(ph)HSSQTQGG(
P02545	406	S	Prelamin-A/C;Lamin-/	LMNA	188.54	_ASSHS(ph)SQTQGG(
P02545	414	S	Prelamin-A/C;Lamin-/	LMNA	132.76	_ASSHSSQTQGGGS(p
P02545	458	S	Prelamin-A/C;Lamin-/	LMNA	228.94	_NKS(ph)NEDQSMGN
P02545	533	S	Prelamin-A/C;Lamin-/	LMNA	43.208	_TALINS(ph)TGEEVAM
P04183	13	S	Thymidine kinase, cyt	TK1	125.23	_(ac)SCINLPTVLPGS(p
P04424	254	S	Argininosuccinate lya	ASL	32.548	_DFVAEFLFWAS(ph)L
P04792	15	S	Heat shock protein be	HSPB1	113.93	_GPS(ph)WDPFR_
P04792	82	S	Heat shock protein be	HSPB1	108.68	_QLS(ph)SGVSEIR_
P04920	173	S	Anion exchange prote	SLC4A2	58.479	_TSPSS(ph)PAPLPHQ
P05114	89	S	Non-histone chromos	HMGN1	31.089	_TEESPAS(ph)DEAGE
P05387	86	S	60S acidic ribosomal	RPLP2	58.012	_LASVPAGGAVAVSAA
P05387	102	S	60S acidic ribosomal	RPLP2;RPLP1	265.7	_KEES(ph)EES(ph)DD
P05387	105	S	60S acidic ribosomal	RPLP2;RPLP1	280.62	_KEES(ph)EES(ph)DD
P05412	63	S	Transcription factor A	JUN	74.793	_NSDLLTS(ph)PDVGL
P05412	243	S	Transcription factor A	JUN	45.349	_EEPQTVPEMPGETP
P05455	92	S	Lupus La protein	SSB	82.87	_S(ph)PSKPLPEVTDE
P05455	366	S	Lupus La protein	SSB	284.21	_FAS(ph)DDEHDEHDE
P05783	7	S	Keratin, type I cytosk	KRT18	96.665	_S(ph)TFSTNYR_
P05783	10	S	Keratin, type I cytosk	KRT18	92.538	_STFS(ph)TNYR_
P05783	15	S	Keratin, type I cytosk	KRT18	174.47	_S(ph)LGSVQAPSYGA
P05783	18	S	Keratin, type I cytosk	KRT18	182.57	_SLGS(ph)VQAPSYGA
P05783	23	S	Keratin, type I cytosk	KRT18	150.39	_SLGSVQAPS(ph)YGA
P05783	31	S	Keratin, type I cytosk	KRT18	198.24	_PVSS(ph)AASVYAGA
P05783	34	S	Keratin, type I cytosk	KRT18	205.96	_PVSSAAS(ph)VYAGA
P05783	36	Y	Keratin, type I cytosk	KRT18	118.5	_PVSSAASVY(ph)AGA
P05783	42	S	Keratin, type I cytosk	KRT18	172.24	_PVSSAASVYAGAGG
P05783	60	S	Keratin, type I cytosk	KRT18	259.25	_GGMGS(ph)GGLATG
P05783	100	S	Keratin, type I cytosk	KRT18	105.65	_VRS(ph)LETENR_
P05783	398	S	Keratin, type I cytosk	KRT18	134.14	_LLEDGEDFNLGDALD
P05783	399	S	Keratin, type I cytosk	KRT18	218.94	_LLEDGEDFNLGDALD
P05783	401	S	Keratin, type I cytosk	KRT18	176.01	_LLEDGEDFNLGDALD
P06400	373	T	Retinoblastoma-asso	RB1	83.871	_KSNLDEEVNVIPPHT

P06454	2	S	Prothymosin alpha;Th	PTMA	81.157	_(ac)S(ph)DAAVDTSSI
P06748	4	S	Nucleophosmin	NPM1	208.34	_(ac)MEDS(ph)MDMDM
P06748	10	S	Nucleophosmin	NPM1	212.39	_(ac)MEDSMDMDMS(p
P06748	70	S	Nucleophosmin	NPM1	309.35	_DELHIVEAEAMNYEG
P06748	125	S	Nucleophosmin	NPM1	258.91	_CGSGPVHISGQHLVA
P07199	156	S	Major centromere aut	CENPB	195.25	_TPAAPAS(ph)PAAVP
P07355	12	S	Annexin A2;Putative a	ANXA2;ANXA2P2	67.11	_LS(ph)LEGDHSTPPS
P07355	19	T	Annexin A2;Putative a	ANXA2;ANXA2P2	139.7	_LSLEGDHST(ph)PPS
P07814	885	S	Bifunctional glutamat	EPRS	183.75	_EYIPGQPPLSQSSDS
P07900	231	S	Heat shock protein H	HSP90AA1	115.8	_DKEVS(ph)DDEAEEK
P07900	263	S	Heat shock protein H	HSP90AA1	381.84	_ESEDKPEIEDVGS(ph
P07910	233	S	Heterogeneous nucle	HNRNPC	227.46	_NDKS(ph)EEEQSSSS
P07910	241	S	Heterogeneous nucle	HNRNPC	112.34	_SEEEQSSSS(ph)VKK
P07910	253	S	Heterogeneous nucle	HNRNPC	333.94	_MES(ph)EGGADDS(p
P07910	260	S	Heterogeneous nucle	HNRNPC	428.08	_MES(ph)EGGADDS(p
P07919	61	S	Cytochrome b-c1 com	UQCRH	167.51	_S(ph)HTEEDCTEELF
P07948	13	S	Tyrosine-protein kina	LYN	152.01	_GKDSLS(ph)DDGVDL
P08047	7	S	Transcription factor S	SP1	111.45	_(ac)SDQDHS(ph)MDE
P08048	270	S	Zinc finger Y-chromos	ZFY;ZFX	51.229	_ADPGEDDLGGTVDIV
P08195	165	S	4F2 cell-surface antig	SLC3A2	127.32	_FTGLS(ph)KEELLK_
P08238	226	S	Heat shock protein H	HSP90AB1	283.64	_EKEIS(ph)DDEAEEE
P08238	255	S	Heat shock protein H	HSP90AB1;HSP9	253.31	_IEDVGS(ph)DEEDDS
P08621	226	S	U1 small nuclear ribo	SNRNP70	132.51	_YDERPGPS(ph)PLPH
P08648	127	S	Integrin alpha-5;Integ	ITGA5	179.42	_LLESSLSS(ph)SEGEI
P08651	323	S	Nuclear factor 1 C-typ	NFIC	229.51	_NWTEDMEGGISS(ph
P08651	333	S	Nuclear factor 1 C-typ	NFIC	144.55	_TEMDKS(ph)PFNSPS
P08651	339	S	Nuclear factor 1 C-typ	NFIC	209.66	_TEMDKS(ph)PFNSPS
P08670	42	S	Vimentin	VIM	91.657	_TYSLGS(ph)ALRPST
P08670	55	S	Vimentin	VIM	168.05	_SLYAS(ph)SPGGVYA
P08670	56	S	Vimentin	VIM	174.87	_SLYASS(ph)PGGVYA
P08670	73	S	Vimentin	VIM	111.26	_LRSS(ph)VPGVR_
P08670	205	S	Vimentin	VIM	135.81	_EEAENTLQS(ph)FR_
P08670	325	S	Vimentin	VIM	178.22	_QVQS(ph)LTCEVDAL
P08670	412	S	Vimentin	VIM	91.657	_IS(ph)LPLPNFSSLNL
P08670	420	S	Vimentin	VIM	185.71	_ISLPLPNFSS(ph)LNL
P08670	430	S	Vimentin	VIM	161.55	_ETNLDS(ph)LPLVDTH
P08670	438	S	Vimentin	VIM	69.088	_ETNLDSLPLVDTHS(p
P08670	459	S	Vimentin	VIM	167.63	_DGQVINETS(ph)QHH
P09496	105	S	Clathrin light chain A	CLTA	42.864	_LQS(ph)EPESIR_
P09651	2	S	Heterogeneous nucle	HNRNPA1	157.54	_(ac)S(ph)KSESPKEPI
P09651	4	S	Heterogeneous nucle	HNRNPA1	136.66	_(ac)SKS(ph)ES(ph)PK
P09651	6	S	Heterogeneous nucle	HNRNPA1	171.73	_SES(ph)PKEPEQLR_
P0C1Z6	180	S	TCF3 fusion partner	TFPT	167.34	_TPAPPEPGS(ph)PAP
P0C1Z6	249	S	TCF3 fusion partner	TFPT	110.6	_LLPYPTLAS(ph)PAS(
P0C1Z6	252	S	TCF3 fusion partner	TFPT	110.6	_LLPYPTLAS(ph)PAS(
P0C7T5	361	S	Ataxin-1-like	ATXN1L	60.561	_KEEPS(ph)PLNLSHH
P0DJ93	58	S	Small integral membr	SMIM13	84.48	_ELVGDTGSQEGDHE
P0DJ93	60	S	Small integral membr	SMIM13	84.48	_ELVGDTGSQEGDHE
P10075	86	S	Zinc finger protein GL	GLI4	123.63	_S(ph)PGSQAPDEGA(
P10398	582	S	Serine/threonine-prot	ARAF;RAF1	112.13	_SAS(ph)EPSLHR_
P10412	2	S	Histone H1.4	HIST1H1E	120.22	_(ac)S(ph)ETAPAAPA
P10412	18	T	Histone H1.4	HIST1H1E	180.21	_SETAPAAPAAPAPAE
P10451	219	S	Osteopontin	SPP1	175.93	_AIPVAQDLNAPSDWI
P10451	224	S	Osteopontin	SPP1	106.4	_GKDS(ph)YETSQLDI

P10451	234	S	Osteopontin	SPP1	106.4	_GKDS(ph)YETSQLDD
P10451	275	S	Osteopontin	SPP1	69.649	_EFHS(ph)HEFHS(ph)I
P10451	280	S	Osteopontin	SPP1	69.649	_EFHS(ph)HEFHS(ph)I
P10644	83	S	cAMP-dependent pro	PRKAR1A	164.41	_EDEIS(ph)PPPPNPV
P10809	70	S	60 kDa heat shock pr	HSPD1	160.81	_TVIIEQSWGS(ph)PK_
P11388	4	S	DNA topoisomerase 2	TOP2A	100.28	_(ac)MEVS(ph)PLQPV
P11388	1106	S	DNA topoisomerase 2	TOP2A	355.17	_VPDEEENEES(ph)DN
P11388	1213	S	DNA topoisomerase 2	TOP2A	189.11	_TQMAEVLPS(ph)PR_
P11388	1247	S	DNA topoisomerase 2	TOP2A	279.95	_NENTEGS(ph)PQEDC
P11388	1332	S	DNA topoisomerase 2	TOP2A	103.02	_FTMDLDS(ph)DEDFS
P11388	1337	S	DNA topoisomerase 2	TOP2A	103.02	_FTMDLDS(ph)DEDFS
P11388	1343	T	DNA topoisomerase 2	TOP2A	98.74	_FTMDLDS(ph)DEDFS
P11388	1351	S	DNA topoisomerase 2	TOP2A	75.46	_FTMDLDS(ph)DEDFS
P11388	1377	S	DNA topoisomerase 2	TOP2A	164.66	_SVVS(ph)DLEADDVK
P11388	1393	S	DNA topoisomerase 2	TOP2A	143.36	_GSVPLSSS(ph)PPAT
P11388	1469	S	DNA topoisomerase 2	TOP2A	86.357	_RKPS(ph)TS(ph)DDS
P11388	1471	S	DNA topoisomerase 2	TOP2A	86.357	_RKPS(ph)TS(ph)DDS
P11388	1474	S	DNA topoisomerase 2	TOP2A	86.357	_RKPS(ph)TS(ph)DDS
P11388	1525	S	DNA topoisomerase 2	TOP2A	142.08	_YLEES(ph)DEDDLF_
P11511	153	S	Cytochrome P450 19	CYP19A1	48.981	_ALS(ph)GPGLVR_
P11717	2409	S	Cation-independent m	IGF2R	239.97	_ALSSLHGDDQDS(ph)
P11717	2484	S	Cation-independent m	IGF2R	272.95	_LVSFHDDS(ph)DEDL
P11831	224	S	Serum response fact	SRF	137.69	_ALIQTCLNSPDS(ph)F
P12270	379	S	Nucleoprotein TPR	TPR	74.525	_GAILSEEELAAMS(ph
P12270	2155	S	Nucleoprotein TPR	TPR	123.12	_TDGFAEAIHS(ph)PQ
P12694	337	S	2-oxoisovalerate dehy	BCKDHA	135.23	_IGHHS(ph)TSDDSSA
P12694	347	S	2-oxoisovalerate dehy	BCKDHA	132.79	_S(ph)VDEVNYWDK_
P12931	17	S	Proto-oncogene tyros	SRC	185.2	_S(ph)LEPAENVHGAG
P12956	222	S	X-ray repair cross-cor	XRCC6	46.156	_DIIS(ph)IAEDEDLR_
P12956	455	T	X-ray repair cross-cor	XRCC6	79.492	_IMAT(ph)PEQVGK_
P13807	645	S	Glycogen [starch] syn	GYS1	60.55	_PASVPPS(ph)PSLSR
P13861	78	S	cAMP-dependent pro	PRKAR2A	186.96	_VADAKGDS(ph)ES(ph
P13861	80	S	cAMP-dependent pro	PRKAR2A	186.96	_VADAKGDS(ph)ES(ph
P14543	600	S	Nidogen-1	NID1	30.564	_DGAS(ph)PSR_
P14618	37	S	Pyruvate kinase isozy	PKM	115.83	_LDIDS(ph)PPITAR_
P14866	101	S	Heterogeneous nucle	HNRNPL	121.21	_TPAS(ph)PVVHIR_
P14923	182	S	Junction plakoglobin	JUP	118.31	_ALMGS(ph)PQLVAAV
P15336	112	S	Cyclic AMP-depende	ATF2	157.74	_MPLDLS(ph)PLATPIIF
P15408	120	S	Fos-related antigen 2	FOSL2	121.45	_RRDEQLS(ph)PEEEE
P15408	200	S	Fos-related antigen 2	FOSL2	137.21	_S(ph)PPAPGLQPMR_
P15408	230	S	Fos-related antigen 2	FOSL2	98.545	_QEPLEEDS(ph)PSSS
P15531	94	T	Nucleoside diphosph	NME1;NME2;NME	85.61	_VMLGET(ph)NPADSK
P15924	2209	S	Desmoplakin	DSP	88.495	_SMS(ph)FQGIR_
P15924	2825	S	Desmoplakin	DSP	77.959	_GLPSPYNMS(ph)SAF
P16070	706	S	CD44 antigen	CD44	196.84	_S(ph)QEMVHLVNK_
P16157	15	S	Ankyrin-1	ANK1	36.417	_EADAATS(ph)FLR_
P16402	2	S	Histone H1.3	HIST1H1D	114.55	_(ac)S(ph)ETAPLAPTII
P16402	18	T	Histone H1.3	HIST1H1D	167.67	_(ac)SETAPLAPTIPAP
P16402	37	S	Histone H1.4;Histone	HIST1H1E;HIST1I	135.18	_KAS(ph)GPPVSELITK
P16402	180	T	Histone H1.3	HIST1H1D	93.096	_KVKT(ph)PQPK_
P16403	2	S	Histone H1.2	HIST1H1C	101.38	_(ac)S(ph)ETAPAAPA
P16615	663	S	Sarcoplasmic/endopl	ATP2A2	146.59	_EFDELNPS(ph)AQR_
P16949	25	S	Stathmin	STMN1	132.79	_ASGQAFELILS(ph)PF
P16949	38	S	Stathmin	STMN1	123.76	_ESVPEFPLS(ph)PPK_

P16989	34	S	Y-box-binding protein	YBX3	120.65	_S(ph)PVGSGAPQAA
P17029	13	S	Zinc finger protein wit	ZKSCAN1	74.147	_EATGLS(ph)PQAAQE
P17029	208	S	Zinc finger protein wit	ZKSCAN1	58.712	_ALPAAHIPAPPHEGS
P17096	36	S	High mobility group pı	HMGA1	110.98	_KQPPVS(ph)PGTALV
P17096	44	S	High mobility group pı	HMGA1	96.068	_KQPPVSPGTALVGS(
P17096	53	T	High mobility group pı	HMGA1	85.554	_EPSEVPT(ph)PK_
P17096	99	S	High mobility group pı	HMGA1	171	_LEKEEEEGIS(ph)QE
P17096	102	S	High mobility group pı	HMGA1	264.44	_LEKEEEEGIS(ph)QE
P17096	103	S	High mobility group pı	HMGA1	209.67	_LEKEEEEGIS(ph)QE
P17252	226	S	Protein kinase C alph	PRKCA	200.58	_STLNPQWNES(ph)F
P17252	497	T	Protein kinase C alph	PRKCA;PRKCB;P	124.19	_T(ph)FCGTPDYIAPEI
P17275	259	S	Transcription factor ju	JUNB	60.325	_DAT(ph)PPVS(ph)PIN
P17480	484	S	Nucleolar transcriptio	UBTF	93.345	_GKLPES(ph)PKR_
P17535	100	S	Transcription factor A	JUN;JUND	104.22	_LAS(ph)PELER_
P17535	255	S	Transcription factor ju	JUND	130.22	_LAALKDEPQTVPDVF
P17535	259	S	Transcription factor ju	JUND	130.22	_DEPQTVPDVPSFGE
P17706	304	S	Tyrosine-protein phos	PTPN2	90.561	_EDLSPAFDHS(ph)PN
P17812	575	S	CTP synthase 1	CTPS1	57.173	_SGSSS(ph)PDSEITE
P17936	148	S	Insulin-like growth fac	IGFBP3	127.49	_SAGS(ph)VESPSVSS
P17980	9	S	26S protease regulat	PSMC3	56.768	_(ac)MNLLPNIES(ph)P
P18054	246	S	Arachidonate 12-lipox	ALOX12	39.625	_RSTS(ph)LPSR_
P18206	290	S	Vinculin	VCL	71.592	_DPSAS(ph)PGDAGE
P18206	721	S	Vinculin	VCL	114.31	_S(ph)LLDASEEAIKK_
P18583	152	S	Protein SON	SON	241.01	_SHDDGNIDLES(ph)D
P18583	1556	S	Protein SON	SON	288.75	_EMEHNTVCAAGTS(p
P18583	1697	S	Protein SON	SON	238.08	_ESDQTLAALLS(ph)PI
P18583	1769	S	Protein SON	SON	157.58	_SAAS(ph)PVVSSMPE
P18583	1782	S	Protein SON	SON	112.85	_ASES(ph)S(ph)SEEKI
P18583	1783	S	Protein SON	SON	112.85	_ASES(ph)S(ph)SEEKI
P18583	1784	S	Protein SON	SON	96.55	_ASESS(ph)S(ph)EEKI
P18583	1948	S	Protein SON	SON	92.943	_S(ph)FS(ph)IS(ph)PSI
P18583	1950	S	Protein SON	SON	70.089	_S(ph)FS(ph)IS(ph)PSI
P18583	1952	S	Protein SON	SON	104.22	_S(ph)FSIS(ph)PSR_
P18583	2009	S	Protein SON	SON	137.62	_S(ph)FS(ph)IS(ph)PVI
P18583	2011	S	Protein SON	SON	107.34	_S(ph)FS(ph)IS(ph)PVI
P18583	2013	S	Protein SON	SON	137.62	_S(ph)FS(ph)IS(ph)PVI
P18583	2029	S	Protein SON	SON	77.744	_RFS(ph)RS(ph)PIR_
P18583	2031	S	Protein SON	SON	77.744	_RFS(ph)RS(ph)PIR_
P18583	2129	S	Protein SON	SON	169.73	_EDDDVIVNKPHVS(ph
P18669	118	S	Phosphoglycerate mu	PGAM1;PGAM4	68.074	_S(ph)YDVPPPPMEPI
P18754	11	S	Regulator of chromos	RCC1	103.76	_S(ph)PPADAIPK_
P18858	51	S	DNA ligase 1	LIG1	95.365	_EWNGVVSESDS(ph)
P18858	66	S	DNA ligase 1	LIG1	255.99	_VLGS(ph)EGEEEDEA
P18858	76	S	DNA ligase 1	LIG1	255.99	_VLGS(ph)EGEEEDEA
P18858	141	S	DNA ligase 1	LIG1	202.16	_TIQEVLEEQS(ph)EDI
P18858	183	T	DNA ligase 1	LIG1	98.196	_EGEDGDQPTT(ph)PI
P18858	195	T	DNA ligase 1	LIG1	181.34	_AET(ph)PTESVSEPE
P18887	241	S	DNA repair protein XF	XRCC1	130.4	_AIGSTSKPQES(ph)PI
P18887	447	S	DNA repair protein XF	XRCC1	192.73	_TKPTQAAGPSS(ph)P
P18887	453	T	DNA repair protein XF	XRCC1	192.73	_TKPTQAAGPSS(ph)P
P19338	67	S	Nucleolin	NCL	149.41	_KVVVS(ph)PTK_
P19338	145	S	Nucleolin	NCL	186.46	_KEDS(ph)DEEEDDDS
P19338	153	S	Nucleolin	NCL	212.98	_KEDS(ph)DEEEDDDS
P19338	206	S	Nucleolin	NCL	117.63	_AAAAAPASEDEDDEI

P19634	703	S	Sodium/hydrogen exc	SLC9A1	51.03	_IGS(ph)DPLAYEPK_
P20020	1178	S	Plasma membrane ca	ATP2B1	111.22	_SS(ph)IHNFMTHPEFI
P20020	1193	S	Plasma membrane ca	ATP2B1	207.72	_IEDS(ph)EPHIPLIDDT
P20042	2	S	Eukaryotic translation	EIF2S2	159.18	_(ac)S(ph)GDEM(ox)IF
P20042	105	S	Eukaryotic translation	EIF2S2	105.35	_IES(ph)DVQEPTEPEI
P20042	111	T	Eukaryotic translation	EIF2S2	132.84	_IESDVQEPT(ph)EPEI
P20700	391	S	Lamin-B1;Lamin-B2	LMNB1;LMNB2	107.53	_LKLS(ph)PS(ph)PSSF
P20700	393	S	Lamin-B1;Lamin-B2	LMNB1;LMNB2	104.55	_LKLS(ph)PS(ph)PSSF
P20700	575	T	Lamin-B1	LMNB1	83.818	_TTIPEEEEEEEEAAG
P20810	243	S	Calpastatin	CAST	223.44	_PIGPDDAIDALSSDFT
P20810	364	S	Calpastatin	CAST	269.92	_S(ph)ESELIDELSEDF
P20810	366	S	Calpastatin	CAST	185.33	_SES(ph)ELIDELSEDF
P20810	575	S	Calpastatin	CAST	85.441	_DTSQSDKDLDDALDK
P21127	47	S	Cyclin-dependent kin	CDK11B;CDK11A	119.87	_RDS(ph)LEEGELR_
P21127	234	S	Cyclin-dependent kin	CDK11B;CDK11A	89.698	_S(ph)PPRPPR_
P21127	283	S	Cyclin-dependent kin	CDK11B;CDK11A	203.99	_DLLSDLQDIS(ph)DSE
P21127	589	S	Cyclin-dependent kin	CDK11B;CDK11A	47.96	_EYGS(ph)PLK_
P21127	595	T	Cyclin-dependent kin	CDK11B	106.66	_AYT(ph)PVVVTLWYR
P21127	752	S	Cyclin-dependent kin	CDK11B;CDK11A	124.09	_GTS(ph)PRPPEGGLC
P21291	192	S	Cysteine and glycine-	CSRP1	94.569	_GFGFGQGAGALVHS
P21333	968	S	Filamin-A	FLNA	100.02	_SPFSVAVSPS(ph)LD
P21333	1084	S	Filamin-A	FLNA	165.49	_AFGPGLQGGSAGS(p
P21333	1459	S	Filamin-A	FLNA	162.69	_CSGPGLS(ph)PGMVI
P21333	2152	S	Filamin-A	FLNA	198.61	_APS(ph)VANVGSHCI
P21333	2180	S	Filamin-A	FLNA	200.3	_IPEISIQDMTAQVTS(p
P21333	2327	S	Filamin-A	FLNA	60.419	_FNEEHIPDSPFVVPV.
P21796	104	S	Voltage-dependent ar	VDAC1	265.56	_LTFDSSFS(ph)PNTGI
P22059	190	S	Oxysterol-binding pro	OSBP	221.13	_MLAES(ph)DES(ph)G
P22059	193	S	Oxysterol-binding pro	OSBP	221.13	_MLAES(ph)DES(ph)G
P22059	351	S	Oxysterol-binding pro	OSBP	198.44	_GDMS(ph)DEDDENEI
P22626	159	T	Heterogeneous nucle	HNRNPA2B1	76.586	_GFGFVT(ph)FDDHDF
P22626	259	S	Heterogeneous nucle	HNRNPA2B1	154.35	_GFGDGYNGYGGGPG
P22626	341	S	Heterogeneous nucle	HNRNPA2B1	185.22	_NMGGPYGGGNYGPG
P22626	344	S	Heterogeneous nucle	HNRNPA2B1	244.1	_NMGGPYGGGNYGPG
P22694	198	T	cAMP-dependent pro	PRKACB;PRKAC(	117.62	_TWT(ph)LCGTPEYLA
P23193	100	S	Transcription elongati	TCEA1	208.24	_EPAITSQNS(ph)PEAI
P23246	521	S	Splicing factor, prolin	SFPQ	67.928	_DKLES(ph)EMEDAYH
P23396	221	T	40S ribosomal proteir	RPS3	152.07	_DEILPTT(ph)PISEQK_
P23497	18	S	Nuclear autoantigen S	SP100	113.15	_LNECIS(ph)PVANEMI
P23497	157	S	Nuclear autoantigen S	SP100	114.96	_LPLQES(ph)EEEERE
P23497	409	S	Nuclear autoantigen S	SP100	61.84	_VIGQDHDFSES(ph)S
P23497	410	S	Nuclear autoantigen S	SP100	61.84	_VIGQDHDFSES(ph)S
P23511	326	S	Nuclear transcription	NFYA	90.757	_EKDS(ph)PHMQDPN(
P23528	3	S	Cofilin-1	CFL1	85.493	_(ac)AS(ph)GVAVSDG
P23588	93	S	Eukaryotic translation	EIF4B	123.65	_S(ph)PPYTAFLGNLP
P23588	406	S	Eukaryotic translation	EIF4B	77.192	_ERHPS(ph)WR_
P23588	409	S	Eukaryotic translation	EIF4B	77.08	_ERHPS(ph)WRS(ph)E
P23588	459	S	Eukaryotic translation	EIF4B	141.45	_EEDCHS(ph)PTSKPP
P24534	106	S	Elongation factor 1-be	EEF1B2	223.09	_DDDDIDLFGS(ph)DD
P24928	1882	S	DNA-directed RNA pc	POLR2A	61.959	_YSPT(ph)SPTYS(ph)F
P24928	1910	S	DNA-directed RNA pc	POLR2A	86.488	_YS(ph)PTSPTYS(ph)F
P24928	1913	S	DNA-directed RNA pc	POLR2A	54.418	_YSPTS(ph)PTYSPTSI
P24928	1919	T	DNA-directed RNA pc	POLR2A	154.48	_YSPTSPTYSPT(ph)SI
P24928	1966	S	DNA-directed RNA pc	POLR2A	47.167	_GSTYSPTSPGYSPTS

P25054	1438	T	Adenomatous polypo	APC	114.56	_SKT(ph)PPPPPQTAC
P25054	1567	S	Adenomatous polypo	APC	96.123	_DLLDDS(ph)DDDDIEI
P25205	672	S	DNA replication licen	MCM3	266.63	_SEDES(ph)ETEDEEE
P25205	711	S	DNA replication licen	MCM3	104.4	_DGDSYDPYDFS(ph)D
P25205	722	T	DNA replication licen	MCM3	104.4	_DGDSYDPYDFS(ph)D
P25440	298	S	Bromodomain-contair	BRD2	73.371	_KADTTTPTPTAILAPG
P25440	301	S	Bromodomain-contair	BRD2	73.371	_KADTTTPTPTAILAPG
P25440	633	S	Bromodomain-contair	BRD2	103.85	_TAPPALPTGYDS(ph)
P25490	118	S	Transcriptional repre	YY1	82.349	_EEVVGGDDS(ph)DGI
P25490	247	S	Transcriptional repre	YY1	143.96	_DIDHETVVEEQIIGEN
P25788	250	S	Proteasome subunit a	PSMA3	156.57	_ESLKEEDES(ph)DDD
P26358	714	S	DNA (cytosine-5)-met	DNMT1	241.29	_EADDDEEVDDNIPEM
P26368	2	S	Splicing factor U2AF	U2AF2	170.68	_(ac)S(ph)DFDEFER_
P26368	79	S	Splicing factor U2AF	U2AF2	180.85	_EEHGGLIRS(ph)PR_
P26599	141	S	Polypyrimidine tract-b	PTBP1	55.314	_TDSS(ph)PNQAR_
P27708	1859	S	CAD protein;Glutamir	CAD	62.055	_IHRAS(ph)DPGLPAEI
P27816	280	S	Microtubule-associate	MAP4	266.83	_DMES(ph)PTKLDVTL
P27816	507	S	Microtubule-associate	MAP4	116.06	_DMS(ph)PLS(ph)ETEI
P27816	510	S	Microtubule-associate	MAP4	95.414	_DMS(ph)PLS(ph)ETEI
P27816	521	T	Microtubule-associate	MAP4	184.99	_DVT(ph)PPPETEVVL
P27816	624	S	Microtubule-associate	MAP4	114.33	_GISEDSHLESLQDVG
P27816	636	S	Microtubule-associate	MAP4	107.57	_KCS(ph)LPAEEDSVL
P27816	787	S	Microtubule-associate	MAP4	115.2	_RAS(ph)PSKPASAPA
P27816	1073	S	Microtubule-associate	MAP4	68.134	_VGS(ph)LDNVGHLPA
P27824	554	S	Calnexin	CANX	312.74	_QKS(ph)DAEEDGGTV
P27824	562	T	Calnexin	CANX	317.01	_SDAEEDGGT(ph)VSC
P27824	564	S	Calnexin	CANX	306.28	_SDAEEDGGTVS(ph)C
P27824	583	S	Calnexin	CANX	235.26	_AEEDEILNRS(ph)PR_
P28290	442	T	Sperm-specific antige	SSFA2	110.94	_SVHIST(ph)PEKEPCA
P28290	737	S	Sperm-specific antige	SSFA2	123.4	_S(ph)QS(ph)LPTTLLS
P28290	739	S	Sperm-specific antige	SSFA2	150.01	_S(ph)QS(ph)LPTTLLS
P28290	1055	S	Sperm-specific antige	SSFA2	82.766	_S(ph)ADNLS(ph)CPS(
P28290	1060	S	Sperm-specific antige	SSFA2	79.426	_S(ph)ADNLS(ph)CPS(
P28290	1063	S	Sperm-specific antige	SSFA2	82.766	_S(ph)ADNLS(ph)CPS(
P28290	1134	S	Sperm-specific antige	SSFA2	33.616	_TGVPSTAS(ph)VGK_
P28290	1156	T	Sperm-specific antige	SSFA2	106.76	_ASVALT(ph)PTAPSR_
P28347	11	S	Transcriptional enhan	TEAD1	205.63	_(ac)MEPSSWSGSES
P28370	116	S	Probable global trans	SMARCA1	97.633	_S(ph)PTSPLNMK_
P28370	118	T	Probable global trans	SMARCA1	92.866	_SPT(ph)SPLNMK_
P28370	119	S	Probable global trans	SMARCA1	106.16	_SPT(ph)S(ph)PLNMK_
P28715	526	S	DNA repair protein co	ERCC5	77.031	_ELTPAS(ph)PTCTNS
P28715	562	S	DNA repair protein co	ERCC5	75.564	_FDSSLLS(ph)S(ph)DD
P28715	563	S	DNA repair protein co	ERCC5	75.564	_FDSSLLS(ph)S(ph)DD
P28749	640	S	Retinoblastoma-like p	RBL1	51.495	_DMQPLS(ph)PISVHE
P29317	897	S	Ephrin type-A recepto	EPHA2	150.76	_LPS(ph)TSGSEGVPF
P29317	901	S	Ephrin type-A recepto	EPHA2	148.33	_LPSTSGS(ph)EGVPF
P29323	776	S	Ephrin type-B recepto	EPHB2	108.96	_FLEDDTS(ph)DPTYTS
P29375	1111	S	Lysine-specific deme	KDM5A	121.46	_DLDLEPLS(ph)DLEE(
P29375	1423	S	Lysine-specific deme	KDM5A	46.001	_KS(ph)PLVPR_
P29375	1666	S	Lysine-specific deme	KDM5A	42.185	_QGPVS(ph)PGPAPPI
P29590	8	S	Protein PML	PML	71.933	_(ac)MEPAPARS(ph)P
P29590	518	S	Protein PML	PML	77.51	_AVS(ph)PPHLDGPPS
P29590	527	S	Protein PML	PML	77.51	_AVS(ph)PPHLDGPPS
P29692	133	S	Elongation factor 1-de	EEF1D	188.16	_ATAPQTQHVS(ph)PM

P29692	147	T	Elongation factor 1-d	EEF1D	200.81	_KPAT(ph)PAEDDEDD
P29692	162	S	Elongation factor 1-d	EEF1D	244.51	_KPAT(ph)PAEDDEDD
P29803	291	S	Pyruvate dehydrogen	PDHA2;PDHA1	156.06	_YHGHS(ph)MSDPGV
P29803	298	S	Pyruvate dehydrogen	PDHA2;PDHA1	99.011	_YHGHS(ph)MSDPGV
P29966	27	S	Myristoylated alanine-	MARCKS	193.96	_GEAAAERPGEAAVA
P29966	101	S	Myristoylated alanine-	MARCKS	120.54	_GEPAAAAAPEAGAS
P29966	118	S	Myristoylated alanine-	MARCKS	65.378	_EAPAEGEAAEPGS(p
P29966	145	S	Myristoylated alanine-	MARCKS	88.335	_AEDGATPS(ph)PSNE
P30050	38	S	60S ribosomal protein	RPL12	76.357	_IGPLGLS(ph)PK_
P30086	52	S	Phosphatidylethanola	PEBP1	81.807	_NRPTS(ph)ISWDGLD
P30414	379	S	NK-tumor recognition	NKTR	103.44	_AYRPPS(ph)GEK_
P30414	463	S	NK-tumor recognition	NKTR	101.32	_ILIPS(ph)DIESSK_
P30414	1077	S	NK-tumor recognition	NKTR	88.781	_HDTVTVSS(ph)DLDQ
P30414	1146	S	NK-tumor recognition	NKTR	74.613	_VEETS(ph)PLGNAR_
P30414	1155	T	NK-tumor recognition	NKTR	75.102	_LDT(ph)PDINIVLK_
P31350	20	S	Ribonucleoside-dipho	RRM2	81.696	_VPLAPITDPQQLQLS
P31751	451	T	RAC-beta serine/thre	AKT2	74.364	_YFDDEFTAQSITIT(ph
P31942	216	S	Heterogeneous nucle	HNRNPH3	25.987	_ATENDIANFFS(ph)PL
P31943	23	S	Heterogeneous nucle	HNRNPH1	66.022	_GLPWSCS(ph)ADEV
P31943	104	S	Heterogeneous nucle	HNRNPH1;HNRN	198.76	_HTGPNS(ph)PDTAND
P31943	310	S	Heterogeneous nucle	HNRNPH1;HNRN	116.27	_ATENDIYNFFS(ph)PL
P33176	933	S	Kinesin-1 heavy chair	KIF5B	124.08	_PIRPGQHPAAS(ph)P
P33527	915	S	Multidrug resistance-	ABCC1	84.712	_QLS(ph)SSSSYSGDI
P33527	930	S	Multidrug resistance-	ABCC1	143.56	_HHNS(ph)TAELQK_
P35125	770	S	Ubiquitin carboxyl-ter	USP6	29.135	_DLCGLNSEQILLAEVI
P35221	641	S	Catenin alpha-1	CTNNA1	373.04	_TPEELDDS(ph)DFET
P35222	191	S	Catenin beta-1	CTNNB1	133.16	_S(ph)PQMVSAIVR_
P35232	109	S	Prohibitin	PHB	95.067	_IFTS(ph)IGEDYDER_
P35240	518	S	Merlin	NF2	86.014	_RLS(ph)MEIEK_
P35251	71	S	Replication factor C s	RFC1	113.54	_IIYDSDS(ph)ESEETL
P35251	156	S	Replication factor C s	RFC1	48.998	_NKPLS(ph)PIK_
P35269	224	S	General transcription	GTF2F1	93.505	_IHDLEDDLEMSSDAS
P35269	385	S	General transcription	GTF2F1	113.3	_GNS(ph)RPGTPSAEC
P35579	1943	S	Myosin-9	MYH9	144.23	_KGAGDGS(ph)DEEVI
P35580	1956	S	Myosin-10	MYH10	136.24	_QLHLEGASLELS(ph)I
P35606	859	S	Coatomer subunit bet	COPB2	265.67	_STAQQELDGKPAS(p
P35611	12	S	Alpha-adducin	ADD1	74.793	_AAVVTS(ph)PPPTTAI
P35611	358	S	Alpha-adducin	ADD1	98.804	_SPGS(ph)PVGEGTGS
P35613	362	S	Basigin	BSG	82.177	_RKPEDVLDDDDAGS
P35658	430	S	Nuclear pore comple	NUP214	156.29	_S(ph)PGSTPTTPTSS
P35658	433	S	Nuclear pore comple	NUP214	188.43	_SPGS(ph)TPTT(ph)PT
P35658	437	T	Nuclear pore comple	NUP214	188.43	_SPGS(ph)TPTT(ph)PT
P35658	678	S	Nuclear pore comple	NUP214	76.761	_ITPPAAKPGS(ph)PQA
P35658	940	S	Nuclear pore comple	NUP214	73.36	_VPAKLS(ph)PMK_
P35658	956	T	Nuclear pore comple	NUP214	93.374	_RKT(ph)PPVR_
P35659	13	T	Protein DEK	DEK	138.82	_(ac)SASAPAAEGEGT
P35659	32	S	Protein DEK	DEK	374.33	_EPEMPGPREES(ph)E
P35659	301	S	Protein DEK	DEK	145.14	_KES(ph)ES(ph)EDS(p
P35659	303	S	Protein DEK	DEK	101.41	_KES(ph)ES(ph)EDS(p
P35659	306	S	Protein DEK	DEK	249.12	_KES(ph)ES(ph)EDS(p
P35659	307	S	Protein DEK	DEK	249.12	_KES(ph)ES(ph)EDS(p
P35680	75	S	Hepatocyte nuclear fa	HNF1B	127.95	_GRLS(ph)GDEGS(ph)
P35680	80	S	Hepatocyte nuclear fa	HNF1B	85.441	_GRLS(ph)GDEGS(ph)
P36578	295	S	60S ribosomal protein	RPL4	147.58	_ILKS(ph)PEIQR_

P36915	51	S	Guanine nucleotide-b	GNL1	116.73	_EEQTDTS(ph)DGESV
P37173	548	S	TGF-beta receptor ty	TGFBR2	60.489	_FSELEHLDRLS(ph)G
P37198	408	S	Nuclear pore glycopr	NUP62	79.837	_ELEDLLS(ph)PLEELV
P38159	58	S	RNA-binding motif pr	RBMX;RBMXL1;R	86.005	_GFAFVTFES(ph)PAD
P38159	88	S	RNA-binding motif pr	RBMX	147.09	_VEQATKPS(ph)FESG
P38159	208	S	RNA-binding motif pr	RBMX;RBMXL1	113.69	_RDVYLS(ph)PR_
P38159	251	S	RNA-binding motif pr	RBMX;RBMXL1	128.1	_DYGHSSS(ph)RDDYI
P38159	273	S	RNA-binding motif pr	RBMX;RBMXL1	144.94	_DRDYS(ph)DHPSGG
P38159	284	S	RNA-binding motif pr	RBMX;RBMXL1	75.695	_DYSDHPSGGSYRDS
P38159	352	S	RNA-binding motif pr	RBMX	108.43	_GLPPS(ph)MER_
P38432	122	T	Coilin	COIL	174.02	_AFQLEEGEET(ph)EP
P38919	12	S	Eukaryotic initiation f	EIF4A3	169.02	_(ac)ATTATMATSGS(p
P39880	1059	S	Homeobox protein cu	CUX1	127.16	_TSASCSPAPES(ph)P
P39880	1237	S	Homeobox protein cu	CUX1	128.73	_HSSVSDSQPCEPPS
P39880	1270	S	Homeobox protein cu	CUX1	78.326	_AYQQKPYPS(ph)PK_
P40189	667	S	Interleukin-6 receptor	IL6ST	160.04	_SHIAQWS(ph)PHT(ph
P40189	670	T	Interleukin-6 receptor	IL6ST	101.53	_SHIAQWS(ph)PHT(ph
P40222	515	S	Alpha-taxilin	TXLNA	126.42	_RPEGPGAQAPSS(ph
P40818	718	S	Ubiquitin carboxyl-ter	USP8	162.32	_SYS(ph)SPDITQAIQE
P41208	20	S	Centrin-2	CETN2	161.35	_MS(ph)PKPELTEEQK
P41212	18	T	Transcription factor E	ETV6	81.718	_ISYT(ph)PPES(ph)PV
P41212	22	S	Transcription factor E	ETV6	81.718	_ISYT(ph)PPES(ph)PV
P42166	66	S	Lamina-associated pc	TMPO;TMPO	174.46	_GPPDFS(ph)S(ph)DE
P42166	67	S	Lamina-associated pc	TMPO;TMPO	174.46	_GPPDFS(ph)S(ph)DE
P42166	74	T	Lamina-associated pc	TMPO;TMPO	190.82	_GPPDFSSDEEREPT(
P42166	160	T	Lamina-associated pc	TMPO;TMPO	138.46	_SST(ph)PLPTISSSAE
P42166	351	S	Lamina-associated pc	TMPO	155.06	_SHISDQS(ph)PLSSK_
P42166	424	S	Lamina-associated pc	TMPO	110.44	_FQETEFLS(ph)PPR_
P42167	208	T	Lamina-associated pc	TMPO	79.23	_AKT(ph)PVTLK_
P42167	306	S	Lamina-associated pc	TMPO	183.77	_HAS(ph)PILPITEFSDI
P42345	1162	T	Serine/threonine-prot	MTOR	63.046	_T(ph)LDQSPELR_
P42356	207	S	Phosphatidylinositol 4	PI4KA	62.002	_TSSVSSISQVS(ph)PE
P42566	814	S	Epidermal growth fac	EPS15	49.188	_LNDPFQPFPGNDS(p
P42677	11	S	40S ribosomal protein	RPS27	105.99	_DLLHPS(ph)PEEEK_
P42684	936	S	Abelson tyrosine-prot	ABL2	60.196	_VPVLIS(ph)PTLK_
P42696	28	S	RNA-binding protein 3	RBM34	103.64	_SVQEGENPDDGVRG
P43243	188	S	Matrin-3	MATR3	151.28	_RDS(ph)FDDRGPSLN
P43243	206	S	Matrin-3	MATR3	79.88	_GPSLNPVLDYDHGS(
P43243	598	S	Matrin-3	MATR3	128.06	_SYS(ph)PDGKESPSD
P43243	604	S	Matrin-3	MATR3	93.342	_SYS(ph)PDGKES(ph)
P43307	268	S	Translocon-associate	SSR1	83.724	_VEMGTSSQNDVDMS
P45880	115	S	Voltage-dependent ar	VDAC2	271.19	_LTFDTTFS(ph)PNTGI
P45880	271	S	Voltage-dependent ar	VDAC2	81.565	_LTLS(ph)ALVDGK_
P45973	11	S	Chromobox protein h	CBX5	74.123	_RTADS(ph)S(ph)S(ph
P45973	12	S	Chromobox protein h	CBX5	74.123	_RTADS(ph)S(ph)S(ph
P45973	13	S	Chromobox protein h	CBX5	74.123	_RTADS(ph)S(ph)S(ph
P45973	14	S	Chromobox protein h	CBX5	183.09	_RTADS(ph)S(ph)S(ph
P46013	308	S	Antigen KI-67	MKI67	100.44	_SGGSGHAVAEPAS(p
P46013	357	S	Antigen KI-67	MKI67	363.8	_TPVQYSQQQNS(ph)I
P46013	579	S	Antigen KI-67	MKI67	106.93	_AQSLVIS(ph)PPAPSI
P46013	584	S	Antigen KI-67	MKI67	138.46	_AQSLVISPPAPS(ph)I
P46013	1131	S	Antigen KI-67	MKI67	102.37	_IACKS(ph)PPPESVD
P46013	1376	S	Antigen KI-67	MKI67	189.11	_MPCESS(ph)PPESAI
P46013	1861	S	Antigen KI-67	MKI67	87.652	_ILCKS(ph)PQSDPAD

P46013	1983	S	Antigen KI-67	MKI67	59.983	_ITEVSCKS(ph)PQPDI
P46013	2105	S	Antigen KI-67	MKI67	82.362	_IACKS(ph)PPPESMD
P46013	2223	S	Antigen KI-67	MKI67	86.987	_S(ph)PQPDPVGTPTII
P46013	2344	S	Antigen KI-67	MKI67	84.707	_IACKS(ph)PQPDPVD
P46013	2466	S	Antigen KI-67	MKI67	118.54	_ITEVSCKS(ph)PQPE
P46013	2708	S	Antigen KI-67	MKI67	160.57	_IPCES(ph)PPLEVVDT
P46013	2827	S	Antigen KI-67	MKI67	183.56	_IPCKS(ph)SPELEDTA
P46060	442	S	Ran GTPase-activatir	RANGAP1	67.799	_ILDPNTGEPAPVLSS(
P46087	67	S	Putative ribosomal RI	NOP2	126.26	_TNKS(ph)PEAKPLPG
P46087	181	S	Putative ribosomal RI	NOP2	191.34	_EAAAGIQWS(ph)EEE
P46087	185	T	Putative ribosomal RI	NOP2	87.28	_EAAAGIQWS(ph)EEE
P46087	732	S	Putative ribosomal RI	NOP2	160.43	_GTDTQTPAVLS(ph)P
P46087	786	S	Putative ribosomal RI	NOP2	134.61	_GPQPPTVS(ph)PIR_
P46100	33	S	Transcriptional regula	ATRX	261.69	_LHDFLAHSSEESEET
P46100	92	S	Transcriptional regula	ATRX	192.27	_YVES(ph)DDEKPLDD
P46100	594	S	Transcriptional regula	ATRX	112.01	_LTPVS(ph)LSNS(ph)F
P46100	598	S	Transcriptional regula	ATRX	128.06	_LTPVS(ph)LSNS(ph)F
P46100	662	T	Transcriptional regula	ATRX	57.55	_VKTT(ph)PLR_
P46100	674	T	Transcriptional regula	ATRX	83.165	_RPTETNPVT(ph)S(ph
P46100	675	S	Transcriptional regula	ATRX	220.41	_RPTETNPVT(ph)S(ph
P46100	677	S	Transcriptional regula	ATRX	219.27	_RPTETNPVTSNS(ph)
P46100	703	S	Transcriptional regula	ATRX	197.79	_NS(ph)SDSAIDNPKPI
P46100	704	S	Transcriptional regula	ATRX	87.275	_NSS(ph)DSAIDNPKPI
P46100	729	S	Transcriptional regula	ATRX	134.26	_QSETVDQNS(ph)DS(
P46100	731	S	Transcriptional regula	ATRX	134.26	_QSETVDQNS(ph)DS(
P46100	819	S	Transcriptional regula	ATRX	137.75	_QTQSESSNYDS(ph)E
P46100	889	S	Transcriptional regula	ATRX	154.1	_ETFS(ph)SAEGTVDK
P46100	1011	S	Transcriptional regula	ATRX	97.049	_MEQQYES(ph)S(ph)S
P46100	1012	S	Transcriptional regula	ATRX	97.049	_MEQQYES(ph)S(ph)S
P46100	1013	S	Transcriptional regula	ATRX	97.049	_MEQQYES(ph)S(ph)S
P46100	1061	S	Transcriptional regula	ATRX	140.96	_KKDELS(ph)DYAEK_
P46100	1348	S	Transcriptional regula	ATRX	159.04	_LTVS(ph)DGES(ph)G
P46100	1352	S	Transcriptional regula	ATRX	159.04	_LTVS(ph)DGES(ph)G
P46100	1527	S	Transcriptional regula	ATRX	184	_EVIEIEDAS(ph)PTK_
P46100	1996	S	Transcriptional regula	ATRX	102.98	_ATSSSNPSS(ph)PAP
P46379	113	S	Large proline-rich pro	BAG6	72.191	_APPQTHLPSGASSG
P46379	973	S	Large proline-rich pro	BAG6	144.5	_ENAS(ph)PAPGTTAE
P46783	146	S	40S ribosomal proteir	RPS10;RPS10P5	87.429	_AEAGAGS(ph)ATEFG
P46821	614	S	Microtubule-associate	MAP1B	188.51	_EVPSKEEPS(ph)PVK
P46821	704	T	Microtubule-associate	MAP1B	123.26	_KET(ph)PPKEVK_
P46821	831	S	Microtubule-associate	MAP1B	172.43	_SLMS(ph)S(ph)PEDL
P46821	832	S	Microtubule-associate	MAP1B	172.43	_SLMS(ph)S(ph)PEDL
P46821	937	S	Microtubule-associate	MAP1B	132.36	_FEDEGAGFEESS(ph)
P46821	995	S	Microtubule-associate	MAP1B	86.08	_ESVAS(ph)GDDRAEE
P46821	1016	S	Microtubule-associate	MAP1B	188.33	_GEAEQS(ph)EEEADE
P46821	1154	S	Microtubule-associate	MAP1B	89.659	_DVMSDETNNEETES(
P46821	1256	S	Microtubule-associate	MAP1B	127.1	_VSPSKS(ph)PSLS(ph
P46821	1258	S	Microtubule-associate	MAP1B	119.37	_SPS(ph)LSPSPPS(ph
P46821	1260	S	Microtubule-associate	MAP1B	148.85	_SPSLS(ph)PSPPS(ph
P46821	1265	S	Microtubule-associate	MAP1B	191.44	_SPSLSPSPPS(ph)PLI
P46821	1282	T	Microtubule-associate	MAP1B	76.158	_SVNFSLT(ph)PNEIK_
P46821	1298	S	Microtubule-associate	MAP1B	122.68	_VSAEAEVAPVS(ph)P
P46821	1312	S	Microtubule-associate	MAP1B	114.22	_VSAEAEVAPVS(ph)P
P46821	1322	S	Microtubule-associate	MAP1B	174.19	_TLEVVS(ph)PSQSVT

P46821	1378	S	Microtubule-associate	MAP1B	175.79	_ASVS(ph)PMDEPVPD
P46821	1389	S	Microtubule-associate	MAP1B	180.21	_ASVSPMDEPVPDSE
P46821	1396	S	Microtubule-associate	MAP1B	139.41	_VLS(ph)PLRS(ph)PPL
P46821	1400	S	Microtubule-associate	MAP1B	139.41	_VLS(ph)PLRS(ph)PPL
P46821	1427	S	Microtubule-associate	MAP1B	55.261	_GAES(ph)PFEEK_
P46821	1501	S	Microtubule-associate	MAP1B	233.26	_LGDVS(ph)PTQIDVS
P46821	1620	S	Microtubule-associate	MAP1B	91.076	_PMSIS(ph)PPDFSPK_
P46821	1625	S	Microtubule-associate	MAP1B	165.45	_PMSISPPDFS(ph)PK_
P46821	1779	S	Microtubule-associate	MAP1B	187.78	_VQSLEGEKLS(ph)PK
P46821	1782	S	Microtubule-associate	MAP1B	138.55	_VQSLEGEKLS(ph)PK
P46821	1785	S	Microtubule-associate	MAP1B	99.539	_SDIS(ph)PLT(ph)PR_
P46821	1788	T	Microtubule-associate	MAP1B	138.55	_SDIS(ph)PLT(ph)PR_
P46821	1793	S	Microtubule-associate	MAP1B	152.47	_ESS(ph)PLYS(ph)PTF
P46821	1797	S	Microtubule-associate	MAP1B	152.47	_ESS(ph)PLYS(ph)PTF
P46821	1818	S	Microtubule-associate	MAP1B	174.28	_TATCHSSS(ph)SPPID
P46821	1819	S	Microtubule-associate	MAP1B	191.44	_TATCHSSSS(ph)PPID
P46821	1915	S	Microtubule-associate	MAP1B	183.36	_TTKS(ph)PSDSGYSY
P46821	1949	T	Microtubule-associate	MAP1B	87.676	_T(ph)PEEGGYSYDIS
P46821	1965	S	Microtubule-associate	MAP1B	93.478	_TTS(ph)PPEVSGYSY
P46821	2098	S	Microtubule-associate	MAP1B	118.62	_TELS(ph)PSFINPNPL
P46821	2209	S	Microtubule-associate	MAP1B	80.412	_HMDPPPAPVQDRS(p
P46821	2211	S	Microtubule-associate	MAP1B	80.412	_HMDPPPAPVQDRS(p
P46937	61	S	Yorkie homolog	YAP1	256.79	_GDS(ph)ETDLEALFN
P46937	109	S	Yorkie homolog	YAP1	87.652	_QAS(ph)TDAGTAGAL
P47712	434	S	Cytosolic phospholipa	PLA2G4A	155.04	_HIVSNDS(ph)SDS(ph
P47712	435	S	Cytosolic phospholipa	PLA2G4A	203.74	_HIVSNDSS(ph)DS(ph
P47712	437	S	Cytosolic phospholipa	PLA2G4A	203.74	_HIVSNDS(ph)SDS(ph
P47755	9	S	F-actin-capping protei	CAPZA2	43.557	_(ac)ADLEEQLS(ph)DE
P48634	342	S	Protein PRRC2A	PRRC2A	142.55	_LKFS(ph)DEEDGRDS
P48634	350	S	Protein PRRC2A	PRRC2A	142.55	_LKFS(ph)DEEDGRDS
P48634	808	S	Protein PRRC2A	PRRC2A	90.15	_PLTS(ph)PLR_
P48634	1089	S	Protein PRRC2A	PRRC2A	94.287	_S(ph)EGSEYEEIPK_
P48634	1092	S	Protein PRRC2A	PRRC2A	52.5	_SEGS(ph)EYEEIPK_
P48634	1219	S	Protein PRRC2A	PRRC2A	86.944	_LIPGPLS(ph)PVAR_
P48651	417	S	Phosphatidylserine sy	PTDSS1	130.49	_TYS(ph)ECEDGTYSP
P48681	768	S	Nestin	NES	141.6	_S(ph)LGEQDQMTLRP
P49321	503	S	Nuclear autoantigenic	NASP	114.79	_S(ph)LQENEEEEIGN
P49327	2204	T	Fatty acid synthase;[A	FASN	165.9	_ADEASELACPT(ph)P
P49407	412	S	Beta-arrestin-1	ARRB1	72.755	_GMKDDKEEEEDGTG
P49450	17	S	Histone H3-like centro	CENPA	74.141	_S(ph)PS(ph)PTPTPGP
P49450	19	S	Histone H3-like centro	CENPA	106.66	_S(ph)PS(ph)PTPTPGP
P49589	19	S	Cysteine--tRNA ligase	CARS	87.676	_VQPQWS(ph)PPAGT
P49590	67	S	Probable histidine--tR	HARS2	91.961	_DLS(ph)PQHMVVR_
P49736	27	S	DNA replication licens	MCM2	109.65	_RGNDPLTSS(ph)PGP
P49736	41	S	DNA replication licens	MCM2	137.62	_RTDALTSS(ph)PGR_
P49736	139	S	DNA replication licens	MCM2	228.08	_GLLYDS(ph)DEEDEE
P49756	583	S	RNA-binding protein 2	RBM25	176.94	_QEPES(ph)EEEEEEK
P49756	677	S	RNA-binding protein 2	RBM25	181.86	_LGASNS(ph)PGQPNS
P49756	703	S	RNA-binding protein 2	RBM25	53.3	_FEDEDS(ph)DDVPR_
P49759	140	S	Dual specificity protei	CLK1	124.51	_S(ph)VEDDEEGHLIC
P49761	157	S	Dual specificity protei	CLK3	169.4	_YRS(ph)PEPDPYLSY
P49761	283	S	Dual specificity protei	CLK3	86.772	_S(ph)VEDDKEGHLVC
P49768	367	S	Presenilin-1;Presenilin	PSEN1	152.57	_AAVQELSSS(ph)ILAG
P49790	334	S	Nuclear pore comple	NUP153	91.401	_IPSIVSS(ph)PLNSPLP

P49790	516	S	Nuclear pore comple›	NUP153	102.89	_VQMTS(ph)PSSTGSF
P49792	788	S	E3 SUMO-protein liga	RANBP2;RGPD4;	68.76	_YSLS(ph)PSK_
P49792	1160	S	E3 SUMO-protein liga	RANBP2	158.37	_NHETDGGS(ph)AHGI
P49792	2246	S	E3 SUMO-protein liga	RANBP2;RGPD4;	120.64	_EDALDDSVSSSSVHA
P49792	2251	S	E3 SUMO-protein liga	RANBP2;RGPD4;	289.76	_EDALDDSVSSSSVHA
P49792	2293	T	E3 SUMO-protein liga	RANBP2;RGPD4;	120.64	_LNQSGTSVGT(ph)DE
P49792	2450	T	E3 SUMO-protein liga	RANBP2;RGPD4;	100.13	_DSLIT(ph)PHVS(ph)R
P49792	2454	S	E3 SUMO-protein liga	RANBP2;RGPD4;	100.13	_DSLIT(ph)PHVS(ph)R
P49792	2668	S	E3 SUMO-protein liga	RANBP2	197.35	_NRPDYVS(ph)EEEEL
P49792	2900	S	E3 SUMO-protein liga	RANBP2	68.616	_VGEDEDGS(ph)DEE\
P49810	22	S	Presenilin-2;Presenili	PSEN2	37.009	_TSLMS(ph)AES(ph)P
P49810	25	S	Presenilin-2;Presenili	PSEN2	125.5	_TSLMSAES(ph)PTPR
P49841	215	S	Glycogen synthase ki	GSK3B;GSK3A	74.611	_GEPNVS(ph)YICSR_
P49841	216	Y	Glycogen synthase ki	GSK3B;GSK3A	77.597	_GEPNVSY(ph)ICSR_
P49916	210	S	DNA ligase 3	LIG3	103.88	_LTTTGQVTS(ph)PVK_
P49959	688	S	Double-strand break r	MRE11A	214.3	_GVDFES(ph)S(ph)ED
P49959	689	S	Double-strand break r	MRE11A	214.3	_GVDFES(ph)S(ph)ED
P50402	8	S	Emerin	EMD	171.06	_(ac)MDNYADLS(ph)D
P50402	49	S	Emerin	EMD	179.19	_RLS(ph)PPSSSAASS
P50402	141	S	Emerin	EMD	116.85	_QSVTSFPDADAFHH(
P50402	142	S	Emerin	EMD	82.033	_QSVTSFPDADAFHH(
P50402	143	S	Emerin	EMD	116.85	_QSVTSFPDADAFHH(
P50402	171	S	Emerin	EMD	153.36	_DSAYQSITHYRPVS(p
P50443	12	S	Sulfate transporter	SLC26A2	98.261	_EQHNVS(ph)PRDS(p
P50443	16	S	Sulfate transporter	SLC26A2	98.261	_EQHNVS(ph)PRDS(p
P50502	75	S	Hsc70-interacting pro	ST13	111.81	_KVEEDLKADEPS(ph)
P50502	76	S	Hsc70-interacting pro	ST13	111.81	_KVEEDLKADEPS(ph)
P50502	79	S	Hsc70-interacting pro	ST13	111.81	_KVEEDLKADEPS(ph)
P50613	170	T	Cyclin-dependent kin	CDK7	74.698	_AYT(ph)HQVVTR_
P51003	23	T	Poly(A) polymerase a	PAPOLA	88.311	_HYGIT(ph)SPISLAAP
P51114	409	S	Fragile X mental retar	FXR1	66.959	_RGPNYTSGYGTNSE
P51114	485	S	Fragile X mental retar	FXR1	165.17	_DPDSNPYSLLDNTES
P51116	598	T	Fragile X mental retar	FXR2	110.78	_T(ph)DGSIS(ph)GDR(
P51116	601	S	Fragile X mental retar	FXR2	139.47	_TDGS(ph)IS(ph)GDR(
P51116	603	S	Fragile X mental retar	FXR2	138.54	_TDGS(ph)IS(ph)GDR(
P51397	51	S	Death-associated pro	DAP	66.884	_DKDDQEWESPS(ph)
P51531	1377	S	Probable global trans	SMARCA2	94.203	_GRPPAEKLS(ph)PNP
P51531	1572	S	Probable global trans	SMARCA2	105.72	_AKPVVSDFDS(ph)DE
P51608	80	S	Methyl-CpG-binding p	MECP2	252.66	_AETSEGSGSAPAVPI
P51608	229	S	Methyl-CpG-binding p	MECP2	137.95	_MPFQTS(ph)PGGK_
P51610	3	S	Host cell factor 1;HCF	HCFC1	61.087	_(ac)AS(ph)AVSPANLF
P51610	6	S	Host cell factor 1;HCF	HCFC1	150.99	_(ac)ASAVS(ph)PANLF
P51610	666	S	Host cell factor 1;HCF	HCFC1	46.953	_S(ph)PISVPGGSALIS
P51610	1507	S	Host cell factor 1;HCF	HCFC1	90.955	_AVTTVTQSTPVPGPS
P51636	18	S	Caveolin-2	CAV2	147.35	_ADVQLFMDDDS(ph)Y
P51636	20	S	Caveolin-2	CAV2	146.83	_ADVQLFMDDDSYS(p
P51636	23	S	Caveolin-2	CAV2	147.35	_ADVQLFMDDDS(ph)Y
P51825	199	S	AF4/FMR2 family me	AFF1	48.669	_ELS(ph)PLISLPS(ph)F
P51825	206	S	AF4/FMR2 family me	AFF1	48.669	_ELS(ph)PLISLPS(ph)F
P51825	212	S	AF4/FMR2 family me	AFF1	48.669	_ELS(ph)PLISLPS(ph)F
P51858	132	S	Hepatoma-derived gr	HDGF	223	_KGNAEGS(ph)S(ph)D
P51858	133	S	Hepatoma-derived gr	HDGF	243.54	_KGNAEGS(ph)S(ph)D
P51858	165	S	Hepatoma-derived gr	HDGF	150.11	_RAGDLLEDS(ph)PK_
P51946	315	T	Cyclin-H	CCNH	101	_SKHEEEEWT(ph)DDI

P51991	14	S	Heterogeneous nucle	HNRNPA3	78.674	_(ac)MEVKPPPGRPQI
P51991	358	S	Heterogeneous nucle	HNRNPA3	213.7	_SSGS(ph)PYGGGYG
P52292	61	T	Importin subunit alph	KPNA2	157.14	_NVSSFPDDAT(ph)SP
P52701	137	S	DNA mismatch repair	MSH6	153.72	_VHVQFFDDS(ph)PTR
P52701	227	S	DNA mismatch repair	MSH6	264.92	_SEEDNEIES(ph)EEE
P52701	252	S	DNA mismatch repair	MSH6	70.761	_VIS(ph)DSESDIGGS(
P52732	926	T	Kinesin-like protein K	KIF11	83.087	_LDIPTGTT(ph)PQR_
P52756	59	S	RNA-binding protein	RBM5	103.01	_YDDYRDYDS(ph)PEF
P52756	78	S	RNA-binding protein	RBM5	142.93	_SEDGYHS(ph)DGDY(
P52756	624	S	RNA-binding protein	RBM5	226.08	_GLVAAYSGDS(ph)DN
P52926	44	S	High mobility group p	HMGA2	159.54	_KQQQEPTGEPS(ph)I
P52948	612	S	Nuclear pore comple	NUP98	183.76	_NLNNSNLFS(ph)PVN
P52948	623	S	Nuclear pore comple	NUP98	231.5	_DSENLAS(ph)PSEYP
P52948	670	T	Nuclear pore comple	NUP98	74.853	_PIPQT(ph)PESAGNK_
P52948	888	S	Nuclear pore comple	NUP98	225.41	_YGLQDS(ph)DEEEEE
P52948	934	S	Nuclear pore comple	NUP98	169.85	_PAPPPQSQS(ph)PEV
P53355	333	S	Death-associated pro	DAPK1	155.1	_S(ph)DDTLDEEDSFV
P53396	455	S	ATP-citrate synthase	ACLY	41.399	_TAS(ph)FSESR_
P53396	481	S	ATP-citrate synthase	ACLY	99.092	_AKPAMPQDSVPS(ph
P53674	8	S	Beta-crystallin B1	CRYBB1	39.905	_AS(ph)ASATVAVNPG
P53999	17	S	Activated RNA polym	SUB1	79.177	_ELVSSSSSGSDS(ph)
P53999	118	S	Activated RNA polym	SUB1	56.29	_EQIS(ph)DIDDAVR_
P54105	102	S	Methylosome subunit	CLNS1A	201.17	_FEEESKEPVADEEEE
P54259	168	S	Atrophin-1	ATN1	78.352	_PYHPPPLFPPS(ph)P
P54259	632	S	Atrophin-1	ATN1	49.216	_TAS(ph)PPGPPPYGK
P54274	11	S	Telomeric repeat-binc	TERF1	78.95	_(ac)AEDVSSAAPS(ph
P54727	160	S	UV excision repair pr	RAD23B	146.65	_QEKPAEKPAETPVAT
P55081	52	S	Microfibrillar-associat	MFAP1	173.95	_RPDYAPMES(ph)S(pI
P55081	53	S	Microfibrillar-associat	MFAP1	173.95	_RPDYAPMES(ph)S(pI
P55081	116	S	Microfibrillar-associat	MFAP1	199.36	_IVEPEVVGES(ph)DS(
P55081	118	S	Microfibrillar-associat	MFAP1	220.46	_IVEPEVVGES(ph)DS(
P55081	132	S	Microfibrillar-associat	MFAP1	239.04	_MEREDS(ph)S(ph)EE
P55081	133	S	Microfibrillar-associat	MFAP1	239.04	_MEREDS(ph)S(ph)EE
P55081	267	T	Microfibrillar-associat	MFAP1	278.24	_SLAALDALNT(ph)DDI
P55196	1182	S	Afadin	MLLT4	57.484	_SSPNVANQPPS(ph)F
P55197	689	S	Protein AF-10	MLLT10	67.385	_S(ph)PVSSLQIR_
P55201	460	S	Peregrin	BRPF1	152.32	_RLPALS(ph)HS(ph)EC
P55201	462	S	Peregrin	BRPF1	152.32	_RLPALS(ph)HS(ph)EC
P55201	1076	S	Peregrin	BRPF1	208.16	_GAGWLS(ph)EDEDSI
P55265	614	S	Double-stranded RNA	ADAR	111.66	_S(ph)PVTTLLECMHK_
P55265	825	S	Double-stranded RNA	ADAR	32.415	_S(ph)PEAQPK_
P55317	331	S	Hepatocyte nuclear fa	FOXA1	75.196	_TGQLEGAPAPGPAA
P55884	154	S	Eukaryotic translation	EIF3B	109.75	_ALENGDADEPSFS(p
P55884	164	S	Eukaryotic translation	EIF3B	109.75	_ALENGDADEPSFS(p
P56181	105	S	NADH dehydrogenas	NDUFV3	81.651	_MPQPSSGRES(ph)PI
P56945	639	S	Breast cancer anti-es	BCAR1	50.473	_PLPS(ph)PPK_
P57059	435	S	Serine/threonine-prot	SIK1	156.59	_PVS(ph)PSSLLDTAIS
P57682	250	S	Krueppel-like factor 3	KLF3	105.17	_RPLPVES(ph)PDTQR
P57739	225	S	Claudin-2	CLDN2	86.803	_SEFNSYS(ph)LTGYV
P57740	86	S	Nuclear pore comple	NUP107	100.9	_QPDISCILGTGGKS(p
P60174	58	S	Triosephosphate ison	TPI1	152.48	_KQS(ph)LGELIGTLNA
P60468	17	S	Protein transport prot	SEC61B	211.14	_PGPTPSGTNVGSSG
P60468	19	S	Protein transport prot	SEC61B	110.53	_PGPTPSGTNVGSSG
P60981	3	S	Destrin	DSTN	107.82	_(ac)AS(ph)GVQVADE

P61244	11	S	Protein max	MAX	104.82	_(ac)SDNDDIEVES(ph)
P61247	263	S	40S ribosomal protein	RPS3A	91.006	_ADGYEPPVQES(ph)\
P61978	116	S	Heterogeneous nuclea	HNRNPK	177.58	_IIPTLEEGLQLPS(ph)I
P61978	216	S	Heterogeneous nuclea	HNRNPK	147.12	_IILDLISES(ph)PIK_
P61978	284	S	Heterogeneous nuclea	HNRNPK	137.4	_RDYDDMS(ph)PR_
P61978	379	S	Heterogeneous nuclea	HNRNPK	40.986	_GS(ph)YGDLGGPIITT
P62070	186	S	Ras-related protein R	RRAS2	197.1	_KFQEQECPPS(ph)PE
P62258	210	S	14-3-3 protein epsilon	YWHAE	92.01	_AAFDDAIAELDTLS(p
P62750	43	S	60S ribosomal protein	RPL23A	74.533	_IRTS(ph)PTFR_
P62805	48	S	Histone H4	HIST1H4A	135.55	_RIS(ph)GLIYEETR_
P62995	2	S	Transformer-2 protein	TRA2B	101.6	_(ac)S(ph)DSGEQNYG
P62995	14	S	Transformer-2 protein	TRA2B	223.11	_(ac)SDSGEQNYGERI
P62995	95	S	Transformer-2 protein	TRA2B	125.22	_RHS(ph)HS(ph)HS(ph
P62995	97	S	Transformer-2 protein	TRA2B	156.52	_RHS(ph)HS(ph)HS(ph
P62995	99	S	Transformer-2 protein	TRA2B	143.97	_HSHS(ph)HS(ph)PMS
P62995	102	S	Transformer-2 protein	TRA2B	110.56	_RHS(ph)HS(ph)HSPM
P62995	201	T	Transformer-2 protein	TRA2B	148.7	_RPHT(ph)PTPGIYMG
P63104	207	S	14-3-3 protein zeta/de	YWHAZ	174	_TAFDEAIAELDTLS(pI
P63165	2	S	Small ubiquitin-relate	SUMO1	198.14	_(ac)S(ph)DQEAKPSTI
P67809	165	S	Nuclease-sensitive el	YBX1	183.23	_NYQQNYQNS(ph)ES(
P67809	174	S	Nuclease-sensitive el	YBX1	108.9	_NEGS(ph)ESAPEGQA
P67809	314	S	Nuclease-sensitive el	YBX1	62.532	_AADPPAENSS(ph)AP
P78310	332	S	Coxsackievirus and a	CXADR	59.248	_TPQS(ph)PTLPPAK_
P78316	146	S	Nucleolar protein 14	NOP14	177.4	_HNDIVDS(ph)DS(ph)D
P78316	148	S	Nucleolar protein 14	NOP14	256.75	_HNDIVDS(ph)DS(ph)D
P78332	362	S	RNA-binding protein 6	RBM6	131.96	_EGETQGVAFEHESPA
P78332	1025	S	RNA-binding protein 6	RBM6	87.216	_LQSFDS(ph)PER_
P78344	395	S	Eukaryotic translation	EIF4G2	95.815	_FS(ph)PTMGR_
P78344	508	T	Eukaryotic translation	EIF4G2	109.5	_TQT(ph)PPLGQTPQL
P78346	251	S	Ribonuclease P prote	RPP30	163.92	_KPRPS(ph)EGDEDCL
P78347	210	S	General transcription	GTF2I	48.216	_SILS(ph)PGGSCGPIK
P78356	322	T	Phosphatidylinositol 5	PIP4K2B	74.3	_AEDEECENDGVGGN
P78356	326	S	Phosphatidylinositol 5	PIP4K2B	74.3	_AEDEECENDGVGGN
P78364	645	S	Polyhomeotic-like pro	PHC1	85.185	_KADS(ph)EEERDDVS
P78527	3205	S	DNA-dependent prote	PRKDC	31.054	_LTPLPEDNS(ph)MNV
P78536	791	S	Disintegrin and metall	ADAM17	167.56	_S(ph)FEDLTDHPVTR_
P78545	215	S	ETS-related transcrip	ELF3	177.22	_SSHSSDSGGS(ph)DV
P80723	164	S	Brain acid soluble pro	BASP1	85.925	_S(ph)DGAPASDSKPC
P82094	344	S	TATA element modul	TMF1	130.77	_SVSEINS(ph)DDELSC
P84022	8	T	Mothers against deca	SMAD3	84.753	_(ac)SSILPFT(ph)PPIV
P84103	5	S	Serine/arginine-rich s	SRSF3	118.51	_(ac)MHRDS(ph)CPLD
P85037	213	S	Forkhead box protein	FOXK1	148.36	_EEAPAS(ph)PLRPLYI
P85037	223	S	Forkhead box protein	FOXK1	91.819	_EEAPAS(ph)PLRPLYI
P85037	243	S	Forkhead box protein	FOXK1	177.82	_SMVSPVPS(ph)PTGT
P85037	257	S	Forkhead box protein	FOXK1	63.261	_SMVSPVPS(ph)PTGT
P85037	416	S	Forkhead box protein	FOXK1	120.71	_S(ph)APAS(ph)PTHP(
P85037	420	S	Forkhead box protein	FOXK1	149.52	_SAPAS(ph)PTHPGLM
P85037	428	S	Forkhead box protein	FOXK1	105.22	_SAPAS(ph)PTHPGLM
P85037	445	S	Forkhead box protein	FOXK1	134.93	_EGS(ph)PIPHDPEFG
P86791	266	S	Vacuolar fusion prote	CCZ1;CCZ1B	52.862	_HIEPELAGRDS(ph)PI
P98175	89	S	RNA-binding protein 1	RBM10	139.34	_HS(ph)PTGPPGFPR_
P98175	718	S	RNA-binding protein 1	RBM10	133.15	_LAS(ph)DDRPSPPR_
P98175	723	S	RNA-binding protein 1	RBM10	147.51	_LASDDRPS(ph)PPR_
P98175	736	S	RNA-binding protein 1	RBM10	170.14	_GLVAAYSGES(ph)DS

P98175	738	S	RNA-binding protein 1	RBM10	270.37	_GLVAAYSGES(ph)DS
Q00341	31	S	Vigilin	HDLBP	121.14	_VATLNS(ph)EEESDP
Q00613	303	S	Heat shock factor pro	HSF1	88.176	_VKEEPPS(ph)PPQS(
Q00613	307	S	Heat shock factor pro	HSF1	88.176	_VKEEPPS(ph)PPQS(
Q00613	363	S	Heat shock factor pro	HSF1	163.8	_GHTDTEGRPPS(ph)F
Q00839	59	S	Heterogeneous nucle	HNRNPU	57.932	_LQAALDDEEAGGRP/
Q00839	271	S	Heterogeneous nucle	HNRNPU	176.87	_AKS(ph)PQPPVEEED
Q01082	2102	S	Spectrin beta chain, r	SPTBN1	122.46	_RPPS(ph)PEPSTK_
Q01082	2138	S	Spectrin beta chain, r	SPTBN1	48.151	_GEQVSQNGLPAEQG
Q01082	2161	S	Spectrin beta chain, r	SPTBN1	175.68	_TS(ph)S(ph)KESS(ph)
Q01082	2164	S	Spectrin beta chain, r	SPTBN1	131.94	_TSS(ph)KES(ph)SPIP
Q01082	2165	S	Spectrin beta chain, r	SPTBN1	175.68	_TSS(ph)KESS(ph)PIP
Q01082	2169	S	Spectrin beta chain, r	SPTBN1	175.68	_TS(ph)SKESS(ph)PIP
Q01082	2320	T	Spectrin beta chain, r	SPTBN1	167.14	_HEVSASTQST(ph)PA
Q01082	2341	S	Spectrin beta chain, r	SPTBN1	184.72	_AQTLPTSVVTITSESS
Q01105	7	S	Protein SET	SET	81.676	_RQS(ph)PLPPQK_
Q01130	206	S	Serine/arginine-rich s	SRSF2	150.5	_S(ph)KS(ph)PPKS(ph
Q01130	208	S	Serine/arginine-rich s	SRSF2	150.5	_S(ph)KS(ph)PPKS(ph
Q01130	212	S	Serine/arginine-rich s	SRSF2	150.5	_S(ph)KS(ph)PPKS(ph
Q01167	373	S	Forkhead box protein	FOXK2	43.922	_SAPAS(ph)PNHAGVL
Q01167	398	S	Forkhead box protein	FOXK2	93.601	_EGS(ph)PAPLEPEPG
Q01518	308	S	Adenylyl cyclase-ass	CAP1	78.552	_PFSAPKPQTS(ph)PS
Q01518	310	S	Adenylyl cyclase-ass	CAP1	78.552	_PFSAPKPQTS(ph)PS
Q01581	495	S	Hydroxymethylglutary	HMGCS1	169.94	_RPTPNDDTLDEGVGI
Q01650	31	S	Large neutral amino a	SLC7A5	65.833	_S(ph)ADGSAPAGEGI
Q01650	35	S	Large neutral amino a	SLC7A5	92.01	_SADGS(ph)APAGEGI
Q01664	124	S	Transcription factor A	TFAP4	163.62	_FIQELSGSS(ph)PK_
Q01813	386	S	6-phosphofructokinas	PFKP	44.311	_S(ph)FAGNLNTYK_
Q01831	94	S	DNA repair protein co	XPC	177	_VIKDEALS(ph)DGDDI
Q01831	122	S	DNA repair protein co	XPC	164.35	_GATMNEDS(ph)NEEI
Q01831	129	S	DNA repair protein co	XPC	164.35	_GATMNEDS(ph)NEEI
Q01831	883	S	DNA repair protein co	XPC	157.47	_SEAAAPHTDAGGGL
Q01831	884	S	DNA repair protein co	XPC	157.47	_SEAAAPHTDAGGGL
Q02040	537	S	A-kinase anchor prote	AKAP17A	98.942	_VVPEDGS(ph)PEKR_
Q02156	729	S	Protein kinase C epsi	PRKCE	91.961	_GFS(ph)YFGEDLMP_
Q02241	867	S	Kinesin-like protein K	KIF23	206.94	_YMLTHQELAS(ph)DG
Q02297	435	S	Pro-neuregulin-1, me	NRG1	68.576	_MS(ph)PVDFHTPSSF
Q02880	1336	S	DNA topoisomerase 2	TOP2B	102.79	_NPWS(ph)DDES(ph)K
Q02880	1340	S	DNA topoisomerase 2	TOP2B	102.79	_NPWS(ph)DDES(ph)K
Q02880	1342	S	DNA topoisomerase 2	TOP2B	102.79	_RNPWS(ph)DDES(ph
Q02880	1344	S	DNA topoisomerase 2	TOP2B	102.79	_NPWS(ph)DDES(ph)K
Q02880	1375	S	DNA topoisomerase 2	TOP2B	136.44	_YTFDFS(ph)EEEDDD
Q02880	1400	S	DNA topoisomerase 2	TOP2B	130.5	_VKAS(ph)PITNDGEDI
Q02880	1403	T	DNA topoisomerase 2	TOP2B	116.98	_ASPIT(ph)NDGEDEF
Q02880	1413	S	DNA topoisomerase 2	TOP2B	126.73	_VKAS(ph)PITNDGEDI
Q02880	1424	S	DNA topoisomerase 2	TOP2B	111.52	_VKAS(ph)PITNDGEDI
Q02880	1461	S	DNA topoisomerase 2	TOP2B	108.95	_SEDDS(ph)AKFDS(ph
Q02880	1466	S	DNA topoisomerase 2	TOP2B	304.44	_FDS(ph)NEEDSASVF
Q02880	1522	S	DNA topoisomerase 2	TOP2B	171.05	_VVEAVNS(ph)DS(ph)
Q02880	1524	S	DNA topoisomerase 2	TOP2B	171.05	_VVEAVNS(ph)DS(ph)
Q02880	1526	S	DNA topoisomerase 2	TOP2B	107.75	_VVEAVNS(ph)DS(ph)
Q02880	1550	S	DNA topoisomerase 2	TOP2B	154.26	_KAS(ph)GSENEGDY
Q02880	1575	T	DNA topoisomerase 2	TOP2B	110.47	_KT(ph)SFDQDS(ph)D
Q02880	1581	S	DNA topoisomerase 2	TOP2B	378.53	_KTSFDQDS(ph)DVDI

Q02880	1613	S	DNA topoisomerase 2	TOP2B	170.89	_YFAES(ph)DEEEDDV
Q02952	285	T	A-kinase anchor prote	AKAP12	156.67	_SAESPT(ph)SPVTSE
Q02952	286	S	A-kinase anchor prote	AKAP12	158.52	_SAESPTS(ph)PVTSE
Q02952	347	S	A-kinase anchor prote	AKAP12	77.646	_EQEPEKVDTEEDGK
Q02952	371	S	A-kinase anchor prote	AKAP12	104.13	_LS(ph)AEYEKVELPSI
Q02952	381	S	A-kinase anchor prote	AKAP12	101.01	_VELPS(ph)EEQVSGS
Q02952	598	S	A-kinase anchor prote	AKAP12	262.09	_GLAEVQQDGEAEEG
Q02952	627	S	A-kinase anchor prote	AKAP12	125.45	_RPS(ph)ESDKEDELD
Q02952	644	S	A-kinase anchor prote	AKAP12	169.41	_SATLS(ph)S(ph)TEST
Q02952	645	S	A-kinase anchor prote	AKAP12	169.41	_SATLS(ph)S(ph)TEST
Q02952	1390	S	A-kinase anchor prote	AKAP12	163.15	_EVS(ph)SLEGSPPPC
Q02952	1395	S	A-kinase anchor prote	AKAP12	167.51	_EVSSLEGS(ph)PPPC
Q03060	287	S	cAMP-responsive ele	CREM	100.82	_APTAALPQGVVMAA
Q03111	292	S	Protein ENL	MLLT1	165.58	_RPATADS(ph)PKPSA
Q03111	475	S	Protein ENL	MLLT1	121.13	_RS(ph)PESCSKPEK_
Q03135	37	S	Caveolin-1	CAV1	51.957	_AMADELS(ph)EK_
Q03164	337	T	Histone-lysine N-meth	MLL	116.63	_DKEGT(ph)PPLTK_
Q03164	1837	S	Histone-lysine N-meth	MLL	77.51	_GPGEPDS(ph)PTPLH
Q03164	2098	S	Histone-lysine N-meth	MLL	126.8	_TIAHS(ph)PTSFTESS
Q03164	2151	S	Histone-lysine N-meth	MLL	76.073	_TPSYS(ph)PTQR_
Q03188	73	S	Centromere protein C	CENPC1	77.068	_IKDTCIQS(ph)PSK_
Q03188	130	T	Centromere protein C	CENPC1	167.97	_ILATDVSSKNT(ph)PD
Q03188	225	S	Centromere protein C	CENPC1	119.76	_IEIDNKVS(ph)DEEDK
Q03188	538	S	Centromere protein C	CENPC1	95.236	_SEES(ph)PVYSNSSV
Q03188	773	S	Centromere protein C	CENPC1	83.312	_PSGGFVISGVLS(ph)I
Q03252	296	S	Lamin-B2	LMNB2	59.606	_LES(ph)LSYQLSGLQ
Q03252	400	S	Lamin-B2	LMNB2	96.773	_ATSS(ph)SSGSLSAT
Q03701	629	S	CCAAT/enhancer-bin	CEBPZ	240.05	_SQLDDHPES(ph)DDE
Q03701	835	S	CCAAT/enhancer-bin	CEBPZ	137.43	_DADEES(ph)IEDVDD
Q04637	314	S	Eukaryotic translation	EIF4G1	74.063	_ETGEPYRLS(ph)PEP
Q04637	1187	S	Eukaryotic translation	EIF4G1	81.565	_SFS(ph)KEVEER_
Q04637	1231	S	Eukaryotic translation	EIF4G1	105.99	_EAALPPVS(ph)PLK_
Q04637	1596	S	Eukaryotic translation	EIF4G1	40.015	_EAEEES(ph)DHN_
Q04656	270	S	Copper-transporting A	ATP7A	92.932	_S(ph)PSYTNDSTATF
Q04726	203	S	Transducin-like enhar	TLE3	115.63	_ESSANNSVS(ph)PSE
Q04726	286	S	Transducin-like enhar	TLE3	68.97	_DAPTS(ph)PASVASS
Q04828	232	S	Aldo-keto reductase f	AKR1C1;AKR1C2	47.286	_EEPWVDPNS(ph)PVI
Q05209	673	S	Tyrosine-protein phos	PTPN12	139.81	_DVDVSEDS(ph)PPPL
Q05397	910	S	Focal adhesion kinas	PTK2	31.488	_LQPQEIS(ph)PPPTAI
Q05519	207	S	Serine/arginine-rich s	SRSF11	101.49	_LNHVAAGLVS(ph)PS
Q05519	434	S	Serine/arginine-rich s	SRSF11	290.57	_DYDEEEQGYDS(ph)E
Q05519	449	S	Serine/arginine-rich s	SRSF11	81.565	_KPIETGS(ph)PK_
Q05519	483	S	Serine/arginine-rich s	SRSF11	31.883	_VNGDDHHEEDMDMS
Q05655	507	T	Protein kinase C delta	PRKCD	67.827	_AST(ph)FCGTPDYIAP
Q05D32	28	S	CTD small phosphata	CTDSPL2	147.76	_KYS(ph)EVDDSLPSG
Q05D32	134	S	CTD small phosphata	CTDSPL2	79.86	_LEDNPSSGS(ph)PPR
Q06210	261	S	Glutamine--fructose-6	GFPT1	170.35	_VDS(ph)TTCLFPVEEI
Q06265	306	S	Exosome complex co	EXOSC9	154.65	_APIDTS(ph)DVEEK_
Q06587	38	S	E3 ubiquitin-protein li	RING1	52.657	_TPQEAIMDGTEIAVS(
Q07021	201	S	Complement compon	C1QBP	78.642	_ALVLDCHYPEDEVG(
Q07157	125	S	Tight junction protein	TJP1	100.75	_VQIPVSRPDPEPVS(
Q07157	131	S	Tight junction protein	TJP1	59.059	_VQIPVSRPDPEPVSD
Q07157	178	S	Tight junction protein	TJP1	94.119	_SVAS(ph)S(ph)QPAK
Q07157	179	S	Tight junction protein	TJP1	93.909	_SVAS(ph)S(ph)QPAK

Q07157	275	S	Tight junction protein	TJP1	109.23	_ATLLNVPDLS(ph)DSI
Q07157	277	S	Tight junction protein	TJP1	163.49	_ATLLNVPDLSDS(ph)I
Q07157	280	S	Tight junction protein	TJP1	163.49	_ATLLNVPDLSDS(ph)I
Q07157	297	S	Tight junction protein	TJP1	235.84	_DDISEIQSLAS(ph)DH
Q07157	300	S	Tight junction protein	TJP1	235.84	_DDISEIQSLAS(ph)DH
Q07157	353	S	Tight junction protein	TJP1	114.54	_ISKPGAVS(ph)TPVK_
Q07157	617	S	Tight junction protein	TJP1	100.45	_S(ph)REDLSAQPVQT
Q07157	810	S	Tight junction protein	TJP1	50.358	_ADGATS(ph)DDLDLH
Q07157	868	T	Tight junction protein	TJP1	183.04	_HTSDYEDTDTEGGA'
Q07157	899	S	Tight junction protein	TJP1	115.54	_EDSSGMHHENQTYP
Q07157	912	S	Tight junction protein	TJP1	134.93	_IDS(ph)PGFKPASQQ
Q07157	968	S	Tight junction protein	TJP1	215.84	_LEEPTPAPSTSYS(ph
Q07157	1111	S	Tight junction protein	TJP1	68.579	_QPYPSRPPFDNQHS
Q07157	1617	S	Tight junction protein	TJP1	174.06	_AIPVS(ph)PSAVEEDE
Q07666	20	S	KH domain-containing	KHDRBS1	102.36	_SGS(ph)MDPSGAHPS
Q07955	199	S	Serine/arginine-rich s	SRSF1	105.19	_VKVDGPRS(ph)PS(ph
Q07955	201	S	Serine/arginine-rich s	SRSF1	88.19	_VDGPRS(ph)PS(ph)Y
Q07955	238	S	Serine/arginine-rich s	SRSF1	45.908	_YS(ph)PRHS(ph)R_
Q07955	242	S	Serine/arginine-rich s	SRSF1	45.908	_YS(ph)PRHS(ph)R_
Q08170	456	S	Serine/arginine-rich s	SRSF4	101.53	_SKPNLPS(ph)ESR_
Q08170	458	S	Serine/arginine-rich s	SRSF4	66.289	_SKPNLPSES(ph)RS(p
Q08170	460	S	Serine/arginine-rich s	SRSF4	66.289	_SKPNLPSES(ph)RS(p
Q08211	87	S	ATP-dependent RNA	DHX9	133.1	_SEEVPAFGVAS(ph)P
Q08495	226	S	Dematin	EPB49	50.358	_RGAEEEEEEEDDDS
Q08499	202	S	cAMP-specific 3',5'-cy	PDE4D;PDE4B	103.76	_SDSDYDLS(ph)PK_
Q08499	348	S	cAMP-specific 3',5'-cy	PDE4D	91.789	_QHEVEIPS(ph)PTQK_
Q08945	444	S	FACT complex subun	SSRP1	306.35	_EGM(ox)NPSYDEYAD
Q08J23	456	S	tRNA (cytosine(34)-C	NSUN2	202.38	_ESTQLS(ph)PADLTE
Q08J23	743	S	tRNA (cytosine(34)-C	NSUN2	72.389	_AGEPNS(ph)PDAEEA
Q08J23	751	S	tRNA (cytosine(34)-C	NSUN2	44.721	_AGEPNS(ph)PDAEEA
Q09161	22	S	Nuclear cap-binding p	NCBP1	289.13	_KTS(ph)DANETEDHL
Q09472	1038	S	Histone acetyltransfer	EP300	114.9	_TEIKEEEDQPSTSAT
Q09666	41	S	Neuroblast differentia	AHNAK	37.025	_DDGVFVQEVTQNS(p
Q09666	93	S	Neuroblast differentia	AHNAK	123.59	_S(ph)PEPGQTWTR_
Q09666	135	S	Neuroblast differentia	AHNAK	222.78	_LKS(ph)EDGVEGDLG
Q09666	177	S	Neuroblast differentia	AHNAK	126.34	_DIDISS(ph)PEFK_
Q09666	210	S	Neuroblast differentia	AHNAK	210.34	_LPS(ph)GSGAASPTG
Q09666	212	S	Neuroblast differentia	AHNAK	147.16	_LPSGS(ph)GAAS(ph)
Q09666	216	S	Neuroblast differentia	AHNAK	250.34	_LPSGSGAAS(ph)PTG
Q09666	490	T	Neuroblast differentia	AHNAK	139	_VKT(ph)PEMIIQKPK_
Q09666	511	S	Neuroblast differentia	AHNAK	139.9	_ISMQDVDLSLGS(ph)
Q09666	570	S	Neuroblast differentia	AHNAK	111.77	_IS(ph)MSEVDLNVAA
Q09666	2397	S	Neuroblast differentia	AHNAK	154.26	_ISMPDLDLHLKS(ph)F
Q09666	3426	S	Neuroblast differentia	AHNAK	125.73	_VSMPDVELNLKS(ph)
Q09666	5110	S	Neuroblast differentia	AHNAK	113.47	_FKAEAPLPS(ph)PK_
Q09666	5448	S	Neuroblast differentia	AHNAK	79.332	_IS(ph)APNVDFNLEGF
Q09666	5731	S	Neuroblast differentia	AHNAK	130.01	_GGVTGS(ph)PEASIS
Q09666	5749	S	Neuroblast differentia	AHNAK	171.17	_AS(ph)LGS(ph)LEGE/
Q09666	5752	S	Neuroblast differentia	AHNAK	219.66	_AS(ph)LGS(ph)LEGE/
Q09666	5763	S	Neuroblast differentia	AHNAK	313.64	_ASLGSLEGEAEAEAS
Q09666	5782	S	Neuroblast differentia	AHNAK	39.625	_SNS(ph)FSDER_
Q09666	5841	S	Neuroblast differentia	AHNAK	222.51	_GHYEVTGS(ph)DDET
Q0JRZ9	394	S	FCH domain only pro	FCHO2	45.598	_HS(ph)PVQMNR_
Q0VDD8	705	S	Dynein heavy chain 1	DNAH14	50.897	_ISS(ph)M(ox)GELT(ph

Q0ZGT2	80	S	Nexilin	NEXN	147.09	_EMLAS(ph)DDEEDVS
Q0ZGT2	365	S	Nexilin	NEXN	107.35	_TIS(ph)QEFLTPGK_
Q12767	445	S	Uncharacterized prote	KIAA0195	75.773	_VEPPHSS(ph)HEDLT
Q12789	739	S	General transcription	GTF3C1	44.683	_TSQPPVPQGEAEED
Q12789	1856	S	General transcription	GTF3C1	224.42	_PLEGSSSEDSPPEG(
Q12830	1300	S	Nucleosome-remodel	BPTF	115.66	_VLDDVSIRS(ph)PETK
Q12830	2370	S	Nucleosome-remodel	BPTF	64.64	_LS(ph)PQMQVHQDK_
Q12857	300	S	Nuclear factor 1 A-type	NFIA	109.77	_S(ph)PGSGSQSSGW
Q12872	283	S	Splicing factor, suppre	SFSWAP	106.1	_SGVSS(ph)DNEDDDI
Q12872	743	S	Splicing factor, suppre	SFSWAP	109.65	_PLPTLEVKPPDRPSS
Q12873	713	S	Chromodomain-helica	CHD3	160.25	_ELQGDGPPSS(ph)PT
Q12873	1601	S	Chromodomain-helica	CHD3	130.37	_METEADAPS(ph)PAF
Q12888	265	S	Tumor suppressor p53	TP53BP1	129.34	_SEDMPFS(ph)PK_
Q12888	294	S	Tumor suppressor p53	TP53BP1	245.92	_S(ph)PEPEVLSTQED
Q12888	366	S	Tumor suppressor p53	TP53BP1	146.1	_SLVQDSLSTNSSDLV
Q12888	380	S	Tumor suppressor p53	TP53BP1	171.35	_STPFIVPSS(ph)PTEC
Q12888	500	S	Tumor suppressor p53	TP53BP1	237.52	_NS(ph)PEDLGLSLTG
Q12888	523	S	Tumor suppressor p53	TP53BP1	108.71	_LMLSTSEYS(ph)QS(p
Q12888	525	S	Tumor suppressor p53	TP53BP1	148.52	_LMLSTSEYS(ph)QS(p
Q12888	552	S	Tumor suppressor p53	TP53BP1	342.18	_IDEDGENTQIEDTEPI
Q12888	580	S	Tumor suppressor p53	TP53BP1	69.142	_FVPAENDSILMNPAQ
Q12888	635	S	Tumor suppressor p53	TP53BP1	171.29	_S(ph)EALS(ph)S(ph)V
Q12888	639	S	Tumor suppressor p53	TP53BP1	179.7	_S(ph)EALS(ph)S(ph)V
Q12888	640	S	Tumor suppressor p53	TP53BP1	179.7	_S(ph)EALS(ph)S(ph)V
Q12888	1056	T	Tumor suppressor p53	TP53BP1	64.224	_SEDPPTT(ph)PIR_
Q12888	1068	S	Tumor suppressor p53	TP53BP1	136.68	_GNLLHFPSS(ph)QGE
Q12888	1094	S	Tumor suppressor p53	TP53BP1	141.64	_QSQQPMKPIS(ph)PV
Q12888	1101	S	Tumor suppressor p53	TP53BP1	141.64	_QSQQPMKPIS(ph)PV
Q12888	1113	S	Tumor suppressor p53	TP53BP1	179.54	_MVIQGPS(ph)SPQGE
Q12888	1114	S	Tumor suppressor p53	TP53BP1	186.71	_M(ox)VIQGPSS(ph)P(
Q12888	1216	S	Tumor suppressor p53	TP53BP1	59.305	_GSGEKPVSAPGDDT
Q12888	1219	S	Tumor suppressor p53	TP53BP1	59.305	_GSGEKPVSAPGDDT
Q12888	1317	S	Tumor suppressor p53	TP53BP1	110.95	_TSS(ph)GTSLSAMHS
Q12888	1362	S	Tumor suppressor p53	TP53BP1	58.313	_GGPGKLS(ph)PR_
Q12888	1430	S	Tumor suppressor p53	TP53BP1	157.17	_ETAVPGPLGIEDISPN
Q12888	1678	S	Tumor suppressor p53	TP53BP1	141.82	_LITSEEERS(ph)PAK_
Q12888	1758	S	Tumor suppressor p53	TP53BP1	79.304	_LPDGPTGS(ph)S(ph)I
Q12888	1759	S	Tumor suppressor p53	TP53BP1	79.304	_LPDGPTGS(ph)S(ph)I
Q12906	62	S	Interleukin enhancer-b	ILF3	141.21	_GSSEQAES(ph)DNMI
Q12906	382	S	Interleukin enhancer-b	ILF3	194.99	_RPMEEDGEEKS(ph)I
Q12906	482	S	Interleukin enhancer-b	ILF3	120.38	_GEDS(ph)AEETEAKP
Q12906	592	T	Interleukin enhancer-b	ILF3	69.331	_LFPDT(ph)PLALDANI
Q12986	50	S	Transcriptional repres	NFX1	52.599	_NYSS(ph)PPPCHLSR
Q12996	691	S	Cleavage stimulation	CSTF3	104.53	_RPNEDS(ph)DEDEEI
Q13029	643	S	PR domain zinc finge	PRDM2	49.448	_TAS(ph)PPALPK_
Q13029	739	S	PR domain zinc finge	PRDM2	74.732	_TSS(ph)PPS(ph)SPQI
Q13029	742	S	PR domain zinc finge	PRDM2	74.732	_TSS(ph)PPS(ph)SPQI
Q13033	257	S	Striatin-3	STRN3	45.993	_SSGDVLETFNFLENA
Q13042	560	S	Cell division cycle pro	CDC16	74.987	_NIIS(ph)PPWDFR_
Q13045	856	S	Protein flightless-1 ho	FLII	63.447	_NAEAVLQS(ph)PGLS
Q13085	29	S	Acetyl-CoA carboxyla	ACACA	69.845	_FIIGSVSEDNS(ph)ED
Q13111	65	S	Chromatin assembly f	CHAF1A	140.55	_S(ph)PDLEASLDTLEI
Q13111	206	S	Chromatin assembly f	CHAF1A	42.21	_S(ph)CPELTSGPR_
Q13112	410	S	Chromatin assembly f	CHAF1B	103.9	_GSS(ph)PGPRPVEG

Q13112	429	S	Chromatin assembly f	CHAF1B	142.58	_TQDPSS(ph)PGTTPP
Q13112	433	T	Chromatin assembly f	CHAF1B	83.077	_TQDPSS(ph)PGTT(ph
Q13123	460	S	Protein Red	IK	91.855	_QLGDFFGMSNSYAE
Q13177	141	S	Serine/threonine-prot	PAK2	145.95	_YLS(ph)FTPPEK_
Q13185	93	S	Chromobox protein h	CBX3	168.05	_RKS(ph)LSDSESDDS
Q13185	176	S	Chromobox protein h	CBX3	135.81	_LTWHS(ph)CPEDEA(
Q13188	316	S	Serine/threonine-prot	STK3	104.66	_ELEEEEENS(ph)DED
Q13200	16	S	26S proteasome non-	PSMD2	172.31	_DKAPVQPQQS(ph)P/
Q13206	7	S	Probable ATP-depen	DDX10	89.467	_TANS(ph)PGSGARPD
Q13206	780	S	Probable ATP-depen	DDX10	89.751	_AKDEEEAFLDWS(ph
Q13242	189	S	Serine/arginine-rich s	SRSF9	95.642	_STS(ph)YGYSR_
Q13242	204	S	Serine/arginine-rich s	SRSF9	85.973	_GRDS(ph)PYQSR_
Q13242	211	S	Serine/arginine-rich s	SRSF9	179.5	_GS(ph)PHYFS(ph)PF
Q13242	216	S	Serine/arginine-rich s	SRSF9	158.35	_GSPHYFS(ph)PFRPY
Q13247	118	S	Serine/arginine-rich s	SRSF4;SRSF5;SF	103.08	_LIVENLS(ph)SR_
Q13247	297	S	Serine/arginine-rich s	SRSF6	78.708	_S(ph)QSRS(ph)NSPL
Q13247	301	S	Serine/arginine-rich s	SRSF6	126.25	_S(ph)NS(ph)PLPVPP
Q13247	303	S	Serine/arginine-rich s	SRSF6	128.74	_S(ph)NS(ph)PLPVPP
Q13247	314	S	Serine/arginine-rich s	SRSF6	99.991	_ARS(ph)VS(ph)PPPK
Q13247	316	S	Serine/arginine-rich s	SRSF6	99.991	_ARS(ph)VS(ph)PPPK
Q13263	19	S	Transcription interme	TRIM28	417.08	_(ac)AASAAAASAAAA
Q13263	49	S	Transcription interme	TRIM28	146.76	_STAPSAAASASASA/
Q13263	50	S	Transcription interme	TRIM28	138.78	_STAPSAAASASASA/
Q13263	473	S	Transcription interme	TRIM28	61.015	_S(ph)GEGEVSGLMR_
Q13283	149	S	Ras GTPase-activatir	G3BP1	170.01	_YQDEVFGGFVTEPQ
Q13283	232	S	Ras GTPase-activatir	G3BP1	228.11	_SSS(ph)PAPADIAQT
Q13286	12	S	Battenin	CLN3	226.23	_RFS(ph)DS(ph)EGEE
Q13286	14	S	Battenin	CLN3	130.83	_RFS(ph)DS(ph)EGEE
Q13330	449	S	Metastasis-associate	MTA1	71.879	_SNMS(ph)PHGLPAR_
Q13371	296	S	Phosducin-like protei	PDCL	51.942	_NSATCHSEDS(ph)DL
Q13402	846	Y	Unconventional myos	MYO7A	29.544	_LWAVLT(ph)VQAY(ph
Q13415	199	S	Origin recognition cor	ORC1	100.04	_SAES(ph)PSWTPAEH
Q13415	311	S	Origin recognition cor	ORC1	151.84	_ETGLSYTEDDKKAS(
Q13425	95	S	Beta-2-syntrophin	SNTB2	129.77	_GLGPPS(ph)PPAPPR
Q13425	110	S	Beta-2-syntrophin	SNTB2	151.59	_GPAGEAGAS(ph)PP\
Q13425	222	S	Beta-2-syntrophin	SNTB2	75.965	_KPSLVSDLPWEGAA
Q13425	231	S	Beta-2-syntrophin	SNTB2	95.227	_KPSLVSDLPWEGAA
Q13425	393	S	Beta-2-syntrophin	SNTB2	158.91	_S(ph)PSLGSDLTFATI
Q13426	327	S	DNA repair protein XF	XRCC4	81.992	_NS(ph)S(ph)PEDLFDI
Q13426	328	S	DNA repair protein XF	XRCC4	129.37	_NS(ph)S(ph)PEDLFDI
Q13427	356	S	Peptidyl-prolyl cis-trar	PPIG	131.17	_S(ph)ET(ph)PPHWR_
Q13427	358	T	Peptidyl-prolyl cis-trar	PPIG	131.17	_S(ph)ET(ph)PPHWR_
Q13427	611	T	Peptidyl-prolyl cis-trar	PPIG	79.201	_ERRT(ph)PPGR_
Q13427	687	S	Peptidyl-prolyl cis-trar	PPIG	80.96	_ADRDQS(ph)PFSK_
Q13427	716	S	Peptidyl-prolyl cis-trar	PPIG	73.834	_IRS(ph)S(ph)VEKENC
Q13427	717	S	Peptidyl-prolyl cis-trar	PPIG	116.58	_IRS(ph)S(ph)VEKENC
Q13427	744	S	Peptidyl-prolyl cis-trar	PPIG	187.73	_KFDHES(ph)SPGTDE
Q13427	753	S	Peptidyl-prolyl cis-trar	PPIG	166.75	_KFDHES(ph)SPGTDE
Q13428	156	S	Treacle protein	TCOF1	122.46	_TVANLLSGKS(ph)PR_
Q13428	171	S	Treacle protein	TCOF1	191.71	_SAEPSANTTLVS(ph)I
Q13428	233	S	Treacle protein	TCOF1	127.57	_ASSVSTKES(ph)PAR
Q13428	381	S	Treacle protein	TCOF1	176.1	_TSQVGAASAPAKES(
Q13428	503	S	Treacle protein	TCOF1	131.56	_S(ph)PQVKPASTMGM
Q13428	906	S	Treacle protein	TCOF1	97.273	_AALAPAKES(ph)PR_

Q13428	967	S	Treacle protein	TCOF1	103.92	_S(ph)PAGPAATPAQA
Q13428	1111	S	Treacle protein	TCOF1	152.01	_TQPSSGVDSAVGTLI
Q13428	1228	S	Treacle protein	TCOF1	131.18	_LDSS(ph)PSVSSTLA
Q13428	1257	S	Treacle protein	TCOF1	177.22	_QEAKPQQAAGMLS(p
Q13428	1378	S	Treacle protein	TCOF1	172.03	_LGAGEGGEASVS(ph
Q13435	309	S	Splicing factor 3B sut	SF3B2	201.97	_SSLGQSAS(ph)ETEE
Q13435	435	S	Splicing factor 3B sut	SF3B2	75.193	_GFEEEHKDSDDDS(p
Q13435	436	S	Splicing factor 3B sut	SF3B2	75.193	_GFEEEHKDSDDDS(p
Q13439	71	S	Golgin subfamily A m	GOLGA4	91.961	_VPS(ph)VESLFR_
Q13439	266	S	Golgin subfamily A m	GOLGA4	202.73	_EENPES(ph)DGEPV
Q13442	60	S	28 kDa heat- and acic	PDAP1	321.49	_SLDS(ph)DES(ph)EDI
Q13442	63	S	28 kDa heat- and acic	PDAP1	283.09	_SLDS(ph)DES(ph)EDI
Q13443	758	S	Disintegrin and metall	ADAM9	86.772	_HVS(ph)PVT(ph)PPR_
Q13443	761	T	Disintegrin and metall	ADAM9	95.477	_HVS(ph)PVT(ph)PPR_
Q13459	1290	S	Unconventional myos	MYO9B	150.68	_VQEKPDS(ph)PGGS
Q13501	269	T	Sequestosome-1	SQSTM1	224.57	_SRLT(ph)PVSPESSS
Q13501	272	S	Sequestosome-1	SQSTM1	133.86	_LTPVS(ph)PESSSTEI
Q13501	328	S	Sequestosome-1	SQSTM1	87.016	_IALESEGRPEEQMES
Q13501	332	S	Sequestosome-1	SQSTM1	87.016	_IALESEGRPEEQMES
Q13501	366	S	Sequestosome-1	SQSTM1	135.16	_EVDPSTGELQSLQMI
Q13523	32	S	Serine/threonine-prot	PRPF4B	110.38	_SINEENGEVS(ph)ED
Q13523	142	S	Serine/threonine-prot	PRPF4B	117.94	_VQSGMGLILQGYES(
Q13523	144	S	Serine/threonine-prot	PRPF4B	80.496	_VQSGMGLILQGYES(
Q13523	257	S	Serine/threonine-prot	PRPF4B	129.29	_ARS(ph)PTDDKVK_
Q13523	277	S	Serine/threonine-prot	PRPF4B	120.87	_KKS(ph)PIINESR_
Q13523	292	S	Serine/threonine-prot	PRPF4B	92.247	_S(ph)RS(ph)PVDLR_
Q13523	294	S	Serine/threonine-prot	PRPF4B	92.247	_S(ph)RS(ph)PVDLR_
Q13523	328	S	Serine/threonine-prot	PRPF4B	89.9	_KPIKS(ph)PSK_
Q13523	366	S	Serine/threonine-prot	PRPF4B	122.66	_S(ph)RS(ph)PLLNDR_
Q13523	368	S	Serine/threonine-prot	PRPF4B	122.66	_S(ph)RS(ph)PLLNDR_
Q13523	427	S	Serine/threonine-prot	PRPF4B	69.765	_S(ph)KDAS(ph)PINRV
Q13523	431	S	Serine/threonine-prot	PRPF4B	99.044	_DAS(ph)PINRWS(ph)
Q13523	437	S	Serine/threonine-prot	PRPF4B	99.044	_S(ph)KDAS(ph)PINRV
Q13523	518	S	Serine/threonine-prot	PRPF4B	44.6	_VEQES(ph)S(ph)S(ph
Q13523	519	S	Serine/threonine-prot	PRPF4B	44.6	_VEQES(ph)S(ph)S(ph
Q13523	520	S	Serine/threonine-prot	PRPF4B	44.6	_VEQES(ph)S(ph)S(ph
Q13523	580	S	Serine/threonine-prot	PRPF4B	145.14	_SPS(ph)PDDILER_
Q13523	849	Y	Serine/threonine-prot	PRPF4B	228.23	_LCDFGSASHVADNDI
Q13547	393	S	Histone deacetylase ´	HDAC1	128.99	_M(ox)LPHAPGVQMQ
Q13547	421	S	Histone deacetylase ´	HDAC1	130.15	_IACEEEFS(ph)DS(ph)
Q13547	423	S	Histone deacetylase ´	HDAC1	130.15	_IACEEEFS(ph)DS(ph)
Q13573	224	S	SNW domain-contain	SNW1	166.34	_GPPS(ph)PPAPVMHS
Q13573	232	S	SNW domain-contain	SNW1	166.34	_GPPS(ph)PPAPVMHS
Q13586	519	S	Stromal interaction m	STIM1	73.948	_DLTHS(ph)DSESSLH
Q13586	575	S	Stromal interaction m	STIM1	78.903	_LPDS(ph)PALAK_
Q13586	618	S	Stromal interaction m	STIM1	263.61	_SHS(ph)PSSPDPDTP
Q13595	2	S	Transformer-2 protein	TRA2A	166.29	_(ac)S(ph)DVEENNFE
Q13595	14	S	Transformer-2 protein	TRA2A	200.71	_(ac)S(ph)DVEENNFE
Q13595	16	S	Transformer-2 protein	TRA2A	111.27	_(ac)SDVEENNFEGRE
Q13595	73	S	Transformer-2 protein	TRA2A	36.514	_S(ph)HS(ph)HSHR_
Q13595	75	S	Transformer-2 protein	TRA2A	36.514	_S(ph)HS(ph)HSHR_
Q13595	84	S	Transformer-2 protein	TRA2A	119.39	_S(ph)RS(ph)YT(ph)PE
Q13595	86	S	Transformer-2 protein	TRA2A	119.39	_S(ph)RS(ph)YT(ph)PE
Q13595	88	T	Transformer-2 protein	TRA2A	119.39	_SYT(ph)PEYR_

Q13595	100	S	Transformer-2 protein	TRA2A	75.764	_SRS(ph)HS(ph)PMSN
Q13595	202	T	Transformer-2 protein	TRA2A	159.5	_AHT(ph)PTPGIYMGR
Q13595	260	S	Transformer-2 protein	TRA2B;TRA2A	138.89	_RS(ph)PS(ph)PYYSR_
Q13595	262	S	Transformer-2 protein	TRA2B;TRA2A	138.89	_RS(ph)PS(ph)PYYSR_
Q13596	32	S	Sorting nexin-1	SNX1	47.884	_LPPPFPGLEPESEGA
Q13596	39	S	Sorting nexin-1	SNX1	47.884	_LPPPFPGLEPESEGA
Q13596	41	T	Sorting nexin-1	SNX1	47.884	_LPPPFPGLEPESEGA
Q13601	3	S	KRR1 small subunit p	KRR1	133.15	_(ac)AS(ph)PSLERPEI
Q13610	50	S	Periodic tryptophan p	PWP1	273.89	_LQEEGGGS(ph)DEEI
Q13625	698	S	Apoptosis-stimulating	TP53BP2	71.176	_IPRPLS(ph)PTK_
Q13769	312	S	THO complex subunit	THOC5	97.55	_ALFKPPEDSQDDES(
Q13769	314	S	THO complex subunit	THOC5	111.05	_ALFKPPEDSQDDES(
Q13790	273	T	Apolipoprotein F	APOF	84.375	_DANISQPET(ph)T(ph)
Q13790	274	T	Apolipoprotein F	APOF	84.375	_DANISQPET(ph)T(ph)
Q13813	1217	S	Spectrin alpha chain,	SPTAN1	124.6	_S(ph)LQQLAEER_
Q13895	98	S	Bystin	BYSL	211.5	_MPQDGS(ph)DDEDE
Q14004	315	S	Cyclin-dependent kin	CDK13	58.274	_S(ph)LS(ph)PLGGR_
Q14004	317	S	Cyclin-dependent kin	CDK13	58.274	_S(ph)LS(ph)PLGGR_
Q14004	383	S	Cyclin-dependent kin	CDK13	56.819	_GGDVS(ph)PSPYSSS
Q14004	400	S	Cyclin-dependent kin	CDK13	139.38	_SPYS(ph)PVLR_
Q14004	437	S	Cyclin-dependent kin	CDK13	86.367	_HSS(ph)IS(ph)PSTLTI
Q14004	439	S	Cyclin-dependent kin	CDK13	173.71	_HSSIS(ph)PSTLTLK_
Q14004	525	S	Cyclin-dependent kin	CDK13	81.854	_IEHAPS(ph)PSSGGTI
Q14004	1246	T	Cyclin-dependent kin	CDK13	118.52	_ILELT(ph)PEPDRPR_
Q14103	83	S	Heterogeneous nucle	HNRNPD	224.67	_NEEDEGHSNSS(ph)F
Q14126	680	S	Desmoglein-2	DSG2	128.01	_VVPSFLPVDQGGS(p
Q14137	126	S	Ribosome biogenesis	BOP1	226.71	_IGDEYAEDS(ph)S(ph
Q14137	127	S	Ribosome biogenesis	BOP1	226.71	_IGDEYAEDS(ph)S(ph
Q14151	207	S	Scaffold attachment f	SAFB2	44.441	_VTPDIEES(ph)LLEPE
Q14151	513	S	Scaffold attachment f	SAFB2	76.605	_HHS(ph)VEIK_
Q14156	694	S	Protein EFR3 homolo	EFR3A	55.208	_LSVPYVPQVTDEDRL
Q14157	454	S	Ubiquitin-associated p	UBAP2L	171.9	_SPAVATSTAAPPPPS
Q14157	467	S	Ubiquitin-associated p	UBAP2L	66.828	_STSAPQMS(ph)PGSS
Q14157	609	S	Ubiquitin-associated p	UBAP2L	143.64	_RYPSSISSS(ph)PQK_
Q14160	504	S	Protein scribble homc	SCRIB	128.19	_SEACPCQPDSGS(ph
Q14160	835	S	Protein scribble homc	SCRIB	138.78	_MVEPENAVTITPLRP
Q14160	1220	S	Protein scribble homc	SCRIB	109.79	_NS(ph)LESISSIDR_
Q14160	1306	S	Protein scribble homc	SCRIB	84.362	_MAESPCSPSGQQPP
Q14160	1309	S	Protein scribble homc	SCRIB	84.362	_MAESPCSPSGQQPP
Q14160	1348	S	Protein scribble homc	SCRIB	41.563	_AFAAVPTSHPPEDAF
Q14160	1448	S	Protein scribble homc	SCRIB	94.973	_QSPAS(ph)PPPLGGC
Q14160	1475	S	Protein scribble homc	SCRIB	119.96	_VQS(ph)PEPPAPER_
Q14160	1486	S	Protein scribble homc	SCRIB	91.636	_ALS(ph)PAELR_
Q14160	1566	S	Protein scribble homc	SCRIB	115.57	_LS(ph)PDFAEELR_
Q14160	1581	S	Protein scribble homc	SCRIB	71.651	_SLEPSPS(ph)PGPQE
Q14181	141	S	DNA polymerase alph	POLA2	90.762	_S(ph)PHQLLSPSSFS
Q14186	23	S	Transcription factor D	TFDP1	97.69	_VFIDQNLS(ph)PGK_
Q14191	1133	S	Werner syndrome AT	WRN	41.684	_SIMVQS(ph)PEK_
Q14202	51	S	Zinc finger MYM-type	ZMYM3	79.426	_GWAPPGPS(ph)PSS
Q14204	4368	S	Cytoplasmic dynein 1	DYNC1H1	105.53	_TDS(ph)TSDGRPAWI
Q14207	207	S	Protein NPAT	NPAT	77.644	_AHASLMS(ph)PGR_
Q14247	401	T	Src substrate cortacti	CTTN	171.83	_TQT(ph)PPVSPAPQF
Q14247	405	S	Src substrate cortacti	CTTN	169.68	_TQT(ph)PPVS(ph)PAI
Q14247	418	S	Src substrate cortacti	CTTN	202.35	_LPSS(ph)PVYEDAAS

Q14258	100	S	E3 ubiquitin/ISG15 lig	TRIM25	129.75	_ASAPS(ph)PNAQVAC
Q14498	97	S	RNA-binding protein 3	RBM39	101.71	_YRS(ph)PYSGPK_
Q14498	136	S	RNA-binding protein 3	RBM39	239.73	_DKS(ph)PVREPIDNLT
Q14498	334	S	RNA-binding protein 3	RBM39	78.708	_TDASS(ph)ASSFLDS
Q14517	4272	S	Protocadherin Fat 1; F	FAT1	61.96	_NNLDRNS(ph)FEGSA
Q14573	1832	S	Inositol 1,4,5-trisphos	ITPR3	48.131	_VAS(ph)FSIPGSSSR_
Q14669	100	S	E3 ubiquitin-protein li	TRIP12	122.53	_ALQHTES(ph)PSETN
Q14669	310	S	E3 ubiquitin-protein li	TRIP12	79.652	_S(ph)ESPPAELPSLR_
Q14669	312	S	E3 ubiquitin-protein li	TRIP12	183.96	_SES(ph)PPAELPSLR_
Q14669	991	S	E3 ubiquitin-protein li	TRIP12	94.781	_DDSLDLS(ph)PQGR_
Q14669	1016	S	E3 ubiquitin-protein li	TRIP12	148.06	_YS(ph)PPRDDDKVDN
Q14669	1317	S	E3 ubiquitin-protein li	TRIP12	191.49	_VREDDEDS(ph)DDDC
Q14669	1322	S	E3 ubiquitin-protein li	TRIP12	191.49	_VREDDEDS(ph)DDDC
Q14676	168	S	Mediator of DNA dam	MDC1	162.44	_LLLAEDS(ph)EEEVDI
Q14676	329	S	Mediator of DNA dam	MDC1	81.144	_AQPFGFIDS(ph)DTDA
Q14676	376	S	Mediator of DNA dam	MDC1	103.85	_GPGAPGLAHLQESQ
Q14676	402	S	Mediator of DNA dam	MDC1	89.391	_SQASMVINS(ph)DT(p
Q14676	404	T	Mediator of DNA dam	MDC1	89.391	_SQASMVINS(ph)DT(p
Q14676	453	S	Mediator of DNA dam	MDC1	109.08	_SQTTTERDS(ph)DT(p
Q14676	455	T	Mediator of DNA dam	MDC1	109.08	_SQTTTERDS(ph)DT(p
Q14676	780	S	Mediator of DNA dam	MDC1	163.75	_ESEDSETQPFDTHLE
Q14676	793	S	Mediator of DNA dam	MDC1	89.979	_AIPGDQHPES(ph)PV
Q14676	1775	S	Mediator of DNA dam	MDC1	82.702	_AAESLTAIPEPAS(ph)
Q14676	1820	S	Mediator of DNA dam	MDC1	57.148	_SLATMDS(ph)PPHQK
Q14677	299	S	Clathrin interactor 1	CLINT1	70.358	_AS(ph)PDQNASTHTF
Q14684	513	S	Ribosomal RNA proc	RRP1B	129.37	_GS(ph)PTGGAQLLK_
Q14684	732	S	Ribosomal RNA proc	RRP1B	105.53	_TPTSS(ph)PASSPLVA
Q14690	1360	S	Protein RRP5 homolc	PDCD11	137.27	_YSHVSQHS(ph)PSKK
Q14692	552	S	Ribosome biogenesis	BMS1	95.067	_AGLS(ph)PANCQSDF
Q14692	639	S	Ribosome biogenesis	BMS1	153.65	_LGPQNFIDETS(ph)DI
Q14694	365	S	Ubiquitin carboxyl-ter	USP10	70.802	_YS(ph)PPAISPLVSEK
Q14694	576	S	Ubiquitin carboxyl-ter	USP10	283.08	_NHSVNEEEQEEQGE
Q14739	99	S	Lamin-B receptor	LBR	77.372	_SAS(ph)ASHQADIK_
Q14764	873	S	Major vault protein	MVP	73.259	_VASGPSPGEGIS(ph)
Q14814	251	S	Myocyte-specific enh	MEF2D	129.2	_VIPAKS(ph)PPPPTHS
Q14839	428	S	Chromodomain-helica	CHD4	204.47	_EDNS(ph)EGEEILEEV
Q14839	515	S	Chromodomain-helica	CHD4	64.002	_WGQPPS(ph)PTPVPI
Q14839	1553	T	Chromodomain-helica	CHD4	43.04	_TPTPSTPGDTQPNT(
Q14966	508	S	Zinc finger protein 63	ZNF638	109.83	_S(ph)RS(ph)PMHYMY
Q14966	510	S	Zinc finger protein 63	ZNF638	109.83	_S(ph)RS(ph)PMHYMY
Q14966	552	S	Zinc finger protein 63	ZNF638	68.49	_NPFRGS(ph)PK_
Q14966	605	S	Zinc finger protein 63	ZNF638	86.243	_GHS(ph)PAQKPK_
Q14966	1100	S	Zinc finger protein 63	ZNF638	120.93	_IDLPEVQIEHDPELEK
Q14966	1401	S	Zinc finger protein 63	ZNF638	73.499	_AVIVSS(ph)PK_
Q14978	366	S	Nucleolar and coiled-l	NOLC1	99.969	_AAESSSDSS(ph)DSD
Q14978	397	S	Nucleolar and coiled-l	NOLC1	71.879	_S(ph)PAVKPAAAPK_
Q14978	538	S	Nucleolar and coiled-l	NOLC1	69.314	_GS(ph)PRPQAPK_
Q14978	607	T	Nucleolar and coiled-l	NOLC1	66.004	_LQT(ph)PNT(ph)FPK_
Q14978	610	T	Nucleolar and coiled-l	NOLC1	66.004	_LQT(ph)PNT(ph)FPK_
Q14980	169	S	Nuclear mitotic appar	NUMA1	133.15	_APVPSTCSSTFPEEL
Q14980	1757	S	Nuclear mitotic appar	NUMA1	205.39	_TQPDGTSVPGEPAS
Q14980	2000	T	Nuclear mitotic appar	NUMA1	182.64	_VSLEPHQGPGT(ph)P
Q15019	218	S	Septin-2	SEPT2	258.2	_IYHLPDAES(ph)DEDE
Q15020	8	S	Squamous cell carcin	SART3	185.85	_(ac)ATAAETS(ph)ASE

Q15020	10	S	Squamous cell carcin	SART3	244.52	_(ac)ATAAETSAS(ph)E
Q15029	19	S	116 kDa U5 small nuc	EFTUD2	178.89	_(ac)MDTDLYDEFGNY
Q15050	5	S	Ribosome biogenesis	RRS1	55.011	_(ac)MEGQS(ph)VEEL
Q15052	488	S	Rho guanine nucleoti	ARHGEF6;ARHGI	84.479	_MS(ph)GFIYQGK_
Q15054	307	S	DNA polymerase delt	POLD3	220.42	_VALS(ph)DDETKETE
Q15057	521	S	Arf-GAP with coiled-c	ACAP2	63.682	_YSISLS(ph)PPEQQK_
Q15059	263	S	Bromodomain-contair	BRD3	75.89	_SES(ph)PPPLSDPK_
Q15061	77	S	WD repeat-containing	WDR43	88.075	_LQAKES(ph)PQRK_
Q15084	428	S	Protein disulfide-isom	PDIA6	100.24	_DGELPVEDDIDLS(ph
Q15118	163	Y	[Pyruvate dehydroger	PDK1	33.547	_HNDVIPTM(ox)AQGV
Q15131	196	T	Cyclin-dependent kin	CDK10	65.038	_AYGVPVKPMT(ph)PK
Q15149	125	S	Plectin	PLEC	193.06	_TPHVQAVQGPLGS(p
Q15149	149	S	Plectin	PLEC	217.82	_ELEEVS(ph)PETPVV
Q15149	1047	S	Plectin	PLEC	64.82	_SWS(ph)LATFR_
Q15149	1352	S	Plectin	PLEC	40.363	_ES(ph)ADPLGAWLQI
Q15149	1435	S	Plectin	PLEC	130.61	_AQLEPVAS(ph)PAK_
Q15149	1721	S	Plectin	PLEC	94.409	_RAS(ph)FAEK_
Q15149	4030	T	Plectin	PLEC	128.95	_QIT(ph)MEELVR_
Q15149	4382	S	Plectin	PLEC	131.56	_S(ph)RSS(ph)S(ph)VC
Q15149	4385	S	Plectin	PLEC	138.28	_SRS(ph)S(ph)S(ph)VC
Q15149	4386	S	Plectin	PLEC	194.08	_S(ph)RSS(ph)S(ph)VC
Q15149	4389	S	Plectin	PLEC	171.91	_SSS(ph)VGS(ph)SSS
Q15149	4396	S	Plectin	PLEC	175.34	_SSSVGSSSSYPIS(ph
Q15149	4406	S	Plectin	PLEC	305.22	_TQLAS(ph)WSDPTEE
Q15149	4408	S	Plectin	PLEC	72.214	_TQLASWS(ph)DPTEE
Q15149	4613	S	Plectin	PLEC	203.33	_GYYS(ph)PYSVSGSC
Q15149	4616	S	Plectin	PLEC	190.79	_GYYSPYS(ph)VSGSC
Q15149	4618	S	Plectin	PLEC	187.76	_GYYSPYSVS(ph)GSC
Q15149	4622	S	Plectin	PLEC	203.33	_GYYSPYSVSGSGS(p
Q15149	4626	S	Plectin	PLEC	197.38	_GYYS(ph)PYSVSGSC
Q15154	65	S	Pericentriolar materia	PCM1	140.8	_VTNDIS(ph)PESSPGV
Q15154	533	S	Pericentriolar materia	PCM1	52.858	_KDEETEES(ph)EYDS
Q15154	537	S	Pericentriolar materia	PCM1	55.74	_KDEETEES(ph)EYDS
Q15154	1730	S	Pericentriolar materia	PCM1	134.14	_ILEDHGS(ph)PAGEID
Q15154	1765	S	Pericentriolar materia	PCM1	72.683	_NVRS(ph)DIS(ph)DQE
Q15154	1768	S	Pericentriolar materia	PCM1	72.683	_NVRS(ph)DIS(ph)DQE
Q15154	1776	S	Pericentriolar materia	PCM1	187.43	_SDISDQEEDEES(ph)
Q15185	113	S	Prostaglandin E synth	PTGES3	318.09	_DWEDDS(ph)DEDMS
Q15185	148	S	Prostaglandin E synth	PTGES3	56.957	_FSEMMNNMGGDEDV
Q15185	151	S	Prostaglandin E synth	PTGES3	145.04	_FSEMMNNMGGDEDV
Q15233	428	T	Non-POU domain-cor	NONO	76.938	_GAMPPAPVPAGTPA
Q15233	450	T	Non-POU domain-cor	NONO	76	_FGQAATMEGIGAIGG
Q15269	891	S	Periodic tryptophan p	PWP2	44.604	_SLDPLGS(ph)EEEAE
Q15269	898	S	Periodic tryptophan p	PWP2	44.604	_SLDPLGS(ph)EEEAE
Q15269	902	S	Periodic tryptophan p	PWP2	44.604	_SLDPLGS(ph)EEEAE
Q15269	913	S	Periodic tryptophan p	PWP2	44.604	_SLDPLGS(ph)EEEAE
Q15345	357	S	Leucine-rich repeat-c	LRRC41	98.21	_S(ph)PSAPAATSSAS
Q15361	65	S	Transcription termina	TTF1	52.599	_DFQHLISS(ph)PLKK_
Q15365	173	S	Poly(rC)-binding prote	PCBP1	115.42	_QICLVMLETLSQS(ph
Q15365	189	S	Poly(rC)-binding prote	PCBP1	165.42	_VMTIPYQPMPAS(ph)
Q15365	190	S	Poly(rC)-binding prote	PCBP1	203.06	_VMTIPYQPMPASS(pl
Q15366	188	S	Poly(rC)-binding prote	PCBP2	139.08	_PSS(ph)SPVIFAGGQ
Q15366	189	S	Poly(rC)-binding prote	PCBP2	121.72	_PKPSSS(ph)PVIFAG(
Q15388	135	S	Mitochondrial import r	TOMM20	94.639	_IVS(ph)AQSLAEDDVI

Q15424	21	S	Scaffold attachment f	SAFB	120.69	_(ac)AETLSGLGDSGA
Q15424	24	S	Scaffold attachment f	SAFB	290.1	_(ac)AETLSGLGDSGA
Q15424	234	S	Scaffold attachment f	SAFB2;SAFB	89.689	_SEPVKEES(ph)SELE
Q15424	247	S	Scaffold attachment f	SAFB2;SAFB	121.9	_SEPVKEESSELEQPF
Q15424	344	S	Scaffold attachment f	SAFB2;SAFB	164.02	_TDCEPVGLEPAVEQS
Q15424	383	S	Scaffold attachment f	SAFB	208.34	_ESSTSEGADQKMS(p
Q15424	384	S	Scaffold attachment f	SAFB	208.34	_ESSTSEGADQKMS(p
Q15424	604	S	Scaffold attachment f	SAFB	66.568	_SVVS(ph)FDK_
Q15459	329	S	Splicing factor 3A sut	SF3A1	76.899	_FGESEEVEMEVES(p
Q15459	359	S	Splicing factor 3A sut	SF3A1	152.23	_AEEPPSQLDQDTQV(
Q15477	256	S	Helicase SKI2W	SKIV2L	107.17	_ASS(ph)LEDLVLK_
Q15554	323	S	Telomeric repeat-binc	TERF2	129.98	_DLVLPTQALPAS(ph)I
Q15637	80	S	Splicing factor 1	SF1	119.78	_TGDLGIPPNPEDRS(p
Q15637	82	S	Splicing factor 1	SF1	119.78	_TGDLGIPPNPEDRS(p
Q15642	296	S	Cdc42-interacting pro	TRIP10	111.45	_APS(ph)DSSLGTPSD
Q15648	770	S	Mediator of RNA poly	MED1	85.214	_MVRLS(ph)S(ph)SDS
Q15648	771	S	Mediator of RNA poly	MED1	127.24	_MVRLS(ph)S(ph)SDS
Q15648	774	S	Mediator of RNA poly	MED1	85.214	_MVRLS(ph)S(ph)SDS
Q15648	1051	T	Mediator of RNA poly	MED1	57.366	_SQT(ph)PPGVATPPIF
Q15648	1156	S	Mediator of RNA poly	MED1	113.05	_NSSQSGGKPGSS(ph
Q15648	1207	S	Mediator of RNA poly	MED1	78.758	_LAS(ph)PMKPVPGT(p
Q15648	1215	T	Mediator of RNA poly	MED1	78.758	_LASPMKPVPGT(ph)P
Q15651	6	S	High mobility group n	HMGN3	115.35	_RKS(ph)PENTEGK_
Q15678	594	S	Tyrosine-protein phos	PTPN14	93.909	_YVSGSS(ph)PDLVTR
Q15696	349	S	U2 small nuclear ribo	ZRSR2	68.786	_DIYLS(ph)PDR_
Q15717	202	S	ELAV-like protein 1	ELAVL1	183.22	_NVALLSQLYHS(ph)P
Q15746	305	S	Myosin light chain kin	MYLK	121.26	_GGS(ph)PPWAANSQ
Q15746	365	S	Myosin light chain kin	MYLK	56.121	_APGLGVLS(ph)PSGE
Q15746	1779	S	Myosin light chain kin	MYLK	42.58	_SSTGSPTS(ph)PLNA
Q15773	238	S	Myeloid leukemia fact	MLF2	130.95	_LAIQGPEDS(ph)PSR
Q15773	240	S	Myeloid leukemia fact	MLF2	93.237	_LAIQGPEDSPS(ph)R
Q15796	8	T	Mothers against deca	SMAD2	103.11	_(ac)SSILPFT(ph)PPV
Q15910	367	T	Histone-lysine N-met	EZH2	134.02	_PST(ph)PTINVLESK_
Q15910	487	T	Histone-lysine N-met	EZH2	129.26	_ESSIIAPAPAEDVDT(
Q15911	2795	S	Zinc finger homeobox	ZFHX3	88.495	_TMELS(ph)PR_
Q15942	267	S	Zyxin	ZYX	58.246	_FS(ph)PVTPK_
Q15942	344	S	Zyxin	ZYX	67.234	_S(ph)PGAPGPLTLK_
Q16181	334	S	Septin-7	SEPT7	79.875	_S(ph)PLAQMEEER_
Q16204	244	S	Coiled-coil domain-co	CCDC6	60.317	_LDQPVS(ph)APPS(ph
Q16512	916	S	Serine/threonine-prot	PKN1	175.43	_TDVSNFDEEFTGEAF
Q16514	51	S	Transcription initiatior	TAF12	85.976	_LS(ph)PENNQVLTK_
Q16629	192	S	Serine/arginine-rich s	SRSF7	135.71	_YFQS(ph)PSR_
Q16629	194	S	Serine/arginine-rich s	SRSF7	116.05	_YFQSPS(ph)RS(ph)R
Q16629	196	S	Serine/arginine-rich s	SRSF7	104.24	_YFQSPS(ph)RS(ph)R
Q16629	215	S	Serine/arginine-rich s	SRSF7	57.785	_SRS(ph)PS(ph)PK_
Q16629	217	S	Serine/arginine-rich s	SRSF7	57.785	_SRS(ph)PS(ph)PK_
Q16629	225	S	Serine/arginine-rich s	SRSF7	68.626	_SPS(ph)GS(ph)PR_
Q16629	227	S	Serine/arginine-rich s	SRSF7	68.626	_SPS(ph)GS(ph)PR_
Q16629	233	S	Serine/arginine-rich s	SRSF7	37.696	_RS(ph)AS(ph)PER_
Q16630	404	T	Cleavage and polyad	CPSF6	79.892	_EMDT(ph)ARTPLSEA
Q16630	407	T	Cleavage and polyad	CPSF6	125.91	_EMDTART(ph)PLSEA
Q16637	25	T	Survival motor neuror	SMN1	52.09	_GT(ph)GQS(ph)DDSD
Q16637	28	S	Survival motor neuror	SMN1	222.18	_GTGQS(ph)DDSDIWD
Q16637	31	S	Survival motor neuror	SMN1	165.53	_GTGQS(ph)DDS(ph)D

Q16643	142	S	Drebrin	DBN1	92.051	_LSS(ph)PVLHR_
Q16643	337	S	Drebrin	DBN1	252.44	_S(ph)PS(ph)DSSTAS
Q16643	339	S	Drebrin	DBN1	262.17	_S(ph)PS(ph)DSSTAS
Q16649	301	S	Nuclear factor interleu	NFIL3	78.964	_GPIHS(ph)PVELK_
Q17RY0	97	S	Cytoplasmic polyader	CPEB4	36.464	_QQLS(ph)PSPGQEA(
Q1ED39	42	S	Lysine-rich nucleolar	KNOP1	190.83	_YSVLNNDDYFADVS(
Q1ED39	310	T	Lysine-rich nucleolar	KNOP1	90.211	_ESGVAGDPWKEETD
Q1KMD3	161	S	Heterogeneous nucle	HNRNPUL2	213.88	_EEDEPEERS(ph)GDE
Q1KMD3	165	T	Heterogeneous nucle	HNRNPUL2	72.207	_EEDEPEERS(ph)GDE
Q1KMD3	228	S	Heterogeneous nucle	HNRNPUL2	157.42	_SKS(ph)PLPPEEEAK
Q1MSJ5	459	S	Centrosome and spin	CSPP1	115.57	_VAASGAQDPEKS(ph
Q27J81	589	S	Inverted formin-2	INF2	124.51	_EHNSMWASLSS(ph)I
Q27J81	1188	S	Inverted formin-2	INF2	156.73	_GARPPAAGPGGDED
Q2KHR2	225	S	DNA-binding protein F	RFX7	51.727	_LQS(ph)PLPGESAAK
Q2KHR3	1211	S	Glutamine and serine	QSER1	121.39	_PSSTTPTPLVSETGG
Q2M2I3	4	S	Protein FAM83E	FAM83E	93.776	_(ac)AAS(ph)QLAALEC
Q2M2I8	606	T	AP2-associated prote	AAK1	76.82	_VQTT(ph)PPPAVQGC
Q2TBE0	479	S	CWF19-like protein 2	CWF19L2	49.448	_STFAGS(ph)PER_
Q3B726	316	S	DNA-directed RNA pc	TWISTNB	115.56	_KHS(ph)EEAEFTPPLI
Q3KQU3	86	S	MAP7 domain-contair	MAP7D1	64.24	_PAPPQEES(ph)PSSE
Q3KQU3	460	S	MAP7 domain-contair	MAP7D1	94.569	_LSASTASELS(ph)PK_
Q3KQU3	496	S	MAP7 domain-contair	MAP7D1	44.6	_PASPCPSPGPGHTLI
Q3KR37	274	S	GRAM domain-contai	GRAMD1B	122.44	_SSIETKPDAS(ph)PQI
Q3L8U1	550	S	Chromodomain-helica	CHD9	63.392	_VMS(ph)PENFPTASV
Q3L8U1	1468	S	Chromodomain-helica	CHD9	72.913	_DELAELS(ph)EAES(p
Q3L8U1	1472	S	Chromodomain-helica	CHD9	103.02	_DELAELS(ph)EAES(p
Q3MHD2	75	T	Protein LSM12 homol	LSM12	100.58	_TET(ph)PPPLASLNVS
Q3YBR2	10	S	Transforming growth	TBRG1	141.82	_(ac)SLLDGLASS(ph)F
Q49AG3	387	S	Zinc finger BED dom	ZBED5	56.258	_IMPTS(ph)LK_
Q4G0J3	258	S	La-related protein 7	LARP7	205.07	_SRPTS(ph)EGS(ph)D
Q4G0J3	261	S	La-related protein 7	LARP7	243.52	_SRPTS(ph)EGS(ph)D
Q4G0J3	300	S	La-related protein 7	LARP7	66.246	_SSS(ph)EDAESLAPR
Q4G0J3	337	S	La-related protein 7	LARP7	140.48	_DIEIS(ph)T(ph)EEEKI
Q4G0J3	338	T	La-related protein 7	LARP7	140.48	_DIEIS(ph)T(ph)EEEKI
Q4KMP7	678	S	TBC1 domain family r	TBC1D10B	86.498	_AAGGAPS(ph)PPPP\
Q53EP0	208	S	Fibronectin type III do	FNDC3B	102.45	_LNS(ph)PPSSIYK_
Q53F19	25	S	Uncharacterized prote	C17orf85	156.08	_AEAPAGPALGLPS(pI
Q53F19	415	S	Uncharacterized prote	C17orf85	58.511	_MISTPS(ph)PK_
Q53F19	500	S	Uncharacterized prote	C17orf85	72.243	_RPHS(ph)PEK_
Q53HL2	219	S	Borealin	CDCA8	82.609	_IYNISGNGS(ph)PLAI
Q56P03	109	S	E2F-associated phos	EAPP	120.32	_YYDDIYFDS(ph)DS(p
Q56P03	111	S	E2F-associated phos	EAPP	120.32	_YYDDIYFDS(ph)DS(p
Q5BKY1	175	S	Leucine-rich repeat-c	LRRC10	34.692	_TIWLS(ph)GNR_
Q5C9Z4	139	S	Nucleolar MIF4G dom	NOM1	71.08	_ARPAPSRDPS(ph)PF
Q5H9F3	1192	S	BCL-6 corepressor-lik	BCORL1	127.2	_KPTKPESQS(ph)PGK
Q5H9R7	617	S	Serine/threonine-prot	PPP6R3	201.15	_IQQFDDGGS(ph)DEE
Q5HYJ3	193	S	Protein FAM76B	FAM76B	148.15	_ISNLS(ph)PEEEQGL\
Q5JSZ5	388	S	Protein PRRC2B	PRRC2B	87.319	_LKFS(ph)DDEEEEEV
Q5JSZ5	556	S	Protein PRRC2B	PRRC2B	63.181	_EVPWS(ph)PSAEK_
Q5JTD0	300	S	Tight junction-associa	TJAP1	105.9	_GS(ph)PEEELPLPAFI
Q5JTH9	1080	S	RRP12-like protein	RRP12	289.43	_GDSIEEILADS(ph)ED
Q5JTV8	143	S	Torsin-1A-interacting	TOR1AIP1	214.65	_LQQQHSEQPPLQPS
Q5JTV8	156	S	Torsin-1A-interacting	TOR1AIP1	338.81	_DSHS(ph)S(ph)EEDE
Q5JTV8	157	S	Torsin-1A-interacting	TOR1AIP1	338.81	_DSHS(ph)S(ph)EEDE

Q5JTV8	220	T	Torsin-1A-interacting	TOR1AIP1	125.97	_VNFSEEGET(ph)EED
Q5JVS0	108	S	Intracellular hyaluron	HABP4	66.36	_SLPAPVAQRPDS(ph)
Q5M775	134	S	Cytospin-B	SPECC1	106.87	_SVSS(ph)PTSSNTPT
Q5M775	847	S	Cytospin-B	SPECC1	47.991	_S(ph)PLSGIPVR_
Q5QJE6	117	S	Deoxynucleotidyltrans	DNTTIP2	173.19	_QILIACS(ph)PVSSVR
Q5QJE6	141	S	Deoxynucleotidyltrans	DNTTIP2	236.5	_ESYTEEIVS(ph)EAES
Q5SNT2	441	S	Transmembrane prot	TMEM201	70.628	_RTS(ph)PSSLPGR_
Q5SSJ5	51	T	Heterochromatin prot	HP1BP3	94.09	_TVNSTRET(ph)PPK_
Q5SSJ5	156	S	Heterochromatin prot	HP1BP3	78.814	_QTPMASS(ph)PRPK_
Q5SSJ5	441	S	Heterochromatin prot	HP1BP3	100.17	_KEPDDSRDEDEDED
Q5SSJ5	442	S	Heterochromatin prot	HP1BP3	55.884	_KEPDDSRDEDEDED
Q5SSJ5	446	S	Heterochromatin prot	HP1BP3	55.884	_KEPDDSRDEDEDED
Q5SW79	356	S	Centrosomal protein	CEP170	89.358	_S(ph)IKS(ph)DVPVYL
Q5SW79	359	S	Centrosomal protein	CEP170	89.358	_S(ph)IKS(ph)DVPVYL
Q5SY16	487	S	Polynucleotide 5'-hyd	NOL9	183.48	_LAAFADALEFADEEK
Q5T035	32	S	Putative uncharacteri	C9orf129;FAM120	56.36	_PVAPQVPS(ph)PGGA
Q5T1M5	956	S	FK506-binding protein	FKBP15	186.54	_RPS(ph)QEQSASAS
Q5T1M5	1162	S	FK506-binding protein	FKBP15	66.152	_SS(ph)LS(ph)GDEED
Q5T1M5	1164	S	FK506-binding protein	FKBP15	66.152	_SS(ph)LS(ph)GDEED
Q5T200	77	S	Zinc finger CCCH dor	ZC3H13	73.834	_RS(ph)PERPTGDLR_
Q5T200	198	S	Zinc finger CCCH dor	ZC3H13	119.39	_KEVS(ph)PEVVR_
Q5T200	207	S	Zinc finger CCCH dor	ZC3H13	74.737	_SKLS(ph)PS(ph)PSLF
Q5T200	209	S	Zinc finger CCCH dor	ZC3H13	95.483	_LSPS(ph)PSLR_
Q5T200	242	S	Zinc finger CCCH dor	ZC3H13	114.31	_TSAVSS(ph)PLLDQQ
Q5T200	263	T	Zinc finger CCCH dor	ZC3H13	128.95	_T(ph)PS(ph)PPPPIPE
Q5T200	265	S	Zinc finger CCCH dor	ZC3H13	128.95	_T(ph)PS(ph)PPPPIPE
Q5T200	318	S	Zinc finger CCCH dor	ZC3H13	143.94	_S(ph)TS(ph)PAGQHH
Q5T200	325	S	Zinc finger CCCH dor	ZC3H13	113.05	_ST(ph)S(ph)PAGQHH
Q5T200	364	T	Zinc finger CCCH dor	ZC3H13	112.41	_TLT(ph)PPLR_
Q5T200	370	S	Zinc finger CCCH dor	ZC3H13	106.22	_S(ph)AS(ph)PYPSHS
Q5T200	372	S	Zinc finger CCCH dor	ZC3H13	143.09	_S(ph)AS(ph)PYPSHS
Q5T200	380	S	Zinc finger CCCH dor	ZC3H13	188.96	_SASPYPSHSLS(ph)S
Q5T200	381	S	Zinc finger CCCH dor	ZC3H13	152.59	_SAS(ph)PYPSHSLSS
Q5T200	642	S	Zinc finger CCCH dor	ZC3H13	79.875	_ERDQRPS(ph)SPIR_
Q5T200	643	S	Zinc finger CCCH dor	ZC3H13	96.464	_ERDQRPSS(ph)PIR_
Q5T200	875	S	Zinc finger CCCH dor	ZC3H13	40.493	_S(ph)LS(ph)PSHLTED
Q5T200	877	S	Zinc finger CCCH dor	ZC3H13	138.21	_SLS(ph)PSHLTEDR_
Q5T200	993	S	Zinc finger CCCH dor	ZC3H13	199.75	_GNIETTSEDGQVFS(
Q5T200	1010	S	Zinc finger CCCH dor	ZC3H13	194.56	_S(ph)KGDSDISDEEA
Q5T200	1017	S	Zinc finger CCCH dor	ZC3H13	107.47	_SKGDSDIS(ph)DEEA
Q5T200	1208	S	Zinc finger CCCH dor	ZC3H13	139.86	_LRS(ph)PSNDSAHR_
Q5T200	1455	S	Zinc finger CCCH dor	ZC3H13	127.09	_LDDAHSLGS(ph)GAG
Q5T200	1465	S	Zinc finger CCCH dor	ZC3H13	127.09	_LDDAHSLGS(ph)GAG
Q5T481	876	S	RNA-binding protein	RBM20	78.814	_EAEFS(ph)DPENTR_
Q5T481	1047	S	RNA-binding protein	RBM20	136.66	_GVESSDVHPAPTVQ
Q5T4S7	2719	S	E3 ubiquitin-protein li	UBR4	122.7	_HVTLPSS(ph)PR_
Q5T5C0	759	S	Syntaxin-binding prot	STXBP5	133.16	_KLS(ph)LPTDLKPDLL
Q5T5U3	1430	S	Rho GTPase-activatir	ARHGAP21	49.66	_AQPS(ph)S(ph)S(ph)E
Q5T5U3	1431	S	Rho GTPase-activatir	ARHGAP21	49.66	_AQPS(ph)S(ph)S(ph)E
Q5T5U3	1432	S	Rho GTPase-activatir	ARHGAP21	49.66	_AQPS(ph)S(ph)S(ph)E
Q5T5U3	1604	S	Rho GTPase-activatir	ARHGAP21	57.148	_LS(ph)PEVQSVAESK
Q5T5Y3	1080	S	Calmodulin-regulated	CAMSAP1	107.06	_APVHFVEPLS(ph)PT
Q5T6F0	15	S	DDB1- and CUL4-ass	DCAF12	56.573	_APAS(ph)PGAGSDA
Q5T8D3	196	S	Acyl-CoA-binding don	ACBD5	271.97	_AESSDS(ph)GAES(ph

Q5T8D3	200	S	Acyl-CoA-binding don	ACBD5	271.97	_AESSDS(ph)GAES(ph
Q5T8D3	262	S	Acyl-CoA-binding don	ACBD5	90.758	_S(ph)TEEVKPIDENLC
Q5T8P6	127	S	RNA-binding protein 2	RBM26	76.358	_LNHS(ph)PPQSSSR_
Q5TAQ9	99	S	DDB1- and CUL4-ass	DCAF8	52.522	_VHDRS(ph)EEEEEEE
Q5TGY3	46	S	AT-hook DNA-binding	AHDC1	69.979	_PLLPTRPPAS(ph)PPI
Q5VSL9	335	S	Striatin-interacting pro	STRIP1	144.82	_AAS(ph)PPASASDLIE
Q5VT06	2460	S	Centrosome-associat	CEP350	89.232	_LLELKS(ph)PTELMK_
Q5VT52	374	S	Regulation of nuclear	RPRD2	216.65	_DVEDMELS(ph)DVED
Q5VT52	485	S	Regulation of nuclear	RPRD2	117.03	_PSPGTPTS(ph)PSNL
Q5VT52	593	S	Regulation of nuclear	RPRD2	185.71	_SFNYS(ph)PNSSTSE
Q5VT52	723	T	Regulation of nuclear	RPRD2	108.94	_GPTSTSIDNIDGT(ph)
Q5VT52	758	S	Regulation of nuclear	RPRD2	118.16	_IIS(ph)PGSSTPSSTR
Q5VTL8	527	S	Pre-mRNA-splicing fa	PRPF38B	153.23	_RRS(ph)QSIEQES(ph
Q5VTL8	534	S	Pre-mRNA-splicing fa	PRPF38B	153.23	_RRS(ph)QSIEQES(ph
Q5VTR2	136	S	E3 ubiquitin-protein li	RNF20	157.22	_ALVVPEPEPDS(ph)D
Q5VTR2	138	S	E3 ubiquitin-protein li	RNF20	106.86	_ALVVPEPEPDSDS(ph
Q5VU43	1302	S	Myomegalin	PDE4DIP	32.858	_EETTSPECEEHNS(ph
Q5VUA4	40	S	Zinc finger protein 31	ZNF318	105.89	_RSS(ph)PPPPPSGSS
Q5VUA4	136	S	Zinc finger protein 31	ZNF318	150.22	_S(ph)PGLCSDSLEK_
Q5VUA4	1037	S	Zinc finger protein 31	ZNF318	78.191	_TKS(ph)PKPAESPQS
Q5VWN6	2009	S	Protein FAM208B	FAM208B	56.081	_ES(ph)PTQISIGAFPS
Q5VWN6	2037	S	Protein FAM208B	FAM208B	82.639	_SRS(ph)PLLVTVVESI
Q5VZ89	732	S	DENN domain-contai	DENND4C	69.492	_HSQPS(ph)PEPHS(ph
Q5VZ89	737	S	DENN domain-contai	DENND4C	93.278	_HSQPS(ph)PEPHS(ph
Q5VZ89	863	S	DENN domain-contai	DENND4C	61.959	_THS(ph)FENVSCHLP
Q5VZK9	1094	S	Leucine-rich repeat-c	LRRC16A	58.093	_SERPPTILMTEEPSS(
Q5VZL5	122	S	Zinc finger MYM-type	ZMYM4	229.89	_VTQHES(ph)DNENEI(
Q63HN8	1258	S	E3 ubiquitin-protein li	RNF213	200.04	_EDQEAAELLS(ph)EP
Q63HN8	2273	S	E3 ubiquitin-protein li	RNF213	146.68	_DFATPSLHTSDQS(ph
Q63ZY3	19	S	KN motif and ankyrin	KANK2	72.073	_(ac)AQVLHVPAPFPG
Q63ZY3	323	S	KN motif and ankyrin	KANK2	58.324	_QADPQPQAWPPPDS
Q63ZY3	375	S	KN motif and ankyrin	KANK2	79.676	_ALAMPGRPES(ph)PF
Q63ZY6	258	T	Putative methyltransf	NSUN5P2	66.152	_ASAPERT(ph)PS(ph)I
Q63ZY6	260	S	Putative methyltransf	NSUN5P2	66.152	_ASAPERT(ph)PS(ph)I
Q641Q2	619	S	WASH complex subu	FAM21A;FAM21B	76.899	_ASALLFS(ph)S(ph)DE
Q641Q2	620	S	WASH complex subu	FAM21A;FAM21B	76.899	_ASALLFS(ph)S(ph)DE
Q66K74	657	S	Microtubule-associate	MAP1S	123.35	_LSLS(ph)PLR_
Q66K74	731	S	Microtubule-associate	MAP1S	102.21	_SAS(ph)PHDVDLCLV
Q66K74	759	S	Microtubule-associate	MAP1S	133.81	_AVPMAPAPAS(ph)PC
Q66PJ3	271	S	ADP-ribosylation fact	ARL6IP4	139.81	_S(ph)AGEEEDGPVLT
Q68CZ2	332	S	Tensin-3	TNS3	115.77	_WDS(ph)YENLSADGI
Q68CZ2	660	S	Tensin-3	TNS3	112.57	_GVGSGPHPPDTQQF
Q68CZ2	969	S	Tensin-3	TNS3	51.505	_PTGS(ph)PLSAEFSG
Q68DK7	205	S	Male-specific lethal 1	MSL1	76.049	_S(ph)PLGGGGGSGA
Q68DK7	362	S	Male-specific lethal 1	MSL1	84.327	_HS(ph)PIKEEPCGSLS
Q68E01	502	S	Integrator complex su	INTS3	117.35	_EKFPEFCSSPS(ph)P
Q68EM7	575	S	Rho GTPase-activatir	ARHGAP17	95.002	_AESSSGGGTVPSSA(
Q68EN5	393	Y	Uncharacterized prote	KIAA0895L	30.612	_DQVY(ph)LDGIVR_
Q69YH5	756	S	Cell division cycle-ass	CDCA2	38.875	_IS(ph)PDLNIK_
Q69YH5	934	S	Cell division cycle-ass	CDCA2	114.01	_TICTFDSSGFES(ph)M
Q69YH5	936	S	Cell division cycle-ass	CDCA2	143.07	_TICTFDSSGFESMS(p
Q69YN4	133	S	Protein virilizer homol	KIAA1429	86.543	_VIS(ph)HDRDSPPPPI
Q69YN4	138	S	Protein virilizer homol	KIAA1429	78.642	_VISHDRDS(ph)PPPPI
Q69YN4	1578	S	Protein virilizer homol	KIAA1429	140.82	_SFLSEPS(ph)SPGR_

Q69YN4	1579	S	Protein virilizer homol	KIAA1429	157.09	_SFLSEPSS(ph)PGR_
Q69YQ0	220	S	Cytospin-A	SPECC1L	239.87	_AQLGINEDHS(ph)EG
Q69YQ0	384	S	Cytospin-A	SPECC1L	56.416	_KGS(ph)SGNASEVS\
Q69YQ0	832	S	Cytospin-A	SPECC1L	120.9	_RSS(ph)TSSEPTPTV
Q6IAA8	27	S	Ragulator complex pr	LAMTOR1	135.81	_LLLDPSS(ph)PPTK_
Q6IAA8	98	S	Ragulator complex pr	LAMTOR1	61.444	_LAVLSSS(ph)LTHWK
Q6IBW4	284	S	Condensin-2 complex	NCAPH2	97.463	_S(ph)PQQSAALPR_
Q6IE81	89	S	Protein Jade-1	PHF17	54.668	_GVQVPVS(ph)PGTIP
Q6IN85	117	S	Serine/threonine-prot	SMEK1	84.478	_DPSVDITQDLVDES(p
Q6IQ22	106	S	Ras-related protein R	RAB12	63.091	_FNS(ph)ITSAYYR_
Q6IQ23	903	S	Pleckstrin homology (	PLEKHA7	74.778	_KVTS(ph)PLQS(ph)P
Q6IQ23	907	S	Pleckstrin homology (	PLEKHA7	74.778	_KVTS(ph)PLQS(ph)P
Q6IQ49	278	S	Protein SDE2 homolo	SDE2	159.86	_VVNTDHGS(ph)PEQL
Q6KC79	350	S	Nipped-B-like protein	NIPBL	99.238	_AAMYDIISS(ph)PSK_
Q6KC79	1089	S	Nipped-B-like protein	NIPBL	112.39	_YAEIS(ph)S(ph)DEDN
Q6KC79	1090	S	Nipped-B-like protein	NIPBL	112.39	_YAEIS(ph)S(ph)DEDN
Q6KC79	1096	S	Nipped-B-like protein	NIPBL	112.39	_YAEIS(ph)S(ph)DEDN
Q6KC79	2658	S	Nipped-B-like protein	NIPBL	156.57	_AITSLLGGGS(ph)PK_
Q6MZP7	310	S	Protein lin-54 homolo	LIN54	78.249	_IAIS(ph)PLKS(ph)PNK
Q6MZP7	314	S	Protein lin-54 homolo	LIN54	78.249	_IAIS(ph)PLKS(ph)PNK
Q6N043	545	S	Zinc finger protein 28	ZNF280D	107.87	_ASVGPLQSGASPTPS
Q6NUK4	210	S	Receptor expression-	REEP3	47.371	_TDEEAEGPYS(ph)DN
Q6NWY9	764	S	Pre-mRNA-processin	PRPF40B	103.75	_GS(ph)PSSHLLGADH
Q6NWY9	832	S	Pre-mRNA-processin	PRPF40B	88.574	_ELQQAELPNRS(ph)P
Q6NYC8	125	S	Phostensin	PPP1R18	82.489	_RPS(ph)PGEMR_
Q6NYC8	224	S	Phostensin	PPP1R18	73.273	_LS(ph)PGESAYQK_
Q6NZI2	202	S	Polymerase I and trar	PTRF	156.9	_EGEELGEGERPEED
Q6NZI2	203	S	Polymerase I and trar	PTRF	156.9	_EGEELGEGERPEED
Q6NZI2	365	S	Polymerase I and trar	PTRF	110.13	_RGS(ph)S(ph)PDVHA
Q6NZI2	366	S	Polymerase I and trar	PTRF	110.13	_RGS(ph)S(ph)PDVHA
Q6NZY4	479	T	Zinc finger CCHC dor	ZCCHC8	75.018	_GT(ph)PPPVFTPPLP
Q6NZY4	598	S	Zinc finger CCHC dor	ZCCHC8	165.58	_SEAGHASS(ph)PDSE
Q6NZY4	658	S	Zinc finger CCHC dor	ZCCHC8	103.35	_IHS(ph)PIPDMSK_
Q6P0N0	365	S	Mis18-binding protein	MIS18BP1	52.576	_NISKLS(ph)PPR_
Q6P158	132	S	Putative ATP-depend	DHX57	138.03	_GLS(ph)GEEEDDEPD
Q6P2E9	723	S	Enhancer of mRNA-d	EDC4	107.38	_GPGQVPTATSALSLE
Q6P2E9	729	S	Enhancer of mRNA-d	EDC4	152.31	_S(ph)PDVISSASTALS
Q6P2E9	879	S	Enhancer of mRNA-d	EDC4	120.3	_DSQDASAEQS(ph)DH
Q6P4E1	332	S	Protein CASC4	CASC4	74.296	_LIPGSNLDS(ph)EPR_
Q6P4R8	228	S	Nuclear factor related	NFRKB	84.687	_SPS(ph)PAVPLR_
Q6P4R8	351	S	Nuclear factor related	NFRKB	122.76	_SEAEDLAEPLSSTEG
Q6P4R8	1291	S	Nuclear factor related	NFRKB	95.205	_AVSTVVVTTAPS(ph)
Q6P6C2	64	S	RNA demethylase AL	ALKBH5	73.072	_YQEDS(ph)DPERS(pl
Q6P6C2	69	S	RNA demethylase AL	ALKBH5	73.072	_YQEDS(ph)DPERS(pl
Q6PCB5	6	S	Round spermatid bas	RSBN1L	71.296	_(ac)AEPPS(ph)PVHC
Q6PCE3	175	S	Glucose 1,6-bisphosp	PGM2L1	109.48	_AVAGVMITAS(ph)HN
Q6PD62	925	T	RNA polymerase-ass	CTR9	168.55	_GGEFDEFVNDDT(ph
Q6PD62	1020	S	RNA polymerase-ass	CTR9	98.135	_AIISSSDDS(ph)S(ph)I
Q6PD62	1021	S	RNA polymerase-ass	CTR9	98.135	_AIISSSDDS(ph)S(ph)I
Q6PID6	197	S	Tetratricopeptide repe	TTC33	95.954	_SEAPAEVTHFS(ph)P
Q6PJF5	177	S	Inactive rhomboid pro	RHBDF2	66.365	_DLELPSQEAPSFQGT
Q6PJG2	461	S	ELM2 and SANT dom	ELMSAN1	157.22	_RAS(ph)QEANLLTLA
Q6PJG2	704	T	ELM2 and SANT dom	ELMSAN1	138.72	_TNSAEVT(ph)PPVLS
Q6PJG2	996	S	ELM2 and SANT dom	ELMSAN1	121.92	_SHESNAPGS(ph)AG

Q6PJT7	409	S	Zinc finger CCCH dor	ZC3H14	122.53	_IS(ph)PPIKEEETKGD
Q6PJT7	515	S	Zinc finger CCCH dor	ZC3H14	145.86	_DLVQPDKPAS(ph)PK
Q6PJT7	527	S	Zinc finger CCCH dor	ZC3H14	50.647	_FIVTLDGVPS(ph)PP(
Q6PJT7	533	S	Zinc finger CCCH dor	ZC3H14	50.647	_FIVTLDGVPS(ph)PP(
Q6PKG0	75	S	La-related protein 1	LARP1	100.44	_ES(ph)PRPLQLPGAE
Q6PKG0	90	S	La-related protein 1	LARP1	162.16	_PLQLPGAEGPAIS(ph
Q6PKG0	548	S	La-related protein 1	LARP1	116.45	_GLSAS(ph)LPDLDSE
Q6PKG0	631	S	La-related protein 1	LARP1	59.732	_NTFT(ph)AWSDEES(
Q6PKG0	766	S	La-related protein 1	LARP1	75.743	_S(ph)LPTTVPES(ph)F
Q6PKG0	774	S	La-related protein 1	LARP1	158.91	_SLPTTVPES(ph)PNY
Q6PKG0	824	S	La-related protein 1	LARP1	205.53	_HSS(ph)NPPLESHVG
Q6PKG0	1071	T	La-related protein 1	LARP1	132.01	_PAAMISQPPT(ph)PP
Q6PL18	327	S	ATPase family AAA d	ATAD2	117.37	_KPNIFYSGPAS(ph)P/
Q6PL18	342	S	ATPase family AAA d	ATAD2	133.34	_LSSAGPRS(ph)PYCK
Q6PL18	1200	S	ATPase family AAA d	ATAD2	159.17	_IES(ph)DTEETQDTS\
Q6SPF0	161	S	Atherin	SAMD1	74.364	_AAAAAATAPPS(ph)P
Q6UB99	276	S	Ankyrin repeat domai	ANKRD11	80.541	_VANS(ph)PTMVNLLL
Q6UB99	834	S	Ankyrin repeat domai	ANKRD11	70.808	_FSLS(ph)DDQR_
Q6UN15	259	S	Pre-mRNA 3'-end-pro	FIP1L1	103.76	_AEFTS(ph)PPSLFK_
Q6UN15	492	S	Pre-mRNA 3'-end-pro	FIP1L1	221.47	_DHS(ph)PTPSVFNS(p
Q6UN15	500	S	Pre-mRNA 3'-end-pro	FIP1L1	227.64	_DHSPTPSVFNS(ph)D
Q6VMQ6	113	S	Activating transcriptio	ATF7IP	171.93	_NKQDDDLNCEPLS(p
Q6VMQ6	673	S	Activating transcriptio	ATF7IP	126.07	_RHEHPPNPPVS(ph)F
Q6WCQ1	220	S	Myosin phosphatase I	MPRIP	171.36	_TKDQPDGSSLS(ph)F
Q6WCQ1	224	S	Myosin phosphatase I	MPRIP	171.36	_TKDQPDGSSLS(ph)F
Q6WCQ1	289	S	Myosin phosphatase I	MPRIP	150.06	_AEEQQLPPPLS(ph)P
Q6WCQ1	292	S	Myosin phosphatase I	MPRIP	106.37	_AEEQQLPPPLS(ph)P
Q6WCQ1	326	S	Myosin phosphatase I	MPRIP	194.56	_AEHMETNAVGPS(ph
Q6WCQ1	362	S	Myosin phosphatase I	MPRIP	173.4	_DFTNEAPPAPLPDAS
Q6WCQ1	365	S	Myosin phosphatase I	MPRIP	186.68	_DFTNEAPPAPLPDAS
Q6WCQ1	619	S	Myosin phosphatase I	MPRIP	133.24	_S(ph)PGLPMSDLK_
Q6WCQ1	891	S	Myosin phosphatase I	MPRIP	146.25	_TLLTGDGGGEATGS(
Q6WCQ1	977	S	Myosin phosphatase I	MPRIP	218.98	_AATEALGEKS(ph)PD
Q6WCQ1	993	S	Myosin phosphatase I	MPRIP	73.082	_SKS(ph)NPDFLK_
Q6WKZ4	202	S	Rab11 family-interact	RAB11FIP1	158.21	_DSGSDTASAIIPSTTF
Q6Y7W6	26	S	PERQ amino acid-ric	GIGYF2	135.33	_ALSSGGSITS(ph)PPL
Q6Y7W6	236	S	PERQ amino acid-ric	GIGYF2	73.927	_WRPHS(ph)PDGPR_
Q6Y7W6	382	T	PERQ amino acid-ric	GIGYF2	202.95	_PGT(ph)PSDHQSQE/
Q6ZN18	18	S	Zinc finger protein AE	AEBP2	204.95	_(ac)AAAITDMADLEEL
Q6ZN18	24	S	Zinc finger protein AE	AEBP2	204.95	_(ac)AAAITDMADLEEL
Q6ZNJ1	225	S	Neurobeachin-like pro	NBEAL2	39.73	_ENGQMAVSDGS(ph)
Q6ZRP7	578	S	Sulfhydryl oxidase 2	QSOX2	251.76	_DNLLDTYSADQGDS(
Q6ZRS2	767	S	Helicase SRCAP	SRCAP	38.783	_WQSLLNFNS(ph)QR_
Q6ZRS2	1859	S	Helicase SRCAP	SRCAP	95.622	_SGPPS(ph)PPSTATS
Q6ZRS2	3016	S	Helicase SRCAP	SRCAP	74.793	_NPPS(ph)PRPSQLPV
Q6ZRV2	5	S	Protein FAM83H	FAM83H	48.892	_RS(ph)QSS(ph)S(ph)(
Q6ZRV2	8	S	Protein FAM83H	FAM83H	48.892	_RS(ph)QSS(ph)S(ph)(
Q6ZRV2	9	S	Protein FAM83H	FAM83H	48.892	_RS(ph)QSS(ph)S(ph)(
Q6ZRV2	523	S	Protein FAM83H	FAM83H	173.25	_HGS(ph)DPAFAPGPF
Q6ZRV2	647	S	Protein FAM83H	FAM83H	47.082	_VPVPGPGS(ph)GGN(
Q6ZRV2	785	S	Protein FAM83H	FAM83H	158.01	_S(ph)LESCLLDLR_
Q6ZRV2	870	S	Protein FAM83H	FAM83H	116.24	_GS(ph)PTSAYPER_
Q6ZRV2	881	S	Protein FAM83H	FAM83H	116.63	_KGS(ph)PTPGFSTR_
Q6ZRV2	892	S	Protein FAM83H	FAM83H	137.61	_RGS(ph)PTTGFIEQK_

Q6ZRV2	914	S	Protein FAM83H	FAM83H	98.676	_RGS(ph)PVPPVPER_
Q6ZRV2	925	S	Protein FAM83H	FAM83H	127.07	_RSS(ph)PVPPVPER_
Q6ZRV2	1003	S	Protein FAM83H	FAM83H	187.56	_RLS(ph)LGQGDSTEA
Q6ZSZ5	1103	S	Rho guanine nucleoti	ARHGEF18	46.129	_SLS(ph)PILPGR_
Q6ZU65	13	S	Ubinuclein-2	UBN2	108.32	_VAFISLS(ph)PVR_
Q6ZUT6	201	S	Uncharacterized prot	C15orf52	126.25	_S(ph)PPTQVAISSDSA
Q6ZV73	721	S	FYVE, RhoGEF and F	FGD6	94.717	_AES(ph)LDDQMLSR_
Q6ZV73	1197	S	FYVE, RhoGEF and F	FGD6	216.67	_S(ph)LDEADSENKEE
Q70E73	5	S	Ras-associated and p	RAPH1	77.868	_(ac)MEQLS(ph)DEEID
Q70E73	17	S	Ras-associated and p	RAPH1	77.868	_(ac)MEQLS(ph)DEEID
Q71DI3	81	T	Histone H3.2;Histone	HIST2H3A;HIST3	106.3	_EIAQDFKT(ph)DLR_
Q71RC2	583	S	La-related protein 4	LARP4	100.62	_DGLNQTTIPVS(ph)PF
Q71RC2	597	S	La-related protein 4	LARP4	159.56	_ASTAS(ph)PCNNNIN/
Q71RC2	722	S	La-related protein 4	LARP4	116.98	_EQYVPPRS(ph)PK_
Q76FK4	365	S	Nucleolar protein 8	NOL8	157.07	_VSCHDS(ph)DDDIMR
Q76FK4	378	S	Nucleolar protein 8	NOL8	84.529	_NDREYDS(ph)GDT(pl
Q76FK4	381	T	Nucleolar protein 8	NOL8	84.529	_NDREYDS(ph)GDT(pl
Q76FK4	890	S	Nucleolar protein 8	NOL8	191.97	_FLETDS(ph)EEEQEE
Q76FK4	1082	S	Nucleolar protein 8	NOL8	122.6	_LQDS(ph)S(ph)S(ph)E
Q76FK4	1083	S	Nucleolar protein 8	NOL8	122.6	_LQDS(ph)S(ph)S(ph)E
Q76FK4	1084	S	Nucleolar protein 8	NOL8	122.6	_LQDS(ph)S(ph)S(ph)E
Q76FK4	1099	S	Nucleolar protein 8	NOL8	99.796	_NSS(ph)PGEASLLEK
Q7KZ85	125	S	Transcription elongati	SUPT6H	183.44	_KMS(ph)DDEDDDEEE
Q7KZI7	212	S	Serine/threonine-prot	MARK2;MARK4;M	47.931	_LDTFCGS(ph)PPYAA
Q7L014	804	S	Probable ATP-depen	DDX46	249.69	_AALGLQDS(ph)DDED
Q7L1V2	61	S	Vacuolar fusion prote	MON1B	87.091	_DKDQPPSPS(ph)PPF
Q7L2J0	69	S	7SK snRNA methylph	MEPCE	189.51	_ES(ph)PGAAATSSSG
Q7L2J0	254	S	7SK snRNA methylph	MEPCE	42.709	_DITDPLSLNTCTDEGI
Q7L4E1	276	S	Protein FAM73B	FAM73B	96.673	_TLMLPLTEGS(ph)LR_
Q7L4I2	17	S	Arginine/serine-rich c	RSRC2	117.18	_DGLAPEKTS(ph)PDR
Q7L4I2	218	S	Arginine/serine-rich c	RSRC2	78.95	_SLS(ph)RT(ph)PS(ph)
Q7L4I2	220	T	Arginine/serine-rich c	RSRC2	78.95	_T(ph)PS(ph)PPPFR_
Q7L4I2	222	S	Arginine/serine-rich c	RSRC2	78.95	_T(ph)PS(ph)PPPFR_
Q7L7X3	421	S	Serine/threonine-prot	TAOK1	82.59	_ASDPQS(ph)PPQVSF
Q7Z2W4	271	S	Zinc finger CCCH-typ	ZC3HAV1	96.247	_S(ph)CTPS(ph)PDQIS
Q7Z2W4	273	T	Zinc finger CCCH-typ	ZC3HAV1	95.57	_SCT(ph)PS(ph)PDQIS
Q7Z2W4	275	S	Zinc finger CCCH-typ	ZC3HAV1	121.45	_SCT(ph)PS(ph)PDQIS
Q7Z2W4	284	S	Zinc finger CCCH-typ	ZC3HAV1	115.8	_AS(ph)LEDAPVDDLT
Q7Z2W4	378	S	Zinc finger CCCH-typ	ZC3HAV1	70.889	_TVFS(ph)PTLPAAR_
Q7Z3B3	268	S	KAT8 regulatory NSL	KANSL1	89.011	_S(ph)PLSSILFSALDS
Q7Z3C6	828	S	Autophagy-related pr	ATG9A	85.518	_HPEPVPEEGS(ph)ED
Q7Z3K3	425	S	Pogo transposable el	POGZ	151	_SLDSEPSVPSAAKPF
Q7Z3K3	1364	S	Pogo transposable el	POGZ	149.22	_LSGEHS(ph)ESSTPR
Q7Z3K3	1368	T	Pogo transposable el	POGZ	111.78	_LSGEHSESST(ph)PR
Q7Z406	1969	S	Myosin-14	MYH14	43.222	_LEEGVAS(ph)DEEAE
Q7Z417	572	S	Nuclear fragile X men	NUFIP2	152.32	_RTS(ph)PQVLGSILK_
Q7Z417	629	S	Nuclear fragile X men	NUFIP2	245.53	_DYEIESQNPLAS(ph)P
Q7Z417	652	S	Nuclear fragile X men	NUFIP2	156	_NDS(ph)WGSFDLR_
Q7Z422	39	S	SUZ domain-containi	SZRD1	76.807	_S(ph)PPKVPIVIQDDS
Q7Z434	152	S	Mitochondrial antiviral	MAVS	112.32	_EKEPSYPMPVQETQ
Q7Z434	165	S	Mitochondrial antiviral	MAVS	151.26	_EKEPSYPMPVQETQ
Q7Z434	222	S	Mitochondrial antiviral	MAVS	203.95	_GPVS(ph)PSVSFQPL
Q7Z478	200	S	ATP-dependent RNA	DHX29	72.316	_FQSPQIQATIS(ph)PF
Q7Z4S6	1212	S	Kinesin-like protein K	KIF21A	62.438	_EKELS(ph)PPPGLPS

Q7Z4V5	137	S	Hepatoma-derived gr(	HDGFRP2	109.37	_GVMAVTAVTATAAS(
Q7Z4V5	366	S	Hepatoma-derived gr(	HDGFRP2	96.626	_GEAERGS(ph)GGS(p
Q7Z4V5	369	S	Hepatoma-derived gr(	HDGFRP2	96.626	_GEAERGS(ph)GGS(p
Q7Z4V5	370	S	Hepatoma-derived gr(	HDGFRP2	96.626	_GEAERGS(ph)GGS(p
Q7Z4V5	395	S	Hepatoma-derived gr(	HDGFRP2	116.84	_GRGPPS(ph)S(ph)S(p
Q7Z4V5	396	S	Hepatoma-derived gr(	HDGFRP2	116.84	_GRGPPS(ph)S(ph)S(p
Q7Z4V5	397	S	Hepatoma-derived gr(	HDGFRP2	116.84	_GRGPPS(ph)S(ph)S(p
Q7Z4V5	399	S	Hepatoma-derived gr(	HDGFRP2	116.84	_GRGPPS(ph)S(ph)S(p
Q7Z4V5	625	S	Hepatoma-derived gr(	HDGFRP2	207.6	_GESAEDKEHEEGRD
Q7Z589	173	S	Protein EMSY	EMSY	52.773	_PAS(ph)PASNVVVLP
Q7Z589	209	S	Protein EMSY	EMSY	80.719	_TNS(ph)SSSSPVVLK_
Q7Z5J4	892	S	Retinoic acid-induced	RAI1	113.8	_PGMQDPLS(ph)PK_
Q7Z5J4	1374	S	Retinoic acid-induced	RAI1	130.98	_GAGGS(ph)PVGVEE(
Q7Z5K2	77	S	Wings apart-like prote	WAPAL	131.68	_VEEESTGDPFGFDS(
Q7Z5K2	221	S	Wings apart-like prote	WAPAL	134.88	_RPES(ph)PSEISPIK_
Q7Z5L9	71	S	Interferon regulatory f	IRF2BP2	115.5	_S(ph)PPGAAASAAAK
Q7Z5L9	175	S	Interferon regulatory f	IRF2BP2	185.09	_LEEPPELNRQS(ph)P
Q7Z5L9	360	S	Interferon regulatory f	IRF2BP2	115.74	_RKPS(ph)PEPEGEVG
Q7Z5L9	406	S	Interferon regulatory f	IRF2BP2	82.169	_IPMTPTSSFVSPPPP
Q7Z5L9	457	S	Interferon regulatory f	IRF2BP2	48.832	_NSNS(ph)PPS(ph)PS
Q7Z5L9	460	S	Interferon regulatory f	IRF2BP2	48.832	_NSNS(ph)PPS(ph)PS
Q7Z6E9	244	S	E3 ubiquitin-protein li(	RBBP6	62.57	_EKPPFLPEEPS(ph)S(
Q7Z6E9	245	S	E3 ubiquitin-protein li(	RBBP6	62.57	_EKPPFLPEEPS(ph)S(
Q7Z6E9	246	S	E3 ubiquitin-protein li(	RBBP6	62.57	_EKPPFLPEEPS(ph)S(
Q7Z6E9	247	S	E3 ubiquitin-protein li(	RBBP6	62.57	_EKPPFLPEEPS(ph)S(
Q7Z6E9	770	S	E3 ubiquitin-protein li(	RBBP6	108.47	_S(ph)RS(ph)PQAFR_
Q7Z6E9	772	S	E3 ubiquitin-protein li(	RBBP6	108.47	_S(ph)RS(ph)PQAFR_
Q7Z6E9	984	T	E3 ubiquitin-protein li(	RBBP6	191.15	_DDAT(ph)PVRDEPMD
Q7Z6E9	1179	S	E3 ubiquitin-protein li(	RBBP6	171.56	_LEVTEIVKPS(ph)PK_
Q7Z6E9	1328	S	E3 ubiquitin-protein li(	RBBP6	219.87	_WDKDDFES(ph)EEEI
Q7Z6E9	1699	S	E3 ubiquitin-protein li(	RBBP6	164.8	_NQSHSSPSVS(ph)PS
Q7Z6Z7	1395	S	E3 ubiquitin-protein li(	HUWE1	43.168	_AES(ph)PEEVACR_
Q7Z6Z7	1907	S	E3 ubiquitin-protein li(	HUWE1	221.34	_GSGTAS(ph)DDEFEN
Q7Z6Z7	3808	S	E3 ubiquitin-protein li(	HUWE1	84.152	_REES(ph)PMDVDQPS
Q7Z6Z7	3816	S	E3 ubiquitin-protein li(	HUWE1	120.98	_REESPMDVDQPS(ph
Q86SQ0	204	S	Pleckstrin homology-l	PHLDB2	45.614	_SGAASMPSS(ph)PK_
Q86SQ0	489	S	Pleckstrin homology-l	PHLDB2	165.66	_LQLS(ph)DEESVFEE
Q86TB9	179	S	Protein PAT1 homolo	PATL1	53.557	_STS(ph)PIIGSPPVR_
Q86U06	149	S	Probable RNA-bindin(	RBM23	96.881	_EKS(ph)PVREPVDNL
Q86U42	150	S	Polyadenylate-bindin(	PABPN1	162.41	_QMNMS(ph)PPPGNA
Q86U86	10	S	Protein polybromo-1	PBRM1	133.76	_ATS(ph)PSSSVSGDF
Q86UE4	298	S	Protein LYRIC	MTDH	62.077	_LSSQIS(ph)AGEEK_
Q86UE4	426	S	Protein LYRIC	MTDH	262.33	_SQEPIPDDQKVS(ph)
Q86UE4	568	S	Protein LYRIC	MTDH	111.94	_SETSWES(ph)PK_
Q86UP2	75	S	Kinectin	KTN1	174.04	_EIQNGNLHES(ph)DS
Q86UP2	1313	S	Kinectin	KTN1	100.23	_AAGDTTVIENSDVS(p
Q86UU0	21	S	B-cell CLL/lymphoma	BCL9L	60.307	_EAPGS(ph)PPLS(ph)I
Q86UU0	25	S	B-cell CLL/lymphoma	BCL9L	60.307	_EAPGS(ph)PPLS(ph)I
Q86UU0	750	S	B-cell CLL/lymphoma	BCL9L	125.5	_GLLS(ph)PPMGQSGL
Q86UU0	946	T	B-cell CLL/lymphoma	BCL9L	101.3	_SPTLSQVHSPLVT(ph
Q86UU0	997	S	B-cell CLL/lymphoma	BCL9L	64.16	_LKS(ph)PSMAVPSPG
Q86UU0	1010	S	B-cell CLL/lymphoma	BCL9L	64.16	_LKS(ph)PSMAVPSPG
Q86UU0	1017	S	B-cell CLL/lymphoma	BCL9L	43.042	_TAMPS(ph)PGVSQNH
Q86V48	659	S	Leucine zipper protein	LUZP1	164.13	_EKPDS(ph)DDDLDIAS

Q86V81	8	S	THO complex subunit	ALYREF	79.639	_MDMS(ph)LDDIIK_
Q86VE0	202	S	Myb-related transcript	MYPOP	115.88	_ERES(ph)PPPSALQP
Q86VM9	6	S	Zinc finger CCCH dor	ZC3H18	111.42	_(ac)MDVAES(ph)PER
Q86VM9	24	S	Zinc finger CCCH dor	ZC3H18	88.292	_(ac)MDVAES(ph)PER
Q86VM9	46	S	Zinc finger CCCH dor	ZC3H18	105.58	_AS(ph)DLEDEESAAR
Q86VM9	67	S	Zinc finger CCCH dor	ZC3H18	155.87	_GPSQEEEDNHS(ph)[
Q86VM9	74	S	Zinc finger CCCH dor	ZC3H18	197.32	_GPSQEEEDNHS(ph)[
Q86VM9	78	S	Zinc finger CCCH dor	ZC3H18	40.064	_GPSQEEEDNHS(ph)[
Q86VM9	83	S	Zinc finger CCCH dor	ZC3H18	131.18	_SQDQDS(ph)EVNELS
Q86VM9	118	S	Zinc finger CCCH dor	ZC3H18	127.2	_TSDLRDEASS(ph)VT
Q86VM9	487	S	Zinc finger CCCH dor	ZC3H18	75.788	_PRS(ph)PQPPSR_
Q86VM9	534	S	Zinc finger CCCH dor	ZC3H18	185.99	_LGVSVS(ph)PSR_
Q86VM9	604	S	Zinc finger CCCH dor	ZC3H18	66.372	_SFSS(ph)SPSPSPTP
Q86VM9	613	S	Zinc finger CCCH dor	ZC3H18	104.67	_SFSSSPSPSPTPS(ph
Q86VM9	677	T	Zinc finger CCCH dor	ZC3H18	75.819	_ERPART(ph)PPR_
Q86VM9	842	S	Zinc finger CCCH dor	ZC3H18	103.4	_YEPSDKDRQS(ph)PF
Q86VR2	258	S	Protein FAM134C	FAM134C	139.6	_AMDNHS(ph)DS(ph)E
Q86VR2	260	S	Protein FAM134C	FAM134C	139.6	_AMDNHS(ph)DS(ph)E
Q86VR2	310	T	Protein FAM134C	FAM134C	60.87	_GQTPLT(ph)EGS(ph)[
Q86VR2	313	S	Protein FAM134C	FAM134C	60.87	_GQTPLT(ph)EGS(ph)[
Q86VR2	320	S	Protein FAM134C	FAM134C	188.47	_GQTPLTEGSEDLDGI
Q86WB0	321	S	Nuclear-interacting pa	ZC3HC1	113.99	_LPLVPES(ph)PRR_
Q86WB0	335	S	Nuclear-interacting pa	ZC3HC1	79.616	_SQDATFS(ph)PGSEC
Q86WB0	344	S	Nuclear-interacting pa	ZC3HC1	94.927	_SQDATFSPGSEQAE[
Q86WB0	359	S	Nuclear-interacting pa	ZC3HC1	90.601	_SWDSSS(ph)PVDRPI
Q86WB0	394	S	Nuclear-interacting pa	ZC3HC1	227.6	_SMGTGDTPGLEVPS
Q86WB0	395	S	Nuclear-interacting pa	ZC3HC1	196.78	_SMGTGDTPGLEVPS
Q86WR0	204	S	Coiled-coil domain-co	CCDC25	43.37	_VENMSSNQDGNDS(
Q86WR7	179	S	Proline and serine-ric	PROSER2	52.576	_APS(ph)PPVEHPR_
Q86X29	530	S	Lipolysis-stimulated li	LSR	70.334	_S(ph)RDDLYDQDDSF
Q86X95	394	S	Corepressor interactir	CIR1	58.511	_SRS(ph)PGSYK_
Q86XN8	514	S	RNA-binding protein I	MEX3D	45.614	_HS(ph)PTLPEPGGLR
Q86XP3	109	S	ATP-dependent RNA	DDX42	127.2	_PVDS(ph)DS(ph)DDD
Q86XP3	111	S	ATP-dependent RNA	DDX42	291.88	_PVDS(ph)DS(ph)DDD
Q86XP3	185	S	ATP-dependent RNA	DDX42	188.4	_YMAENPTAGVVQEE
Q86Y91	413	S	Kinesin-like protein K	KIF18B	61.141	_LQVYEGGGQPPPQD
Q86YD1	36	S	Prostate tumor-overe	PTOV1	46.994	_S(ph)WPASPR_
Q86YP4	100	S	Transcriptional repres	GATAD2A	107.25	_RPPS(ph)PDVIVLS(pl
Q86YP4	107	S	Transcriptional repres	GATAD2A	107.25	_RPPS(ph)PDVIVLS(pl
Q86YP4	114	S	Transcriptional repres	GATAD2A	107.25	_RPPS(ph)PDVIVLS(pl
Q86YS7	260	S	C2 domain-containing	C2CD5	96.55	_LSSPAAFLPACNS(ph
Q86YS7	295	S	C2 domain-containing	C2CD5	71.879	_NQTYSFS(ph)PSK_
Q86YV5	743	S	Tyrosine-protein kina	SGK223	97.384	_VSQGSAESLS(ph)PS
Q86YV5	780	S	Tyrosine-protein kina	SGK223	115.01	_TCSDGGPSSELAHS(
Q8IU68	522	S	Transmembrane char	TMC8	61.691	_ASS(ph)RPFR_
Q8IU81	436	S	Interferon regulatory f	IRF2BP1	104.7	_NVAEALGHS(ph)PKD
Q8IU81	453	S	Interferon regulatory f	IRF2BP1	114.87	_AGGAS(ph)PAASSTA
Q8IUR7	512	S	Armadillo repeat-cont	ARMC8	53.237	_SLS(ph)TEQLFR_
Q8IV50	24	S	LysM and putative pe	LYSMD2	54.823	_PSAPS(ph)PPPR_
Q8IVF2	260	S	Protein AHNAK2	AHNAK2	66.962	_ERLS(ph)WPK_
Q8IVF2	280	S	Protein AHNAK2	AHNAK2	143.58	_SHS(ph)SSEAYEPR_
Q8IVF2	294	S	Protein AHNAK2	AHNAK2	268.76	_DAHDVS(ph)PTSTDT
Q8IVF2	593	S	Protein AHNAK2	AHNAK2	138.35	_IPSLGWS(ph)PSK_
Q8IVF2	842	S	Protein AHNAK2	AHNAK2	113.53	_MPS(ph)FGVSAPGK_

Q8IVF2	1172	S	Protein AHNAK2	AHNAK2	79.614	_MPS(ph)FGASAPGK_
Q8IVF2	3408	S	Protein AHNAK2	AHNAK2	113.4	_VDLKS(ph)PQVDIK_
Q8IVF2	4477	S	Protein AHNAK2	AHNAK2	157.23	_MPSFGMLS(ph)PGK_
Q8IVP5	13	S	FUN14 domain-conta	FUNDC1	143.47	_NPPPQDYES(ph)DDI
Q8IVT2	284	S	Uncharacterized prote	C19orf21	138.82	_AVPTWASVQVVDDP
Q8IVT2	287	T	Uncharacterized prote	C19orf21	117.26	_AVPTWASVQVVDDP
Q8IVT2	377	T	Uncharacterized prote	C19orf21	139.88	_AST(ph)PDWVSEGP(
Q8IVT2	394	S	Uncharacterized prote	C19orf21	222.96	_ALS(ph)SDSILSPAPI
Q8IVT2	400	S	Uncharacterized prote	C19orf21	129.2	_ALSSDSILS(ph)PAPI
Q8IVT2	471	S	Uncharacterized prote	C19orf21	136.39	_HLS(ph)ESSGKPLST
Q8IVT2	541	S	Uncharacterized prote	C19orf21	46.88	_S(ph)QSSDLLER_
Q8IVT2	543	S	Uncharacterized prote	C19orf21	73.435	_SQS(ph)SDLLER_
Q8IVT2	575	S	Uncharacterized prote	C19orf21	176.53	_NALFPEVFS(ph)PTPI
Q8IVT2	577	T	Uncharacterized prote	C19orf21	174.03	_NALFPEVFSPT(ph)PI
Q8IW50	115	S	Protein FAM219A	FAM219A	121.98	_GYSSLDQSPDEKPL\
Q8IWA0	779	S	WD repeat-containing	WDR75	99.708	_EIPEDVDMEEEKES(p
Q8IWA0	782	S	WD repeat-containing	WDR75	153.02	_EIPEDVDMEEEKES(p
Q8IWA0	796	S	WD repeat-containing	WDR75	150.36	_VQDTS(ph)NTGLGEI
Q8IWI9	449	S	MAX gene-associated	MGA	77.22	_WLPSS(ph)PSGVAK_
Q8IWI9	924	S	MAX gene-associated	MGA	86.699	_SILPYPVS(ph)PK_
Q8IWS0	155	S	PHD finger protein 6	PHF6	254.6	_TAHNSEADLEESFNE
Q8IWW6	231	T	Rho GTPase-activatin	ARHGAP12	66.378	_ATT(ph)PPNQGRPDS
Q8IWW6	240	S	Rho GTPase-activatin	ARHGAP12	66.378	_ATT(ph)PPNQGRPDS
Q8IWX8	815	S	Calcium homeostasis	CHERP	108.23	_S(ph)RS(ph)PT(ph)PF
Q8IWX8	817	S	Calcium homeostasis	CHERP	108.23	_S(ph)RS(ph)PT(ph)PF
Q8IWX8	819	T	Calcium homeostasis	CHERP	108.23	_S(ph)RS(ph)PT(ph)PF
Q8IWZ8	485	S	SURP and G-patch do	SUGP1	162.49	_AVQQHQHGYDS(ph)
Q8IX15	451	T	Homeobox and leucin	HOMEZ	67.217	_AET(ph)PPLPIPPPPF
Q8IX21	701	S	Protein FAM178A	FAM178A	57.249	_GIKS(ph)PIR_
Q8IXJ6	368	S	NAD-dependent prote	SIRT2	130.8	_EHASIDAQSGAGVPI
Q8IXM2	96	S	Chromatin complexes	BAP18	130.47	_VYEDSGIPLPAES(ph
Q8IXQ4	105	S	Uncharacterized prote	KIAA1704	99.219	_QDDS(ph)PPRPIIGPA
Q8IXT5	250	S	RNA-binding protein 1	RBM12B	105.79	_EGDVLRRS(ph)EEHS
Q8IXT5	254	S	RNA-binding protein 1	RBM12B	105.79	_EGDVLRRS(ph)EEHS
Q8IXT5	278	S	RNA-binding protein 1	RBM12B	115.26	_S(ph)RS(ph)PLGFYVI
Q8IXT5	280	S	RNA-binding protein 1	RBM12B	115.26	_S(ph)RS(ph)PLGFYVI
Q8IXT5	562	S	RNA-binding protein 1	RBM12B	95.502	_HSS(ph)EDFR_
Q8IXT5	575	S	RNA-binding protein 1	RBM12B	143.28	_FPPEDFRHS(ph)PED
Q8IXT5	591	S	RNA-binding protein 1	RBM12B	121.32	_EEDFRRPS(ph)EEDF
Q8IXT5	638	S	RNA-binding protein 1	RBM12B	119.34	_RS(ph)PTEDFR_
Q8IXT5	640	T	RNA-binding protein 1	RBM12B	78.149	_SPT(ph)EDFR_
Q8IXT5	710	S	RNA-binding protein 1	RBM12B	123.55	_RPPEEDFRHS(ph)PE
Q8IXT5	718	S	RNA-binding protein 1	RBM12B	141.07	_HSPEEDFRQS(ph)PC
Q8IXT5	798	S	RNA-binding protein 1	RBM12B	77.14	_S(ph)REEDFR_
Q8IXT5	829	S	RNA-binding protein 1	RBM12B	44.788	_HPPDEDFRS(ph)PQE
Q8IXT5	874	S	RNA-binding protein 1	RBM12B	54.656	_LPDNFRPPGEDFRS(
Q8IXZ2	408	S	Zinc finger CCCH dor	ZC3H3	96.773	_DHASQLS(ph)PVLSR
Q8IY17	345	S	Neuropathy target est	PNPLA6	83.137	_LFPS(ph)PGLPTR_
Q8IY67	14	S	Ribonucleoprotein PT	RAVER1	262	_(ac)AADVSVTHRPPL
Q8IY67	463	T	Ribonucleoprotein PT	RAVER1	133.29	_EALGLGPPAAQLT(ph
Q8IY81	335	S	pre-rRNA processing	FTSJ3	141.45	_ALDISLS(ph)S(ph)GE
Q8IY81	336	S	pre-rRNA processing	FTSJ3	141.45	_ALDISLS(ph)S(ph)GE
Q8IY81	347	S	pre-rRNA processing	FTSJ3	104.97	_ALDISLS(ph)S(ph)GE
Q8IY81	471	S	pre-rRNA processing	FTSJ3	109.49	_DDIYVSDVEDDGDDT

Q8IY81	584	S	pre-rRNA processing FTSJ3	161.99	_TEIMS(ph)PLYQDEAI
Q8IY92	584	S	Structure-specific enc SLX4	48.928	_RS(ph)PALHGTPTAG
Q8IY92	1185	S	Structure-specific enc SLX4	62.463	_ALEIS(ph)PR_
Q8IY92	1469	S	Structure-specific enc SLX4	73.386	_S(ph)PGLLDTTPIR_
Q8IYB3	220	T	Serine/arginine repeti SRRM1	165.49	_KEKT(ph)PELPEPSVI
Q8IYB3	234	S	Serine/arginine repeti SRRM1	119.16	_VKEPS(ph)VQEATST
Q8IYB3	292	S	Serine/arginine repeti SRRM1	75.738	_S(ph)PSHTRPR_
Q8IYB3	294	S	Serine/arginine repeti SRRM1	79.148	_SPS(ph)HTRPR_
Q8IYB3	389	S	Serine/arginine repeti SRRM1	126.09	_RLS(ph)PS(ph)AS(ph)
Q8IYB3	391	S	Serine/arginine repeti SRRM1	95.854	_RLS(ph)PS(ph)AS(ph)
Q8IYB3	393	S	Serine/arginine repeti SRRM1	126.09	_RLS(ph)PS(ph)AS(ph)
Q8IYB3	402	S	Serine/arginine repeti SRRM1	94.639	_HRPS(ph)PPAT(ph)PI
Q8IYB3	406	T	Serine/arginine repeti SRRM1	99.069	_HRPS(ph)PPAT(ph)PI
Q8IYB3	414	S	Serine/arginine repeti SRRM1	127.62	_TRHS(ph)PTPQQSNF
Q8IYB3	450	S	Serine/arginine repeti SRRM1	148.85	_RES(ph)PS(ph)PAPKI
Q8IYB3	452	S	Serine/arginine repeti SRRM1	117.08	_RES(ph)PS(ph)PAPKI
Q8IYB3	463	S	Serine/arginine repeti SRRM1	154.48	_KVELS(ph)ES(ph)EEI
Q8IYB3	465	S	Serine/arginine repeti SRRM1	244.89	_KVELS(ph)ES(ph)EEI
Q8IYB3	530	S	Serine/arginine repeti SRRM1	61.679	_SAS(ph)PS(ph)PR_
Q8IYB3	532	S	Serine/arginine repeti SRRM1	42.718	_SAS(ph)PS(ph)PR_
Q8IYB3	549	S	Serine/arginine repeti SRRM1	78.985	_RRS(ph)PS(ph)PPPTI
Q8IYB3	551	S	Serine/arginine repeti SRRM1	78.985	_RRS(ph)PS(ph)PPPTI
Q8IYB3	560	S	Serine/arginine repeti SRRM1	104.09	_RRS(ph)PS(ph)PAPPI
Q8IYB3	562	S	Serine/arginine repeti SRRM1	104.09	_RRS(ph)PS(ph)PAPPI
Q8IYB3	572	T	Serine/arginine repeti SRRM1	90.697	_RRT(ph)PT(ph)PPPR_
Q8IYB3	574	T	Serine/arginine repeti SRRM1	90.697	_RRT(ph)PT(ph)PPPR_
Q8IYB3	581	T	Serine/arginine repeti SRRM1	81.565	_RRT(ph)PS(ph)PPPR_
Q8IYB3	583	S	Serine/arginine repeti SRRM1	81.565	_RRT(ph)PS(ph)PPPR_
Q8IYB3	597	S	Serine/arginine repeti SRRM1	123.51	_RYS(ph)PPIQR_
Q8IYB3	605	S	Serine/arginine repeti SRRM1	84.605	_RYS(ph)PS(ph)PPPK_
Q8IYB3	607	S	Serine/arginine repeti SRRM1	69.795	_RYS(ph)PS(ph)PPPK_
Q8IYB3	614	T	Serine/arginine repeti SRRM1	77.24	_T(ph)AS(ph)PPPPPKI
Q8IYB3	616	S	Serine/arginine repeti SRRM1	89.301	_T(ph)AS(ph)PPPPPKI
Q8IYB3	626	S	Serine/arginine repeti SRRM1	112.08	_RAS(ph)PS(ph)PPPKI
Q8IYB3	628	S	Serine/arginine repeti SRRM1	112.08	_RAS(ph)PS(ph)PPPKI
Q8IYB3	636	S	Serine/arginine repeti SRRM1	86.911	_RVS(ph)HS(ph)PPPK_
Q8IYB3	638	S	Serine/arginine repeti SRRM1	60.157	_RVS(ph)HS(ph)PPPK_
Q8IYB3	653	S	Serine/arginine repeti SRRM1	84.169	_RRS(ph)PSLSSK_
Q8IYB3	683	S	Serine/arginine repeti SRRM1	82.85	_RHS(ph)PS(ph)PRPR
Q8IYB3	685	S	Serine/arginine repeti SRRM1	82.85	_RHS(ph)PS(ph)PRPR
Q8IYB3	695	S	Serine/arginine repeti SRRM1	160.65	_APQTSS(ph)SPPPVR
Q8IYB3	696	S	Serine/arginine repeti SRRM1	181.26	_APQTSSS(ph)PPPVR
Q8IYB3	705	S	Serine/arginine repeti SRRM1	28.232	_GAS(ph)SS(ph)PQR_
Q8IYB3	707	S	Serine/arginine repeti SRRM1	68.626	_GASSS(ph)PQR_
Q8IYB3	713	S	Serine/arginine repeti SRRM1	83.37	_RQS(ph)PS(ph)PSTR
Q8IYB3	715	S	Serine/arginine repeti SRRM1	91.62	_QSPS(ph)PSTRPIR_
Q8IYB3	725	S	Serine/arginine repeti SRRM1	79.283	_RVS(ph)RT(ph)PEPK_
Q8IYB3	738	S	Serine/arginine repeti SRRM1	113.61	_AAS(ph)PSPQSVR_
Q8IYB3	740	S	Serine/arginine repeti SRRM1	89.189	_AASPS(ph)PQSVR_
Q8IYB3	769	S	Serine/arginine repeti SRRM1	128	_KPPAPPS(ph)PVQSC
Q8IYB3	773	S	Serine/arginine repeti SRRM1	90.287	_KPPAPPSPVQS(ph)C
Q8IYB3	775	S	Serine/arginine repeti SRRM1	173.03	_KPPAPPSPVQSQS(p
Q8IYB3	777	S	Serine/arginine repeti SRRM1	153.25	_KPPAPPS(ph)PVQSC
Q8IYB3	778	T	Serine/arginine repeti SRRM1	72.687	_KPPAPPS(ph)PVQS(

Q8IYB3	781	S	Serine/arginine repeti	SRRM1	128	_KPPAPPS(ph)PVQSC
Q8IYB3	795	S	Serine/arginine repeti	SRRM1	160.83	_SPTPS(ph)PSPPRNS
Q8IYB3	797	S	Serine/arginine repeti	SRRM1	151.05	_SPTPSPS(ph)PPR_
Q8IYB3	802	S	Serine/arginine repeti	SRRM1	160.83	_SPTPS(ph)PSPPRNS
Q8IYB3	872	T	Serine/arginine repeti	SRRM1	290.71	_KET(ph)ES(ph)EAEDI
Q8IYB3	874	S	Serine/arginine repeti	SRRM1	357.57	_KET(ph)ES(ph)EAEDI
Q8IZ21	118	S	Phosphatase and acti	PHACTR4	110.6	_SSS(ph)PVQVEEEPV
Q8IZ73	68	S	RNA pseudouridylate	RPUSD2	124.62	_VELS(ph)PGPPKPAG
Q8IZD4	283	S	mRNA-decapping enz	DCP1B	71.085	_RHS(ph)PPIEK_
Q8IZL8	481	S	Proline-, glutamic aci	PELP1	161.08	_GS(ph)PDGSLQTGKF
Q8IZL8	745	T	Proline-, glutamic aci	PELP1	76.937	_AGSNEDPILAPSGT(p
Q8IZP0	183	S	Abl interactor 1	ABI1	127.74	_TNPPTQKPPS(ph)PP
Q8IZT6	1252	Y	Abnormal spindle-like	ASPM	30.308	_VVIT(ph)Y(ph)LSFLC/
Q8N0Y2	235	S	Zinc finger protein 44	ZNF444	77.53	_DTHPGSPGS(ph)PGF
Q8N0Z3	760	S	Spindle and centriole-	SPICE1	69.704	_LVGLNLS(ph)PPMS(p
Q8N0Z3	764	S	Spindle and centriole-	SPICE1	69.704	_LVGLNLS(ph)PPMS(p
Q8N122	863	S	Regulatory-associate	RPTOR	149.64	_VLDTSSLTQSAPAS(p
Q8N122	877	S	Regulatory-associate	RPTOR	123.51	_GVHIHQAGGS(ph)PF
Q8N128	70	S	Protein FAM177A1	FAM177A1	73.758	_VIHFVSGETMEEYS(p
Q8N128	71	T	Protein FAM177A1	FAM177A1	73.758	_VIHFVSGETMEEYS(p
Q8N163	484	T	DBIRD complex subu	KIAA1967	106.23	_NAET(ph)PEATTQQE
Q8N163	675	S	DBIRD complex subu	KIAA1967	235.68	_S(ph)VAS(ph)NQS(ph
Q8N163	678	S	DBIRD complex subu	KIAA1967	283.72	_S(ph)VAS(ph)NQS(ph
Q8N163	681	S	DBIRD complex subu	KIAA1967	175	_S(ph)VAS(ph)NQS(ph
Q8N1F7	767	S	Nuclear pore comple	NUP93	44.614	_GTS(ph)PSSSSR_
Q8N1F8	610	S	Serine/threonine-prot	STK11IP	67.827	_S(ph)PRPTGSDLLPG
Q8N1F8	772	S	Serine/threonine-prot	STK11IP	100.36	_AKNS(ph)PPQAPSTR
Q8N1G0	183	S	Zinc finger protein 68	ZNF687	103.78	_TPLDLFAHFGPEPGD
Q8N1G0	253	S	Zinc finger protein 68	ZNF687	89.079	_ATDIPASAS(ph)PPP\
Q8N1G0	1057	S	Zinc finger protein 68	ZNF687	57.173	_HGLQLGAQS(ph)PGF
Q8N1G0	1191	S	Zinc finger protein 68	ZNF687	50.799	_SDPDGGDS(ph)PLPA
Q8N1G4	518	S	Leucine-rich repeat-c	LRRC47	169.39	_EEGS(ph)LSDTEADA
Q8N201	307	S	Integrator complex su	INTS1	78.548	_LS(ph)PEQEGQLMPF
Q8N2M8	285	S	CLK4-associating ser	CLASRP	105.2	_KIS(ph)PPSYAR_
Q8N2M8	294	S	CLK4-associating ser	CLASRP	86.498	_RDS(ph)PTYDPYK_
Q8N2M8	501	S	CLK4-associating ser	CLASRP	84.188	_SSWSLS(ph)PSR_
Q8N2M8	667	S	CLK4-associating ser	CLASRP	57.785	_S(ph)RS(ph)PHYR_
Q8N2M8	669	S	CLK4-associating ser	CLASRP	57.785	_S(ph)RS(ph)PHYR_
Q8N392	66	S	Rho GTPase-activatir	ARHGAP18	83.639	_SIS(ph)QDS(ph)LDEL
Q8N392	69	S	Rho GTPase-activatir	ARHGAP18	83.639	_SIS(ph)QDS(ph)LDEL
Q8N3D4	191	S	EH domain-binding pr	EHBP1L1	83.917	_PSDVGNLDDFAES(p
Q8N3E9	496	S	1-phosphatidylinositol	PLCD3	165	_ALS(ph)DREEEEEDD
Q8N3F8	578	S	MICAL-like protein 1	MICALL1	88.19	_VEQMPQAS(ph)PGL/
Q8N3V7	263	S	Synaptopodin	SYNPO	105.9	_VAS(ph)EEEEVPLVV
Q8N3V7	525	S	Synaptopodin	SYNPO	76.533	_APAPQPPSLPDRS(p
Q8N3V7	580	S	Synaptopodin	SYNPO	151.95	_S(ph)PPSYSVLYPSS
Q8N3V7	685	S	Synaptopodin	SYNPO	186.35	_DRAS(ph)PAAAEEVV
Q8N3V7	754	S	Synaptopodin	SYNPO	112.17	_CPS(ph)PTMSLPSSV
Q8N3V7	819	S	Synaptopodin	SYNPO	215.51	_PSLFVLS(ph)PIKEPA
Q8N3V7	828	S	Synaptopodin	SYNPO	165.48	_PSLFVLS(ph)PIKEPA
Q8N3V7	833	S	Synaptopodin	SYNPO	148.36	_AAS(ph)PAKPSSLDL'
Q8N3V7	854	S	Synaptopodin	SYNPO	82.069	_GALPPS(ph)PALPR_
Q8N3V7	882	S	Synaptopodin	SYNPO	53.519	_SS(ph)PGLYTSPGQD
Q8N3X1	18	S	Formin-binding protei	FNBP4	145.49	_RPILQLS(ph)PPGPR_

Q8N3X1	499	S	Formin-binding protei	FNBP4	316.7	_IDENS(ph)DKEMEVE
Q8N3X1	508	S	Formin-binding protei	FNBP4	316.7	_IDENS(ph)DKEMEVE
Q8N442	51	S	Translation factor GU	GUF1	41.704	_LYSS(ph)AEFK_
Q8N4C8	763	S	Misshapen-like kinas	MINK1	50.271	_SDSVLPASHGHLPQ/
Q8N556	265	S	Actin filament-associ	AFAP1	132.8	_EAYSGCSGPVDSEC
Q8N556	664	S	Actin filament-associ	AFAP1	85.837	_SGTS(ph)SPQSPVFR
Q8N556	668	S	Actin filament-associ	AFAP1	160.46	_SGTSSPQS(ph)PVFR
Q8N565	213	S	Melanoregulin	MREG	122.69	_ELHYLPFPS(ph)P_
Q8N5F7	149	S	NF-kappa-B-activatin	NKAP	139.44	_IGELGAPEVWGLS(pl
Q8N5F7	157	S	NF-kappa-B-activatin	NKAP	69.704	_NPEPDS(ph)DEHT(ph
Q8N5F7	161	T	NF-kappa-B-activatin	NKAP	69.704	_NPEPDS(ph)DEHT(ph
Q8N5I9	178	S	Uncharacterized prot	C12orf45	88.075	_IEVLDS(ph)PASK_
Q8N655	273	S	Uncharacterized prot	C10orf12	164.03	_EDNPEEPSKEITSHE
Q8N6N3	158	S	UPF0690 protein C1c	C1orf52	133.76	_LLPEGEETLES(ph)DI
Q8N6T7	294	T	NAD-dependent prote	SIRT6	120.29	_ALPPLPRPPT(ph)PK_
Q8N6T7	338	S	NAD-dependent prote	SIRT6	70.197	_ERPTS(ph)PAPHRPP
Q8N7R7	344	S	Cyclin-Y-like protein 1	CCNYL1	180.11	_SFS(ph)ADNFIGIQR_
Q8N8A6	83	S	ATP-dependent RNA	DDX51	125.91	_VNDAEPGS(ph)PEAF
Q8N9T8	97	S	Protein KRI1 homolo	KRI1	130.05	_TASSSDS(ph)EEDPE
Q8N9T8	136	S	Protein KRI1 homolo	KRI1	191.36	_YVDEENS(ph)DGETS
Q8N9T8	171	S	Protein KRI1 homolo	KRI1	65.801	_AFVEDS(ph)EDEDGA
Q8N9T8	628	S	Protein KRI1 homolo	KRI1	187.49	_QLPALDGSLMGPES(
Q8N9T8	639	S	Protein KRI1 homolo	KRI1	81.723	_QLPALDGSLMGPES(
Q8NAF0	483	S	Zinc finger protein 57	ZNF579	104.38	_AAALQALQAQAPTS(
Q8NAP3	309	S	Zinc finger and BTB d	ZBTB38	75.682	_SKS(ph)PNNEGDVHF
Q8NAV1	193	S	Pre-mRNA-splicing fa	PRPF38A	164.4	_VSALEEDMDDVES(p
Q8NAV1	194	S	Pre-mRNA-splicing fa	PRPF38A	164.4	_VSALEEDMDDVES(p
Q8NB78	247	S	Lysine-specific histon	KDM1B	117.65	_AAATGNAS(ph)PGKL
Q8NBN3	540	S	Transmembrane prot	TMEM87A	172.92	_WVEENVPSSVTDVA
Q8NBU5	317	S	ATPase family AAA d	ATAD1	103.27	_EYVNS(ph)TSEESHD
Q8NBU5	319	S	ATPase family AAA d	ATAD1	79.209	_EYVNSTS(ph)EESHD
Q8NC06	166	S	Acyl-CoA-binding don	ACBD4	160.5	_EPAPPS(ph)PESHSP
Q8NC44	385	S	Protein FAM134A	FAM134A	179.1	_QALDS(ph)EEEEEDV
Q8NC51	25	S	Plasminogen activato	SERBP1	133.16	_FDQLFDDES(ph)DPF
Q8NC51	234	S	Plasminogen activato	SERBP1	72.935	_GGSGSHNWGTVKDI
Q8NC51	330	S	Plasminogen activato	SERBP1	97.291	_SKS(ph)EEAHAEDSV
Q8NC56	5	S	LEM domain-containi	LEMD2	84.053	_(ac)AGLS(ph)DLELR_
Q8NC56	138	S	LEM domain-containi	LEMD2	95.429	_ASVRGS(ph)SEEDEI
Q8NC56	499	S	LEM domain-containi	LEMD2	90.498	_WTKPSSFS(ph)DSEF
Q8NCN4	403	S	E3 ubiquitin-protein li	RNF169	97.597	_VLS(ph)PLIIK_
Q8NCN5	302	S	Pyruvate dehydrogen	PDPR	36.417	_NWQGGILS(ph)GGFE
Q8ND30	387	S	Liprin-beta-2	PPFIBP2	56.205	_LSCS(ph)LEDLR_
Q8ND56	183	S	Protein LSM14 homol	LSM14A	99.752	_SS(ph)PQLDPLR_
Q8ND56	192	S	Protein LSM14 homol	LSM14A	293.01	_S(ph)PTMEQAVQTAS
Q8ND56	216	S	Protein LSM14 homol	LSM14A	200.9	_S(ph)PVSTRPLPSAS
Q8ND76	326	S	Cyclin-Y	CCNY	127.3	_SAS(ph)ADNLTLPR_
Q8ND82	80	S	Zinc finger protein 28	ZNF280C	35.349	_SEPHS(ph)PGIPEIFR
Q8NDC0	15	S	MAPK-interacting anc	MAPK1IP1L	202.52	_(ac)SDEFSLADALPEI
Q8NDI1	171	S	EH domain-binding pr	EHBP1	85.737	_ATDEDMQS(ph)LAS(
Q8NDI1	174	S	EH domain-binding pr	EHBP1	84.707	_ATDEDMQS(ph)LAS(
Q8NDI1	335	S	EH domain-binding pr	EHBP1	82.765	_EVQTPQYLNPFDEPE
Q8NDI1	436	S	EH domain-binding pr	EHBP1	69.98	_PSPIPS(ph)PVLGR_
Q8NDT2	265	S	Putative RNA-binding	RBM15B	83.869	_S(ph)LS(ph)PVAAPPL
Q8NDT2	267	S	Putative RNA-binding	RBM15B	83.869	_S(ph)LS(ph)PVAAPPL

Q8NDT2	532	T	Putative RNA-binding	RBM15B	129.88	_DRT(ph)PPHLLYSDR
Q8NDT2	552	S	Putative RNA-binding	RBM15B	149.59	_TFLEGDWTS(ph)PSK
Q8NDT2	562	S	Putative RNA-binding	RBM15B	74.15	_RNS(ph)LEGYSR_
Q8NDT2	609	S	Putative RNA-binding	RBM15B	83.137	_TTHS(ph)PYEER_
Q8NDX5	315	S	Polyhomeotic-like pro	PHC3	38.14	_HQQIPLHS(ph)PPSK_
Q8NDX5	609	T	Polyhomeotic-like pro	PHC3	150.06	_MDRT(ph)PPPPTLS(p
Q8NDX5	616	S	Polyhomeotic-like pro	PHC3	150.06	_MDRT(ph)PPPPTLS(p
Q8NDX5	761	S	Polyhomeotic-like pro	PHC3	179.06	_HADNS(ph)S(ph)DTE
Q8NDX5	762	S	Polyhomeotic-like pro	PHC3	179.06	_HADNS(ph)S(ph)DTE
Q8NE71	105	S	ATP-binding cassette	ABCF1	102.21	_KLS(ph)VPT(ph)S(ph)
Q8NE71	108	T	ATP-binding cassette	ABCF1	102.21	_KLS(ph)VPT(ph)S(ph)
Q8NE71	109	S	ATP-binding cassette	ABCF1	119.38	_KLS(ph)VPT(ph)S(ph)
Q8NE71	228	S	ATP-binding cassette	ABCF1	334.63	_KAEQGS(ph)EEEGE(
Q8NEA6	623	S	Zinc finger protein GL	GLIS3	49.306	_FAPSAPSPHHIS(ph)F
Q8NEF9	203	S	Serum response fact	SRFBP1	181.86	_AVTIANS(ph)PSKPSE
Q8NEJ9	142	S	Neuroguidin	NGDN	209.44	_LS(ph)S(ph)EDEEEDI
Q8NEJ9	143	S	Neuroguidin	NGDN	209.44	_LS(ph)S(ph)EDEEEDI
Q8NEN9	521	S	PDZ domain-containi	PDZD8	168.12	_AQNEFKDEAQSLSHS
Q8NEN9	538	S	PDZ domain-containi	PDZD8	55.789	_PLGAIS(ph)PVLNR_
Q8NEY8	121	S	Periphilin-1	PPHLN1	91.867	_ERS(ph)PYKR_
Q8NEY8	133	S	Periphilin-1	PPHLN1	142.57	_DNTFFRES(ph)PVGR
Q8NEZ4	4267	S	Histone-lysine N-meth	MLL3	104.09	_ESIPSLPQS(ph)PMR_
Q8NF91	8223	S	Nesprin-1	SYNE1	101.05	_LPLPDDEHDLS(ph)D
Q8NF91	8280	S	Nesprin-1	SYNE1	71.882	_DTPASVDS(ph)IPLEV
Q8NF91	8360	T	Nesprin-1	SYNE1	117.65	_SKT(ph)PTGPELDTS
Q8NFC6	482	S	Biorientation of chrom	BOD1L1	60.621	_YYS(ph)DS(ph)DDEL
Q8NFC6	484	S	Biorientation of chrom	BOD1L1	60.621	_YYS(ph)DS(ph)DDEL
Q8NFC6	3019	S	Biorientation of chrom	BOD1L1	89.731	_TQLS(ph)PSIK_
Q8NFH5	73	S	Nucleoporin NUP53	NUP35	118.36	_SPLLAGGS(ph)PPQP
Q8NFH5	259	S	Nucleoporin NUP53	NUP35	111.58	_CALSS(ph)PSLAFTPI
Q8NFJ5	301	S	Retinoic acid-induced	GPRC5A	119.28	_AYS(ph)QEEITQGFEI
Q8NFJ5	345	S	Retinoic acid-induced	GPRC5A	102.08	_AHAWPS(ph)PYK_
Q8NG27	70	S	E3 ubiquitin-protein li	PJA1	52.132	_SRS(ph)PFSTTR_
Q8NHQ9	544	S	ATP-dependent RNA	DDX55	160.91	_KREEGS(ph)DIEDED
Q8NHQ9	594	S	ATP-dependent RNA	DDX55	105.41	_TVDLGIS(ph)DLEDD(
Q8NHV4	516	S	Protein NEDD1	NEDD1	210.4	_LVTSGAESGNLNTS(
Q8NHW5	304	S	60S acidic ribosomal	RPLP0P6;RPLP0	244.18	_VEAKEES(ph)EES(ph
Q8NHW5	307	S	60S acidic ribosomal	RPLP0P6;RPLP0	228.35	_VEAKEES(ph)EES(ph
Q8NI27	1393	S	THO complex subunit	THOC2	184.21	_TPVSGSLKS(ph)PVP
Q8NI27	1417	S	THO complex subunit	THOC2	112.58	_KIDTHPS(ph)PSHSS
Q8NI27	1516	S	THO complex subunit	THOC2	148.06	_SES(ph)PCESPYPNE
Q8TAD8	35	S	Smad nuclear-interac	SNIP1	126.91	_QERLS(ph)PEVAPPA
Q8TAD8	49	S	Smad nuclear-interac	SNIP1	61.039	_RPDHS(ph)GGS(ph)P
Q8TAD8	52	S	Smad nuclear-interac	SNIP1	148.68	_RPDHSGGS(ph)PSPI
Q8TAD8	54	S	Smad nuclear-interac	SNIP1	123.32	_RPDHSGGS(ph)PS(p
Q8TAD8	99	S	Smad nuclear-interac	SNIP1	138.55	_NRS(ph)PHHSTVK_
Q8TAD8	153	S	Smad nuclear-interac	SNIP1	86.8	_RTS(ph)NERPGSGQ(
Q8TAP8	84	T	Protein phosphatase	PPP1R35	62.287	_FRLT(ph)PPS(ph)PVF
Q8TAP8	87	S	Protein phosphatase	PPP1R35	62.287	_FRLT(ph)PPS(ph)PVF
Q8TAQ2	283	S	SWI/SNF complex su	SMARCC2	196.15	_TLTDEVNS(ph)PDSD
Q8TAQ2	302	S	SWI/SNF complex su	SMARCC2	164.01	_KRS(ph)PS(ph)PSPTI
Q8TAQ2	304	S	SWI/SNF complex su	SMARCC2	164.01	_KRS(ph)PS(ph)PSPTI
Q8TAQ2	347	S	SWI/SNF complex su	SMARCC2	87.652	_DMDEPS(ph)PVPNVE
Q8TB61	427	S	Adenosine 3'-phosph	SLC35B2	50.46	_AVPVES(ph)PVQK_

Q8TB72	102	S	Pumilio homolog 2	PUM2	61.238	_SESGGLGVSMVEYV
Q8TB72	136	S	Pumilio homolog 2	PUM2	105.19	_GKAS(ph)PFEEDQNF
Q8TB72	182	S	Pumilio homolog 2	PUM2	101.56	_QAS(ph)PTEVVER_
Q8TBA6	116	S	Golgin subfamily A m	GOLGA5	131.97	_KKS(ph)EPDDELLFD
Q8TBE0	184	S	Bromo adjacent hom	BAHD1	94.339	_DLS(ph)PEPAPDEGP
Q8TBE7	409	S	Solute carrier family 3	SLC35G2	114.63	_QDYQEILDS(ph)PIK_
Q8TC44	321	S	POC1 centriolar prote	POC1B	35.473	_LHFDS(ph)PPHLLDIY
Q8TCJ2	498	S	Dolichyl-diphosphooli	STT3B	98.957	_ENPPVEDS(ph)S(ph)
Q8TCJ2	499	S	Dolichyl-diphosphooli	STT3B	98.957	_ENPPVEDS(ph)S(ph)
Q8TD16	582	S	Protein bicaudal D ho	BICD2	56.258	_S(ph)PILLPK_
Q8TDB6	3	S	E3 ubiquitin-protein li	DTX3L	55.755	_(ac)AS(ph)HLRPPSPL
Q8TDB6	9	S	E3 ubiquitin-protein li	DTX3L	110.77	_(ac)ASHLRPPS(ph)PL
Q8TDD1	39	S	ATP-dependent RNA	DDX54	70.358	_GS(ph)DSEDGEFEIQ
Q8TDD1	75	S	ATP-dependent RNA	DDX54	166.27	_PLPTFPTSECTS(ph)I
Q8TDM6	264	S	Disks large homolog !	DLG5	128.76	_NLLQQS(ph)WEDMK
Q8TDM6	1000	S	Disks large homolog !	DLG5	52.654	_IDYLLPGPGPAHS(ph
Q8TDM6	1011	T	Disks large homolog !	DLG5	67.136	_AGPLT(ph)PPKPPR_
Q8TDY2	624	S	RB1-inducible coiled-	RB1CC1	34.781	_AAQS(ph)LDEMSQTI
Q8TE67	231	S	Epidermal growth fac	EPS8L3	117.38	_SSS(ph)PEDPERDEE
Q8TE77	9	S	Protein phosphatase	SSH3	88.976	_S(ph)PPGSGASTPVC
Q8TEA8	197	S	D-tyrosyl-tRNA(Tyr) d	DTD1	81.016	_SASS(ph)GAEGDVSS
Q8TEH3	523	S	DENN domain-contai	DENND1A	42.947	_TSVPS(ph)PEQPQPY
Q8TEK3	374	S	Histone-lysine N-met	DOT1L	61.16	_VAGPADAPMDS(ph)(
Q8TEK3	834	S	Histone-lysine N-met	DOT1L	85.563	_PLS(ph)PGALQLAGE
Q8TEK3	1104	S	Histone-lysine N-met	DOT1L	80.236	_ASAGTPSLSAGVS(p
Q8TEM1	1844	T	Nuclear pore membra	NUP210	97.223	_DLAVPAALT(ph)PR_
Q8TF01	211	S	Arginine/serine-rich p	PNISR	159.77	_QRS(ph)PIALPVK_
Q8TF01	290	S	Arginine/serine-rich p	PNISR	239.45	_SKFDS(ph)DEEEEDT
Q8TF01	563	S	Arginine/serine-rich p	PNISR	63.216	_SRS(ph)PTIK_
Q8TF72	910	S	Protein Shroom3	SHROOM3	77.53	_DRPGS(ph)PESPLLD
Q8TF76	147	S	Serine/threonine-prot	GSG2	81.884	_DSGRLS(ph)PDLSVC
Q8WUA2	178	S	Peptidyl-prolyl cis-trar	PPIL4	147.36	_INHTVILDDPFDDPPD
Q8WUA4	167	S	General transcription	GTF3C2	72.898	_DLDRPESQS(ph)PK_
Q8WUA4	893	S	General transcription	GTF3C2	197.49	_AHFNAMFQPSS(ph)F
Q8WUA4	901	S	General transcription	GTF3C2	65.809	_RPGFS(ph)PTSHR_
Q8WUB8	297	S	PHD finger protein 10	PHF10	59.041	_YLPLNTALYEPPLDPI
Q8WUB8	301	S	PHD finger protein 10	PHF10	59.041	_YLPLNTALYEPPLDPI
Q8WUQ7	71	S	Cactin	CACTIN	74.772	_S(ph)RSPPRPK_
Q8WUZ0	126	S	B-cell CLL/lymphoma	BCL7C	68.143	_GTEPSPGGTPQPSR
Q8WVB6	871	S	Chromosome transmi	CHTF18	121.41	_VENSPQVDGS(ph)PF
Q8WVC0	10	S	RNA polymerase-ass	LEO1	158.94	_(ac)ADMEDLFGS(ph)
Q8WVC0	14	S	RNA polymerase-ass	LEO1	205.78	_(ac)ADMEDLFGS(ph)
Q8WVC0	66	S	RNA polymerase-ass	LEO1	143.54	_ELFGDDS(ph)EDEGA
Q8WVC0	188	T	RNA polymerase-ass	LEO1	114.24	_MQNT(ph)DDEERPQI
Q8WVC0	197	S	RNA polymerase-ass	LEO1	114.24	_MQNT(ph)DDEERPQI
Q8WVC0	294	S	RNA polymerase-ass	LEO1	118.9	_NAIAS(ph)DSEADS(p
Q8WVC0	300	S	RNA polymerase-ass	LEO1	118.9	_NAIASDSEADS(ph)D
Q8WVC0	607	S	RNA polymerase-ass	LEO1	122.34	_IYS(ph)SDSDEGS(ph
Q8WVC0	610	S	RNA polymerase-ass	LEO1	119.18	_IYSSDS(ph)DEGSEE
Q8WVC0	614	S	RNA polymerase-ass	LEO1	208.28	_IYSSDSDEGS(ph)EE
Q8WVC0	658	S	RNA polymerase-ass	LEO1	113.99	_YVIS(ph)DEEEEDDD_
Q8WVM7	20	S	Cohesin subunit SA-1	STAG1	140.4	_(ac)MITSELPVLQDST
Q8WVM7	24	S	Cohesin subunit SA-1	STAG1	105.51	_(ac)MITSELPVLQDST
Q8WVV4	98	S	Protein POF1B	POF1B	127.15	_TTSSYQNLVWSDHS

Q8WVV4	123	S	Protein POF1B	POF1B	77.522	_ISTCAPSTLHITQNTE
Q8WW12	119	S	PEST proteolytic sign	PCNP	127.15	_TLSVAAAFNEDEDS(p
Q8WWI1	276	S	LIM domain only prot	LMO7	76.378	_EGFES(ph)DTDSEFT
Q8WWI1	805	S	LIM domain only prot	LMO7	138.28	_MYS(ph)FDDVLEEGK
Q8WWI1	867	S	LIM domain only prot	LMO7	169.13	_VTTEIQLPSQS(ph)P\
Q8WWI1	960	S	LIM domain only prot	LMO7	171.88	_TPNNVVSTPAPS(ph)
Q8WWI1	988	S	LIM domain only prot	LMO7	193.23	_LPS(ph)PTSPFSSLS(
Q8WWI1	990	T	LIM domain only prot	LMO7	128.06	_LPS(ph)PT(ph)SPFSS
Q8WWI1	991	S	LIM domain only prot	LMO7	184.34	_LPS(ph)PTS(ph)PFSS
Q8WWI1	1026	S	LIM domain only prot	LMO7	338.32	_ATLSSTSGLDLMSES
Q8WWI1	1048	T	LIM domain only prot	LMO7	63.473	_ISINQT(ph)PGK_
Q8WWI1	1493	S	LIM domain only prot	LMO7	100.28	_SAS(ph)VNKEPVSLP
Q8WWI1	1586	S	LIM domain only prot	LMO7	145.99	_TSTTGVATTQS(ph)P
Q8WWI1	1593	S	LIM domain only prot	LMO7	171.26	_SHS(ph)PSASQSGS(
Q8WWM7	111	S	Ataxin-2-like protein	ATXN2L	181.34	_GPPQS(ph)PVFEGV\
Q8WWM7	449	S	Ataxin-2-like protein	ATXN2L	73.841	_MYPPRS(ph)PK_
Q8WWM7	559	S	Ataxin-2-like protein	ATXN2L	89.831	_LQPSSS(ph)PENSLD
Q8WWM7	594	S	Ataxin-2-like protein	ATXN2L	247.64	_EKEVDGLLTSEPMGS
Q8WWQ0	911	S	PH-interacting protein	PHIP	122.75	_VNEEKDGPIS(ph)PK_
Q8WWQ0	1281	S	PH-interacting protein	PHIP	259.71	_VLS(ph)DS(ph)EDEEI
Q8WWQ0	1283	S	PH-interacting protein	PHIP	259.71	_VLS(ph)DS(ph)EDEEI
Q8WWQ0	1315	S	PH-interacting protein	PHIP	151.74	_AQS(ph)YDIQAWK_
Q8WWQ0	1783	S	PH-interacting protein	PHIP	237.46	_TAFYNEDDS(ph)EEE
Q8WX92	557	S	Negative elongation f	NELFB	145.26	_KPS(ph)PAQAAETPA
Q8WX93	893	S	Palladin	PALLD	98.253	_IAS(ph)DEEIQGTK_
Q8WX93	1104	S	Palladin	PALLD	59.198	_S(ph)PSGHPHVR_
Q8WXF0	105	S	Serine/arginine-rich s	SRSF12	99.283	_HPCS(ph)PSDHR_
Q8WXF1	477	S	Paraspeckle compon	PSPC1	108.37	_FPQGPPSQMGS(ph)I
Q8WXH0	4136	S	Nesprin-2	SYNE2	52.862	_AEPS(ph)PQSWSSL\
Q8WXH0	6361	S	Nesprin-2	SYNE2	60.834	_LTSCTPGLEDEKEAS
Q8WXI2	325	S	Connector enhancer	CNKSR2	78.272	_S(ph)PTSSVATPSST
Q8WXI9	120	T	Transcriptional repres	GATAD2B	76.481	_GRLT(ph)PS(ph)PDII\
Q8WXI9	122	S	Transcriptional repres	GATAD2B	76.481	_GRLT(ph)PS(ph)PDII\
Q8WY36	844	S	HMG box transcriptio	BBX	99.859	_VS(ph)PAGGTLDDKF
Q8WYA6	545	S	Beta-catenin-like prot	CTNNBL1	54.764	_EYAENIGDGRS(ph)P
Q8WYH8	118	S	Inhibitor of growth pr	ING5	137.69	_DKMEGS(ph)DFESS(
Q8WYL5	897	S	Protein phosphatase	SSH1	85.849	_S(ph)PPPFFYR_
Q8WYL5	937	S	Protein phosphatase	SSH1	78.529	_SSS(ph)SDSIHSVR_
Q8WYP5	528	S	Protein ELYS	AHCTF1	80.96	_CLVAGLLS(ph)PR_
Q8WYP5	1142	S	Protein ELYS	AHCTF1	65.224	_S(ph)PLYLVSR_
Q8WYP5	1222	S	Protein ELYS	AHCTF1	162.32	_STPLASPSPSPGRS(
Q8WYP5	1283	S	Protein ELYS	AHCTF1	99.927	_TTSFFLNS(ph)PEK_
Q8WYP5	1295	S	Protein ELYS	AHCTF1	163.45	_EHQEMDEGS(ph)QS
Q8WYP5	1297	S	Protein ELYS	AHCTF1	153.88	_EHQEMDEGSQS(ph)
Q8WYP5	1513	S	Protein ELYS	AHCTF1	131.32	_LPISDS(ph)PPDTQEI
Q8WYP5	1541	S	Protein ELYS	AHCTF1	65.423	_NLS(ph)FNELYPSGT
Q8WYP5	2212	S	Protein ELYS	AHCTF1	63.754	_ESAWS(ph)PPPIEIR_
Q8WYQ5	377	S	Microprocessor comp	DGCR8	109.98	_EQSSDLTPSGDVS(p
Q8WZ42	27928	Y	Titin	TTN	35.541	_IT(ph)HY(ph)IVEK_
Q8WZ73	229	S	E3 ubiquitin-protein li	RFFL	131.42	_VPAEDETQSIDS(ph)I
Q8WZ73	240	S	E3 ubiquitin-protein li	RFFL	218.88	_RAS(ph)LSDLTDLEDI
Q92466	26	S	DNA damage-binding	DDB2	172.93	_S(ph)PLELEPEAK_
Q92508	1646	S	Piezo-type mechanos	PIEZO1	144.7	_TAS(ph)ELLLDR_
Q92522	2	S	Histone H1x	H1FX	64.589	_(ac)S(ph)VELEEALPV

Q92522	31	S	Histone H1x	H1FX	102.64	_AGGSAALS(ph)PSKK
Q92538	1298	S	Golgi-specific brefeldi	GBF1	198.21	_ADAPDAGAQS(ph)DS
Q92538	1318	S	Golgi-specific brefeldi	GBF1	125.23	_GYTS(ph)DSEVYTDH
Q92541	53	S	RNA polymerase-ass	RTF1	57.802	_VVIDS(ph)DT(ph)EDS
Q92541	55	T	RNA polymerase-ass	RTF1	34.437	_VVIDS(ph)DT(ph)EDS
Q92541	58	S	RNA polymerase-ass	RTF1	76.889	_VVIDSDTEDS(ph)GS(
Q92541	60	S	RNA polymerase-ass	RTF1	76.889	_VVIDSDTEDS(ph)GS(
Q92576	1133	S	PHD finger protein 3	PHF3	99.834	_MAPPVDDLS(ph)PK_
Q92576	1614	S	PHD finger protein 3	PHF3	70.771	_QLQEDQENNLQDNQ
Q92576	1642	S	PHD finger protein 3	PHF3	99.283	_S(ph)PQFINLK_
Q92598	809	S	Heat shock protein 10	HSPH1	73.499	_IES(ph)PKLER_
Q92610	573	S	Zinc finger protein 59	ZNF592	61.03	_VLHSSNPVPLYAPNL
Q92610	1089	S	Zinc finger protein 59	ZNF592	95.662	_VKPPGGHS(ph)PQVI
Q92610	1264	S	Zinc finger protein 59	ZNF592	55.188	_LLGPAPEDDGGHND
Q92613	85	S	Protein Jade-3	PHF16	46.953	_GVQVPAS(ph)PDTVF
Q92613	566	S	Protein Jade-3	PHF16	107.31	_NSSTETDQQPHS(ph
Q92614	83	S	Unconventional myos	MYO18A	104.3	_VASGSDLHLTDIDS(p
Q92614	140	S	Unconventional myos	MYO18A	90.263	_RFS(ph)FSQR_
Q92614	1970	S	Unconventional myos	MYO18A	165.53	_NKLEGDS(ph)DVDSE
Q92614	2007	S	Unconventional myos	MYO18A	138.25	_SSS(ph)PTSYWK_
Q92614	2020	S	Unconventional myos	MYO18A	216.51	_SLAPDRS(ph)DDEHD
Q92614	2041	S	Unconventional myos	MYO18A	225.01	_YSHSYLS(ph)DS(ph)I
Q92614	2043	S	Unconventional myos	MYO18A	269.59	_YSHSYLS(ph)DS(ph)I
Q92615	601	S	La-related protein 4B	LARP4B	121.09	_SPS(ph)PAHLPDDPK
Q92615	718	S	La-related protein 4B	LARP4B	109.36	_RPAGGRPS(ph)PSAM
Q92616	956	T	Translational activato	GCN1L1	41.242	_AVMLLHT(ph)HT(ph)I
Q92625	663	S	Ankyrin repeat and S/	ANKS1A	59.625	_SPS(ph)FASEWDEIE
Q92667	150	S	A-kinase anchor prote	AKAP1	129.38	_SIPLECPLS(ph)SPK_
Q92667	429	S	A-kinase anchor prote	AKAP1	74.021	_TVLGPDTAEPATAEA
Q92667	445	S	A-kinase anchor prote	AKAP1	91.549	_SLLSS(ph)PTK_
Q92674	284	S	Centromere protein I	CENPI	74.987	_NRGPS(ph)PEPLK_
Q92692	410	T	Poliovirus receptor-re	PVRL2	76.97	_KEQTLQGAEEDEDLE
Q92692	433	S	Poliovirus receptor-re	PVRL2	69.016	_LEAQEMPSQLFTLGA
Q92733	157	S	Proline-rich protein PI	PRCC	169.96	_IAAPELHKGDS(ph)DS
Q92733	159	S	Proline-rich protein PI	PRCC	169.96	_IAAPELHKGDS(ph)DS
Q92733	267	S	Proline-rich protein PI	PRCC	237.66	_QITQEEDDS(ph)DEE
Q92754	434	S	Transcription factor A	TFAP2C	46.337	_SYMNPGDQS(ph)PAI
Q92766	161	S	Ras-responsive elem	RREB1	105.46	_DPNSATATAPPS(ph)
Q92766	1219	S	Ras-responsive elem	RREB1	40.951	_FSPFLQTAEDNTQDE
Q92766	1320	S	Ras-responsive elem	RREB1	99.396	_QVAGDAPVEQATAE
Q92766	1475	S	Ras-responsive elem	RREB1	139.44	_LAEETEGPS(ph)DGE
Q92769	394	S	Histone deacetylase 2	HDAC2	141.07	_M(ox)LPHAPGVQM(o
Q92769	422	S	Histone deacetylase 2	HDAC2	239.22	_IACDEEFS(ph)DS(ph)
Q92769	424	S	Histone deacetylase 2	HDAC2	239.22	_IACDEEFS(ph)DS(ph)
Q92794	1113	S	Histone acetyltransfe	KAT6A	187.76	_SKDEEEDEES(ph)DD
Q92797	1171	S	Symplekin	SYMPK	149.63	_LKPGGVGAPSSSS(p
Q92797	1243	S	Symplekin	SYMPK	195.15	_EERS(ph)PQTLAPVG
Q92797	1259	S	Symplekin	SYMPK	128.39	_TPS(ph)PAAEDAREP
Q92878	690	T	DNA repair protein R/	RAD50	98.21	_VFQT(ph)EAELQEVIS
Q92882	202	S	Osteoclast-stimulatin	OSTF1	153.45	_TLS(ph)NAEDYLDDE
Q92882	213	S	Osteoclast-stimulatin	OSTF1	153.45	_TLS(ph)NAEDYLDDE
Q92887	283	S	Canalicular multispec	ABCC2	106.39	_NQSQS(ph)QDALVLE
Q92887	878	S	Canalicular multispec	ABCC2	231.92	_HTGPEEEATVHDGS(
Q92890	247	S	Ubiquitin fusion degra	UFD1L	73.012	_GVEPSPS(ph)PIKPG

Q92922	310	S	SWI/SNF complex su	SMARCC1	104.59	_NEEPVRS(ph)PERR_
Q92922	328	S	SWI/SNF complex su	SMARCC1	125.03	_KHS(ph)PS(ph)PPPP
Q92922	330	S	SWI/SNF complex su	SMARCC1	125.03	_KHS(ph)PS(ph)PPPP
Q92945	181	S	Far upstream elemen	KHSRP	133.86	_VQIS(ph)PDSGGLPE
Q93009	18	S	Ubiquitin carboxyl-ter	USP7	107.61	_AGEQQLS(ph)EPEDM
Q93074	635	S	Mediator of RNA poly	MED12	71.988	_GDLAFGAPGPRPPS
Q969F1	9	S	General transcription	GTF3C6	77.373	_(ac)AAAADERS(ph)P
Q969H6	154	S	Ribonuclease P/MRP	POP5	119.62	_SCLLEEEEES(ph)GE
Q969R5	67	S	Lethal(3)malignant br	L3MBTL2	121.33	_EAGELPTS(ph)PLHLI
Q96A00	128	S	Protein phosphatase	PPP1R14A	51.31	_QPS(ph)PSHDGSLSF
Q96A49	248	T	Synapse-associated p	SYAP1	76.679	_T(ph)PPVVIK_
Q96A57	24	S	Transmembrane prot	TMEM230	94.203	_LSS(ph)TDDGYIDLQF
Q96AE4	630	S	Far upstream elemen	FUBP1	220.53	_QQAAYYAQTS(ph)PC
Q96AQ6	43	S	Pre-B-cell leukemia tr	PBXIP1	67.187	_ALQAPHS(ph)PSK_
Q96AT1	50	S	Uncharacterized prot	KIAA1143	87.772	_IQPQPPDEDGDHS(p
Q96B23	66	S	Uncharacterized prot	C18orf25	64.714	_RDS(ph)SESQLASTE
Q96B36	88	S	Proline-rich AKT1 sub	AKT1S1	69.485	_AATAARPPAPPPAPC
Q96B36	92	S	Proline-rich AKT1 sub	AKT1S1	69.485	_AATAARPPAPPPAPC
Q96B54	99	S	Zinc finger protein 42	ZNF428	40.798	_S(ph)PLGEAPPGTPP
Q96BY7	255	S	Autophagy-related pr	ATG2B	42.336	_LS(ph)PSWNPK_
Q96BY7	1579	S	Autophagy-related pr	ATG2B	40.689	_SYIS(ph)PHS(ph)SPS
Q96C19	74	S	EF-hand domain-cont	EFHD2	185.25	_RADLNQGIGEPQS(p
Q96C57	179	S	Uncharacterized prot	C12orf43	181.14	_EAAVSASDILQESAIH
Q96CP2	21	S	FLYWCH family mem	FLYWCH2	51.39	_ASQEPS(ph)PKPGTE
Q96D71	540	S	RalBP1-associated E	REPS1	116.13	_SHSGT(ph)S(ph)PDN
Q96DF8	292	S	Protein DGCR14	DGCR14	86.014	_ELIPQES(ph)PR_
Q96EB6	14	S	NAD-dependent prote	SIRT1	127.66	_(ac)ADEAALALQPGG
Q96EL2	16	S	28S ribosomal proteir	MRPS24	55.975	_VLS(ph)WS(ph)RELP
Q96EL2	18	S	28S ribosomal proteir	MRPS24	55.975	_VLS(ph)WS(ph)RELP
Q96EV2	41	S	RNA-binding protein 3	RBM33	171.25	_AADEDWDS(ph)ELEI
Q96EV2	205	S	RNA-binding protein 3	RBM33	251.1	_DIKEES(ph)DEEEEDI
Q96EV2	765	S	RNA-binding protein 3	RBM33	51.726	_VKPAS(ph)PVAQPK_
Q96EZ8	282	S	Microspherule protein	MCRS1	202.19	_GDQVLNFS(ph)DAEI
Q96F44	85	S	E3 ubiquitin-protein li	TRIM11	54.764	_LHPPS(ph)PVPQGVC
Q96F63	212	S	Coiled-coil domain-co	CCDC97	79.407	_TPTHQPPKPGS(ph)F
Q96FF9	21	S	Sororin	CDCA5	96.171	_APS(ph)PTKPLR_
Q96FF9	209	S	Sororin	CDCA5	50.226	_PWAPDMTLPGIS(ph)
Q96FJ0	242	S	AMSH-like protease	STAMBPL1	110.56	_SDATNYASHS(ph)PP
Q96FV9	2	S	THO complex subunit	THOC1	97.095	_(ac)MS(ph)PTPPLFSL
Q96FV9	560	S	THO complex subunit	THOC1	58.087	_TGEDEDEEDNDALLK
Q96G74	64	S	OTU domain-containi	OTUD5	100.39	_AS(ph)PPPQGPLPGF
Q96GN5	21	S	Cell division cycle-as	CDCA7L	209.24	_EVADIFNAPS(ph)DDI
Q96GN5	117	S	Cell division cycle-as	CDCA7L	175.23	_ASLVS(ph)EEEEDEE
Q96HA7	719	S	Tonsoku-like protein	TONSL	59.418	_VS(ph)PGQAAPAMAI
Q96HC4	360	S	PDZ and LIM domain	PDLIM5	71.98	_S(ph)PSWQRPNQGV
Q96HR8	315	S	H/ACA ribonucleopro	NAF1	178.76	_NDQEPPPEALDFS(p
Q96HS1	80	S	Serine/threonine-prot	PGAM5	70.47	_NVES(ph)GEEELASK
Q96HS1	87	S	Serine/threonine-prot	PGAM5	127.58	_NVESGEEELAS(ph)K
Q96I13	144	S	Abhydrolase domain-	ABHD8	50.226	_LAPGSAGS(ph)GSG
Q96I15	129	S	Selenocysteine lyase	SCLY	105.41	_GHTGGHHS(ph)PVK_
Q96I25	71	T	Splicing factor 45	RBM17	110.56	_QIVDT(ph)PPHVAAG
Q96I25	155	S	Splicing factor 45	RBM17	270.73	_RPDPDS(ph)DEDED
Q96I25	222	S	Splicing factor 45	RBM17	255.83	_S(ph)PTGPSNSFLAN
Q96IG2	417	T	F-box/LRR-repeat pro	FBXL20	75.773	_VHAYFAPVT(ph)PPP

Q96IY1	4	S	Kinetochore-associat	NSL1	144.55	_(ac)AGS(ph)PELVVLI
Q96JM3	87	S	Chromosome alignme	CHAMP1	71.279	_HAS(ph)PDKWNDKPI
Q96JM3	103	T	Chromosome alignme	CHAMP1	65.905	_ET(ph)DPVKSPPLPE
Q96JM3	108	S	Chromosome alignme	CHAMP1	117.12	_ETDPVKS(ph)PPLPE
Q96JM3	204	S	Chromosome alignme	CHAMP1	127.95	_LAPVPS(ph)PEPQKP
Q96JM3	214	S	Chromosome alignme	CHAMP1	127.95	_LAPVPS(ph)PEPQKP
Q96JM3	282	S	Chromosome alignme	CHAMP1	211.62	_KPS(ph)PSES(ph)PEI
Q96JM3	286	S	Chromosome alignme	CHAMP1	121.19	_KPS(ph)PSES(ph)PEI
Q96JM3	297	S	Chromosome alignme	CHAMP1	90.559	_KPSPSES(ph)PEPWI
Q96JM3	308	S	Chromosome alignme	CHAMP1	122.67	_RPAPAVS(ph)PGSWI
Q96JM3	319	S	Chromosome alignme	CHAMP1	122.67	_RPAPAVS(ph)PGSWI
Q96JM3	405	S	Chromosome alignme	CHAMP1	113.53	_TAPTLS(ph)PEHWK_
Q96JM3	416	S	Chromosome alignme	CHAMP1	92.792	_AVPPVS(ph)PELR_
Q96JM3	427	S	Chromosome alignme	CHAMP1	113.37	_KPGPPLS(ph)PEIRS(
Q96JM3	432	S	Chromosome alignme	CHAMP1	79.278	_KPGPPLS(ph)PEIRS(
Q96JM3	436	S	Chromosome alignme	CHAMP1	79.278	_KPGPPLS(ph)PEIRS(
Q96JM3	443	S	Chromosome alignme	CHAMP1	118.85	_KPS(ph)GSPDLWK_
Q96JM3	445	S	Chromosome alignme	CHAMP1	182.03	_KPSGS(ph)PDLWK_
Q96JM3	452	S	Chromosome alignme	CHAMP1	182.03	_KPS(ph)GSPDLWKLS
Q96JM3	459	S	Chromosome alignme	CHAMP1	133.62	_KTS(ph)PASLDFPES(
Q96JM3	476	S	Chromosome alignme	CHAMP1	73.499	_GGS(ph)PDLWK_
Q96JM3	507	S	Chromosome alignme	CHAMP1	83.252	_KPGPSGPSES(ph)PK
Q96JM3	603	S	Chromosome alignme	CHAMP1	122.44	_CDILVQEELLAS(ph)P
Q96JP2	1025	S	Putative unconventior	MYO15B	51.998	_AVPS(ph)PPPPPIVK_
Q96JP5	83	S	E3 ubiquitin-protein li	ZFP91	122.79	_RSS(ph)PSARPPDVP
Q96JQ2	635	S	Calmin	CLMN	122.3	_MDKHEPHQDS(ph)G
Q96K21	144	S	Zinc finger FYVE dor	ZFYVE19	87.895	_WS(ph)PPQNYK_
Q96K21	354	S	Zinc finger FYVE dor	ZFYVE19	151.87	_LPDS(ph)DDDEDEET
Q96K49	469	S	Transmembrane prot	TMEM87B	96.052	_YAFMPLIDDS(ph)DDI
Q96K49	534	S	Transmembrane prot	TMEM87B	106.88	_WVEENIPSSFTDVAL
Q96KC8	430	S	DnaJ homolog subfar	DNAJC1	155.31	_EDAEGVAAEEEQEG
Q96KC8	479	S	DnaJ homolog subfar	DNAJC1	146.39	_DFDIAEQNES(ph)S(p
Q96KC8	480	S	DnaJ homolog subfar	DNAJC1	146.39	_DFDIAEQNES(ph)S(p
Q96KM6	409	S	Zinc finger protein 51	ZNF512B	65.231	_AAGPAS(ph)PPEEDP
Q96KQ7	140	S	Histone-lysine N-met	EHMT2	132.79	_S(ph)PPSVQSLAMR_
Q96KR1	1054	S	Zinc finger RNA-bindi	ZFR	222.13	_RRDS(ph)DGVDGFEA
Q96L73	2471	S	Histone-lysine N-met	NSD1	126.8	_AAS(ph)PHQVTPQAI
Q96L91	736	S	E1A-binding protein p	EP400	62.633	_ALS(ph)PVTSR_
Q96LT9	108	S	RNA-binding protein 4	RNPC3	101.2	_VHS(ph)PCPTSGSEK
Q96MG7	64	S	Melanoma-associate	NDNL2	168.81	_GPGGSQGSQGPS(p
Q96MH2	29	S	Protein HEXIM2	HEXIM2	121.03	_TSGAPGS(ph)PQTPP
Q96MH2	51	S	Protein HEXIM2	HEXIM2	78.385	_MES(ph)HS(ph)EDED
Q96MH2	53	S	Protein HEXIM2	HEXIM2	78.385	_MES(ph)HS(ph)EDED
Q96MU7	294	S	YTH domain-containi	YTHDC1	35.037	_SGSGTDGS(ph)DEK_
Q96MU7	308	S	YTH domain-containi	YTHDC1	158.02	_GIS(ph)PIVFDR_
Q96MU7	424	S	YTH domain-containi	YTHDC1	201.79	_LSSESHHGGS(ph)PII
Q96MY1	130	S	Uncharacterized prot	C20orf112	105.96	_TTPES(ph)PPYSSGS
Q96MY1	400	S	Uncharacterized prot	C20orf112	86.539	_PVPTAQLS(ph)PTEIS
Q96N64	81	S	PWWP domain-conta	PWWP2A	150.27	_S(ph)PEAVGPELEAE
Q96N67	900	S	Dedicator of cytokine	DOCK7	158.88	_SLSNS(ph)NPDISGTP
Q96NB3	351	S	Zinc finger protein 83	ZNF830	40.101	_KEEENADS(ph)DDEC
Q96NY9	95	S	Crossover junction en	MUS81	51.388	_TSGGDHAPDS(ph)PS
Q96PK6	206	T	RNA-binding protein 1	RBM14	151.66	_QPT(ph)PPFFGR_
Q96PK6	215	S	RNA-binding protein 1	RBM14;RBM4;RB	65.157	_DRS(ph)PLRR_

Q96PK6	572	T	RNA-binding protein 1	RBM14	168.3	_GQPGNAYDGAGQPS
Q96PK6	582	S	RNA-binding protein 1	RBM14	89.047	_TRLS(ph)PPR_
Q96PU4	667	S	E3 ubiquitin-protein li	UHRF2	166.77	_RPIS(ph)DDDCPSAS
Q96PY5	171	S	Formin-like protein 2	FMNL2	133.86	_S(ph)IEDLHR_
Q96Q05	789	T	Trafficking protein pa	TRAPPC9	55.353	_VATFT(ph)INIK_
Q96Q42	492	S	Alsin	ALS2	86.488	_LSLPGLLSQVS(ph)PI
Q96QC0	313	S	Serine/threonine-prot	PPP1R10	73.138	_VLS(ph)PTAAKPSPFI
Q96QC0	545	S	Serine/threonine-prot	PPP1R10	59.118	_LIPLDEECSMDETPY
Q96QR8	101	S	Transcriptional activa	PURB	83.639	_DSLGDFIEHYAQLGP
Q96QT6	586	T	PHD finger protein 12	PHF12	62.193	_PLT(ph)PPAAGGLQN
Q96QT6	671	T	PHD finger protein 12	PHF12	83.733	_VLT(ph)PPQAAGDGI
Q96RK0	173	S	Protein capicua homc	CIC	45.115	_TQS(ph)LSALPK_
Q96RK0	496	S	Protein capicua homc	CIC	52.391	_KVFS(ph)PVIR_
Q96RK0	1373	S	Protein capicua homc	CIC	80.116	_FAELPEFRPEEVLPS
Q96RL1	653	S	BRCA1-A complex su	UIMC1	82.922	_VPS(ph)PGMEEAGC
Q96RT1	440	S	Protein LAP2	ERBB2IP	94.632	_TEDVMFIS(ph)DNES
Q96RT1	602	S	Protein LAP2	ERBB2IP	56.882	_HIVNHDDVFEESEEL
Q96RT1	603	S	Protein LAP2	ERBB2IP	56.882	_HIVNHDDVFEESEEL
Q96S55	153	S	ATPase WRNIP1	WRNIP1	137.68	_RPAAAAAAGSAS(ph
Q96S66	438	S	Chloride channel CLI	CLCC1	87.429	_FQTGNKS(ph)PEVLR
Q96S82	230	S	Ubiquitin-like protein	UBL7	78.913	_DMPGGFLFEGLS(ph
Q96SB3	100	S	Neurabin-2	PPP1R9B	102.89	_ASS(ph)LNENVDHSA
Q96SB3	203	S	Neurabin-2	PPP1R9B	81.329	_LDADAVS(ph)PTVSQ
Q96SB4	51	S	SRSF protein kinase	SRPK1	138.24	_GSAPHSESDLPEQEI
Q96SB4	311	S	SRSF protein kinase	SRPK1	128.44	_QEESES(ph)PVERPL
Q96SK2	533	Y	Transmembrane prot	TMEM209	28.812	_NNMFHTLLM(ox)FLY
Q96SN8	613	S	CDK5 regulatory subu	CDK5RAP2	92.112	_TLEEQIS(ph)EIR_
Q96ST2	198	S	Protein IWS1 homolo	IWS1	131.45	_HQASDS(ph)ENEEPF
Q96ST2	235	S	Protein IWS1 homolo	IWS1	215.32	_HQAS(ph)DS(ph)ENE
Q96ST2	237	S	Protein IWS1 homolo	IWS1	215.32	_HQAS(ph)DS(ph)ENE
Q96ST2	287	S	Protein IWS1 homolo	IWS1	166.69	_NQAS(ph)DS(ph)ENE
Q96ST2	289	S	Protein IWS1 homolo	IWS1	166.69	_NQAS(ph)DS(ph)ENE
Q96ST2	438	S	Protein IWS1 homolo	IWS1	143.83	_TIAS(ph)DS(ph)EEEA
Q96ST2	440	S	Protein IWS1 homolo	IWS1	143.83	_TIAS(ph)DS(ph)EEEA
Q96ST3	277	S	Paired amphipathic h	SIN3A	68.216	_S(ph)PPVQPHTPVTI
Q96ST3	832	S	Paired amphipathic h	SIN3A	266.4	_GDLS(ph)DVEEEEEE
Q96ST3	940	S	Paired amphipathic h	SIN3A	84.759	_DKSDS(ph)PAIQLR_
Q96T23	397	S	Remodeling and spac	RSF1	134.61	_LSDDFDS(ph)PVK_
Q96T23	604	S	Remodeling and spac	RSF1	146.67	_LS(ph)PIPEEVPK_
Q96T23	617	S	Remodeling and spac	RSF1	124.07	_STLES(ph)EKPGSPE
Q96T23	622	S	Remodeling and spac	RSF1	171.03	_STLESEKPGS(ph)PE
Q96T23	629	S	Remodeling and spac	RSF1	137.47	_STLESEKPGS(ph)PE
Q96T23	1277	S	Remodeling and spac	RSF1	196	_GRS(ph)T(ph)DEYS(p
Q96T23	1278	T	Remodeling and spac	RSF1	196	_GRS(ph)T(ph)DEYS(p
Q96T23	1282	S	Remodeling and spac	RSF1	196	_GRS(ph)T(ph)DEYS(p
Q96T23	1305	T	Remodeling and spac	RSF1	346.24	_IET(ph)DEEES(ph)CD
Q96T23	1310	S	Remodeling and spac	RSF1	205.46	_IET(ph)DEEES(ph)CD
Q96T23	1345	S	Remodeling and spac	RSF1	211.39	_IES(ph)DEEEDFENV
Q96T37	127	S	Putative RNA-binding	RBM15	122.55	_LHSYS(ph)SPSTK_
Q96T37	128	S	Putative RNA-binding	RBM15	112.02	_LHSYSS(ph)PSTK_
Q96T37	257	S	Putative RNA-binding	RBM15	130.45	_S(ph)RS(ph)PLDKDT
Q96T37	259	S	Putative RNA-binding	RBM15	130.45	_S(ph)RS(ph)PLDKDT
Q96T37	292	S	Putative RNA-binding	RBM15	62.469	_S(ph)LS(ph)PGGAAL
Q96T37	294	S	Putative RNA-binding	RBM15	140.31	_S(ph)LS(ph)PGGAAL

Q96T37	568	T	Putative RNA-binding	RBM15	140.91	_DRT(ph)PPLLYR_
Q96T37	656	S	Putative RNA-binding	RBM15	134.88	_HLDRS(ph)PESDRPF
Q96T37	670	S	Putative RNA-binding	RBM15	174.62	_HCAPS(ph)PDRS(ph)
Q96T37	674	S	Putative RNA-binding	RBM15	174.62	_HCAPS(ph)PDRS(ph)
Q96T37	700	S	Putative RNA-binding	RBM15	160.48	_LLLERPS(ph)PIRDR_
Q96T37	741	S	Putative RNA-binding	RBM15	130.21	_TTAPTEGKS(ph)PLK
Q96T58	725	S	Msx2-interacting prot	SPEN	77.387	_S(ph)QS(ph)PVHLR_
Q96T58	727	S	Msx2-interacting prot	SPEN	83.499	_S(ph)QS(ph)PVHLR_
Q96T58	736	S	Msx2-interacting prot	SPEN	119.37	_RPQS(ph)PGAS(ph)P
Q96T58	740	S	Msx2-interacting prot	SPEN	140.22	_RPQSPGAS(ph)PSQ
Q96T58	1222	S	Msx2-interacting prot	SPEN	123.24	_SLVHEVGKPPQDVT
Q96T58	1278	S	Msx2-interacting prot	SPEN	84.249	_HGSFHEDEDPIGS(p
Q96T58	1380	S	Msx2-interacting prot	SPEN	91.416	_DLEPGEVPS(ph)DS(
Q96T58	1382	S	Msx2-interacting prot	SPEN	91.416	_DLEPGEVPS(ph)DS(
Q96T58	1910	T	Msx2-interacting prot	SPEN	114.74	_SVYAT(ph)MGDHENF
Q96T58	1918	S	Msx2-interacting prot	SPEN	109.25	_SVYATMGDHENRS(
Q96T58	2120	S	Msx2-interacting prot	SPEN	105.71	_ESGVVAVS(ph)PEKS
Q96T58	2126	S	Msx2-interacting prot	SPEN	105.71	_ESGVVAVS(ph)PEKS
Q96T58	2159	S	Msx2-interacting prot	SPEN	75.695	_SDPVDPDKEPEKED
Q96T60	118	T	Bifunctional polynucle	PNKP	222.4	_TPESQPDT(ph)PPGT
Q96T88	91	S	E3 ubiquitin-protein li	UHRF1	135.84	_ERDSELS(ph)DTDSG
Q96T88	287	S	E3 ubiquitin-protein li	UHRF1	132.76	_IERPGEGS(ph)PMVD
Q96TA1	692	S	Niban-like protein 1	FAM129B	109.44	_AAPEASS(ph)PPASP
Q96TA1	696	S	Niban-like protein 1	FAM129B	109.44	_AAPEASS(ph)PPAS(
Q96TC7	46	S	Regulator of microtub	RMDN3	171.23	_SQS(ph)LPNSLDYTQ
Q96TC7	212	S	Regulator of microtub	RMDN3	87.04	_KDS(ph)LDLEEEAAS
Q99081	386	S	Transcription factor 1	TCF12	69.248	_PGGQAPSS(ph)PSYE
Q99442	341	S	Translocation protein	SEC62	116.28	_VGPGNHGTEGSGGE
Q99442	375	T	Translocation protein	SEC62	322.61	_EELEQQT(ph)DGDCE
Q99460	273	T	26S proteasome non-	PSMD1	108.73	_TVGT(ph)PIASVPGS
Q99543	47	S	DnaJ homolog subfar	DNAJC2	114.63	_NAS(ph)ASFQELEDK
Q99543	60	S	DnaJ homolog subfar	DNAJC2	137.29	_KELS(ph)EES(ph)EDE
Q99543	63	S	DnaJ homolog subfar	DNAJC2	137.29	_KELS(ph)EES(ph)EDE
Q99549	51	S	M-phase phosphopro	MPHOSPH8	219.18	_GAEAFGDS(ph)EEDC
Q99549	85	S	M-phase phosphopro	MPHOSPH8	185.16	_GYTS(ph)DDDTWEPI
Q99549	164	S	M-phase phosphopro	MPHOSPH8	94.023	_QREEKS(ph)PDDLK_
Q99549	319	S	M-phase phosphopro	MPHOSPH8	134.22	_AGQDMGLEHGFEKP
Q99549	403	S	M-phase phosphopro	MPHOSPH8	189.56	_GLWSTDS(ph)AEEDK
Q99567	35	S	Nuclear pore comple	NUP88	59.818	_NQS(ph)PTEAEKPAS
Q99567	50	S	Nuclear pore comple	NUP88	71.117	_NQSPTEAEKPASSSL
Q99567	517	S	Nuclear pore comple	NUP88	134.06	_EDVEVAES(ph)PLR_
Q99569	221	S	Plakophilin-4	PKP4	81.807	_AQS(ph)PSYVISTGV
Q99569	273	S	Plakophilin-4	PKP4	55.718	_AAS(ph)PYSQRPAS(
Q99569	281	S	Plakophilin-4	PKP4	55.718	_AAS(ph)PYSQRPAS(
Q99569	314	S	Plakophilin-4	PKP4	133.87	_VGS(ph)PLTLTDAQT
Q99569	512	S	Plakophilin-4;Catenin	PKP4;CTNND2	32.263	_SPS(ph)IDSIQK_
Q99569	776	S	Plakophilin-4	PKP4	59.539	_LLGLNELDDLLGKES
Q99569	1099	S	Plakophilin-4	PKP4	155.92	_PSPIYISSYS(ph)SPA
Q99575	730	S	Ribonucleases P/MR	POP1	41.53	_VQAYEEPSVASS(ph)
Q99590	405	S	Protein SCAF11	SCAF11	203.82	_SSSNDS(ph)VDEETA
Q99590	413	S	Protein SCAF11	SCAF11	175.85	_SSSNDSVDEETAES(
Q99590	608	S	Protein SCAF11	SCAF11	267.39	_TEELIES(ph)PKLESS
Q99590	776	S	Protein SCAF11	SCAF11	114.87	_VETVSQPSES(ph)PK
Q99590	796	S	Protein SCAF11	SCAF11	173.01	_FHS(ph)PSTTWSPNK

Q99590	802	S	Protein SCAF11	SCAF11	173.01	_FHS(ph)PSTTWS(ph)
Q99590	816	S	Protein SCAF11	SCAF11	83.53	_KRPQS(ph)PS(ph)PR
Q99590	818	S	Protein SCAF11	SCAF11	113.61	_KRPQS(ph)PS(ph)PR
Q99607	188	S	ETS-related transcrip	ELF4	86.288	_STS(ph)PVTDPSIPIR_
Q99613	39	S	Eukaryotic translation	EIF3C;EIF3CL	153.92	_QPLLLS(ph)EDEEDTI
Q99638	387	S	Cell cycle checkpoint	RAD9A	69.03	_SPQGPSPVLAEDS(p
Q99700	772	S	Ataxin-2	ATXN2	142.72	_ENIKPNETS(ph)PSFS
Q99733	125	S	Nucleosome assembl	NAP1L4	268.45	_EFITGDVEPTDAESE
Q99848	3	T	Probable rRNA-proce	EBNA1BP2	51.811	_(ac)MDT(ph)PPLSDSI
Q99848	16	S	Probable rRNA-proce	EBNA1BP2	82.6	_(ac)MDTPPLSDSESE
Q99959	151	S	Plakophilin-2	PKP2	105.53	_RLEIS(ph)PDS(ph)S(p
Q99959	154	S	Plakophilin-2	PKP2	126.07	_RLEIS(ph)PDS(ph)S(p
Q99959	155	S	Plakophilin-2	PKP2	126.07	_RLEIS(ph)PDS(ph)S(p
Q99973	397	S	Telomerase protein c	TEP1	105.19	_S(ph)PGMEPPFSHR_
Q9BPX3	674	S	Condensin complex s	NCAPG	317.05	_TLHCEGTEINS(ph)DI
Q9BPX3	1015	S	Condensin complex s	NCAPG	93.478	_LNLAQFLNEDLS(ph)_
Q9BQ52	199	S	Zinc phosphodiestera	ELAC2	96.247	_HQPWQS(ph)PERPL
Q9BQ67	119	S	Glutamate-rich WD re	GRWD1	142.86	_MHNLHGTKPPPS(ph
Q9BQ67	122	S	Glutamate-rich WD re	GRWD1	142.86	_MHNLHGTKPPPS(ph
Q9BQA1	5	T	Methylosome protein	WDR77	98.281	_KET(ph)PPPLVPPAA
Q9BQA9	173	S	Uncharacterized prote	C17orf62	45.983	_LITSFLELHCLESPT(p
Q9BQA9	175	S	Uncharacterized prote	C17orf62	54.003	_LITSFLELHCLESPT(p
Q9BQA9	176	S	Uncharacterized prote	C17orf62	54.003	_LITSFLELHCLESPT(p
Q9BQA9	178	S	Uncharacterized prote	C17orf62	54.003	_LITSFLELHCLESPT(p
Q9BQF6	443	S	Sentrin-specific prote	SENP7	36.449	_GHNEGNQSLISAEPI
Q9BQF6	444	S	Sentrin-specific prote	SENP7	36.449	_GHNEGNQSLISAEPI
Q9BQG0	11	S	Myb-binding protein 1	MYBBP1A	199.97	_DPAQPMS(ph)PGEA
Q9BQG0	775	S	Myb-binding protein 1	MYBBP1A	279.02	_ALGGEDS(ph)ENEEE
Q9BQG0	1163	S	Myb-binding protein 1	MYBBP1A	130.95	_EIPSATQS(ph)PISK_
Q9BRD0	139	S	BUD13 homolog	BUD13	66.267	_HGTPDPS(ph)PR_
Q9BRD0	159	T	BUD13 homolog	BUD13	75.764	_HDT(ph)PDPS(ph)PLI
Q9BRD0	163	S	BUD13 homolog	BUD13	113.61	_HDT(ph)PDPS(ph)PLI
Q9BRD0	201	S	BUD13 homolog	BUD13	78.964	_HDSPDPS(ph)PPR_
Q9BRD0	214	S	BUD13 homolog	BUD13	94.007	_RPQHNSSGAS(ph)PI
Q9BRD0	248	S	BUD13 homolog	BUD13	60.196	_RVHNNS(ph)PDTSR_
Q9BRD0	271	S	BUD13 homolog	BUD13	101.92	_HDS(ph)PDLAPNVTY
Q9BRD0	325	S	BUD13 homolog	BUD13	136.6	_YEYDPDIS(ph)PPR_
Q9BRD0	364	S	BUD13 homolog	BUD13	107.31	_HKQS(ph)PGHQDSD
Q9BRD0	375	S	BUD13 homolog	BUD13	107.31	_HKQS(ph)PGHQDSD
Q9BRD0	391	S	BUD13 homolog	BUD13	122.52	_SSDSDLS(ph)PPRR_
Q9BRJ6	175	S	Uncharacterized prote	C7orf50	125.86	_ELDEEGS(ph)DPPLP
Q9BRK4	570	S	Leucine zipper putativ	LZTS2	105.66	_AAAGVGGS(ph)LR_
Q9BRL6	158	S	Serine/arginine-rich s	SRSF8	50.806	_S(ph)PYSRS(ph)PYSI
Q9BRL6	161	S	Serine/arginine-rich s	SRSF8	94.781	_SPYS(ph)RS(ph)PYSI
Q9BRL6	163	S	Serine/arginine-rich s	SRSF8	94.781	_SPYS(ph)RS(ph)PYSI
Q9BRR8	6	S	G patch domain-cont	GPATCH1	126.91	_(ac)AARDS(ph)DS(ph
Q9BRR8	8	S	G patch domain-cont	GPATCH1	126.91	_(ac)AARDS(ph)DS(ph
Q9BRT9	12	S	DNA replication comp	GINS4	55.662	_(ac)TEEVDFLGQDS(p
Q9BRT9	16	S	DNA replication comp	GINS4	55.662	_(ac)TEEVDFLGQDS(p
Q9BRY0	125	S	Zinc transporter ZIP3	SLC39A3	97.068	_EKPSFIDLETFNAGS(
Q9BRY0	129	S	Zinc transporter ZIP3	SLC39A3	97.068	_EKPSFIDLETFNAGS(
Q9BSJ6	131	S	Protein FAM64A	FAM64A	135.14	_GSGS(ph)PTHSLSQK
Q9BSJ8	820	S	Extended synaptotagı	ESYT1	80.596	_HLS(ph)PYATLTVGD
Q9BSJ8	1034	S	Extended synaptotagı	ESYT1	63.473	_TLS(ph)PEFNER_

Q9BTA9	511	S	WW domain-containir	WAC	30.484	_QQGHEPVS(ph)PR_
Q9BTC0	805	S	Death-inducer obliter	DIDO1	133.72	_QEAIPDLEDS(ph)PP
Q9BTC0	809	S	Death-inducer obliter	DIDO1	133.72	_QEAIPDLEDS(ph)PP
Q9BTC0	898	S	Death-inducer obliter	DIDO1	83.854	_HDSSAPDPAPDS(ph
Q9BTC0	1040	S	Death-inducer obliter	DIDO1	163.8	_S(ph)PPEGDTTLFLSI
Q9BTC0	1260	S	Death-inducer obliter	DIDO1	55.49	_YPLCSADAAVST(ph)
Q9BTC0	1456	S	Death-inducer obliter	DIDO1	184.43	_RNS(ph)VERPAEPVA
Q9BTC0	1714	S	Death-inducer obliter	DIDO1	131.54	_SSS(ph)PAGETEGDF
Q9BTK6	237	S	PAXIP1-associated g	PAGR1	223.07	_DLFSLDSEDPSPAS(
Q9BTU6	44	S	Phosphatidylinositol 4	PI4K2A	142.56	_VAAAAGS(ph)GPSPF
Q9BTU6	47	S	Phosphatidylinositol 4	PI4K2A	246.32	_VAAAAGSGPS(ph)PF
Q9BTU6	51	S	Phosphatidylinositol 4	PI4K2A	246.32	_VAAAAGSGPS(ph)PF
Q9BTU6	462	S	Phosphatidylinositol 4	PI4K2A	36.752	_SSS(ph)ESYTQSFQS
Q9BTX1	406	S	Nucleoporin NDC1	TMEM48	101.24	_KLNS(ph)PEETAFQT
Q9BU19	231	S	Zinc finger protein 69	ZNF692	36.447	_LLPS(ph)PVTCTPK_
Q9BU76	123	S	Multiple myeloma tum	MMTAG2	58.246	_LLGLGS(ph)ASGSVG
Q9BU76	217	S	Multiple myeloma tum	MMTAG2	129.74	_RPAEATSS(ph)PT(ph
Q9BU76	220	S	Multiple myeloma tum	MMTAG2	111.11	_RPAEATS(ph)SPTS(
Q9BU76	235	S	Multiple myeloma tum	MMTAG2	113.33	_HHHHDSDSNS(ph)P(
Q9BUA3	308	S	Uncharacterized prot	C11orf84	88.706	_AES(ph)PSPAPPPGL
Q9BUH6	148	S	Uncharacterized prot	C9orf142	113.47	_LAAAEETAVS(ph)PR_
Q9BUJ2	194	S	Heterogeneous nucle	HNRNPUL1	189.97	_S(ph)PQPPAEEDEDI
Q9BUQ8	14	S	Probable ATP-depen	DDX23	64.64	_DAS(ph)PSKEER_
Q9BUR4	54	S	Telomerase Cajal bo	WRAP53	111.15	_GDPPRLS(ph)PDPVA
Q9BUR4	491	S	Telomerase Cajal bo	WRAP53	111.64	_VFPEPTES(ph)GDEG
Q9BUZ4	426	S	TNF receptor-associa	TRAF4	66.826	_GS(ph)LDESSLGFGY
Q9BV36	266	S	Melanophilin	MLPH	181.71	_AEGLEEADTGASGC
Q9BV36	314	S	Melanophilin	MLPH	205.26	_NEQLPLQYLADVDTS
Q9BV36	337	S	Melanophilin	MLPH	51.771	_ASS(ph)ESQIFELNK_
Q9BV36	458	T	Melanophilin	MLPH	108.56	_TT(ph)DEELSELEDR_
Q9BVC5	189	S	Ashwin	C2orf49	77.191	_S(ph)PPLSPVGTTPV
Q9BVG4	197	S	Protein PBDC1	PBDC1	103.04	_GADS(ph)GEEKEEGI
Q9BVG9	16	S	Phosphatidylserine s	PTDSS2	97.384	_DAGGPRPES(ph)PVF
Q9BVJ6	29	S	U3 small nucleolar R	UTP14A	119.41	_DYLLS(ph)ES(ph)EDE
Q9BVJ6	31	S	U3 small nucleolar R	UTP14A	119.41	_DYLLS(ph)ES(ph)EDE
Q9BVJ6	405	S	U3 small nucleolar R	UTP14A	116.68	_EAATQEDPEQLPELE
Q9BVJ6	453	S	U3 small nucleolar R	UTP14A	57.148	_DSGS(ph)QEVLSELR
Q9BW71	84	T	HIRA-interacting prot	HIRIP3	65.467	_RPPT(ph)PCS(ph)DP
Q9BW71	87	S	HIRA-interacting prot	HIRIP3	65.467	_RPPT(ph)PCS(ph)DP
Q9BW71	196	S	HIRA-interacting prot	HIRIP3	139.64	_EES(ph)EESEAEPVC
Q9BW71	223	S	HIRA-interacting prot	HIRIP3	202.61	_SLKES(ph)EQES(ph)I
Q9BW71	227	S	HIRA-interacting prot	HIRIP3	202.61	_SLKES(ph)EQES(ph)I
Q9BW71	530	S	HIRA-interacting prot	HIRIP3	94.594	_TLDS(ph)DEERPRPA
Q9BWF3	86	S	RNA-binding protein 4	RBM4	108.18	_LHVGNIS(ph)PTCTNI
Q9BWT3	648	S	Poly(A) polymerase g	PAPOLG	82.202	_SHS(ph)PSIDGTPK_
Q9BWU0	82	S	Kanadaptin	SLC4A1AP	37.657	_KPALPVS(ph)PAAR_
Q9BWU0	312	S	Kanadaptin	SLC4A1AP	209.9	_MLGEDS(ph)DEEEEM
Q9BWU0	466	S	Kanadaptin	SLC4A1AP	256.33	_NWEDEDFYDS(ph)DI
Q9BX79	404	S	Stimulated by retinoic	STRA6	35.054	_GAALDLS(ph)PLHR_
Q9BX95	112	S	Sphingosine-1-phosp	SGPP1	189.59	_RNS(ph)LTGEEGQLA
Q9BXF6	307	S	Rab11 family-interact	RAB11FIP5	96.745	_TYS(ph)DEANQMR_
Q9BXF6	538	S	Rab11 family-interact	RAB11FIP5	85.044	_DPTQKPSPHPVKPLS
Q9BXK5	426	S	Bcl-2-like protein 13	BCL2L13	140.28	_EESLVEELS(ph)PASI
Q9BXP5	67	S	Serrate RNA effector	SRRT	96.143	_ERFS(ph)PPRHELS(

Q9BXP5	74	S	Serrate RNA effector	SRRT	137.95	_HELS(ph)PPQKR_
Q9BXP5	544	T	Serrate RNA effector	SRRT	135.22	_TQLWASEPGT(ph)PF
Q9BXS9	752	S	Solute carrier family 2	SLC26A6	107.93	_PVPDS(ph)PVSVTR_
Q9BXS9	755	S	Solute carrier family 2	SLC26A6	60.489	_PVPDS(ph)PVS(ph)V
Q9BXY0	197	S	Protein MAK16 homo	MAK16	120.44	_ALEQQEAES(ph)DS(
Q9BXY0	199	S	Protein MAK16 homo	MAK16	120.44	_ALEQQEAES(ph)DS(
Q9BXY0	200	S	Protein MAK16 homo	MAK16	116.24	_ALEQQEAES(ph)DS(
Q9BXY0	202	T	Protein MAK16 homo	MAK16	115.45	_ALEQQEAES(ph)DS(
Q9BY44	506	S	Eukaryotic translation	EIF2A	173.89	_SDKS(ph)PDLAPTPA
Q9BY89	600	T	Uncharacterized prote	KIAA1671	178.77	_GGSSVEAPCPSDVT(
Q9BY89	749	S	Uncharacterized prote	KIAA1671	98.817	_VHSEAIS(ph)PAPEEI
Q9BY89	1059	T	Uncharacterized prote	KIAA1671	56.504	_KIT(ph)PPSS(ph)PHS
Q9BY89	1224	S	Uncharacterized prote	KIAA1671	71.531	_RS(ph)PTVEPSTLPR_
Q9BY89	1488	S	Uncharacterized prote	KIAA1671	77.899	_ERPLQQVS(ph)PVAS
Q9BYG3	223	T	MKI67 FHA domain-ir	MKI67IP	116.68	_VSGTLDT(ph)PEK_
Q9BYG3	234	T	MKI67 FHA domain-ir	MKI67IP	140.41	_TVDSQGPT(ph)PVCT
Q9BYG3	238	T	MKI67 FHA domain-ir	MKI67IP	140.41	_TVDSQGPT(ph)PVCT
Q9BZ95	606	T	Histone-lysine N-meth	WHSC1L1	57.175	_EQVET(ph)VPQAT(ph
Q9BZ95	611	T	Histone-lysine N-meth	WHSC1L1	57.175	_EQVET(ph)VPQAT(ph
Q9BZL4	509	S	Protein phosphatase	PPP1R12C	50.783	_IPEPES(ph)PAKPNVI
Q9C086	63	S	INO80 complex subur	INO80B	75.743	_HHQEEDAGPTQPS(p
Q9C086	97	S	INO80 complex subur	INO80B	80.475	_SVPTFTVIPEGPRS(p
Q9C086	99	S	INO80 complex subur	INO80B	80.475	_SVPTFTVIPEGPRS(p
Q9C086	132	S	INO80 complex subur	INO80B	163.79	_AWLDEDSNLSPS(ph
Q9C086	351	S	INO80 complex subur	INO80B	45.873	_LGGPEGPGS(ph)PLL
Q9C0B5	380	S	Palmitoyltransferase Z	ZDHHC5	98.175	_GDS(ph)LKEPTSIAES
Q9C0B5	554	S	Palmitoyltransferase Z	ZDHHC5	76.423	_LLRQS(ph)PPLPGRE
Q9C0B5	621	S	Palmitoyltransferase Z	ZDHHC5	72.21	_GVGS(ph)PEPGPTAI
Q9C0C2	178	S	182 kDa tankyrase-1-	TNKS1BP1	87.719	_KEVLAS(ph)PDR_
Q9C0C2	228	S	182 kDa tankyrase-1-	TNKS1BP1	90.581	_GWSQEGPVKS(ph)P
Q9C0C2	353	S	182 kDa tankyrase-1-	TNKS1BP1	52.351	_HTPS(ph)PGLPAEGA
Q9C0C2	494	S	182 kDa tankyrase-1-	TNKS1BP1	187.41	_LDS(ph)PPPS(ph)PIT
Q9C0C2	498	S	182 kDa tankyrase-1-	TNKS1BP1	179.19	_LDS(ph)PPPS(ph)PIT
Q9C0C2	601	S	182 kDa tankyrase-1-	TNKS1BP1	238.07	_YESQEPLAGQES(ph
Q9C0C2	672	S	182 kDa tankyrase-1-	TNKS1BP1	79.317	_AS(ph)PEPPGPESSS
Q9C0C2	691	S	182 kDa tankyrase-1-	TNKS1BP1	102.66	_WLDDLLAS(ph)PPPS
Q9C0C2	836	S	182 kDa tankyrase-1-	TNKS1BP1	190.44	_S(ph)QEADVQDWEF
Q9C0C2	893	S	182 kDa tankyrase-1-	TNKS1BP1	212.36	_RDS(ph)LGAYASQDA
Q9C0C2	1024	S	182 kDa tankyrase-1-	TNKS1BP1	121.5	_GS(ph)GGLFSPSTAH
Q9C0C2	1554	S	182 kDa tankyrase-1-	TNKS1BP1	110.78	_SPS(ph)QDFSFIEDTE
Q9C0C2	1620	S	182 kDa tankyrase-1-	TNKS1BP1	186.01	_VPS(ph)S(ph)DEEVV
Q9C0C2	1621	S	182 kDa tankyrase-1-	TNKS1BP1	186.01	_VPS(ph)S(ph)DEEVV
Q9C0C2	1666	S	182 kDa tankyrase-1-	TNKS1BP1	159.01	_NRS(ph)AEEGELAES
Q9C0E2	521	S	Exportin-4	XPO4	103.4	_HQQQLLAS(ph)PGSS
Q9C0H2	522	S	Protein tweety homol	TTYH3	114.25	_YLATSQPRPDSSGS(
Q9C0J8	7	S	pre-mRNA 3' end pro	WDR33	130.16	_(ac)ATEIGS(ph)PPR_
Q9C0J8	1210	S	pre-mRNA 3' end pro	WDR33	62.082	_DTPRPDHPPHDGHS
Q9C0J8	1279	S	pre-mRNA 3' end pro	WDR33	52.862	_SSS(ph)LDGEHHDGY
Q9GZR7	82	S	ATP-dependent RNA	DDX24	164.53	_KAQAVS(ph)EEEEEE
Q9GZR7	94	S	ATP-dependent RNA	DDX24	283.56	_AQAVSEEEEEEGK
Q9GZR7	295	S	ATP-dependent RNA	DDX24	108.09	_SPGKAEAES(ph)DAL
Q9GZT3	102	S	SRA stem-loop-intera	SLIRP	144.53	_LPQTS(ph)DDEKKDF
Q9GZY8	115	T	Mitochondrial fission	MFF	164.01	_PADLDLIQSTPFKPLA
Q9GZY8	155	S	Mitochondrial fission	MFF	139.7	_ERS(ph)MSENAVR_

Q9H019	238	S	Mitochondrial fission r	MTFR1L	96.135	_ASS(ph)FADMMGILK
Q9H0B6	582	S	Kinesin light chain 2	KLC2	37.144	_ASS(ph)LNFLNK_
Q9H0C8	13	S	Integrin-linked kinase	ILKAP	124.51	_(ac)MDLFGDLPEPER
Q9H0D6	448	S	5'-3' exoribonuclease	XRN2	97.235	_NS(ph)PGSQVASNPF
Q9H0D6	499	S	5'-3' exoribonuclease	XRN2	292.49	_KAEDS(ph)DS(ph)EP
Q9H0D6	501	S	5'-3' exoribonuclease	XRN2	292.49	_KAEDS(ph)DS(ph)EP
Q9H0E9	579	S	Bromodomain-contair	BRD8	52.455	_TEAS(ph)PESMLS(ph
Q9H0G5	33	S	Nuclear speckle splici	NSRP1	77.024	_TQQLHPVLQKPSVF(
Q9H0G5	248	S	Nuclear speckle splici	NSRP1	126.07	_VEENPDADS(ph)DFI
Q9H0H5	203	S	Rac GTPase-activatir	RACGAP1	113.54	_S(ph)IGSAVDQGNES
Q9H0H5	342	T	Rac GTPase-activatir	RACGAP1	91.883	_DRCPLPCIPTLIGT(ph
Q9H0S4	9	S	Probable ATP-depen	DDX47	225.65	_(ac)AAPEEHDS(ph)P
Q9H116	613	S	GDNF-inducible zinc	GZF1	64.52	_SFLVIVDGS(ph)PK_
Q9H1A4	688	S	Anaphase-promoting	ANAPC1	60.561	_NFDFEGSLS(ph)PVIA
Q9H1B7	215	S	Interferon regulatory f	IRF2BPL	48.551	_QS(ph)PNSSSAAASV
Q9H1B7	547	S	Interferon regulatory f	IRF2BPL	166.91	_KAS(ph)PEPPDSAEG
Q9H1B7	622	S	Interferon regulatory f	IRF2BPL	107.55	_TTPPES(ph)APQNGF
Q9H1B7	639	S	Interferon regulatory f	IRF2BPL	107.55	_TTPPES(ph)APQNGF
Q9H1B7	657	S	Interferon regulatory f	IRF2BPL	99.378	_RNS(ph)SS(ph)PVS(p
Q9H1B7	659	S	Interferon regulatory f	IRF2BPL	99.378	_NSSS(ph)PVSPASVP
Q9H1B7	662	S	Interferon regulatory f	IRF2BPL	99.378	_NSSS(ph)PVS(ph)PA
Q9H1C4	547	S	Protein unc-93 homol	UNC93B1	149.48	_YLEEDNS(ph)DES(ph
Q9H1C4	550	S	Protein unc-93 homol	UNC93B1	157.5	_YLEEDNS(ph)DES(ph
Q9H1E3	19	S	Nuclear ubiquitous ca	NUCKS1	315.14	_VVDYSQFQES(ph)DI
Q9H1E3	79	S	Nuclear ubiquitous ca	NUCKS1	154.08	_KDDSHSAEDS(ph)EI
Q9H1E3	113	S	Nuclear ubiquitous ca	NUCKS1	311.95	_EMLMEDVGS(ph)EEI
Q9H1E3	130	S	Nuclear ubiquitous ca	NUCKS1	117.8	_DS(ph)GSDEDFLMEI
Q9H1E3	132	S	Nuclear ubiquitous ca	NUCKS1	306.98	_DSGS(ph)DEDFLMEI
Q9H1E3	144	S	Nuclear ubiquitous ca	NUCKS1	306.98	_DSGS(ph)DEDFLMEI
Q9H1E3	181	S	Nuclear ubiquitous ca	NUCKS1	80.69	_ATVTPS(ph)PVK_
Q9H1E3	202	T	Nuclear ubiquitous ca	NUCKS1	207.72	_EKT(ph)PS(ph)PKEEI
Q9H1E3	204	S	Nuclear ubiquitous ca	NUCKS1	207.72	_EKT(ph)PS(ph)PKEEI
Q9H1E3	214	S	Nuclear ubiquitous ca	NUCKS1	298.11	_TPSPKEEDEEPES(pl
Q9H2H9	52	S	Sodium-coupled neut	SLC38A1	136.53	_S(ph)LTNSHLEK_
Q9H2J7	687	S	Sodium-dependent ne	SLC6A15	86.548	_IPSEMPS(ph)PNFGK
Q9H2P0	921	S	Activity-dependent ne	ADNP	177.41	_VIPEDAS(ph)ESEEKI
Q9H2P0	953	S	Activity-dependent ne	ADNP	168.35	_LMHNAS(ph)DS(ph)E
Q9H2P0	955	S	Activity-dependent ne	ADNP	168.35	_LMHNAS(ph)DS(ph)E
Q9H2Y7	861	S	Zinc finger protein 10	ZNF106	86.944	_SLS(ph)ESSVIMDR_
Q9H2Y7	1025	S	Zinc finger protein 10	ZNF106	89.659	_ATGDGS(ph)S(ph)PE
Q9H2Y7	1026	S	Zinc finger protein 10	ZNF106	89.659	_ATGDGS(ph)S(ph)PE
Q9H2Y7	1279	S	Zinc finger protein 10	ZNF106	52.52	_ENS(ph)PSSQSAGLS
Q9H2Y7	1328	S	Zinc finger protein 10	ZNF106	39.244	_EPHS(ph)PADQPEQ(
Q9H307	100	S	Pinin	PNN	136.66	_QES(ph)DPEDDDVKI
Q9H307	347	S	Pinin	PNN	176.9	_EIAIVHS(ph)DAEKEC
Q9H307	381	S	Pinin	PNN	208.64	_QQDS(ph)QPEEVMD
Q9H307	413	S	Pinin	PNN	44.391	_VES(ph)VEPSENEAS
Q9H307	441	S	Pinin	PNN	132.09	_S(ph)LS(ph)PGKENV
Q9H307	443	S	Pinin	PNN	181.64	_S(ph)LS(ph)PGKENV
Q9H3N1	247	S	Thioredoxin-related tr	TMX1	392.53	_VEEEQEADEEDVS(p
Q9H3P2	363	S	Negative elongation fa	NELFA	57.798	_EASRPPEEPSAPS(pl
Q9H3U1	15	T	Protein unc-45 homol	UNC45A	100.43	_PAT(ph)PGASSVEQL
Q9H3Z4	10	S	DnaJ homolog subfar	DNAJC5	247.18	_SLS(ph)TSGESLYHV
Q9H410	30	S	Kinetochore-associat	DSN1	74.561	_THDHQLESSLS(ph)P

Q9H410	58	S	Kinetochore-associat	DSN1	82.417	_IHLGSS(ph)PK_
Q9H410	81	S	Kinetochore-associat	DSN1	88.471	_SLHLS(ph)PQEQSAS
Q9H4A3	2029	S	Serine/threonine-prot	WNK1	140.04	_DVDDGSGS(ph)PHS(
Q9H4A3	2032	S	Serine/threonine-prot	WNK1	220.91	_DVDDGSGS(ph)PHS(
Q9H4G0	430	S	Band 4.1-like protein	EPB41L1	115.29	_S(ph)LDGAEFSR_
Q9H4G0	441	S	Band 4.1-like protein	EPB41L1	122.57	_SLDGAEFSRPAS(ph)
Q9H4G0	461	S	Band 4.1-like protein	EPB41L1	116.59	_PASVSENHDAGPDG
Q9H4G0	466	S	Band 4.1-like protein	EPB41L1	177.18	_DEDGESGGQRS(ph)
Q9H4G0	475	T	Band 4.1-like protein	EPB41L1	126.69	_SEAEEGEVRT(ph)PT
Q9H4G0	650	S	Band 4.1-like protein	EPB41L1	214.58	_SDS(ph)DTEGLLFSR
Q9H4G0	678	S	Band 4.1-like protein	EPB41L1	141.36	_GAPSQDDESGGIEDS
Q9H4G0	686	T	Band 4.1-like protein	EPB41L1	48.288	_GACST(ph)PDMPQFE
Q9H4G0	784	S	Band 4.1-like protein	EPB41L1	99.973	_SLS(ph)PIIGK_
Q9H4L4	169	S	Sentrin-specific prote	SENP3	121.56	_NHLS(ph)PQQGGATF
Q9H4L4	181	S	Sentrin-specific prote	SENP3	78.025	_NHLS(ph)PQQGGATF
Q9H4L4	212	S	Sentrin-specific prote	SENP3	77.221	_GS(ph)PPVPSGPPME
Q9H4L5	437	S	Oxysterol-binding pro	OSBPL3	37.77	_ALVHQLS(ph)NESR_
Q9H4L7	124	S	SWI/SNF-related mat	SMARCAD1	54.626	_DTVIIVS(ph)EPS(ph)E
Q9H4L7	127	S	SWI/SNF-related mat	SMARCAD1	54.626	_DTVIIVS(ph)EPS(ph)E
Q9H4Z3	30	S	Phosphorylated CTD-	PCIF1	75.945	_EEASLLSHSPGTSNC
Q9H501	198	S	ESF1 homolog	ESF1	195.86	_TLDSGTSEIVKS(ph)F
Q9H501	311	T	ESF1 homolog	ESF1	72.755	_GNIET(ph)S(ph)S(ph)
Q9H501	312	S	ESF1 homolog	ESF1	72.755	_GNIET(ph)S(ph)S(ph)
Q9H501	313	S	ESF1 homolog	ESF1	72.755	_GNIET(ph)S(ph)S(ph)
Q9H501	657	S	ESF1 homolog	ESF1	192.15	_ALAEEAS(ph)EEELPS
Q9H501	663	S	ESF1 homolog	ESF1	192.15	_ALAEEAS(ph)EEELPS
Q9H5H4	83	S	Zinc finger protein 76	ZNF768	109.95	_FEPES(ph)PGFESR_
Q9H5H4	90	S	Zinc finger protein 76	ZNF768	87.24	_S(ph)PGLVPPS(ph)PI
Q9H5H4	97	S	Zinc finger protein 76	ZNF768	87.24	_S(ph)PGLVPPS(ph)PI
Q9H5H4	125	S	Zinc finger protein 76	ZNF768	112.08	_YEPQS(ph)PGYEPR_
Q9H5I1	381	S	Histone-lysine N-met	SUV39H2	147.08	_GSGDIS(ph)SDS(ph)I
Q9H5I1	384	S	Histone-lysine N-met	SUV39H2	147.08	_GSGDIS(ph)SDS(ph)I
Q9H5I1	388	S	Histone-lysine N-met	SUV39H2	164.74	_GSGDISSDSIDHS(ph
Q9H694	612	S	Protein bicaudal C ho	BICC1	100.95	_VLSANHGDPSIQTSG
Q9H6F5	18	S	Coiled-coil domain-co	CCDC86	189.54	_LGGLRPES(ph)PESL
Q9H6F5	21	S	Coiled-coil domain-co	CCDC86	60.54	_LGGLRPES(ph)PES(p
Q9H6F5	42	T	Coiled-coil domain-co	CCDC86	187.21	_ALVEFESNPEET(ph)I
Q9H6F5	47	S	Coiled-coil domain-co	CCDC86	240.4	_ALVEFESNPEETREP
Q9H6F5	58	S	Coiled-coil domain-co	CCDC86	111.49	_AGLGS(ph)PERPPK_
Q9H6F5	66	S	Coiled-coil domain-co	CCDC86	76.762	_AGLGS(ph)PERPPKT
Q9H6F5	69	S	Coiled-coil domain-co	CCDC86	111.49	_AGLGS(ph)PERPPKT
Q9H6F5	80	S	Coiled-coil domain-co	CCDC86	293.54	_LQQGAGLES(ph)PQC
Q9H6F5	91	S	Coiled-coil domain-co	CCDC86	330.51	_LQQGAGLES(ph)PQC
Q9H6F5	102	S	Coiled-coil domain-co	CCDC86	178.69	_QQDLHLES(ph)PQRC
Q9H6F5	110	S	Coiled-coil domain-co	CCDC86	178.69	_QQDLHLES(ph)PQRC
Q9H6F5	113	S	Coiled-coil domain-co	CCDC86	150.34	_QPEYSPES(ph)PR_
Q9H6H4	152	S	Receptor expression-	REEP4	79.659	_SFS(ph)MQDLR_
Q9H6S3	570	S	Epidermal growth fac	EPS8L2	84.892	_YWGPAS(ph)PTHK_
Q9H6X2	362	S	Anthrax toxin recepto	ANTXR1	73.781	_EVPPPPAEES(ph)EE
Q9H6Y2	14	S	WD repeat-containing	WDR55	189.93	_TCEERPAEDGS(ph)D
Q9H6Y2	382	S	WD repeat-containing	WDR55	267.18	_EEGEDSMAQEEKEE
Q9H6Z4	100	S	Ran-binding protein 3	RANBP3	63.79	_SAGGS(ph)S(ph)PEG
Q9H6Z4	101	S	Ran-binding protein 3	RANBP3	63.79	_SAGGS(ph)S(ph)PEG
Q9H6Z4	108	S	Ran-binding protein 3	RANBP3	65.801	_SAGGS(ph)S(ph)PEG

Q9H6Z4	333	S	Ran-binding protein 3	RANBP3	125.51	_VLS(ph)PPKLNEVSS
Q9H792	281	S	Pseudopodium-enrich	PEAK1	72.321	_ANTLS(ph)PVR_
Q9H792	1036	S	Pseudopodium-enrich	PEAK1	114.76	_SHSS(ph)PSQIPK_
Q9H7D0	1756	S	Dedicator of cytokine	DOCK5	66.246	_APEPDLMS(ph)PTR_
Q9H7D0	1789	S	Dedicator of cytokine	DOCK5	63.606	_LSPFHGSSPPQSTPL
Q9H7D0	1834	S	Dedicator of cytokine	DOCK5	97.797	_NS(ph)TELAPPLPVR_
Q9H7F0	817	S	Probable cation-trans	ATP13A3	125.45	_LVHDS(ph)LEDLQMT
Q9H7L9	32	S	Sin3 histone deacetyl	SUDS3	52.762	_(ac)SAAGLLAPAPAQ
Q9H7L9	234	S	Sin3 histone deacetyl	SUDS3	146.94	_RPAS(ph)PS(ph)SPE
Q9H7L9	236	S	Sin3 histone deacetyl	SUDS3	140.45	_RPASPS(ph)S(ph)PE
Q9H7L9	237	S	Sin3 histone deacetyl	SUDS3	146.94	_RPAS(ph)PSS(ph)PE
Q9H7N4	498	S	Splicing factor, arginir	SCAF1	140.51	_QRS(ph)PS(ph)PAPA
Q9H7N4	500	S	Splicing factor, arginir	SCAF1	140.67	_QRS(ph)PS(ph)PAPA
Q9H7N4	548	S	Splicing factor, arginir	SCAF1	177.73	_EAASSSSGTQPAPP/
Q9H7N4	564	S	Splicing factor, arginir	SCAF1	53.3	_KPGS(ph)HASSSAR_
Q9H7N4	734	S	Splicing factor, arginir	SCAF1	164.01	_REVLYDS(ph)EGLS(p
Q9H7N4	738	S	Splicing factor, arginir	SCAF1	136.34	_REVLYDS(ph)EGLS(p
Q9H7N4	874	S	Splicing factor, arginir	SCAF1	111.63	_S(ph)PFLKPDER_
Q9H7N4	965	S	Splicing factor, arginir	SCAF1	112.17	_GAEETSWS(ph)GEE
Q9H7N4	989	T	Splicing factor, arginir	SCAF1	104.81	_AAPPPPALT(ph)PDS
Q9H8G2	203	S	Caspase activity and	CAAP1	198.93	_ILEGDNGMDS(ph)DM
Q9H8G2	312	S	Caspase activity and	CAAP1	262.94	_SVNEILGLAESS(ph)F
Q9H8Y8	222	T	Golgi reassembly-sta	GORASP2	89.011	_ISLPGQMAGT(ph)PIT
Q9H972	224	S	Uncharacterized prot	C14orf93	97.163	_QLS(ph)PATQLAIQR_
Q9H9J4	754	S	Ubiquitin carboxyl-ter	USP42	62.052	_DAEPQPGS(ph)PAAE
Q9H9J4	856	S	Ubiquitin carboxyl-ter	USP42	186.01	_DSALAEAPEGLS(ph)
Q9H9J4	1007	S	Ubiquitin carboxyl-ter	USP42	100.76	_HAPEHHPGHGDRLS
Q9H9J4	1166	S	Ubiquitin carboxyl-ter	USP42	110.77	_RHDS(ph)VENSDSH\
Q9H9J4	1226	S	Ubiquitin carboxyl-ter	USP42	85.805	_HQQDSDLSAACS(ph
Q9HAN9	117	S	Nicotinamide mononu	NMNAT1	48.773	_LEASDCDHQQNS(ph
Q9HAU0	855	S	Pleckstrin homology c	PLEKHA5	98.3	_AKS(ph)PTPESSTIAS
Q9HAZ1	136	S	Dual specificity protei	CLK4	91.1	_S(ph)RS(ph)IEDDEEC
Q9HAZ1	138	S	Dual specificity protei	CLK4	97.5	_S(ph)RS(ph)IEDDEEC
Q9HAZ1	339	S	Dual specificity protei	CLK1;CLK4	164.46	_VVDFGSATYDDEHH
Q9HB09	243	S	Bcl-2-like protein 12	BCL2L12	63.426	_LSS(ph)DSFAR_
Q9HB58	244	S	Sp110 nuclear body p	SP110	214.05	_DKEDPQEMPHS(ph)F
Q9HB58	380	S	Sp110 nuclear body p	SP110	131.3	_VTQGAAS(ph)PGHGI
Q9HB90	2	S	Ras-related GTP-binc	RRAGC	81.844	_(ac)S(ph)LQYGAEETI
Q9HB90	15	S	Ras-related GTP-binc	RRAGC	81.844	_(ac)S(ph)LQYGAEETI
Q9HBR0	802	S	Putative sodium-coup	SLC38A10	154.41	_S(ph)LEHSEGPVGR_
Q9HC35	144	S	Echinoderm microtub	EML4	104.45	_AS(ph)PS(ph)PQPSS
Q9HC35	146	S	Echinoderm microtub	EML4	126.84	_AS(ph)PS(ph)PQPSS
Q9HC52	311	S	Chromobox protein h	CBX8	96.096	_HGS(ph)GPPSSGGG
Q9HC56	932	S	Protocadherin-9	PCDH9	94.019	_FDWGPAPPTTFKPN
Q9HC78	305	T	Zinc finger and BTB c	ZBTB20	121.24	_YLSTT(ph)PETTHCR_
Q9HCD5	6	S	Nuclear receptor coa	NCOA5	104.95	_(ac)MNTAPS(ph)RPS
Q9HCD5	9	S	Nuclear receptor coa	NCOA5	102.65	_(ac)MNTAPSRPS(ph)
Q9HCD6	1442	S	Protein TANC2	TANC2	83.312	_PSQGLPVIQS(ph)PP
Q9HCD6	1517	S	Protein TANC2	TANC2	32.478	_FS(ph)PPPVGGQGK_
Q9HCK8	2046	S	Chromodomain-helic	CHD8	64.52	_VS(ph)PSDTTPLVSR_
Q9HCK8	2519	S	Chromodomain-helic	CHD8	52.451	_APGYPSS(ph)PVTTA
Q9HCN4	338	S	GPN-loop GTPase 1	GPN1	288.83	_GTLDEEDEEADS(ph)
Q9HCS5	389	S	Band 4.1-like protein	EPB41L4A	43.604	_IIAPS(ph)PVK_
Q9HD20	899	S	Probable cation-trans	ATP13A1	38.399	_DS(ph)PTLSNSGIR_

Q9NP66	105	S	High mobility group p	HMG20A	114.39	_S(ph)PLTGYVR_
Q9NPF5	445	T	DNA methyltransfera	DMAP1	133.21	_DTIIDVVGAPLT(ph)P
Q9NPI1	289	S	Bromodomain-contair	BRD7	115.5	_EREDSGDAEAHAFK
Q9NPQ8	436	S	Synembryn-A	RIC8A	64.856	_GLMAGGRPEGQYS(
Q9NPQ8	441	T	Synembryn-A	RIC8A	64.856	_GLMAGGRPEGQYS(
Q9NPQ8	528	S	Synembryn-A	RIC8A	49.141	_GHLTSLQDAMCETM
Q9NQ55	359	S	Suppressor of SWI4 1	PPAN	174.35	_VGGS(ph)DEEASGIP
Q9NQ92	66	S	Coordinator of PRMT5	COPRS	38.261	_GTQSIPNDS(ph)PAR
Q9NQC3	7	S	Reticulon-4	RTN4	170.19	_(ac)MEDLDQS(ph)PL
Q9NQC3	15	S	Reticulon-4	RTN4	263.15	_(ac)M(ox)EDLDQSPL
Q9NQC3	107	S	Reticulon-4	RTN4	42.057	_QPS(ph)WDPSPVSS
Q9NQC3	181	S	Reticulon-4	RTN4	112.12	_RGS(ph)S(ph)GSVDE
Q9NQG5	132	S	Regulation of nuclear	RPRD1B	65.374	_LSMEDS(ph)KSPPPK
Q9NQG5	134	S	Regulation of nuclear	RPRD1B	115.38	_LSMEDSKS(ph)PPPK
Q9NQG6	59	S	Mitochondrial dynami	SMCR7L	92.039	_AISAPTS(ph)PTR_
Q9NQQ7	335	S	Solute carrier family 3	SLC35C2	120.54	_GLGS(ph)SPDLELLL
Q9NQR1	181	T	N-lysine methyltransf	SETD8	66.137	_SEAAEPPKT(ph)PPS
Q9NQS1	94	S	Cell death regulator A	AVEN	108.23	_REPGGWGAGASAP
Q9NQS3	465	S	Poliovirus receptor-re	PVRL3	107.47	_ESQIDVLQQDELDS(
Q9NQS7	263	S	Inner centromere prot	INCENP	117.25	_IAQVS(ph)PGPR_
Q9NQS7	275	S	Inner centromere prot	INCENP	94.717	_DSPAFPDS(ph)PWR_
Q9NQS7	306	S	Inner centromere prot	INCENP	110.4	_HS(ph)PIAPSSPSPQ
Q9NQS7	312	S	Inner centromere prot	INCENP	100.94	_HS(ph)PIAPSS(ph)PS
Q9NQS7	314	S	Inner centromere prot	INCENP	100.94	_HS(ph)PIAPSS(ph)PS
Q9NQS7	421	S	Inner centromere prot	INCENP	197	_PAASS(ph)PETPSAG
Q9NQS7	899	S	Inner centromere prot	INCENP	123.59	_TSSAVWNS(ph)PPLC
Q9NQW6	182	S	Actin-binding protein	ANLN	76.237	_AAS(ph)PPRPLLSNA
Q9NQW6	323	S	Actin-binding protein	ANLN	89.886	_TPIS(ph)PLK_
Q9NQZ2	365	S	Something about silei	UTP3	132.28	_TSAAACAVTDLS(ph)
Q9NQZ2	368	S	Something about silei	UTP3	293.88	_TSAAACAVTDLSDDS
Q9NR09	480	S	Baculoviral IAP repea	BIRC6	171.78	_LEGDSDDLLEDS(ph)
Q9NR19	30	S	Acetyl-coenzyme A s	ACSS2	88.101	_SWS(ph)PPPEVSR_
Q9NR30	71	S	Nucleolar RNA helica	DDX21	163.11	_KAEPSEVDMNS(ph)F
Q9NR30	89	S	Nucleolar RNA helica	DDX21	185.25	_KKEEPSQNDIS(ph)PI
Q9NR30	121	S	Nucleolar RNA helica	DDX21	151.41	_NEEPS(ph)EEEIDAPI
Q9NR30	171	S	Nucleolar RNA helica	DDX21	44.747	_LKNGFPHPEPDCNP
Q9NR30	173	S	Nucleolar RNA helica	DDX21	44.747	_LKNGFPHPEPDCNP
Q9NRA8	564	S	Eukaryotic translation	EIF4ENIF1	116.71	_APS(ph)PPLSQVFQT
Q9NRG9	495	S	Aladin	AAAS	85.38	_FS(ph)PVLGR_
Q9NRL2	731	T	Bromodomain adjace	BAZ1A	248.7	_ELDQDMVT(ph)EDE
Q9NRL2	1413	S	Bromodomain adjace	BAZ1A	118.5	_KRQS(ph)PEPSPVTL
Q9NRY4	1179	S	Rho GTPase-activatir	ARHGAP35	151.95	_TSFSVGS(ph)DDELG
Q9NS56	98	S	E3 ubiquitin-protein li	TOPORS	101.54	_LQQTVPADAS(ph)PD
Q9NS69	15	S	Mitochondrial import r	TOMM22	181.13	_(ac)AAAVAAAGAGEF
Q9NSY1	1076	S	BMP-2-inducible prot	BMP2K	35.66	_PFHS(ph)PDLSWHPF
Q9NTI5	1166	S	Sister chromatid cohe	PDS5B	317.06	_METVSNASSSSNPS
Q9NTI5	1182	S	Sister chromatid cohe	PDS5B	148.31	_LDSSEMDHS(ph)ENE
Q9NTI5	1257	S	Sister chromatid cohe	PDS5B	264.66	_GHTAS(ph)ESDEQQ
Q9NTI5	1283	S	Sister chromatid cohe	PDS5B	311.77	_LKEDILENEDEQNS(p
Q9NTI5	1358	S	Sister chromatid cohe	PDS5B	234.8	_AES(ph)PESSAIEST
Q9NTI5	1370	T	Sister chromatid cohe	PDS5B	110.32	_AES(ph)PESSAIEST
Q9NTI5	1381	T	Sister chromatid cohe	PDS5B	120.11	_GRPSKT(ph)PS(ph)P
Q9NTI5	1383	S	Sister chromatid cohe	PDS5B	120.11	_GRPSKT(ph)PS(ph)P
Q9NTJ3	41	S	Structural maintenanc	SMC4	255.82	_TES(ph)PATAAETAS

Q9NU22	4752	S	Midasin	MDN1	56.313	_MHDGELEEQEEDDE
Q9NU22	4754	S	Midasin	MDN1	56.313	_MHDGELEEQEEDDE
Q9NVI7	2	S	ATPase family AAA d	ATAD3A	34.087	_(ac)S(ph)WLFGINK_
Q9NVM9	626	S	Protein asunder hom	ASUN	175.15	_GKEELAEAEIIKDSPD
Q9NVR2	231	S	Integrator complex su	INTS10	122.13	_STQIENQHQGAQDT
Q9NVU0	503	S	DNA-directed RNA pc	POLR3E	43.336	_IKEEPVS(ph)EEGEEI
Q9NVU7	585	S	Protein SDA1 homolo	SDAD1	166.28	_YIEIDS(ph)DEEPR_
Q9NVW2	230	S	E3 ubiquitin-protein li	RLIM	79.613	_SRS(ph)PLHPMSEIPI
Q9NW82	638	S	WD repeat-containing	WDR70	91.416	_TMFAQVES(ph)DDEE
Q9NWB6	77	S	Arginine and glutama	ARGLU1	45.368	_ASS(ph)PPDR_
Q9NWH9	11	S	SAFB-like transcriptic	SLTM	68.569	_(ac)AAATGAVAAS(ph
Q9NWH9	144	S	SAFB-like transcriptic	SLTM	80.69	_ELLS(ph)AEENKR_
Q9NWH9	289	S	SAFB-like transcriptic	SLTM	190.83	_DGQDAIAQS(ph)PEK
Q9NWH9	550	S	SAFB-like transcriptic	SLTM	87.151	_IS(ph)S(ph)KSPGHM
Q9NWH9	551	S	SAFB-like transcriptic	SLTM	124.32	_ISS(ph)KS(ph)PGHM
Q9NWH9	553	S	SAFB-like transcriptic	SLTM	174.39	_S(ph)PGHM(ox)VILDC
Q9NWH9	590	S	SAFB-like transcriptic	SLTM	72.321	_ERAS(ph)LDKK_
Q9NWH9	748	S	SAFB-like transcriptic	SLTM	59.155	_KLS(ph)LDTDAR_
Q9NWS9	137	S	Zinc finger protein 44	ZNF446	141.38	_TEEPLGS(ph)PHPSG
Q9NWT1	320	S	p21-activated protein	PAK1IP1	48.376	_ESLPPAAEPS(ph)PV
Q9NX40	108	S	OCIA domain-contain	OCIAD1	142.4	_LENS(ph)PLGEALR_
Q9NX40	123	S	OCIA domain-contain	OCIAD1	98.898	_RSS(ph)PPGHYYQK_
Q9NX63	50	S	Coiled-coil-helix-coile	CHCHD3	132.03	_YS(ph)GAYGASVSDE
Q9NXC5	766	S	WD repeat-containing	MIOS	65.231	_GFSQYGVSGS(ph)P
Q9NXE4	753	S	Sphingomyelin phosp	SMPD4	88.495	_HLLS(ph)PVGR_
Q9NXE8	218	S	Pre-mRNA-splicing fa	CWC25	73.36	_MANSS(ph)PVLSK_
Q9NXG2	86	S	THUMP domain-cont	THUMPD1	174.89	_FTDKDQQPS(ph)GS(
Q9NXG2	88	S	THUMP domain-cont	THUMPD1	158.25	_FTDKDQQPS(ph)GS(
Q9NXX6	61	S	Non-structural mainte	NSMCE4A	92.48	_EAPERPSLEDTEPS(
Q9NXX6	63	S	Non-structural mainte	NSMCE4A	92.48	_EAPERPSLEDTEPS(
Q9NY27	226	S	Serine/threonine-prot	PPP4R2	250.93	_NHSDSSTSESEVSS
Q9NY61	316	S	Protein AATF	AATF	103.34	_YLVDGTKPNAGS(ph)
Q9NY61	320	S	Protein AATF	AATF	103.34	_YLVDGTKPNAGS(ph)
Q9NY61	321	S	Protein AATF	AATF	103.34	_YLVDGTKPNAGS(ph)
Q9NYB0	154	S	Telomeric repeat-binc	TERF2IP	53.773	_S(ph)PSSVTGNALW
Q9NYB0	203	S	Telomeric repeat-binc	TERF2IP	189.59	_YLLGDAPVS(ph)PSS
Q9NYB9	183	S	Abl interactor 2	ABI2	72.09	_TTPPTQKPPS(ph)PP
Q9NYF8	177	S	Bcl-2-associated tran	BCLAF1	211.26	_KAEGEPQEES(ph)PL
Q9NYF8	183	S	Bcl-2-associated tran	BCLAF1	138.34	_S(ph)QEEPKDTFEHD
Q9NYF8	198	S	Bcl-2-associated tran	BCLAF1	174.22	_DTFEHDPSES(ph)IDE
Q9NYF8	222	S	Bcl-2-associated tran	BCLAF1	201.21	_SSATSGDIWPGLSA
Q9NYF8	228	S	Bcl-2-associated tran	BCLAF1	148.97	_SPHS(ph)PSPIATPP
Q9NYF8	230	S	Bcl-2-associated tran	BCLAF1	129.26	_SPHS(ph)PS(ph)PIAT
Q9NYF8	234	T	Bcl-2-associated tran	BCLAF1	146.6	_SPHSPSPIAT(ph)PP
Q9NYF8	237	S	Bcl-2-associated tran	BCLAF1	148.98	_SPHSPSPIATPPS(ph
Q9NYF8	243	S	Bcl-2-associated tran	BCLAF1	112.91	_SPHS(ph)PS(ph)PIAT
Q9NYF8	257	T	Bcl-2-associated tran	BCLAF1	184.12	_NT(ph)PSQHSHSIQH
Q9NYF8	259	S	Bcl-2-associated tran	BCLAF1	155.25	_NTPS(ph)QHS(ph)HS
Q9NYF8	262	S	Bcl-2-associated tran	BCLAF1	126.4	_NTPS(ph)QHS(ph)HS
Q9NYF8	264	S	Bcl-2-associated tran	BCLAF1	114.55	_NTPSQHSHS(ph)IQH
Q9NYF8	268	S	Bcl-2-associated tran	BCLAF1	255.63	_NTPSQHSHSIQHS(p
Q9NYF8	285	S	Bcl-2-associated tran	BCLAF1	162.44	_YS(ph)PSQNS(ph)PI
Q9NYF8	287	S	Bcl-2-associated tran	BCLAF1	95.837	_YSPS(ph)QNS(ph)PI
Q9NYF8	290	S	Bcl-2-associated tran	BCLAF1	162.44	_YS(ph)PSQNS(ph)PI

Q9NYF8	319	S	Bcl-2-associated tran	BCLAF1	49.613	_GRS(ph)SFYPDGGD(
Q9NYF8	385	S	Bcl-2-associated tran	BCLAF1	367.27	_AEGEWEDQEALDYF
Q9NYF8	397	S	Bcl-2-associated tran	BCLAF1	322.71	_FNDS(ph)EGDDT(ph)
Q9NYF8	402	T	Bcl-2-associated tran	BCLAF1	233.34	_FNDSEGDDT(ph)EET
Q9NYF8	512	S	Bcl-2-associated tran	BCLAF1	203.32	_LKDLFDYS(ph)PPLHI
Q9NYF8	531	S	Bcl-2-associated tran	BCLAF1	114.79	_STFREES(ph)PLR_
Q9NYF8	648	S	Bcl-2-associated tran	BCLAF1	85.533	_QKS(ph)PEIHR_
Q9NYF8	658	S	Bcl-2-associated tran	BCLAF1	228.78	_IDIS(ph)PSTLR_
Q9NYL2	637	S	Mitogen-activated pro	MLTK	62.287	_SSS(ph)PTQYGLTK_
Q9NYL9	25	S	Tropomodulin-3	TMOD3	147.23	_YKDLDEDELLGNLS(
Q9NYM9	9	S	BET1-like protein	BET1L	95.954	_AQS(ph)PGAVEEILDI
Q9NYV4	80	S	Cyclin-dependent kin	CDK12	55.276	_DMGLVTPEAASLGT\
Q9NYV4	249	S	Cyclin-dependent kin	CDK12	224.43	_QDDSPSGASYGQDY
Q9NYV4	274	S	Cyclin-dependent kin	CDK12	118.63	_RQS(ph)VS(ph)PPYK
Q9NYV4	276	S	Cyclin-dependent kin	CDK12	118.63	_RQS(ph)VS(ph)PPYK
Q9NYV4	385	S	Cyclin-dependent kin	CDK12	103.42	_HSSIS(ph)PVR_
Q9NYV4	420	S	Cyclin-dependent kin	CDK12	96.866	_ES(ph)KGSPVFLPR_
Q9NYV4	423	S	Cyclin-dependent kin	CDK12	78.939	_GS(ph)PVFLPR_
Q9NYV4	681	S	Cyclin-dependent kin	CDK12	134.15	_HLLTDLPLPPELPGG
Q9NYV4	685	S	Cyclin-dependent kin	CDK12	112.08	_HLLTDLPLPPELPGG
Q9NYV4	692	T	Cyclin-dependent kin	CDK12	84.605	_AIT(ph)PPQQPYK_
Q9NYV4	893	T	Cyclin-dependent kin	CDK12	88.637	_LYNSEESRPYT(ph)N
Q9NYV4	1244	T	Cyclin-dependent kin	CDK12	61.437	_RT(ph)PTMPQEEAA
Q9NZ09	146	S	Ubiquitin-associated	UBAP1	65.719	_VLS(ph)PPHIK_
Q9NZ56	345	T	Formin-2	FMN2	115.36	_GAGDT(ph)DEEGEE
Q9NZ63	261	S	Uncharacterized prot	C9orf78	149.53	_VGDTEKPEPERS(ph
Q9NZH5	165	S	Securin-2;Securin	PTTG2;PTTG1	47.037	_LFQLGPPS(ph)PVK_
Q9NZI8	181	S	Insulin-like growth fac	IGF2BP1	104.09	_QGS(ph)PVAAGAPAI
Q9NZM3	884	S	Intersectin-2	ITSN2	58.272	_TVS(ph)PGSVS(ph)P
Q9NZM3	889	S	Intersectin-2	ITSN2	74.819	_TVS(ph)PGSVS(ph)P
Q9NZN4	438	S	EH domain-containin	EHD2	278.86	_GPDEAMEDGEEGS(
Q9NZT2	315	S	Opioid growth factor r	OGFR	107.01	_KVEEEGS(ph)PGDPI
Q9NZT2	378	S	Opioid growth factor r	OGFR	160.31	_SQGDEAGGHGEDRF
Q9P035	114	S	Very-long-chain (3R)-	PTPLAD1	209.43	_WLDES(ph)DAEMELF
Q9P0K7	249	T	Ankycorbin	RAI14	120.56	_ISQDADLKT(ph)PTKF
Q9P0K7	281	S	Ankycorbin	RAI14	139.28	_KAPPPPIS(ph)PTQLS
Q9P0K7	286	S	Ankycorbin	RAI14	130.81	_KAPPPPISPTQLS(ph
Q9P0K7	297	T	Ankycorbin	RAI14	82.651	_SITST(ph)PLS(ph)GK
Q9P0K7	300	S	Ankycorbin	RAI14	82.651	_SITST(ph)PLS(ph)GK
Q9P0K7	327	S	Ankycorbin	RAI14	127.8	_DRLS(ph)DSTTGADS
Q9P0K7	340	S	Ankycorbin	RAI14	136.71	_LSDSTTGADSLLDIS(
Q9P0K7	341	S	Ankycorbin	RAI14	136.71	_LSDSTTGADSLLDIS(
Q9P0K7	412	S	Ankycorbin	RAI14	108.38	_SS(ph)PSVLIHSLGK_
Q9P0L0	214	S	Vesicle-associated m	VAPA	71.853	_VAHSDKPGS(ph)TST
Q9P0M6	129	S	Core histone macro-H	H2AFY2	101.2	_SETILS(ph)PPPEK_
Q9P0P8	106	S	Uncharacterized prot	C6orf203	92.01	_VDEEDS(ph)DEESHI
Q9P1Q5	190	S	Olfactory receptor 1A	OR1A1	38.3	_LSCS(ph)DIHFHVK_
Q9P1Y6	867	S	PHD and RING finger	PHRF1	67.385	_TISINS(ph)PK_
Q9P1Y6	915	S	PHD and RING finger	PHRF1	165	_GAVAAEGAS(ph)DTE
Q9P1Y6	973	S	PHD and RING finger	PHRF1	183.48	_TVTCVTVVEPEAPPS
Q9P1Y6	991	S	PHD and RING finger	PHRF1	101.39	_VVELRPPS(ph)R_
Q9P1Y6	1034	S	PHD and RING finger	PHRF1	122.33	_SAS(ph)PSVGEERPF
Q9P1Y6	1124	S	PHD and RING finger	PHRF1	55.721	_ECS(ph)PTSSLER_
Q9P1Y6	1202	S	PHD and RING finger	PHRF1	152.66	_EAS(ph)PAPLAQGEF

Q9P1Y6	1229	S	PHD and RING finger	PHRF1	232.57	_LPALGEAHVS(ph)PE
Q9P1Y6	1359	S	PHD and RING finger	PHRF1	69.361	_AEAPS(ph)S(ph)PDV
Q9P1Y6	1360	S	PHD and RING finger	PHRF1	69.361	_AEAPS(ph)S(ph)PDV
Q9P206	545	S	Uncharacterized prot	KIAA1522	95.264	_GLAGPPAS(ph)PGK_
Q9P206	669	S	Uncharacterized prot	KIAA1522	66.474	_DQS(ph)PPPS(ph)PP
Q9P206	673	S	Uncharacterized prot	KIAA1522	66.474	_DQS(ph)PPPS(ph)PP
Q9P206	929	S	Uncharacterized prot	KIAA1522	87.352	_LQLERPVS(ph)PETQ
Q9P206	979	S	Uncharacterized prot	KIAA1522	59.574	_KPSVGVPPPAS(ph)P
Q9P212	721	S	1-phosphatidylinositol	PLCE1	44.045	_ELCEVLDGAS(ph)GL
Q9P246	523	S	Stromal interaction m	STIM2	60.157	_SIVPSS(ph)PQPQR_
Q9P275	871	S	Ubiquitin carboxyl-ter	USP36	59.908	_QPGS(ph)PMYR_
Q9P275	952	S	Ubiquitin carboxyl-ter	USP36	211.75	_HSCSPMGDGDPEAM
Q9P2B4	488	S	CTTNBP2 N-terminal	CTTNBP2NL	58.246	_DLS(ph)PTLIDNSAAK
Q9P2D0	1045	S	Inhibitor of Bruton tyr	IBTK	141.64	_DLQS(ph)PDFTTGFH
Q9P2D1	2559	S	Chromodomain-helica	CHD7	41.621	_NIPS(ph)PGQLDPDTI
Q9P2E9	1277	S	Ribosome-binding pro	RRBP1	112.64	_SHVEDGDIAGAPASS
Q9P2F8	1461	S	Signal-induced prolife	SIPA1L2	90.348	_LMLPDS(ph)PLVEEG
Q9P2F8	1488	S	Signal-induced prolife	SIPA1L2	124.24	_TLS(ph)DESICSNR_
Q9P2I0	419	S	Cleavage and polyad	CPSF2	102.28	_EADIDS(ph)S(ph)DES
Q9P2I0	420	S	Cleavage and polyad	CPSF2	102.28	_EADIDS(ph)S(ph)DES
Q9P2I0	423	S	Cleavage and polyad	CPSF2	102.28	_EADIDS(ph)S(ph)DES
Q9P2K3	156	S	REST corepressor 3	RCOR3	39.723	_HNQGDS(ph)DDDVE
Q9P2K5	17	S	Myelin expression fac	MYEF2	262.29	_AEVPGATGGDS(ph)F
Q9P2K8	667	T	Eukaryotic translation	EIF2AK4	91.238	_HERPAGPGT(ph)PPF
Q9P2M7	149	S	Cingulin	CGN	79.639	_SNS(ph)MLELAPK_
Q9P2M7	159	S	Cingulin	CGN	135.63	_VAS(ph)PGSTIDTAPL
Q9P2M7	332	S	Cingulin	CGN	78.548	_KVS(ph)LVLEK_
Q9P2R6	1106	S	Arginine-glutamic aci	RERE	68.763	_EEALDDAEEPES(ph)
Q9P2R6	1113	S	Arginine-glutamic aci	RERE	68.763	_EEALDDAEEPES(ph)
Q9P2R6	1115	S	Arginine-glutamic aci	RERE	68.763	_EEALDDAEEPES(ph)
Q9P2R6	1266	S	Arginine-glutamic aci	RERE	67.548	_PHVMS(ph)PTNR_
Q9UBB9	59	S	Tuftelin-interacting pr	TFIP11	138.78	_EEATYGVWAERDS(p
Q9UBB9	98	S	Tuftelin-interacting pr	TFIP11	204.41	_GAAEEAELEDS(ph)D
Q9UBB9	210	S	Tuftelin-interacting pr	TFIP11	258.87	_TTQSMQDFPVVDS(p
Q9UBC2	229	S	Epidermal growth fac	EPS15L1	36.454	_TVFPGAVPVLPAS(ph
Q9UBC2	255	S	Epidermal growth fac	EPS15L1	73.68	_STPSHGSVSSLNSTC
Q9UBC2	366	T	Epidermal growth fac	EPS15L1	57.738	_GT(ph)PGPDSSGSLC
Q9UBC2	593	S	Epidermal growth fac	EPS15L1	50.102	_GS(ph)FGAMDDPFK_
Q9UBF8	428	S	Phosphatidylinositol 4	PI4KB	104.84	_S(ph)VENLPECGITHE
Q9UBL3	623	S	Set1/Ash2 histone m	ASH2L	57.149	_RS(ph)PPWEP_
Q9UBQ5	217	S	Eukaryotic translation	EIF3K	53.255	_IDFDSVSSIMASS(ph)
Q9UER7	495	S	Death domain-associ	DAXX	72.801	_DGDKS(ph)PMSSLQI
Q9UER7	739	S	Death domain-associ	DAXX	121.35	_TSVATQCDPEEIIVLS
Q9UEW8	385	S	STE20/SPS1-related	STK39	196.31	_TEDGDWEWS(ph)DD
Q9UEY8	677	S	Gamma-adducin	ADD3	107.75	_IEEVLSPEGS(ph)PSI
Q9UEY8	681	S	Gamma-adducin	ADD3	160.81	_IEEVLSPEGSPSKS(p
Q9UFC0	212	S	Leucine-rich repeat a	LRWD1	115.54	_ANS(ph)PEKPPEAGA
Q9UFC0	243	S	Leucine-rich repeat a	LRWD1	116.61	_RPDDVPLSLS(ph)PS
Q9UFC0	251	S	Leucine-rich repeat a	LRWD1	117.04	_ACAS(ph)PSAQVEGS
Q9UGH3	75	T	Solute carrier family 2	SLC23A2	150.36	_SSLAET(ph)LDSTGS(
Q9UGH3	78	S	Solute carrier family 2	SLC23A2	265.13	_SSLAETLDS(ph)TGS(
Q9UGH3	79	T	Solute carrier family 2	SLC23A2	171.13	_SSLAETLDST(ph)GSI
Q9UGH3	81	S	Solute carrier family 2	SLC23A2	265.13	_SSLAET(ph)LDSTGS(
Q9UGU5	502	S	HMG domain-contain	HMGXB4	130.83	_S(ph)PPTTMLLPAS(p

Q9UGU5	512	S	HMG domain-contain	HMGXB4	130.83	_S(ph)PPTTMLLPAS(p
Q9UGV2	331	S	Protein NDRG3	NDRG3	84.107	_THS(ph)TSSSLGSGE
Q9UHB6	132	S	LIM domain and actin	LIMA1	118.21	_LRS(ph)PPEALVQGR
Q9UHB6	225	S	LIM domain and actin	LIMA1	126.64	_KIS(ph)ENSYSLDDLE
Q9UHB6	362	S	LIM domain and actin	LIMA1	165.38	_SEVQQPVHPKPLS(p
Q9UHB6	490	S	LIM domain and actin	LIMA1	169.67	_ETPHS(ph)PGVEDAF
Q9UHB7	180	S	AF4/FMR2 family me	AFF4	114.92	_SSS(ph)PGKPQAVSS
Q9UHB7	487	S	AF4/FMR2 family me	AFF4	95.459	_VNPHKVS(ph)PASSV
Q9UHB7	694	S	AF4/FMR2 family me	AFF4	65.056	_MFS(ph)PMEEK_
Q9UHB7	703	S	AF4/FMR2 family me	AFF4	145.44	_ELLS(ph)PLSEPDDR
Q9UHB7	706	S	AF4/FMR2 family me	AFF4	61.537	_ELLSPLS(ph)EPDDR
Q9UHB7	814	S	AF4/FMR2 family me	AFF4	91.589	_EKDLLPS(ph)PAGPV
Q9UHB7	1058	S	AF4/FMR2 family me	AFF4	99.941	_AVGMPSPVS(ph)PK_
Q9UHD8	30	S	Septin-9	SEPT9	223.5	_S(ph)FEVEEVETPNS
Q9UHL9	448	S	General transcription	GTF2IRD1	66.448	_LEPAS(ph)PPEDTSA
Q9UHR4	255	S	Brain-specific angiog	BAIAP2L1	126.51	_TPASTPVS(ph)GTPQ
Q9UHR4	261	S	Brain-specific angiog	BAIAP2L1	152.07	_TPASTPVSGTPQAS(
Q9UHR5	77	S	SAP30-binding protei	SAP30BP	160.01	_QSEDDDS(ph)ETEKF
Q9UHV7	890	S	Mediator of RNA poly	MED13	50.04	_IEVDEGFCS(ph)PKP
Q9UIF9	509	S	Bromodomain adjace	BAZ2A	90.601	_ASPVTSPAAAFPTAS
Q9UIF9	1207	S	Bromodomain adjace	BAZ2A	91.069	_HLKS(ph)PVR_
Q9UIF9	1397	S	Bromodomain adjace	BAZ2A	100.85	_AGDPGEMPQS(ph)P
Q9UIF9	1542	S	Bromodomain adjace	BAZ2A	34.432	_GWTCPS(ph)PDSTR_
Q9UIF9	1783	S	Bromodomain adjace	BAZ2A	125.29	_YSEEGLS(ph)PSKR_
Q9UIG0	158	S	Tyrosine-protein kina	BAZ1B	219.7	_SDGACDS(ph)PSS(pl
Q9UIG0	161	S	Tyrosine-protein kina	BAZ1B	224.83	_SDGACDSPSS(ph)DH
Q9UIG0	361	S	Tyrosine-protein kina	BAZ1B	81.789	_S(ph)PEEHLEEMMK_
Q9UIG0	705	S	Tyrosine-protein kina	BAZ1B	127.33	_RSDVQEES(ph)EGS(
Q9UIG0	708	S	Tyrosine-protein kina	BAZ1B	120.12	_RSDVQEES(ph)EGS(
Q9UIG0	710	T	Tyrosine-protein kina	BAZ1B	127.33	_RSDVQEES(ph)EGSD
Q9UIG0	945	T	Tyrosine-protein kina	BAZ1B	136.39	_DHT(ph)VSGDEDYCF
Q9UIG0	947	S	Tyrosine-protein kina	BAZ1B	128.74	_DHTVS(ph)GDEDYCF
Q9UIG0	1342	S	Tyrosine-protein kina	BAZ1B	97.163	_RQS(ph)LELQK_
Q9UIG0	1468	S	Tyrosine-protein kina	BAZ1B	235.5	_LAEDEGDS(ph)EPEA
Q9UIS9	295	S	Methyl-CpG-binding d	MBD1	86.577	_RRPGAQPLPPPPPS(
Q9UIS9	297	S	Methyl-CpG-binding d	MBD1	124.57	_RRPGAQPLPPPPPS(
Q9UIS9	311	S	Methyl-CpG-binding d	MBD1	106.6	_ALAPS(ph)PPAEFIYY
Q9UJM3	251	S	ERBB receptor feedb	ERRFI1	97.095	_SHS(ph)GPAGSFNKF
Q9UJV9	21	S	Probable ATP-depen	DDX41	65.152	_TDEVPAGGS(ph)RS(
Q9UJV9	23	S	Probable ATP-depen	DDX41	161.51	_S(ph)EAEDEDDEDYV
Q9UJX2	588	S	Cell division cycle pro	CDC23	172.82	_RVS(ph)PLNLSSVTP_
Q9UJX2	596	T	Cell division cycle pro	CDC23	132.14	_RVS(ph)PLNLSSVT(p
Q9UJX5	777	S	Anaphase-promoting	ANAPC4	141.23	_IKEEVLS(ph)ESEAEN
Q9UJZ1	327	T	Stomatin-like protein	STOML2	111.77	_APVPGT(ph)PDSLSS
Q9UK58	330	T	Cyclin-L1	CCNL1	78.974	_GLNPDGTPALST(ph)
Q9UK58	335	S	Cyclin-L1	CCNL1	151.24	_GLNPDGTPALSTLGC
Q9UK58	342	S	Cyclin-L1	CCNL1	114.77	_GLNPDGTPALSTLGC
Q9UK58	352	S	Cyclin-L1	CCNL1	203.53	_AEEKS(ph)PISINVK_
Q9UK58	445	S	Cyclin-L1	CCNL1	110.14	_HHNHGS(ph)PHLK_
Q9UK61	979	S	Protein FAM208A	FAM208A	124.63	_SSDYQFPSS(ph)PFT
Q9UK61	1103	S	Protein FAM208A	FAM208A	68.877	_GGNLPPVS(ph)PNDS
Q9UK76	87	S	Hematological and ne	HN1	230.18	_RNS(ph)SEASSGDFL
Q9UK76	131	S	Hematological and ne	HN1	72.051	_GEGDIHENVDTDLPG
Q9UKJ3	740	S	G patch domain-cont	GPATCH8	116.73	_GPKPEPPGSGS(ph)P

Q9UKJ3	974	S	G patch domain-cont	GPATCH8	136.39	_S(ph)RS(ph)TTAHSW
Q9UKJ3	976	S	G patch domain-cont	GPATCH8	136.39	_S(ph)RS(ph)TTAHSW
Q9UKJ3	1009	S	G patch domain-cont	GPATCH8	107.35	_S(ph)WGHES(ph)PEE
Q9UKJ3	1014	S	G patch domain-cont	GPATCH8	107.35	_S(ph)WGHES(ph)PEE
Q9UKJ3	1035	S	G patch domain-cont	GPATCH8	70.908	_SQS(ph)PHYFR_
Q9UKJ3	1107	S	G patch domain-cont	GPATCH8	81.807	_KPS(ph)VSEEVQATP
Q9UKL0	257	S	REST corepressor 1	RCOR1	79.278	_EREES(ph)EDELEEA
Q9UKM9	135	S	RNA-binding protein F	RALY	148.48	_LS(ph)PVPVPR_
Q9UKM9	286	T	RNA-binding protein F	RALY	202.61	_TRDDGDEEGLLT(ph)
Q9UKM9	288	S	RNA-binding protein F	RALY	182.23	_TRDDGDEEGLLT(ph)
Q9UKM9	295	S	RNA-binding protein F	RALY	101.33	_TRDDGDEEGLLTHS(
Q9UKM9	298	T	RNA-binding protein F	RALY	169.84	_TRDDGDEEGLLTHS(
Q9UKN8	611	S	General transcription	GTF3C4	233.2	_ILLVDS(ph)PGMGNA
Q9UKV3	216	S	Apoptotic chromatin c	ACIN1	195.09	_SSSISEEKGDS(ph)D
Q9UKV3	240	S	Apoptotic chromatin c	ACIN1	89.979	_LS(ph)EGS(ph)QPAE
Q9UKV3	243	S	Apoptotic chromatin c	ACIN1	89.979	_LS(ph)EGS(ph)QPAE
Q9UKV3	410	S	Apoptotic chromatin c	ACIN1	118.9	_ASLVALPEQTAS(ph)
Q9UKV3	414	T	Apoptotic chromatin c	ACIN1	142.65	_ASLVALPEQTASEEE
Q9UKV3	478	S	Apoptotic chromatin c	ACIN1	189.11	_ELLVSQHTVQLVGGL
Q9UKV3	490	S	Apoptotic chromatin c	ACIN1	197.39	_AES(ph)PAEKVPEES
Q9UKV3	657	S	Apoptotic chromatin c	ACIN1	98.254	_SLS(ph)PGVSR_
Q9UKV3	682	T	Apoptotic chromatin c	ACIN1	59.372	_DPSSGQEVAT(ph)PF
Q9UKV3	710	S	Apoptotic chromatin c	ACIN1	138.31	_RLS(ph)QPESAEK_
Q9UKV3	729	S	Apoptotic chromatin c	ACIN1	58.511	_LQPERGS(ph)PK_
Q9UKV3	838	S	Apoptotic chromatin c	ACIN1	104.45	_GVPAGNS(ph)DTEG
Q9UKV3	1004	S	Apoptotic chromatin c	ACIN1	140.78	_TAQVPS(ph)PPR_
Q9ULD2	399	S	Microtubule-associate	MTUS1	166.43	_DLGTQNHTSELILSS(
Q9ULD2	443	S	Microtubule-associate	MTUS1	112.34	_VTFSVS(ph)PIEATEK
Q9ULD2	1245	S	Microtubule-associate	MTUS1	77.27	_RS(ph)PTSSAIPLQSF
Q9ULD2	1266	S	Microtubule-associate	MTUS1	128.64	_NSGSFPSPS(ph)ISPF
Q9ULD2	1268	S	Microtubule-associate	MTUS1	119.99	_NSGSFPSPSIS(ph)PF
Q9ULD4	17	S	Bromodomain and PH	BRPF3	69.345	_RS(ph)PS(ph)PYSLK_
Q9ULD4	19	S	Bromodomain and PH	BRPF3	69.345	_RS(ph)PS(ph)PYSLK_
Q9ULF5	591	S	Zinc transporter ZIP1	SLC39A10	101.9	_LNETELTDLEGQQES
Q9ULH0	918	S	Kinase D-interacting s	KIDINS220	55.721	_QMS(ph)FDLTK_
Q9ULH0	1526	S	Kinase D-interacting s	KIDINS220	231.17	_LPSDEDES(ph)GTEE
Q9ULH0	1555	S	Kinase D-interacting s	KIDINS220	112.96	_S(ph)PEHSAEPIR_
Q9ULI0	1347	S	ATPase family AAA d	ATAD2B	59.227	_LEPGS(ph)DVEVK_
Q9ULJ8	190	S	Neurabin-1	PPP1R9A	76.051	_GSTDS(ph)LDS(ph)LS
Q9ULJ8	199	S	Neurabin-1	PPP1R9A	149	_TEAVS(ph)PTVSQLS
Q9ULJ8	338	S	Neurabin-1	PPP1R9A	148.06	_SEIPS(ph)PQSQLLED
Q9ULJ8	840	S	Neurabin-1	PPP1R9A	96.866	_RTS(ph)LGEVSK_
Q9ULL5	487	S	Proline-rich protein 12	PRR12	130.83	_HPPLYQAGLTPPLS(
Q9ULL5	560	S	Proline-rich protein 12	PRR12	110.94	_NLETLPSFS(ph)S(ph)
Q9ULL5	561	S	Proline-rich protein 12	PRR12	110.94	_NLETLPSFS(ph)S(ph)
Q9ULL5	884	T	Proline-rich protein 12	PRR12	109.14	_APAPPPKPET(ph)PE
Q9ULT8	1772	S	E3 ubiquitin-protein li	HECTD1	61.444	_QFS(ph)ALVPAFDPR
Q9ULU4	406	S	Protein kinase C-bind	ZMYND8	181.67	_LNFDMTAS(ph)PK_
Q9ULU4	425	S	Protein kinase C-bind	ZMYND8	125.46	_RIS(ph)LSDMPR_
Q9ULU4	547	S	Protein kinase C-bind	ZMYND8	65.064	_ELSESVQQQSTPVPI
Q9ULU4	668	S	Protein kinase C-bind	ZMYND8	243.99	_DKAS(ph)PEPEKDFS
Q9ULU4	746	T	Protein kinase C-bind	ZMYND8	72.573	_QDVVGKT(ph)PPS(ph
Q9ULU4	756	S	Protein kinase C-bind	ZMYND8	125.91	_QDVVGKT(ph)PPSTT
Q9ULW0	738	S	Targeting protein for X	TPX2	82.877	_SSDQPLTVPVS(ph)P

Q9ULX3	201	S	RNA-binding protein N	NOB1	179.2	_KDDS(ph)DDDGGGW
Q9UMN6	2083	T	Histone-lysine N-meth	WBP7	84.046	_GQGT(ph)PPSGPGV'
Q9UMS6	902	S	Synaptopodin-2	SYNPO2	134.14	_AQS(ph)PTPSLPASW
Q9UMY4	73	S	Sorting nexin-12	SNX12	52.821	_RYS(ph)DFEWLK_
Q9UMZ2	752	S	Synergin gamma	SYNRG	121.26	_QLS(ph)LEGSGLGVE
Q9UN86	141	S	Ras GTPase-activatin	G3BP2	132.62	_YEDEVFGDS(ph)EPE
Q9UN86	149	S	Ras GTPase-activatin	G3BP2	132.62	_YEDEVFGDS(ph)EPE
Q9UNS1	1173	S	Protein timeless hom	TIMELESS	137.69	_QLLDS(ph)DEEQEED
Q9UNZ2	114	S	NSFL1 cofactor p47	NSFL1C	150.23	_S(ph)PNELVDDLFK_
Q9UP95	967	S	Solute carrier family 1	SLC12A4	117.62	_LESLYS(ph)DEEDES
Q9UPN3	1376	S	Microtubule-actin cros	MACF1	72.568	_MLS(ph)SSDAITQEFI
Q9UPN3	3927	S	Microtubule-actin cros	MACF1	57.525	_RQGS(ph)FSEDVISH
Q9UPN3	4521	S	Microtubule-actin cros	MACF1	58.079	_AFLAELEQNS(ph)PK
Q9UPN6	617	S	Protein SCAF8	SCAF8	153.98	_ETVQTTQS(ph)PTPV
Q9UPN7	531	S	Serine/threonine-prot	PPP6R1	102.21	_NMVDLVNTHHLHSS
Q9UPN9	1102	T	E3 ubiquitin-protein li	TRIM33	49.737	_TFAPLPEFEQEEDDG
Q9UPN9	1105	S	E3 ubiquitin-protein li	TRIM33	49.737	_TFAPLPEFEQEEDDG
Q9UPP1	857	S	Histone lysine demeth	PHF8	85.062	_DAEYIYPSLES(ph)DI
Q9UPQ0	169	S	LIM and calponin hon	LIMCH1	76.358	_KDTDDIES(ph)PKR_
Q9UPQ0	192	S	LIM and calponin hon	LIMCH1	108.47	_SDSLS(ph)PPR_
Q9UPQ0	204	S	LIM and calponin hon	LIMCH1	77.746	_DDSFDS(ph)LDSFGS
Q9UPQ0	215	T	LIM and calponin hon	LIMCH1	86.213	_SRQT(ph)PS(ph)PDV
Q9UPQ0	217	S	LIM and calponin hon	LIMCH1	86.213	_SRQT(ph)PS(ph)PDV
Q9UPQ0	226	S	LIM and calponin hon	LIMCH1	100.04	_GSS(ph)DGRGS(ph)D
Q9UPQ0	231	S	LIM and calponin hon	LIMCH1	112.36	_GSSDGRGS(ph)DS(p
Q9UPQ0	233	S	LIM and calponin hon	LIMCH1	108.94	_GSSDGRGS(ph)DS(p
Q9UPQ0	718	S	LIM and calponin hon	LIMCH1	202.84	_S(ph)PEPEATLTFPFL
Q9UPQ0	973	S	LIM and calponin hon	LIMCH1	73.928	_SINHQIES(ph)PSER_
Q9UPT8	159	S	Zinc finger CCCH dor	ZC3H4	126.86	_EYS(ph)PPYAPSHQC
Q9UPT8	1114	S	Zinc finger CCCH dor	ZC3H4	101.36	_AAKPGPAEAPSPTAS
Q9UPT8	1275	S	Zinc finger CCCH dor	ZC3H4	81.643	_TGSGSPFAGNS(ph)F
Q9UPU5	2047	S	Ubiquitin carboxyl-ter	USP24	59.634	_VSDQNS(ph)PVLPK_
Q9UPU5	2561	S	Ubiquitin carboxyl-ter	USP24	180.44	_TIS(ph)AQDTLAYATA
Q9UPX8	67	S	SH3 and multiple ank	SHANK2	101.42	_SLS(ph)PQLLQQMPS
Q9UPX8	1330	S	SH3 and multiple ank	SHANK2	142.43	_RAPS(ph)PVVSPTEM
Q9UPY5	26	S	Cystine/glutamate tra	SLC7A11	85.67	_LPS(ph)LGNK_
Q9UQ35	204	S	Serine/arginine repeti	SRRM2	49.418	_SESSS(ph)PR_
Q9UQ35	295	S	Serine/arginine repeti	SRRM2	208.61	_THTTALAGRS(ph)PS
Q9UQ35	297	S	Serine/arginine repeti	SRRM2	208.61	_THTTALAGRS(ph)PS
Q9UQ35	323	S	Serine/arginine repeti	SRRM2	221.5	_GEGDAPFSEPGTTS'
Q9UQ35	353	S	Serine/arginine repeti	SRRM2	99.686	_SATRPSPS(ph)PER_
Q9UQ35	377	S	Serine/arginine repeti	SRRM2	170.24	_HGGS(ph)PQPLATTF
Q9UQ35	384	T	Serine/arginine repeti	SRRM2	120.92	_HGGSPQPLATT(ph)F
Q9UQ35	398	S	Serine/arginine repeti	SRRM2	170.24	_HGGS(ph)PQPLATTF
Q9UQ35	408	S	Serine/arginine repeti	SRRM2	143.58	_SPPKS(ph)PEKLPQS
Q9UQ35	424	S	Serine/arginine repeti	SRRM2	226.67	_LPQSSSSESSPPS(pl
Q9UQ35	435	S	Serine/arginine repeti	SRRM2	162.61	_HAS(ph)S(ph)S(ph)PE
Q9UQ35	436	S	Serine/arginine repeti	SRRM2	153.65	_HAS(ph)S(ph)S(ph)PE
Q9UQ35	437	S	Serine/arginine repeti	SRRM2	153.65	_HAS(ph)S(ph)S(ph)PE
Q9UQ35	440	S	Serine/arginine repeti	SRRM2	197.79	_HAS(ph)S(ph)S(ph)PE
Q9UQ35	476	T	Serine/arginine repeti	SRRM2	58.592	_SHSHT(ph)PSR_
Q9UQ35	484	S	Serine/arginine repeti	SRRM2	108.35	_S(ph)RS(ph)PATAK_
Q9UQ35	486	S	Serine/arginine repeti	SRRM2	108.35	_S(ph)RS(ph)PATAK_
Q9UQ35	508	S	Serine/arginine repeti	SRRM2	81.95	_S(ph)RS(ph)PQWR_

Q9UQ35	510	S	Serine/arginine repeti	SRRM2	81.95	_S(ph)RS(ph)PQWR_
Q9UQ35	534	S	Serine/arginine repeti	SRRM2	109.14	_S(ph)RS(ph)PQRPGV
Q9UQ35	536	S	Serine/arginine repeti	SRRM2	109.14	_S(ph)RS(ph)PQRPGV
Q9UQ35	839	S	Serine/arginine repeti	SRRM2	70.373	_QSHSSSS(ph)PHPK_
Q9UQ35	864	S	Serine/arginine repeti	SRRM2	89.043	_QGSITSPQANEQS(pl
Q9UQ35	866	T	Serine/arginine repeti	SRRM2	189.07	_QGSITSPQANEQSVT
Q9UQ35	871	S	Serine/arginine repeti	SRRM2	97.797	_S(ph)CFESSPDPELK
Q9UQ35	875	S	Serine/arginine repeti	SRRM2	114.31	_SCFES(ph)SPDPELK
Q9UQ35	876	S	Serine/arginine repeti	SRRM2	131.96	_SCFESS(ph)PDPELK
Q9UQ35	914	S	Serine/arginine repeti	SRRM2	48.794	_SSS(ph)PQPK_
Q9UQ35	952	S	Serine/arginine repeti	SRRM2	84.046	_S(ph)VS(ph)PCSNVE
Q9UQ35	954	S	Serine/arginine repeti	SRRM2	132.09	_S(ph)VS(ph)PCSNVE
Q9UQ35	983	T	Serine/arginine repeti	SRRM2	81.525	_VKPET(ph)PPR_
Q9UQ35	990	S	Serine/arginine repeti	SRRM2	78.564	_QSHS(ph)GSISPYPK
Q9UQ35	994	S	Serine/arginine repeti	SRRM2	116.49	_QSHSGSIS(ph)PYPK
Q9UQ35	1003	T	Serine/arginine repeti	SRRM2	108.77	_AQT(ph)PPGPSLSGS
Q9UQ35	1010	S	Serine/arginine repeti	SRRM2	92.886	_AQTPPGPSLS(ph)GS
Q9UQ35	1014	S	Serine/arginine repeti	SRRM2	84.515	_AQT(ph)PPGPSLSGS
Q9UQ35	1064	S	Serine/arginine repeti	SRRM2	47.712	_GQSQTS(ph)PDHR_
Q9UQ35	1083	S	Serine/arginine repeti	SRRM2	196.18	_QSHSES(ph)PSLQSK
Q9UQ35	1099	S	Serine/arginine repeti	SRRM2	116.85	_S(ph)RS(ph)SS(ph)PV
Q9UQ35	1101	S	Serine/arginine repeti	SRRM2	129.37	_S(ph)RS(ph)SS(ph)PV
Q9UQ35	1103	S	Serine/arginine repeti	SRRM2	133.15	_S(ph)RS(ph)SS(ph)PV
Q9UQ35	1122	S	Serine/arginine repeti	SRRM2	51.064	_GEFS(ph)ASPMLK_
Q9UQ35	1124	S	Serine/arginine repeti	SRRM2	133.02	_GEFSAS(ph)PMLK_
Q9UQ35	1179	S	Serine/arginine repeti	SRRM2	164.93	_MALPPQEDATAS(ph)
Q9UQ35	1188	S	Serine/arginine repeti	SRRM2	98.21	_DKFS(ph)PFPVQDRF
Q9UQ35	1208	T	Serine/arginine repeti	SRRM2	97.463	_DTLRT(ph)PPRER_
Q9UQ35	1227	S	Serine/arginine repeti	SRRM2	83.312	_EQNS(ph)ALPTSSQD
Q9UQ35	1320	S	Serine/arginine repeti	SRRM2	124.08	_ELSNS(ph)PLR_
Q9UQ35	1326	S	Serine/arginine repeti	SRRM2	111.55	_ENS(ph)FGSPLEFR_
Q9UQ35	1329	S	Serine/arginine repeti	SRRM2	139.86	_ENSFGS(ph)PLEFR_
Q9UQ35	1378	S	Serine/arginine repeti	SRRM2	297.36	_S(ph)SGHSSSELSPD
Q9UQ35	1382	S	Serine/arginine repeti	SRRM2	255.22	_SSGHS(ph)SSELSPD
Q9UQ35	1383	S	Serine/arginine repeti	SRRM2	207.43	_SSGHSS(ph)SELSPD
Q9UQ35	1387	S	Serine/arginine repeti	SRRM2	200.99	_SSGHSSSELS(ph)PD
Q9UQ35	1462	S	Serine/arginine repeti	SRRM2	141.58	_HSLSGS(ph)S(ph)PG
Q9UQ35	1463	S	Serine/arginine repeti	SRRM2	141.58	_HSLSGS(ph)S(ph)PG
Q9UQ35	1472	T	Serine/arginine repeti	SRRM2	59.198	_DIPRT(ph)PSR_
Q9UQ35	1492	T	Serine/arginine repeti	SRRM2	90.64	_ALPQT(ph)PRPR_
Q9UQ35	1497	S	Serine/arginine repeti	SRRM2	120.32	_S(ph)RS(ph)PSSPELI
Q9UQ35	1499	S	Serine/arginine repeti	SRRM2	124.04	_S(ph)RS(ph)PSSPELI
Q9UQ35	1531	T	Serine/arginine repeti	SRRM2	67.997	_TVART(ph)PLGQR_
Q9UQ35	1539	S	Serine/arginine repeti	SRRM2	241.52	_S(ph)GSSQELDVKPS
Q9UQ35	1541	S	Serine/arginine repeti	SRRM2	125.37	_SGS(ph)S(ph)QELDV
Q9UQ35	1542	S	Serine/arginine repeti	SRRM2	118.05	_SGS(ph)S(ph)QELDV
Q9UQ35	1550	S	Serine/arginine repeti	SRRM2	96.723	_SGSSQELDVKPS(ph)
Q9UQ35	1652	S	Serine/arginine repeti	SRRM2	280.2	_GPSPEGS(ph)SSTES
Q9UQ35	1653	S	Serine/arginine repeti	SRRM2	256.8	_GPSPEGSS(ph)STES
Q9UQ35	1655	T	Serine/arginine repeti	SRRM2	150.36	_GPSPEGSSST(ph)ES
Q9UQ35	1657	S	Serine/arginine repeti	SRRM2	208.16	_GPSPEGSSSTES(ph)
Q9UQ35	1658	S	Serine/arginine repeti	SRRM2	288.31	_GPSPEGSSSTES(ph)
Q9UQ35	1727	S	Serine/arginine repeti	SRRM2	121.82	_S(ph)PSVSSPEPAEK
Q9UQ35	1729	S	Serine/arginine repeti	SRRM2	120.99	_RSPS(ph)VSSPEPAE

Q9UQ35	1731	S	Serine/arginine repeti	SRRM2	154.19	_SPSVS(ph)SPEPAEK
Q9UQ35	1854	S	Serine/arginine repeti	SRRM2	90.697	_S(ph)RT(ph)SPAPWK
Q9UQ35	1856	T	Serine/arginine repeti	SRRM2	90.697	_SRT(ph)S(ph)PAPWK
Q9UQ35	1857	S	Serine/arginine repeti	SRRM2	70.889	_S(ph)RTS(ph)PAPWK
Q9UQ35	1869	S	Serine/arginine repeti	SRRM2	101.71	_AS(ph)PATHR_
Q9UQ35	1876	S	Serine/arginine repeti	SRRM2	78.564	_S(ph)RS(ph)RT(ph)PL
Q9UQ35	1878	S	Serine/arginine repeti	SRRM2	95.162	_S(ph)RT(ph)PLISR_
Q9UQ35	1880	T	Serine/arginine repeti	SRRM2	95.162	_S(ph)RT(ph)PLISR_
Q9UQ35	1916	S	Serine/arginine repeti	SRRM2	60	_SRAS(ph)PVSR_
Q9UQ35	1974	T	Serine/arginine repeti	SRRM2	73.951	_SRT(ph)SPITR_
Q9UQ35	1986	T	Serine/arginine repeti	SRRM2	111.86	_SRT(ph)SPVTR_
Q9UQ35	2020	S	Serine/arginine repeti	SRRM2	97.734	_S(ph)RT(ph)PPAIR_
Q9UQ35	2022	T	Serine/arginine repeti	SRRM2	97.734	_S(ph)RT(ph)PPAIR_
Q9UQ35	2032	S	Serine/arginine repeti	SRRM2	107.03	_S(ph)RT(ph)PLLPR_
Q9UQ35	2034	T	Serine/arginine repeti	SRRM2	107.03	_S(ph)RT(ph)PLLPR_
Q9UQ35	2044	S	Serine/arginine repeti	SRRM2	122.7	_S(ph)RS(ph)RS(ph)PL
Q9UQ35	2046	S	Serine/arginine repeti	SRRM2	122.7	_S(ph)RS(ph)RS(ph)PL
Q9UQ35	2067	S	Serine/arginine repeti	SRRM2	118.88	_S(ph)LT(ph)RS(ph)PP
Q9UQ35	2069	T	Serine/arginine repeti	SRRM2	145.49	_S(ph)LT(ph)RS(ph)PP
Q9UQ35	2071	S	Serine/arginine repeti	SRRM2	145.49	_S(ph)LT(ph)RS(ph)PP
Q9UQ35	2100	S	Serine/arginine repeti	SRRM2	78.272	_NHS(ph)GS(ph)RT(ph
Q9UQ35	2102	S	Serine/arginine repeti	SRRM2	111.66	_NHS(ph)GS(ph)RT(ph
Q9UQ35	2104	T	Serine/arginine repeti	SRRM2	125.82	_T(ph)PPVALNSSR_
Q9UQ35	2123	S	Serine/arginine repeti	SRRM2	158.25	_PSMS(ph)PTPLDR_
Q9UQ35	2132	S	Serine/arginine repeti	SRRM2	114.31	_S(ph)PGMLEPLGSSF
Q9UQ35	2155	S	Serine/arginine repeti	SRRM2	102.16	_TPMSVLQQAGGS(ph
Q9UQ35	2272	S	Serine/arginine repeti	SRRM2	132.9	_TPAAAAAMNLAS(ph)
Q9UQ35	2335	S	Serine/arginine repeti	SRRM2	117.07	_TPQAPAS(ph)ANLVG
Q9UQ35	2343	S	Serine/arginine repeti	SRRM2	87.088	_S(ph)AHATAPVNIAGS
Q9UQ35	2382	S	Serine/arginine repeti	SRRM2	140.22	_MAPALSGANLTS(ph)
Q9UQ35	2398	S	Serine/arginine repeti	SRRM2	61.679	_TS(ph)PPLLDR_
Q9UQ35	2407	S	Serine/arginine repeti	SRRM2	101.08	_S(ph)RT(ph)PPSAPS(
Q9UQ35	2409	T	Serine/arginine repeti	SRRM2	113.52	_S(ph)RT(ph)PPSAPS(
Q9UQ35	2449	S	Serine/arginine repeti	SRRM2	87.544	_S(ph)PVPSAFSDQSR
Q9UQ35	2581	S	Serine/arginine repeti	SRRM2	89.189	_VPS(ph)PTPAPK_
Q9UQ35	2688	S	Serine/arginine repeti	SRRM2	107.46	_KPIDSLRDS(ph)R_
Q9UQ35	2690	S	Serine/arginine repeti	SRRM2	102.73	_S(ph)LS(ph)YS(ph)PV
Q9UQ35	2692	S	Serine/arginine repeti	SRRM2	105.66	_S(ph)LS(ph)YS(ph)PV
Q9UQ35	2694	S	Serine/arginine repeti	SRRM2	120.77	_SLSYS(ph)PVER_
Q9UQ35	2702	S	Serine/arginine repeti	SRRM2	128.1	_RRPS(ph)PQPSPR_
Q9UQ80	2	S	Proliferation-associat	PA2G4	250.81	_(ac)S(ph)GEDEQQEC
Q9UQN3	199	S	Charged multivesicul	CHMP2B	47.621	_ATIS(ph)DEEIER_
Q9UQR0	267	S	Sex comb on midleg-l	SCML2	144.63	_TESSPSEASQHSMQ
Q9UQR0	499	S	Sex comb on midleg-l	SCML2	76.237	_S(ph)PQQTVPYVVPL
Q9UQR0	511	S	Sex comb on midleg-l	SCML2	76.237	_RS(ph)PQQTVPYVVF
Q9UQR0	590	S	Sex comb on midleg-l	SCML2	72.935	_SVPGTTSSPLVGDIS
Q9Y232	88	S	Chromodomain Y-like	CDYL	86.208	_GYDS(ph)EDDTWEP
Q9Y232	201	S	Chromodomain Y-like	CDYL	78.043	_ILVPKS(ph)PVK_
Q9Y277	4	T	Voltage-dependent ar	VDAC3	76.759	_(ac)CNT(ph)PTYCDL(
Q9Y2D5	152	S	A-kinase anchor prote	AKAP2	139.46	_DALGDSLQVPVS(ph)
Q9Y2D5	393	S	A-kinase anchor prote	AKAP2	142.4	_S(ph)PGALETPSAAG
Q9Y2D5	778	S	A-kinase anchor prote	AKAP2	94.841	_VKPPPS(ph)PTTEGP
Q9Y2F5	533	S	Uncharacterized prote	KIAA0947	105.65	_SELCSS(ph)PLGK_
Q9Y2F5	925	S	Uncharacterized prote	KIAA0947	93.766	_SIS(ph)PEVSASR_

Q9Y2F5	1642	T	Uncharacterized prot	KIAA0947	89.457	_QEVGPPLPPLLAPLI
Q9Y2F5	1712	S	Uncharacterized prot	KIAA0947	38.995	_VVPS(ph)PLQFCAAT
Q9Y2F5	1903	S	Uncharacterized prot	KIAA0947	38.744	_SCSSPAVSAVSQLPL
Q9Y2H5	777	S	Pleckstrin homology d	PLEKHA6	130.5	_TKS(ph)PTDDEVTPS
Q9Y2K7	28	S	Lysine-specific deme	KDM2A	191.97	_YEDDGIS(ph)DDEIEC
Q9Y2K7	558	S	Lysine-specific deme	KDM2A	70.828	_LTPVRPAAAS(ph)PIV
Q9Y2K7	692	S	Lysine-specific deme	KDM2A	107.97	_KMEES(ph)DEEAVQA
Q9Y2K7	713	T	Lysine-specific deme	KDM2A	107.71	_SCDEPLT(ph)PPPHS
Q9Y2K7	718	S	Lysine-specific deme	KDM2A	107.71	_SCDEPLT(ph)PPPHS
Q9Y2U8	259	S	Inner nuclear membra	LEMD3	143.91	_ENYS(ph)DSEEEDDD
Q9Y2V2	30	S	Calcium-regulated he	CARHSP1	74.562	_ERS(ph)PSPLR_
Q9Y2V2	41	S	Calcium-regulated he	CARHSP1	89.747	_GNVVPS(ph)PLPTR_
Q9Y2V2	52	S	Calcium-regulated he	CARHSP1	111.06	_TFS(ph)ATVR_
Q9Y2W1	55	S	Thyroid hormone rece	THRAP3	80.755	_SYS(ph)PAHNR_
Q9Y2W1	217	S	Thyroid hormone rece	THRAP3	109.91	_AS(ph)ESSKPWPDA
Q9Y2W1	237	S	Thyroid hormone rece	THRAP3	104.24	_AS(ph)AVSELSPR_
Q9Y2W1	240	S	Thyroid hormone rece	THRAP3	85.006	_ASAVS(ph)ELS(ph)PI
Q9Y2W1	243	S	Thyroid hormone rece	THRAP3	188.48	_ASAVSELS(ph)PR_
Q9Y2W1	248	S	Thyroid hormone rece	THRAP3	177.6	_ERS(ph)PALKS(ph)PL
Q9Y2W1	253	S	Thyroid hormone rece	THRAP3	177.6	_ERS(ph)PALKS(ph)PL
Q9Y2W1	264	S	Thyroid hormone rece	THRAP3	76.165	_S(ph)PRPS(ph)PVPK_
Q9Y2W1	268	S	Thyroid hormone rece	THRAP3	65.219	_S(ph)PRPS(ph)PVPK_
Q9Y2W1	310	S	Thyroid hormone rece	THRAP3	135.5	_PSPPLSSTSQMGSTL
Q9Y2W1	315	S	Thyroid hormone rece	THRAP3	184.57	_S(ph)PVGKS(ph)PPS
Q9Y2W1	320	S	Thyroid hormone rece	THRAP3	203.72	_SPVGKS(ph)PPSTGS
Q9Y2W1	379	S	Thyroid hormone rece	THRAP3	109.64	_GSFS(ph)DTGLGDGK
Q9Y2W1	406	S	Thyroid hormone rece	THRAP3	102.47	_TDSEKPFRGS(ph)QS
Q9Y2W1	408	S	Thyroid hormone rece	THRAP3	102.47	_TDSEKPFRGS(ph)QS
Q9Y2W1	535	S	Thyroid hormone rece	THRAP3	62.582	_SSS(ph)PPPR_
Q9Y2W1	575	S	Thyroid hormone rece	THRAP3	92.856	_MDS(ph)FDEDLAR_
Q9Y2W1	624	S	Thyroid hormone rece	THRAP3	72.99	_SPS(ph)ELFAQHIVTI
Q9Y2W1	672	S	Thyroid hormone rece	THRAP3	147.62	_NKKS(ph)PEIHR_
Q9Y2W1	682	S	Thyroid hormone rece	THRAP3	234.39	_IDIS(ph)PSTFR_
Q9Y2W1	698	S	Thyroid hormone rece	THRAP3	173.71	_KHGLAHDEMKS(ph)F
Q9Y2W1	928	S	Thyroid hormone rece	THRAP3	169.13	_WAHDKFS(ph)GEEG
Q9Y2W1	939	S	Thyroid hormone rece	THRAP3	364.17	_FSGEEGEIEDDES(ph
Q9Y2W2	237	S	WW domain-binding p	WBP11	119.38	_RRDEDMLYS(ph)PEL
Q9Y2X3	105	S	Nucleolar protein 58	NOP58	38.808	_LNLS(ph)CIHS(ph)PV
Q9Y2X3	109	S	Nucleolar protein 58	NOP58	38.808	_LNLS(ph)CIHS(ph)PV
Q9Y2X3	502	S	Nucleolar protein 58	NOP58	265.97	_HIKEEPLS(ph)EEEPC
Q9Y2X3	514	S	Nucleolar protein 58	NOP58	260.38	_HIKEEPLS(ph)EEEPC
Q9Y2X7	388	S	ARF GTPase-activati	GIT1	55.999	_SQSDLDDQHDYDSV
Q9Y2X9	651	S	Zinc finger protein 28	ZNF281	108.5	_VDLHTSGEHSELVQE
Q9Y320	288	S	Thioredoxin-related tr	TMX2	42.393	_AGDNIPEEQPVASTF
Q9Y388	148	S	RNA-binding motif pr	RBMX2	162.98	_TPSPSLSES(ph)S(ph
Q9Y388	149	S	RNA-binding motif pr	RBMX2	162.98	_TPSPSLSES(ph)S(ph
Q9Y3B9	266	S	RRP15-like protein	RRP15	164.64	_DWDKES(ph)DGPDD
Q9Y3B9	280	S	RRP15-like protein	RRP15	213.09	_DWDKES(ph)DGPDD
Q9Y3E7	200	S	Charged multivesicula	CHMP3	115.11	_VTDALPEPEPPGAM
Q9Y3T9	49	S	Nucleolar complex pr	NOC2L	164.89	_EAARS(ph)PDKPGGS
Q9Y3T9	56	S	Nucleolar complex pr	NOC2L	144.44	_EAARS(ph)PDKPGGS
Q9Y3T9	672	S	Nucleolar complex pr	NOC2L	317.1	_DLFDLNS(ph)S(ph)EE
Q9Y3T9	673	S	Nucleolar complex pr	NOC2L	300.38	_DLFDLNS(ph)S(ph)EE
Q9Y3X0	80	S	Coiled-coil domain-co	CCDC9	99.069	_S(ph)PGTPRPPGASK

Q9Y3X0	521	S	Coiled-coil domain-co	CCDC9	47.155	_TTHLAGALS(ph)PGE
Q9Y3Z3	33	S	SAM domain and HD	SAMHD1	83.944	_TPSNTPSAEADWS(p
Q9Y446	314	S	Plakophilin-3	PKP3	100.82	_LSS(ph)GFDDIDLPSA
Q9Y463	273	Y	Dual specificity tyrosi	DYRK1B;DYRK1A	100.98	_IYQY(ph)IQSR_
Q9Y487	695	S	V-type proton ATPase	ATP6V0A2	133.29	_KDS(ph)EEEVSLLGS
Q9Y4B5	263	S	Protein SOGA2	SOGA2	63.095	_GAPPGS(ph)PEPPAL
Q9Y4B5	622	S	Protein SOGA2	SOGA2	132.84	_DHAPSIPTS(ph)PFGI
Q9Y4B5	776	S	Protein SOGA2	SOGA2	113.31	_REGPVGGES(ph)DSI
Q9Y4B5	1417	T	Protein SOGA2	SOGA2	114.28	_EDVT(ph)PPLS(ph)PI
Q9Y4B5	1421	S	Protein SOGA2	SOGA2	114.28	_EDVT(ph)PPLS(ph)PI
Q9Y4B5	1514	S	Protein SOGA2	SOGA2	87.568	_VLHS(ph)PPAVR_
Q9Y4E1	333	S	WASH complex subu	FAM21A;FAM21C	71.202	_RTPS(ph)DDEEDNLF
Q9Y4E1	498	S	WASH complex subu	FAM21A;FAM21B	37.169	_AVAS(ph)PEATVSQT
Q9Y4E1	539	S	WASH complex subu	FAM21C	198.47	_GLFS(ph)DEEDSEDL
Q9Y4E8	229	S	Ubiquitin carboxyl-ter	USP15	84.41	_S(ph)PGASNFSTLPK
Q9Y4F1	889	S	FERM, RhoGEF and	FARP1	211.5	_SPDEATAADQES(ph)
Q9Y4G6	1843	T	Talin-2	TLN2	64.104	_LDEGT(ph)PPEPK_
Q9Y4H2	306	S	Insulin receptor subst	IRS2	88.976	_SKS(ph)QSSGSSATH
Q9Y4H2	388	S	Insulin receptor subst	IRS2	88.945	_PVSVAGS(ph)PLS(ph
Q9Y4H2	391	S	Insulin receptor subst	IRS2	143.99	_PVSVAGS(ph)PLS(ph
Q9Y4H2	577	S	Insulin receptor subst	IRS2	74.611	_TYS(ph)LTTPAR_
Q9Y4H2	915	S	Insulin receptor subst	IRS2	109.5	_S(ph)PGEYINIDFGEF
Q9Y4H2	1176	S	Insulin receptor subst	IRS2	73.498	_HNSAS(ph)VENVSLR
Q9Y4H2	1203	S	Insulin receptor subst	IRS2	144.35	_SSEGGVGVGPGGGI
Q9Y4I1	600	S	Unconventional myos	MYO5A	55.097	_AIS(ph)PTSATSSGR_
Q9Y4I1	1652	S	Unconventional myos	MYO5A	131.98	_TSS(ph)IADEGTYTLI
Q9Y4W2	560	S	Ribosomal biogenesis	LAS1L	159.66	_AQQQEEQGS(ph)VN
Q9Y4W2	617	S	Ribosomal biogenesis	LAS1L	167.98	_MEVGPFSTGQES(ph
Q9Y519	402	S	Transmembrane prot	TMEM184B	48.944	_TLLLS(ph)S(ph)DDEF
Q9Y519	403	S	Transmembrane prot	TMEM184B	48.944	_TLLLS(ph)S(ph)DDEF
Q9Y520	878	S	Protein PRRC2C	PRRC2C	91.151	_S(ph)VEDVRPHHTDA
Q9Y520	924	S	Protein PRRC2C	PRRC2C	183.06	_S(ph)VSHGSNHTQKP
Q9Y520	1248	S	Protein PRRC2C	PRRC2C	110.38	_SES(ph)S(ph)DFEVVI
Q9Y520	1249	S	Protein PRRC2C	PRRC2C	81.448	_SES(ph)S(ph)DFEVVI
Q9Y520	2105	S	Protein PRRC2C	PRRC2C	171.2	_LPDLS(ph)PVENK_
Q9Y520	2673	T	Protein PRRC2C	PRRC2C	89.663	_AFGSGIDIKPGT(ph)F
Q9Y5B0	740	S	RNA polymerase II su	CTDP1	41.824	_ENS(ph)PAAFPDR_
Q9Y5B0	869	S	RNA polymerase II su	CTDP1	97.744	_EDLESMDKEVDDILG
Q9Y5B0	872	S	RNA polymerase II su	CTDP1	97.744	_EDLESMDKEVDDILG
Q9Y5B6	557	S	PAX3- and PAX7-bin	PAXBP1	115.74	_MADHLEGLS(ph)S(ph
Q9Y5B6	558	S	PAX3- and PAX7-bin	PAXBP1	115.74	_MADHLEGLS(ph)S(ph
Q9Y5J1	121	S	U3 small nucleolar RN	UTP18	236.94	_VQEHEDS(ph)GDS(p
Q9Y5J1	124	S	U3 small nucleolar RN	UTP18	292.09	_VQEHEDS(ph)GDS(p
Q9Y5J1	205	S	U3 small nucleolar RN	UTP18	337.94	_KTS(ph)S(ph)DDES(p
Q9Y5J1	206	S	U3 small nucleolar RN	UTP18	298.55	_KTS(ph)S(ph)DDES(p
Q9Y5J1	210	S	U3 small nucleolar RN	UTP18	298.55	_TSS(ph)DDES(ph)EEI
Q9Y5Q9	43	S	General transcription	GTF3C3	173.25	_GKLS(ph)AEENPDDS
Q9Y5S2	1690	S	Serine/threonine-prot	CDC42BPB	112.34	_HSTPSNSSNPSGPPS
Q9Y5S9	56	S	RNA-binding protein 8	RBM8A	178.2	_MREDYDS(ph)VEQD(
Q9Y606	426	T	tRNA pseudouridine s	PUS1	90.099	_VPSPLEGSEGDGDT(
Q9Y608	328	S	Leucine-rich repeat fli	LRRFIP2	224.53	_RGS(ph)GDTSSLIDPI
Q9Y613	523	S	FH1/FH2 domain-con	FHOD1	44.511	_EPLIPAS(ph)PK_
Q9Y618	149	S	Nuclear receptor core	NCOR2	99.319	_LEPVS(ph)PPS(ph)PI
Q9Y618	152	S	Nuclear receptor core	NCOR2	99.319	_LEPVS(ph)PPS(ph)PI

Q9Y618	939	S	Nuclear receptor core	NCOR2	80.382	_LLS(ph)PRPSLLTPTG
Q9Y618	956	S	Nuclear receptor core	NCOR2	135.08	_ANAS(ph)PQKPLDLK
Q9Y618	1487	S	Nuclear receptor core	NCOR2	57.149	_SLIGS(ph)PGR_
Q9Y618	1786	S	Nuclear receptor core	NCOR2	118.15	_HSSSPLS(ph)PGGPT
Q9Y618	1869	S	Nuclear receptor core	NCOR2	57.798	_PASHSHAHQHS(ph)P
Q9Y618	1872	S	Nuclear receptor core	NCOR2	84.249	_PASHSHAHQHSPIS(p
Q9Y618	2016	S	Nuclear receptor core	NCOR2	83.871	_NLAPHHAS(ph)PDPP
Q9Y618	2057	S	Nuclear receptor core	NCOR2	114.2	_SLGYHGSSYS(ph)PE
Q9Y618	2065	S	Nuclear receptor core	NCOR2	120.69	_SLGYHGSSYSPEGVP
Q9Y618	2068	S	Nuclear receptor core	NCOR2	95.319	_SLGYHGSSYSPEGVP
Q9Y618	2214	S	Nuclear receptor core	NCOR2	85.177	_GSPHSEGGKRS(ph)P
Q9Y618	2234	S	Nuclear receptor core	NCOR2	140.36	_TSVLGGGEDGIEPVS
Q9Y618	2269	S	Nuclear receptor core	NCOR2	189.77	_S(ph)PGNTSQPPAFF
Q9Y618	2424	S	Nuclear receptor core	NCOR2	107.19	_S(ph)PAPGLASGDRP
Q9Y666	30	T	Solute carrier family 1	SLC12A7	80.355	_TEAPGT(ph)PEGPEP
Q9Y6D5	218	S	Brefeldin A-inhibited g	ARFGEF2	88.814	_ELEKPIQSKPQS(ph)P
Q9Y6D5	227	S	Brefeldin A-inhibited g	ARFGEF2	95.988	_PQSPVIQAAAVS(ph)P
Q9Y6D5	277	S	Brefeldin A-inhibited g	ARFGEF2	103.9	_GSS(ph)LSGTDDGAG
Q9Y6G9	207	S	Cytoplasmic dynein 1	DYNC1LI1	192.58	_DFQEYVEPGEDFPAS
Q9Y6G9	421	S	Cytoplasmic dynein 1	DYNC1LI1	50.752	_SVSSNVASVS(ph)PP
Q9Y6G9	510	S	Cytoplasmic dynein 1	DYNC1LI1	90.475	_KPVTVS(ph)PTTPTSP
Q9Y6G9	516	S	Cytoplasmic dynein 1	DYNC1LI1	138.04	_KPVTVSPTTPTS(ph)P
Q9Y6I3	435	S	Epsin-1	EPN1	115.12	_S(ph)PGAFDMSGVR_
Q9Y6I3	454	S	Epsin-1	EPN1	78.978	_GSLAEAVGS(ph)PPP
Q9Y6I3	470	T	Epsin-1	EPN1	94.295	_T(ph)PESFLGPNAAL
Q9Y6M7	84	S	Sodium bicarbonate c	SLC4A7	222.24	_ESDKEDGRES(ph)PS
Q9Y6M7	242	S	Sodium bicarbonate c	SLC4A7	64.224	_KHS(ph)DPHLLER_
Q9Y6Q9	214	S	Nuclear receptor coa	NCOA3	81.788	_TPHDILEDINAS(ph)P
Q9Y6R0	263	S	Numb-like protein	NUMBL	68.58	_KAEAAAAPTVAPGPA
Q9Y6X9	615	S	MORC family CW-typ	MORC2	91.549	_S(ph)PPLPAVIR_
Q9Y6X9	743	S	MORC family CW-typ	MORC2	64.377	_SVAVS(ph)DEEEVEE

Mass error [ppm]	Intensity L	Intensity H	Ratio L/H
0.14468	363470000	267300000	1.201
0.14468	147070000	90390000	1.401
0.83035	340820000	298620000	0.956
0.94653	1143000000	946040000	0.786
1.6217	738120000	571510000	1.019
1.6217	1250600000	1031200000	0.978
0.59595	88269000	74300000	0.888
-0.21481	76163000	22055000	6.398
1.4771	673780000	221600000	2.066
1.4771	673780000	221600000	2.066
-0.51466	14643000	4432000	1.87
0.18394	67428000	19345000	4.372
-0.87437	823380000	545810000	2.077
-0.75733	802430000	550500000	1.365
1.7997	160590000	62308000	2.025
0.0076582	138020000	54058000	2.188
-0.48531	22752000	6312000	2.88
0.19105	29084000	16438000	1.441
1.2952	46886000	576650000	0.263
1.2952	57703000	590270000	0.475
0.40829	192570000	135400000	1.205
-0.03703	55063000	97776000	0.69
-0.61524	21269000	17478000	1.144
1.1373	180430000	102060000	1.904
-2.1981	14251000	4252600	2.644
0.3859	102410000	102820000	0.814
-0.40877	22914000	12603000	2.24
-0.19713	1822500000	2183700000	0.724
1.6014	151680000	163840000	0.774
-0.045677	2365700000	1988500000	0.988
-0.24535	8530900000	6168200000	0.98
-1.1829	195240000	64584000	1.769
-1.1829	195240000	64584000	1.769
0.85985	13411000	7697000	2.913
0.26562	64839000	75163000	1.152
-1.9089	8219400	8084600	1.568
-1.1738	33025000	26422000	1.186
-1.7777	15170000	33526000	0.309
0.12473	330170000	170420000	1.695
-0.037415	48466000	30330000	1.4
1.1549	1911800000	2033200000	0.824
1.2169	961190000	673740000	0.87
1.2169	521500000	393390000	0.717
1.2169	1122200000	833210000	0.971
-0.10716	1062800000	893940000	0.785
-1.2314	76149000	61764000	1.472
-0.11647	4155100000	3882300000	0.907
-0.11647	5914500000	4931200000	1.004
1.1054	890830000	398730000	0.922
1.1054	1957800000	1068300000	1.33
0.69304	41040000	23347000	1.495
1.674	55609000	12755000	2.65

-0.52769	24826000	10130000	3.824
-0.31799	540140000	334530000	1.279
0.9138	42772000	54668000	0.692
-0.52916	319280000	225190000	1.125
2.1971	128170000	86396000	1.333
-0.43495	117170000	90196000	0.89
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0.33217	1640700	5887400	0.328
0.8329	70109000	56505000	0.926
0.8329	70109000	56505000	0.926
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-0.69309	118020000	38166000	3.99
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-0.21958	1064400000	397470000	2.218
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0.94397	371540000	125560000	2.67
0.94397	19661000	12218000	1.707
0.72652	7740900	34917000	0.167
3.006	34964000	17060000	2.012
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0.25367	16523000	21345000	0.653
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-1.1012	16680000	10373000	1.346
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-0.18655	20165000	11332000	0.887
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0.20531	31319000	16333000	1.887
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1.7233	5635700	2798500	1.033
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-0.42373	12293000	12065000	0.664

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-0.99988	50312000	40325000	2.059
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-0.30777	191060000	127600000	0.824
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-0.24454	34869000	15033000	2.235
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-0.88949	16623000	14679000	1.046
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2.9889	92332000	87514000	0.509
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-1.4827	221540000	249490000	1.188
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0.39508	26727000	24409000	0.714
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0.34119	27952000	12376000	2.495
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1.2068	70193000	15821000	3.108
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0.34853	36403000	45991000	0.73
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0.23072	18646000	17623000	0.831
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0.039453	13437000	8245400	1.017
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0.068386	0	0	
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0.82276	58245000	7305200	4.352
0.82276	58245000	7305200	4.621
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0.43497	0	0	
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-0.95595	68555000	61016000	1.103
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0.71906	126790000	127970000	0.968
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1.0075	473020000	59186000	4.997
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0.19157	101090000	21179000	4.072
0.19157	101090000	21179000	4.072
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-0.28238	622010000	416350000	0.963
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-0.57273	44208000	54295000	0.72
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-2.2594	80786000	146320000	0.577
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0.18237	620840000	853340000	0.339
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0.10059	349960000	171180000	1.787
0.10059	349960000	171180000	1.787
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0.39862	122440000	48671000	1.376
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-0.17547	114550000	14817000	6.327
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0.21425	138820000	54647000	1.943
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-0.43207	362100000	205950000	1.727
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1.5	29152000	18754000	1.724
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1.125	84876000	164140000	0.437
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0.63235	46576000	42517000	1.218
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-1.549	153870000	86563000	1.908
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3.6334	12883000	6269200	1.825
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0.58221	48654000	10805000	2.428
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0.55686	2610200000	1387300000	1.374
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0.23654	877070000	582750000	0.679
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0.58662	157430000	76826000	1.331
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-0.95302	9735800	2477300	5.26
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2.3304	31049000	6105200	2.256
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1.0791	576150000	342900000	1.442
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1.2632	242440000	186710000	1.152
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1.271	23083000	17593000	1.151
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0.42972	58684000	50477000	0.838
0.42972	58684000	50477000	0.838
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-1.7593	11577000	7966600	1.631
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1.0383	1001100000	675970000	1.287
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-1.5573	92358000	40743000	1.638
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0.13119	16978000	4826100	3.565
0.13119	16978000	4826100	3.565
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0.041953	152450000	139940000	0.803
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-0.80188	109440000	126790000	0.885
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0.32542	7048500	3849800	1.779
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0.26215	14851000	15235000	1.015
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0.41256	10045000	397970	10.526
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0.10762	71270000	33651000	1.502
0.10762	71270000	33651000	1.502
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0.33025	88362000	116560000	0.602
0.33025	88362000	116560000	0.602
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-0.11264	20651000	10574000	1.349
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-0.27379	582300000	163240000	3.501
-0.27379	582300000	163240000	3.501
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-1.6819	24908000	15342000	1.05
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1.6635	474670000	325640000	1.305
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0.56424	10832000	2861200	2.767
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-0.55496	198920000	146680000	1.124
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0.080319	16597000	14258000	1.003
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-1.4878	25852000	15518000	0.729
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-0.17889	1250000000	873140000	1.122
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0.88718	18554000	11870000	0.849
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1.1659	136420000	123070000	0.393
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0.7304	610080000	353070000	1.633
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-2.2584	11489000	81035000	0.104
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-0.56722	142770000	39181000	4.007
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2.0933	6132400	8194600	0.78
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-2.3818	11384000	5420300	1.65
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-1.4344	27430000	33059000	0.866
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-0.021067	62113000	8070400	3.436
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0.21184	116930000	187190000	0.731
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-1.2902	36843000	19801000	2.133
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0.57991	178980000	83211000	2.747
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-0.0030591	42368000	19825000	1.61
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0.026742	1251100000	1125800000	1.125
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-0.54648	23325000	18597000	1.626
-0.54648	23325000	18597000	1.626

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-0.67192	10884000	7289900	1.995
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-0.46186	27989000	28174000	0.842
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-4.1436	22474000	17263000	1.107
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-0.8264	163900000	79905000	1.957
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-1.4861	26739000	17587000	1.423
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-0.13009	286020000	219450000	1.023
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0.87053	12000000	8859400	1.169
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-0.094756	23740000	8133900	3.573
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-0.22605	57521000	24803000	1.785
-0.22605	57521000	24803000	1.785
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-0.56049	24605000	16480000	0.969
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-0.078387	6882700	3281800	2.877
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-0.79547	99659000	43768000	1.722
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1.0604	631300000	637190000	0.595
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0.82186	3412400000	2140600000	0.989
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1.3395	66210000	22478000	1.735
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-1.5585	410110000	488010000	0.429
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-0.049302	128730000	60724000	1.876
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0.05845	706680000	187960000	1.329

-3.206	0	0	
-0.98674	59105000	25225000	3.999
1.444	54800000	113250000	0.501
0.83244	297430000	151170000	1.524
0.41094	249010000	118240000	1.514
0.50899	30256000	10386000	2.358
-1.3907	73971000	46390000	0.943
-1.211	21443000	19961000	0.79
-0.81704	102220000	91184000	1.245
-0.81704	102220000	91184000	1.245
-0.046662	64186000	45069000	1.355
-0.50823	14105000	8638500	0.772
-0.8735	12837000	6848300	1.244
-4.0616	23740000	19479000	1.047
-0.010301	48611000	41907000	1.651
-0.54748	17148000	14976000	1.795
1.3082	20887000	12194000	2.164
-0.69842	26378000	54487000	0.301
-1.2816	13247000	24270000	0.368
-1.2816	168670000	142830000	1.923
0.6313	39063000	101720000	0.286
-1.6847	45127000	110060000	0.309
2.4013	9821900	30052000	0.233
0.039651	33654000	84438000	0.323
0.16482	147290000	23854000	2.412
0.62962	74971000	46053000	1.187
-0.6247	249290000	180170000	1.041
0.77706	6153500	15959000	0.937
-0.98944	0	0	
-0.98944	0	0	
-1.1638	138040000	62798000	1.455
-0.029669	68613000	22092000	2.943
-0.67938	92435000	33961000	2.224
-0.95898	10289000	5645000	1.968
3.4786	53670000	17284000	3.06
2.2736	95779000	14714000	5.658
-0.56903	10168000	13503000	1.096
-0.25489	66219000	54317000	1.252
1.9728	66219000	54317000	1.252
-0.34775	489450000	438780000	0.968
-0.34775	489450000	438780000	0.968
-0.023877	1346800000	1058400000	0.6
-0.023877	1732800000	1453700000	0.686
0.42918	488370000	251670000	0.732
0.42918	474060000	265900000	1.403
-0.58478	604070000	380160000	1.382
0.17342	118770000	68243000	1.451
-0.74804	25447000	26951000	0.92
-0.4072	152070000	197470000	0.656
-1.3765	0	0	
0.060808	599120000	536230000	0.701
0.42785	11038000	10993000	1.152
0.95759	393850000	227320000	1.463
0.95759	393850000	227320000	1.463

0.081247	10831000	5473000	2.275
0.023635	475760000	95389000	5.578
0.61534	50820000	41556000	1.542
0.22222	45371000	27910000	1.246
0.39549	6749900	3394100	1.938
-0.62518	22085000	12347000	1.661
-0.26646	339780000	165630000	1.67
2.2251	160350000	49104000	1.911
0.054872	515390000	236590000	1.905
0.03823	84804000	44867000	2.007
1.0236	38356000	18956000	1.472
0.53949	452490000	197610000	1.619
1.2081	564880000	541220000	1.366
-0.67772	430550000	157430000	1.58
0.26562	95162000	86762000	0.929
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0.37477	187150000	195910000	0.838
1.1916	55017000	97925000	0.69
-0.06722	208540000	176530000	1.159
2.1048	13185000	5747300	1.471
-0.21546	51396000	47602000	1.31
0.60572	79868000	82511000	0.965
-0.22435	26031000	18841000	1.152
1.8231	33952000	8201300	2.752
-1.9923	20806000	20034000	1.45
-0.34931	692380000	341230000	1.915
-0.048904	52638000	59752000	0.73
0.36042	14081000	12067000	1.421
0.0014752	48853000	26786000	2.202
-0.26019	343750000	188760000	1.442
-0.86661	13259000	14670000	0.999