Peak Area %CV	abundan		compared to	the			
.5 25 42 71	timepoint PSM	with the minimum					
5 >100 >10	_	_		RajiB E E E			Commen
Protein Name 14-3-3 epsilon		Phosphosites S210	9 2 2	ā 5 5	Ascor 13.4	MOWSE 57.0	Sequence K.AAFDDAIAELDTLS*EESYK.D
14-3-3 epsilon	YWHAE	T208		<u></u>	9.1	53.4	K.AAFDDAIAELDT*LSEESYK.D
14-3-3 Eta		<b>S</b> 46			37.7	36.8	R.NLLS*VAYK.N
14-3-3 theta	YWHAQ	S230			16.9	27.8	R.DNLTLWTS*DSAGEECDAAEGAEN
14-3-3 theta		S232			15.3	38.5	R.DNLTLWTSDS*AGEECDAAEGAEN
14-3-3 zeta		S207			24.1	93.9	K.TAFDEAIAELDTLS*EESYK.D
14-3-3 zeta		T205			10.2	43.5	K.TAFDEAIAELDT*LSEESYK.D
3 Phosphoinositide dependent protein kinase 1		S241			57.2	129.2	R.ANS*FVGTAQYVSPELLTEK.S
3 Phosphoinositide dependent protein kinase 1 5 azacytidine induced 1		T245		-	9.2	38.2	R.ANSFVGT*AQYVSPELLTEK.S
5 azacytidine induced 1		S89			10.1	59.8	R.SGS*PRPTEPTDFLMLFEGSPSGK.K  R.S*GSPRPTEPTDFLMLFEGS*PSGK.K
	CEP131	\$87\$105 \$89\$105			11.3	35.9	R.SGS*PRPTEPTDFLMLFEGS*PSGKK.R
5 azacytidine induced 1		T96S105			9.8	15.7	R.SGSPRPTEPT'DFLMLFEGS'PSGKK.R
5 azacytidine induced 1		T93	-		9.8	37.1	R.SGSPRPT*EPTDFLMLFEGSPSGK.K
5 azacytidine induced 1		T96S107			9.6	21.5	R.SGSPRPTEPT*DFLMLFEGSPS*GKK.R
5`-3` exoribonuclease 2	XRN2	S448			46.9	26.4	R.NS*PGSQVASNPR.Q
5`-3` exoribonuclease 2	XRN2	S499S501		• •	100.0	105.2	R.KAEDS*DS*EPEPEDNVR.L
5`-3` exoribonuclease 2	XRN2	T478			15.2	59.4	R.MQNNSSPSISPNT*SFTSDGSPSPLGGIK.R
5`-3` exoribonuclease 2	XRN2	<b>S</b> 473			8.4	133.5	R.MQNNSSPS*ISPNTSFTSDGSPSPLGGIK.R
5`-3` exoribonuclease 2	XRN2	<b>S</b> 482			-0.2	19.5	R.MQNNSSPSISPNTSFTS*DGSPSPLGGIK.R
5`-3` exoribonuclease 2	XRN2	<b>S471</b>			2.3	86.7	R.MQNNSS*PSISPNTSFTSDGSPSPLGGIK.R
5`-3` exoribonuclease 2	XRN2	<b>S</b> 475		•	6.0	63.6	R.MQNNSSPSIS*PNTSFTSDGSPSPLGGIK.R
5`-3` exoribonuclease 2		S471S473			12.3	79.6	R.MQNNSS*PS*ISPNTSFTSDGSPSPLGGIK.R
5`-3` exoribonuclease 2	XRN2	S475T478		·	3.2	79.5	R.MQNNSSPSIS*PNT*SFTSDGSPSPLGGIK.R
5'-3' exoribonuclease 2		\$473\$475		÷		11.4	R.MQNNSSPS*IS*PNTSFTSDGSPSPLGGIK.R
5'-3' exoribonuclease 2		\$471\$475			2.4	90.4	R.MQNNSS*PSIS*PNTSFTSDGSPSPLGGIK.R
5'-3' exoribonuclease 2		\$470\$471			11.3	38.1	R.MQNNS*S*PSISPNTSFTSDGSPSPLGGIK.R
5'-3' exoribonuclease 2		T478S479	<u> </u>		13.6	11.8	R.MQNNSSPSISPNT*S*FTSDGSPSPLGGIK.R
5'-3' exoribonuclease 2		S470	=		7.4	25.7	R.MQNNS*SPSISPNTSFTSDGSPSPLGGIK.R  R.MQNNSS*PSISPNT*SFTSDGSPSPLGGIK.R
5', 3'-Nucleotidase, cytosolic		\$471T478 \$182	_		51.2	73.1 58.2	RII S'WSDNWR F
6-phosphofructo-2 kinase/fructose-2,6-		S466			51.2	50.9	R.RNS*FTPLSSSNTIR.R
biphosphatase 2 6-phosphofructo-2 kinase/fructose-2,6-	PFKFB2	Y482	•••		9.0	14.5	R.NY*SVGSRPLKPLSPLR.A
6-phosphofructo-2 kinase/fructose-2,6-	PFKFB2	S483			24.1	33.3	R.NYS*VGSRPLKPLSPLR.A
6-phosphofructo-2 kinase/fructose-2,6- biphosphatase 2	PFKFB2	\$486\$493			37.9	18.0	R.NYSVGS*RPLKPLS*PLR.A
6-phosphofructo-2 kinase/fructose-2,6- biphosphatase 2	PFKFB2	S483S493			13.0	21.2	R.NYS*VGSRPLKPLS*PLR.A
6-phosphofructo-2 kinase/fructose-2,6- biphosphatase 2	PFKFB2	S486			16.1	33.2	R.NYSVGS*RPLKPLSPLR.A
6-phosphofructo-2 kinase/fructose-2,6- biphosphatase 2	PFKFB2	Y482S493			8.3	14.2	R.NY*SVGSRPLKPLS*PLR.A
60S ribosomal protein L22-like 1	RPL22L1	S117			12.1	40.6	R.YFQISQDEDES*ESED
7-dehydrocholesterol reductase	DHCR7	S14	ij.		46.8	13.8	K.S*LDGVTNDR.T
A kinase anchor protein 11	AKAP11	S1337S1340			10.6	23.5	K.YPS*CES*VTDEYAGHLIQILK.Q
A kinase anchor protein 11		Y1335S1340			23.9	58.3	K.Y*PSCES*VTDEYAGHLIQILK.Q
A kinase anchor protein 11		S1242			-0.5	22.1	R.SVS*PTFLNPSDENLK.T
A kinase anchor protein 2		S383	•		17.8	82.0	R.DALGDSLQVPVS*PSSTTSSR.C
A kinase anchor protein 2		S951			33.6	63.1	R.TLS*MIEEEIR.A
A kinase anchor protein 2  A kinase anchor protein 2		S979	-		39.3	31.6	R.QVLQSTQS*PR.T
A kinase anchor protein 2  A kinase anchor protein 2		T949			10.6	60.7	R.T*LSMIEEEIR.A  R.DALGDSLQVPVSPS*STTSSR.C
A kinase anchor protein 2  A kinase anchor protein 2		S385 T1012	ببعد		7.8	47.0	K.VKPPPSPTT*EGPSLQPDLAPEEAAGTQRPK.N
A kinase anchor protein 2		\$1012 \$1016			1.6	12.1	K.VKPPPSPTTEGPS*LQPDLAPEEAAGTQRPK.N
A kinase anchor protein 2		S862	-		13.4	12.9	R.DGAEQQGPEATVEEAEAAAFGSEKPQSMFEPPQVSS*PVQEK.R
A kinase anchor protein 2		T837				16.3	R.DGAEQQGPEAT*VEEAEAAAFGSEKPQSMFEPPQVSSPVQEK.R
A kinase anchoring protein 13		S2732			19.8	56.2	K.SGSLDSELSVS*PK.R
A kinase anchoring protein 13	AKAP13	S1880	·	• •	104.4	85.5	R.S*AVLLVDETATTPIFANR.R
A kinase anchoring protein 13	AKAP13	S1931S1936	• •		14.4	22.5	K.FLS*HSTDS*LNK.I
A kinase anchoring protein 13	AKAP13	<b>S</b> 1559		•	9.9	16.7	R.SLS'PFRR.H
A kinase anchoring protein 13	AKAP13	<b>S</b> 1910			5.1	28.6	K.SVS*IQNITGVGNDENMSNTWK.F
A kinase anchoring protein 13	AKAP13	S1931S1933			14.7	17.6	K.FLS*HS*TDSLNK.I
A kinase PRKA anchor protein 8 like	AKAP8L	\$297\$300\$302			1.7	68.6	R.TDCS'DNS'DS'DNDEGTEGEATEGLEGTEAVEK.G
A kinase PRKA anchor protein 8 like	AKAP8L	S297S302T308			2.4	40.3	R.TDCS*DNSDS*DNDEGT*EGEATEGLEGTEAVEK.G
A_Raf	ARAF	<b>S</b> 299	•		9.8	27.1	R.DS*GYYWEVPPSEVQLLK.R
A_Raf	ARAF	T213		•	-0.3	41.3	R.ST*STPNVHMVSTTAPMDSNLIQLTGQSFSTDAAGSR.G

Peak Area	%CV V	Vhite do	ts-Significant cha	nge in pepti	de the			
-5 -3 0	29 ti 42 F	imepoint PSM	with the minimum	peak area f	or a given			
5 >10	>100	_		CarT E E E	RajiB E E E			Common
	Protein Name G A_Raf AF		Phosphosites S212	9 2 4	2 4 2	Ascor 11.5	MOWSE 39.9	Sequence R.S'TSTPNVHMVSTTAPMDSNLIQLTGQSFSTDAAGSR.G
	ABL interactor 1 AB	BI1	S231	Ţ.		11.4	24.0	R.TAS*LNQRPR.T
	sent in melanoma 1 <sub>Cl</sub>		T20	Ţ.		-0.1	44.5	K.ST*DSPGADAELPESAAR.D
	carboxylase alpha A(		S117			22.5	62.3	R.SSMS*GLHLVK.Q
	carboxylase alpha A(		S62		•	10.9	61.9	R.FIIGSVS*EDNSEDEISNLVK.L
	carboxylase alpha A(		\$60\$66 \$62\$66	•••		46.7	105.3	R.FIIGS'VSEDNS'EDEISNLVK.L  R.FIIGSVS'EDNS'EDEISNLVK.L
	carboxylase alpha A		S60S62			41.9	115.7	R.FIIGS*VS*EDNSEDEISNLVK.L
	carboxylase alpha A(		T1249S1253		=	6.5	11.6	R.MSFSSNLNHYGMT*HVAS*VSDVLLDNSFTPPCQR.M
Acetyl-CoA	carboxylase alpha A(	CACA	S87S90			3.1	38.3	K.EGSLS*PAS*VGSDTLSDLGISSLQDGLALHIR.S
Acetyl-CoA	carboxylase alpha A	CACA	S85S87S90	• • •		1.2	43.1	K.EGS*LS*PAS*VGSDTLSDLGISSLQDGLALHIR.S
Acetyl-CoA	carboxylase alpha A(	CACA	S85S87S93		<u> </u>	5.4	32.8	K.EGS*LS*PASVGS*DTLSDLGISSLQDGLALHIR.S
Acetyl-CoA	carboxylase alpha A(	CACA	S1296			7.4	11.5	R.IFDEVMGCFSDS*PPQSPTFPEAGHTSLYDEDKVPR.D
	carboxylase alpha A(		S1296T1302			22.2	70.5	R.IFDEVMGCFSDS*PPQSPT*FPEAGHTSLYDEDKVPR.D
	carboxylase alpha A(		S1296S1300	-		26.0	52.8	R.IFDEVMGCFSDS*PPQS*PTFPEAGHTSLYDEDKVPR.D
	carboxylase alpha A		S1294S1296	<b></b>			46.6	R.IFDEVMGCFS*DS*PPQSPTFPEAGHTSLYDEDKVPR.D
	carboxylase alpha A(		S85S87			7.3	43.4	K.EGS*LS*PASVGSDTLSDLGISSLQDGLALHIR.S  K.EGS*LSPAS*VGSDTLSDLGISSLQDGLALHIR.S
	carboxylase alpha A(		\$85\$90			12.2	63.9	K.EGS*LSPAS*VGSDTLSDLGISSLQDGLALHIR.S  K.EGS*LS*PAS*VGSDT*LSDLGISSLQDGLALHIR.S
	carboxylase alpha A		\$85\$87\$90T95 \$87\$90\$93\$97			5.0	57.3	K.EGS.LS*PAS*VGSDI*LSDLGISSLQDGLALHIR.S  K.EGSLS*PAS*VGS*DTLS*DLGISSLQDGLALHIR.S
	carboxylase alpha A		S66		-	9.1	74.6	R.FIIGSVSEDNS*EDEISNLVK.L
	carboxylase alpha A(		S60			5.5	69.1	R.FIIGS*VSEDNSEDEISNLVK.L
Acetyl-CoA	carboxylase alpha A(	CACA	S1253S1255			2.2	24.5	R.MSFSSNLNHYGMTHVAS*VS*DVLLDNSFTPPCQR.M
Acetyl-CoA	carboxylase alpha A(	CACA	S1238T1249		•	2.5	24.2	R.MS*FSSNLNHYGMT*HVASVSDVLLDNSFTPPCQR.M
Acetyl-CoA	carboxylase alpha A(	CACA	Y1246S1255	i i		10.0	58.8	R.MSFSSNLNHY*GMTHVASVS*DVLLDNSFTPPCQR.M
	carboxylase alpha A(		Y1246T1249		•	3.3	12.8	R.MSFSSNLNHY'GMT'HVASVSDVLLDNSFTPPCQR.M
	carboxylase alpha A(		S1238S1240	<b>H</b>		2.2	23.7	R.MS*FS*SNLNHYGMTHVASVSDVLLDNSFTPPCQR.M
	carboxylase alpha A(		S1300T1302			27.8	17.3	R.IFDEVMGCFSDSPPQS*PT*FPEAGHTSLYDEDKVPR.D
Acetyl-CoA	carboxylase alpha A(		S1294T1302			11.9	38.0	R.IFDEVMGCFS*DSPPQSPT*FPEAGHTSLYDEDK.V
Acetyl-CoA	carboxylase alpha A(	CACA	\$1294\$1300 \$85T95			6.4	20.2	K.EGS*LSPASVGSDT*LSDLGISSLQDGLALHIR.S
	carboxylase alpha A(		S87S90S93		=	5.8	36.6	K.EGSLS*PAS*VGS*DTLSDLGISSLQDGLALHIR.S
Acetyl-CoA	carboxylase alpha A(	CACA	\$85\$87\$93T95			17.0	71.4	K.EGS'LS'PASVGS'DT'LSDLGISSLQDGLALHIR.S
Acetylserotonin met	hyltransferase-like A	SMTL	S239			66.0	120.0	K.HDSIPAADTFEDLS*DVEGGGSEPTQR.D
Acetylserotonin met	hyltransferase-like As	SMTL	T234			16.5	13.0	K.HDSIPAADT*FEDLSDVEGGGSEPTQR.D
	Acheron F	AM27E3	S247S248		<u> </u>	100.0	28.2	R.RIS'S'R.G
TRAF3-interact	ting JNK-activating TR modulator	RAF3IP3	S110			100.0	30.6	R.RIS*SPR.E
	ACINUS A		T563	•		18.4	41.9	R.RASHT*LLPSHR.L
	ACINUS A		S1004			71.2	36.0	R.TAQVPS'PPR.G
	ACINUS A		\$490			121.6	70.3	K.AES*PAEKVPEESVLPLVQK.S
	ACINUS A		T408			7.9	58.3	K.ASLVALPEQT'ASEEETPPPLLTK.E  K.ASLVALPEQT'ASEEET'PPPLLTK.E
	ACINUS A		T408T414 S386S388	<del></del>		32.4	27.7	K.SKS'PS'PPR.L
	ACINUS A		S729			100.0	29.5	R.LQPERGS*PK.K
	ACINUS A	CIN1	S605			35.1	25.1	R.SHS*PLR.S
	ACINUS A	CIN1	S898			61.4	57.3	R.IS*EDETER.N
	ACINUS A	CIN1	<b>S</b> 710			46.5	54.6	R.RLS*QPESAEK.H
	ACINUS A	CIN1	S655S657			60.8	48.6	K.S*LS*PGVSR.D
	ACINUS A		\$478\$482			26.4	48.8	R.ELLVSQHTVQLVGGLS*PLSS*PSDTK.A
	ACINUS A		S478S481			24.0	60.3	R.ELLVSQHTVQLVGGLS*PLS*SPSDTK.A
	ACINUS AC		S216			16.9	63.3	K.SSSISEEKGDS*DDEKPR.K
	ACINUS A		\$895 \$467T470\$479			44.6	24.2	K.SLIPDIKPLAGQEAVVDLHADDS'RISEDETER.N  R.
	ACINUS A		\$467T470\$478 \$1329\$1331T1			100.0	20.2	R.S*RS*T*PVRDR.G
	ACINUS A		S166S169			14.0	20.2	R.EAAELEEAS*AES*EDEM#HPEGVASLLPPDFQSSLERPELELSR.
	ACINUS A		S1331T1332			10.4	23.9	R.SRS*T*PVRDR.G
	ACINUS A	CIN1	S603			24.6	27.8	R.S'HSPLR.S
	ACINUS A	CIN1	S561	Ę.		25.8	32.8	R.RAS*HTLLPSHR.L
	ACINUS A	CIN1	S240S243	<b>—</b>		61.8	39.1	K.LS*EGS*QPAEEEEDQETPSR.N
	ACINUS A		S410			2.2	67.7	K.ASLVALPEQTAS*EEETPPPLLTK.E
	ACINUS A		S410T414		<u> </u>	3.8	22.7	K.ASLVALPEQTAS*EEET*PPPLLTK.E
	ACINUS A	CIN1	S1284		•	100.0	12.9	K.RREHS'R.E

Peak Area	%CV 0 29 42	abundanc	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
0 3 6	71 86 >100			CarT	RajiB			
>10 <mark></mark>	Protein Name ACINUS		Phosphosites \$365	9m 5m 5m	2 m m	Ascor 9.1	MOWSE 24.9	Sequence K.TTS*PLEEEER.E
	ACINUS ,	ACIN1	S657S661	Ţ		8.4	12.4	K.SLS*PGVS*R.D
	ACINUS		<b>S</b> 478			24.4	17.0	R.ELLVSQHTVQLVGGLS*PLSSPSDTK.A
Antin alab	ACINUS,		S210			11.9	42.3	K.SSSIS*EEKGDSDDEKPR.K
	ing LIM protein 1		Y242 \$452		<del></del> .	-0.3	93.2	R.SY*ELPDGQVITIGNER.F  R.STS*QGSINSPVYSR.H
	ling LIM protein 1,		\$452 \$655			13.8	76.7	K.TAS'LPGYGR.N
Actin bind	ling LIM protein 1	ABLIM1	S431			25.3	80.5	R.TLS*PTPSAEGYQDVR.D
Actin bind	ling LIM protein 1	ABLIM1	S185			98.4	40.1	R.S'PQHFHRPDQGINIYR.K
Actin bind	ling LIM protein 1	ABLIM1	<b>S</b> 352			9.8	53.6	R.TS*SESIYSRPGSSIPGSPGHTIYAK.V
Actin bino	ling LIM protein 1	ABLIM1	\$352\$367			16.1	35.1	R.TS*SESIYSRPGSSIPGS*PGHTIYAK.V
	ling LIM protein 1		\$367			38.4	24.9	R.TSSESIYSRPGSSIPGS*PGHTIYAK.V
	ling LIM protein 1,		\$353	<u> </u>		1.3	32.2	R.TSS*ESIYSRPGSSIPGSPGHTIYAK.V  R.TSS*ESIYSRPGSSIPGS*PGHTIYAK.V
	ssociated protein 1		\$353\$367 \$342\$343	=		13.8	21.9	K.KKPSTDEQTS*S*AEEDVPTCGYLNVLSNSR.W
	Actin gamma 1		\$232	•		28.2	12.3	K.LCYVALDFEQEMATAAS*SSSLEK.S
Actin-bundling pro	otein with BAIAP2	MTSS1L	S639T643			20:2	13.1	K.RLS*LPNT*AWGSPSPEAAGYPGAGAEDEQQQLAANRHSLVEK.L
Actin-bundling pro	homology otein with BAIAP2 homology	MTSS1L	\$639\$673	•		10.1	12.0	K.RLS'LPNTAWGSPSPEAAGYPGAGAEDEQQQLAANRHS'LVEK.L
	Actin-like 6A	ACTL6A	<b>S</b> 233			100.0	34.2	R.EGS*PANWK.R
Activating tran	scription factor 1	PKP4	<b>S</b> 63			13.9	19.2	R.RPS*YR.K
	scription factor 2		T69T71	•		16.4	37.6	R.NDSVIVADQT*PT*PTR.F
	BCR related Gene		T30S33			15.3	49.0	K.VLEDEDVFLLEECELGT*PTS*PGSGSPFLVAVK.V
	BCR related Gene		S33	•••		10.3	45.3	K.VLEDEDVFLLEECELGTPTS*PGSGSPFLVAVK.V
	nt neuroprotector		\$953\$955 \$1058			100.0	57.7	K.LMHNAS'DS'EVDQDDVVEWK.D  R.LS'NPQIEWQNSTIDSEDGEQFDNMTDGVAEPMHGSLAGVK.L
	nt neuroprotector		\$1058 \$1071			7.4	69.1	R.LSNPQIEWQNSTIDS*EDGEQFDNMTDGVAEPMHGSLAGVK.L
Activity depende	nt neuroprotector	ADNP	S1067			7.7	23.4	R.LSNPQIEWQNS*TIDSEDGEQFDNMTDGVAEPMHGSLAGVK.L
Activity depende	nt neuroprotector,	ADNP	T1068S1071			3.5	42.7	R.LSNPQIEWQNST*IDS*EDGEQFDNMTDGVAEPMHGSLAGVK.L
Activity depende	nt neuroprotector,	ADNP	S1058S1067				14.8	R.LS*NPQIEWQNS*TIDSEDGEQFDNMTDGVAEPMHGSLAGVK.L
Activity depende	nt neuroprotector,	ADNP	T1068			4.2	61.0	R.LSNPQIEWQNST*IDSEDGEQFDNMTDGVAEPMHGSLAGVK.L
	ADAM17	ADAM17	S791			58.9	35.5	K.S*FEDLTDHPVTR.S
		AP3D1	\$632\$634\$636			100.0	27.0	K.KVPVPEGLDLDAWINEPLS*DS*ES*EDERPR.A
	Adaptin, delta		\$758\$759				17.2	R.  UC*C*I DTECNENIADA/ON/DIA/TECMDENIAI DENENDA/DBN/DDVD A  K.FRTPS*FLKK.S
	Adducin 1 alpha		\$757 \$431			13.9	23.5 69.7	K.YSDVEVPASVTGYSFASDGDSGTCS*PLR.H
	Adducin 1 alpha	ADD1	S358			39.1	91.8	R.SPGS*PVGEGTGSPPK.W
	Adducin 1 alpha	ADD1	T364			18.1	15.5	R.SPGSPVGEGT*GSPPKWQIGEQEFEALMR.M
	Adducin 1 alpha	ADD1	\$358\$366	Ė		14.9	82.6	R.SPGS*PVGEGTGS*PPKWQIGEQEFEALMR.M
	Adducin 1 alpha	ADD1	<b>S</b> 465			17.0	48.3	R.GDEASEEGQNGSS*PK.S
	Adducin 1 alpha		\$423\$436			-0.2	21.7	K.YSDVEVPASVTGYSFAS*DGDSGTCSPLRHS*FQK.Q
	Adducin 1 alpha		\$355\$366			12.0	58.6	R.S'PGSPVGEGTGS'PPKWQIGEQEFEALMR.M
	Adducin 1 alpha		\$355\$358			17.2	48.3	R.S'PGS'PVGEGTGSPPKWQIGEQEFEALMR.M  R.S'PGSPVGEGT'GSPPKWQIGEQEFEALMR.M
	Adducin 1 alpha		\$355T364 \$512			11.8	14.2	K.S PGSPVGEGI GSPFAWQIGEQEFEALWK.W
	Adducin 1 alpha		\$700T702T706			6.5	14.5	К.
	Adducin 1 alpha		S436			2.0	16.6	K.YSDVEVPASVTGYSFASDGDSGTCSPLRHS*FQK.Q
	Adducin 1 alpha	ADD1	T511	ij		-6.1	23.6	K.EDGHRT*STSAVPNLFVPLNTNPK.E
	Adducin 1 alpha	ADD1	\$366			6.6	45.8	R.SPGSPVGEGTGS*PPKWQIGEQEFEALMR.M
	Adducin 1 alpha		T364S366			2.3	59.4	R.SPGSPVGEGT*GS*PPKWQIGEQEFEALMR.M
	Adducin 3		S673S677S681			19.2	21.3	K.IEEVLS*PEGS*PSKS*PSK.K
	Adducin 3		\$402\$423			30.4	56.8	R.HKS*DVEIPATVTAFSFEDDTVPLS*PLK.Y
	Adducin 3		\$423 \$677\$681			23.1	55.1	K.SDVEIPATVTAFSFEDDTVP <mark>LS*P</mark> LK.Y  K.IEEVLSPEGS*PSKS*PSK.K
	Adducin 3		\$677\$681 \$461			21.2	10.9	R.NGETS*PR.T
	Adducin 3		S42	=		100.0	21.1	R.NMS*PDLR.Q
	Adducin 3	ADD3	T460				13.7	R.NGET*SPR.T
	Adducin 3	ADD3	<b>S</b> 600			3.5	46.6	R.KQQGLEDAEQELLSDDASSVSQIQSQTQS*PQNVPEK.L
	Adducin 3	ADD3	S585				33.0	R.KQQGLEDAEQELLS*DDASSVSQIQSQTQSPQNVPEK.L
Adenosine deamin			S825			100.0	34.1	R.S*PEAQPK.T
Adenosine deamin			S614			37.8	75.0	K.S*PVTTLLECMHK.L
Adenosine monophosp  Adenylyl cyclase-a			S190		-	-0.3	32.1	K.TDS*DSDLQLYK.E  R.SGPKPFSAPKPQTS*PSPK.R
		UMP'I	\$308			16.4	54.9	N. GOF REFOREREY IO FORK.K

<-10 -5 29	abundano timepoint	ts-Significant char e at 5%FDR or with the minimum p	ompared to	the			
3 42 71 3 86	PSM		CarT	RajiB			
>10 >100 Protein Name		Phosphosites	8 # # 8	8 E E	Ascor	MOWSE	Sequence
Adenylyl cyclase-associated protein (		\$308\$310			17.7	22.0	R.SGPKPFSAPKPQTS*PS*PK.R  R.SGPKPFSAPKPQT*SPSPK.R
Adenylyl cyclase-associated protein (		T307 T307S310	==		10.4	32.7	R.SGPKPFSAPKPQT*SPS*PK.R
Adenylyl cyclase-associated protein (		S310	•••		2.4	12.7	R.SGPKPFSAPKPQTSPS*PK.R
ADP ribosylation factor GTPase activating protein 1	ARFGAP1	<b>S</b> 361			-0.4	53.1	R.SS*DSWEVWGSASTNR.N
ADP ribosylation factor GTPase activating protein 1	ARFGAP1	<b>S</b> 363			6.1	31.0	R.SSDS*WEVWGSASTNR.N
ADP ribosylation factor guanine nucleotide exchange factor 2	ARFGEF2	<b>S</b> 277		Ė	11.9	86.4	R.GSS*LSGTDDGAQEVVK.D
ADP ribosylation factor guanine nucleotide a exchange factor 2					20.0	46.3	K.HLDVDLDRQSLS*S*IDKNPSER.G
ADP ribosylation factor guanine nucleotide ; exchange factor 2					4.8	26.2	K.HLDVDLDRQSLS*S*IDKNPS*ER.G
ADP ribosylation factor guanine nucleotide exchange factor 2					7.2	69.0	R.RCSVTSMESTVSSGT*QT*TVQDDPEQFEVIK.Q
ADP ribosylation factor guanine nucleotide exchange factor 2  ADP ribosylation factor guanine nucleotide				•••	26.0	21.5	R.GS*SLSGTDDGAQEVVK.D  K.HLDVDLDRQS*LS*S*IDKNPSER.G
ADP ribosylation factor guanine nucleotide					1.9	68.9	R.RCS*VTS*MESTVSSGTQTTVQDDPEQFEVIK.Q
ADP ribosylation factor guanine nucleotide					5.1	15.7	R.RCSVTS*MESTVSSGTQT*TVQDDPEQFEVIK.Q
exchange factor 2  ADP ribosylation factor like 3 /	ARL3	<b>S</b> 5	•••		100.0	38.7	M.GLLS*ILR.K
ADP-ribosylation factor interacting protein (1)	ARFIP1	<b>S</b> 39			54.5	87.5	K.HSLPS*GLGLSETQITSHGFDNTK.E
ADP-ribosylation factor interacting protein (1)	ARFIP1	S44			13.6	49.8	K.HSLPSGLGLS*ETQITSHGFDNTK.E
ADP-ribosylation factor interacting protein (1) (arfaptin 1)		S100	<del>-</del>		20.7	28.0	R.KWS*LNTYK.C
ADP-ribosyltransferase like 1 p		S1335			55.8	55.5	R.AHS*PASLSFASYR.Q
AF10;	VILLT10	\$705	<b>#</b>		55.9	32.9	R.S'PVSSLQIR.Y
AF5Q31,		\$84 \$703\$706			28.4 42.5	48.7 26.1	K.ELLS*PLS*EPDDRYPLIVK.I
AF5Q31 /		S1062	• • •		9.8	65.5	K.LS*PGNSGNYSSGASSASASGSSVTIPQK.I
AF6 /	AFDN	S1067		•	30.2	75.3	R.TSS*VVTLEVAK.Q
AF6 /	AFDN	S1185			29.7	65.4	K.ITSVS*TGNLCTEEQTPPPRPEAYPIPTQTYTR.E
AF6,	AFDN	S1259		•••	100.0	41.6	R.S*QEELREDK.A
AF6 /	AFDN	S1183			8.0	41.7	K.ITS*VSTGNLCTEEQTPPPRPEAYPIPTQTYTR.E
AF6 /		S1185T1195			12.0	14.8	K.ITSVS*TGNLCTEEQT*PPPRPEAYPIPTQTYTR.E
Aftiphilin /		S411			7.3	70.8	R.KFTNFQSPNIDPTEENDLDDSLS*VK.N
Aftiphilin /		\$409		•••	48.1	81.0	R.KFTNFQSPNIDPTEENDLDDS*LSVK.N  K.RS*S*RHPR.R
AKAP95 /		\$2403\$2404 \$339			100.0	67.4	R.S*GDEEFKGEDELCDSGR.Q
AKAP95 /		S328			47.8	105.6	R.VDSEGDFS*ENDDAAGDFR.S
AKAP95 ,	AKAP8	\$323\$328			100.0	156.6	R.VDS*EGDFS*ENDDAAGDFR.S
AKT1 /	AKT1	S124	• • •		20.6	80.3	R.SGS*PSDNSGAEEMEVSLAKPK.H
AKT1 /	AKT1	S122S129		<b>i</b>	9.7	98.5	R.S*GSPSDNS*GAEEMEVSLAKPK.H
AKT1 /		S124S129	<b>.</b>		6.6	77.0	R.SGS*PSDNS*GAEEMEVSLAKPK.H
AKT1 /		S124S126S129		<b></b>	35.1	66.7	R.SGS*PS*DNS*GAEEMEVSLAKPK.H
AKT1 /		Y315	•		5.6	61.0	K.TFCGTPEY*LAPEVLEDNDYGR.A
AKT1,		Y474S477			9.7	68.2	R.RPHFPQFSY*SAS*GTA  R.RPHFPQFS*YSASGT*A
AKT1,		\$473T479 \$473Y474			10.1	25.2	R.RPHFPQFS*Y*SASGTA
AKT1,		S477T479			6.9	62.5	R.RPHFPQFSYSAS*GT*A
AKT1 /	AKT1	\$475T479			9.2	30.8	R.RPHFPQFSYS*ASGT*A
AKT1 ,	AKT1	Y474S475			-0.3	20.9	R.RPHFPQFSY*S*ASGTA
AKT1 /	AKT2	T308	Ħ.		5.4	64.2	K.T*FCGTPEYLAPEVLEDNDYGR.A
AKT1 substrate 1 /		T246		• •	19.1	33.9	R.LNT*SDFQK.L
AKT1 substrate 1		S88S92			25.4	23.6	R.AATAARPPAPPPAPQPRS*PTPS*PPRPTLAR.E
AKT1 substrate 1 ,		\$183			42.4	54.2	K.S*LPVSVPVWGFK.E  R.SS*DEENGPPSS*PDLDR.I
AKT1 substrate 1 /		\$203\$212 \$202\$203\$212			18.7	18.2	R.TEARS*S*DEENGPPSS*PDLDR.I
AKT1 substrate 1 /		\$88T97		•	12.9	10.8	R.AATAARPPAPPPAPQPRS*PTPSPPRPT*LAR.E
Aladin ,		<b>S</b> 495			100.0	26.7	R.FS*PVLGR.A
AlkB, alkylation repair homolog 5 /	ALKBH5	S64S69			28.0	18.6	K.YQEDS'DPERS'DYEEQQLQK.E
AlkB, alkylation repair homolog 5	ALKBH5	S361			44.4	71.5	R.RGS*FSSENYWR.K
AlkB, alkylation repair homolog 5 /		S64Y71	<b></b>		24.7	25.7	R.KYQEDS*DPERSDY*EEQQLQK.E
AlkB, alkylation repair homolog 5 /		S363	<b></b>		-0.2	36.9	R.RGSFS*SENYWR.K
Alpha, and gamma-adaptin-binding protein		Y60S69			7.4	11.1	R.KY*QEDSDPERS*DYEEQQLQK.E
Alpha- and gamma-adaptin-binding protein p34  Alpha-2-HS glycoprotein p		\$310\$311			100.0	57.1	R.DEIEGLS*S*DEEH  K.CDSSPDS*AEDVRK.V
Alpna-2-HS glycoprotein /		\$138 \$483\$492	البيد		37.0 55.7	70.3	R.RLS*LPGLLSQVS*PR.L
Alsin ,		S1464		•	-0.7	57.6	R.SES*PEPGYVVTSSGLLLPVLLPR.L
				-			

<-10 0	oundance at	ificant change 5%FDR comp	pared to the	he			
-5 25 UI -3 42 P 0 71 3	nepoint with th SM	minimum peal					
>100 >100 Protein Name G	ene Phos		E E	E E E	Ascor	MOWSE	Sequence
Alsin AL	0140	_			13.1	35.3	R.S*ESPEPGYVVTSSGLLLPVLLPR.L
Amida TF				<del>-</del>	20.6	48.1	R.SESPEPGY*VVTSSGLLLPVLLPR.L  K.LLPYPTLASPAS*D
Amida TF		252			31.0	44.2	KLLPYPTLAS'PAS'D
	PT T246	252			8.3	41.5	K.LLPYPT*LASPAS*D
Amida TF	PT <b>Y</b> 244	252	<del></del>		8.9	47.2	K.LLPY*PTLASPAS*D
Amida TF		246			5.7	26.0	K.LLPY*PT*LASPASD
AMP deaminase 3 AM		130		<u> </u>	9.8	12.4	K.GPPAAS*PAMSPTTPVVTGATSLPT*PAPYAMPEFQR.V
AMP deaminase 3 AM					1.2	44.8	K.GPPAAS*PAMSPTT*PVVTGATSLPTPAPYAMPEFQR.V  K.GPPAASPAMS*PT*TPVVTGATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM					4.1	40.6 31.5	K.GPPAASPAMS*PTTPVVT*GATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM					-1.7	26.0	K.GPPAASPAMS*PTTPVVTGATS*LPTPAPYAMPEFQR.V
AMP deaminase 3 AM	IPD3 <b>S</b> 112	118			4.9	40.7	K.GPPAAS*PAMSPT*TPVVTGATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM	IPD3 \$112	123			6.2	38.4	K.GPPAAS*PAMSPTTPVVT*GATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM		116		<b></b>	0.5	32.8	K.GPPAAS*PAMS*PTTPVVTGATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM				<u>=</u>	-1.7	36.2	K.GPPAASPAMSPTT*PVVTGATS*LPTPAPYAMPEFQR.V
AMP deaminase 3 AM  AMP deaminase 3 AM				Ξ	1.9	23.6	K.GPPAAS'PAM#SPTTPVVTGATS'LPTPAPYAMPEFQR.V  K.GPPAASPAMSPT*TPVVT*GATSLPTPAPYAMPEFQR.V
AMP deaminase 3 AM				-	12.2	25.9 38.2	K.GPPAASPAMS*PTT*PVVTGATSLPTPAPYAMPEFQR.V
Amphiphysin II BII		_			6.2	74.2	K.SPS*QSS*LPAVVVETFPATVNGTVEGGSGAGR.L
Amphiphysin II BII	N1 \$300	305			12.6	70.3	K.S'PSQSS*LPAVVVETFPATVNGTVEGGSGAGR.L
Amphiphysin II BII	N1 \$302	304			4.3	55.0	K.SPS*QS*SLPAVVVETFPATVNGTVEGGSGAGR.L
Amphiphysin II Bil	N1 \$304	305	÷.		5.4	50.4	K.SPSQS*S*LPAVVVETFPATVNGTVEGGSGAGR.L
Amphiphysin II Bil					1.8	35.7	K.SPS*QSSLPAVVVETFPATVNGTVEGGSGAGR.L
Amphiphysin II BII		304			4.8	28.2	K.S*PSQS*SLPAVVVETFPATVNGTVEGGSGAGR.L
AMPK alpha 1 pp					26.0	29.5	K.DFYLAT*SPPDSFLDDHHLTRPHPER.V  R.SDS*DAEAQGK.S
AMPK beta 2 pp		_	•		10.2	61.5	R.DLSS*SPPGPYGQEMYAFR.S
AMPK beta1 PF				i	137.2	42.4	R.S*HNNFVAILDLPEGEHQYK.F
Amyotrophic lateral sclerosis 2 FA	M117B S170	173		• • •	8.3	86.7	R.SQSVS*PTS*FLTISNEGSEESPCSADDLLVDPR.D
Amyotrophic lateral sclerosis 2 FA chromosome region, candidate 13	M117B S170	176			6.7	50.0	R.SQSVS*PTSFLT*ISNEGSEESPCSADDLLVDPR.D
Anaphase promoting complex subunit 5 AN					100.0	49.2	K.EELDVS*VR.E
Anaphase promoting complex, subunit 1 <sub>AN</sub>			=		24.1	58.1	R.NFDFEGSLS*PVIAPK.K
Anaphase promoting complex, subunit 1 <sub>AN</sub> Anaphase promoting complex, subunit 1 <sub>AN</sub>		-			32.9	63.5	K.LLGS*LDEVVLLSPVPELRDSS*K.L  R.QLQPASELWSS*DGAAGLVGS*LQEVTIHEK.Q
Anaphase promoting complex, subunit 1 <sub>AN</sub>		•			25.4	47.5	R.QLQPASELWS*SDGAAGLVGS*LQEVTIHEK.Q
Anaphase promoting complex, subunit 1 AN	IAPC1 S547	563		• •	42.3	31.7	K.LLGS*LDEVVLLSPVPELRDS*SK.L
Anaphase promoting complex, subunit 1 <sub>AN</sub>	IAPC1 S547	5555	÷		100.0	40.3	K.LLGS*LDEVVLLS*PVPELR.D
Anaphase promoting complex, subunit 3 CD	IC27 \$364				52.0	78.0	R.EVTPILAQTQSSGPQTSTTPQVLS*PTITSPPNALPR.R
Anaphase promoting complex, subunit 3 CD	IC27 T343		Image: Control of the			44.1	R.EVT*PILAQTQSSGPQTSTTPQVLSPTITSPPNALPR.R
Anaphase promoting complex, subunit 4 <sub>AN</sub>				_		34.6	
Anaphase promoting complex, subunit 8 CE	C23 \$588						K.IKEEVLS*ESEAENQQAGAAALAPEIVIK.V
Androgen induced proliferation inhibitor pr	IS5B \$125		•		23.4	19.8	K.IKEEVLS*ESEAENQQAGAAALAPEIVIK.V  R.RVS*PLNLSSVTP  R.AES*PESSAIESTQSTPQK.G
Androgen induced proliferation inhibitor p		_			23.4 45.3 31.2	19.8 105.4 70.7	R.RVS*PLNLSSVTP
Androgen induced proliferation inhibitor p		8T1370	-	•••	45.3	105.4	R.RVS*PLNLSSVTP R.AES*PESSAIESTQSTPQK.G
Androgen induced proliferation inhibitor p	S5B S135	3T1370			45.3 31.2	105.4 70.7	R.RVS*PLNLSSVTP R.AES*PESSAIESTQSTPQK.G R.AES*PESSAIESTQST*PQK.G
Androgen induced proliferation inhibitor PE	S5B S135 S5B S128 S5B S118	BT1370			45.3 31.2 100.0	105.4 70.7 51.4	R.RVS*PLNLSSYTP.  R.AES*PESSAIESTQSTPQK.G  R.AES*PESSAIESTQST*PQK.G  R.LKEDILENEDEONS*PPKK.G
Androgen induced proliferation inhibitor pc PC Androgen induced proliferation inhibitor pc Androgen induced proliferation inhibitor pc Androgen induced proliferation inhibitor pc	S5B S135 S5B S128 S5B S118 S5B S117 S5B S117	3 3 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			45.3 31.2 100.0 11.5	105.4 70.7 51.4 24.3	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTOSTPOK.G  R.AES*PESSAIESTOST*POK.G  R.LKEDILENEDEONS*PPKK.G  R.LDSSEMDHS*ENEDYTMSSPLPGKK.S
Androgen induced proliferation inhibitor pc	SSB S135 SSB S128 SSB S118 SSB S117 SSB T138 SSB S116	BT1370			45.3 31.2 100.0 11.5 -1.8 20.3 22.5	70.7 51.4 24.3 18.3 21.5	R RVS*PLNLSSVTP.  R AES*PESSAIESTÖSTPÖK.G  RAES*PESSAIESTÖST*PÖK.G  RLIKEDILENEDEONS*PPKK.G  RLIDSSEMDHS*ENEDYTMSSPLPGKK.S  RLDS*SEMDHSENEDYTMSSPLPGKK  K.T*PSPSQPK.K  R METVSNASSSSNPSS*PGR.I
Androgen induced proliferation inhibitor pc	SSB S135 SSB S128 SSB S118 SSB S117 SSB T138 SSB S116 SSB S135	8T1370 8 2 6 6 8 8S1369			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2	105.4 70.7 51.4 24.3 18.3 21.5 84.9	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTOSTPOK.G  R.AES*PESSAIESTOSTPOK.G  R.LKEDILENEDEONS*PPKK.G  R.LDSSEMDHS*ENEDYTMSSPLPGKK.S  R.LDS*SEMDHSENEDYTMSSPLPGKK  K.T*PSPSOPK.K  R.METVSNASSSSNPSS*PGR.I  R.AES*PESSAIESTOS*TPOK.G
Androgen induced proliferation inhibitor pc	SSB S135 SSB S128 SSB S128 SSB S118 SSB S117/ SSB S116 SSB S116 SSB S135 SSB S116	811370			45.3 31.2 100.0 11.5 -1.8 20.3 22.5	70.7 51.4 24.3 18.3 21.5	R RVS*PLNLSSVTP.  R AES*PESSAIESTÖSTPÖK.G  RAES*PESSAIESTÖST*PÖK.G  RLIKEDILENEDEONS*PPKK.G  RLIDSSEMDHS*ENEDYTMSSPLPGKK.S  RLDS*SEMDHSENEDYTMSSPLPGKK  K.T*PSPSQPK.K  R METVSNASSSSNPSS*PGR.I
Androgen induced proliferation inhibitor pc	SSSB S128 SSSB S128 SSSB S118 SSSB S117 SSSB S117 SSSB S116 SSSB S116 SSSB S135 SSSB S135 SSSB S135 SSSB S135	811370			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTQSTPQK.G  R.AES*PESSAIESTQST*PQK.G  R.LDSSEMDHS*ENEDYTMSSPLPGKK.S  R.LDS*EMDHS*ENEDYTMSSPLPGKK.S  R.LDS*EMDHSENEDYTMSSPLPGKK  K.T*PSPSQPK.K  R.METVSNASSSSNPSS*PGR.I  R.AES*PESSAIESTQS*TPQK.G
Androgen induced proliferation inhibitor pc	\$55B \$135\$ \$135B \$135B \$128\$ \$55B \$118\$ \$55B \$118\$ \$55B \$1170\$ \$55B \$1160\$ \$55B \$135\$ \$55B \$1160\$ \$55B \$1170\$ \$55B \$1170\$ \$55B \$1170\$ \$55B \$1170\$	811370 • 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTQST*PQK.G  R.AES*PESSAIESTQST*PQK.G  R.LDSSEMDHS*ENEDYTMSSPLPGK.S  R.LDS*EMDHS*ENEDYTMSSPLPGK.K  K.T*PSPSQPK.K  R.METVSNASSSSNPSS*PGR.I  R.AES*PESSAIESTQS*TPQK.G  R.METVSNASSSSNPS*SPGR.I  R.DS*S*EMDHSENEDYTMSSPLPGK.S
Androgen induced proliferation inhibitor pc	SSSB S135 SSSB S128 SSSB S118 SSSB S117 SSSB S116 SSSB S116 SSSB S116 SSSB S116 SSSB S116 SSSB S116 SSSB S117 SSSB S117 SSSB S117 SSSB S118 SSSB S118 SSSB S118 SSSB S118 SSSB S118	\$11370 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3 \$3			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTQSTPQK.G  R.AES*PESSAIESTQST*PQK.G  R.LDSSEMDHS*ENEDYTMSSPLPGK.S  R.LDS*SEMDHS*ENEDYTMSSPLPGK.K  K.T*PSPSQPK.K  R.METVSNASSSSNPS*PGR.I  R.AES*PESSAIESTQS*TPQK.G  R.METVSNASSSSNPS*PGR.I  R.AES*PESSAIESTQS*TPQK.G  R.METVSNASSSSNPS*SPGR.I  R.LDS*S*EMDHSENEDYTMSSPLPGKK.S  K.TPS*PSQPK.K
Androgen induced proliferation inhibitor pc	SSSB S1355SB S1288SSB S1188SSB S1178SSB S1178SSB S1178SSB S1178SSB S1178SSB S1178SSB S1178SSSB S1178SSB S117	\$11370 \$3 \$2 \$5 \$6 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2 30.7	R RVS*PLNLSSVTP.  R AES*PESSAIESTOSTPOK.G  R AES*PESSAIESTOSTPOK.G  R LIKEDILENEDEONS*PPKK.G  R LIDSSEMDHS*ENEDYTMSSPLPGKK.S  R LDS*SEMDHS*ENEDYTMSSPLPGKK  K.T*PSPSQPK.K  R METVSNASSSSNPS*PGR.I  R AES*PESSAIESTQS*TPQK.G  R METVSNASSSSNPS*SPGR.I  R LDS*S*EMDHSENEDYTMSSPLPGKK.S  K.TPS*PSSAIESTQS*TPQK.G  K.TYSPSSAIESTQS*TPQK.G  K.S*CS*PSPVSPVSPQVQPQAADTISDSVAVPASLLGMR.R  K.S*CS*PSPVSPQVQPQAADTISDSVAVPASLLGMR.R  K.S*CS*PSPVSPQVQPQAADTISDSVAVPASLLGMR.R
Androgen induced proliferation inhibitor pc Anillin actin binding protein (Fragment) St.	SSSB S128-SSSB S118-SSSB S116-SSSB S117-SSSB S118-SSSB S118-SSSB S118-SSSB S118-SSSB S138-SSSB S118-SSSB S138-SSSB S118-SSSB S138-SSSB S118-SSSB S138-SSSB S138-SSB S138-SB	\$11370 \$3 \$2 \$5 \$6 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8 9.3 8.5 10.8	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2 30.7 35.6 20.9	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTOSTPOK.G  R.AES*PESSAIESTOSTPOK.G  R.LKEDILENEDEONS*PPKK.G  R.LDSSEMDHS*ENEDYTMSSPLPGKK.S  R.LDS*SEMDHSENEDYTMSSPLPGKK.K  K.T*PSPSOPK.K  R.METVSNASSSSNPS*PGR.I  R.AES*PESSAIESTOS*TPOK.G  R.METVSNASSSSNPS*SPGR.I  R.LDS*S*EMDHSENEDYTMSSPLPGKK.S  K.TPS*PSOPK.K  K.SCS*PS*PVS*POVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PS*PVS*POVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PSPVS*POVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PSPVS*POVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PSPVS*POVOPQAADTISDSVAVPASLLGMR.R  R.NGILASPQS*APGNLDNSK.S
Androgen induced proliferation inhibitor pc Anillin actin binding protein Ah Anillin act	SSB S1355B S128SSB S118SSB S118SSB S118SSB S116SSB S1177SSSB S116SSB S117SSSB S116SSSB S116SSSB S116SSSB S116SSSB S117SSSB S116SSSB S117SSSB S117SSB S117SB S1	ST1370			45.3 31.2 100.0 111.5 -1.8 20.3 22.5 24.2 15.8 39.8 9.3 8.5 10.8 13.9	105.4 70.7 71.4 24.3 21.5 24.3 21.5 84.9 19.5 44.5 43.2 33.2 20.9 41.2	R RVS*PLNLSSVTP.  R AES*PESSAIESTOSTPOK.G  R AES*PESSAIESTOSTPOK.G  R LIKEDILENEDEONS*PPKK.G  R LIDSSEMDHS*ENEDYTMSSPLPGKK.S  R LDS*SEMDHS*ENEDYTMSSPLPGKK  K.T*PSPSQPK.K  R METVSNASSSSNPS*PGR.I  R AES*PESSAIESTQS*TPQK.G  R METVSNASSSSNPS*SPGR.I  R LDS*S*EMDHSENEDYTMSSPLPGKK.S  K.TPS*PSSAIESTQS*TPQK.G  K.TYSPSSAIESTQS*TPQK.G  K.S*CS*PSPVSPVSPQVQPQAADTISDSVAVPASLLGMR.R  K.S*CS*PSPVSPQVQPQAADTISDSVAVPASLLGMR.R  K.S*CS*PSPVSPQVQPQAADTISDSVAVPASLLGMR.R
Androgen induced proliferation inhibitor pc Anillin actin binding protein (Fragment) St.	SSB S1355B S1288 S155B S1288 S155B S1188 S155B S1177 S155B S1177 S155B S116 S155B S116 S155B S116 S155B S1177 S155B S1177 S177 S177 S177 S177 S177 S177 S17	ST1370			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8 9.3 8.5 10.8	105.4 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2 30.7 35.6 20.9	R.RVS*PLNLSSVTP.  R.AES*PESSAIESTGSTPOK.G  R.AES*PESSAIESTGSTPOK.G  R.LKEDILENEDEONS*PPKK.G  R.LDSSEMDHS*ENEDYTMSSPLPGKK.S  R.LDS*SEMDHS*ENEDYTMSSPLPGKK.K  K.T*PSPSOPK.K  R.METVSNASSSSNPS*PGR.I  R.AES*PESSAIESTGS*TPOK.G  R.METVSNASSSSNPS*PGR.I  R.LDS*S*EMDHSENEDYTMSSPLPGKK.S  K.TPS*PSOPK.K  K.SCS*PS*PVSPOVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PS*PVSPOVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PSPVS*POVOPQAADTISDSVAVPASLLGMR.R  K.SCS*PSPVS*POVOPQAADTISDSVAVPASLLGMR.R  R.NGILASPQS*APGNLDNSK.S
Androgen induced proliferation inhibitor pc Androgen induced proli	SSB S1355B S1288 SSSB S1288 SSSB S1188 SSSB S1188 SSSB S1177 SSSB S1177 SSSB S1168 SSSB S1168 SSSB S1168 SSSB S1168 SSSB S1168 SSSB S1177 SSSB	ST1370			45.3 31.2 100.0 111.5 -1.8 20.3 22.5 24.2 15.8 39.8 9.3 8.5 10.8 13.9 33.2 6.8	105.4 70.7 70.7 51.4 24.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2 20.9 41.2 33.8 51.8	R. R
Androgen induced proliferation inhibitor pc Androgen induced proli	SSSB S1355SS S1288SSSB S1188SSB S1178SSSB S1178SSB S1178SB S1178SB S1178SSB S1178SB S1178SB S1178SB S1178SB S1178SB S1178SB S1178SB S1178SB S	ST1370			45.3 31.2 100.0 11.5 -1.8 20.3 22.5 24.2 15.8 9.3 8.5 10.8 13.9 33.2 6.8	105.4 70.7 70.7 71.4 24.3 18.3 18.3 21.5 84.9 19.5 44.5 43.2 33.2 33.7 35.6 20.9 41.2 33.8 51.8	R. RES'PESSAIESTOSTPOK.G  R. AES'PESSAIESTOSTPOK.G  R. LES'PESSAIESTOSTPOK.G  R. LES'PESSAIESTOST'POK.G  R. LDSSEMDHS'ENEDYTMSSPLPGK.K.S  R. LDS'SEMDHSENEDYTMSSPLPGK.K.  K. T'PSPSOPK.K  R. METVSNASSSSNPS'PGR.I  R. AES'PESSAIESTOS'TPOK.G  R. METVSNASSSSNPS'SPGR.I  R. LDS'S'EMDHSENEDYTMSSPLPGK.K.S  K. TPS'PSOPK.K  K. SCS'PS'PVSPOVOPQAADTISDSVAVPASLLGMR.R  K. SCS'PS'PVSPOVOPQAADTISDSVAVPASLLGMR.R  K. SCS'PSPVS'POVOPQAADTISDSVAVPASLLGMR.R  R. K. SCS'PSPVS'POVOPQAADTISDSV

Peak Area %CV White do	ts-Significant cha	inge in pepti compared to	de the			
.5 25 timepoint .3 42 PSM	with the minimum	peak area f	or a given			
3 86 5 5 >100 5 10		CarT	RajiB			
Protein Name Gene Ankyrin repeat and KH domain containing 1 ANKHD1	Phosphosites S95	£ £ £	5 th 9	Ascor 12.1	MOWSE 90.8	Sequence  R.TGGGGGASGS*DEDEVSEVESFILDQEDLDNPVLK.T
Ankyrin repeat and KH domain containing 1 ANKHD1				-1.2	13.2	R.T*GGGGGASGSDEDEVSEVESFILDQEDLDNPVLK.T
Ankyrin repeat and KH domain containing 1 ANKHD1	S93			6.0	51.3	R.TGGGGGAS*GSDEDEVSEVESFILDQEDLDNPVLK.T
Ankyrin repeat domain 11 ANKRD11	S1792			18.9	13.0	R.SVS*VDIR.R
Ankyrin repeat domain 28 ANKRD28	S1048			5.2	43.7	R.NEPSSYCSFNNIGGEQEYLYTDVDELNDS*DSETY
Ankyrin repeat domain 28 ANKRD28	T1040			0.7	27.1	R.NEPSSYCSFNNIGGEQEYLYT*DVDELNDSDSETY
Ankyrin repeat domain 28 ANKRD28	Y1037	<u> </u>		12.6	38.4	R.NEPSSYCSFNNIGGEQEY*LYTDVDELNDSDSETY
Ankyrin repeat domain protein 17 ANKRD17	T5				63.9	K.AT*VPVAAATAAEGEGSPPAVAAVAGPPAAAEVGGGVGGSSRA
Ankyrin repeat domain protein 17 ANKRD17	S19			9.9	35.8	K.ATVPVAAATAAEGE©*PPAVAAVAGPPAAAEVGGGVGGSSR.A
Ankyrin repeat domain protein 17 ANKRD17	S2041S2047			5.9	18.2	K.EHYPVS*SPSSPS*PPAQPGGVSR.N
Anti silencing function 1B <sub>ASF1B</sub>	S198			100.0	24.0	K.GLGLPGCIPGLLPENS*MDCI
Anti-silencing function 1A ASF1A	S166			25.9	63.3	K.LEDAESS*NPNLQSLLSTDALPSASK.G
Anti-silencing function 1A ASF1A	S165			48.3	57.1	K.LEDAES*SNPNLQSLLSTDALPSASK.G
Antigen identified by monoclonal antibody MKI67 Ki-67  Antigen identified by monoclonal antibody MKI67	\$2002		• •	100.0	25.0	R.LKIS*LGK.V
Ki-67  Antigen identified by monoclonal antibody MKI67	S584	•		29.9	84.7	K.AUSLVISPPAPS*PR.K  K.TPVQYSQQQNS*PQK.H
Ki-67  Antigen identified by monoclonal antibody MKI67	\$357 \$352	==		48.5	25.7	K.TPVQYS*QQQNSPQK.H
Ki-67  Antigen identified by monoclonal antibody MKI67	S1131			20.0	30.3	K.S*PPPESVDTPTSTK.Q
Ki-67  Antigen identified by monoclonal antibody MKI67	S2223	•		37.2	38.9	R.S*PQPDPVGTPTIFKPQSK.R
Ki-67 Antisense ERCC1 CD3EAP	S126S136		•	42.7	42.6	R.ILEGPQQSLS*GSPLQPIPAS*PPPQIPPGLRPR.F
Antisense ERCC1 CD3EAP	S124S136	•		26.1	16.9	R.ILEGPQQS*LSGSPLQPIPAS*PPPQIPPGLRPR.F
Antisense ERCC1 CD3EAP	S128S136	•		34.5	52.1	R.ILEGPQQSLSGS*PLQPIPAS*PPPQIPPGLRPR.F
Antisense ERCC1 CD3EAP	S124S126	•			35.5	R.ILEGPQQS*LS*GSPLQPIPASPPPQIPPGLRPR.F
AP2 associated kinase 1 AAK1	T620S624			12.5	25.9	K.VGSLT*PPSS*PK.T
AP2 associated kinase 1 AAK1	S623S624			12.2	24.6	K.VGSLTPPS*S*PK.T
AP2 associated kinase 1 AAK1	T640			13.8	48.5	R.ILSDVT*HSAVFGVPASK.S
AP2 associated kinase 1 AAK1	T653			-0.3	83.5	K.ST*QLLQAAAAEASLNK.S
AP2 associated kinase 1 AAK1	S637			61.2	65.4	R.ILS*DVTHSAVFGVPASK.S
AP47 AP1M1	T154			16.2	37.3	K.LETGAPRPPATVT*NAVSWR.S
AP47 AP1M1	T152T154			34.9	29.3	K.LETGAPRPPAT*VT*NAVSWR.S
APBB2 APBB2	S123		•	53.8	21.5	K.NLS*PTAVINITSEK.L
APC APC	S2837	•			16.8	K.RHSGS*YLVTSV
APC APC APG4 autophagy 4 homolog B ATG4B	\$780			36.4	41.0	K.ALEAELDAQHLSETFDNIDNLS*PK.A  R.FFDS*EDEDFEILSL
Apoptosis antagonizing transcription factor AATF	\$383 \$203			107.9	48.6	R.AGDRNS*EDDGVVMTFSSVK.V
Apoptosis antagonizing transcription factor AATF	\$320\$321			107.9	31.4	R.YLVDGTKPNAGSEEIS*S*EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	T310S316S321		==	12.0	23.7	R.YLVDGT*KPNAGS*EEISS*EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	S316S320S321		-	28.0	66.1	R.YLVDGTKPNAGS*EEIS*S*EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	T310S316S320			9.7	17.1	R.YLVDGT*KPNAGS*EEIS*SEDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	T310S320S321	•		3.9	22.9	R.YLVDGT*KPNAGSEEIS*S*EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	Y305T310S316		•	9.0	34.5	R.Y*LVDGT*KPNAGS*EEISSEDDELVEEK.K
Apoptosis antagonizing transcription factor AATF	\$169\$170\$178			100.0	49.0	K.GMDDLGS*S*EEEEDEES*GMEEGDDAEDS*QGES*EEDR.A
Apoptosis antagonizing transcription factor AATF	T310S321			20.0	11.6	R.YLVDGT*KPNAGSEEISS*EDDELVEEK.K
Apoptosis inhibitor 5 API5	\$462			13.9	69.4	R.ASEDTTS*GSPPKK.S
Apoptosis inhibitor 5 API5	S464		<u>.</u> .	7.8	46.1	R.ASEDTTSGS*PPKK.S
Apoptotic chromatin condensation inducer ACIN1 in the nucleus (Fragment)	S125			3.4	30.2	K.EAVVDLHADDS*RISEDETER.N
Apoptotic chromatin condensation inducer ACIN1 in the nucleus (Fragment)	S128			9.2	24.2	K.EAVVDLHADDSRIS*EDETER.N
Aprataxin APTX	S132		₽.₽	22.2	42.2	R.S*GNSDSIER.D
ANP32B	T244			100.0	28.3	R.ET*DDEGEDD
Arachidonate 12-oxidoreductase ALOX12	S246		-	10.2	27.2	R.RSTS*LPSR.L
Arachidonate 12-oxidoreductase ALOX12  Arf-GAP with dual PH domain-containing ADAP1	S244			15.4	13.3	R.RS*TSLPSR.L  K.IAPS*ER.K
protein 1 (Fragment)  Arginine/serine-rich coiled-coil 2 RSRC2	\$71 \$216\$210T220			100.0	14.7	R.S'LS'RT"PS"PPPFR.G
Arginine/serine-rich colled-coil 2 RSRC2	\$216\$218T220 \$32			100.0	43.7	K.EQSEVSVS*PR.A
Arginine/serine-rich colled-coil 2 RSRC2	S41			6.5	11.7	K.HHYS'R.S
Arginine/serine-rich coiled-coil 2 RSRC2	S30S32			10.5	14.7	K.EQSEVS*VS*PR.A
Arginine/serine-rich coiled-coil 2 RSRC2	Y40		•	-	17.0	K.HHY*SR.S
Arginine/serine-rich splicing factor 10 TRA2B	<b>S</b> 39			26.3	27.8	R.S*KEDSRR.S
Arginine/serine-rich splicing factor 10 TRA2B	T201			32.0	33.5	K.RPHT*PTPGIYMGRPTYGSSR.R
Arginine/serine-rich splicing factor 10 TRA2B	T201Y213			17.1	23.8	K.RPHT"PTPGIYMGRPTY"GSSR.R
Arginine/serine-rich splicing factor 10 TRA2B	T201T212			8.5	22.2	K.RPHT*PTPGIYMGRPT*YGSSR.R
Arginine/serine-rich splicing factor 10 TRA2B	S29T33			100.0	17.6	K.S*ARHT*PAR.S

Peak Area	o abundan		compared to	the			
-5 -3 0	timepoint PSM 71	with the minimum	peak area f	or a given			
3 5 >10	>100		CarT	RajiB			
Arginine/serine-rich	Protein Name Gene splicing factor 10 TRA2B	Phosphosites T69	8 4 5	9m 2m 5m		MOWSE 34.7	Sequence R.RHYT*R.S
	splicing factor 10 TRA2B	S95S97S99	===		13.9	34.5	R.RHS*HS*PMSTR.R
	splicing factor 10 TRA2B	S95S97			14.9	38.8	R.RHS*HS*HSPMSTR.R
	splicing factor 10 TRA2B	S95S99				21.8	R.RHS*HSHS*PMSTR.R
	splicing factor 10 TRA2B	S97S99			13.7	25.6	R.RHSHS*HS*PMSTR.R
	splicing factor 10 TRA2B	T201Y207			7.3	25.4	K.RPHT*PTPGIY*MGRPTYGSSR.R
	splicing factor 10 TRA2B	T201S215	=		11.8	19.8	K.RPHT*PTPGIYMGRPTYGS*SR.R
	splicing factor 10 TRA2B	\$97\$102T103	_		15.3	18.6	R.RHSHS*HSPMS*T*RR.R
	splicing factor 10 TRA2B	T203Y207			19.0	25.8	K.RPHTPT*PGIY*MGRPTYGSSR.R
	splicing factor 10 TRA2B	T201T203			10.4	23.5	K.RPHT*PT*PGIYMGRPTYGSSR.R
	splicing factor 10 TRA2B	S43	=		-0.2	19.7	R.SKEDS*RR.S
Arginine/serine-rich	splicing factor 10 TRA2B	T203T212			3.9	17.4	K.RPHTPT*PGIYMGRPT*YGSSR.R
Arginine/serine-rich	splicing factor 10 TRA2B	S102T103		-	21.5	17.3	R.RHSHSHSPMS*T*R.R
	splicing factor 10 TRA2B	S97S99S102		• •	3.3	12.6	R.RRHSHS*HS*PMS*TR.R
	splicing factor 10 TRA2B	S39S43			100.0	15.1	R.S*KEDS*RR.S
	splicing factor 10 TRA2B		_				K.RPHTPTPGIY*MGRPTYGSSR.R
	splicing factor 10 TRA2B	Y207 Y68			8.9	11.9	R.RHY*TR.S
	ARID1B ARID1B	Y68 S1550			22.4		R.MS*PSKSPFLPSMK.M
	ARL6IP4 ARL6IP4	\$1550 \$252			32.1	108.6	R.S*AGEEEDGPVLTDEQK.S
Armadillo re	epeat containing 1 ARMC1				90.9		K.LLASEIYDILQSSNMADGDS*FNEMNSR.R
	ARPP-21 ARPP21	\$120 \$383			24.9	61.9	K.TAS*FGGITVLTR.G
	ARPP-21 ARPP21				15.1	76.2	K.DCS*QEYTDSTGIDLHEFLINTLK.N
	ARPP19 ENSA	S138 S62	-		35.2	46.6	K.YFDS*GDYNMAK.A
Arconito re				• • •	35.2	66.6	R.ERFS*PPR.H
	sistance protein 2 SRRT	<b>S</b> 67			100.0	23.0	
	sistance protein 2 SRRT	T544			26.7	58.1	R.TQLWASEPGT*PPLPTSLPSQNPILK.N
Arsenite res	ASH1L ASH1L	S74	•••		100.0	29.1	R.HELS'PPQKR.M
		S1162S1170			25.4	23.5	R.RLS*PPTLLPNS*PSHLSELTSLK.E
	ASH2 like ASH2L	S623			100.0	28.0	R.S*PPWEP
	ASK1 MAP3K5	S1029S1033		•	12.1	14.7	R.TLFLGIPDENFEDHS*APPS*PEEK.D
	motif containing 1 <sub>AHDC1</sub>	S846S849			29.5	53.6	R.SLLDS*DDS*SDLLDFALSASRPESR.K
	motif containing 1 <sub>AHDC1</sub>	S842S849		-	13.3	39.4	R.S*LLDSDDS*SDLLDFALSASRPESR.K
	motif containing 1 <sub>AHDC1</sub>	S842S846	Ļ		5.0	15.4	R.S*LLDS*DDSSDLLDFALSASRPESR.K
	anscription factor AKNA	S1170S1173			13.1	60.5	R.LS*LSS*ESELPSLPLFSEK.S
	anscription factor AKNA	S534S537			9.7	44.4	R.GDLS*PSS*LTSMPTLGWLPENR.D
	anscription factor AKNA	S534T539		•	2.2	23.3	R.GDLS*PSSLT*SMPTLGWLPENR.D
	anscription factor AKNA	S1172S1173		•	16.5	79.9	R.LSLS*S*ESELPSLPLFSEK.S
	anscription factor AKNA	T539	-		6.0	29.2	R.GDLSPSSLT*SMPTLGWLPENR.D
	anscription factor AKNA	S1170S1175		-	3.5	19.7	R.LS*LSSES*ELPSLPLFSEK.S
	anscription factor AKNA	S534			11.0	86.6	R.GDLS*PSSLTSMPTLGWLPENR.D
	anscription factor AKNA	S540			4.8	38.7	R.GDLSPSSLTS*MPTLGWLPENR.D
	anscription factor AKNA	S534S536		<u> </u>	1.4	21.6	R.GDLS*PS*SLTSMPTLGWLPENR.D
	anscription factor AKNA	S536	<b>—</b>		-0.2	42.5	R.GDLSPS*SLTSMPTLGWLPENR.D
	ractive domain 1A ARID1A	S1600			16.7	52.4	R.TS*PSKSPFLHSGMK.M
	ractive domain 1A ARID1A	<b>S</b> 696			53.8	80.1	R.GPS*PSPVGSPASVAQSR.S
	ractive domain 1A ARID1A	S1754	ij.			78.3	K.VS*SPAPMEGGEEEELLGPK.L
AT rich inte	ractive domain 1A ARID1A	S1600S1602	-		12.8	24.1	R.TS*PS*KSPFLHSGMK.M
AT rich inte	ractive domain 1A <sub>ARID1A</sub>	S363	÷		31.6	74.8	R.SHHAPMS*PGSSGGGGQPLAR.T
AT rich inter	ractive domain 1A ARID1A	<b>S</b> 769			15.6	35.7	R.NPQMPQYSSPQPGS*ALSPR.Q
AT rich inter	ractive domain 1A ARID1A	S772	<b>—</b>		3.5	25.9	R.NPQMPQYSSPQPGSALS*PR.Q
AT rich inter	ractive domain 3A <sub>ARID3A</sub>	S77S81S88			100.0	58.3	R.AAAAGLGHPAS*PGGS*EDGPPGS*EEEDAAR.E
	ATAD2 <sub>ATAD2</sub>	<b>S</b> 327			45.3	61.5	R.KPNIFYSGPAS*PARPR.Y
	ATAD2 <sub>ATAD2</sub>	Y750			4.3	70.8	K.TLDSDISCPLLESDLAY*SDDDVPSVYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	S746Y750			51.4	47.3	K.TLDSDISCPLLES*DLAY*SDDDVPSVYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	S746S757			7.3	51.5	K.TLDSDISCPLLES*DLAYSDDDVPS*VYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	Y750S751			29.7	52.7	K.TLDSDISCPLLESDLAY*S*DDDVPSVYENGLSQK.S
-	ATAD2 <sub>ATAD2</sub>	Y750S757			8.2	33.4	K.TLDSDISCPLLESDLAY*SDDDVPS*VYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	<b>S</b> 757	Ħ.		13.8	45.8	K.TLDSDISCPLLESDLAYSDDDVPS*VYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	<b>S</b> 746			1.2	40.6	K.TLDSDISCPLLES*DLAYSDDDVPSVYENGLSQK.S
	ATAD2 <sub>ATAD2</sub>	<b>S</b> 751	-		4.6	40.5	K.TLDSDISCPLLESDLAYS*DDDVPSVYENGLSQK.S
	Ataxin 10 ATXN10	<b>S</b> 12			100.0	47.1	R.LS*GVMVPAPIQDLEALR.A
	Ataxin 2 ATXN2	S848S850S865	- •		5.8	14.3	K.DSFIENS*SS*NCTSGSSKPNSPSIS*PSILSNTEHK.R
	Ataxin 2 ATXN2	S667		•	-0.3	82.2	R.TS*PSGGTWSSVVSGVPR.L
			-				

Peak Area <-10 -6 -3 -3	0 abundano	ts-Significant cha e at 5%FDR of with the minimum	compared to peak area fo	the or a given			
5 >10	>100 Protein Name Gene	Phosphosites	E E E	RajiB E E E	Ascor	MOWSE	Sequence
	Ataxin 2 ATXN2	S667S684			16.2	28.1	R.TS*PSGGTWSSVVSGVPRLS*PK.T
	Ataxin 2 ATXN2  Ataxin 2 ATXN2	\$697 \$850\$861\$865				36.0	R.QNS*IGNTPSGPVLASPQAGIIPTEAVAMPIPAASPTPASPASNR.A  K.DSFIENSSS*NCTSGSSKPNS*PSIS*PSILSNTEHK.R
Ataxi		\$238			11.9	47.5	R.WEGGDSNS*DDYDLESDMSNGWDPNEMFK.F
Ataxi	in 2 domain protein ATXN2L	S236S238		•••	24.7	64.4	R.WEGGDS*NS*DDYDLESDMSNGWDPNEMFK.F
Ataxi	in 2 domain protein ATXN2L	Y241S245			11.9	45.0	R.WEGGDSNSDDY*DLES*DMSNGWDPNEMFK.F
Ataxi	in 2 domain protein ATXN2L	S684	•		12.2	32.3	K.STSTPTS*PGPR.T
		S236Y241		•	7.5	36.2	R.WEGGDS*NSDDY*DLESDMSNGWDPNEMFK.F
	in 2 domain protein ATXN2L	S594	Ė		5.1	15.6	K.EVDGLLTSEPMGS*PVSSK.T
	in 2 domain protein ATXN2L	\$452	•			58.5	K.
	in 2 domain protein ATXN2L	\$236 Y241\$248			11.8	38.6	R.WEGGDS'NSDDYDLESDMSNGWDPNEMFK.F  R.WEGGDSNSDDY'DLESDMS'NGWDPNEMFK.F
	in 2 domain protein ATXN2L	S111			66.2	31.3	K.GPPQS*PVFEGVYNNSR.M
Ataxi	in 2 domain protein ATXN2L	\$236\$245			7.0	32.7	R.WEGGDS*NSDDYDLES*DMSNGWDPNEMFK.F
Ataxi	in 2 domain protein ATXN2L	T31				19.6	R. DDDCCT/SDDA(CC) DCDI ATSAADDCDDAAASSDCI CD//AAASSCI D
Ataxi	in 2 domain protein ATXN2L	T31S32				31.6	R.  DDDCCT*C*DDMCCI DCDI ATSAADDCDDAAASDCI CDMAAACSCI
Ataxi	in 2 domain protein ATXN2L	\$452\$459	<b>.</b> .			32.5	K.
		S236S248	ij.		7.6	37.5	R.WEGGDS*NSDDYDLESDMS*NGWDPNEMFK.F
	acid trehalase-like 1 PGGHG	S552			10.7	43.2	R.DPLQSPLWVTLGSSSPTES*LTVDPASE
	acid trehalase-like 1 PGGHG	T550 S547			2.8	41.4	R.DPLQSPLWVTLGSSSPT*ESLTVDPASE  R.DPLQSPLWVTLGSS*SPTESLTVDPASE
	acid trehalase-like 1 <sub>PGGHG</sub>	T543	==		7.4	19.5	R.DPLQSPLWVT*LGSSSPTESLTVDPASE
	acid trehalase-like 1 PGGHG	S546			7.0	18.1	R.DPLQSPLWVTLGS*SSPTESLTVDPASE
ATH1, a	acid trehalase-like 1 PGGHG	T554			7.3	18.7	R.DPLQSPLWVTLGSSSPTESLT*VDPASE
ATP t	binding cassette 50 ABCF1	S105	•		6.6	69.9	K.LS*VPTSDEEDEVPAPKPR.G
ATP t	binding cassette 50 <sub>ABCF1</sub>	T108	•		17.6	44.9	K.LSVPT*SDEEDEVPAPKPR.G
	binding cassette 50 <sub>ABCF1</sub>	S228			178.6	159.3	K.AEQGS*EEEGEGEEEEEGGESK.A
	binding cassette 50 <sub>ABCF1</sub>	T108S109			20.8	19.9	KLSVPT*S*DEEDEVPAPKPR.G
	binding cassette 50 ABCF1	S140			100.0	38.9	K.GGNVFAALIQDQS*EEEEEEEKHPPKPAKPEK.N  K.KLS*VPT*S*DEEDEVPAPKPR.G
	binding cassette 50 <sub>ABCF1</sub>	\$105T108\$109 \$109			100.0 5.5	36.8	KLSVPTS*DEEDEVPAPKPR.G
	binding cassette 50 ABCF1	S105T108			7.3	38.5	K.LS*VPT*SDEEDEVPAPKPR.G
ATP binding cassette, su	ubfamily C, member ABCC4	T646			13.9	30.3	K.DNEESEQPPVPGT*PTLR.N
ATP binding cassette, su	ubfamily C, member ABCC4	S664S668		•••	19.0	46.3	R.TFSESSVWSQQS*SRPS*LK.D
ATP binding cassette, su	ubfamily C, member ABCC4	S664S665			6.5	18.3	R.TFSESSVWSQQS*S*RPSLK.D
	ATP citrate lyase ACLY	S481			28.4	45.6	K.AKPAMPQDSVPS*PR.S
	ATP citrate lyase ACLY	S455			29.9	52.5	R.TAS*FSESR.A
	lent RNA helicase A <sub>DHX9</sub>	<b>S</b> 77				42.3	K.S'EEVPAFGVASPPPLTDTPDTTANAEGDLPTTMGGPLPPHLALK.  K.S'RFSGGFGAR.D
	NA helicase DDX3X DDX3X	\$590 \$593			11.2	37.7	K.SRFS*GGFGAR.D
	ATP7A <sub>ATP7A</sub>	S272	•		-0.6	54.6	R.SPS*YTNDSTATFIIDGMHCK.S
ATPa	ase classVI type11B ATP11B	S1154			13.8	52.4	R.SWS*ASDPFYTNDR.S
ATPase family AAA	domain-containing ATAD2B protein 2B	S727T731	Ţ.		2.8	13.1	K.EDIETLILEDSEDENALS*IFET*NCHSGSPK.K
	protein 2B	\$727\$735			2.0	16.2	K.EDIETLILEDSEDENALS*IFETNCHS*GSPK.K
ATPase H+ transpo	orting lysosomal V0 ATP6V0A2 subunit a isoform	S695			53.6	46.7	R.KDS*EEEVSLLGSQDIEEGNHQVEDGCR.E
	ATPase II ATP8A1	S25T28S29			38.4	78.1	K.TDDVS*EKT*S*LADQEEVR.T
	ATPase II ATP8A1	T21T28S29			11.3	49.5	K.T*DDVSEKT*S*LADQEEVR.T  R.TVS*EIR.S
	ATPase II ATP8A1	T21S25T28		•	5.6	36.8	K.T*DDVS*EKT*SLADQEEVR.T
ATPase	01	\$445			17.8	11.4	K.GVTQEVDGLS*QTDGTLTYFDK.V
	Autoantigen La SSB	S366	•	-	137.7	75.6	K.FAS*DDEHDEHDENGATGPVKR.A
	Autoantigen RCD8 EDC4	<b>S</b> 879			25.3	77.2	R.DSQDASAEQS*DHDDEVASLASASGGFGTK.V
	Autoantigen RCD8 EDC4	S723		•••	6.6	79.0	K.GPGQVPTATSALSLELQEVEPLGLPQAS*PSR.T
	Autoantigen RCD8 EDC4	S729S741			45.8	56.4	R.TRS*PDVISSASTALS*QDIPEIASEALSR.G
	Autoantigen RCD8 EDC4	S729			7.6	93.4	R.TRS*PDVISSASTALSQDIPEIASEALSR.G
	Autoantigen RCD8 EDC4	\$708\$723			34.2	67.8	K.GPGQVPTATSALS*LELQEVEPLGLPQAS*PSR.T
	Autoantigen RCD8 EDC4  Autoantigen RCD8 EDC4	S875			12.4	36.2	R.DSQDAS*AEQSDHDDEVASLASASGGFGTK.V  R.T*RSPDVISSASTALSQDIPEIASEALSR.G
	Autoantigen RCD8 EDC4	T727			15.8	98.8	R.T'RSPDVISSASTALSQDIPEIASEALSR.G  K.GPGQVPTAT'SALSLELQEVEPLGLPQAS'PSR.T
	Autoantigen RCD8 EDC4	\$729\$737	-		26.1	49.2	R.S'PDVISSAS'TALSQDIPEIASEALSR.G
	Autoantigen RCD8 EDC4	T702				46.5	K.GPGQVPT*ATSALSLELQEVEPLGLPQASPSR.T
	Autoantigen RCD8 EDC4	\$705\$723			12.1	34.1	K.GPGQVPTATS*ALSLELQEVEPLGLPQAS*PSR.T

<-10 0	abundance at		compared to	the			
-5 29 ti	imepoint with PSM	the minimum					
>100	·		CarT	RajiB E E E	Ascor	MOWSE	Sequence
Protein Name (C Autoantigen RCD8 E		osphosites 34	0 0 0	. 2 2	0.5	29.7	R.SPDVIS*SASTALSQDIPEIASEALSR.G
Autoantigen RCD8 E		29 <mark>\$</mark> 735			21.7	38.3	R.S*PDVISS*ASTALSQDIPEIASEALSR.G
Autoantigen RCD8 E		27 <mark>\$</mark> 741		•	6.4	18.7	R.T*RSPDVISSASTALS*QDIPEIASEALSR.G
Autophagy related 9 homolog A A:  Autophagy related 9 homolog A A:				<u>::</u>	7.6	67.9	R.SAS*YPCAAPRPGAPETTALHGGFQR.R  R.HPEPVPEEGS*EDELPPQVHKV
B cell CLL/lymphoma 9 like B		480		•	100.0	23.1	R.SVS*LDSQMGYLPAPGGMANLPF
B cell CLL/lymphoma 9 like B					7.2	44.4	K.S*PTLSQVHSPLVTSPSANLK.S
B cell CLL/lymphoma 9 like B	CL9L S7	50			54.7	53.0	R.GLLS*PPMGQSGLR.E
B cell CLL/lymphoma 9 like B	CL9L S1	478	•	•••	10.0	32.8	R.S*VSLDSQMGYLPAPGGMANLPF
B cell lymphoma 6 protein B	CL6 S3	07 <b>S</b> 308			100.0	31.9	K.EEERPS'S'EDEIALHFEPPNAPLNR.K
B-lymphocyte cell-surface antigen B1 M		53			6.1	38.6	K.EEVVGLTETS*SQPK.N
B-lymphocyte cell-surface antigen B1 M				==	51.9	75.4	R.NS*VNGTFPAEPMK.G  K.S*NIVLLSAEEKK.E
B-lymphocyte cell-surface antigen B1 <sub>M</sub>	IS4A1 S2	25 52 <mark>\$</mark> 254			101.1	64.7	K.S*NIVLLSAEEKK.E  K.EEVVGLTET*SS*QPK.N
	IS4A1 S3			===	-0.1	53.6 64.2	R.MSS*LVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1 M		5 <b>S</b> 36			68.1	86.9	R.MS*S*LVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1 M	IS4A1 S2	95			30.5	26.4	K.NEEDIEIIPIQEEEEEETETNFPEPPQDQESSPIENDS*SP
B-lymphocyte cell-surface antigen B1 M	IS4A1 S2	5	•••		100.0	37.0	K.GPIAMQS*GPKPLFR.R
M	IS4A1 S3	5			27.6	61.6	R.RM#S*SLVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1 M	IS4A1 S2	88			4.6	18.6	K.NEEDIEIIPIQEEEEEETETNFPEPPQDQES*SPIENDSSP
B-lymphocyte cell-surface antigen B1 M		52 <mark>\$</mark> 253			9.3	29.7	K.EEVVGLTET*S*SQPK.N
B-lymphocyte cell-surface antigen B1 <sub>M</sub> B-lymphocyte cell-surface antigen B1 <sub>M</sub>			•••		6.1	23.1	K.NEEDIEIIPIQEEEEEET*ETNFPEPPQDQESSPIENDSSP
B-lymphocyte cell-surface antigen B1 M		54 50T252			7.2	35.6	K.EEVVGLT'ET'SSQPK.N
B-lymphocyte cell-surface antigen B1 <sub>M</sub>				==	0.5	30.7	K.EEVVGLTET*SSQPK.N
B-lymphocyte cell-surface antigen B1 M	IS4A1 T2	50 <b>S</b> 254			3.5	26.1	K.EEVVGLT*ETSS*QPK.N
B-lymphocyte cell-surface antigen B1 M	IS4A1 S2	53 <mark>S</mark> 254			8.9	39.1	K.EEVVGLTETS*S*QPK.N
B-lymphocyte cell-surface antigen B1 M	IS4A1 S3	5 <mark>8</mark> 43		ij	-0.5	24.3	R.RMS*SLVGPTQS*FFM#R.E
B-lymphocyte cell-surface antigen B1 M	IS4A1 S2	89	·		5.5	12.0	K.NEEDIEIIPIQEEEEEETETNFPEPPQDQESS*PIENDSSP
B-Raf <sub>Bl</sub>		46			92.2	50.0	R.RDS*SDDWEIPDGQITVGQR.I
B-Raf <sub>B</sub>	RAF S3				23.6	77.7	R.SSS*APNVHINTIEPVNIDDLIR.D  R.SS*SAPNVHINTIEPVNIDDLIR.D
B-Raf Bi					-0.3 9.0	52.5 55.0	R.RDSS*DDWEIPDGQITVGQR.I
B-Raf <sub>Bl</sub>			•		70.5	53.2	K.T*PIQAGGYGAFPVH
B-Raf B					9.5	42.8	R.SAS*EPSLNR.A
B-Raf B	RAF \$3	63		•••	1.8	39.8	R.DRS*SSAPNVHINTIEPVNIDDLIR.D
B-Raf B	RAF T3	73		<b>—</b>	-5.3	17.5	R.SSSAPNVHINT*IEPVNIDDLIR.D
Baculoviral IAP repeat containing protein 6 B		52			18.4	42.4	K.LEGDSDDLLEDS*DSEEHSR.S
Baculoviral IAP repeat containing protein 6B		689 <mark>S</mark> 4691T46	-		28.9	12.6	R.GT*PS*GT*QSSR.E
Baculoviral IAP repeat containing protein 6 B				Ξ.	12.0	80.7	K.FEINAYDPAIVQQLILSGDPSSGVDS*R.R  K.NAEEES*ESEAEEGD
Basic leucine zipper and W2 domains 1 <sub>B</sub>		45 <b>S</b> 347			100.0	92.9	K.NAEEES*ES*EAEEGD
		12 <b>S</b> 414	•		100.0	48.7	K.FVEWLQNAEEES'ES'EGEEN
Basic transcription factor 3 g	TF3 S1	58			15.8	52.9	K.QLTEMLPSILNQLGADS*LTSLR.R
BAT2 domain containing 1p	RRC2C S8	78		••	25.7	47.1	R.S*VEDVRPHHTDANNQSACFEAPDQK.T
BAT2 domain containing 1 <sub>P</sub>	RRC2C S1	248S1249			3.1	42.3	R.SES*S*DFEVVPK.R
BAT2 domain containing 1p		542		. =	15.3	14.3	R.S*FSSQRPVDR.Q
BAT2 domain containing 1 p		246S1249			7.4	35.0	R.S*ESS*DFEVVPK.R
BAT2 domain containing 1 p		246S1248			5.5	37.7	R.S*ES*SDFEVVPK.R  K.LPDLS*PVENK.E
Bcl 2 related proline rich protein B				-	100.0	35.2	R.LS*SDSFAR.L
BCL11A <sub>B</sub>		25 <b>S</b> 630	三		23.8	59.8	K.LLLGS*PSSLS*PFSK.R
BCL2 antagonist of cell death B,					53.1	28.4	R.RMS*DEFVDSFKK.G
BCL2 antagonist of cell death B	AD S9	9	• •		100.0	39.6	R.S*APPNLWAAQR.Y
BCL2 associated athanogene 2 <sub>B/</sub>	AG2 S1	9	-	•	-0.4	34.4	R.SS'SMADR.S
BCL2 associated athanogene 2 B		0			9.6	14.3	R.SSS*MADR.S
BCL2 associated transcription factor 1 B					100.0	33.3	K.AEGEPQEES*PLK.S
BCL2 associated transcription factor 1 B		85 <b>S</b> 287			16.4	36.3	R.YS*PS*QNSPIHHIPSRR.S
BCL2 associated transcription factor 1 Bi		87 <b>S</b> 297			12.4	17.4	R.YSPS'QNSPIHHIPS'RR.S  R.Y'SPS'QNSPIHHIPSRR.S
	Y2	84S287			17.6	29.0	
BCL2 associated transcription factor 1 Bi	CLAF1 \$2	85 <mark>S</mark> 290			19.5	52.6	R.YS*PSQNS*PIHHIPSRR.S
			•		19.5 55.7	52.6 87.2	R.YS'PSQNS'PIHHIPSRR.S  K.QKFNDS'EGDDTEETEDYR.Q

Peak Area %CV10 0 293 42	abundano	ots-Significant cha be at 5%FDR c with the minimum	ompared to	the			
3 88 88 100 100 100 100 100 100 100 100 1			CarT	RajiB			
Protein Name BCL2 associated transcription factor 1		Phosphosites Y284S290	5 2 G	9m 2m 5m	Ascor 13.4	MOWSE 64.1	Sequence R.Y*SPSQNS*PIHHIPSR:R
	BCLAF1	S285			22.0	78.3	R.YS*PSQNSPIHHIPSR.R
BCL2 associated transcription factor 1		\$397T402			63.3	125.1	K.FNDS*EGDDT*EETEDYR.Q
BCL2 associated transcription factor 1	BCLAF1	S658	•		32.3	61.5	R.IDIS*PSTLR.K
BCL2 associated transcription factor 1	BCLAF1	Y383		• • •	5.2	75.2	R.AEGEWEDQEALDY*FSDKESGK.Q
BCL2 associated transcription factor 1	BCLAF1	S385S389			6.0	47.8	R.AEGEWEDQEALDYFS*DKES*GK.Q
BCL2 associated transcription factor 1	BCLAF1	S222			39.4	55.8	K.SSATSGDIWPGLSAYDNS*PR.S
BCL2 associated transcription factor 1	BCLAF1	Y219			22.6	66.1	K.SSATSGDIWPGLSAY*DNSPR.S
BCL2 associated transcription factor 1	BCLAF1	S385			22.8	107.8	R.AEGEWEDQEALDYFS*DK.E
BCL2 associated transcription factor 1	BCLAF1	S121			13.8	29.5	R.SVS*SQR.S
BCL2 associated transcription factor 1	BCLAF1	S121S122			13.8	23.7	R.SVS*S*QR.S
BCL2 associated transcription factor 1	BCLAF1	S119S122			7.8	20.3	R.S*VSS*QR.S
BCL2 associated transcription factor 1	BCLAF1	S119S121			13.0	24.0	R.S*VS*SQR.S
BCL2 associated transcription factor 1	BCLAF1	S102S104			100.0	14.5	R.RHS*RS*PR.R
	BCLAF1	<b>S</b> 496			27.7	45.3	K.KETQS*PEQVK.S
BCL2 associated transcription factor 1	BCLAF1	T257S268			35.6	40.9	K.NT*PSQHSHSIQHS*PER.S
BCL2 associated transcription factor 1	BCLAF1	S531			100.0	49.0	R.EES*PLR.I
	BCLAF1	Y284S285	<b></b>		12.3	16.8	R.Y*S*PSQNSPIHHIPSRR.S
BCL2 associated transcription factor 1	BCLAF1	S339			100.0	15.1	K.FLKS*PPLHK.N
BCL2 associated transcription factor 1	BCLAF1	S287			37.7	78.4	R.YSPS*QNSPIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S119S121S122			100.0	12.7	R.S*VS*S*QRS*R.S
BCL2 associated transcription factor 1	BCLAF1	T494			10.9	18.1	K.ET*QSPEQVK.S
BCL2 associated transcription factor 1	BCLAF1	S183			14.9	37.8	K.S*QEEPKDTFEHDPSESIDEFNK.S
BCL2 associated transcription factor 1	BCLAF1	Y383S385		<u> </u>	13.8	61.9	R.AEGEWEDQEALDY*FS*DKESGK.Q
BCL2 associated transcription factor 1	BCLAF1	<b>S</b> 217			7.3	61.6	K.SSATSGDIWPGLS*AYDNSPR.S
BCL2 associated transcription factor 1	BCLAF1	T257S264			30.1	18.0	K.NT*PSQHSHS*IQHSPER.S
BCL2 associated transcription factor 1	BCLAF1	S281S287			9.0	16.1	R.SGSGSVGNGS*SRYSPS*QNSPIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S132Y133S135			5.7	19.6	R.RS*Y*RS*SR.S
BCL2 associated transcription factor 1	BCLAF1	Y133S135S136			11.8	13.1	R.RSY*RS*S*R.S
BCL2 associated transcription factor 1	BCLAF1	Y383S389			4.5	48.3	R.AEGEWEDQEALDY*FSDKES*GK.Q
BCL2 associated transcription factor 1	BCLAF1	S259S268			16.6	16.5	K.NTPS*QHSHSIQHS*PER.S
BCL2 associated transcription factor 1	BCLAF1	S648	Ħ.		100.0	36.9	R.QKS*PEIHR.R
BCL2 associated transcription factor 1	BCLAF1	S268			6.5	32.9	K.NTPSQHSHSIQHS*PER.S
BCL2 associated transcription factor 1	BCLAF1	S276S281			3.8	12.0	R.SGSGS*VGNGS*SRYSPSQNSPIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S225S228	: ا		16.0	52.3	R.S*PHS*PSPIATPPSQSSSCSDAPMLSTVHSAK.
BCL2 associated transcription factor 1	BCLAF1	S259			9.4	23.5	K.NTPS*QHSHSIQHSPER.S
BCL2 associated transcription factor 1	BCLAF1	S225T234			9.6	49.5	R.S*PHSPSPIAT*PPSQSSSCSDAPMLSTVHSAK.
BCL2 associated transcription factor 1		S36			16.9	16.3	K.RYSS*R.S
BCL2 associated transcription factor 1	BCLAF1	S276S287	-		3.8	14.1	R.SGSGS*VGNGSSRYSPS*QNSPIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S264			7.9	24.7	K.NTPSQHSHS*IQHSPER.S
BCL2 associated transcription factor 1	BCLAF1	S290	<b>—</b>		8.3	30.4	R.YSPSQNS*PIHHIPSR.R
BCL2 associated transcription factor 1		Y284		■.■	26.0	75.0	R.Y*SPSQNSPIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S225S230		÷.	9.0	54.0	R.S*PHSPS*PIATPPSQSSSCSDAPMLSTVHSAK.
BCL2 associated transcription factor 1		S660	<u> </u>		13.9	10.9	R.RIDISPS*TLRK.H
BCL2 associated transcription factor 1	BCLAF1	S512	<b>.</b>		7.4	20.3	K.LKDLFDYS*PPLHK.N
BCL2 associated transcription factor 1	BCLAF1	Y511				12.9	K.DLFDY*SPPLHK.N
BCL2 associated transcription factor 1	BCLAF1	S276S290			21.6	11.9	R.SGSGS*VGNGSSRYSPSQNS*PIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S287S290			25.1	42.3	R.YSPS*QNS*PIHHIPSR.R
BCL2 associated transcription factor 1	BCLAF1	S119S121S122			100.0	13.0	R.S*VS*S*QR.S
BCL2-like 11 (apoptosis facilitator)	BCL2L11	<b>S</b> 77	• •		100.0	64.8	R.S*PLFIFMR.R
BCL2-like 11 (apoptosis facilitator)	BCL2L11	S86S87S90			100.0	20.8	R.RS*S*LLS*R.S
BCL2-like 11 (apoptosis facilitator)	BCL2L11	S94			7.6	33.7	R.SSS*GYFSFDTDR.S
BCL2L13	BCL2L13	S371			-0.3	74.5	K.SS*PATSLFVELDEEEVK.A
BCL6 corepressor	BCOR	S747S749	<u> </u>		100.0	11.2	R.S*RS*HER.A
BCR	BCR	S1264			42.3	21.6	K.RQS*ILFSTEV
BCR	BCR	S315Y316			10.9	13.5	R.RS*Y*SPR.S
Beta adaptin 3A	AP3B1	<b>S</b> 276			39.3	30.1	K.NFYES*DDDQKEK.T
Beta adaptin 3A	AP3B1	Y274			1.0	19.1	K.EGDELEDNGKNFY*ESDDDQKEK.T
Beta adaptin 3A	AP3B1	S750S752			100.0	57.3	K.GKS*DS*EDGEKENEK.S
Beta cysteine string protein	DNAJC5B	T16			10.3	28.1	R.TLSTT*GEALYEILGLHK.G
BHC110	KDM1A	S166	<b>—</b>		58.7	39.7	K.LPPPPPQAPPEEENES*EPEEPSGVEGAAFQSR
BHC110	KDM1A	S131S137			26.0	111.9	R.EMDESLANLS'EDEYYS'EEER.N

Peak Area	0 abundano	ts-Significant cha e at 5%FDR c with the minimum	ompared to	the			
-5 -3 0	42 PSM	with the minimum					
5 >10	>100  Protein Name Gene	Phosphosites	CarT	RajiB E E E	Ascor	MOWSE	Sequence
	BHC110 KDM1A	Y136S137			9.9	32.9	R.EMDESLANLSEDEYY*S*EEER.N
	BHC110 KDM1A	S126S137			12.5	50.2	R.EMDES'LANLSEDEYYS'EEER.N
	BHC110 KDM1A	\$126\$131 \$849		•	4.4	11.3	R.EMDES*LANLS*EDEYYSEEER.N  R.QATPGVPAQQS*PSM
	BHC80 PHF21A	T446S455	-		19.3	25.6	K.YNAVLGFGALTPT*SPQSSHPDS*PENEK.T
		T446S451			5.7	27.6	K.YNAVLGFGALTPT*SPQSS*HPDSPENEK.T
	BHC80 PHF21A	T446S450			4.3	25.5	K.YNAVLGFGALTPT*SPQS*SHPDSPENEK.T
	BHC80 PHF21A	\$447\$455			19.2	15.8	K.YNAVLGFGALTPTS*PQSSHPDS*PENEK.T
	BIG1 ARFGEF1	S1569			73.2	39.7	K.S*VDIHDSIQPR.S
	BIG1 ARFGEF1				4.3	67.9	R.Y*GSLNSLES*TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1				3.0	97.6	R.YGS'LNSLESTSSSGIGS'YSTQMSGTDNPEQFEVLK.Q
	BIG1 AREGEE1				7.6	98.1	R.YGS*LNSLES*TSSSGIGSYSTQMSGTDNPEQFEVLK.Q  R.YGSLNS*LES*TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1				3.7	92.9	R.YGS*LNS*LES*TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1			• • • •	0.4	88.4	R.YGS*LNSLESTSSSGIGSYS*TQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1		•		-4.5	33.2	R.YGSLNSLESTSSSGIGS*Y*STQM#SGTDNPEQFEVLK.Q
	BIG1 ARFGEF1			•	2.0	92.8	R.YGS*LNSLESTSSS*GIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1	S664Y679			4.7	66.8	R.YGS*LNSLESTSSSGIGSY*STQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1	S670S673T681			4.9	17.0	R.YGSLNSLES*TSS*SGIGSYST*QMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1			•	3.6	53.0	R.Y"GSLNS"LESTSSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1			-	4.6	38.2	R.YGSLNSLESTSSSGIGS*YS*TQMSGTDNPEQFEVLK.Q
	BIG1 AREGEE1				5.1	31.5	R.YGSLNSLES'T'SSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1 BIG1 ARFGEF1				6.2	19.5	R.YGSLNSLES*TSS*SGIGSYS*TQMSGTDNPEQFEVLK.Q  R.YGSLNSLES*TS*SSGIGS*YSTQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1				5.2	20.8	R.YGSLNSLES'T'SSSGIGS'Y'STQMSGTDNPEQFEVLK.Q
	BIG1 ARFGEF1				2.5	70.1	R.YGS*LNSLEST*SSSGIGSYSTQMSGTDNPEQFEVLK.Q
	BIN2 BIN2	S458	•	•	7.8	48.4	R.ASLGTGTAS*PR.T
	BIN2 BIN2	<b>S</b> 357			24.4	35.4	R.AKS*QEEVLPSSTTPSPGGALSPSGQPSSSATEVVLR.T
	BIN2 BIN2	\$273\$277			10.3	32.4	R.TATVSS*PLTS*PTSPSTLSLK.S
	BIN2 BIN2	S259	• •		67.1	35.7	R.S*LVISPPVR.T
	BIN2 BIN2	T454	÷		8.4	35.4	R.ASLGT*GTASPR.T
	eracting 3, homolog MEPCE	S254			39.4	31.1	K.DITDPLSLNTCTDEGHVVLAS*PLK.T  R.DEVVS*PLPSALQGPSGSLSAPPAASVISAPPSSSSR.H
	eracting 3, homolog MEPCE	\$330 \$334			7.7	71.1 52.6	R.DEVVSPLPS*ALQGPSGSLSAPPAASVISAPPSSSSR.H
	eracting 3, homolog MEPCE	S342			-0.3	42.8	R.DEVVSPLPSALQGPSGS*LSAPPAASVISAPPSSSSR.H
Blo	ck of proliferation 1 <sub>BOP1</sub>	S126S127			91.4	114.9	R.IGDEYAEDS*S*DEEDIR.N
Blo	ck of proliferation 1 <sub>BOP1</sub>	Y122S126			6.3	27.6	R.IGDEY*AEDS*SDEEDIR.N
Blo	ck of proliferation 1 <sub>BOP1</sub>	S126T135	· -		10.5	17.8	R.IGDEYAEDS*SDEEDIRNT*VGNVPLEWYDDFPHVGYDLDGR.R
		T63S65	-		73.4	48.2	R.VAGEAAET*DS*EPEPEPEPTAAPR.D
	cible protein kinase BMP2K	<b>S</b> 949			35.1	68.7	K.SES*NEDLFGLVPFDEITGSQQQK.V
BMP2 indu	cible protein kinase BMP2K	S947		<del></del>	10.0	108.7	K.S'ESNEDLFGLVPFDEITGSQQQK.V
DWG4 ""	BMS1	S639	=		3.1	33.4	K.LGPQNFIDETS*DIENLLKEEEDYKEENNDSK.E
	ne assembly protein BMS1	T638				58.0	K.LGPONFIDET'SDIENLLK.E  R.DMPGGFLFEGLS'DDEDDFHPNTR.S
	like nteracting protein 1 MAP1S	S230 T782			123.4	71.6	R.
	nteracting protein 1 <sub>MAP1S</sub>	T638S640			36.2	71.6	ACCI CAEET*BDTCVCECI DTI CHCHDI/DI ADCIANCENENTECECI/
	nteracting protein 1 MAP1S	S731			-0.4	14.7	R.SAS'PHDVDLCLVSPCEFEHRK.A
BPY2 i	nteracting protein 1 <sub>MAP1S</sub>	<b>S</b> 657			26.0	29.5	RLSLS*PLR.G
BPY2 i	nteracting protein 1 <sub>MAP1S</sub>	<b>S</b> 729			5.5	29.2	R.S*ASPHDVDLCLVSPCEFEHR.K
BPY2 i	nteracting protein 1 MAP1S	<b>S</b> 759		-	25.4	34.7	K.AVPMAPAPAS*PGSSNDSSAR.S
del	hain alpha-ketoacid BCKDK nvdrogenase kinase	T32		Ţ.	-0.3	44.2	R.ST*SATDTHHVEMAR.E
del	hain alpha-ketoacid BCKDK nydrogenase kinase	<b>S</b> 31			7.4	13.1	R.S*TSATDTHHVEMAR.E
E1	ncid dehydrogenase BCKDHA I. alpha polypeptide	Y353			7.1	11.1	R.SVDEVNY*WDKQDHPISR.L
E1	I, alpha polypeptide	\$347			90.2	61.3	R.S'VDEVNYWDK.Q  R.IGHHS'TSDDSSAYR.S
E1	I. alpha polypeptide  BRCA1 BRCA1	\$337 \$1217\$1218			26.0	87.6	R.IGHHS'TSDDSSAYR.S  K.KLESSEENLS'S'EDEELPCFQHLLFGK.V
	BRCA1 BRCA1	\$1217\$1218 \$1189\$1191			36.9	79.7	R.S'PS'PFTHTHLAQGYR.R
	BRCA1 BRCA1	S1189T1194			19.1	30.9	R.S'PSPFT'HTHLAQGYR.R
	BRCA1 BRCA1	S1212S1218			3.5	10.8	K.LESS*EENLSS*EDEELPCFQHLLFGK.V
	BRCA1 BRCA1	S1189		•	20.5	51.1	R.S'PSPFTHTHLAQGYR.R
	BRCA1 BRCA1	\$1211\$1212\$12			100.0	30.1	K.KLES"S"EENLS"S"EDEELPCFQHLLFGK.V
BRCA2 and CDKN1A	interacting protein BCCIP	<b>S</b> 42			100.0	79.8	R.DEEEEKEVENEDEDDDDS*DKEK.D

<-10 o abundan	ots-Significant cha ce at 5%FDR of with the minimum	compared to	the			
3 42 PSM			RajiB			
>100 >100 >100 Protein Name Gene	Phosphosites	- 2 5 B		Ascor	MOWSE	Sequence
BRCA2 and CDKN1A interacting protein BCCIP	S112S115			8.9	39.9	K.QTDVS*EDS*NDDMDEDEVFGFISLLNLTER.K
Brefeldin A-inhibited guanine nucleotide-ARFGEF exchange protein 2				40.9	39.0	R.ELEKPIQSKPQS*PVIQAAAVS*PK.F
Brefeldin A-inhibited guanine nucleotide-ARFGEF.				71.3	66.7	R.ELEKPIQSKPQSPVIQAAAVS*PK.F
BRG1 associated factor 180 KD PBRM1  BRG1 associated factor 180 KD PBRM1	S10S14			15.1	58.3	R.ATS*PSSS*VSGDFDDGHHSVSTPGPSR.K  R.ATS*PS*S*VSGDFDDGHHSVSTPGPSR.K
BRG1 associated factor 180 KD PBRM1	\$10\$12\$13\$14 \$371\$375T377			7.4	39.3	R.YEEGES'EAES'IT'SFMDVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	S371S375S378			12.0	26.6	R.YEEGES*EAES*ITS*FMDVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	S375T377S378			6.8	10.9	R.YEEGESEAES*IT*S*FMDVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	\$353\$355	•		9.3	84.8	R.LSAITMALQYGS'ES'EEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1	Y351S353			9.8	45.1	R.LSAITMALQY*GS*ESEEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1	T9S10S12S14		• •	5.0	14.5	R.AT*S*PS*SS*VSGDFDDGHHSVSTPGPSR.K
BRG1 associated factor 180 KD PBRM1	S10S13S14S16	-		6.4	31.9	R.ATS*PSS*S*VS*GDFDDGHHSVSTPGPSR.K
PBRM1	S375T377			2.7	63.3	R.YEEGESEAES*IT*SFM#DVSNPFYQLYDTVR.S
PBRM1	S371S375			3.6	50.9	R.YEEGES*EAES*ITSFM#DVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	T346Y351		•	4.3	12.0	R.LSAIT*MALQY*GSESEEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1  BRG1 associated factor 180 KD PBRM1	Y366S371			4.4	63.2	R.Y*EEGES*EAESITSFMDVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1  BRG1 associated factor 180 KD PBRM1	Y366T377 S178		-	3.9	13.2	R.Y*EEGESEAESIT*SFMDVSNPFYQLYDTVR.S  K.GEADDEDDDEDGQDNQGTVTEGSS*PAYLK.E
BRG1 associated factor 180 KD PBRM1	\$178 \$343T346	•		10.3	43.1	R.LS*AIT*MALQYGSESEEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1	T346S353			6.7	23.4	R.LSAIT*MALQYGS*ESEEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1	Y351S355			6.5	51.5	R.LSAITMALQY*GSES*EEDAALAAAR.Y
BRG1 associated factor 180 KD PBRM1	<b>S</b> 177		•	18.0	40.1	K.GEADDEDDDEDGQDNQGTVTEGS*SPAYLK.E
BRG1 associated factor 180 KD PBRM1	S371T377	÷		8.4	78.0	R.YEEGES*EAESIT*SFM#DVSNPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	S371S383			4.5	41.8	R.YEEGES*EAESITSFMDVS*NPFYQLYDTVR.S
BRG1 associated factor 180 KD PBRM1	\$375\$378			6.3	12.8	R.YEEGESEAES*ITS*FMDVSNPFYQLYDTVR.S
Bromo adjacent homology domain BAHD1 containing 1	S121			100.0	106.3	R.LAS'LNAEALNNLLLER.E
Bromodomain adjacent to zinc finger BAZ1A domain 1A	S820			58.5	76.8	R.NSTADIS*IGEEER.E
Bromodomain adjacent to zinc finger BAZ1A domain 1A	S420			45.1	40.5	K.IAEQDFSYFFPDDPPTFIFS*PANR.R
Bromodomain adjacent to zinc finger BAZ1A domain 1A  Bromodomain adjacent to zinc finger BAZ1A	T731			28.9	22.4	K.ELDQDMVT*EDEDDPGSHKR.G  R.KRQS*PEPSPVTLGR.R
domain 1A  Bromodomain adjacent to zinc finger BAZ1A	\$1531 \$349	-		56.4	41.3	K.K.LSGS*PLK.V
domain, 1B  Bromodomain adjacent to zinc finger BAZ1B	S1468			113.7	145.4	R.LAEDEGDS*EPEAVGQSR.G
domain. 1B  Bromodomain adjacent to zinc finger BAZ1B	\$708T710	===		3.5	64.2	R.SDVQEESEGS*DT*DDNKDSAAFEDNEVQDEFLEK.L
domain. 1B  Bromodomain adjacent to zinc finger BAZ1B domain, 1B	T710S716			4.0	64.3	R.SDVQEESEGSDT*DDNKDS*AAFEDNEVQDEFLEK.L
Bromodomain adjacent to zinc finger BAZ1B domain, 1B	S705S708	•		2.9	40.0	R.SDVQEES*EGS*DTDDNKDSAAFEDNEVQDEFLEK.L
Bromodomain and PHD finger containing 1 BRPF1	S238		•	14.1	36.5	R.KTEGVS*PIPQEIFEYLMDR.L
Bromodomain containing 1 BRD1	\$1052\$1055			17.4	36.6	R.VHGEPTS*DLS*DID
Bromodomain containing 4 BRD4	S1117		•	100.0	26.7	K.IHS'PIIR.S
BRD4	S1064S1083			13.9	10.7	R.EAPS*PLM#IHSPQMSQFQSLTHQS*PPQQNVQPK.K
Bromodomain containing 4BRD4	S1070S1083			24.3	23.2	R.EAPSPLMIHS*PQMSQFQSLTHQS*PPQQNVQPK.K
Bromodomain containing 4 BRD4	\$1064\$1070\$1		• • •	35.3	18.8	R.EAPS*PLMIHS*PQMSQFQSLTHQS*PPQQNVQPK.K
Bromodomain containing 4 <sub>BRD4</sub>	T1080 S1078S1083			21.4	27.0	R.EAPSPLMIHSPQMSQFQSLT*HQSPPQQNVQPK.K  R.EAPSPLMIHSPQMSQFQS*LTHQS*PPQQNVQPK.K
Bromodomain containing 4 BRD4	\$1078\$1083 \$1083			7.2	11.0	R.EAPSPLMIHSPQMSQFQSLTHQS*PPQQNVQPK.K
Bromodomain containing 8 BRD8	T264S268			27.8	45.1	KAT*PPPS*PLLSELLK.K
Bromodomain containing 8 BRD8	T264			41.9	52.1	K.AT*PPPSPLLSELLK.K
Bromodomain containing 8 BRD8	S268S272			1.6	38.8	KATPPPS*PLLS*ELLK.K
BTB POZ domain containing 14B NACC1	S140S151	• -	•	2.5	21.0	K.VSSPSCDSQGLHAEEAPS*SEPQSPVAQTS*GWPACSTPLPLVSR.
BTB POZ domain containing 14B NACC1	T150S151		• •	6.9	21.7	K.VSSPSCDSQGLHAEEAPSSEPQSPVAQT*S*GWPACSTPLPLVSR.
BTB POZ domain containing 14B NACC1	S127S130		•	6.6	25.1	K.VSSPS*CDS*QGLHAEEAPSSEPQSPVAQTSGWPACSTPLPLVSR.
BTB POZ domain containing 14B NACC1	S124S125		•		28.6	K.VS*S*PSCDSQGLHAEEAPSSEPQSPVAQTSGWPACSTPLPLVSR.
BTB POZ domain containing 14B NACC1	S124	<u> </u>			18.5	K.VS*SPSCDSQGLHAEEAPSSEPQSPVAQTSGWPACSTPLPLVSR.
BTB POZ domain containing 14B NACC1	S140S141			4.6	31.9	K.VSSPSCDSQGLHAEEAPS*S*EPQSPVAQTSGWPACSTPLPLVSR.
BTKI <sub>IBTK</sub>	S1045		==	44.5	59.3	R.DLQS*PDFTTGFHSDKIEAK.V  R.IDTTSSASWVAGSFS*PVS*PPVVDLR.T
BTKI	S1113S1116 Y996			9.0	19.2	R.SDSSGGY*NLSDIQSPSSTGLLK.S
BTKI IBTK	Y996 S1111S1116			19.6	44.7	R.IDTTSSASWVAGS*FSPVS*PPVVDLR.T
	S992			5.1	22.6	R.SDS*SGGYNLSDIIQSPSSTGLLK.S
BTKI <sub>IBTK</sub>			•	8.0	23.3	R.SDSS*GGYNLSDIIQSPSSTGLLK.S
BTKI IBTK	S993					
	S993 T1102S1116			2.4	12.1	R.IDTT*SSASWVAGSFSPVS*PPVVDLR.T
BTKI <sub>IBTK</sub>			-	2.4	12.1	R.IDTT*SSASWVAGSFSPVS*PPVVDLR.T  K.SPGDFTS*AAQLASTPFHK.L
BTKI <sub>IBTK</sub>	T1102S1116		<u>.</u>			

Peak Area	abundan	kts-Significant cha ce at 5%FDR of with the minimum	compared to peak area f	the or a given			
5 >100	otein Name Gene	Phosphosites		RajiB E E E	Ascor	MOWSE	Sequence
	BUB1 BUB1	S596	- 11 10		1.8	38.8	K.S*PGDFTSAAQLASTPFHK.L
Butyrate induced	transcript 1 HACD3	S114	••••		100.0	74.2	R.WLDES*DAEMELR.A
	Bystin BYSL	S98			110.5	96.3	R.MPQDGS*DDEDEEWPTLEKA  K.QTEVETVMS*EVS*GFPMPQLDPR.V
	Bystin BYSL	\$167\$170 \$167			13.1	52.2 60.8	K.QTEVETVMS-EVSGFPMPQLDPR.V
	Bystin BYSL	T164S170			7.0	15.0	K.QTEVET*VMSEVS*GFPMPQLDPR.V
	Bystin BYSL	T164	•		12.8	23.7	K.QTEVET*VMSEVSGFPMPQLDPR.V
	Bystin BYSL	T160		•	6.7	22.6	K.QT*EVETVMSEVSGFPMPQLDPR.V
c-Mpl bin	ding protein LARP4	T601			9.5	89.2	R.AST*ASPCNNNINAATAVALQEPR.K
c-Mpl bin	ding protein LARP4	S603			15.8	65.4	R.ASTAS*PCNNNINAATAVALQEPR.K
	ding protein LARP4	S589	-		37.7	38.4	K.DGLNQTTIPVS*PPSTTKPSR.A
c-Mpl bin	c-Myb MYB	\$600		<u> </u>	7.4	50.2	R.AS'TASPCNNNINAATAVALQEPRK  R.HSIYS'S'DEDDEDFEMCDHDYDGLLPK.S
	c-Myc <sub>MYC</sub>	S11S12 T73S77			13.7	29.1 35.5	K.KFELLPT'PPLS'PSRR.S
	c-Myc <sub>MYC</sub>	S86	•		22.3	53.4	R.SGLCS*PSYVAVTPFSLR.G
	c-Myc MYC	T73S79			24.7	17.6	K.FELLPT*PPLSPS*RR.S
	c-Src SRC	<b>S</b> 17	•		125.2	55.9	R.S*LEPAENVHGAGGGAFPASQTPSKPASADGHR.G
C-X-C chemokine rec	eptor type 5 CXCR5	<b>S</b> 359			13.4	20.7	R.RSS*LSESENATSLTTF
	iced protein FAM117A				100.0	71.6	R.S*LEGLNQELEEVFVK.E
	iced protein FAM117A	\$305\$317\$319			8.7	12.2	K.AS*SPGHPAFLEDGS*PS*PVLAFAAS*PRPNHSYIFK.R
	orf3 protein CEP55	S428			14.0	115.0	K.S'PTAALNESLVECPK.C
	rf47 protein PROSER2	T430	-		3.9	62.6 37.8	K.SPT"AALNESLVECPK.C  R.AQVLATIHGHAGAFPAAGDAGEGAPGGGS"SPER.V
	rf69 protein ERLIN1	S323			153.9	37.8	R.ES*SLPSK.E
	rf69 protein ERLIN1	S324			13.9	38.2	R.ESS*LPSK.E
C10a	rf86 protein NSMCE4#	A \$30\$32		• • • •	30.3	22.1	R.S'RS'PLSPR.S
C10a	rf86 protein NSMCE4A	A S63S72			4.9	28.6	R.EAPERPSLEDTEPSDS*GDEMMDPAS*LEAEADQGLCR.Q
C10c	rf86 protein NSMCE4A	T58S61S72			5.1	33.6	R.EAPERPSLEDT"EPS"DSGDEMMDPAS"LEAEADQGLCR.Q
	rf23 protein PPP6R3	<b>S</b> 537			100.0	131.5	R.IQQFDDGGS*DEEDIWEEK.H
	orf5 protein TIGAR	S159			8.0	53.4	K.EQFSQGSPS*NCLETSLAEIFPLGK.N
	orf5 protein TIGAR	S157			21.4	53.5	K.EQFSQGS'PSNCLETSLAEIFPLGK.N  K.NSVHEQEAINS'DPELSNCENFOK.T
	orf3 protein SKA3	S119 S155			71.2	81.1	R.S*POLSDFGLERY
	orf8 protein CHAMP1	S476			100.0	49.3	R.GGS*PDLWK.S
C13	orf8 protein CHAMP1				67.7	14.4	K.LAPVPS*PEPQKPAPVS*PESVK.A
C13	orf8 protein CHAMP1	<b>S</b> 627		•	16.9	79.1	K.DNQESS*DAELSSSEYIK.T
C13	orf8 protein CHAMP1	S445S452			40.6	53.2	R.KPSGS*PDLWKLS*PDQR.K
	orf8 protein CHAMP1				54.2	34.0	R.RPAPA\S*PGSWKPGPPGS*PRPWK.S
	orf8 protein CHAMP1				29.7	68.2	R.KPSPSES*PEPWKPFPAVSPEPR.R
	orf8 protein CHAMP1				18.4	52.0	R.KPS*PSESPEPWKPFPAVSPEPRR
	orf8 protein CHAMP1	\$282\$297 \$282\$284			56.8	29.6	R.KPS'PSESPEPWKPFPAVS'PEPR.R  R.KPS'PS'ESPEPWKPFPAVSPEPR.R
	orf8 protein CHAMP1	\$282\$284 \$282\$286			21.7	34.2 40.8	R.KPS'PSES'PEPWKPFPAVSPEPRR  R.KPS'PSES'PEPWKPFPAVSPEPRR
	orf8 protein CHAMP1	S652S653			7.6	67.1	K.GQESS'S'DQEQVDVESIDFSK.E
C13	orf8 protein CHAMP1	S651S653		<del></del>	49.6	130.4	K.GQES*SS*DQEQVDVESIDFSK.E
C13	orf8 protein CHAMP1	\$432\$436	<del></del>		100.0	41.1	R.S*PAGS*PELR.K
	orf8 protein CHAMP1		-		63.3	45.3	R.KPS'GSPDLWKLS'PDQR.K
	orf8 protein CHAMP1				20.3	70.1	R.KPSPS'ESPEPWKPFPAVSPEPR.R
	orf8 protein CHAMP1				55.5	61.7	K.DNQES*SDAELSSSEYIK.T
	orf8 protein CHAMP1				68.5	52.6	K.GQES'S'SDQEQVDVESIDFSK.E
	orf8 protein CHAMP1				22.5	30.6 41.0	R.TTS*PEPRK  R.KTS*PASLDFPESQK.S
	orf8 protein CHAMP1	\$459 \$445			16.9 5.9	38.5	R.KPSGS*PDLWK.L
	orf8 protein CHAMP1	S627S632		-	13.0	84.2	K.DNQESS'DAELS'SSEYIK.T
C13	orf8 protein CHAMP1	\$427\$432\$436			100.0	13.0	R.KPGPPLS*PEIRS*PAGS*PELR.K
C13	orf8 protein CHAMP1	S284S286			20.1	34.7	R.KPSPS*ES*PEPWKPFPAVSPEPR.R
C13	orf8 protein CHAMP1	\$282\$286\$297	•		24.8	19.4	R.KPS'PSES'PEPWKPFPANS'PEPR.R
	orf8 protein CHAMP1	T274		-	-0.2	28.9	R.TT*SPEPR.K
	orf8 protein CHAMP1	S627S633		<u> </u>	8.7	79.5	K.DNQESS*DAELSS*SEYIK.T
	orf8 protein CHAMP1	\$626\$632		_	7.6	30.4	K.DNQES*SDAELS*SSEYIK.T
	orf8 protein CHAMP1	S311S319	-		24.9	29.0	R.RPAPAVSPGS*WKPGPPGS*PRPWK.S  K.DNQES*S*DAELSSSEYIK.T
		S626S627		-	4.1	30.2	Connect of Dribbook Lines

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-3 0 3	42 PSM 71 86		CarT	RajiB			
5 >10	>100 Protein Name Gene	Phosphosites	5 E E		Ascor	MOWSE	Sequence
	C13orf8 protein CHAMP1	S286S297			49.6	26.6	R.KPSPSES"PEPWKPFPAVS"PEPR.R
	C13orf8 protein CHAMP1	S626S633		<u>.</u>	12.4	48.2	K.DNQES'SDAELSS'SEYIK.T
	C14orf103 protein ATG2B	S1018T1022		_=	7.4	27.0	K.SAVHYDEESGS*EEET*LQYFSTVDPNYR.S
	C14orf103 protein ATG2B	\$1016\$1018 \$1016\$1022			7.8	34.2 25.8	K.SAVHYDEES'GS'EEETLQYFSTVDPNYR.S  K.SAVHYDEES'GSEEET'LQYFSTVDPNYR.S
	C14orf106 protein MIS18BP				13.5	27.5	R.NTSNIPVILEPET'EES'ENEFYIK.Q
	C14orf11 protein EAPP	S109S111	=		48.4	67.9	R.YYDDIYFDS*BEDDR.A
	C14orf11 protein EAPP	Y106S111	=		21.1	28.7	R.YYDDIY'FDSDS'EDEDRA
	C14orf11 protein EAPP	Y106S109	•		9.7	62.9	R.YYDDIY'FDS'DSEDEDRA
	C14orf11 protein EAPP	\$17\$24\$25\$26	_		41.5	23.6	R.LPDDYDPYAVEEPS'DEEPALS'S'S'EDEVDVLLHGTPDQK.R
	NGDN	S142S143			131.4	103.2	K.LS"S"EDEEEDEAEDDQSEASGK.K
	C14orf133 protein VIPAS39		-		13.7	67.9	R.TRPGS*FQSLSDALSDTPAK.S
	C14orf133 protein VIPAS39				22.6	67.1	R.T'RPGSFQSLSDALSDTPAK.S
	C14orf133 protein VIPAS39		-		7.3	31.3	R.TRPGSFQS*LSDALSDTPAK.S  R.NS*FSSYAQLPKPT*S*TYSLSSFFR.G
	C14orf133 protein VIPAS39				13.1	12.8	R.NSFSYSYAQLPKPT'STYSLSSFFR.G
	C14orf133 protein VIPAS39		-		15.2	16.4	R.NS'FS'S'YAQLPKPTSTYSLSSFFR.G
	C14orf133 protein VIPAS39				4.4	14.1	R.NS'FSSYAQLPKPTS'TYSLSSFFR.G
	C14orf133 protein VIPAS39				12.9	13.0	RNS'FSS'Y'AQLPKPTSTYSLSSFFR.G
	C14orf133 protein VIPAS39				20.3	22.6	R NS'FSSYAQLPKPT'STYSLSSFFR.G
	C14orf133 protein VIPAS39	S96T104S105			12.9	13.6	R.NSFSS*YAQLPKPT*S*TYSLSSFFR.G
	C14orf171 protein TMEM630	S77S80	•		17.4	46.6	RLALLIHNDS*LTS*LIYGEQSEK.T
	C14orf171 protein TMEM630	S77T79			15.1	44.5	RLALLIHNDS'LT'SLIYGEQSEK.T
	C14orf35 protein NAA30	<b>S</b> 55			40.2	15.7	R.S'PAGGESATVAAK.G
	C14orf4 protein IRF2BPL	S615S639	<u> </u>		6.8	12.6	R.TTPPES'APQNGPSPMAALMSVADTLGTAHS'PK.D
	C18orf25 protein C18orf25				29.4	31.7	R.RDS*SES*QLASTESDKPTTGR.V
	C18orf25 protein C18orf25	S67S69	÷.		8.6	11.4	R.RDSS*ES*QLASTESDKPTTGR.V
	C19orf14 protein WDR62	T1021S1022	•••			23.6	R.FAT'S'LPHFPGCAGPTEDELSLPEGPSVPSSSLPQTPEQEK.F
	C19orf14 protein WDR62	S1228	<u></u>		16.8	157.1	R.SIS*LGDSEGPIVATLAQPLR.R
	C19orf14 protein WDR62	S1249	===		5.8	79.9	R RPSS*VGELASLGQELQAITTATTPSLDSEGQEPALR S  R.RPS*SVGELASLGQELQAITTATTPSLDSEGQEPALR S
	C19orf14 protein WDR62	S1248			29.8	55.1	R.FATSLPHFPGCAGPTEDELSLPEGPSVPSS*SLPQT*PEQEK.F
	C19orf14 protein WDR62	\$1048T1053 \$1248T1268			24.3	15.7	R.RPS*SVGELASLGQELOAITTATT*PSLDSEGGEPALR.S
	C19orf14 protein WDR62	\$1249T1268	==		6.2	30.7	R.RPSS*VGELASLGQELQAITTATT*PSLDSEGQEPALR.S
	C19orf14 protein WDR62	S1255T1264			15.0	30.9	R.RPSSVGELAS*LGQELQAIT*TATTPSLDSEGQEPALR.S
	C19orf14 protein WDR62	S1248S1249			6.6	14.8	R.RPS'S'VGELASLGQELQAITTATTPSLDSEGQEPALR.S
	C1orf16 protein SMG7	S520		•	34.0	60.2	K.ENLILQETSVIESLAADGS*PGLK.S
	C1orf24 protein FAM129A	S579T584	•		1.2	37.5	K.HNLFEDNMALPSES*VSSLT*DLKPPTGSNQASPAR.R
	C1orf24 protein FAM129A	S577S581			2.9	37.7	K.HNLFEDNMALPS'ESVS'SLTDLKPPTGSNQASPARR
	C1orf24 protein FAM129A	S577S592S596			7.9	24.5	K,HNLFEDNMALPS'ESVSSLTDLKPPTGS'NQAS'PAR.R
	C1orf24 protein FAM129A				4.9	70.2	K.HNLFEDNMALPSES*VSS*LTDLKPPTGSNQASPARR
	C1orf24 protein FAM129A				3.6	48.5	K.HNLFEDNMALPSES"VS"SLTDLKPPTGSNQASPARR
	C1orf24 protein FAM129A				10.2	30.8	K.HNLFEDNMALPSESVS*SLTDLKPPTGS*NQAS*PAR.R
	C1orf24 protein FAM129A				11.0	17.1	K.HNLFEDNMALPSES'VSSLT'DLKPPT'GSNQAS'PAR.R
	C1orf24 protein FAM129A				1.8	13.8	KKHNLFEDNMALPS'ESVSS'LTDLKPPTGSNQASPAR.R
	C1orf24 protein FAM129A				9.9	45.6	K.HNLFEDNMALPSESVSSLTDLKPPTGS*NQAS*PARR
	C1orf24 protein FAM129A				15.9	25.5	K-HNLFEDNMALPSES'VSSLTDLKPPT'GSNQAS'PAR.R  K-HNLFEDNMALPSESVSSLT'DLKPPT'GSNQAS'PAR.R
	C1orf24 protein FAM129A				4.2	14.3	K.HNLFEDNMALPSESVSSLT*DLKPPT*GSNQAS*PAR.R  K.HNLFEDNMALPSESVS*LT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein FAM129A				14.5	25.2	K.HNLFEDNMALPSESVS'S'LTDLKPPTGSNQASPARR
	C1orf24 protein FAM129A				5.7	46.1	K.HNLFEDNMALPS*ES*VSSLTDLKPPTGSNQASPAR.R
	C1orf24 protein FAM129A				2.7	15.8	K.HNLFEDNMALPSES'VSSLTDLKPPT'GSNQASPAR.R
	C1orf24 protein FAM129A				12.5	34.3	K.HNLFEDNMALPSES'VSSLTDLKPPTGS'NQAS'PAR.R
	C1orf24 protein FAM129A	S579S581S592			2.0	17.2	K.HNLFEDNMALPSES*VS*SLTDLKPPTGS*NQAS*PARR
	C1orf24 protein FAM129A	S581T584T590			2.1	29.5	K.HNLFEDNMALPSESVS*SLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein FAM129A	S577S579T590			1.2	14.7	K.HNLFEDNMALPS'ES'VSSLTDLKPPT'GSNQAS'PAR.R
	C1orf24 protein FAM129A	S582T584			3.6	30.7	K.HNLFEDNMALPSESVSS'LT'DLKPPTGSNQASPARR
	C1orf24 protein FAM129A				16.8	19.2	K.HNLFEDNMALPS'ESVSSLT'DLKPPT'GSNQAS'PARR
	C1orf24 protein FAM129A				5.9	15.9	K.HNLFEDNMALPS'ESVSSLT'DLKPPTGS'NQAS'PARR
	C1orf35 protein MMTAG2		<b>=</b>		-0.4	13.2	R.RPAEATSS'PT'SPERPRH
	C1orf35 protein MMTAG2	S216T219			7.7	13.6	R.RPAEATS'SPT'SPERPR.H
	C1orf52 protein C1orf52	S158	<b></b>		4.3	65.7	R LLPEGEETLES'DDEKDEHTSK.K

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>10 Protein Name Gene C1orf52 protein C1orf52	Phosphosites T155	9 J J	§ 5 8	Ascor 50.1	MOWSE 50.4	Sequence RLLPEGEET*LESDDEKDEHTSK.K
C200RF1 protein TPX2	S486	•		100.0	39.3	K.S*PAFALK.N
C200RF1 protein TPX2	S738			32.7	35.0	K.SSDQPLTVPVS*PK.F
C20ORF121 protein TTPAL	S13S16			3.8	10.9	R.TSPS*VAS*LSENELPPPPEPPGYVCSLTEDLVTK.A
C20ORF121 protein TTPAL	S11S16	-		2.6	13.5	R.TS*PSVAS*LSENELPPPPEPPGYVCSLTEDLVTK.A
C20orf14 protein PRPF6	T275S279			24.4	52.1	K.GYLT*DLNS*MIPTHGGDINDIKK.A
C20orf14 protein PRPF6 C20orf14 protein PRPF6	T205T212T227T	•	-	9.0	18.1	R.QT*QFGGLNT*PYPGGLNTPYPGGMT*PGLMT*PGTGELDMR.K  K.GYLT*DLNSMIPT*HGGDINDIKK.A
C20orf6 protein ESF1	S153			18.8	49.4	K.FKIDSNIS*PK.K
C20orf6 protein ESF1	S663			95.5	77.6	K.ALAEEASEEELPS*DVDLNDPYFAEEVK.Q
C20orf6 protein ESF1	S657		<del></del>	40.8	63.0	K.ALAEEAS*EEELPSDVDLNDPYFAEEVK.Q
C20orf6 protein ESF1	S657S663			98.3	79.4	K.ALAEEAS*EEELPS*DVDLNDPYFAEEVK.Q
C20orf6 protein ESF1	T311S312T319			108.5	63.7	R.GKGNIET'S'SEDEDDT'ADLFPEESGFEHAWR.E
C20orf6 protein ESF1	S312S313T319 T311S313T319			6.9	49.0 30.5	R.GKGNIETS*S*EDEDDT*ADLFPEESGFEHAWR.E  K.GNIET*SS*EDEDDT*ADLFPEESGFEHAWR.E
C20orf6 protein ESF1	\$75\$77\$79\$82			21.7	51.1	R.FYDLS'DS'DS'NLS'GEDSK.A
C20orf6 protein ESF1	T311S312S313			15.9	23.2	R.GKGNIET*S*S*EDEDDTADLFPEESGFEHAWR.E
C20orf6 protein ESF1	T311T319	·-			43.9	R.GKGNIET*SSEDEDDT*ADLFPEESGFEHAWRE
C200RF77 protein RPRD1B	S164			42.4	76.2	R.TFQQIQEEEDDDYPGS*YSPQDPSAGPLLTEELIK.A
C200RF77 protein RPRD1B				6.6	46.7	R.TFQQIQEEEDDDY*PGSYSPQDPSAGPLLTEELIK.A
C20ORF77 protein RPRD1B	Y165			13.9	83.5	R.TFQQIQEEEDDDYPGSY*SPQDPSAGPLLTEELIK.A
C200RF77 protein RPRD1B	T149 S166		==		51.8	R.T*FQQIQEEEDDDYPGSYSPQDPSAGPLLTEELIK.A  R.TFQQIQEEEDDDYPGSYS*PQDPSAGPLLTEELIK.A
C21orf66 protein PAXBP1	\$557T563		•	13.5	83.5	K.M#ADHLEGLS*SDDEET*STDITNFNLEK.D
C21orf66 protein PAXBP1	S557S558	•••		22.5	97.5	K.MADHLEGLS*S*DDEETSTDITNFNLEK.D
C21orf66 protein PAXBP1	S558T563			11.6	24.9	K.MADHLEGLSS*DDEET*STDITNFNLEK.D
C22orf5 protein TMEM18	4 S402S403	<u> </u>		37.8	20.8	K.TLLLS*S*DDEF
C22orf9 protein KIAA093				35.2	63.4	R.NNRPAFFS*PSLKR.K
C22orf9 protein KIAA093	S367			40.6	39.6	R.SLVGS*WLK.L
C4orf9 protein NOP14  C4orf9 protein NOP14	T155S157	=		25.5	26.0	K.HNDIVDSDSDAEDRGT*LS*AELTAAHFGGGGGLLHK.K  K.HNDIVDS*DSDAEDRGT*LSAELTAAHFGGGGGLLHK.K
C4orf9 protein NOP14	S146T155 S146T161			5.9	12.2	K.HNDIVDS*DSDAEDRGTLSAELT*AAHFGGGGGLLHK.K
C4orf9 protein NOP14	S148T155			4.3	13.1	K.HNDIVDSDS*DAEDRGT*LSAELTAAHFGGGGGLLHK.K
NOP14	S146S148				35.3	K.HNDIVDS*DS*DAEDRGTLSAELTAAHFGGGGGLLHKK.T
C4orf9 protein NOP14	S148S157			1.5	14.1	K.HNDIVDSDS*DAEDRGTLS*AELTAAHFGGGGGLLHK.K
C5orf3 protein FAM114/		<u>.</u> :		37.0	66.1	K.ENENS*SPVAGAFGVFSTISTAVQSTGK.S
C5orf6 protein FAM53C				15.7	18.5	R.RFS*LSPS*LGPQASR.F
C5orf6 protein FAM53C	\$232\$234 \$209			31.3	14.9	R.RFS'LS'PSLGPQASR.F  R.LSQNSVNLSPSS'HANNLSVVTYSK.G
C6orf106 protein C6orf106				9.1	72.8	R.LSQNSVNLS*PSSHANNLSVVTYSK.G
C6orf106 protein C6orf106			•	1.2	14.2	R.LSQNS*VNLSPSSHANNLSVVTYSK.G
C6orf111 proteinPNISR	S290S304T309	•		24.3	58.0	R.SKFDS*DEEEEDTENVEAAS*SGKVT*R.S
C6orf111 protein PNISR	T297\$304T309	-		8.1	13.5	R.SKFDSDEEEEDT*ENVEAAS*SGKVT*R.S
C6orf111 protein PNISR	S290			18.8	61.5	R.SKFDS*DEEEEDTENVEAASSGK.V
C6orf111 proteinPNISR  C6orf111 proteinPNISR	\$290T309			11.8	55.2	R.SKFDS*DEEEEDTENVEAASSGKVT*R.S  R.SKFDS*DEEEEDTENVEAASS*GKVTR.S
C6orf111 proteinPNISR	\$290\$305 \$211			100.0	15.6 44.5	R.StPIALPVK.Q
C6orf111 protein <sub>PNISR</sub>	S393S396			4.3	27.3	K.QLAQSSALASLTGLGGLGGYGS*GDS*EDER.S
C6orf111 protein PNISR	S611S613			100.0	16.2	R.NRS'PS'RER.R
C6orf111 protein <sub>PNISR</sub>	S672		• • •	100.0	35.9	R.S'IDKDR.K
C6orf111 protein PNISR	S601			15.7	14.5	R.SNRNS*IER.E
C6orf111 protein PNISR	S726			25.8	57.5	R.SGS*ISVK.I
C6orf111 proteinPNISR  C6orf111 proteinPNISR	\$670\$672			100.0	22.9	R.S'RS'IDKDR.K
C6orf111 proteinpNISR	T383S396 S290S304			11.7	47.8 26.9	K.QLAQSSALASLT*GLGGLGGYGSGDS*EDER.S  R.SKFDS*DEEEEDTENVEAAS*SGK.V
C6orf111 protein PNISR	Y391S396			23.8	77.8	K.QLAQSSALASLTGLGGLGGY'GSGDS'EDER.S
C6orf111 protein PNISR	S311S313T326			12.8	11.3	R.S*PS*PVPQEEHSDPEMT*EEEKEYQMMLLTK.M
C6orf111 protein PNISR	\$290\$304\$305		<del></del>	25.9	47.6	R.SKFDS*DEEEEDTENVEAAS*S*GKVT*R.S
PNISR	S311S313S321		•	73.6	29.8	R.S'PS'PVPQEEHS'DPEMTEEEKEYQMMLLTK.M
C6orf111 protein PNISR	S724			20.3	47.3	R.S'GSISVK.I
C6orf113 protein ZUFSP	S253	<u> </u>	-	20.2	16.1	R.RSEES*R.Q
C6orf32 protein RIPOR2	T522			10.8	59.9	R.LT*SAEVPMATDR.L

Peak Area	%cv	White do	ts-Significant cha	nge in pept	ide			
10 -5 -3	0 29 42 71		e at 5%FDR o					
3 5	86 >100			CarT	RajiB			
>10	Protein Name		Phosphosites	§ 2 g	9 H H	Ascor	MOWSE	Sequence
	C6orf32 protein		S473	<u>==</u>			35.9	R. DOC! GOAGAEUI EI ENDWAEAL I OEGEEAGEI VOWEI DTGEGNITV O
	C6orf32 protein		S19			18.0	61.4	R.S'QSFAGFSGLQER.R
	C6orf32 protein		S21			33.7	62.6	R.SQS*FAGFSGLQER.R
	C6orf32 protein		\$535\$538	_		45.1	64.1	R.LLS*EGS*VGGESEGCR.S
	C6orf32 protein		S344T350			15.7	16.0	R.RMSMYS*QGTPET*PTFK.D
	C6orf32 protein		S523	=		13.9	19.8	RLTS'AEVPMATDR.L
	C7orf25 protein		Y343T350			12.2	23.1	R.RMSMY*SQGTPET*PTFK.D  R.GDIVAVNALLDHPEELQPS*ES*ES*DDEGPELLQVTR.V
	C8orf20 protein		\$208\$210\$212 \$152			65.4	43.0	R.SFS*MQDLR.S
	C8orf20 protein		\$194T196\$202			15.1	13.5	R.AGGLQDS*DT*EDECWS*DTEAVPR.A
	C8orf20 protein		S150			10.5	33.3	R.S*FSMQDLR.S
	C9orf25 protein	FAM219A				27.6	33.2	K.GYSSLDQSPDEKPLVALDT*DS*DDDFDMSR.Y
	C9orf42 protein	FAM122A	S143S147			21.9	52.3	K.RIDFIPVS*PAPS*PTR.G
	C9orf42 protein	FAM122A	T47		• • • •	34.7	56.4	R.SNSAPLIHGLSDT*SPVFQAEAPSAR.R
	C9orf42 protein	FAM122A	<b>S</b> 37			18.8	62.2	R.SNS*APLIHGLSDTSPVFQAEAPSAR.R
	C9orf42 protein	FAM122A	S45			16.9	51.9	R.SNSAPLIHGLS*DTSPVFQAEAPSAR.R
	C9orf42 protein	FAM122A	S143T149			20.9	48.2	K.RIDFIPVS*PAPSPT*R.G
	C9orf42 protein	FAM122A	<b>S</b> 270	Ħ		48.0	56.1	K.VSTTTDSPVS*PAQAASPFIPLDELSSK-
	C9orf42 protein	FAM122A	S276			1.8	19.3	K.VSTTTDSPVSPAQAAS*PFIPLDELSSK
	C9orf42 protein	FAM122A	T263S270			4.2	46.9	K.VST*TTDSPVS*PAQAASPFIPLDELSSK
	C9orf42 protein	FAM122A	\$267\$270	<del>ب</del>		-3.1	27.1	K.VSTTTDS*PVS*PAQAASPFIPLDELSSK
	C9orf42 protein	FAM122A	<b>S</b> 76	·		100.0	36.4	R.HGLLLPAS*PVR.M
	C9orf42 protein	FAM122A	S189			-0.2	56.3	R.SQS*PINCIRPSVLGPLK.R
	C9orf42 protein	FAM122A	S35		-	26.2	49.4	R.S*NSAPLIHGLSDTSPVFQAEAPSAR.R
	C9orf42 protein					41.4	34.0	K.VSTTTDSPVS*PAQAAS*PFIPLDELSSK
	C9orf42 protein			•		-5.3	21.1	K.VSTTTDS*PVSPAQAAS*PFIPLDELSSK
	C9orf42 protein				-	16.9	45.0	R.RNS*TTFPSR.H
	C9orf42 protein					5.5	19.8	K.VS*TTTDSPVS*PAQAASPFIPLDELSSK-
	C9orf55 protein					16.9	42.1	R.SIS*LSALVR.S  R.KSSTGS*IS*NVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein					27.6	55.6	R. SS*PVPEMI FESOELLEPVVDDVPK T
	C9orf55 protein				• • •	-0.3	35.7	R.SSPVPEMLEES*QELLEPVVDDVPK.T
			S769S774T775			8.1	35.6	R.KSSTGSIS*NVLFS*T*QDPVEDAVFGEATNLK.K
	C9orf55 protein					8.8	57.6	R.KSS*T*GSISNVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein					17.8	41.9	R.SHS*VGGPLQNIDFT*QRPFHGISTVSLPNSLQEVVDPLGK.R
			S763S764T765			5.4	35.4	R.KS*S*T*GSISNVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein	DENND4C	S763S764S774			2.8	28.7	R.KS*S*TGSISNVLFS*TQDPVEDAVFGEATNLKK.N
	C9orf55 protein	DENND4C	S1404S1423S1		•	16.4	23.0	R.SHS*VGGPLQNIDFTQRPFHGIS*TVSLPNS*LQEVVDPLGK.R
	C9orf55 protein	DENND4C	S1404T1415T14			10.9	36.4	R.SHS*VGGPLQNIDFT*QRPFHGIST*VSLPNSLQEVVDPLGK.R
	C9orf55 protein	DENND4C	S763S769			16.5	64.5	R.KS*STGSIS*NVLFSTQDPVEDAVFGEATNLK.K
	C9orf55 protein	DENND4C	S763S764	•			25.9	R.KS*S*TGSISNVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein	DENND4C	T765 <b>S</b> 769			6.6	15.8	R.KSST*GSIS*NVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein			-		-0.4	30.6	R.ST*SLSALVR.S
			T765S769S774			9.0	31.7	R.KSST*GSIS*NVLFS*TQDPVEDAVFGEATNLKK.N
	C9orf55 protein			<del></del>		28.3	31.0	R.KSSTGSISNVLFS*T*QDPVEDAVFGEATNLKK.N
	C9orf55 protein				•	2.0	41.5	R.KS'STGS'ISNVLFSTQDPVEDAVFGEATNLK.K
			T765S767S769	Ţ		9.5	25.5	R.KSST*GS*IS*NVLFSTQDPVEDAVFGEATNLK.K
	C9orf55 protein				. :	24.9	20.0	K.HSQPS*PEPHS*PTEPPAWGSSIVK.V
	C9orf55 protein			-		25.3	48.8	R.SHS*VGGPLQNIDFTQRPFHGIS*TVSLPNSLQEVVDPLGK.R  R.SHS*VGGPLQNIDFTQRPFHGIST*VS*LPNSLQEVVDPLGK.R
	C9orf55 protein					10.3	48.3 26.3	R.SHS*VGGPLQNIDFTQRPFHGIST*VS*LPNSLQEVVDPLGK.R  R.KSST*GS*ISNVLFSTQDPVEDAVFGEATNLKK.N
	C9orf55 protein					9.3	57.2	R.KSS*TGSIS*NVLFSTQDPVEDAVFGEATNLK.K
			T765S767S774		•	8.4	17.4	R.KSST*GS*ISNVLFS*TQDPVEDAVFGEATNLK.K
	C9orf55 protein					9.8	42.7	R.SHS*VGGPLQNIDFTQRPFHGISTVS*LPNSLQEVVDPLGK.R
			S261			92.1	23.6	R.VGDTEKPEPERS'PPNR.K
			S15S17			68.5	89.7	R.RRGDS*ES*EEDEQDSEEVR.L
	C9orf88 protein	FAM129B	S691S696			24.0	37.3	K.AAPEAS*SPPAS*PLQHLLPGK.A
	C9orf88 protein					8.7	48.1	K.QVVSVVQDEEVGLPFEASPES*PPPAS*PDGVTEIR.G
	C9orf88 protein	FAM129B	\$692\$696			26.1	33.5	K.AAPEASS*PPAS*PLQHLLPGK.A
	Calcipressin 1	RCAN1	S163S167	<u> </u>		100.0	70.3	K.QFLIS*PPAS*PPVGWK.Q
Calcium channel, voltag	ge dependent, P/C alpha 1A subunit	CACNA1A	S2457			6.6	14.8	R.S*PRTPR.A
Calcium regulated hea			S52		•	33.6	40.6	R.TFS*ATVR.A

<-10	abundance	s-Significant char	ompared to	the			
-5 29		with the minimum					
3 86 5 >100			CarT	RajiB			
>10 Protein Name Calcium regulated heat stable protein 1 (		Phosphosites	5 F B	8 % E		MOWSE	Sequence B GNWVPS*PI PTRR T
Calcium regulated heat stable protein 1 (					41.9	24.4	R.GNVVPS*PLPTRR.T  K.HETWSGHVIS*S
Calcium regulated heat stable protein 1 (					-0.4	28.0	
Calcium regulated heat stable protein 1 C					45.0	22.7	RERS'PS'PLRGNVVPS'PLPTR.R  RERS'PS'PLRG
					100.0	31.8	
Calcium regulated heat stable protein 1					3.5	13.8	R TRT FSATVRA
Calcium regulated heat stable protein 1 (			=		23.1	27.5	R.ERS*PSPLRGNVVPS*PLPTR.R
Calcium/calmodulin dependent protein (kinase IV		S360			100.0	47.9	R.DPS*PIQDGNEDMK.A
Calmodulin regulated spectrin-associated (					16.3	74.3	K.SPNS*HDSEPWTLLR.Q
Calmodulin regulated spectrin-associated of protein 1					39.0	34.5	R.S*PQGQLDTSESKPDSFFLEPLMPAVLKPAK.E
Calmodulin regulated spectrin-associated of protein 1				-	-2.7	36.1	R.SPQGQLDTSESKPDS*FFLEPLMPAVLKPAK.E
Calmodulin regulated spectrin-associated of protein 1					8.2	45.1	R.SPQGQLDTSES*KPDSFFLEPLMPAVLKPAK.E
Calmodulin regulated spectrin-associated ( protein 1			•		15.0	80.1	K.S'PNSHDSEPWTLLR.Q
Calmodulin regulated spectrin-associated ( protein 1				<u> </u>	0.2	29.1	K.SPNSHDS*EPWTLLR.Q
Calmodulin regulated spectrin-associated oprotein 1			-		183.2	72.5	R.QDS*DS*DVVDIEEAEHDFMGEAHPVVFSR.Y
Calmodulin regulated spectrin-associated ( protein 1-like 1		S404		•	-0.1	21.7	R.SS*SMSYVDGFIGTWPK.E
Calnexin (	CANX	<b>S</b> 583	-		100.0	49.3	K.AEEDEILNRS'PR.N
Calnexin (	CANX	T562S564			15.5	66.7	K.QKSDAEEDGGT*VS*QEEEDRKPK.A
C	CANX	S554	<b></b>		28.6	66.4	K.QKS*DAEEDGGTVSQEEEDR.K
Calnexin (	CANX	S554T562	<b></b>		8.3	56.4	K.QKS*DAEEDGGT*VSQEEEDRKPK.A
Calnexin (	CANX	T562			6.5	37.7	K.QKSDAEEDGGT*VSQEEEDR.K
Calnexin (	CANX	<b>S</b> 564			17.8	65.8	K.SDAEEDGGTVS*QEEEDR.K
Calpastatin (	CAST	S326	•		25.9	68.9	K.KEGITGPPADSSKPIGPDDAIDALSSDFTCGS*PTAAGK.K
Calpastatin (	CAST	T299				63.0	K.KEGIT*GPPADSSKPIGPDDAIDALSSDFTCGSPTAAGK.K
Calpastatin (	CAST	<b>S</b> 449		-	-0.2	55.6	R.SES*ELIDELSEDFDR.S
Calpastatin (	CAST	T323			5.6	13.4	K.EGITGPPADSSKPIGPDDAIDALSSDFT*CGSPTAAGK.K
CAP-GLY domain containing linker protein	CLIP1	S348			27.7	98.3	R.KIS'GTTALQEALK.E
1 CAP-GLY domain containing linker protein		S147			1.4	77.2	R.ATS*PLCTSTASMVSSSPSTPSNIPQKPSQPAAK.E
1 CAP-GLY domain containing linker protein		S195S200S204			20.3	55.8	K.TASES*ISNLS*EAGS*IK.K
1 CAP-GLY domain containing linker protein		\$200\$204 \$200\$204			26.7	67.7	K.TASESISNLS*EAGS*IK.K
1 CAP-GLY domain containing linker proteing		\$147\$160					RATS*PLCTSTASMVSSS*PSTPSNIPQKPSQPAAK.E
1 CAP-GLY domain containing linker protein					-0.5	18.3	RAIS-PLCTSTASMVS-SSPSTPSNIPURPSUPAAK.E  RAIS-PLCTSTASMVS-SSPSTPSNIPURPSUPAAK.E
1		S147S158			3.6	20.5	RATS:PLCTSTASMVS*SSPSTPSNIPQKPSQPAAK.E  K.TASESIS*NLSEAGS*IK.K
CAP-GLY domain containing linker protein		S197S204			19.3	42.0	
CAP-GLY domain containing linker protein		S195S197S204			2.8	24.2	K.TASES'IS'NLSEAGS'IK.K
CapZ-interacting protein		<b>S</b> 75	•••		75.7	69.2	K.LQANLTFDPAALLPG <mark>AS*P</mark> K.S
Carboxypeptidase D (		T1368T1370	<u> </u>		27.6	63.7	K.SLLSHEFQDET*DT*EEETLYSSKH,-
Cardiac lineage protein 1		T236S237S252			1.9	35.3	K.SDDT*S*DDDFMEEGGEEDGGS*DGMGGDGSEFLQR.D
Cask-interacting protein 2 (	CASKIN2	S471	-		102.6	44.1	R.S*GEQIFTQDVRPEQLLEGK.D
Cask-interacting protein 2	CASKIN2	T252			10.5	73.0	R.NT*YNQTALDIVNQFTTSQASR.E
Cask-interacting protein 2 (	CASKIN2	S358			11.1	28.9	RLPS'APTPLRPGFSR.T
Cask-interacting protein 2 (	CASKIN2	Y253			16.9	68.8	R.NTY*NQTALDIVNQFTTSQASR.E
CasL interacting molecule	MICAL1	S872S875S876	-		66.5	63.9	K.EEKES'PFS'S'EEEEEDVPLDSDVEQALQTFAK.T
CasL interacting molecule		S876		_ <del></del>	5.3	75.0	K.ESPFSS*EEEEEDVPLDSDVEQALQTFAK.T
CasL interacting molecule		S875			12.3	81.1	K.ESPFS*SEEEEEDVPLDSDVEQALQTFAK.T
CasL interacting molecule		S875S876				86.6	K.ESPFS'S'EEEEDVPLDSDVEQALQTFAK.T
CasL interacting molecule					9.4		K.ESKES*PFS*SEEEEEDVPLDSDVEQALQTFAK.T
		\$872\$875			29.7	56.5	
Caspase 2 (		S157			39.9	48.3	KLRLS*TDTVEHSLDNK.D
Caspase 2 (		T160	·		4.5	32.2	KLRLSTDT*VEHSLDNK.D
CASPR4 (		S520		•	22.4	23.9	RLIS*ISGK.V
Catalase (		<b>S</b> 515		ı.	1.9	30.5	K.NAIHTFVQS*GSHLAAR.E
Catenin alpha 1 <sub>C</sub>	CTNNA1	S641	÷.		49.2	74.8	R.TPEELDDS*DFETEDFDVR.S
CBF1 interacting corepressor (	CIR1	S202			28.3	104.9	R.NLTANDPSQEYVAS*EGEEDPEVEFLK.S
CBF1 interacting corepressor	CIR1	Y199			9.2	42.3	R.NLTANDPSQEY*VASEGEEDPEVEFLK.S
CBFA2 <sub>F</sub>	RUNX1	T41S48	بجب	•	41.4	45.1	R.RFT*PPSTALS*PGK.M
CBFA2 F	RUNX1	S276S303			22.9	41.4	R.QIQPS*PPWSYDQSYQYLGSIASPSVHPATPB*PGR.A
CBFA2 <sub>F</sub>	RUNX1	S48			55.8	67.8	R.RFTPPSTALS*PGK.M
CBFA2 F	RUNX1	S276S280				19.0	R.QIQPS*PPWS*YDQSYQYLGSIASPSVHPATPISPGR.A
CBFA2 <sub>F</sub>		S239			7.7	18.5	R.TAMRVS*PHHPAPTPNPR.A
CBFA2 <sub>F</sub>		S303					R.QIQPSPPWSYDQSYQYLGSIASPSVHPATPS*PGR.A
CBL					11.4	26.8	R.HS'LPFSLPSQMEPRPDVPR.L
CBL		S619	_		60.9	28.3	
	NCBP1	S22			19.1	66.1	R.KTS*DANETEDHLESLICK.V
CBP80 N			_				
CBP80 N	NCBP1	T27	Ħ.		11.9	28.8	R.RKTSDANET 'EDHLESLICK.V
	NCBP1	T27 S367	<u>.</u>		11.9 17.8	28.8 26.5	R.RKTSDANET'EDHLESLICKV R.RSSMS'VEAETTTTFSP.

Peak Area <-10	%CV White do	ts-Significant cha	inge in pepti compared to	de the			
-5 -3 0	25 timepoint 42 PSM 71	with the minimum	peak area f	or a given			
3 5 >10	86		CarT	RajiB			
	Protein Name Gene receptor type 7 CCR7	Phosphosites	9 H H	9 % E	Ascor	MOWSE	Sequence R.RS*SMSVEAETTTTFSP
	eceptor type 7 CCR7	\$364 \$365		Ξ	32.4	17.9	R.RSS*MSVEAETTTTFSP
	binding factor CEBPZ	S629			14.7	35.7 83.9	R.SQLDDHPES*DDEENFIDANDDEDMEK.F
	binding factor CEBPZ	T33			34.9	56.8	K.RPWRPEEAVEDPDEEDEDNT*SEAENGFSLEEVLR.L
	binding factor CEBPZ	S34		• •	29.5	83.8	K.RPWRPEEAVEDPDEEDEDNTS*EAENGFSLEEVLR.L
	binding factor CEBPZ	S973			38.4	54.8	R.NLNDS*SLFVSAEEFGHLLDENMGSK.F
CCAAT/Enhancer bindin		S229		• • •	12.1	26.7	R.AYLGYQAVPSGSSGSLSTS85*SSPPGTPSPADAK.A
CCAAT/Enhancer bindin		S228T235			10.9	15.5	R.AYLGYQAVPSGSSGSLSTSS*SSSPPGT*PSPADAK.A
CCAAT/Enhancer bindin		S218T235			9.0	23.2	R.AYLGYQAVP8*GSSGSLSTSSSSSPPGT*PSPADAK.A
	CTCF	\$609\$610\$612	-		3.0	18.4	K.EDS*S*DS*ENAEPDLDDNEDEEEPAVEIEPEPEPQPVTPAPPPAK.
CCR4-NOT transcription com		S473				41.9	K.
CCR4-NOT transcription com	plex, subunit 3 CNOT3	S506			14.6	34.0	K
CCR4-NOT transcription comp	plex, subunit 3 <sub>CNOT3</sub>	S358				13.1	K.
CCR4-NOT transcription com	plex, subunit 3 CNOT3	S507			5.3	47.8	к.
	CD19 CD19	S499	•••		13.9	106.5	REATSLGSQS*YEDMR.G
	CD19 CD19	\$494\$499			13.2	80.5	R.EATS*LGSQS*YEDMR.G
	CD19 CD19	T493S497		• • •	27.3	68.6	R.EAT*SLGS*QSYEDMR.G
	CD19 CD19	Y531			-0.3	65.7	R.GQPGPNHEEDADSY*ENMDNPDGPDPAWGGGGR.M
	CD19 CD19	T493S494S499			6.0	53.2	R.EAT*S*LGSQS*YEDMR.G
	CD19 CD19	S530			-	59.0	R.GQPGPNHEEDADS*YENMDNPDGPDPAWGGGGR.M
	CD19 CD19	T493S497S499			11.3	56.2	R.EAT*SLGS*QS*YEDMR.G
	CD19 <sub>CD19</sub>	\$494\$497		• • •	12.8	61.8	R.EATS*LGS*QSYEDMR.G
	CD19 CD19	\$494\$497\$499			9.7	55.8	R.EATS*LGS*QS*YEDMR.G
	CD19 CD19	T493S499			20.8	78.3	R.EAT*SLGSQS*YEDMR.G
CD2 antigen bir	nding protein 2 <sub>CD2BP2</sub>	S195	•	•	9.8	41.4	R.KGPGQPSS*PQR.L
	CD2BP2	S194	•			11.3	R.KGPGQPS*SPQRLDR.L
CD2 antigen bir	nding protein 2 CD2BP2	<b>S</b> 49		•	36.0	124.2	K.HSLDS*DEEEDDDDGGSSK.Y
CD2 asso	ociated protein CD2AP	S233			7.9	51.8	R.TSS*SETEEKKPEKPLILQSLGPK.T
CD2 asso	ociated protein CD2AP	S458	• •	•	78.4	69.9	K.S*VDFDSLTVR.T
CD2 asso	ociated protein CD2AP	S86			25.8	45.6	R.IS*TYGLPAGGIQPHPQTK.N
CD2 asso	ociated protein CD2AP	T87	=		12.6	50.0	R.IST*YGLPAGGIQPHPQTK.N
CD2 asso	ociated protein CD2AP	Y88			12.9	47.1	R.ISTY*GLPAGGIQPHPQTK.N
	CD28	S189			7.9	22.4	R.LLHS*DYMNMTPR.R
	CD28	Y191			11.1	26.5	R.LLHSDY*MNMTPR.R
	CD3 gamma CD3G	T152	•		1.3	39.0	R.ASDKQT*LLPNDQLYQPLK.D
	CD3 gamma CD3G	S148			4.4	22.2	R.AS*DKQTLLPNDQLYQPLK.D
	CD40 CD40	S272			100.0	37.7	R.IS'VQER.Q
	CD5 <sub>CD5</sub>	S428			14.9	89.0	R.QWIGPTGMNQNMS*FHR.N
	CD5 CD5	\$482\$483\$485			16.6	34.6	R.SSMQPDNS*S*DS*DYDLHGAQR.L
	CD5 CD5	T421			2.6	84.9	R.QWIGPT*GMNQNMSFHR.N
	CD5 CD5	<b>S</b> 439			31.3	35.5	R.S*HAENPTASHVDNEYSQPPR.N
	CD5 <sub>CD5</sub>	S476S482			3.3	50.9	R.SS*MQPDNS*SDSDYDLHGAQR.L
	CD5 CD5	\$476\$482\$483			2.8	34.0	R.SS*MQPDNS*S*DS*DYDLHGAQR.L
	CD7 CD7	S228			10.7	52.6	K.NSAACVVYEDMSHS*R.C
	CD7 CD7	S226			-0.4	50.1	K.NSAACVVYEDMS*HSR.C
	CD74 antigen CD74	S25			100.0	58.3	R.DLIS*NNEQLPMLGR.R
	CD80 antigen CD80	S284			100.0	20.5	R.LRRES'VRPV
	CDC 25B CDC25B	S396	•	•	61.1	53.4	K.S*LCHDEIENLLDSDHR.E
	CDC 25B CDC25B	S344			22.3	29.1	R.SPS*MPCSVIRPILK.R
CD	C like kinase 3 <sub>CDCA5</sub>	S27	•-		23.9	21.0	R.RSYS'R.L
CD	C like kinase 3 CDCA5	\$25 <b>Y</b> 26			13.9	17.8	R.RS"Y"SR.L
CD	C like kinase 3 <sub>CLK3</sub>	S49S51	اب		30.5	13.0	R.S'RS'HDRLPYQR.R
	CDC2 CDK1	Y15			16.9	61.0	K.IGEGTY*GVVYK.A
	CDC2 <sub>CDK1</sub>	T14Y15			50.2	60.6	K.IGEGT*Y*GVVYK.A
CDC2 related po	rotein kinase 7 CDK12	S274S276			46.0	38.2	R.RQS"VS"PPYKEPSAYQSSTR.S
CDC2 related pr	rotein kinase 7 CDK12	\$333\$334			8.3	32.2	R.SS*S*PFLSK.R
CDC2 related po	rotein kinase 7 CDK12	S382S385			21.3	43.5	R.HS*SIS*PVRLPLNSSLGAELSR.K
CDC2 related po	rotein kinase 7 CDK12	\$383\$385			35.8	48.9	R.HSS*IS*PVRLPLNSSLGAELSR.K
CDC2 related po	rotein kinase 7 CDK12	S681S685			126.6	39.6	R.HLLTDLPLPPELPGGDLS*PPDS*PEPK.A
CDC2 related po	rotein kinase 7 CDK12	\$301\$303			38.3	25.5	R.S'VS'PYSR.R
CDC2 related po	rotein kinase 7 CDK12	Y892	•••		5.8	23.0	R.LYNSEESRPY*TNK.V
CDC2 related po	rotein kinase 7 CDK12	\$379\$382\$383			39.9	19.0	R.S'RHS'S'IS'PVRLPLNSSLGAELSR.K
				• •			

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3 5 >100 >10		CarT				
Protein Name Gene CDC2 related protein kinase 7 CDK12	Phosphosites S77S78S80S84	5 E E	£ £ £	Ascor 7.9	MOWSE 26.2	Sequence K.DMGLVTPEAASLGTVIKPLVEYDDIS'S'DS'DTFS'DDMAFK.L
CDC2 related protein kinase 7 CDK12	Y73S78T82S84		•	5.6	15.2	K.DMGLVTPEAASLGTVIKPLVEY*DDISS*DSDT*FS*DDMAFK.L
CDC2 related protein kinase 7 CDK12	T57S62T65Y73	÷		4.1	16.4	K.DMGLVT*PEAAS*LGT*VIKPLVEY*DDISSDSDTFSDDMAFK.L
CDC2 related protein kinase 7 CDK12	S332S333	•		10.0	39.0	R.S*S*SPFLSK.R
CDC2 related protein kinase 7 CDK12	S62T65S77S84		•	2.0	22.1	K.DMGLVTPEAAS*LGT*VIKPLVEYDDIS*SDSDTFS*DDMAFK.L
CDC2 related protein kinase 7 CDK12	\$382\$383			17.9	43.7	R.HS*S*ISPVRLPLNSSLGAELSR.K
CDC2 related protein kinase 7 CDK12	S77S78T82S84		•	6.6	11.4	K.DMGLVTPEAASLGTVIKPLVEYDDIS*S*DSDT*FS*DDMAFK.L
CDC2 related protein kinase 7 CDK12	Y73S78S80T82			4.4	23.0	K.DMGLVTPEAASLGTVIKPLVEY*DDISS*DS*DT*FSDDMAFK.L
CDC2 related protein kinase 7 CDK12	S1083		<u> </u>	11.2	61.4	K.NSS*PAPPQPAPGK.V
CDC2 related protein kinase 7 CDK12  CDC2 related protein kinase 7 CDK12	\$383\$393 \$681		<u> </u>	12.2	29.3	R.HSS*ISPVRLPLNS*SLGAELSR.K  R.HLLTDLPLPPELPGGDLS*PPDSPEPK.A
CDC2 related protein kinase 7 CDK12	T893		-	40.0	35.8	R.LYNSEESRPYT'NK.V
CDC2 related protein kinase 7 CDK12	S276Y279			5.3	12.2	R.RQSVS*PPY*KEPSAYQSSTR.S
CDC2 related protein kinase 7 CDK12	Y73S78S80S84			7.1	22.7	K.DMGLVTPEAASLGTVIKPLVEY*DDISS*DS*DTFS*DDMAFK.L
CDC2 related protein kinase 7 CDK12	S62T65Y73S84			3.6	24.2	K.DMGLVTPEAAS*LGT*VIKPLVEY*DDISSDSDTFS*DDMAFK.L
CDC25C CDC25C	S263		•	6.6	64.7	K.TVS*LCDITITQMLEEDSNQGHLIGDFSK.V
CDC26 CDC26	<b>S</b> 42	••		48.1	47.6	K.QKEDVEVVGGS*DGEGAIGLSSDPK.S
CDC42 effector protein 4 CDC42Ef	° 89		<u> </u>	20.1	15.4	K.QLVS*SSVHSK.R
CDC5 CDC5L	T373T377T396			18.1	12.6	R.ILQEAQNLMALT*NVDT*PLKGGLNTPLHESDFSGVT*PQR.Q
CDCA5 CDCA5	<b>S</b> 35			-0.2	36.2	K.SGS*ELPSILPEIWPK.T
Cdk5 and Abl enzyme substrate 2 CABLES	S105	•		5.5	38.5	R.TPAPQGLLS*PTQVPTGLGLDGQR.Q
CDP-DAG synthase 2 <sub>CDS2</sub>	S33		■. ₽	49.2	65.4	K.VDGETAS*DSESR.A
Cell death regulator Aven AVEN	S94	<b>-</b>		6.9	76.2	R.REPGGWGAGASAPVEDDS*DAETYGEENDEQGNYSK.R
Cell death regulator Aven AVEN  Cell division cycle 2 like 1 CDK11B	T98			6.5	11.6	R.REPGGWGAGASAPVEDDSDAET*YGEENDEQGNYSK.R  -MEITIRNSPY*R.R
Cell division cycle 2 like 1 CDK11B	Y67 T595	•		9.5	11.3 55.6	KAYT*PVWTLWYRA
Cell division cycle 2 like 1 CDK11B	S589T595		• • •	16.0	88.3	R.EYGS*PLKAYT*PVVVTLWYRA
Cell division cycle 2 like 1 CDK11B	Y587S589	• • • •		24.9	67.4	R.EY*GS*PLKAYTPVVVTLWYRA
Cell division cycle 2 like 1 CDK11B	Y594T595			24.0	60.4	R.EYGSPLKAY*T*PVVVTLWYR.A
Cell division cycle 2 like 1 CDK11B	Y587Y594			10.6	57.7	R.EY*GSPLKAY*TPVVVTLWYR.A
Cell division cycle 2 like 1 CDK11B	S589Y594	ij		14.5	34.4	R.EYGS*PLKAY*TPVVVTLWYR.A
Cell division cycle 2 like 1 CDK11B	Y587T595			12.3	59.2	R.EY*GSPLKAYT*PVVVTLWYRA
Cell division cycle 2 like 1 CDK11B	<b>S</b> 65			16.1	20.5	-MEITIRNS*PYR.R
Cell division cycle 2 like 2 CDK11B	S574	:		26.0	35.4	R.EYGS*PLK.A
Cell division cycle 2 like 2 CDK11B	T736S737	•		73.0	26.9	K.RGT*S*PRPPEGGLGYSQLGDDDLK.E
Cell division cycle 2 like 2 CDK11A	T580		<del>.</del>	16.8	55.4	KAYT*PVVVTQWYRA
Cell division cycle 2 like 2 CDK11B  Cell division cycle 2 like 2 CDK11A	S271	•		16.8	59.3	R.DLLSDLQDIS*DSER.K  R.EYGSPLKAY*T*PVVVTQWYR.A
Cell division cycle 2 like 2 CDK11A	Y579T580 Y572Y579			16.6	76.2	R.EY*GSPLKAY*TPVVVTQWYRA
Cell division cycle 2 like 2 CDK11B	S265S271			38.0	89.0	R.DLLS*DLQDIS*DSER.K
Cell division cycle 2 like 2 CDK11B	\$363\$366T377	•••			14.7	R. ENDROGEREE AEEE VOERT DOGG AN TERROVIDERDAL SPIEL V
Cell division cycle 2 like 2 CDK11B	S222	•		100.0	23.5	R.S*PPRPPR.L
Cell division cycle 2 like 2 CDK11A	S574T580			11.2	74.9	R.EYGS*PLKAYT*PVVVTQWYR.A
Cell division cycle 2 like 2 CDK11A	Y572T580			12.0	61.9	R.EY*GSPLKAYT*PVVVTQWYR.A
Cell division cycle 2 like 2 CDK11A	Y572S574	Ţ		13.5	20.6	R.EY*GS*PLKAYTPVVVTQWYR.A
Cell division cycle 2 like 5 CDK13	T1056T1058			0.3	39.1	R.KDLSLGLDDSRT*NT*PQGVLPSSQLK.S
Cell division cycle 2 like 5 CDK13	\$437\$439			20.0	57.7	R.HSS*IS*PSTLTLK.S
Cell division cycle 2 like 5 CDK13	S1054T1056			5.9	32.7	R.KDLSLGLDDS*RT*NTPQGVLPSSQLK.S
Cell division cycle 2 like 5 CDK13  Cell division cycle 2 like 5 CDK13	\$436\$437			8.5	42.5	R.HS'S'ISPSTLTLK.S
	S315S317			100.0	29.8	R.S'LS'PLGGR.D
Cell division cycle 2 like 5 CDK13  Cell division cycle 2 like 5 CDK13	\$1054T1058			6.8	35.5	R.S'LS'PLGGRDDS'PVSHR.A
Cell division cycle 2 like 5 CDK13	\$315\$317\$325 \$383			31.4	13.4	R.GGDVS*PSPYSSSSWR.R
Cell division cycle 2 like 5 CDK13	\$436\$439			13.4	45.5	R.HS'SIS'PSTLTLK.S
Cell division cycle and apoptosis regulator CCAR1	S333			100.0	20.6	R.ERS*PQR.K
Centaurin beta 1 ACAP1	T739			46.2	33.9	R.SHDLHT*L
Centaurin beta 5 ACAP3	T454S456				11.4	R.KPT*AS*SSRQDK.E
Centaurin delta 2 <sub>ARAP1</sub>	<b>S</b> 229	•		39.3	91.2	R.LFPEFDDS*DYDEVPEEGPGAPAR.V
Centaurin delta 2 <sub>ARAP1</sub>	Y231		•••	22.6	19.6	R.LFPEFDDSDY*DEVPEEGPGAPAR.V
Centaurin delta 2 <sub>ARAP1</sub>	<b>S</b> 1195			81.4	71.2	R.S*VAAFTADPLSLLR.N
Centromeric protein a CENPA	S17S19			27.5	32.7	R.RRS*PS*PTPTPGPSR.R
Centromeric protein c1 CENPC	S316			52.5	33.3	R.S*WITIPR.K
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Peak Area	o abundani						
-5 -3  0	timepoint PSM	with the minimum	peak area f	or a given			
3 5 >10	>100			RajiB			
Cer	Protein Name Gene	Phosphosites S1259	8 4 5	£ £ £	Ascor	MOWSE 22.5	Sequence R.RSVS*EK.T
Cen	ntromeric protein E CENPE	S1257			9.5	16.9	R.RS*VSEK.T
Cer	ntromeric protein F CENPF	S1651			8.9	29.9	R.LQLQGLDLS*SR.S
Centroso	omal protein 72kDa CEP72	S237			60.5	27.6	R.HLLS*PQLVQYQCGDSGK.Q
Cer	ntrosome protein 4 CEP135	S1125S1132		•	4.5	20.4	R.HGLATPPLS*STLRSPS*HSPEHR.N
Cer	Centrosome protein 4 CEP135			• •	9.6	14.6	R.DRS*PSRLDTFLK.G
Cer	Centrosome protein 4 <sub>ELOA2</sub>				28.7	40.3	R.SPS*HS*PEHR.N
Cer	ntrosome protein 4 CEP135	S1125S1126		=	0.8	13.2	R.HGLATPPLS*S*TLRSPSHSPEHR.N
Cer	ntrosome protein 4 CEP135	T1127S1130			2.2	12.5	R.HGLATPPLSST*LRS*PSHSPEHR.N
Cer	ntrosome protein 4 CEP135	S439S441		•	100.0	14.7	R.RDRS*PS*R.L
Cer	ntrosome protein 4 CEP135	S441			7.9	13.3	R.DRSPS*RLDTFLK.G
	CEP135	S1130S1132			5.1	13.7	R.HGLATPPLSSTLRS*PS*HSPEHR.N
Cer	ntrosome protein 4 CEP135	T1127S1132			-0.2	16.6	R.HGLATPPLSST*LRSPS*HSPEHR.N
Ce	eramide synthase 4 CERS4	S291S296S298		•	100.0	55.3	K.DIRS*DVEES*DS*S*EEAAAAQEPLQLK.N
Ce	ramide synthase 4 CERS4	S291S296S298			14.7	37.9	R.S*DVEES*DS*SEEAAAAQEPLQLK.N
Ce	eramide synthase 4 CERS4	S291S299			24.7	18.4	K.DIRS*DVEESDSS*EEAAAAQEPLQLK.N
Ce	eramide synthase 4 CERS4	S291S296S299			8.5	42.6	R.S*DVEES*DSS*EEAAAAQEPLQLK.N
Ce	eramide synthase 4 CERS4	S291S298		-	14.4	13.2	K.DIRS*DVEESDS*SEEAAAAQEPLQLK.N
Ce	eramide synthase 4 CERS4	S291S296			14.1	11.7	K.DIRS*DVEES*DSSEEAAAAQEPLQLK.N
Ce	eramide synthase 4 CERS4	S291S298S299			14.6	52.5	K.DIRS*DVEESDS*S*EEAAAAQEPLQLK.N
Cerebellar de	generation-related CDR2	S311			10.9	53.4	R.SSS'ETILSSLAGSDIVK.G
	autoantiden 2	S310			-0.2	45.7	R.SS*SETILSSLAGSDIVK.G
(	autoantigen 2 Cerebral protein 11 TMCC3	S438			100.0	64.7	R.NKFGS*ADNIAHLK.D
	CGI-07 protein NMD3	\$468 <b>T</b> 470		•	48.4	38.5	R.DSAIPVES*DT*DDEGAPR.I
	CGI-07 protein NMD3	T470			9.1	59.4	R.DSAIPVESDT*DDEGAPR.I
	CGI-79 protein RBMX2	S187		•	13.9	11.5	R.EVQAEQPSSS*SPR.R
	CGI-79 protein RBMX2	S188	i		9.8	24.6	R.EVQAEQPSSSS*PR.R
	CGI115 protein RRP15	\$266\$276\$280	•		8.9	21.7	K.DWDKES*DGPDDSRPES*ASDS*DT*
	CGI115 protein RRP15	\$272\$276\$280			0.6	18.1	K.DWDKESDGPDDS*RPES*ASDS*DT*
Chemokine, CX	C motif, receptor 4 CXCR4	S321S324	•		4.0	14.5	K.TSAQHALTSVS*RGS*SLK.I
Chemokine, CX	C motif, receptor 4 CXCR4	T318S319S324	•		12.1	15.5	K.TSAQHALT"S"VSRGS"SLK.I
Chemokine, CX	C motif, receptor 4 CXCR4	S347			5.8	46.9	K.RGGHSSVSTESESS*SFHSS
Chemokine, CX	C motif, receptor 4 CXCR4	S324S325			31.3	32.1	K.TSAQHALTSVSRGS*S*LK.I
Chemokine, CX	C motif, receptor 4 CXCR4	T311S312			2.1	12.4	K.T*S*AQHALTSVSRGSSLK.I
	CHERP CHERP	S813S815S817			47.5	83.2	R.S'RS'RS'PT'PPSSAGLGSNSAPPIPDSR.L
	CHERP CHERP	S815S817T819			11.2	61.5	R.S'RS"PT"PPSSAGLGSNSAPPIPDSR.L
	CHERP CHERP	S815S817S823	•••	-	10.1	45.0	R.S*RS*PTPPSS*AGLGSNSAPPIPDSR.L
	CHERP CHERP	T819S822S823		• • • •	13.8	50.6	R.SRSPT*PPS*S*AGLGSNSAPPIPDSR.L
	CHERP CHERP	S815T819S823	•••		7.6	49.6	R.S*RSPT*PPSS*AGLGSNSAPPIPDSR.L
	CHERP CHERP	\$802\$804\$806		••	15.2	14.4	R.S'KS'YS'PGRR.R
	CHERP CHERP	S815T819S822	-	-	9.1	37.7	R.S*RSPT*PPS*SAGLGSNSAPPIPDSR.L
	CHERP CHERP	S817T819S823		=	9.3	36.3	R.SRS*PT*PPSS*AGLGSNSAPPIPDSR.L
	CHERP CHERP	S815T819S822			7.7	17.0	R.S*RSPT*PPS*S*AGLGSNSAPPIPDSR.L
	CHERP CHERP	S813S815S817			9.3	10.7	R.S'RS'RS'PT'PPS'SAGLGSNSAPPIPDSR.L
	CHERP CHERP	S815S817T819	Ė		10.1	27.4	R.S*RS*PT*PPS*SAGLGSNSAPPIPDSR.L
	CHERP CHERP	S813S815S817			11.8	22.1	R.S'RS'RS'PTPPS'SAGLGSNSAPPIPDSR.L
	CHERP CHERP	S813S815S817		Ė	6.5	36.4	R.S'RS'RS'PTPPSS'AGLGSNSAPPIPDSR.L
	CHERP CHERP	S817T819S822		-	2.0	47.9	R.SRS'PT'PPS"SAGLGSNSAPPIPDSR.L
	CHERP CHERP	S815S817S822			2.6	61.0	R.S*RS*PTPPS*SAGLGSNSAPPIPDSR.L
	CHL12 CHTF18	S871			65.8	102.3	R.VENSPQVDGS*PPGLEGLLGGIGEK.G
СНМІ	P family, member 7 <sub>CHMP7</sub>	S417			100.0	80.7	R.IS*DAELEAELEK.L
Chondrocyte protein	with a poly proline MTFR1 region	S119			84.9	68.5	R.QIS*LPDLSQEEPQLK.T
Chondroitin sulf	ate proteoglycan 6 SMC3	S1081			11.5	39.4	R.GS*GSQSSVPSVDQFTGVGIR.V
C	hr2 synaptotagmin <sub>ESYT2</sub>	S665			2.8	35.2	K.SHMSGS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
C	hr2 synaptotagmin ESYT2	T656S660S663			5.0	33.5	R.KT*SIKS*HMS*GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
C	hr2 synaptotagmin ESYT2	T656S657S660				59.6	R.KT*S*IKS*HMSGSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
C	hr2 synaptotagmin ESYT2	S710			23.5	91.8	R.SSS*SLLASPGHISVK.E
C	hr2 synaptotagmin ESYT2	S708			11.6	46.5	R.S*SSSLLASPGHISVK.E
C	hr2 synaptotagmin ESYT2	S710S711			23.3	66.1	R.SSS*S*LLASPGHISVK.E
C	hr2 synaptotagmin ESYT2	S733	-		9.1	36.0	K.EPTPSIASDIS*LPIATQELR.Q
C	hr2 synaptotagmin ESYT2	S730			37.7	118.8	K.EPTPSIAS*DISLPIATQELR.Q
C	hr2 synaptotagmin ESYT2	S730S733	-		9.1	72.1	K.EPTPSIAS*DIS*LPIATQELR.Q

s <sub>-10</sub> abundar	ots-Significant cha nce at 5%FDR c t with the minimum	compared to	the .			
.3 42 PSM		CarT	RajiB			
>100 >10 Protein Name Gene	Phosphosites		£ £ £	Ascor	MOWSE	Sequence
Chr2 synaptotagmin ESYT2	\$727 <b>\$</b> 730			7.7	62.1	KEPTPS'IAS'DISLPIATQELR.Q
Chr2 synaptotagmin ESYT2	T725S730			9.9	43.1	K.EPT'PSIAS'DISLPIATQELR.Q
Chr2 synaptotagmin ESYT2  Chr2 synaptotagmin ESYT2	\$727\$730\$733			23.9	117.1	KEPTPS'IAS'DIS'LPIATQELR.Q  KEPT'PS'IAS'DISLPIATQELR.Q
Chr2 synaptotagmin ESYT2	T725S727S730 S648			9.8	37.9 29.7	K.R.P.S.V.S.K.E
Chr2 synaptotagmin ESYT2	T656S660S665			5.1	58.6	R.KT*SIKS*HMSGS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	T656S660S663			4.6	28.9	R.KT*SIKS*HMS*GS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	T656S657S660				27.8	R.KT*S*IKS*HMS*GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	<b>S</b> 711			12.6	60.8	R.SSSS*LLASPGHISVK.E
Chr2 synaptotagmin ESYT2	S709S711			11.8	76.8	R.SS*SS*LLASPGHISVK.E
Chr2 synaptotagmin ESYT2	\$708\$709			12.3	44.1	R.S'S'SSLLASPGHISVK.E
Chr2 synaptotagmin ESYT2	\$727 <b>\$</b> 733			6.2	64.3	K.EPTPS'IASDIS'LPIATQELR.Q
Chr2 synaptotagmin ESYT2  Chr2 synaptotagmin ESYT2	T725S727S733	==		6.6	65.0	K.EPT*PS'IASOIS'LPIATOELR.Q  R.SS'SSLLASPGHISVKE
Chr2 synaptotagmin ESYT2	\$709 \$657\$660\$665			-0.3	37.7	R.KTS'IKS'+IMSGS'PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	T725S733			12.3	35.9	K.EPT*PSIASDIS*LPIATQELR.Q
Chr2 synaptotagmin ESYT2	\$657\$660\$663			3.5	46.4	R.KTS*IKS*HMS*GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	\$663\$665			17.6	43.1	K.SHMS*GS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	\$657\$660\$663			31.8	26.8	R.KTS*IKS*HMS*GS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	T725			2.8	19.4	K.EPT*PSIASDISLPIATQELR.Q
Chr2 synaptotagmin ESYT2	T725S727	<b></b>		9.0	48.3	K.EPT*PS*IASDISLPIATQELR.Q
Chr2 synaptotagmin <sub>ESYT2</sub>	\$660\$663\$665	<u> </u>		30.2	25.7	R.KTSIKS"+IMS"GS"PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	T725S730S733			23.2	76.1	K.EPT*PSIAS*DIS*LPIATQELR.Q  K.SHMS*GSPGPGGSNTAPSTPVIGGSDKPGMEEKA
Chr2 synaptotagmin ESYT2	S663 T656S657			7.3	11.9	R.KT'S'IKSHMSGSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	\$709\$710			5.0	40.0	R.SS'S'SLLASPGHISVK.E
Chr2 synaptotagmin ESYT2	T656S657S665			-0.6	23.6	R.KT*S*IKSHMSGS*PGPGGSNTAPSTPVIGGSDKPGMEEK.A
Chr2 synaptotagmin ESYT2	\$708\$710			1.2	45.8	R.S*SS*SLLASPGHISVK.E
Chromatin accessibility complex, subunit 1 CHRAC1	S124			20.4	41.8	R.EEDEENDNDNES'DHDEADS
Chromatin assembly factor 1 subunit A CHAF1A	<b>S</b> 772	<b>.</b>		29.8	70.2	RGLLSNHTGS*PRS
Chromatin assembly factor 1 subunit A CHAF1A				12.0	54.3	R.SPS*TTYLHTPTPSEDAAIPSK.S
Chromatin assembly factor 1 subunit A CHAF1A				108.3	81.3	K.S'PDLEASLDTLENNCHVGSDIDFRPK.L
Chromatin assembly factor 1 subunit A CHAF1A  Chromatin assembly factor 1 subunit A CHAF1A				22.0	44.8 50.6	R.GLISNHT*GSPR.S  R.S*PSTTYLHTPTPSEDAAIPSK.S
Chromatin assembly factor 1 subunit A CHAF1A				7.2	45.3	R.SPSTTYLHTPTPSEDAAIPSK.S
Chromatin assembly factor 1 subunit A CHAF1A				56.6	32.9	R.S*CPELTSGPR.M
Chromatin assembly factor 1 subunit B CHAF1B	<b>S</b> 429			12.1	67.6	RTQDPSS'PGTTPPQARQ
Chromatin assembly factor 1 subunit B <sub>CHAF1B</sub>	\$428T433			23.4	44.5	R.TQDPS*SPGTT*PPQAR.Q
Chromatin assembly factor 1 subunit B CHAF1B	S538	<u> </u>		42.1	33.6	K.TDTPPSSVPTSVISTPSTEEIQSETPGDAQGS*PPELK.R
Chromatin assembly factor 1 subunit B CHAF1B	<b>S</b> 410			6.6	25.3	R.GSS*PGPRPVEGTPASR.T
Chromatin assembly factor 1 subunit B CHAF1B				35.2	54.0	R.TQDPS'SPGTTPPQAR.Q
Chromatin assembly factor 1 subunit B CHAF1B		=		17.7	10.9	RTQDPSS*PGTT*PPQAR.Q
Chromobox homolog 3 <sub>CBX3</sub>	S176			24.6	35.9	RLTWHS*CPEDEAQ  K.RKS*LS*DSESDDSK.S
CBX3	\$93\$95 \$95\$97			13.6	58.9 38.9	K.SLS*DS*ESDDSK.S
Chromobox homolog 3 CBX3	S95			28.9	62.3	K.SLS*DSESDDSK.S
Chromobox homolog 3 <sub>CBX3</sub>	S95S97S99		• • •	12.2	38.1	K.SLS'DS'ES'DDSK.S
Chromobox homolog 3 CBX3	S93			12.2	23.9	K.S'LSDSESDDSK.S
Chromobox homolog 3 CBX3	S93S95S97	T.		10.9	24.1	K.S'LS'DS'ESDDSK.S
Chromobox homolog 7 <sub>CBX7</sub>	Y28			100.0	21.4	R.KGKVEY*LVK.W
Chromodomain helicase DNA binding CHD1 protein 1	T250S252	Ļ		109.3	31.4	K.EDEEMKT*DS*DDLLEVCGEDVPQPEEEFETIER.F
Chromodomain helicase DNA binding CHD2 protein 2	S1364				32.7	R.LKEEHGIELS*SPR.H
Chromodomain helicase DNA binding CHD3 protein 3  Chromodomain helicase DNA binding CHD4	S1646S1650			27.6	20.4	K.METEADAPS*PAPS*LGER.L
Chromodomain helicase DNA binding CHD4 protein 4  Chromodomain helicase DNA binding CHD4	\$512\$528 \$306\$307\$316			38.4	95.7	K.WGQPPS*PTPVPRPPDADPNTPS*PKPLEGRPER.Q  R.KRSS*S*EDDDLDVES*DFDDASINSYSVSDGSTSR.S
Chromodomain helicase DNA binding CHD4	\$306\$307\$316 \$305\$306\$307			19.5	119.1	R.KRS'S'S'EDDDLDVES'DFDDASING/SVSDGSTSRS
Chromodomain helicase DNA binding CHD4	\$1360\$1364\$1			12.4	84.3	R.DWQDDQS'DNQS'DYS'VAS'EEGDEDFDER.S
Chromodomain helicase DNA binding CHD4	S1364Y1366S1			9.2	87.5	R.DWQDDQSDNQS'DY'S'VAS'EEGDEDFDER.S
Chromodomain helicase DNA binding CHD4 protein 4	\$307\$322			2.3	61.0	R.SSS'EDDDLDVESDFDDAS'INSYSVSDGSTSR.S
Chromodomain helicase DNA binding CHD4 protein 4	\$307\$316		•••	6.3	20.5	R.SSS*EDDDLDVES*DFDDASINSYSVSDGSTSR.S
Chromodomain helicase DNA binding CHD4 protein 4	S425	<b>H</b>		100.0	103.8	K.EDNS*EGEEILEEVGGDLEEEDDHHMEFCR.V
Chromodomain helicase DNA binding CHD4 protein 4	S1560	<b></b>		13.9	38.7	K.MSQPGS'PSPK.T

Peak Area	0	abundance		ompared to	the			
-5 -3		timepoint v PSM	vith the minimum	peak area fo	or a given			
5 >10	>100			CarT				_
Chromodomain he	Protein Name elicase DNA binding ( protein 4		Phosphosites S1556S1560	2 12 2	£ £ £	Ascor 16.4	MOWSE 43.2	Sequence K.KMS*QPGS*PSPK.T
Chromodomain he	licase DNA binding ( protein 4	CHD4	S1360S1364Y1			12.2	90.0	R.DWQDDQS"DNQS"DY"SVAS"EEGDEDFDER.S
Chromodomain he	licase DNA binding ( protein 4	CHD4	\$305\$307\$316			18.7	62.6	R.KRS*SS*EDDDLDVES*DFDDASINSYSVSDGSTSR.S
	elicase DNA binding ( protein 4		\$306\$307			-0.4	12.5	R.SS*S*EDDDLDVESDFDDASINSYSVSDGSTSR.S
	licase DNA binding ( protein 4		T1574T1578			12.6	23.9	K.TPTPSTPGDT*QPNT*PAPVPPAEDGIK.I
	licase DNA binding ( protein 4		S1360Y1366S1		•	4.7	42.3	R.DWQDDQS'DNQSDY'S'VAS'EEGDEDFDER.S  R.DWQDDQS'DNQS'DY'S'VASEEGDEDFDER.S
	protein 4		\$1360\$1364Y1 \$305\$306			6.0	49.1 35.3	R.S'S'SEDDLDVESDFDDASINSYSVSDGSTSR.S
	protein 4		S305S307S316			8.7	63.0	R.KRS*SS*EDDDLDVES*DFDDAS*INSYSVSDGSTSR.S
	protein 4		S1556	•		15.4	15.6	K.MS*QPGSPSPK.T
Chromodomain he	protein 4 licase DNA binding ( protein 7	CHD7	S2559			49.0	27.6	R.NIPS*PGQLDPDTRIPVINLEDGTR.L
Chromodomain he	licase DNA binding o	CHD7	S2956			35.7	44.0	K.DGETLEGS*DAEESLDK.T
Chromodomain he	licase DNA binding ( protein 7	CHD7	S2983			38.4	46.0	K.TAESSLLEDEIAQGEELDS*LDGGDEIENNENDE
Chromodomain he	licase DNA binding ( protein 7	CHD7	S1577S1581			1.5	12.6	K.EDELMEFS'DLES'DSEEKPCAKPR.R
	(	CHD8	S1141S1145	-		18.4	73.4	R.HFSTLKDDDLVEFS*DLES*EDDERPR.S
	licase DNA binding ( protein 8		T1714S1716				28.4	R.T*AS*PLPLRPDAPVEKSPEETATQVPSLESLTLK.L
	licase DNA binding ( protein 8		S1716T1733	•		6.3	32.8	R.TAS*PLPLRPDAPVEKSPEET*ATQVPSLESLTLK.L
	licase DNA binding ( protein 8		S1940S1944		===	8.4	70.2	R.SS'SAAS'MAEEEASAVSTAAAQFTK.L
	licase DNA binding ( protein 8 licase DNA binding (		S1940S1941			3.6	34.0	R.SS'S'AASMAEEASAVSTAAAQFTKL  R.TAS'PLPLRPDAPVEKS'PEETATQVPSLESLTLKL
	protein 8		S1716S1729 T1925Y1929			11.4	57.1	R.SQEMVTGGILGPGNHLLDSPSLT*PGEY*GDSPVPTPR.S
	protein 8 licase DNA binding		T1908S1932	-		10.7	17.9	R.SQEMVT'GGILGPGNHLLDSPSLTPGEYGDS'PVPTPR.S
	protein 8 licase DNA binding (		S1921S1932T1			25.6	24.9	R.SQEMVTGGILGPGNHLLDS*PSLTPGEYGDS*PVPT*PR.S
Chromodomain he	protein 8	CHD8	S1941S1944			2.2	41.4	R.SSS*AAS*MAEEEASAVSTAAAQFTK.L
Chromodomain he	protein 8 licase DNA binding (	CHD8	S1697			37.8	66.7	R.MNYMQNHQAGAPAPS*LSR.C
Chromodomain he	licase DNA binding (	CHD8	S1716T1735		•	9.4	24.1	R.TAS*PLPLRPDAPVEKSPEETAT*QVPSLESLTLK.L
Chromodomain he	licase DNA binding (	CHD8	S1699	Ė		7.3	20.5	R.MNYMQNHQAGAPAPSLS*R.C
Chromodomain he	licase DNA binding ( protein 8	CHD8	S1939S1944			4.1	25.8	R.S'SSAAS'MAEEEASAVSTAAAQFTK.L
D	licase-DNA-binding ( rotein 3 (Fragment)		S371S375			35.8	63.4	R.GRPPAQALGPAAS*PPPS*PPLGPSLG
D	licase-DNA-binding ( rotein 3 (Fragment)		S371S381	-		14.9	26.1	R.GRPPAQALGPAAS*PPPSPPLGPS*LG
	licase-DNA-binding ( protein 4		S96S98S101			6.0	22.7	K.ELGDSSGEGPEFVEEEEEVALRS*DS*EGS*DYTPGK.K
	licase-DNA-binding ( protein 4		S78S96S98S10			6.6	17.2	K.ELGDS*SGEGPEFVEEEEEVALRS*DS*EGS*DYTPGK.K
Chromosome 1 open			S37S39			62.2	60.4	K.S'KS'PPKVPIVIQDDSLPAGPPPQIR.I  K.S'PPKVPIVIQDDSLPAGPPPQIR.I
Chromosome 1 open			\$39 \$51			2.3	72.2	K.SKSPPKVPIVIODDS*LPAGPPPQIR.I
Chromosome 1 open			S105			2.8	39.8	R.ILGS*ASPEEEQEKPILDRPTR.I
Chromosome 1 open	n reading frame 144 s	SZRD1	<b>S</b> 37			6.2	15.6	K.S*KSPPKVPIVIQDDSLPAGPPPQIR.I
Chromosome 1 open	n reading frame 218	DENND1B	T270S275	•		9.5	45.5	R.E.T*LSQIS*DDLLIPGLGR.H
Chromosome 1 ope	en reading frame 25	TRMT1L	S31	÷			11.8	R. DESACUTABRADESAL DEADTRACADARADA AGADAL EDEL AGADET.
Chromosome 1 op	oen reading frame 9 s	SUCO	S1377	<u> </u>		10.2	60.9	K.SGS*LPSLHDIIK.G
	F	FAM208B	S1243			25.3	16.4	R.S*PLLVTVVESDPRPQGQPR.R
Chromosome 10 op	oen reading frame 7	CDC123	T54S56	<u> </u>			15.4	R.DDPPT"HS"QPDSDDEAEEIQWSDDENTATLTAPEFPEFATK.V
	oen reading frame 7 (		S56T75		-	3.2	19.7	R.DDPPTHS*QPDSDDEAEEIQWSDDENT*ATLTAPEFPEFATK.V
	oen reading frame 7		T54S70		-	5.6	22.1	R.DDPPT*HSQPDSDDEAEEIQWS*DDENTATLTAPEFPEFATK.V
	pen reading frame 7		\$60\$70		-	5.8	32.9	R.DDPPTHSQPDS*DDEAEEIQWS*DDENTATLTAPEFPEFATK.V
	pen reading frame 7 (		S60T75		•	8.8	21.9	R.DDPPTHSQPDS*DDEAEEIQWSDDENT*ATLTAPEFPEFATK.V  K.S*LFINHHPPGQIAR.K
	pen reading frame 9 (		\$83 \$326			100.0	31.3	R.SAS'ADNLTLPR.W
	pen reading frame 2		Y660S663			6.0	35.3	R.Y"APS"YTPSAPMDTNLLSNIQK.L
Chromosome 11 op	pen reading frame 2		S663Y664			3.0	42.4	R.YAPS*Y*TPSAPMDTNLLSNIQK.L
Chromosome 11 op	pen reading frame 2	VPS51	Y660S667			9.3	23.1	R.Y*APSYTPS*APMDTNLLSNIQK.L
Chromosome 11 op	oen reading frame 2	VPS51	Y664S667			4.8	34.7	R.YAPSY*TPS*APMDTNLLSNIQK.L
Chromosome 12 ope	en reading frame 41 p	KANSL2	<b>S</b> 47		•	4.2	18.1	R.ILDEDSWS*DGEQEPITVDQTWR.G
Chromosome 12 ope	en reading frame 41 <sub>h</sub>	KANSL2	S45S47	•		25.2	28.8	R.ILDEDS*WS*DGEQEPITVDQTWR.G
Chromosome 12 ope			\$66\$70\$73	-		100.0	62.9	R.GDPDS'EADS'IDS'DQEDPLK.H
Chromosome 12 ope					-	19.2	47.2	R.EAAVSASDILQESAIHS*PGTVEK.E
Chromosome 12 ope			S138			100.0	35.9	R.EKEES'POPR.R
Chromosome 12 ope			S278S279	<u> </u>		12.2	11.8	K.MLIS"S"EYSR.A
Chromosome 13 ope			S270S273			12.0	59.9	K YSLGSITSPS*PIS*SPTFSPIEFQIGETPLSEQR K
Chromosome 13 ope			\$270\$274			7.9	60.4	K.YSLGSITSPS*PISS*PTFSPIEFQIGETPLSEQR.K  K.YSLGSITSPSPIS*SPTFS*PIEFQIGETPLSEQR.K
Chromosome 14 open			\$273\$278 \$56			1.5	76.8	R.EHNSMWASLSS*PDAEAVEPDFSSIER.L
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in the second se								

<-10 0 abu	ite dots-Significant chandance at 5%FDR point with the minimum	compared to	the			
-3 42 PSM						
5 >100 >10			RajiB			_
Protein Name Ger Chromosome 14 open reading frame 173 INF2		5 2 9	F 2 E	Ascor 22.8	MOWSE 50.2	Sequence R.EHNSMWASLS*SPDAEAVEPDFSSIER.L
Chromosome 14 open reading frame 173 INF2	S614		•	14.7	93.0	K.DPTSLLGVLQAEADS*TSEGLEDAVHSR.G
Chromosome 14 open reading frame 43 ELM	SAN1 Y654S661			39.3	25.2	R.SFELPPY*TPPPILS*PVR.E
Chromosome 14 open reading frame 43 ELM	SAN1 T655S661			30.6	28.8	R.SFELPPYT*PPPILS*PVR.E
Chromosome 14 open reading frame 43 ELM	SAN1 T704T715			26.9	63.8	R.TNSAEVT*PPVLSVMGEAT*PVSIEPR.I
Chromosome 14 open reading frame 43 ELM	SAN1 \$700T704T715	i	-	10.9	36.2	R.TNS*AEVT*PPVLSVMGEAT*PVSIEPR.I
Chromosome 14 open reading frame 43 ELM	SAN1 S461	•		46.2	26.1	R.RAS*QEANLLTLAQK.A
Chromosome 14 open reading frame 43 ELM	SAN1 T704S709			6.5	23.4	R.TNSAEVT*PPVLS*VMGEATPVSIEPR.I
Chromosome 14 open reading frame 43 ELM	SAN1 S148			36.6	15.6	K.GS*PHPGVGVPTYYNHPEALKR.E
Chromosome 14 open reading frame 46 LIN5	2 <b>S</b> 28			75.2	42.1	R.AS'PDLWPEQLPGVAEFAASFK.S
Chromosome 14 open reading frame 92 TOX	4 S178S182			9.7	36.2	R.LSTTPS*PTSS*LHEDGVEDFRR.Q
Chromosome 14 open reading frame 92 TOX	4 S178S181			14.7	45.7	R.LSTTPS*PTS*SLHEDGVEDFRR.Q
Chromosome 14 open reading frame 92 TOX	4 T176S178S182	!		9.3	14.5	R.LSTT*PS*PTSS*LHEDGVEDFRR.Q
Chromosome 14 open reading frame 92 TOX	4 T176S178T180			23.2	19.1	R.LSTT*PS*PT*SSLHEDGVEDFRR.Q
Chromosome 15 open reading frame 42 TICR	R \$1750			122.0	54.1	R.TPILEDFELEGVCQLPDQS*PPR.N
Chromosome 16 open reading frame 53 PAG	R1 T138S143S148	-		100.0	12.6	R.RPPT*PEAQS*EEERS*DEEPEAK.E
Chromosome 17 open reading frame 49 BAP	18 <b>S</b> 96		•	29.2	38.7	K.VYEDSGIPLPAES*PK.K
Chromosome 17 open reading frame 62 C17c				7.3	34.5	K.LITSFLELHCLESPTELSQSSDS*EAGDPASQS
Chromosome 17 open reading frame 62 C17c				16.5	31.7	K.LITSFLELHCLESPTELSQSS*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c				9.8	21.0	K.LITSFLELHCLESPTELS*QSS*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c				7.5	30.4	K.LITSFLELHCLESPTELSQS*S*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c				19.7	24.8	K.LITSFLELHCLESPTELS*QS*S*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c				4.5	11.5	K.LITSFLELHCLES*PT*ELSQSS*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c				9.4	12.8	K.LITSFLELHCLESPT*ELS*QSS*DSEAGDPASQS
Chromosome 17 open reading frame 62 C17c		-		19.4	39.3	K.LITSFLELHCLESPTELS*QS*S*DS*EAGDPASQS
Chromosome 17 open reading frame 62 C17c				9.6	16.4	K.LITSFLELHCLESPT*ELS*QS*S*DSEAGDPASQS
Chromosome 18 open reading frame 9 CEP				17.4	18.2	K.ELNFVTDSVEQELPS*SPKQPICFDR.Q
Chromosome 19 open reading frame 13 LSM				-0.3	33.4	R.SS*PQLDPLR.K
Chromosome 19 open reading frame 13 LSM				31.8	87.4	K.S*PTMEQAVQTASAHLPAPAAVGR.R
Chromosome 19 open reading frame 13 LSM				36.6	61.9	R.S*PVSTRPLPSASQK.A
Chromosome 19 open reading frame 13 LSM	01000102	-		11.0	33.3	R.SS*PQLDPLRKS*PTMEQAVQTASAHLPAPAAVGR.R
Chromosome 19 open reading frame 13 LSM	CIGEOTOE			6.4	25.6	R.S*SPQLDPLRKS*PTM#EQAVQTASAHLPAPAAVGR.R
Chromosome 19 open reading frame 13 LSM				12.8	57.2	K.SPT"M#EQAVQTASAHLPAPAAVGR.R
Chromosome 19 open reading frame 13 LSM			_	-1.6	41.2	K.SPTMEQAVQT*ASAHLPAPAAVGR.R
Chromosome 19 open reading frame 13 LSM  Chromosome 19 open reading frame 13 LSM			-	26.9	26.0	K.TQLS'QGR.S  R.S'S'PQLDPLRKSPTMEQAVQTASAHLPAPAAVGR.R
Chromosome 19 open reading frame 29 CAC		=			30.9	R.RS'DS'EEER.W
Chromosome 19 open reading frame 29 CAC		•		100.0	12.4	
Chromosome 19 open reading frame 43 TRIF					84.7	R. WARDON TO PROPERTY OF A COMMUNICATION OF THE TAX
Chromosome 19 open reading frame 43 TRIF			•		16.9	R.WAES*GSGTSPESGDEEVSGAGSSPVSGGVNLFANDGSFLELFK.
Chromosome 19 open reading frame 43 TRIF					38.1	R.
Chromosome 19 open reading frame 43 TRIF					69.6	R.WAESGSGTSPES*GDEEVSGAGSSPVSGGVNLFANDGSFLELFK.
Chromosome 19 open reading frame 47 C19c				6.3	71.2	R.LGATPETDEDLAWDS*DNDSSSSVLQYAGVIK.K
Chromosome 19 open reading frame 47 C19c				34.2	110.6	R.LGATPETDEDLAWDS DNDSSSSVLQYAGVLK.K
chromosome 19 open reading frame 7 ZC3			-	27.4	11.4 84.1	K.TGSGS*PFAGNS*PAR.E
chromosome 19 open reading frame 7 ZC3				27.1	74.4	K.TGS'GSPFAGNS'PAR.E
chromosome 19 open reading frame 7 ZC3				3.0	18.7	R.AAKPGPAEAPSPT*ASPSGDAS*PPATAPYDPR.V
chromosome 19 open reading frame 7 ZC3				19.2	35.4	R.AAKPGPAEAPS*PTASPS*GDASPPATAPYDPR.V
chromosome 19 open reading frame 7 ZC3				19.2	88.9	R.ENEEGDTGNWYS*S*DEDEGGSSVTSILK.T
chromosome 19 open reading frame 7 ZC3	14 T802S808			2.9	27.7	R.ENEEGDT*GNWYSS*DEDEGGSSVTSILK.T
chromosome 19 open reading frame 7 ZC3			•	30.1	28.8	R.EYS*PPYAPSHQQYPPSHATPLPK.K
chromosome 19 open reading frame 7 ZC3				100.0	12.9	K.HHS'DS'DEEK.S
chromosome 19 open reading frame 7 ZC3				5.6	29.7	R.AAKPGPAEAPS*PTASPSGDAS*PPATAPYDPR.V
chromosome 19 open reading frame 7 ZC3				12.9	88.1	R.ENEEGDTGNWY*S*SDEDEGGSSVTSILK.T
chromosome 19 open reading frame 7 ZC3				1.9	30.7	R.AAKPGPAEAPSPT*ASPS*GDASPPATAPYDPR.V
chromosome 19 open reading frame 7 ZC3				9.2	17.2	R.ENEEGDT*GNWY*SSDEDEGGSSVTSILK.T
chromosome 19 open reading frame 7 ZC3				12.4	61.9	R.ENEEGDT*GNWYS*SDEDEGGSSVTSILK.T
Chromosome 2 open reading frame 17 RET				37.6	29.1	K.NAPPGGDEPLAET*ES*ES*EAELAGFSPVVDVK.K
Chromosome 2 open reading frame 17 RET				100.0	69.0	R.QALDS*EEEEEDVAAK.E
Chromosome 2 open reading frame 49 C2or				5.1	26.4	R.KSPSGPVKS*PPLS*PVGTTPVK.L
Chromosome 2 open reading frame 49 C2or				4.8	32.3	R.KLSNS*SSSVSPLILSSNLPVNNK.T
Chromosome 20 open reading frame 172 DSN	1 <b>S</b> 81			16.3	47.7	K.SLHLS*PQEQSASYQDR.R
protein		•••				

Peak Area %CV <-10 0	abundano	ts-Significant cha e at 5%FDR o with the minimum	compared to	the		
-3 42 71 3 86 5 >100	PSM			RajiB		
>10			5 m m	5 2 m	_	
Chromosome 20 open reading fra	Name Gene me 172 DSN1 protein	Phosphosites \$57	2 4 2	0 0 10	Ascor 8.2	MOWS 17.9
Chromosome 20 open reading fra	me 172 DSN1 protein	S27S28			12.5	36.3
Chromosome 20 open reading fr	ame 74 RALGAPA	S820S821			10.6	45.1
Chromosome 20 open reading fr	ame 74 RALGAPA	<b>S</b> 696			33.6	38.5
Chromosome 20 open reading fr	ame 74 RALGAPA	S373S375			10.1	33.8
Chromosome 22 open reading fr	ame 19 THOC5 protein	T328			100.0	33.0
Chromosome 22 open reading fr	ame 19 THOC5 protein	\$307\$312	<b>F</b>		2.0	16.1
Chromosome 22 open reading fr	ame 19 THOC5 protein	S312S314	<u> </u>		25.5	45.6
Chromosome 22 open reading fr	ame 19 THOC5 protein	S307S314			8.2	26.8
Chromosome 5 open reading fr	rame 22 C5orf22	Y435			11.9	43.4
Chromosome 5 open reading fr	ame 22 C5orf22	Y427	-		0.1	16.4
Chromosome 5 open reading fr		S53	-		20.3	58.6
Chromosome 6 open reading fra	me 108 DNPH1	S169			32.7	56.7
Chromosome 6 open reading fra		S12			29.9	42.3
Chromosome 6 open reading fra	me 203 C6orf203	S110S116			12.2	35.3
Chromosome 6 open reading fra	me 203 C6orf203	S106S116			24.3	43.7
Chromosome 6 open reading fra		T30			92.0	12.5
Chromosome 6 open reading fra	me 209 LMBRD1	S528S531			6.6	15.3
Chromosome 6 open reading fr	ame 93 LTV1	S352S355	•••		13.6	34.8
Chromosome 6 open reading fr	ame 93 LTV1	\$352\$355Y357			19.7	19.0
Chromosome 6 open reading fr	ame 93 LTV1	S331			12.7	23.3
Chromosome 6 open reading fr	ame 93 <sub>LTV1</sub>	T314			13.9	18.7
Chromosome 6 open reading fr	ame 93 LTV1	S355T356Y357			0.3	12.4
Chromosome 7 open reading fr	rame 47 PPP1R35	<b>S</b> 52			42.6	28.2
Chromosome 7 open reading fr	rame 47 PPP1R35	T84S87			100.0	22.4
Chromosome 7 open reading fr		S175			100.0	46.9
Chromosome 9 open reading fra	me 142 PAXX	S148	•		32.3	51.9
Chromosome 9 open reading fra		S152			100.0	35.8
	protein	S203	•		106.6	108.6
	protein	S312			8.9	29.3
	protein	S311			111.6	38.6
Chromosome 9 open reading fr		S597S598	•		54.3	80.9
Chromosome 9 open reading fr		\$382\$384	<u> </u>		100.0	84.7
Chromosome 9 open reading fr		S411S421T425			8.1	42.6
Chromosome 9 open reading fr		S553T556			100.0	84.9
Chromosome 9 open reading fr	ame 86 RABL6	\$411T425\$427			0.2	35.3
Chromosome 9 open reading fr		S411S421S428			14.3	33.1
Chromosome 9 open reading fr	ame 86 <sub>RABL6</sub>	\$411\$427\$428			16.6	56.7
Chromosome 9 open reading fr	ame 86 RABL6	S411T425S428	÷		12.4	19.7
Chromosome associated kinesin	KIF4A KIF4A	T1161			17.2	40.2

Chromosome associated kinesin KIF4A KIF4A T799S801

Chromosome condensation 1 RCC1 S11

Chromosome condensation protein G NCAPG T968S973

NCAPG \$1015

S1373S1382

S1373S1378

T1375S1382

S1373T1381

S1182S1191

S301

Chromosome associated kinesin KIF4A KIF4A S801

Chromosome condensation protein G NCAPG S674

Chromosome condensation protein G NCAPG \$390

Chromosome condensation protein G NCAPG \$1002

Chromosome condensation protein G NCAPG 8973S975

CIC CIC

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CIC CIC

Cingulin CGN

Cisplatin resistance associated LUC7L3 T419S431 overexpressed protein

Cisplatin resistance associated LUC7L3 S425S431 overexpressed protein

Cisplatin resistance associated LUC7L3 S425T429 overexpressed protein

Citron CIT

Claspin CLSPN S225

Claspin CLSPN T217

Cingulin CGN \$338

R.IHLGS\*SPK.K

K.THDHQLES\*S\*LSPVEVFAK.T

R.RSS\*S\*PAELDLKDDLQQTQGK.C

R.RLS\*NS\*SLCSIEEEHR.M
R.RRPT\*LGVQLDDK.R

R.ALY\*GNLDLQVYAAESPPS.-R.ISTIHDILHSQGNNS\*EVR.E

R.YFEADPPGQVAAS\*PDPTT.-

R.ASLLT\*SLMLVK.R

K.SVIEGVDEDS\*DIS\*DDEPSVYSA.-

R.FRLT\*PPS\*PVR.S

R.ELDEEGS\*DPPLPGR.A

R.LAAAEETAVS\*PR.K

R.KS\*PRPAGPQLFLPDPDPQR.G

K.ILEGDNGMDS\*DMEEEADDGSK.M

K.SVNEILGLAESS\*PNEPK.A

K.AAQQDS\*DS\*DGEALGGNPMVAGFQDDVDLEDQPR.G

R.GS\*PPLPAGPVPS\*QDIT\*LSSEEEAEVAAPTK.G
R.DDPS\*DVT\*DEDEGPAEPPPPPK.L

R.GS\*PPLPAGPVPSQDIT\*LS\*SEEEAEVAAPTK.G

R.GS\*PPLPAGPVPS\*QDITLSS\*EEEAEVAAPTK.G

R.GS\*PPLPAGPVPSQDITLS\*S\*EEEAEVAAPTK.G

R.GS\*PPLPAGPVPSQDIT\*LSS\*EEEAEVAAPTK.G

K.LEDPTEVTPGLSFFNPVCAT\*PNSK.I

R.RRT\*FS\*LTEVR.G

R.TFS\*LTEVR.G

R.S\*PPADAIPK.S

R.GDFS\*YIGNLMTK.E

K.LNLAQFLNEDLS\*.

K.S\*KLNLAQFLNEDLS.-

K.TLHCEGTEINS\*DDEQESK.E

R.CQT\*AEADS\*ESDHEVPEPESEMK.M

R.CQTAEADS\*ES\*DHEVPEPESEMK.M

R.FAELPEFRPEEVLPS\*PTLQSLATS\*PR.A

R.FAELPEFRPEEVLPS\*PTLQS\*LATSPR.A

R.FAELPEFRPEEVLPSPT\*LQSLATS\*PR.A

R.FAELPEFRPEEVLPS\*PTLQSLAT\*SPR.A

K.NEVNGT\*SEDIKSEGDTQS\*N.-

K.NEVNGTSEDIKS\*EGDTQS\*N.-

R.SMS\*ETGTAAAPGVSSELLSVAAQTLLSSDTK.A

K.NEGLSSDEEFDS\*VYDPSSIAS\*LLTESNLQTSSC.-

K.NSWVS\*SSPCQLSPSGFSGEELPFVGFSYSK.A

K.DLFETGLEDENNS\*PLEDEESLESIR.A

K.DLFET\*GLEDENNSPLEDEESLESIR.A

30.0 24.6

100.0 13.0

21.0 29.7

100.0 69.0

9.2 34.7

7.7 12.9

17.4 47.3

39.1 57.4

41.9 56.8

25.8 30.3

17.5 31.0

7.7 18.2

-0.4 31.7

19.1 25.2

12.8 15.6

10.8

2.3 11.4

10.7 11.9

41.7 83.1

2.8 24.9

100.0 40.9

10.0 29.2

K.SVNEILGLAES\*SPNEPK.A

R.LKNDSDLFGLGLEEAGPKES\*S\*EEGK.E

K.ALFKPPEDS\*QDDES\*DSDAEEEQTTKR.R

K.ALFKPPEDSQDDES\*DS\*DAEEEQTTK.R

K.ALFKPPEDS\*QDDESDS\*DAEEEQTTKR.R

R.ALYGNLDLQVY\*AAESPPS.-

K.VDEEDSDEES"HHDEMS"EQEEELEDDPTVVK.N K.VDEEDS"DEESHHDEMS"EQEEELEDDPTVVK.N

K.EKWDCES\*ICS\*TYSNLYNHPQLIK.Y

K.EKWDCES\*ICS\*TY\*S\*NLYNHPQLIK.Y

K.EKWDCESICS\*T\*Y\*S\*NLYNHPQLIK.Y

R.APVPEPGLDLSLSPRPDS\*PQPR.H

K.LNT'LEPLEDQDLPM#NELDES'EEEEMITVVLEEAK.E

K.LNT'LEPLEDQDLPM#NELDESEEEEMITVVLEEAK.E

Peak Area <-10 -5 -3 0	%CV 0 29 42 71	abundand	ts-Significant cha se at 5%FDR c with the minimum	ompared to peak area f	the			
>10 Clathrin,	Protein Name		Phosphosites \$1494		5 2 3 5 2 3	Ascor 28.9	MOWSE	Sequence R.TSIDAYDNFDNIS*LAQR.L
	Claudin 12	CLDN12	S231			3.2	27.3	R.SRLS*AIEIDIPVVSHTT
Cleavage and polyader	nylation specificity factor 2	CPSF2	\$419\$420\$423			114.1	83.3	K.EADIDS*S*DES*DIEEDIDQPSAHK.T
Cleavage and polyader		CPSF6	T444			33.8	96.2	R.T*PLSEAEFEEIMNR.N
Cleavage stimulation		CSTF2	T507				45.0	R.QVPVMQGT*GMQGASIQGGSQPGGFSPGQNQVTPQDHEK.A
Cleavage stimulation	on factor subunit 2	CSTF2	S524			27.3	31.7	R.QVPVMQGTGMQGASIQGGSQPGGFS*PGQNQVTPQDHEK.A
Cleavage stimulation	on factor subunit 2	CSTF2	S518			9.4	23.1	R.QVPVMQGTGMQGASIQGGS*QPGGFSPGQNQVTPQDHEK.A
Cleavage stimulation	on factor subunit 2	CSTF2	T531			-4.7	20.3	R.QVPVMQGTGMQGASIQGGSQPGGFSPGQNQVT*PQDHEK.A
Cleavage stimulation f	actor, 3 Prime pre- L subunit 3. 77kDa	CSTF3	S691			100.0	33.2	K.RPNEDS*DEDEEK.G
CLIP as	ssociated protein 1	CLASP1	<b>S</b> 600			9.3	88.1	R.SRS*DIDVNAAASAK.S
CLIP as	ssociated protein 1	CLASP1	S1196	<b>—</b>		100.0	32.2	R.S'QEDLNEPIKR.D
CLIP as	ssociated protein 1		<b>S</b> 572			10.5	36.8	R.S*PTGSTTSR.A
	CLN6 protein		S31			35.4	44.1	R.HGS*VSADEAAR.T
	CLNS1A		S102	<b></b> :		111.9	144.1	K.EPVADEEEEDS*DDDVEPITEFR.F
		NAT8B	T83	=		100.0	11.1	K.KPWT'R.Y
		NCAPH	T541	ļ I			31.3	R. VET*EUVEEENVNAMDAINTENEODOL OAANONNENI NNI EUODV
Coatomer protein comp			T861			9.7	66.3	R.STAQQELDGKPASPT*PVIVASHTANK.E
Coatomer protein comp			S859	-		58.1	35.8	R.STAQQELDGKPAS*PTPVIVASHTANKEEK.S
Coatomer protein comple			S45			12.1	40.1	KLSSPERD  KLSSPERD
Coatomer protein comple			S44	<del></del>		9.8	30.9	
	COBL like 1		S441			110.8	65.0	K.S'QDIPFVSTDINTLK.N  K.SGSTES'LNPRPOT'TISPADLHGMWYPTVR.R
	COG3		S536T543			6.5	40.8	K.SGSTES*LNPRPQT*TISPADLHGMWYPTVR.R  K.SGS*T*ESLNPRPQTTISPADLHGMWYPTVR.R
Coiled coil de	omain containing 6		S533T534			-0.8	22.7	K.SGS*T*ESLNPRPQTTISPADLHGMWYPTVR.R  K.LDQPVS*APPS*PR.D
	omain containing 6		S240S244		_	100.0	58.9	R.TVS*SPIPYTPS*PSSSRPIS*PGLSYASHTVGFTPPTSLTR.A
	omain containing 6		S351S359S367 T427S431		<u> </u>	23.8	16.9	K.
	omain containing 6		\$352\$359\$367			13.4	11.5	R.TVSS*PIPYTPS*PSSSRPIS*PGLSYASHTVGFTPPTSLTRA
	omain containing 6		S419			6.1	23.9	R.RSNS*PDKFK.R
	omain containing 6		S254			28.4	30.5	R.DISMEIDS*PENMMR.H
Coiled coil do	omain containing 6	CCDC6	S351S352S363		•	7.6	11.8	R.TVS*S*PIPYTPSPSSS*RPISPGLSYASHTVGFTPPTSLTR.A
Coiled coil do	omain containing 6	CCDC6	T349S351	•			17.7	R.T"VS"SPIPYTPSPSSSRPISPGLSYASHTVGFTPPTSLTR.A
Coiled coil do	omain containing 6	CCDC6	\$351\$359\$363		•	14.5	13.5	R.TVS*SPIPYTPS*PSSS*RPISPGLSYASHTVGFTPPTSLTR.A
Coiled coil do	omain containing 6	CCDC6	S352S361	•	•	1.1	16.5	R.TVSS*PIPYTPSPS*SSRPISPGLSYASHTVGFTPPTSLTR.A
Coiled coil do	omain containing 6	CCDC6	\$352\$362	•		4.8	13.7	R.TVSS*PIPYTPSPSS*SRPISPGLSYASHTVGFTPPTSLTRA
Coiled coil do	omain containing 6	CCDC6	S351S363			7.6	22.7	R.TVS*SPIPYTPSPSSS*RPISPGLSYASHTVGFTPPTSLTR.A
Coiled coil do	omain containing 9	CCDC9	S521		•	42.2	25.2	R.TTHLAGALS*PGEAWPFESV
Coiled-coil dom	ain containing 131	ZFC3H1	S1046			49.2	69.2	R.S*FLESNYFTKPNLK.H
Coiled-coil dom	ain containing 131	ZFC3H1	S28			60.5	91.1	K.EEGELEDGEIS*DDDNNSQIR.S
Coiled-coil dom	ain containing 131	ZFC3H1	S1301S1303			15.4	50.4	R.KPISDNS*FS*SDEEQSTGPIK.Y
Coiled-coil dom	ain containing 132	VPS50	Y96S98			19.7	29.3	K.SAYQEY*DS*DSDVPEELKR.D
	ain containing 132		Y96S100	<b></b>		14.1	29.3	K.SAYQEY'DSDS'DVPEELKR.D
	ain containing 132		Y93S98			3.2	26.2	K.SAY'QEYDS'DSDVPEELKR.D
	ain containing 132		S91			6.6	33.6	K.S'AYQEYDSDSDVPEELKR.D
	main containing 14		S598S602			17.3	17.9	K.QDS*DEGS*ETMALIEDEHNLDNTIYIPFAR.S
	in containing 144B		S632	<u></u>		19.8	31.0	K.DS*ASLPR.I
Coiled-coil dor	main containing 16		S351			97.8	71.2	K.EEENADS*DDEGELQDLLSQDWR.V
0-8-1 9 -		CCDC25	S204			21.1	26.0	K.VENMSSNQDGNDS*DEFM#.
	main containing 25		S196			10.0	28.2	K.VENMS*SNQDGNDSDEFM#
	main containing 43		T139	<u> </u>		17.5	28.6	K.AALLAQYADVT*DEEDEADEKDDSGATTMNIGSDK.L  KLVGLNLS*PPMS*PVQLPLR.A
	main containing 52		\$760\$764			100.0	69.1	K.VEENPDADS'DFDAKS'S'ADDEIEETR.V
		NSRP1	\$248\$254\$255 \$33			91.4	78.4 58.0	K.VEENPDAUS DEDAKS S ADDEIEE IK.V  K.KTQQLHPVLQKPSVFGNDS DDDDETSVSESLQR.E
Coiled-coil dor	main containing 55		\$33 \$27			13.9	13.6	K.TQQLHPVLQKPS*VFGNDSDDDDETSVSESLQR.E
	main containing 55		T16			.3.8	46.8	K.T'QQLHPVLQKPSVFGNDSDDDDETSVSESLQR.E
	main containing 86		S91			122.6	45.8	R.LQQGAGLESPQGQPEPGAAS*PQR.Q
	main containing 86		S80S91			100.0	41.8	R.LQQGAGLES*PQGQPEPGAAS*PQR.Q
	main containing 86		S102S113			14.6	30.1	R.QQDLHLES'PQRQPEYSPES'PR.C
	main containing 86		S18			32.3	58.0	R.LGGLRPES*PESLTSVSR.T
	main containing 86		T42			6.4	22.2	R.ALVEFESNPEET*REPGSPPSVQR.A
	main containing 86		S47			6.0	19.7	R.ALVEFESNPEETREPGS*PPSVQR.A
	main containing 86		S58			100.0	20.5	R.AGLGS*PERPPK.T
Coiled-coil dor	main containing 86	CCDC86	T65S66			21.8	15.9	R.AGLGSPERPPKT'S'PGSPR.L

<-10 0 abundano		ompared to	the			
	with the minimum	peak area f	or a given			
5 >10 = -	Phoenic "	CarT	RajiB E E E	A	MOWSE	Sequence
Protein Name Gene Coiled-coil domain containing 86 CCDC86	Phosphosites \$102Y109	0 0 0	0 0 0	Ascor 2.7	21.5	R.QQDLHLES'PQRQPEY"SPESPR.C
Coiled-coil domain containing 86 CCDC86	\$102\$110		■.	14.9	31.9	R.QQDLHLES*PQRQPEYS*PESPR.C
Colled-coil domain containing 86 CCDC86	S217	•		8.9	48.8	R.KGS*SSQAPASK.K
Coiled-coil domain containing 86 CCDC86  Coiled-coil domain containing 94 CCDC94	T146 S211S213				15.6	K.EELT*PGAPQHQLPPVPGSPEPYPGQQAPGPEPSQPLLELTPI
Coiled-coil domain containing 94 CCDC94	\$305\$306\$316			6.7	53.8	K.EANPTPLTPGAS*S*LSQLGAYLDS*DDSNGSN
CCDC94	\$308Y313\$316			15.7	36.6	K.EANPTPLTPGASSLS*QLGAY*LDS*DDSNGSN
Coiled-coil domain containing 94 CCDC94	Y313S316S322			6.5	15.6	K.EANPTPLTPGASSLSQLGAY*LDS*DDSNGS*N
Coiled-coil domain containing 94 CCDC94	\$308Y313\$319			1.3	23.0	R.KEANPTPLTPGASSLS*QLGAY*LDSDDS*NGSN
Coiled-coil domain containing 94 CCDC94	Y313S316			13.5	25.7	K.EANPTPLTPGASSLSQLGAY*LDS*DDSNGSN
CCDC94  Coiled-coil domain containing 94 CCDC94	Y313S316S319	-		12.5	34.2	K.EANPTPLTPGASSLSQLGAY*LDS*DDS*NGSN  R.LLEDS*DS*EDEAAPS*PLQPALRPNPTAILDEAPKPK.R
Coiled-coil domain containing 94 CCDC94	S211S213S220 S319	-		57.9	14.1	K.EANPTPLTPGASSLSQLGAYLDSDDS*NGSN
Coiled-coil domain containing 94 CCDC94	\$308\$316			7.8	27.2	K.EANPTPLTPGASSLS*QLGAYLDS*DDSNGSN
Coiled-coil domain containing 94 CCDC94	Y313S319S322			0.8	27.2	R.KEANPTPLTPGASSLSQLGAY*LDSDDS*NGS*N
Coiled-coil domain containing 94 CCDC94	\$308Y313\$322			3.7	25.1	R.KEANPTPLTPGASSLS*QLGAY*LDSDDSNGS*N
Coiled-coil domain containing 94 CCDC94	\$308\$316\$319		•	1.3	18.1	R.KEANPTPLTPGASSLS*QLGAYLDS*DDS*NGSN
Coiled-coil domain containing 97 CCDC97	S257	<b>.</b>		100.0	49.9	R.LLQQQEEEEACLEEEEEEDS*DEEDQR.S
Coiled-coil domain containing 97 CCDC97	S221			17.5	37.1	R.TPTHQPPKPGSPGRPACPLS*NLLLQSYEER.E
Colled-coil domain containing 97 CCDC97	S212			22.9	37.2	R.TPTHQPPKPGS*PGRPACPLSNLLLQSYEER.E
Coiled-coil domain containing 97 CCDC97  Coiled-coil domain containing 97 CCDC97	T202T204 T204S212			-2.9	30.1	R.T*PT*HQPPKPGSPGRPACPLSNLLLQSYEER.E  R.TPT*HQPPKPGS*PGRPACPLSNLLLQSYEER.E
Coiled-coil domain containing 97 CCDC97	S337			98.3	22.6	R.YFDEEEPEDAPS*PELDGD
Coiled-coil domain containing 98 ABRAXAS		• • •		100.0	36.1	K.MS*S*PET*DEEIEK.M
Coiled-coil domain-containing protein 149 CCDC149	T337S341S354		•••	1.6	11.5	R.T'LEVS'GLWSLPGLSYNVS'VGFGRGK.D
Coiled-coil-helix-coiled-coil-helix domain CHCHD3	<b>S</b> 50	<del>ii</del>		13.9	111.3	R.YS*GAYGASVSDEELK.R
Coiled-coil-helix-coiled-coil-helix domain CHCHD3 containing 3	<b>Y</b> 49	Ŧ.		32.8	85.2	R.Y*SGAYGASVSDEELK.R
Coilin COIL	T122			100.0	35.0	R.AFQLEEGEET*EPDCK.Y
Cold shock domain protein AYBX3	\$201\$203\$204			54.1	45.5	R.NYAGEEEEEGS*GS*S*EGFDPPATDR.Q
Cold shock domain protein AYBX3  Cold shock domain protein AYBX3	\$203\$204			8.7	26.6	R.NYAGEEEEGSGS*S*EGFDPPATDR.Q  R.NYAGEEEEGSGSS*EGFDPPATDR.Q
Cold shock domain protein AYBX3	\$204 \$203			-0.2	19.7	R.NYAGEEEEEGSGS*SEGFDPPATDR.Q
Cold shock domain protein AYBX3	Y192S201S203			50.7	15.8	R.NY*AGEEEEEGS*GS*SEGFDPPATDR.Q
Collagen type IV alpha 3 binding protein COL4A3B	\$132\$147	•	•	8.8	31.2	R.HGS*MVSLVSGASGYSATS*TSSFKK.G
Collagen type IV alpha 3 binding protein COL4A3B	S132T146	Ė		5.7	13.2	R.HGS*MVSLVSGASGYSAT*STSSFKK.G
Conserved nuclear protein NHN1 ZC3H18	<b>S</b> 46			104.3	73.5	R.AS*DLEDEESAAR.G
Conserved nuclear protein NHN1 ZC3H18	S534			17.8	51.6	K.LGVSVS*PSR.A
Conserved nuclear protein NHN1 ZC3H18	S78			63.6	78.6	K.S*QDQDSEVNELSR.G
Conserved nuclear protein NHN1 ZC3H18  Conserved nuclear protein NHN1 ZC3H18	\$532\$534			15.5	31.7	K.LGVS*VS*PSR.A  R.S*PQPPSR.Q
Conserved nuclear protein NHN1 ZC3H18	\$487 \$868			100.0	37.2 46.1	RLGS*PKPER.Q
Conserved nuclear protein NHN1 ZC3H18	\$78\$83			71.2	41.6	K.S'QDQDS'EVNELSR.G
Conserved nuclear protein NHN1 ZC3H18	S118			6.5	12.4	R.DEASS*VTR.E
Conserved nuclear protein NHN1 ZC3H18	S67S74	-		14.9	20.7	R.GPSQEEEDNHS'DEEDRAS'EPK.S
Conserved nuclear protein NHN1 ZC3H18	S59S67S74				11.1	R.GPS*QEEEDNHS*DEEDRAS*EPKSQDQDSEVNELSR.G
Conserved nuclear protein NHN1 ZC3H18	S59S67S74S78	·			16.7	R.GPS*QEEEDNHS*DEEDRAS*EPKS*QDQDSEVNELSR.G
Conserved nuclear protein NHN1 ZC3H18	S746			40.7	17.4	R.S'PAPAQTR.K
Conserved nuclear protein NHN1 ZC3H18  Conserved nuclear protein NHN1 ZC3H18	S117 S59S67S78		•	13.8	23.8	R.DEAS*SVTR.E  R.GPS*QEEEDNHS*DEEDRASEPKS*QDQDSEVNELSR.G
Conserved nuclear protein NHN1 ZC3H18	S59S67S78 S532			-7.3	14.7 45.6	K.KKLGVS*VSPSR.A
Conserved nuclear protein NHN1 ZC3H18	S67S74S78S83			8.5	11.9	R.GPSQEEEDNHS'DEEDRAS'EPKS'QDQDS'EVNELSR.G
Conserved nuclear protein NHN1 ZC3H18	T851				15.3	K.RPNT*SPDR.G
Conserved oligomeric Golgi complex COG1 subunit 1 (Fragment)	S113S114T115			100.0	13.5	R.RS'S'T'AWLPR.S
Conserved oligomeric Golgi complex COG1 subunit 1 (Fragment)	S113S114			5.2	23.7	R.RS*S*TAWLPR.S
Conserved oligomeric Golgi complex COG1 subunit 1 (Fragment)	S114T115	<del></del>		6.7	16.8	R.RSS*T*AWLPR.S
Copper homeostasis protein cutC homolog CUTC	<b>S</b> 17			100.0	18.6	R.ARIPS*GK.A
Core binding factor, beta subunit CBFB  Coronin 7 CORO7-	\$173 \$21			46.9	89.0	R.QQDPS*PGSNLGGGDDLK.L  R.RES*WISDIR.A
Coronin 7 CORO7-	\$21 \$462			39.8	18.5	R.S'LQSLLGPSSK.F
CRDBP IGF2BP1	S181		•	100.0	79.9	R.QGS*PVAAGAPAK.Q
CRK CRK	T42			6.5	97.1	R.DSST*SPGDYVLSVSENSR.V
CRK CRK	<b>S</b> 40			7.8	14.0	R.DS*STSPGDYVLSVSENSR.V
	_		_	_		

Peak Area <-10 -5 -3 0 3	o abundani	ts-Significant cha ce at 5%FDR c with the minimum	ompared to peak area f	the			
>10	Protein Name Gene CRK CRK	Phosphosites		2 H E		MOWSE	Sequence R.DSS*TSPGDYVLSVSENSR.V
	CRKLCRKL	S41 S107		<b>-</b> .	9.5	74.5	R.YPS*PPMGSVSAPNLPTAEDNLEYVR.T
	CRKL CRKL	S112			10.6	49.2	R.YPSPPMGS*VSAPNLPTAEDNLEYVR.T
	CRKL CRKL	S195				13.8	R. MC-MICYGIDEDAUAYAODOTTTDI DAVEGGDGAAITDI DETOMICDIJEA
Cross immune rea	ction antigen PCIA1 DDA1	<b>S</b> 95			50.6	54.7	R.TDS*PDMHEDT
	CRSP2 <sub>MED14</sub>	S995		<b></b>	12.0	16.1	R.SVNEDDNPPSPIGGDMMDS*LISQLQPPPQQQPFPK.Q
	CRSP2 <sub>MED14</sub>	S998			37.2	17.8	R.SVNEDDNPPSPIGGDMMDSLIS*QLQPPPQQQPFPK.Q
	CRSP2 <sub>MED14</sub>	S986		==	2.6	20.3	R.SVNEDDNPPS'PIGGDMMDSLISQLQPPPQQQPFPK.Q  R.S'VNEDDNPPSPIGGDMMDSLISQLQPPPQQQPFPK.Q
	CRSP2 MED14	S977 S977S995			2.2	10.9	R.S'VNEDDNPPSPIGGDMMDS'LISQLQPPPQQQPFPK.Q
CTD pho	sphatase, subunit 1 CTDP1	S869S872	-		24.7	39.7	K.EVDDILGEGS*DS*DSEK.R
	CTP synthetase 2 CTPS2	S568S571			13.4	27.2	KLSSSDRYS*DAS*DDSFSEPR.I
	CTP synthetase 2 CTPS2	S562S563S576		<u> </u>	3.3	11.1	K.LS*S*SDRYSDASDDSFS*EPR.I
	CTP synthetase 2 CTPS2	S563Y567S574			1.6	15.5	KLSS*SDRY*SDASDDS*FSEPR.I
	CTP synthetase 2 CTPS2	Y567S568S574			0.3	11.6	K.LSSSDRY*S*DASDDS*FSEPR.I
	CTP synthetase 2 CTPS2	S571S574S576		<u></u>	15.0	21.7	K.LSSSDRYSDAS*DDS*FS*EPR.I
	CTP synthetase 2 CTPS2	S563S571			2.4	34.9	KLSS*SDRYSDAS*DDSFSEPR.I  KLSS*SDRY*S*DASDDSFSEPR.I
	CTP synthetase 2 CTPS2	\$563Y567\$568 \$563Y567		<u> </u>	6.3	14.9	K.LSS'SDRY'SDASDDSFSEPR.I
	CTP synthetase 2 CTPS2	\$563\$564Y567		<u> </u>	1.1	15.9	K.LSS'S'DRY'SDASDDSFSEPR.I
	CTP synthetase 2 CTPS2	S564S571			2.5	17.6	K.LSSS*DRYSDAS*DDSFSEPR.I
	CTP synthetase 2 CTPS2	S568S571S574		•	7.4	18.8	K.LSSSDRYS*DAS*DDS*FSEPR.I
	ike family member 1 CELF1 (Fragment)	S22		-	19.1	24.0	K.LDFLPEMMVDHCSLNSS*PVSK.K
CUGBP Elav-li	ike family member 1 CELF1 (Fragment)	S18	ı.		26.1	11.4	K.LDFLPEMMVDHCS*LNSSPVSK.K
	Cullin 4A CUL4A	S10			29.8	70.3	R.KGS*FSALVGR.T
	noma tumor antigen RBM26 se70-2 noma tumor antigen RBM26	S127			20.7	11.7	R.LNHS*PPQSSSR.Y  R.EGSTQQLQT*TSPKPLVQQPILPVVK.Q
	se70-2	T614 S65	•		-0.3	11.0 59.7	R.SS*SLSDFSWSQR.K
	CYBR CYTIP	S66		=	30.2	70.3	R.SSS'LSDFSWSQR.K
Cyclic GMP inhibited p	hosphodiesterase B PDE3B	S295S296		· <del></del> -	32.9	69.6	R.RRS*S*CVSLGETAASYYGSCK.I
Cyclic GMP inhibited p	hosphodiesterase B PDE3B	S981	Ė		-0.1	12.2	R.SS*PQLAK.L
Cyclic nucleotide g	ated channel beta 1 CNGB1	T1021		•	25.1	17.2	K.SVLVT*LK.A
	Cyclin A1 CCNA1	T96T102			100.0	14.6	R.RT*CGQGIT*R.I
Cyclin	Cyclin B2 CCNB2V	S92			32.3	59.7	K.GPS*PTPEDVSMKEENLCQAFSDALLCK.I
	dependent kinase 7 CDK7	T160 S164	-		10.2 45.1	42.2	R.TYT*HEVVTLWYR.A  K.SFGS*PNR.A
	CDKN3	S14S15	•		21.4	77.0	M.KPPSSIQTSEFDS*S*DEEPIEDEQTPIHISWLSLSR.V
Cyclin depende	nt kinase inhibitor 3 <sub>CDKN3</sub>	S10S14			19.0	46.8	M.KPPSSIQTS*EFDS*SDEEPIEDEQTPIHISWLSLSR.V
Cyclin depende	nt kinase inhibitor 3 CDKN3	S5S6				60.3	M.KPPS*S*IQTSEFDSSDEEPIEDEQTPIHISWLSLSR.V
Cyclin	G associated kinase GAK	S826S829	. •		25.8	52.4	R.DES*EVS*DEGGSPISSEGQEPR.A
	CCNH	T315	<u> </u>		67.5	56.6	K.HEEEEWT*DDDLVESL
	Cyclin L1 CCNL1	S445	<u></u>		100.0	30.3	R.HHNHGS'PHLK.A
	Cyclin L1 CCNL1	S352	-		27.8	67.6	K.AEEKS'PISINVK.T  K.GLNPDGTPALSTLGGFSPASKPS'SPR.E
	Cyclin L1 CCNL1	S335S341			23.3	13.1	K.GLNPDGTPALSTLGGFSPASKPS*SPR.E  K.GLNPDGTPALSTLGGFS*PASKPS*SPR.E
	Cyclin L1 CCNL1	S335S338	• • •		14.0	14.0	K.GLNPDGTPALSTLGGFS*PAS*KPSSPR.E
	Cyclin L1 CCNL1	S335S342			18.6	19.4	K.GLNPDGTPALSTLGGFS*PASKPSS*PR.E
	Cyclin L1 CCNL1	S338S341	÷		15.0	11.0	K.GLNPDGTPALSTLGGFSPAS*KPS*SPR.E
	Cyclin L2 CCNL2	S330			14.2	32.2	R.GLLPGGTQVLDGTSGFS*PAPK.L
	Cyclin L2 <sub>CCNL2</sub>	S327		-	6.5	34.3	R.GLLPGGTQVLDGTS*GFSPAPK.L
	Cyclin Y-like 1 CCNYL1	S274			25.1	85.8	R.SFS*ADNFIGIQR.S
Cyclin deserted	Cyclin Y-like 1 CCNYL1	S272	<u> </u>		14.0	73.7	R.S*FSADNFIGIQR.S
	kinase 9 (Fragment) CDK9	\$56 \$26			12.2	44.9 64.1	R.  R.
	kinase 9 (Fragment) CDK9	S26			12.2	64.1	R.
	natosis gene protein CYLD	S418S422	•		37.2	26.0	R.FHS'LPFS'LTK.M
	natosis gene protein CYLD	S398			15.1	18.2	K.SLTEISTDFDRS*SPPLQPPPVNSLTTENR.F
Cylindron	natosis gene protein CYLD	S399	<u> </u>		4.0	35.5	K.SLTEISTDFDRSS*PPLQPPPVNSLTTENR.F
Cylindron	natosis gene protein CYLD	S392			-0.1	25.6	K.SLTEIS*TDFDRSSPPLQPPPVNSLTTENR.F
	lycine rich protein 1 CSRP1	S192			100.0	72.0	K.GFGFGQGAGALVHS*E
	steine string protein DNAJC5	S12		•••	1.4	84.6	R.SLSTS*GESLYHVLGLDK.N
Су	steine string protein DNAJC5	S10			25.6	139.0	R.SLS*TSGESLYHVLGLDK.N

Peak Area	o abundano		compared to	the			
.5 -3	timepoint PSM	with the minimum	peak area fo	or a given			
3 5 >10	>100		CarT	RajiB			
	Protein Name Gene Cysteine string protein DNAJC5	Phosphosites T11S12	8 4 4	# # #	Ascor 8.9	MOWSE 77.1	Sequence R.SLST*S*GESLYHVLGLDK.N
	Cysteine string protein DNAJC5	\$10\$15		• • •	14.2	90.6	R.SLS*TSGES*LYHVLGLDK.N
	Cysteine string protein DNAJC5	T11			-0.3	82.3	R.SLST*SGESLYHVLGLDK.N
	Cysteine string protein DNAJC5	T11S15		<del></del>	21.6	114.2	R.SLST*SGES*LYHVLGLDK.N
	Cysteine string protein DNAJC5	S12S15			12.9	104.8	R.SLSTS*GES*LYHVLGLDK.N
	Cysteine string protein DNAJC5	\$10T11			7.9	64.8	R.SLS*T*SGESLYHVLGLDK.N
	Cysteine string protein DNAJC5	S10S12			6.6	37.2	R.SLS*TS*GESLYHVLGLDK.N
	Cysteine string protein DNAJC5	S8S15		•	4.0	44.1	R.S*LSTSGES*LYHVLGLDK.N
	triphosphate synthetase CTPS1	S574S575	•		14.3	108.2	R.SGSS*S*PDSEITELKFPSINHD
	triphosphate synthetase CTPS1	S571S574S575			15.6	63.9	R.S*GSS*S*PDSEITELKFPSINHD
	triphosphate synthetase CTPS1	S571S573S574	•••		18.0	47.8	R.DTYSDRS'GS'S'S'PDSEITELKFPSINHD  R.DTYS'DRSGS'S'S'PDSEITELKFPSINHD
	triphosphate synthetase CTPS1	\$568\$573\$574			-0.4	25.5	R.SGS*S*SPDSEITELKFPSINHD
	triphosphate synthetase CTPS1	\$573\$574 \$568			16.9	45.0 21.9	R DIVSTOR S
	triphosphate synthetase CTPS1	S571S574			6.0	24.8	R.S'GSS'SPDSEITELKFPSINHD
	triphosphate synthetase CTPS1	S571S578			4.4	18.2	R.S'GSSSPDS'EITELKFPSINHD
	triphosphate synthetase CTPS1	Y567S568S573			8.3	30.4	R.DTY*S*DRSGS*SS*PDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	Y567S568S571			13.2	46.7	R.DTY"S"DRS"GSSS"PDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	S571S573			9.1	87.0	R.S'GS'SSPDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	S571S573S574			9.4	63.6	R.S'GS'S'SPDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	Y567S571S574			6.7	11.6	R.DTY*SDRS*GSS*S*PDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	Y567S573S574	•		13.1	27.6	R.DTY*SDRSGS*S*S*PDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	\$573 <b>\$</b> 575	-		5.3	115.3	R.SGS*SS*PDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	S571S573S574	÷.		21.7	35.1	R.DTYSDRS*GS*S*SPDS*EITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	S562	ij.		100.0	28.6	K.GCRLS*PR.D
	CTPS1	<b>S</b> 575	·		10.8	64.2	R.SGSSS*PDSEITELK.F
	triphosphate synthetase CTPS1	S574	•		13.8	96.1	R.SGSS*SPDSEITELKFPSINHD
	triphosphate synthetase CTPS1	<b>S</b> 573			10.6	70.7	R.SGS*SSPDSEITELKFPSINHD
Cytidine 5-prime t	triphosphate synthetase CTPS1	\$573\$574\$575			11.6	21.7	R.DTYSDRSGS*S*S*PDS*EITELKFPSINHD
Catidina F prima 6	CTPS1 triphosphate synthetase CTPS1	\$573\$574\$575		-	9.2	59.3	R.SGS'S'S'PDSEITELK.F  R.DTYS'DRS'GS'S'SPDSEITELKFPSINHD
	triphosphate synthetase CTPS1	S568S571S573			2.0	29.4	R.S'GSS'S'PDS'EITELKFPSINHD
		\$571\$574\$575 \$81			11.4	42.1	R.EAEALLQSMGLTPESPIVPPPMS*PSSK.S
	(Fragment) n 1 intermediate chain 2 DYNC1 2	S83	••••		9.8 5.3	20.2	R.EAEALLQSMGLTPESPIVPPPM#SPS*SK.S
	(Fragment) ker associated protein 2 CLASP2	S603		•	9.3	84.3	R.SRS*DIDVNAAAGAK.A
Cytoplasmic lin	ker associated protein 2 CLASP2	S758S762	==		15.6	25.4	R.IPRPSVS*QGCS*R.E
Cytoplasmic lini	ker associated protein 2 CLASP2	S1224			26.5	43.5	K.ASLLHSMPTHS*SPR.S
Cytoplasmic lini	ker associated protein 2 <sub>CLASP2</sub>	S808			56.2	90.8	R.VLNTGS*DVEEAVADALKKPAR.R
Cytoplasmic lini	ker associated protein 2 CLASP2	S1164	<u> </u>		54.8	66.7	R.GVTEAIQNFS*FR.S
Cytoplasmic lin	ker associated protein 2 CLASP2	T806			11.1	54.8	R.VLNT*GSDVEEAVADALKKPAR.R
Cytoplasmic lini	ker associated protein 2 CLASP2	S1113S1118S11	•		5.7	100.4	R.S'PANWS'S'PLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
Cytoplasmic lin	ker associated protein 2 CLASP2	S1113S1118T11			9.7	100.4	R.S'PANWS"SPLT"SPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
	ker associated protein 2 CLASP2	S1113T1131S11	-		3.8	48.1	R.S'PANWSSPLTSPTNTSQNT'LS'PSAFDYDTENMNSEDIYSSLR.G
	ker associated protein 2 CLASP2	S1241	•		16.1	55.5	R.DYNPYNYSDSIS*PFNK.S
	ker associated protein 2 CLASP2	S1113T1125T11	÷		2.9	94.3	R.S'PANWSSPLTSPT*NTSQNT*LSPSAFDYDTENMNSEDIYSSLR.G
	ker associated protein 2 CLASP2	S774			21.2	12.9	R.DTS*PVR.S
	ker associated protein 2 CLASP2	S756S758	-		6.8	17.5	R.IPRPS*VS*QGCSR.E
	ker associated protein 2 CLASP2	S1113S1128T11			2.6	52.2	R.S*PANWSSPLTSPTNTS*QNT*LSPSAFDYDTENMNSEDIYSSLR.G
	ker associated protein 2 CLASP2	\$1113\$1119T11	•••		5.4	89.2	R.S*PANWSS*PLT*SPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
	ker associated protein 2 <sub>CLASP2</sub>	\$1225		<u> </u>	40-	19.6	K.ASLLHSMPTHSS*PR.S  R.S*PILLPK.G
	homolog 2 ble PHD fingers family 2 DPF2	\$582 \$142			100.0	92.8	R.S*PILLPK.G  R.VDDDS*LGEFPVTNSR.A
	ble PHD fingers family 2 DPF2	T176			27.3	92.8	R.ILEPDDFLDDLDDEDYEEDT*PK.R
	ble PHD fingers family 2 DPF2	S244T248			23.0	53.5	K.NRPGLSYHYAHSHLAEEEGEDKEDS*QPPT*PVSQR.S
	ble PHD fingers family 2 DPF2	S225Y226				36.0	K.NRPGLS*Y*HYAHSHLAEEEGEDKEDSQPPTPVSQR.S
	c DNA binding protein 2 DDB2	S24			6.0	41.2	R.S*RSPLELEPEAK.K
	c DNA binding protein 2 DDB2	S24S26			100.0	36.3	R.S'RS'PLELEPEAK.K
Damage specifi	c DNA binding protein 2 <sub>DDB2</sub>	<b>S</b> 26			100.0	77.5	R.S*PLELEPEAK.K
	Daxx DAXX	\$737\$739			82.8	32.2	K.TSVATQCDPEEIIVLS*DS*D
	Daxx DAXX	S668S671			18.1	50.4	K.ICTLPS*PPS*PLASLAPVADSSTR.V
	Daxx DAXX	\$668 <b>\$</b> 675			9.0	43.9	K.ICTLPS*PPSPLAS*LAPVADSSTR.V
	Daxx DAXX	<b>S</b> 495			46.9	42.5	K.DGDKS*PMSSLQISNEK.N

<-10 0 abunda		compared to	the .			
.s 29 timepoi .a 42 PSM	nt with the minimum	peak area t	for a given			
3 86 86 5100 510			RajiB			
Protein Name Gene Daxx DAXX	Phosphosites S671	5 E B	5 F E	Ascor 4.5	MOWSE 11.6	Sequence K.ICTLPSPPS'PLASLAPVADSSTR.V
Daxx DAXX	\$690\$702			29.3	11.4	R.VDSPS*HGLVTSSLCIPS*PAR.L
DBC1 <sub>CCAR2</sub>	S124			100.0	85.8	K.S*PAPPLLHVAALGQK.Q
DBC1 CCAR2	S678S681			20.9	126.1	R.SVAS*NQS*EMEFSSLQDMPK.E
DBC1 CCAR2	S675S678			46.8	127.0	R.S*VAS*NQSEMEFSSLQDMPK.E
DBC1 CCAR2	\$675\$678\$681		•••	88.7	172.4	R.S'VAS'NQS'EMEFSSLQDMPK.E
DBC1 CCAR2	\$678 \$675\$681	•		7.9	35.3	R.SVAS*NQSEMEFSSLQDMPK.E  R.S*VASNQS*EMEFSSLQDMPK.E
DDHD domain containing 1 DDHD1	S723S727		=	16.8	22.9	K.EPTSVSENEGISTIPS*PVLS*PVLSR.R
DDX16 DHX16	S103S106		<del></del>	23.8	101.3	R.LLEDS*EES*SEETVSR.A
DDX16 DHX16	\$103\$106\$107			38.3	76.9	R.LLEDS*EES*S*EETVSR.A
DDX18 DDX18	\$86			29.8	19.0	K.VTKS*PQK.S
DDX21 DDX21	S121		•••	100.0	79.8	K.NEEPS*EEEIDAPKPK.K
DDX21 DDX21	\$164\$171\$173		•	2.2	14.8	K.LKNGFPHPEPDCNPS*EAASEES*NS*EIEQEIPVEQK.E
DDX21 DDX21 DDX21	\$168\$171\$173			41.3	63.1	K.NGFPHPEPDCNPSEAAS*EES*NS*EIEQEIPVEQK.E  K.KKEEPSQNDIS*PK.T
DDX21	\$89 \$164\$168\$171			55.6	48.9	K.NGFPHPEPDCNPS*EAAS*EES*NSEIEQEIPVEQK.E
DDX23 DDX23	S14			32.2	50.2	R.Das*PSKEER.K
DDX23	S107S109			14.6	26.9	K.RSS*LS*PGR.G
DDX23 DDX23	S106S109			6.8	14.0	R.KRS*SLS*PGR.G
DDX23 DDX23	\$106\$107				16.1	R.KRS*S*LSPGR.G
DDX23 DDX23	T25		-	100.0	15.3	R.T'PDRER.D
DDX24 DDX24	T302	-		9.4	67.4	R.SPGKAEAESDALPDDT*VIESEALPSDIAAEAR.A
DDX24 DDX24 DDX24 DDX24 DDX24 DDX24	S295	-		16.7	22.0	R.SPGKAEAES*DALPDDTVIESEALPSDIAAEAR.A
DDX24 DDX24	\$82\$94 \$82			100.0	103.2	K.AQAVS*EEEEEEGKSSS*PK.K  K.AQAVS*EEEEEEEGK.S
DDX24 DDX24	S82S93			26.7	35.6	KAQAVS*EEEEEEGKSS*SPK.K
DDX3 DDX3X	<b>S</b> 90			21.2	31.8	K.SSFFSDRGS*GSR.G
DDX3 DDX3X	S594	•••		100.0	48.6	R.FS*GGFGAR.D
DDX3 DDX3X	S654			7.3	11.6	R.GFGGGGYGGFYNSDGYGGNYNS*QGVDWWGN
DDX39 DDX39A	S426			3.2	42.2	R.FEVNVAELPEEIDISTYIEQS*R
DDX3Y DDX3Y	\$588		Ţ.	16.5	19.4	K.S*NRFSGGFGAR.D
DDX3Y DDX3Y	S592		-	21.0	30.0	K.SNRFS'GGFGAR.D
DDX41 DDX41  DDX41 DDX41	S66S68			52.3	45.4	K.GAAEEEQQDS*GS*EPRGDEDDIPLGPQSNVSLLDQHQHLK.E  R.S*EAEDEDDEDYVPYVPLR.Q
DDX41 DDX41	\$23 \$21\$23			107.2 33.8	135.8 35.2	R.TDEVPAGGS*RS*EAEDEDDEDYVPYVPLR.Q
DDX41 DDX41	S21			34.2	22.9	R.TDEVPAGGS*R.S
DDX42 DDX42	S104S111			16.0	72.0	R.QQFHS*KPVDSDS*DDDPLEAFMAEVEDQAAR.D
DDX42 DDX42	S751S754	•••		11.3	10.8	K.AGSSAAGASGWTSAGSLNSVPTNSAQQGHNS*PDS*PVTSAAK.
DDX42 DDX42	S109S111		•	26.5	71.3	R.QQFHSKPVDS*DS*DDDPLEAFMAEVEDQAAR.D
DDX42 DDX42	S104S109	-		7.0	44.9	R.QQFHS*KPVDS*DSDDDPLEAFMAEVEDQAAR.D
DDX42 DDX42	S754	<del>-</del>		12.0	67.4	K.AGSSAAGASGWTSAGSLNSVPTNSAQQGHNSPDS*PVTSAAK.G
DDX42  DDX42 DDX42	S185			28.4	57.3	R.YMAENPTAGVVQEEEEDNLEYDS*DGNPIAPTK.K  K.AGS*SAAGASGWTSAGSLNSVPTNSAQQGHNSPDSPVTSAAK.G
DDX42 DDX42 DDX42	\$723 \$104			7.9	16.4	R.QQFHS*KPVDSDSDDDPLEAFMAEVEDQAAR.D
DDX42 DDX42	S751			8.6	24.7	K.AGSSAAGASGWTSAGSLNSVPTNSAQQGHNS*PDSPVTSAAK.G
DDX42 DDX42	T7428754			6.4	21.5	K.AGSSAAGASGWTSAGSLNSVPT*NSAQQGHNSPDS*PVTSAAK.
DDX42 DDX42	S733S754		ij	5.9	11.6	K.AGSSAAGASGWTS*AGSLNSVPTNSAQQGHNSPDS*PVTSAAK.
DDX42 DDX42	T742S744		Ė	-0.4	16.6	K.AGSSAAGASGWTSAGSLNSVPT*NS*AQQGHNSPDSPVTSAAK.
DDX46 DDX46	S24S26			18.7	20.1	R.S'RS'PSDKR.S
DDX46 DDX46	S804			145.3	89.5	K.AALGLQDS*DDEDAAVDIDEQIESM#FNSK.K
DDX46 DDX46	S295S296		<u></u>	10.6	48.4	K.GELMENDQDAMEYS'S'EEEEVDLQTALTGYQTK.Q
DDX46 DDX46 DDX51 DDX51	Y294S295 S83			26.8	24.9 53.8	K.GELMENDQDAMEY"S"SEEEEVDLQTALTGYQTK.Q  R.VNDAEPGS"PEAPQGK.R
DEAD (Asp-Glu-Ala-Asp) box polypeptide DDX17	S599			100.0	22.9	R.RDS'ASYR.D
DEAD box polypeptide 55 DDX55	S544			144.0	87.8	R.EEGS*DIEDEDMEELLNDTR.L
DEAD-box protein 54 DDX54	<b>S</b> 75	•		20.8	43.5	K.LGPGRPLPTFPTSECTS*DVEPDTR.E
DEAD-box protein 54 DDX54	T74		•	42.1	35.0	R.KLGPGRPLPTFPTSECT*SDVEPDTR.E
DEAD-box protein 54 DDX54	S39S41			100.0	114.8	R.GS*DS*EDGEFEIQAEDDAR.A
DEAD-box protein 54 DDX54	S782			73.4	28.8	K.IDDRDS*DEEGASDR.R
DEAH box polypeptide 57 DHX57	S127			100.0	70.7	R.DLQEQDADAGS*ER.G
Death associated protein DAP	<b>S</b> 51			58.6	84.7	K.DKDDQEWESPS*PPKPTVFISGVIAR.G

Peak Area	0	abundano		ompared to	the	
-5 -3	42 71	timepoint of PSM	with the minimum	peak area fo	r a given	
3 5 >10	>100			CarT	RajiB	
	Protein Name		Phosphosites	5 m m	9 # E	Asco
Deat	th associated protein [	DAP	S49S51			84.1
	th associated protein [		T56	<b>—</b>		5.2
Deat	th associated protein [	DAP	S51T56			12.0
	1	DIDO1	T151S152S154			14.6
Death associated to	transcription factor 1	DIDO1	S1040		•••	38.5
Death associated to	transcription factor 1	DIDO1	S1254S1260		Ţ.	4.9
	1	DIDO1	T1256S1260		•	9.7
Death associated t	transcription factor 1	DIDO1	\$805\$809			51.5
Death associated to	transcription factor 1	DIDO1	S1254T1255		•	2.2
	1	DIDO1	T1255S1260		•	18.4
Death associated to	transcription factor 1	DIDO1	S1242Y1244	4		
Death associated t	transcription factor 1	DIDO1	S1456	•		40.1
De	eath-inducing-protein (	GRAMD4	S24S28	-		29.0
Decap	ping enzyme hDcp1b [	OCP1B	S276			16.9
Deca	pping enzyme hDcp2 [	DCP2	S246S247S249			45.3
Dedica	ator of cytokinesis 11	OOCK11	<b>S</b> 440			31.0
Dedic	cator of cytokinesis 2	OOCK2	S1706			-0.4
Dedic	cator of cytokinesis 2	OOCK2	S587	-		13.6
Dedic	cator of cytokinesis 2	OOCK2	S1731			27.8
Dedic	cator of cytokinesis 2	OOCK2	T1786	•		7.7
	cator of cytokinesis 2		S1685			32.3
Dedic	cator of cytokinesis 2 [	OOCK2	T1733			2.8
Dedic	cator of cytokinesis 2	OOCK2	S1784		•	4.4
Dedic	cator of cytokinesis 2	OOCK2	S1705			
Dedic	cator of cytokinesis 2 [	OOCK2	S586			-0.3
Dedic	cator of cytokinesis 7 [	OOCK7	S898			12.6
Dedic	cator of cytokinesis 7	OOCK7	\$862			6.0
Dedic	cator of cytokinesis 7	OOCK7	<b>S</b> 190	•••		44.4
Dedic	cator of cytokinesis 7	OOCK7	S863			6.2
Dedic	cator of cytokinesis 7	OOCK7	S864			-0.5
Dedic	cator of cytokinesis 7	OOCK7	T935	<b></b>		7.3

Dedicator of cytokinesis 7 DOCK7 \$882

Dedicator of cytokinesis 7 DOCK7 \$933

Dedicator of cytokinesis 7 DOCK7

Dedicator of cytokinesis 7 DOCK7 S180S190

Dedicator of cytokinesis 7 DOCK7 S180T186S190

DEF6 DEF6

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Delangin NIPBL

Delangin NIPBL

Delangin NIPBL

Delangin NIPBL

Deltex1 DTX1

DENN domain-containing protein 1B DENND1B S653

DENN domain-containing protein 1B DENND1B S652

DENN domain-containing protein 1B DENND1B \$652\$653

DENN domain-containing protein 1B DENND1B 8653S654

Deoxycytidine kinase DCK

Density regulated protein DENR \$73

DEP domain containing 1B DEPDC1B S160

DEP domain containing 5 DEPDC5 85798582

Desmoglein 2 DSG2 S680

DGCR14 DGCR14 T453

S590

S580

S581

S301S303S306

S243S244S251

T220S227S230

S2482S2490S2

S306

**S**305

S2658

Delangin NIPBL \$1089\$1090\$1

Dedicator of cytokinesis 7 DOCK7

39.4

36.4

70.4

13.8

65.1

25.6

31.8

46.1

36.4 49.1

60.0

46.5

74.6 68.1

11.8 64.4

37.5 29.3

46.0

26.1

63.8

55.3

23.1

38.0

7.0 59.0

40.0

7.2 29.7

48.7

12.1

58.7

58.6

55.8 58.1

100.0 23.5

100.0 62.2

13.1 23.8

-0.2 15.9

14.3

50.1 49.5

6.9 17.8

12.0 54.6

20.1 99.0

16.4 45.4

10.8 102.2

10.6 29.4

18.8 45.8

35.2

. .

36.8 20.3

100.0 35.0

47.9 59.7

44.5

100.0 97.1

100.0 45.6

14.8 29.1

27.7 21.7

4.1 11.3

1.8 43.2

4.6

• •

K.DKDDQEWES\*PS\*PPKPT\*VFISGVIAR.G

K.DKDDQEWESPS\*PPKPT\*VFISGVIAR.G

K.VKGGDDHDDT\*S\*DS\*DSDGLTLK.E

K.KPSKYPLCSADAAVS\*TTPPGS\*PPPPPPPPPPPVLK.V

K.YPLCSADAAVSTT\*PPGS\*PPPPPPPPPPVLK.V

K.YPLCSADAAVS\*T\*TPPGSPPPPPPPPPPPVLK.V

K.KPS\*KY\*PLCSADAAVSTTPPGSPPPPPPLPEPPVLK.V R.RNS\*VERPAEPVAGAATPSLVEQQK.M

R.DDFLDLAES\*PNAS\*DTECSDEIPLKVPR.T

R.RFGDS\*S\*DS\*DNGFSSTGSTPAKPTVEK.L

R.EMLWGSSTQLASDGS\*PK.G

R.SLS\*YEEPR.R

R.SS\*VVFADEK.A

R.SSS\*SVGGLSVSSR.D

R.KHEFM#S\*DTNLSEHAAIPLK.A

R.LSQT\*FLQLSDGDKK.T

R.VEQEEPIS\*PGSTLPEVK.L

R.KHEFMSDT\*NLSEHAAIPLK.A

R.LS\*QTFLQLSDGDKK.T
K.RS\*SVVFADEK.A

R.SS\*SSVGGLSVSSR.D

R.SLS\*NSNPDISGTPTSPDDEVR.S

R.GS\*WACSIFDLK.N

R.MSSHT\*ETSSFLQTLTGR.L

R.SLSNS\*NPDISGTPTSPDDEVR.S

R.S\*MSIDDTPRGS\*WACSIFDLK.N

R.S\*MSIDDT\*PRGS\*WACSIFDLK.N

R.MSS\*HTETSSFLQTLTGR.L

R.MSSHTETSS\*FLQTLTGR.L

R.S\*QHRELQQALEGQLR.E

R.TPS\*PNSNEQQK.S

R.EES\*EEEEDEDDEEEEEEKEK.S

K.KES\*ES\*EDS\*S\*DDEPLIKK.L

K.EES\*S\*DDEDKES\*EEEPPKK.T

R.T\*KCPEILS\*DES\*SS\*DEDEKK.N

K.GSRPPLILQSQSLPCSS\*PR.D

K.GSRPPLILQSQSLPCS\*SPR.D

R.KS\*SPSKENES\*S\*DS\*EEEVSRPR.K

K.SQS\*WPVGASSGQPCSCQQCLLVNSTR.A

K.YAEIS\*S\*DEDNDS\*DEAFESSR.K

K.AITSLLGGGS\*PK.N

R.VSS\*SGLTDSLFILK.E

K.RVS\*S\*SGLTDSLFILK.E

R.VS\*SSGLTDSLFILK.E

K.RVSS\*S\*GLTDSLFILK.E

R.WCNVQSTQDEFEELTMS\*QK.N

R.FHVGS\*AES\*MLHVRPGGYTPQR.A

K.VVPSFLPVDQGGS\*LVGR.N

R.TPLT\*QDPASITDNLLQLPAR.R

K.LTVENS\*PK.Q

R.WGS\*QGNR.T

R.DS\*SLKR.L

R.DSS\*LKR.L

R.S\*AVRPASLNLNR.S

R.LPNTYPNS\*SSPGPGGLGGSVHYATMAR.S

R.LPNTYPNSS\*SPGPGGLGGSVHYATMAR.S

R.LPNTYPNSSS\*PGPGGLGGSVHYATMAR.S

R.QEAIPDLEDS\*PPVS\*DSEEQQESAR.A

R.S\*PPEGDTTLFLSR.L

Peak Area %CV	abundan		compared to	the			
.5 .3 .42 .71 .3	PSM	with the minimum					
5 >100 >10 Protein Name	Gene	Phosphosites	CarT_		Ascor	MOWSE	Sequence
Diacylglycerol kinase, eta		T26S27S31				39.0	MACACCOULIDBOAACCAAACACAAAT**C**AAAC**ACDCEDESDSE
Diacylglycerol kinase, zeta  DiGeorge syndrome critical region gene is		\$52\$53 \$35	=		133.6	58.9 75.3	R.RRS'S'AQLQGCLLSCGVR.A
DiGeorge syndrome critical region gene		S275T279			21.5	12.9	K.YGGDSDHPS*DGET*SVQPMMTK.I
DiGeorge syndrome critical region gene	BDGCR8	<b>S</b> 377			6.8	27.7	R.EQSSDLTPSGDVS*PVKPLSR.S
DiGeorge syndrome critical region gene	BDGCR8	S373			14.0	14.6	R.EQSSDLTPS'GDVSPVKPLSR.S
Dihydropyrimidinase-related protein 2		<b>S</b> 27			24.1	45.6	K.NLGSGS'PKPR.Q
Dihydrouridine synthase 3-like		T273S276			19.3	39.5	R.QENCGAQQVPAGPGTST*PPS*SPVR.T  R.QENCGAQQVPAGPGTS*TPPS*SPVR.T
Dihydrouridine synthase 3-like		S272S276 T273S277			17.7	26.4	R.QENCGAQQVPAGPGTST*PPSS*PVR.T
DIS	3 DIS3	<b>S730</b>			20.9	49.4	K.SLAESLDQAES'PTFPYLNTLLR.I
Disabled homolog 2-interacting protein	DAB2IP	S35T37			100.0	16.1	R.S'RT'RPAR.E
Discs large associated protein a		S127		-	5.3	50.0	R.KLSS*IGIQVDCIQPVPK.E
Discs, large homolog		S332	•		71.8	70.1	R.S'ANAFLTPSYTWTPLK.T  K.SLTTECHLLDS'PGLNCS'NPFTQLER.R
Discs, large homolog		\$806\$812 \$148\$149			100.0	11.2	KAIPS*S*VR.I
Disrupter of silencing 1	O <sub>UTP3</sub>	\$365\$368		•	38.6	88.4	K.TSAAACAVTDLS*DDS*DFDEK.A
Disrupter of silencing 1	OUTP3	T362S368			33.7	44.0	K.TSAAACAVT*DLSDDS*DFDEK.A
Disrupter of silencing 1		T362S365	-		20.4	20.6	K.TSAAACAVT*DLS*DDSDFDEK.A
DKFZP434C212 protein		S757T762	===		11.2	82.0	R.EVS*SRPST*PGLSVVSGISATSEDIPNK.I
DKFZP434C212 protein  DKFZP434C212 protein		\$757\$758 T762\$766			9.8	43.0	R.EVS*S*RPSTPGLSVVSGISATSEDIPNKIEDLR.S  R.EVSSRPST*PGLS*VVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein		S761T762			5.5	63.7	R.EVSSRPS*T*PGLSVVSGISATSEDIPNK.I
DKFZP434C212 protein	GAPVD1	S757S766			5.4	54.1	R.EVS*SRPSTPGLS*VVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein	GAPVD1	S757S761	-		16.6	85.5	R.EVS*SRPS*TPGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein		S758T762	-		9.8	32.4	R.EVSS'RPST'PGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein		\$761\$766 \$930	-		5.2	39.4	R.EVSSRPS*TPGLS*VVSGISATSEDIPNKIEDLR.S  R.SS*DIVSSVR.R
DKFZP434C212 protein		S929			-0.3	36.0	R.S*SDIVSSVR.R
DKFZP434C212 protein	GAPVD1	\$757\$769			1.9	30.6	R.EVS*SRPSTPGLSVVS*GISATSEDIPNK.I
DKFZP434C212 protein	GAPVD1	S758S761			4.5	35.6	R.EVSS'RPS'TPGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein		0014			4.8	15.2	R.ELPPAAAIGATSLVAAPHSS*SSSPSK.D
DKFZP434P1750 protein  DKFZP434P1750 protein					22.5	60.8	R.QQPPLGPSSS'tLSLPGLK.S  R.QQPPLGPSSS'tLS'tPGLK.S
DKFZP434P1750 proteir					17.7	51.9	R.QQPPLGPSS*SLLS*LPGLK.S
DKFZP434P1750 protein	TBC1D10	B \$382\$383			5.9	45.4	R.QQPPLGPSS'S'LLSLPGLK.S
DKFZP434P1750 protein	TBC1D10	B T422			-3.2	20.9	R.ASAGPAPGPVVT*AEGLHPSLPSPTGNSTPLGSSK.E
	TBC1D10				69.2	46.9	R.AS*AGPAPGPVVTAEGLHPSLPSPTGNSTPLGSSK.E
DKFZP434P1750 protein				•	11.1	30.1	R.QQPPLGPS*SSLLSLPGLK.S
DKFZP434P1750 protein					6.8	13.3	R.RAS'AGPAPGPVVTAEGLHPSLPS'PTGNSTPLGSSK.E  R.QQPPLGPS'SSLLS'LPGLK.S
DKFZP564C186 protein		S672S673	-		59.4	101.1	K.DLFDLNS*S*EEDDTEGFSER.G
DKFZP564C186 protein	NOC2L	S22S26S30		<del>;</del>	16.5	39.9	R.LAELTVDEFLAS*GFDS*ESES*ESENSPQAETR.E
DKFZP564C186 protein		<b>S</b> 672			13.9	87.6	K.DLFDLNS*SEEDDTEGFSER.G
DKFZP564C186 protein		<b>S</b> 49			35.4	16.5	R.S*PDKPGGSPSASR.R
DKFZP564C186 protein		\$93\$98\$100\$1 \$49\$56			18.3	55.1 28.8	R.S'PDKPGGS'PSASR.R
DKFZP564O123 proteir		S199			11.0	42.0	KATIS*DEEIER.Q
DKFZp761A052 protein	OTUD5	<b>S</b> 177			26.0	125.8	R.EEVGAGYNS*EDEYEAAAAR.I
DKFZp761A052 protein	OTUD5	<b>S</b> 64	<del></del>		100.0	46.8	R.AS*PPPQGPLPGPPGALHR.W
DKFZp761A052 protein		T507			67.4	29.9	R.AT*SPLVSLYPALECR.A
	DMAP1	T445			9.8	37.2	K.DTIIDVVGAPLT*PNSR.K
Dmx like Dmx like DnA damage inducible protein		T573		Ţ	-0.5 9.1	73.8	R.ST*SMLISSGHNK.S  R.IDFSSIAVPGT*SSPR.Q
DNA damage inducible protein		S194			100.0	73.8	RLFS*ADPFDLEAQAK.I
DNA dependent protein kinase catalyti subuni	PRKDC	T2609S2612			22.1	68.5	R.STVLTPMFVET*QAS*QGTLQTR.T
DNA dependent protein kinase catalytic subuni	PRKDC	S2612		• •	7.4	43.6	R.STVLTPMFVETQAS*QGTLQTR.T
DNA Ligase II		S210	<u></u>		1.0	74.0	K.LTTTGQVTS*PVKGASFVTSTNPR.K
DNA Ligase II	LIG3	S241			7.8	14.1	R.KFSGFSAKPNNSGEAPS*SPTPK.R  K.LTTTGQVT*SPVK.G
DNA methyltransferase 1		T209 S714	-		100.0	20.6 86.5	K.EADDDEEVDDNIPEMPS*PK.K
DNA methyltransferase		S394			21.2	28.5	K.LSIFDANES*GFESYEALPQHK.L
			-				

<-10 0 abundan	ots-Significant cha ce at 5%FDR of t with the minimum	ompared to peak area f	the or a given			
5 >100 >10		CarT				
Protein Name Gene DNA mismatch repair protein PMS2 PMS2	Phosphosites S523	9 4 2	£ £ £	Ascor -11.2	MOWSE 48.5	Sequence K.DSGHGSTSVDSEGFSIPDTGSHCSSEYAASS*PGDR.G
DNA mismatch repair protein PMS2 PMS2	S522			44.0	60.2	K.DSGHGSTSVDSEGFSIPDTGSHCSSEYAAS*SPGDR.G
DNA mismatch repair protein PMS2 PMS2	<b>S</b> 517			8.3	23.9	K.DSGHGSTSVDSEGFSIPDTGSHCSS*EYAASSPGDR.G
DNA polymerase delta interacting protein 3 POLDIP3	S127			-0.3	42.7	R.SS'PAAFINPPIGTVTPALK.L
DNA polymerase subunit B	S141			35.2	70.5	R.S*PHQLLSPSSFSPSATPSQK.Y
DNA Polymerase, alpha POLA1	S186			49.8	79.6	R.S*IGASPNPFSVHTATAVPSGK.I
DNA primase large subunit PRIM2	Y504	<u> </u>		8.8	33.3	K.DASSALASLNSSLEMDMEGLEDY*FSEDS
XRCC4	S327S328			100.0	26.6	R.NS'S'PEDLFDEL-
DNA replication licensing factor MCM4 <sub>MCM4</sub>	S131	<del></del>		58.4	86.5	K.GLQVDLQ8*DGAAAEDIVASEQSLGQK.L
DNA topoisomerase II alpha TOP2A	S1469T1470S1	• • •	•	27.8	19.6	R.KPS'T'S'DDS'DSNFEK.I
DNA topoisomerase II alpha TOP2A	S1392		•••	7.2	42.6	K.GSVPLSS*SPPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	S1377			23.4	62.9	K.SVVS*DLEADDVK.G
DNA topoisomerase II alpha TOP2A	S1377S1391			6.5	40.4	K.SVVS*DLEADDVKGSVPLS*SSPPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	S1525			35.3	35.7	K.YLEES'DEDDLF
DNA topoisomerase II alpha TOP2A	S1332S1337T1			22.2	36.5	K.FTMDLDS*DEDFS*DFDEKT*DDEDFVPSDAS*PPK.T
DNA topoisomerase II alpha TOP2A	S1332S1337T1			36.4	28.5	K.FTMDLDS*DEDFS*DFDEKT*DDEDFVPS*DAS*PPK.T
DNA topoisomerase II alpha TOP2A	T1112			3.9	71.1	K.VPDEEENEESDNEKET*EKSDSVTDSGPTFNYLLDMPLWYLTK.E
DNA topoisomerase II alpha TOP2A	<b>S</b> 1115			4.3	71.0	K.VPDEEENEESDNEKETEKS*DSVTDSGPTFNYLLDMPLWYLTK.E
DNA topoisomerase II alpha TOP2A	T1124			-0.7	25.5	K.VPDEEENEESDNEKETEKSDSVTDSGPT*FNYLLDMPLWYLTK.E
TOP2A	S1106		•	40.3	65.3	K.VPDEEENEES'DNEKETEK.S
DNA topoisomerase II alpha TOP2A	S1247			22.8	107.9	K.NENTEGS*PQEDGVELEGLK.Q
DNA topoisomerase II alpha TOP2A	S1391			32.8	33.3	K.GSVPLS*SSPPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	S1377S1392			7.4	36.3	K.SVVS*DLEADDVKGSVPLSS*SPPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	S1121	•		7.5	51.9	K.VPDEEENEESDNEKETEKSDSVTDS*GPTFNYLLDMPLWYLTK.E
DNA topoisomerase II alpha TOP2A	S1393		• •	5.3	24.7	K.GSVPLSSS*PPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	S1332S1337			17.7	55.5	K.FTMDLDS*DEDFS*DFDEK.T
DNA topoisomerase II alpha TOP2A	S1332S1337T1	•		24.4	53.9	K.FTMDLDS'DEDFS'DFDEKT'DDEDFVPSDASPPK.T
DNA topoisomerase II alpha TOP2A	S1332S1337T1		•	16.3	31.8	K.FTMDLDS'DEDFS'DFDEKT'DDEDFVPS'DASPPK.T
DNA topoisomerase II alpha TOP2A	T1327S1332S1			18.2	13.7	K.FT*MDLDS*DEDFS*DFDEKT*DDEDFVPS*DASPPK.T
DNA topoisomerase II alpha TOP2A	S1117		•	0.8	67.4	K.VPDEEENEESDNEKETEKSDS*VTDSGPTFNYLLDMPLWYLTK.E
DNA topoisomerase II alpha TOP2A	\$1387\$1392			3.1	10.8	K.SVVSDLEADDVKGS*VPLSS*SPPATHFPDETEITNPVPK.K
DNA topoisomerase II alpha TOP2A	T1119			7.0	48.9	K.VPDEEENEESDNEKETEKSDSVT*DSGPTFNYLLDMPLWYLTK.E
DNA-binding protein RFX7 RFX7	T1025S1028		•	26.8	33.3	R.HHDTHFGRLT"PVS"PVQHQGATVNNTNK.Q
DNA-binding protein RFX7 RFX7	T1019T1025			5.3	10.8	R.HHDT*HFGRLT*PVSPVQHQGATVNNTNK.Q
DnaJ homology subfamily A member 5 DNAJC2	S283			100.0	26.5	K.EFGDGS*DENEMEEHELK.D
DOCK10 DOCK10	S318S322		•	18.3	32.1	K.IPRPLS*LIGS*TLR.F
DOCK10 DOCK10	S289S292			9.4	32.3	R.AS*LAS*LDSNPSTNEK.S
DOCK8 DOCK8	S1177	•		20.1	54.9	R.TSGS*DEEQEGAGAINQNVALAIAGNNFNLK.T
DOCK8 DOCK8	S1175S1177		•••	16.2	65.3	R.YRTS'GS*DEEQEGAGAINQNVALAIAGNNFNLK.T
DOCK8 DOCK8	T1174S1175			14.0	50.9	R.YRT*S*GSDEEQEGAGAINQNVALAIAGNNFNLK.T
DOCK8 DOCK8	T1174S1177			11.2	64.3	R.YRT*SGS*DEEQEGAGAINQNVALAIAGNNFNLK.T
Docking protein 3 DOK3	S330			27.6	73.0	RATS*LPSLDTPGELRE
Docking protein 3 DOK3	<b>S</b> 425			13.1	69.6	R.S*PTTSPIYHNGQDLSWPGPANDSTLEAQYRR
Docking protein 3 DOK3	<b>S</b> 439			1.1	48.9	R.SPTTSPIYHNGQDLS*WPGPANDSTLEAQYRR
Docking protein 3 DOK3	T427T428			5.8	40.4	R.SPT'T'SPIYHNGQDLSWPGPANDSTLEAQYR.R
Docking protein 3 DOK3	\$429\$439			1.6	18.7	R.SPTTS*PIYHNGQDLS*WPGPANDSTLEAQYR.R
Docking protein 3 <sub>DOK3</sub>	S429			1.8	14.2	R.SPITS*PIYHNGQDLSWPGPANDSTLEAQYRR
Docking protein 3 DOK3	S425Y432			7.2	69.2	R.S'PTTSPIY'HNGQDLSWPGPANDSTLEAQYR.R
Docking protein 4 <sub>DOK4</sub>	S35			16.9	25.9	R.KSS*SKGPQR.L
Double strand break repair protein MRE11A <sub>MRE11</sub>	S688S689			141.5	138.0	K.GVDFES*S*EDDDDDPFMNTSSLR.R
Double strand break repair protein MRE11A <sub>MRE11</sub>	S649			45.7	84.5	K.NYSEVIEVDES*DVEEDIFPTTSK.T
Down regulated in metastasis UTP20	S2601			64.7	21.0	K.AES*DGEEKEEVKEELGRPATLLWLIQK.L
Downregulator of transcription 1 <sub>DR1</sub>	S157			2.2	73.6	R.
Downregulator of transcription 1 <sub>DR1</sub>	\$166\$167			-0.6	32.2	R.
Downregulator of transcription 1 <sub>DR1</sub>	\$157\$159			-5.0	35.2	R.
Downregulator of transcription 1 <sub>DR1</sub>	\$1575159 \$159\$161			24	28.7	R.
Drebrin E DBN1				2.1		COOAEI AOGEMI OMOGAAGOAGI AAASAS'AS'AS'ANGAGSSODEED  R.SPS'DSSTASTPVAEQIER.A
Drebrin E DBN1	S341			4.0	90.8	RLS*SPVLHRL
Drebrin E DBN1	S143			12.1	47.9	R.IS'SPVLHRL  R.S'PSDSSTASTPVAEQIER A
Drebrin EDBN1	S339			21.2	96.2	K.S'ESEVEEAAAIIAQRPDNPR.E
Dual adapter for phosphotyrosine and 3-DAPP1	S274	-		8.4	20.0	R.SRS'FIFK-
Dual adapter for phosphotyrosine and 3-DAPP1  phosphotyrosine and 3-phosphoinositide  Dual-specificity protein phosphatase 22 DUSP22	S276			7.6	13.2	
proton prosprietase 22 DUSP22	S86			13.8	32.7	R.RWSS'FPALAPLTYDNYTTET

<-10 0 -5 29	abundanc timepoint	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
3 42 71 3 86 5 >100	PSM	mainulli	CarT	RajiB			
>10 Protein Name of dUTP pyrophosphatase of		Phosphosites	- 2 g	£ £ £		MOWSE	Sequence M.PCSEETPAIS*PSKR.A
Dynamin 2		S11 S736			16.1	71.4	K.EALNIIGDIS*TSTVSTPVPPPVDDTWLQSASSHSPTPQR.R
Dynamin 2	NM2	T762			8.8	36.6	K.EALNIIGDISTSTVSTPVPPPVDDTWLQSASSHSPT*PQR.R
Dynamin 2	NM2	<b>S</b> 760			12.2	31.1	K.EALNIIGDISTSTVSTPVPPPVDDTWLQSASSHS*PTPQR.R
Dynamin 2		<b>S</b> 757			4.7	12.5	K.EALNIIGDISTSTVSTPVPPPVDDTWLQSAS*SHSPTPQR.R
Dynamin 2		\$758				13.5	K.EALNIIGDISTSTVSTPVPPPVDDTWLQSASS*HSPTPQR.R
Dynamin related protein 1 p		\$616 \$616			43.6	25.2	K.SKPIPIMPAS*PQK.G  R.KPVTVSPTTPTS*PTEGEAS
Dynein light chain A					13.9	64.7	R.KPVTVSPTTPT*SPTEGEAS
Dynein light chain A					39.3	19.0	R.DFQEYVEPGEDFPAS*PQRR.N
Dynein light chain A					9.5	11.2	R.KPVTVSPTT'PT'SPTEGEAS
Dynein light chain A	YNC1LI1	S510T515			8.5	14.8	R.KPVTVS*PTTPT*SPTEGEAS
Dynein, axonemal, heavy polypeptide 8 [		S4103T4106			100.0	11.2	K.GVS"WNT"VR.Y
Dynein, cytoplasmic, heavy polypeptide 1				•	6.5	44.1	R.TDST*SDGRPAWMR.T
Dynein, cytoplasmic, heavy polypeptide 1					-0.4	32.7	R.TDS*TSDGRPAWMR.T
Dynein, cytoplasmic, heavy polypeptide 2 p					10.9	12.6	K.PFT*ISK.E  K.DFQDYMEPEEGCQGS*PQRR.G
polypenti, cytopiasmic, light intermediate polypeptide 2		\$194 Y273		•	34.8	35.2	R.IYQY*IQSR.F
DYRK1B [		Y271			15.1	47.6	R.IY'QYIQSR.F
Dyskerin [	KC1	<b>S</b> 494		• • •	19.8	80.6	K.AGLESGAEPGDGDS*DTTK.K
Dyskerin [	KC1	S451S455			30.9	36.9	R.KRES*ESES*DETPPAAPQLIK.K
	KC1	S513			100.0	42.9	K.EVELVS*E
Dyskerin [		\$451\$453\$455	<b></b>		14.0	33.9	R.KRES'ES'DETPPAAPQLIK.K
Dyskerin :		\$451\$455T458			8.8	28.9	R.KRES'ESES'DET'PPAAPQLIK.K
Dyskerin p		\$21 \$461\$462T469			126.1	49.7	K.S*LPEEDVAEIQHAEEFLIKPESK.V  R.KRES*ES*ESDET*PPAAPQLIK.K
Dyskerin [		\$451\$453T458 \$451T458			14.8	15.7	R.KRES'ESESDET"PPAAPQLIK.K
Dyskerin [		\$453\$455			-0.1	26.4	R.KRESES*ES*DETPPAAPQLIK.K
Dyskerin [	KC1	\$451\$453\$455			100.0	21.7	R.KRES'ES'ES'DET'PPAAPQLIK.K
Dyskerin [	KC1	S451S453		-	12.4	45.6	R.ES*ESDETPPAAPQLIK.K
Dystrobrevin alpha	TNA	S564		. •	-0.3	14.8	R.SS*PSHTISRPIPMPIR.S
Dystrophin [		S291			30.2	35.2	R.TSS*PKPR.F
Dystrophin		T289			10.0	13.4	R.T'SSPKPR.F
E1A binding protein p300 <sub>E</sub>		T1906T1909			11.0	57.6	K.AAGQVT*PPT*PPQTAQPPLPGPPPAAVEMAMQIQR.A  K.AAGQVTPPT*PPQT*AQPPLPGPPPAAVEMAMQIQR.A
E1A binding protein p400g		T1909T1913 S23S37			11.4	31.4 50.3	R.
E1A binding protein p400 <sub>E</sub>		\$315T320			8.5	43.3	ACDGS*EGEEDDAUDNIDDBS*DAADEADGASDGADGGSSVOIGOI M  R.TPGVLLPGAGGAAGFGMTS*PPPPT*SPSRT
E1A binding protein p400 <sub>E</sub>		T320			12.6	50.9	R.TPGVLLPGAGGAAGFGMTSPPPPT*SPSR.T
E1A binding protein p400 g	P400	T314S321	-		6.0	18.7	R.TPGVLLPGAGGAAGFGMT*SPPPPTS*PSR.T
E1A binding protein p400 <sub>E</sub>	P400	T314T320		÷	25.3	38.1	R.TPGVLLPGAGGAAGFGMT*SPPPPT*SPSR.T
E1A binding protein p400 <sub>E</sub>		S904T908	<b>!!!</b>		23.0	14.4	R.KAS*ISLT*DDEVDDEEETIEEEEANEGVVDHQTELSNLAK.E
E2-230K L		\$87\$89\$98\$99	<b>—</b>		100.0	13.0	R.LIHGEDS'DS'EGEEEGRGS'S'GCS'EAGGAGHEEGR.A
E2-230K <sub>L</sub>		S839			17.8	71.5	K.NMTVEQLLTGSPTS*PTVEPEKPTR.E  K.NMTVEQLITGSPT*SPTVEPEKPTR.E
E2-230K L		T838 S836S839			19.3	47.5 54.9	K.NMTVEQLLTGSPT*SPTVEPEKPTR.E  K.NMTVEQLLTGS*PTS*PTVEPEKPTR.E
E2-230K L		\$836\$839 \$115			11.5	23.2	R.AS'PLRR.G
E2-230K <sub>L</sub>		S87S89		•••	100.0	39.7	R.LIHGEDS*DS*EGEEEGR.G
E2-230K L	IBE2O	S836			15.4	55.0	K.NMTVEQLLTGS*PTSPTVEPEKPTR.E
E2-230K <sub>U</sub>	IBE2O	T838S839			7.0	14.7	K.NMTVEQLLTGSPT*S*PTVEPEKPTR.E
E2-230K <sub>L</sub>	IBE2O	T834T838	<u> </u>		20.1	23.8	K.NMTVEQLLT"GSPT"SPTVEPEKPTR.E
E2-230K <sub>L</sub>		S836T838	Ţ.		1.9	25.4	K.NMTVEQLLTGS*PT*SPTVEPEKPTR.E
E2-230K L		S515			42.8	33.1	R.KKS*IPLSIK.N
E2-230K L		T834			7.8	15.4	K.NMTVEQLLT*GSPTSPTVEPEKPTR.E
E3 ubiquitin-protein ligase RNF213 g		\$1307 \$1166\$1167			51.3	77.2	K.EDQEAAELLS'EPEEESER.H
enzvme (E3-independent) E2 ubiquitin-conjugating (		\$1166\$1167 \$1166\$1167\$11				16.6	K.
enzvme E6 targeted protein 1 g		S258		•	-0.4	46.1	K.GSGFS'LDVIDGPISQR.E
E6 targeted protein 1 g	IPA1L1	S208S211			1.8	58.4	R.EYGS*TSS*IDKQGTSGESFFDLLK.G
E6 targeted protein 1 g	iPA1L1	T209S210			5.0	58.4	R.EYGST*S*SIDKQGTSGESFFDLLK.G
E6 targeted protein 1 g	IPA1L1	Y206S208		-	13.6	12.6	R.EY'GS'TSSIDKQGTSGESFFDLLK.G
EBNA2 coactivator p100 g		S426			24.1	77.0	K.VNVTVDYIRPAS*PATETVPAFSER.T
Echinoderm microtubule associated protein E	ML3	S176			33.8	79.5	KAIS*SANLLVR.S

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5 >100	Discount of the second		RajiB E E E		MOWEE	Sociano
Protein Name Ge Echinoderm microtubule-associated EMI protein-like 2		ŭņĢ	0 4 5	Ascor 44.7	MOWSE 25.0	Sequence R.YLS'PERL
EF hand calcium binding protein 1 NEC		<b>—</b>		100.0	12.0	K.KDY*QEAS*NLEQFVT*RFLLK.E
EF hand domain family member D2 <sub>EFF</sub>				6.9	22.2	R.ADLNQGIGEPQS*PSR.R
EH domain binding protein 1-like 1 EHE				0.8	10.8	R. ATDRIMOSI ACH MCN/KDCND/GMI DREAESDEDEAUGDGADEAD
EH domain binding protein 1-like 1 <sub>EHE</sub>				7.0	30.4	R.  ATDIDIMOST AST MONZOSTNOMI DISASSTOREAD
EH domain containing 1 <sub>EHE</sub>				16.1	15.6 32.5	ATHORMOSI ASI MSW/DSDW/ANI DDEASCREAD
elF 4G1 ElFa		•		32.2	77.5	R.S*FSKEVEER.S
elF 4G1 EIF4				9.5	28.3	K.ITKPGSIDS*NNQLFAPGGR.L
elF 4G1 <sub>ElF-</sub>	4G1 <b>S</b> 704			100.0	31.8	R.S'QQGPR.K
EIF	4G1 <b>S</b> 1209			42.4	57.2	K.AAS*LTEDR.D
eIF 4G1 EIF	4G1 <u>\$1077</u>			15.8	40.7	K.ITKPGS*IDSNNQLFAPGGR.L
elF 4G1 EIF	4G1 \$236\$253\$255				17.4	R.  COGANIADDES DESEUS PESECODES DESTRUCTURES DE CECEDAN
elF 4G1 EIF4	4G1 S1185S1187			100.0	46.3	R.S'FS'KEVEER.S
elF 4G1 EIF	4G1 S1596			100.0	37.9	R.EAEEES'DHN
elF 4G1 EIF				8.5	93.4	K.IT*KPGSIDSNNQLFAPGGR.L
elF-2B epsilon EIF;				100.0	62.1	R.GGS*PQMDDIK.V
elF-2B epsilon EIF;				100.0	16.4	K.EAEEES'S'EDD
elF-2B epsilon EIF;					15.8	R.  SHIRT TROUBLEDGENITI DECORRE LIDEDAFFDEDGEFEDDOFFEDDOFFEDDO
elF2beta EjF;				20.8	68.7	K.IES*DVQEPTEPEDDLDIMLGNK.K  K.IESDVQEPT*EPEDDLDIMLGNK.K
EIF3S4 <sub>EIF</sub>			•	48.0	71.6	K.GIPLATGDT'SPEPELLPGAPLPPPK.E
EIF3S4 EIF3				5.3	19.3	K.GIPLAT*GDT*SPEPELLPGAPLPPPK.E
EIF3S4 EIF;				5.8	30.2	K.GIPLATGDTS*PEPELLPGAPLPPPK.E
EIF3S4 <sub>EIF</sub> ;			•	14.7	39.9	K.GIPLATGDT*S*PEPELLPGAPLPPPK.E
EIF3S4 EIF	3G T38S42			-1.4	21.4	K.GIPLAT*GDTS*PEPELLPGAPLPPPK.E
EIF3S5 EIF	3F S258			51.4	27.0	K.TCFS*PNR.V
EIF3S5 EIF	3F T255	•••		9.2	28.4	K.T*CFSPNR.V
EIF3S7 EIF	3D <b>S</b> 160			7.0	28.4	R.DS*SVEVR.S
EIF3S8 EIF;	3C <b>S</b> 39			67.6	57.6	K.QPLLLS*EDEEDTKR.V
EIF3S8 EIF;			•	7.9	15.0	R.FFTT*GS*DSESESSLSGEELVTKPVGGNYGK.Q
EIF3S8 EIF;				68.9	68.8	K.QNPEQS*ADEDAEKNEEDS*EGS*S*DEDEDEDGVSAATFLK.K
EIF3S8 EIF;				69.9	54.3	K.NEEDS'EGS'S'DEDEDEDGVSAATFLK.K
EIF3S8 EIF3			•	7.7	13.8	R FFTTGSDBSES <mark>S'S'L</mark> SGEELVTKPVGGNYGK Q  R.FFTTGS'DS'ESESSLSGEELVTKPVGGNYGK Q
EIF3S8 EIF3			-	3.6	77.2 49.0	K.QNPEQS*ADEDAEK.N
EIF4G2 EIF4			-	100.0 32.3	40.7	R.FS'PTMGR.H
EIF4G2 EIF.		•••		6.9	25.2	K.ALFQVNQWLTWLET*AEEEESEEEAD
EIF4G2 EIF4	4G2 T508			19.9	60.6	R.TQT*PPLGQTPQLGLK.T
EIF4G2 EIF4	4G2 S381				28.0	K.MDRDPLGGLADMFGQMPGS*GIGTGPGVIQDRFSPTMGR.H
EIF4G2 EIF4	4G2 T397			28.6	39.0	R.DPLGGLADMFGQMPGSGIGTGPGVIQDRFSPT*MGR.H
EIF4G2 EIF4	4G2 \$902	Ţ,		4.3	17.0	K.ALFQVNQWLTWLETAEEEBS'EEEAD
EIF4G3 EIF4		===		96.1	55.3	R.S"PVPAQIAITVPK.T
<b>ELAC</b> ELA				2.2	17.1	R.LS'PERS'S'DS'ESNENEPHLPHGVSQR.R
ELAC ELA				41.3	19.4	K.HQPWQS*PERPLSR.L
ELAC ELA				13.4	18.9	RLS*PERSS*DS*ES*NENEPHLPHGVSQRR
ELAC ELA				16.2	16.3	R.LS'PERS'SDS'ES'NENEPHLPHGVSQR.R  R.LSPERS'S'DS'ES'NENEPHLPHGVSQR.R
ELF4 ELF		<del></del>		-0.5 8.4	14.4	R.S'PTPAPFS'PENPTSLIK.M
ELL associated factor 1 <sub>EAF</sub>				22.6	40.8	K.T'SPLKDNPS'PEPQLDDIKR.E
ELL associated factor 1 <sub>EAF</sub>				19.9	38.4	K.TS*PLKDNPS*PEPQLDDIKR.E
Embryonic lethal abnormal vision like 1 ELA				35.4	96.9	K.NVALLSQLYHS*PARR
Embryonic lethal abnormal vision like 1 ELA	VL1 Y200			17.2	48.3	K.NVALLSQLY"HSPAR.R
Embryonic lethal abnormal vision like 1 <sub>ELA</sub>	VL1 <u>\$</u> 197			15.7	28.9	K.NVALLS*QLYHSPAR.R
Emerin <sub>EM</sub> (	D Y167	-		4.8	39.8	R.DSAYQSITHY*RPVSASR.S
Emerin <sub>EM</sub>	D \$141\$143			8.5	13.9	R QSVTSFPDADAFHHQVHDDDLLS*SS*EEECKDR.E
Emerin <sub>EM</sub> [	S120S141S142			3.1	13.8	R.QS*VTSFPDADAFHHQVHDDDLLS*S*SEEECKDR.E
Emerin <sub>EM</sub> [				4.1	43.4	R.DSAYQSIT*HYRPVSASR.S
Emerin EMI				4.2	29.0	R.DS*AYQSITHYRPVSASR.S
Emerin <sub>EMI</sub>				14.9	33.8	R DSAY'QSITHYRPVSASR.S  R DSAYQS'ITHYRPVSASR.S
Emerin EMI				15.0	39.8	R.DSAYOS*TIHYRPVSASR.S  R.QSVTSFPDADAFHHQVHDDDLLS*S*SEEECKDR.E
- ··· Livit	J 14 10 142			24.7	7	

Peak Area <-10 -5 -3 0 3 5	o abundanc	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
>10	Protein Name Gene	Phosphosites	5 m m	F # E	Ascor	MOWSE	Sequence
	Emerin EMD	\$53 \$171			40.4	67.0	R.RLSPPSS'SAASSYSFSDLNSTR.G  R.DSAYQSITHYRPVS'ASR.S
	Emerin <sub>EMD</sub>	S60	•		6.8	38.1	R.LSPPSSSAASSYS*FSDLNSTR.G
	Emerin <sub>EMD</sub>	Y59		_	6.5	68.1	R.LSPPSSSAASSY*SFSDLNSTR.G
	Emerin <sub>EMD</sub>	<b>S</b> 49		-	9.8	62.7	R.RLS*PPSSSAASSYSFSDLNSTR.G
	Emerin <sub>EMD</sub>	S173			14.9	25.8	R.DSAYQSITHYRPVSAS*R.S
	Emerin <sub>EMD</sub>	S123S141S143			4.0	12.5	R.QSVTS*FPDADAFHHQVHDDDLLS*SS*EEECKDR.E
	Emerin <sub>EMD</sub>	S141S142S143			14.4	14.3	R.QSVTSFPDADAFHHQVHDDDLLS*S*S*EEECKDR.E
	Emerin <sub>EMD</sub>	<b>S</b> 176			-0.4	54.3	R.SS*LDLSYYPTSSSTSFMSSSSSSSSWLTR.R
	EMK1 <sub>MARK2</sub>	S452		•	32.1	36.1	R.SRNS*PLLER.A
	EML4 <sub>EML4</sub>	S144S146			24.5	65.4	R.AS*PS*PQPSSQPLQIHR.Q
	EML4 EML4	S895T899			34.3	83.9	K.APVSSTESVIQS*NTPT*PPPSQPLNETAEEESR.I
	EML4EML4	T897T899 S144			37.1	88.9 42.1	R.AS*PSPOPSSOPLOIHR.Q
	EML4 EML4	S919S934S938			4.2	55.6	R
	EML4 <sub>EML4</sub>	S917S918S919				39.0	R.
	EML4 <sub>EML4</sub>	S917S918S919				21.3	R.
	EMSY Protein EMSY	S168S173	عبر	•	13.8	24.7	K.S'PRPAS'PASNVVVLPSGSTVYVK.S
	EMSY Protein EMSY	S173S176			6.1	20.9	K.SPRPAS'PAS'NVVVLPSGSTVYVK.S
	EMSY Protein EMSY	S168S176			9.4	32.7	K.S*PRPASPAS*NVVVLPSGSTVYVK.S
Ena vasodilator stimulat	ted phosphoprotein EVL like protein	S262	-		25.3	94.0	K.SDANRASS*GGGGGGLMEEMNK.L
Ena vasodilator stimulat	like protein	S261	• •		16.9	91.0	R.AS'SGGGGGLMEEMNK.L
Ena vasodilator stimulat	like protein	S333			20.4	75.2	R.SNS*VEKPVSSILSR.T
Ena vasodilator stimulat	like protein	\$333\$343	•		9.3	54.9	R.SNS*VEKPVSSILS*R.T
Ena vasodilator stimulat	like protein	\$371			100.0	82.1	R.MKPAGS*VNDMALDAFDLDR.M
Ena vasodilator stimulat	like protein	\$347\$351 \$306			33.2	36.2 57.9	R.TPS*VAKS*PEAK.S  K.KEDESQMEDPSTS*PSPGTR.A
	like protein  donuclease III-like1 NTHL1	S71			7.0	50.7	R.VAYEGS*DSEKGEGAEPLKVPVWEPQDWQQQLVNIRA
	donuclease III-like1 NTHL1	S73			-0.4	27.9	R.VAYEGSDS*EKGEGAEPLKVPVWEPQDWQQQLVNIR.A
	ENSA	S109			13.9	67.1	R.KSS*LVTSK.L
Endothelial di	fferentiation gene 1 S1PR1	S351			100.0	36.3	K.RPIIAGMEFS*R.S
Endothelial di	fferentiation gene 5 <sub>S1PR2</sub>	\$330\$331\$332			39.5	18.7	R.GGTPGHHLLPLRS*S*S*SLER.G
Endothelial di	fferentiation gene 5 <sub>S1PR2</sub>	S331S332			-0.3	11.8	R.SS*S*SLER.G
Endothelial di	fferentiation gene 5 <sub>S1PR2</sub>	\$330\$331			53.4	13.3	R.GGTPGHHLLPLRS*S*SSLER.G
	fferentiation gene 5 <sub>S1PR2</sub>	\$330\$333		•	9.5	15.4	R.GGTPGHHLLPLRS*SSS*LER.G
	fferentiation gene 5 <sub>S1PR2</sub>	\$333		<u>=</u>	6.5	23.0	R.SSSS*LER.G
	fferentiation gene 5 <sub>S1PR2</sub>	\$331\$332\$333		_	2.2	11.0	R.GGTPGHHLLPLRSS'S'S'LER.G  R.SSS'S'LER.G
	fferentiation gene 5 <sub>S1PR2</sub>	\$332\$333 \$332			6.1	12.1	R.SSS'SLER.G
	onverting enzyme 1 <sub>ECE1</sub>	T25S34			12.6	49.8	R.AT*LDEEDLVDS*LSEGDAYPNGLQVNFHSPR.S
Endothelin co	onverting enzyme 1 <sub>ECE1</sub>	T25S36			8.5	43.6	R.AT*LDEEDLVDSLS*EGDAYPNGLQVNFHSPR.S
Endothelin co	onverting enzyme 1 <sub>ECE1</sub>	S34			6.0	46.2	R.ATLDEEDLVDS*LSEGDAYPNGLQVNFHSPR.S
Endothelin co	onverting enzyme 1 ECE1	<b>S</b> 36			4.2	65.9	R.ATLDEEDLVDSLS*EGDAYPNGLQVNFHSPR.S
Engulfmen	at and cell motility 1 ELMO1	S342			12.1	61.9	R.IAFDAESEPNNSS*GSMEK.R
Enhancer of mRNA de	capping 3 homolog EDC3	S131	•		53.2	80.4	K.SQDVAVS*PQQQQCSK.S
	Enolase 1 ENO1	Y257			2.1	47.6	R.SGKY*DLDFK.S
	Enolase 1 ENO1	S254			12.2	24.7	R.S*GKYDLDFK.S
	Enolase 1 ENO1	<b>S</b> 419		<u> </u>	100.0	25.9	R.IEEELGS*K.A
Enovi CoA hydr	Enolase 1 ENO1	T26		-	40.4	21.6	R.GNPTVEVDLFT*SK.G  R.IS*WYLR.D
,. sociajui	EP4 receptor PTGER4	\$139 \$390T391			8.0	16.2 42.3	K.EISS*T*SQTLLPDLSLPDLSENGLGGR.N
	EP4 receptor PTGER4	\$390\$400	• •		2.3	20.0	K.EISS'TSQTLLPDLS'LPDLSENGLGGR.N
	Eplin <sub>LIMA1</sub>	S686			50.3	117.3	K.EGHSLEMENENLVENGADS*DEDDNSFLK.Q
	Eps15 <sub>EPS15</sub>	S324			9.8	104.2	K.NIIGSS'PVADFSAIK.E
	Eps15 <sub>EPS15</sub>	S851			49.2	67.7	K.EADPSNFANFSAYPS*EEDMIEWAK.R
	Eps15 <sub>EPS15</sub>	S323			55.8	59.6	K.NIIGS*SPVADFSAIK.E
	Eps15 <sub>EPS15</sub>	\$796\$814			59.4	22.6	R.SINKLDS'PDPFKLNDPFQPFPGNDS'PK.E
	Eps15 <sub>EPS15</sub>	S605				50.7	K.EEDPFNVDS*SSLTGPVADTNLDFFQSDPFVGSDPFKDDPFGK.I
	Eps15 <sub>EPS15</sub>	S563	<u> </u>		-0.5	54.3	R.SS*PELLPSGVTDENEVTTAVTEK.V
	Eps15 <sub>EPS15</sub>	<b>S</b> 569	,		13.7	21.9	R.SSPELLPS*GVTDENEVTTAVTEK.V
	Eps15 EPS15	\$606		•	-0.0	32.9	K.EEDPFNVDSS*SLTGPVADTNLDFFQSDPFVGSDPFKDDPFGK.I
	Fhe19Eh212	S562		•	11.5	76.5	R.S'SPELLPSGVTDENEVTTAVTEK.V

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0 71 3 86	PSM		CarT	RaiiB			
>100 >100 Protein Name	Gene	Phosphosites		E E E	Ascor	MOWSE	Sequence
EPS15R E					6.0	12.6	R.STPSHGSVSSLNSTGSLS*PK.H
EPS15R <sub>E</sub>	PS15L1	S246S255			7.8	44.5	R.STPSHGSVS*SLNSTGSLS*PK.H
EPS15R E	PS15L1	<b>S</b> 575			6.0	29.7	R.SLEQYDQVLDGAHGAS*LTDLANLSEGVSLAER
EPS15R E	PS15L1	T577			8.9	60.1	R.SLEQYDQVLDGAHGASLT*DLANLSEGVSLAEF
EPS15R E	PS15L1	S804			6.9	47.7	K.STPVSQLGS*ADFPEAPDPFQPLGADSGDPFQ8
EPS15R E	PS15L1	T797			-0.3	50.9	K.ST*PVSQLGSADFPEAPDPFQPLGADSGDPFQ
EPS15R E	PS15L1	S253			25.4	18.6	R.STPSHGSVSSLNSTGS*LSPK.H
EPS15R E	PS15L1	S247S255			5.9	21.3	R.STPSHGSVSS*LNSTGSLS*PK.H
EPS15R E	PS15L1	S246S253			5.3	40.1	R.STPSHGSVS*SLNSTGS*LSPK.H
EPS15R E	PS15L1	S241S255			7.3	53.0	R.STPS*HGSVSSLNSTGSLS*PK.H
Epsin 1 <sub>E</sub>	PN1	T444			53.6	61.0	K.T*PESFLGPNAALVDLDSLVSRPGPTPPGAK.A
Epsin 1 <sub>E</sub>	PN1	T390		. =	52.7	78.9	R.TALPT*SGSSAGELELLAGEVPAR.S
Epsin 1 <sub>E</sub>	PN1	S391			24.2	34.4	R.TALPTS*GSSAGELELLAGEVPAR.S
Epsin 1 <sub>E</sub>		<b>S</b> 447			5.5	44.0	K.TPES*FLGPNAALVDLDSLVSRPGPTPPGAK.A
Epsin 1 <sub>E</sub>		T444T468			31.5	14.9	K.T*PESFLGPNAALVDLDSLVSRPGPT*PPGAK.A
Epsin 1 <sub>E</sub>		<b>S</b> 409	Ţ.		99.0	64.1	R.S*PGAFDMSGVR.G
Epsin 1 <sub>E</sub>		S393		I	10.7	28.7	R.TALPTSGS*SAGELELLAGEVPAR.S
Epsin 1 <sub>E</sub>	PN1	S394			15.7	24.0	R.TALPTSGSS*AGELELLAGEVPAR.S
Epsin 4 <sub>C</sub>	CLINT1	S299		<u> </u>	-3.9	12.8	K.TIDLGAAAHYTGDKAS*PDQNASTHTPQSSVK.T
Epsin 4 <sub>C</sub>	CLINT1	T294			6.5	19.3	K.TIDLGAAAHYT*GDKASPDQNASTHTPQSSVK.T
Epsin 4 C		S305			7.4	11.1	K.TIDLGAAAHYTGDKASPDQNAS*THTPQSSVK.T
Epstein Barr virus induced gene 2 G		S328S330			24.2	63.1	K.RQVS*VS*ISSAVK.S
Epstein Barr virus induced gene 2 G		\$330\$333			13.4	34.4	R.QVSVS*ISS*AVK.S
Epstein Barr virus induced gene 2 G		S328S330S333			17.8	31.3	R.QVS*VS*ISS*AVK.S
Epstein Barr virus induced gene 2 G		S337			27.8	22.1	K.S*APEENSR.E
Epstein Barr virus induced gene 2 G	SPR183	S328S333			9.9	61.5	K.RQVS*VSISS*AVK.S
Epstein Barr virus induced gene 2 G	SPR183	<b>S</b> 333			8.2	53.6	R.QVSVSISS*AVK.S
Epstein Barr virus induced gene 2 G	SPR183	S328		•	35.4	83.4	R.QVS*VSISSAVK.S
Epstein Barr virus induced gene 2 G	SPR183	<b>S</b> 343		•	9.5	17.2	K.SAPEENS*R.E
Epstein Barr virus induced gene 2 G	SPR183	\$332 <b>\$</b> 333			5.4	35.1	R.QVSVSIS*S*AVK.S
Epstein Barr virus induced gene 2 G		S332		-	16.1	52.4	R.QVSVSIS*SAVK.S
Epstein Barr virus induced gene 2 G	SPR183	\$328\$330\$332			10.4	31.9	R.QVS*VS*IS*SAVK.S
Epstein Barr virus induced gene 2 G	SPR183	\$330\$332\$333		÷.	7.9	13.3	R.QVSVS*IS*S*AVK.S
Erbin <sub>E</sub>	RBIN	\$602\$603			5.5	69.8	K.HIVNHDDVFEESEELS*S*DEEMK.M
Erbin <sub>E</sub>	RBIN	S598S602			12.5	57.7	K.HIVNHDDVFEES*EELS*SDEEMK.M
E	RBIN	T917S932			15.0	57.8	R.SKSAT*LLYDQPLQVFTGSSS*SSDLISGTK.A
Erbin <sub>E</sub>	RBIN	S915S932			12.9	49.8	K.S*ATLLYDQPLQVFTGSSS*SSDLISGTK.A
Erbin <sub>E</sub>	RBIN	S915			20.4	108.1	K.S*ATLLYDQPLQVFTGSSSSSDLISGTK.A
Erbin <sub>E</sub>	RBIN	S915S933			14.1	54.8	K.S*ATLLYDQPLQVFTGSSSS*SDLISGTK.A
Erbin	RBIN	T917S933			13.6	49.2	K.SAT*LLYDQPLQVFTGSSSS*SDLISGTK.A
Erbin	RBIN	T917S930	•		12.2	39.5	R.SKSAT*LLYDQPLQVFTGS*SSSSDLISGTK.A
Erbin	RBIN	T917	•		12.2	41.4	R.SKSAT*LLYDQPLQVFTGSSSSSDLISGTK.A
Erbin	RBIN	<b>S</b> 440			3.9	53.8	R.TEDVMFIS*DNESFNPSLWEEQR.K
Erbin	RBIN	S440S444			30.8	34.9	R.TEDVMFIS*DNES*FNPSLWEEQR.K
ERCC5 B	BIVM-	S384			9.1	64.4	R.NAPAAVDEGSIS*PR.T
ERCC5 B	BIVM-	S562S563		<del>ii</del>	31.2	30.6	K.FDSSLLS*S*DDETK.C
ERCC5 B	BIVM-	S156S157		• • •	41.7	16.9	R.ENDLYVLPPLQEEEKHS*S*EEEDEKEWQER.M
ERF E	RF	Y16	•		6.0	34.9	K.TPADTGFAFPDWAY*KPESSPGSR.Q
ERF		T3S21	••		35.7	36.7	MKT*PADTGFAFPDWAYKPESS*PGSR.Q
ERF		T3S24	•••		38.0	38.5	MKT*PADTGFAFPDWAYKPESSPG5*R.Q
ERF		T3S20			26.4	12.7	MKT*PADTGFAFPDWAYKPES*SPGSR.Q
ERF E	RF	S20			7.1	23.9	K.TPADTGFAFPDWAYKP®*SPGSR.Q
ERK1 <sub>N</sub>	ларкз	Y204	• •		25.5	98.4	R.IADPEHDHTGFLTEY*VATR.W
ERK1 <sub>N</sub>	ЛАРК3	T202Y204			38.3	92.7	R.IADPEHDHTGFLT*EY*VATR.W
ERK1 <sub>N</sub>		T198Y204			11.9	33.6	R.IADPEHDHT*GFLTEY*VATR.W
ERK2 <sub>N</sub>	MAPK1	Y187			27.8	98.3	R.VADPDHDHTGFLTEY*VATR.W
ERK2 N		T185Y187	• •		49.5	88.6	R.VADPDHDHTGFLT*EY*VATR.W
ERK2 N		T181Y187			13.2	18.6	R.VADPDHDHT*GFLTEY*VATR.W
Erythrocyte membrane protein band 4.1 E		S684		•	20.7	40.8	K.HHAS*ISELKK.N
Erythrocyte membrane protein band 4.1 E		S709			18.0	21.8	K.RLS*THSPFR.T
Erythrocyte membrane protein band 4.1 E		S84			9.8	31.9	R.LFS*SFLK.R
Erythrocyte membrane protein band 4.1 E		S84S85			100.0	34.2	RLFS*S*FLK.R
					.50.0		

ETS translocation variant 6 ETV6 \$232\$257 27.1 16.4 R.AQGPRPHQENNHQES*YPLSVSPMENNHCPASSESHPKPSS*PR.  ETS translocation variant 6 ETV6 \$213 100.0 27.2 R.RLS*PAERA  ETS translocation variant 6 ETV6 \$165 3.3 19.1 R.TPRPS*VDNVHNPPTIELLHR.S  ETS translocation variant 6 ETV6 T18\$22\$29 10.7 41.4 R.ISYT*PPES**PVPSYAS*STPL*VPVPRA  ETS translocation variant 6 ETV6 \$232\$251 15.6 14.4 R.AGGPRPHQENNHQES**YPLSVSPMENNHCPASSES*HPKPSSPR.  ETS translocation variant 6 ETV6 Y233\$256 11.0 10.8 R.AGGPRPHQENNHGES**PLSVSPMENNHCPASSES*HPKPS*SPR.	Peak Area	o abundanc		compared to	the			
March   Marc	-5 -3 0		with the minimum	peak area f				
Company and marker of part of the Company and Compan	5 >10	>100						
Part	Erythrocyte membrane			2 4 2	ăĸŏ			
Expression invalidate pression band 4 (1999 1991)   1991   1992	Erythrocyte membrane	protein band 4.1 EPB41	<b>S</b> 510			8.9	14.6	K.FRYS*GR.T
Page	Erythrocyte membrane	protein band 4.1 EPB41	Y509	•			14.1	K.FRY*SGR.T
Spirecyla manuface spans had 4 ching graph. 1 (20)			S85	•••		9.8	32.5	
Systems of members and a finis graphic 19 (a)		2		<b></b>		16.9	46.8	
### Part		2		===				
Transcript medical medical enterlands   1861   1862   18		2						
Descript motion motionates (DE)   100   8,3		2						
Estropen receptor binding protein (CUTTIPS   SELECTION   1.1								R.LLS*S*ES*EDEEEFIPLAQR.L
Estrogen receptor binding protein/curriery (1950-1950-1950)  Estrogen receptor binding protein/curriery (1950-1950-1950-1950-1950-1950-1950-1950-	Essential meiotic	endonuclease 1 EME1	\$84 <b>\$</b> 87	i		12.1	20.2	RLLS'SES'EDEEEFIPLAQR.L
European receptor binding protein (CUTTP2   SERVICES)   SERVICES	Estrogen receptor	r binding protein DNTTIP2	S141S148			13.0	63.8	K.ESYTEEIVS*EAESHVS*GISR.I
Entropen receptor bending profession(CNTTP2   \$1451466   123   44   KESYTEROPECEPHOLOGICAL	Estrogen receptor	r binding protein DNTTIP2	S141S145S148			11.8	41.2	K.ESYTEEIVS*EAES*HVS*GISR.I
Edingum receptor binding protein (CKTTP2   ST41556	Estrogen receptor	r binding protein DNTTIP2	\$528\$532\$533	-		44.6	45.4	K.EEEEDEKS*EEDS*S*DHDENEDEFS*DEEDFLNSTK.A
Eutropie receptor bending protein (CNTTPD)   \$14111						21.8	60.3	K.ESYTEEIVS*EAES*HVSGISR.I
Editiogen recipitor bendra protein (CRTTP2 1725-1626-164						12.9	42.4	K.ESY*TEEIVSEAES*HVSGISR.I
Estrogen receptor bending protein (CHTPS   1706-1460-146   110   23   14   KESYTEROSACESPHOYOGES					•	20.7	56.0	
Europen receptor binding protein Central 2   133   337   KERYTENSEARCHWOODER					•			
Entrogen receptor binding protein control 2 1 2 2 40 3 SEPT/TERISEAEIN/GOSPT    Entrogen receptor binding protein control 2 1 2 2 40 3 SEPT/TERISEAEIN/GOSPT    Entrogen receptor binding protein control 2 1 2 2 2 40 3 SEPT/TERISEAEIN/GOSPT    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISEAEIN/GOSPT    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISEAEIN/GOSPT    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISEAEIN/GOSPT    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISEAEIN/GOSPT    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER    ETT brandocation variant 6 2 1 2 2 2 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 4 4 4 3 SEPT/TERISPONYS ASSITTANOPPER     ETT brandocation variant 6 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2								
Editiogen records binding protein putting   125   13   15   15   15   15   15   15   1				-				
### To be added consistent of Eq. (1)  ### To be added co								
### 1832 ###			Y233S251				15.4	R.AQGPRPHQENNHQESY*PLSVSPMENNHCPASSES*HPKPSSPR.
### ### ##############################	ETS transle	ocation variant 6 ETV6	S203	_		100.0	40.7	R.S*PLDNMIR.R
### 12 ##	ETS transle	ocation variant 6 ETV6	T18S22			36.4	68.3	R.ISYT*PPES*PVPSYASSTPLHVPVPR.A
### 225 41.3 R8/TYPESPUPSYASSTPUPSYARS PUPPYRA  #### 225 41.3 R8/TYPESPUPSYASSTPUPSYARS PUPPYRA  #### 225 41.3 R8/TYPESPUPSYASSTPUPSYARS  ###################################	ETS transle	ocation variant 6 ETV6	S16S22	<del>;</del>		15.1	38.1	R.IS*YTPPES*PVPSYASSTPLHVPVPR.A
ETS transdocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6	Y17S22S29			22.9	54.0	R.ISY*TPPES*PVPSYAS*STPLHVPVPR.A
### 124   52.1 RISYTPPESPYPSYASTRIANPUPRA   ### 124   52.1 RISYTPPESPYPSYASTRIANPUPRA   ### 125 translocation variant 6 ETV6   \$160.00   \$12.00   \$160.00   \$1			Y17S22T31			22.5	41.3	R.ISY*TPPES*PVPSYASST*PLHVPVPR.A
ET8 translocation variant 6 ETV6			T161	<b>.</b>		3.7	28.5	
ET8 translocation variant 6 ETV6								
### ETS translocation variant 6 ETV0   11.5   38.1   R.BYTPPES PVPS VASTIFLY PVPR A   ETS translocation variant 6 ETV0   117.272.20   10.3   34.4   R.BYTPPES PVPS VASTIFLY PVPR A   ETS translocation variant 6 ETV0   117.522   26.9   44.2   R.BYTPPES PVPS VASTIFLY PVPR A   ETS translocation variant 6 ETV0   117.522.50   30.2   32.7   R.BYTPPES PVPS VASTIFLY PVPR A   ETS translocation variant 6 ETV0   117.522.50   11.9   36.0   R.BYTPPES PVPS VASTIFLY PVPR A   ETS translocation variant 6 ETV0   232.2033   11.3   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.2033   13.8   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20257   27.1   16.4   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   231.3   19.1   R.TERPS VINVH-NNPTELLIR S   ETS translocation variant 6 ETV0   232.20251   16.9   16.7   41.4   R.BYTPPES PVPS VAS TPLVPVPR A   ETS translocation variant 6 ETV0   232.20251   16.6   14.4   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.6   14.4   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.6   14.4   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.0   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.0   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.0   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.0   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   ETS translocation variant 6 ETV0   232.20251   16.0   R.AGGREPHOENNHOES VPLSVEPMENNHOPAS SES VPPVS SEP   R.AGGREPHOENNHOES VP				-	_			
ETS translocation variant 6ETV0					<del>.</del>			
### ### ##############################								
ETS translocation variant 6 ETV8	ETS transle	ocation variant 6 ETV6						R.ISY*TPPES*PVPSYASSTPLHVPVPR.A
ETS translocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6	S26Y27S29			30.2	32.7	R.ISYTPPESPVPS"Y"AS"STPLHVPVPR.A
ETS translocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6	Y17S22S30			17.9	36.0	R.ISY*TPPES*PVPSYASS*TPLHVPVPR.A
ETS translocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6	S248S251			16.9	15.3	R.AQGPRPHQENNHQESYPLSVSPMENNHCPAS*SES*HPKPSSPR.
ETS translocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6	S232Y233				13.8	R.AQGPRPHQENNHQES*Y*PLSVSPMENNHCPASSESHPKPSSPR.
ETS translocation variant 6ETV6			\$232\$257			27.1	16.4	R.AQGPRPHQENNHQES"YPLSVSPMENNHCPASSESHPKPSS"PR.
ETS translocation variant 6 ETV6			S213		ı.	100.0	27.2	
ETS translocation variant 6 ETV6				==				
ETS translocation variant 6 ETV6								
ETS translocation variant 6 ETV6								n
ETS translocation variant 6 ETV6	ETS transle	ocation variant 6 ETV6						R.AQGPRPHQENNHQESY*PLSVSPMENNHCPASSESHPKPSS*PR.
### ##################################	ETS transle	ocation variant 6 ETV6					11.9	R.S'RS'PITTNHRPSPDPEQRPLR.S
### ### ##############################		ETS1 <sub>ETS1</sub>	Y283		•	9.8	34.0	R.VPSY*DSFDSEDYPAALPNHKPK.G
ETS1 ETS1 S282 7.3 34.8 R. VPSYDS*FDSEDYPAALPNHKPK.G  ETS1 ETS1 S282 7.4 15.2 R. VPS*YDS*FDSEDYPAALPNHKPK.G  ETS1 ETS1 S282 7.4 15.2 R. VPS*YDS*FDSEDYPAALPNHKPK.G  ETS1 ETS1 S41 7.8 23.2 K. VDLELFPSPDMECADVPLLTPS*KE  ETS1 ETS1 S40 3.5 20.0 K. VDLELFPSPDMECADVPLLTPS*KE  EUkaryotic translation elongation factor 1 EEF182 Y79 bts1 2 79.6 K. Y*GPADVEDITGS*GATDS*KDDDDIDLFGS*DDEESEEAK.R beta 2 8.4 6.7 K. YGPADVEDITGS*GATDS*KDDDDIDLFGS*DDEESEEAK.R beta 2 8.4 K. YGPADVEDITGS*GATDS*KDDDDIDLFGS*DDEESEEAK.R beta 2		ETS1 <sub>ETS1</sub>	T38	نبة		7.3	29.2	K.VDLELFPSPDMECADVPLLT*PSSK.E
ETS1 ETS1 S282 7.4 15.2 R. VPS*YDS*FDSEDYPAALPNHKPK.G  ETS1 ETS1 S282 7.4 15.2 R. VPS*YDS*FDSEDYPAALPNHKPK.G  ETS1 ETS1 S41 7.8 23.2 K.VDLELFPSPDMECADVPLLTPS*K.E  EUkaryotic translation elongation factor 1 EEF182 779 beta 2 79.6 K.Y**GPADVEDTTGSGATDSKDDDDIDLFGSDDEESEEAK.R beta 2 58.4 K.Y**GPADVEDTTGS**GATDS**KDDDDIDLFGS**DDEESEEAK.R beta 2 58.4 K.Y**GPADVEDTTGS**GATDS**KDDDDDIDLFGS**DDEESEEAK.		ETS1 <sub>ETS1</sub>	S26T38			43.2	32.0	K.VDLELFPS*PDMECADVPLLT*PSSK.E
ETS1 ETS1 S41 7.4 15.2 R. VPS*/VDSFDSEDYPALIPNHKPK.G  ETS1 ETS1 S41 7.8 23.2 K. VDLELFPSPDMECADVPLLTPSS*K.E  EUkaryotic translation elongation factor 1 EEF182 779 bts1 2 78.6 K.Y**GPADVEDITGSGATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 5106 bts1 2 58.4 K.Y**GPADVEDITGSGATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 5106 bts1 2 58.4 K.Y**GPADVEDITGSGATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 5106 bts1 2 58.4 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 58.6 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 58.6 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 58.6 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGS*DDEESEEAK.R bts1 2 58.6 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGSDDEESEEAK.R bts1 2 58.6 K.Y**GPADVEDITGS*GATDSKDDDDIDLFGS*DDEESEEAK.R bts1		ETS1 <sub>ETS1</sub>	S285			7.3	34.8	R.VPSYDS*FDSEDYPAALPNHKPK.G
ETS1 ETS1 S41 7.8 23.2 KVDLELFPSPDMECADVPLLTPSS*KE  EUkaryotic translation elongation factor 1 EEF182 5106 5106 5106 5106 510 510 510 510 510 510 510 510 510 510			S282S285			22.9	28.6	
Eukaryotic translation elongation factor 1 EEF182 5106 78.6 K.YGPADVEDITGSGATDSKDDDDIDLFGSDDEESSEAK.R beta 2 58.4 K.YGPADVEDITGSGATDSKDDDDDIDLFGSDDEESSEAK.R beta 2 58.4 K.YGPADVEDITGSGATDSKDDDDDIDLFGSDDEESSEAK.R beta 2 58.4 K.YGPADVEDITGSGATDSKDDDDDIDLFGSDDEESSEAK.R beta 2 58.4 K.YGPADVEDITGSGATDSKDDDDDIDLFGSDDEESSEAK.R beta 2 58.4 K.YGPADVEDITGSGATDSKDDDDDIDLFGSDDEESSE			S282		<u>.</u>	7.4	15.2	
Eukaryotic translation elongation factor 1 EEF182				-				
Eukaryotic translation elongation factor 1 EEF182 5106 51.4 46.7 K.YGPADVEDTTGSGATDSKDDDDIDLFGS*DDEESEEAK.R beta 2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESEEAK.R beta 2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESEEAK.R beta 2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESEEAK.R beta 2 78.8 5106 51.2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESEEAK.R beta 2 78.8 5106 51.2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESEEAK.R beta 2 78.8 5106 51.2 58.4 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESEEAK.R beta 2 78.8 5106 51.2 51.2 51.2 51.2 51.2 51.2 51.2 51.2	Eukaryotic translation -1-					3.5		
Eukaryotic translation elongation factor 1 EEF182 58056 6.2 58.4 K.YGPADVEDTTGS*GATDS*KDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 788106 12.0 46.5 K.YGPADVEDTT*GSGATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590 4.3 38.0 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590 4.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  Eukaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKaryotic translation elongation factor 1 EEF182 590733 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R beta 2  EUKARYOTIC TRANSLATION FACT		beta 2				35.4		
Eukaryotic translation elongation factor 1 EEF182 590 12.0 46.5 K.YGPADVEDITIGS'GATDSKDDDDIDLFGS'DDEESEEAK.R beta 2 12.0 46.5 K.YGPADVEDITIGS'GATDSKDDDDIDLFGSDDEESEEAK.R beta 2 14.3 39.0 K.YGPADVEDITIGS'GATDSKDDDDIDLFGSDDEESEEAK.R beta 2 16.8 69.3 K.YGPADVEDITIGS'GATDSKDDDDIDLFGS'DDEESEEAK.R beta 2 16.8 69.3 K.YGPADVEDITIGS'GATDSKDDDDAFGS'DDEESEEAK.R beta 2 16.8 69.3 K.YGPADVEDITIGS'GATDSKDDDDDAFGS'DDEESEEAK.R beta 2 16.8 69.3 K.YGPADVEDTIGS'GATDSKDDDD		beta 2 ongation factor 1 EEF1B2						
Eukaryotic translation elongation factor 1 EEF1B2 S90 4.3 39.0 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESSEAK.R beta 2 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESSEAK.R beta 2 16.8 69.3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 2 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 3 K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEESSEAK.R beta 4 K.YGPADVEDTTGS*GATDSKDDDDDFGS*DDEESSEAK.R beta 4 K.YGPADVEDTTGS*GATDSKDDDDD*GATDSKDDDD*GATDSKDDDD*GATDSKDDDD*GATDSKDDDD*GATDSKDDDD*GATDSKDDDD*GATD		beta 2 ongation factor 1 EEF1B2			•			
Eukaryotic translation elongation factor 1 EEF182 S90193 In 8.8 69.3 K.YGPADVEDITGS*GAT*DSKDDDDIDLFGSDDEEESEAK.R. beta 2  Eukaryotic translation elongation factor 1 EEF182 S90193 In 8.8 69.3 K.YGPADVEDITGS*GAT*DSKDDDDIDLFGS*DDEEESEAK.R. K.YGPADVEDITGS*GATDSKDDDDIDLFGS*DDEEESEAK.R. K.YGPADVEDTGS*DDEEESEAK.R. K.YGPADVEDTGS*DDEEESEAK.R. K.YGPADVEDTGS*DDEEESEAK.R. K.YGPADVEDTGS*DDEEESEAK.R. K.YGPADVEDTGS*DDEEESEAK.R. K.YGPADVEDTGS*GATDSKDDDD*GATDS*DDEEESEAK.R. K.YGPADVEDTGS*GATDS*DDEEESEAK.R. K.YGPADVEDTGS*GATDS*DDEEESEAK.R. K.YGPADVEDTGS*GATDS*DD*GATDS*DDE*GATDS*DD*G		beta 2 ongation factor 1 EEF1B2		-				K.YGPADVEDTTGS*GATDSKDDDDIDLFGSDDEEESEEAK.R
Eukaryotic translation elongation factor 1 EEF182 SQNS10R 49.0 78.9 K. YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R	Eukaryotic translation eld	ongation factor 1 EEF1B2	S90T93			16.8	69.3	K.YGPADVEDTTGS*GAT*DSKDDDDIDLFGSDDEEESEEAK.R
••	Eukaryotic translation eld	ongation factor 1 EEF1B2	\$90\$106			19.0	78.9	K.YGPADVEDTTGS*GATDSKDDDDIDLFGS*DDEEESEEAK.R
<u> </u>								

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3 42 PSM		CarT				
>100 >10 Protein Name Gene	Phosphosites	9 m m m		Ascor	MOWSE	Sequence
Eukaryotic translation elongation factor 1 EEF1B2 beta 2  Eukaryotic translation elongation factor 1 EEF1B2	\$95\$106 \$95	_		18.6	69.1	K.YGPADVEDTTGSGATDS'KDDDDIDLFGS'DDEEESEAK.R  K.YGPADVEDTTGSGATDS'KDDDDIDLFGSDDEEESEAKR.L
beta 2  Eukaryotic translation elongation factor 1 EEF1B2	T93			2.4	13.5	K.YGPADVEDTTGSGAT*DSKDDDDIDLFGSDDEESEEAKR.L
beta 2  Eukaryotic translation elongation factor 1 EEF1B2	T87			-0.0	28.1	K.YGPADVEDT*TGSGATDSKDDDDIDLFGSDDEEESEEAK.R
beta 2  Eukaryotic translation elongation factor 1 EEF1G	T46	•	-	100.0	40.0	R.T'PEFLR.K
eamma  Eukaryotic translation elongation factor 1, EEF1D	S528			161.4	105.0	K.KPATPAEDDEDDDDLFGS*DNEEEDK.E
delta  Eukaryotic translation elongation factor 1, EEF1D	T513S528	=		100.0	71.5	K.KPAT*PAEDDEDDDIDLFGS*DNEEEDKEAAQLR.E
delta  Eukaryotic translation elongation factor 1, EEF1D delta	\$499			19.1	37.0	R.ATAPQTQHVS*PMR.Q
Eukaryotic translation elongation factor 1, EEF1D	T495			5.3	26.8	R.ATAPQT"QHVSPMR.Q
Eukaryotic translation elongation factor 1, EEF1D delta	T491	•••	•	11.0	58.2	R.AT'APQTQHVSPMR.Q
Eukaryotic translation elongation factor 2 EEF2	T57T59		•	100.0	21.3	R.FT*DT*RKDEQER.C
Eukaryotic translation initiation factor 2A EIF2A	<b>S</b> 503	<u> </u>		6.3	38.8	R.S*DKSPDLAPTPAPQSTPR.N
Eukaryotic translation initiation factor 2A EIF2A	S506	•		6.5	37.4	R.SDKS*PDLAPTPAPQSTPR.N
Eukaryotic translation initiation factor 3 EIF3K subunit k	S217			11.2	23.5	K.IDFDSVSSIMASS*Q
Eukaryotic translation initiation factor 3 EIF3K subunit k	S216			60.7	25.4	K.IDFDSVSSIMAS*SQ
Eukaryotic translation initiation factor 3, EIF3A subunit 10	S882			12.1	45.0	RLGDSS*LSRK
Eukaryotic translation initiation factor 3, EIF3A subunit 10	S881	_		2.3	12.6	RLGDS*SLSR.K
Eukaryotic translation initiation factor 3, EIF3E subunit 6 48kDa  Eukaryotic translation initiation factor 3, EIF3B	S399			27.8	27.2	KLGHVVMGNNAVS*PYQQVIEK.T
subunit 9 eta, 116kDa  Eukaryotic translation initiation factor 3, EIF3B	T68 T68S78				38.5	R. TEPDAACACAASCOSCOSCODAACELDOSLACODIVOACCCAOCCCA
subunit 9 eta. 116kDa  Eukaryotic translation initiation factor 3, EIF3B	S152S164			42.0	43.9	R. TYEDAACACAACAGDECEDEDBAAEEI DAGUAEDDURAAACAADACAA R.ALENGDADEPS'FSDPEDFVDDVS'EEELLGDVLK.D
subunit 9 eta. 116kDa  Eukaryotic translation initiation factor 3, FIE3B	S152			78.9	103.5	R.ALENGDADEPS*FSDPEDFVDDVSEEELLGDVLK.D
subunit 9 eta, 116kDa  Eukaryotic translation initiation factor 3, EIF3B	T68S78S81S83			70.0	30.9	R. TERRATAFAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
subunit 9 eta, 116kDa  Eukaryotic translation initiation factor 3, EIF3B	S154S164			49.7	99.9	R.ALENGDADEPSFS*DPEDFVDDVS*EEELLGDVLK.D
subunit 9 eta. 116kDa  Eukaryotic translation initiation factor 3, EIF3B	S152S154			82.9	132.5	R.ALENGDADEPS*FS*DPEDFVDDVSEEELLGDVLK.D
subunit 9 eta. 116kDa  Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta. 116kDa	S152S154S164			100.0	99.6	R.ALENGDADEPS*FS*DPEDFVDDVS*EEELLGDVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S83S85	•	• • •	13.6	16.8	R. TERRALAZARAROROFONDORASTEI DONIASTEDI/DAGOCARDOSOA
Eukaryotic translation initiation factor 4B EIF4B	<b>S</b> 445	•		58.9	75.3	K.S'LENETLNK.E
Eukaryotic translation initiation factor 4B EIF4B	<b>S</b> 597	•••		37.6	73.8	K.YAALS*VDGEDENEGEDYAE
Eukaryotic translation initiation factor 4B EIF4B	<b>S</b> 409			28.8	29.8	R.S'EETQER.E
Eukaryotic translation initiation factor 4B EIF4B	<b>T</b> 97			5.8	75.6	K.SPPYT*AFLGNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	S93			30.1	135.8	K.S'PPYTAFLGNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	Y96			11.8	60.1	K.SPPY*TAFLGNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	S422	••••		15.0	118.0	R.TGS'ESSQTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	\$498\$504			15.9	84.1	R.SQSS*DTEQQS*PTSGGGK.V
Eukaryotic translation initiation factor 4B <sub>EIF4B</sub> Eukaryotic translation initiation factor 4B <sub>EIF4B</sub>	T420S425	•••		20.8	70.9	R.T'GSESS'QTGTSTTSSR.N
Eukaryotic translation initiation factor 48 EIF4B	\$406 \$504			100.0	26.8	R.SOSSDTEQQS*PTSGGGK.V
Eukaryotic translation initiation factor 48 EIF4B	T500S504	_		4.6	13.6	R.SOSSDT'EQGS'PTSGGGKV
Eukaryotic translation initiation factor 4B EIF4B	S497			14.0	121.1	R.SQS*SDTEQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	T500			9.8	59.2	R.SQSSDT*EQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	\$497 <b>T</b> 500		•	11.8	33.2	R.SQS*SDT*EQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	\$424\$425	_	•	6.8	29.1	R.TGSES'S'QTGTSTTSSRN
Eukaryotic translation initiation factor 4B EIF4B	S489	-		16.9	24.3	K.R.S.*NPPAR.S
Eukaryotic translation initiation factor 4B EIF4B	S498			11.7	72.0	R.SQSS*DTEQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	\$422\$425			5.9	35.7	R.TGS*ESS*QTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S422S424			-0.4	11.1	R.TGS"ES"SQTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S424			-0.4	54.4	R.TGSES'SQTGTSTTSSRN
Eukaryotic translation initiation factor 4B EIF4B	\$497\$504			13.9	29.7	R.SQS*SDTEQQS*PTSGGGK.V
Eukaryotic translation initiation factor 4E <sub>EIF4EBP1</sub> binding protein 1				14.0	61.7	K.T*PPRDLPTIPGVTSPSSDEPPMEASQSHLR.N
EIF4EBP1				19.7	25.6	R.RVVLGDGVQLPPGDYST*TPGGTLFS*TTPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1				14.4	22.3	R.R.VVLGDGVQLPPGDYST*TPGGTLFST*TPGGTR1
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP1				20.7	23.2	R.WILGDGVQLPPGDYSTT*PGGTLFS*TTPGGTRI
binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP1  Eukaryotic translation initiation factor 4E EIF4EBP1				24.5	72.3	K.TPPRDLPT*IPGVTSPSSDEPPMEASQSHLR.N  R.VVLGDGVQLPPGDYS*TTPGGTLFS*TTPGGTR.I
binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP1  Eukaryotic translation initiation factor 4E EIF4EBP1				10.5	32.6	R.VVLGDGVQLPPGDYS*TIPGGTLFS*TIPGGTR.I
binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP1				4.3	13.8	R.WLGDGVQLPPGDYSTTPGGTLFS'TTPGGTR.I
binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP1				9.4	26.7	R.R.W.LGDGVQLPPGDYS*TTPGGTLFST*TPGGTRI
binding protein 1  Eukaryotic translation initiation factor 4E EIF4EBP2				17.8	34.2	R.TVAISDAAQLPHDYCTT*PGGTLFS*TTPGGTRJ
binding protein 2  Eukaryotic translation initiation factor 4E EIF4EBP2				24.7	34.0	R.TVAISDAAQLPHDYCT*TPGGTLFST*TPGGTR.I
binding protein 2  Eukaryotic translation initiation factor 4E <sub>EIF4EBP2</sub> binding protein 2		• • • •		6.7	24.7	R.TVAISDAAQLPHDYCT-TPGGTLFSTT-PGGTR.I
Eukaryotic translation initiation factor 4E <sub>EIF4EBP2</sub>	S25S44		• •	13.0	25.5	R.TVAS*DAAQLPHDYCTTPGGTLFS*TTPGGTRJ

Peak Area %CV	White do	ts-Significant cha	nge in pepti	de the			
<-10 -5 -3 -3 -3	abundand timepoint PSM	e at 5%FDR o with the minimum					
0 71 3 86 5 >100			CarT	RajiB			
>10 Protein Name		Phosphosites	F E E	5 m 9 m	Ascor	MOWSE	Sequence
Eukaryotic translation initiation factor 4 binding protein	E EIF4EBP2				26.8	25.2	R.NSPMAQT*PPCHLPNIPGVTSPGTLIEDSK.V
	EIF4EBP2				43.7	31.4	R.NS*PM#AQT*PPCHLPNIPGVTSPGTLIEDSK.V
Eukaryotic translation initiation factor 4 binding protein	2				21.6	35.8	R.TVAISDAAQLPHDYCTT*PGGTLFST*TPGGTR.I
Eukaryotic translation initiation factor 4 binding protein	E EIF4EBP2 2	T36S44			6.2	22.3	R.TVAISDAAQLPHDYCT*TPGGTLFS*TTPGGTR.I
Eukaryotic translation initiation factor 4 binding protein	E EIF4EBP2 2	S65			29.4	51.0	R.NS*PMAQTPPCHLPNIPGVTSPGTLIEDSK.V
Eukaryotic translation initiation factor 4 binding protein	2				11.4	26.0	R.TVAIS*DAAQLPHDYCTTPGGTLFST*TPGGTR.I
Eukaryotic translation initiation factor 4 binding protein	2				22.8	16.0	R.TVAISDAAQLPHDYCTTPGGTLFST*TPGGTR.I
Eukaryotic translation initiation factor 4 binding protein	2			-	2.3	22.9	R.TVAIS*DAAQLPHDYCTTPGGTLFSTT*PGGTR.I
Eukaryotic translation initiation factor 4 binding protein	2				4.9	14.2	R.TVAISDAAQLPHDYCT*TPGGTLFSTTPGGT*R.I
Eukaryotic translation initiation factor 4 binding protein	2				19.4	17.7	R.RNS*PMAQTPPCHLPNIPGVT*SPGTLIEDSK.V
Eukaryotic translation initiation factor 4 binding protein	2			•	5.0	21.2	R.TVAISDAAQLPHDY*CTTPGGTLFST*TPGGTR.I
Eukaryotic translation initiation factor 4 binding protein	2				3.5	17.4	R.TVAISDAAQLPHDY*CTTPGGTLFS*TTPGGTR.I
Eukaryotic translation initiation factor 4 nuclear import factor	1				39.9	51.1	K.WHASLYPAS*GR.S
Eukaryotic translation initiation factor 4 nuclear import factor	1				82.3	68.8	R.APS*PPLSQVFQTR.A
Eukaryotic translation initiation factor 4 nuclear import factor	1				-0.3	34.3	R.SS*PVESLKK.E
Eukaryotic translation initiation factor 4 nuclear import factor	1				30.2	61.6	R.SSS*PVGLAK.W
Eukaryotic translation initiation factor 4 nuclear import factor	1		-		6.8	22.8	R.GNSS*SPAPAASITS*MLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S679S690			8.4	19.4	R.GNS*SSPAPAASITS*MLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S301		-	100.0	37.6	R.DAVLPEQS*PGDFDFNEFFNLDK.V
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S69			8.2	42.7	K.YDSDGVWDPEKWHAS*LYPASGR.S
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1		<b></b>		9.1	28.2	R.GNSS*SPAPAASITSMLS*PSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S345			9.5	15.1	R.WFSNPS'R.S
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	Y71			-0.7	25.9	K.YDSDGVWDPEKWHASLY*PASGR.S
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S681S693		<b>—</b>	6.3	16.7	R.GNSSS*PAPAASITSMLS*PSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S342				13.1	R.WFS*NPSR.S
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	Y382			4.1	14.0	R.LAGLEQAILSPGQNSGNY*FAPIPLEDHAENKVDILEMLQK.A
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S374	<b>—</b>			23.5	R.LAGLEQAILS*PGQNSGNYFAPIPLEDHAENKVDILEMLQK.A
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S680S687			3.9	20.1	R.GNSS*SPAPAAS*ITSMLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S679S687			6.5	24.3	R.GNS*SSPAPAAS*ITSMLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	T689			-10.9	22.1	R.GNSSSPAPAASIT*SMLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S687S690			4.5	18.4	R.GNSSSPAPAAS*ITS*MLSPSFTPTSVIR.K
Eukaryotic translation initiation factor 4 nuclear import factor	E EIF4ENIF1	S950		•	-0.6	27.6	R.SS*SPVGLAK.W
Eukaryotic translation initiation factor		\$389\$390			107.4	76.1	K.EAEEES*S*GGEEEDEDENIEVVYSK.A
Eukaryotic translation initiation factor 5	B <sub>EIF5B</sub>	S113			43.8	110.0	K.KQSFDDNDS*EELEDKDSK.S
Eukaryotic translation initiation factor 5	B EIF5B	\$107\$113			94.5	70.2	K.KQS*FDDNDS*EELEDKDSK.S
Eukaryotic translation initiation factor 5	B <sub>EIF5B</sub>	\$588\$589\$591			20.2	60.8	K.EMS*S*DS*EYDS*DDDRTK.E
Eukaryotic translation initiation factor 5	B EIF5B	S214			147.1	111.7	K.NKPGPNIES*GNEDDDASFK.I
Eukaryotic translation initiation factor 5	B <sub>EIF5B</sub>	S135S137			11.2	69.3	K.VEMYS*GS*DDDDFNKLPK.K
Eukaryotic translation initiation factor 5	B <sub>EIF5B</sub>	\$182\$183\$186	•••		112.4	114.3	R.INS'S'GES'GDES'DEFLQSR.K
Eukaryotic translation initiation factor 5	B EIF5B	S511			34.6	63.3	K.EETPPPVEPEEEEDTEDAGLDDWEAMAS*DEETEK.V
Eukaryotic translation initiation factor 5	B EIF5B	S164			115.1	74.4	K.WDGS*EEDEDNSK.K
Eukaryotic translation initiation factor 5	B EIF5B	\$588\$589\$591			8.6	36.5	K.EMS*S*DS*EY*DSDDDRTK.E
Eukaryotic translation initiation factor 5	B EIF5B	\$182\$183\$186			60.1	116.0	R.INS*S*GES*GDESDEFLQSR.K
Eukaryotic translation initiation factor 5	B EIF5B	T498S511	Ļ		43.0	43.4	K.EETPPPVEPEEEEDT*EDAGLDDWEAMAS*DEETEK.V
Eukaryotic translation initiation factor 5	B EIF5B	S107			4.8	58.6	K.QS*FDDNDSEELEDKDSK.S
Eukaryotic translation initiation factor 5	B EIF5B	S589S591Y593	=		14.9	13.1	K.EMSS*DS*EY*DS*DDDRTK.E
Eukaryotic translation initiation factor 5	B EIF5B	Y134S135	•		5.7	37.4	K.VEMY*S*GSDDDDFNKLPK.K
Eukaryotic translation initiation factor	6 EIF6	T245			16.9	30.2	K.LNEAQPSTIATSMRDSLIDSLT*
Eukaryotic translation initiation factor	6 EIF6	S239			6.6	29.5	K.LNEAQPSTIATSMRDS*LIDSLT
Eukaryotic translation initiation factor	6 <sub>EIF6</sub>	S243			13.0	13.3	K.LNEAQPSTIATSMRDSLIDS*LT
EVER	1 <sub>TMC6</sub>	S62			9.5	29.5	R.EVTGS*SQQTLWRPEGTQSTATLR.I
EVER	1 <sub>TMC6</sub>	T60			21.6	21.0	R.EVT*GSSQQTLWRPEGTQSTATLR.I
EVER	1 <sub>TMC6</sub>	S63			6.5	43.0	R.EVTGSS*QQTLWRPEGTQSTATLR.I
EVER2 protei	n TMC8	S521		•	12.1	28.1	R.AS*SRPFR.A
EVER2 protei	n <sub>TMC8</sub>	S722	•		100.0	29.4	R.FRFPS*GAEL
EVER2 protei	n TMC8	S522	•	• •	8.2	31.0	R.ASS*RPFR.A
EVI2	B <sub>EVI2B</sub>	S271	•••		-1.0	21.5	K.RTSIIS"LTPWKPSK.S
EVI2	B <sub>EVI2B</sub>	T267S268			6.8	43.6	K.RT*S*IISLTPWKPSK.S
EVI2	B EVI2B	S268S271			16.5	26.9	R.TS*IIS*LTPWKPSK.S
EVI2	B <sub>EVI2B</sub>	T267			9.1	23.6	K.RT*SIISLTPWKPSK.S
EVI2	B EVI2B	S294			16.9	119.8	K.LFES*SENIEDSNNPK.T
EVI2	B EVI2B	S268			-0.4	31.3	R.TS*IISLTPWKPSK.S
				•			

<.10 0 abundanc	ts-Significant cha be at 5%FDR of with the minimum	compared to	the			
42 PSM 0 71 3 86		CarT	RajiB			
>10 Protein Name Gene Excision repair cross-complementing ERCC6	Phosphosites \$486\$489	5 E E	8 g g	Ascor	MOWSE	Sequence K.LEDDS'EES'DAEFDEGFKVPGFLFK.K
rodent repair deficiency. complementation  Exocyst complex component 1 EXOC1	S470S473	•		15.3	41.1	K.LTGS*TSS*LNK.L
Exocyst complex component 1 EXOC1	S448			19.1	65.0	K.KFGLHGS*SGK.L
Exocyst complex component 1 EXOC1	S470T471		•••	9.0	31.6	K.LTGS*T*SSLNK.L
Exocyst complex component 1 EXOC1	S499			1.7	44.1	R.SQSSSLLDMGNMS*ASDLDVADR.T
Exocyst complex component 1 EXOC1	T471S473		-	8.9	42.1	K.LTGST*SS*LNK.L
Exocyst complex component 1 EXOC1  Exocyst complex component 1 EXOC1	S472S473		•	10.0	26.0	K.LTGSTS*S*LNK.L  R.SQSS*SLI DMGNMSASDI DVADR T
Exocyst complex component 1 EXOC1	\$490 \$501			17.7	35.8	R.SQSSSLLDMGNMSAS*DLDVADR.T
Exocyst complex component 1 EXOC1	T471S472	•		4.4	37.6	K.LTGST*S*SLNK.L
Exocyst complex component 1 EXOC1	\$470\$472		•	7.6	32.4	K.LTGS*TS*SLNK.L
Exocyst complex component 4 EXOC4	S226			67.3	61.3	K.DAS*VPLIDVTNLPTPR.K
Exportin 6 XPO6	T210S211		-	24.2	99.6	K.HSVTAATPPPSPT*S*GESGDLLSNLLQSPSSAK.L
Exportin 6 XPO6	T204S208			37.3	116.0	K.HSVTAAT*PPPS*PTSGESGDLLSNLLQSPSSAK.L
Exportin 6 XPO6	S208S214			7.6	49.8	K.HSVTAATPPPS*PTSGES*GDLLSNLLQSPSSAK.L
Exportin 6 XPO6	T204S211		==	13.5	101.9	K.HSVTAAT*PPPSPTS*GESGDLLSNLLQSPSSAK.L  K.HSVTAATPPPSPT*SGES*GDLLSNLLQSPSSAK.L
Exportin 6 XPO6	T210S214 T201T204			1.2	40.9	K.HSVT*AAT*PPPSPTSGES*GDLLSNLLQSPSSAK.L
Exportin 6 XPO6	S208S211			13.7	20.3 54.9	K.HSVTAATPPPS*PTS*GESGDLLSNLLQSPSSAK.L
Exportin 6 XPO6	T204S219			10.2	46.0	K.HSVTAAT*PPPSPTSGESGDLLS*NLLQSPSSAK.L
Exportin 6 <sub>XPO6</sub>	T204T210	بجيا	• • •	6.7	26.3	K.HSVTAAT*PPPSPT*SGESGDLLSNLLQSPSSAK.L
Exportin 6 <sub>XPO6</sub>	S199T201	Ė			31.9	K.HS*VT*AATPPPSPTSGESGDLLSNLLQSPSSAK.L
Exportin 6 XPO6	S208S219		•	7.5	39.0	K.HSVTAATPPPS*PTSGESGDLLS*NLLQSPSSAK.L
Exportin 6 XPO6	S208			4.2	25.3	K.HSVTAATPPPS*PTSGESGDLLSNLLQSPSSAK.L
Exportin 6 XPO6	S214S219		÷	2.3	31.2	K.HSVTAATPPPSPTSGES*GDLLS*NLLQSPSSAK.L
Exportin 6 XPO6  EZH2 protein EZH2	T204S214			23.0	14.0	K.HSVTAAT*PPPSPTSGES*GDLLSNLLQSPSSAK.L
EZH2 protein EZH2	\$367\$371 \$371T372			8.6	17.2	R.GRLPNNS*SRPS*TPTINVLESK.D  R.GRLPNNSSRPS*T*PTINVLESK.D
EZH2 protein EZH2	T372T374			3.2	14.8	R.GRLPNNSSRPST*PT*INVLESK.D
EZH2 protein EZH2	\$367\$368			0.8	16.3	R.GRLPNNS*S*RPSTPTINVLESK.D
EZH2 protein EZH2	S368S371			6.1	13.0	R.GRLPNNSS*RPS*TPTINVLESK.D
EZH2 protein EZH2	S367T372			4.0	24.0	R.LPNNS*SRPST*PTINVLESK.D
F box and leucine rich repeat protein 11 KDM2A	T713S718S731	•		22.0	11.7	R.SCDEPLT*PPPHS*PTSMLQLIHDPVS*PR.G
F box and leucine rich repeat protein 11 KDM2A	S869			100.0	98.5	R.GDEEGLGGEEEEEEEEEEDDS*AEEGGAAR.L
F box and leucine rich repeat protein 11 KDM2A  F box and leucine rich repeat protein 11 KDM2A	T713S718			21.8	23.6	R.SCDEPLT*PPPHS*PTSMLQLIHDPVSPR.G
F box and leucine rich repeat protein 11 KDM2A	\$718\$731 \$721\$731	-		12.8	13.1	R.SCDEPLTPPPHS*PTSMLQLIHDPVS*PR.G  R.SCDEPLTPPPHSPTS*MLQLIHDPVS*PR.G
F box and leucine rich repeat protein 11 KDM2A	T713S721S731		-	13.4	12.3	R.SCDEPLT*PPPHSPTS*MLQLIHDPVS*PR.G
F-box and leucine rich repeat protein 10 KDM2B	Y490T493			10.9	24.4	K.STTLAVDY*PKT*PTGSPATEVSAK.W
F-box and leucine rich repeat protein 10 KDM2B	T493T495		•	20.3	17.8	K.STTLAVDYPKT*PT*GSPATEVSAK.W
F-box and leucine rich repeat protein 10 KDM2B	T493S497			14.6	24.0	K.STTLAVDYPKT*PTGS*PATEVSAK.W
F-box and leucine-rich repeat protein 20, FBXL20 isoform CRA a	S4	<u> </u>		100.0	14.6	M.APS*RDR.L
F-box protein 42 <sub>FBXO42</sub>	T5398545			17.0	47.7	R.HPPEQTNGVHT*PPHVAS*ALAGAVSPGALR.R
F-box protein 42 <sub>FBXO42</sub>	T5398552			53.7	54.2	R.HPPEQTNGVHT*PPHVASALAGAVS*PGALR.R
F-box protein 42 FBXO42  F-box protein 42 FBXO42	\$365\$373	=		24.4	43.5	R.APLS*PSLNSRPS*PISATPPALVPETR.E  R.APLS*PSLNSRPSPIS*ATPPALVPETR.E
F-box protein 42 FBXO42	\$365\$376 \$365\$367			13.5	12.8 36.1	R.APLS*PSLNSRPSPISATPPALVPETR.E
FACTp140 SUPT16H				100.0	25.1	K.ES*LGS*EEES*GKDWDELEEEAR.K
FADD FADD	S197	•		-0.3	16.9	R.SGAMSPMS*WNSDASTSEAS
FAM40A STRIP1	Y62			5.6	52.7	R.KDSEGY*SESPDLEFEYADTDK.W
Family with sequence similarity 123C AMER3	<b>S</b> 97			7.3	15.7	R.KCKTHDS*M#SGAGR.A
Family with sequence similarity 126, FAM126B member B	S430			100.0	17.1	K.HLS*LPAGQVVPK.I
Family with sequence similarity 128, MZT2B member B	S152			13.9	34.2	K.GGGPGKS*PTR.G
Family with sequence similarity 133, FAM133B member B  Family with sequence similarity 29, member HAUS6				28.8	75.0	K.MYSEDKPLS*S*ES*LS*ESEYIEEVR.A  K.GWTPSVDLLPPMS*PLSFDPASEEVYAK.S
Family with sequence similarity 44, member BOD1L1	\$406 \$482\$484			15.6 31.3	36.0	K.YYS*DS*DDELTVEQR.R
Family with sequence similarity 44, member BOD1L1	S1077			01.0	14.4	R.RGS*LSQEMAK.G
Family with sequence similarity 44, member BOD1L1	S2779S2780			10.8	45.7	R.KQHYLS*S*EDEPDDNPDVLDSR.I
Family with sequence similarity 53, member FAM53B	S167	•-		12.0	48.0	R.SSS*FSLPSR.A
Family with sequence similarity 53, member FAM53B B	S166			-0.3	39.1	R.SS*SFSLPSR.A
Family with sequence similarity 53, member FAM53B B	S118			33.6	58.7	R.SLS*FSDEMSSCR.T
Family with sequence similarity 53, member FAM53B B	S165	<b>—</b>		17.0	35.5	R.S*SSFSLPSR.A

<-10 0 abundance		compared to	the			
.5 25 timepoint	with the minimum					
>100 >100		CarT	RajiB E E E			•
Protein Name Gene Family with sequence similarity 54, member MTFR1L B	Phosphosites S103	# # # # # #	0 0 0	Ascor 100.0	MOWSE 36.1	Sequence R.NAS*VPNLR.G
Family with sequence similarity 54, member MTFR1L B	S238			30.2	67.2	K.ASS*FADMMGILK.D
Family with sequence similarity 54, member MTFR1L B	S41			22.1	55.4	R.AS*FETLPNISDLCLR.D
В	S237				60.6	K.AS*SFADMM#GILK.D
Family with sequence similarity 65, member RIPOR1  A  Family with sequence similarity 65, member RIPOR1	S22			6.4	42.5	R.SQS*FAGVLGSHER.G  R.S*QSFAGVLGSHER.G
Α	\$20 \$193		• •	12.2 52.0	87.8 61.1	K.ISNLS*PEEEQGLWK.Q
Family with sequence similarity 82, member RMDN2	S128S129			100.0	13.3	R.RRFS*S*R.K
Family with sequence similarity 82, member RMDN3	S46	•		8.3	39.8	R.SQS*LPNSLDYTQTSDPGR.H
Family with sequence similarity 83, member FAM83G	<b>S</b> 127	•		51.9	57.8	R.S*IPQLDLGWPDTIAYR.G
Family with sequence similarity 91, member FAM91A1	<b>S</b> 829			25.6	75.4	R.SPSS*LLIANLHLQ
Family with sequence similarity 91, member FAM91A1				13.8	53.5	R.SPS*SLLIANLHLQ
Family with sequence similarity 91, member FAM91A1	S671S674			100.0	21.2	R.KLS'DAS'DER.G
Far upstream element binding protein FUBP1  Far upstream element binding protein FUBP1	S630	<u></u>		-0.4	21.7	R.QQAAYYAQTS*PQGM#PQHPPAPQGQ
Far upstream element binding protein FUBP1	T629			30.1	72.4	R.QQAAYYAQI*SPQGMPQHPPAPQGQ R.QQAAYY*AQTSPQGMPQHPPAPQGQ
FAS associated factor 1 FAF1	Y626 S320			84.4	64.7	K.S*PMMPENAENEGDALLQFTAEFSSR.Y
FAS associated factor 1 FAF1	S278T283			04.4	66.4	R.
Fas receptor FAS	<b>S</b> 212	_		21.4	60.5	K.ENQGSHES*PTLNPETVAINLSDVDLSK.Y
Fas receptor FAS	<b>S</b> 209			5.6	44.9	K.ENQGS*HESPTLNPETVAINLSDVDLSK.Y
Fas receptor FAS	T214		<del>, i</del>	-2.2	62.9	K.ENQGSHESPT*LNPETVAINLSDVDLSK.Y
Fatty acid synthase FASN	S974		•	14.9	40.2	R.LFDHPES*PTPNPTEPLFLAQAEVYK.E
Fatty acid synthase FASN	T976			2.3	46.5	R.LFDHPESPT*PNPTEPLFLAQAEVYK.E
FBP3 FUBP3	S258			24.3	36.7	R.QQVAFYGQTLGQAQAHS*QEQ
FBP3 FUBP3	S538			24.4	65.5	K.QSHAASAAPQAS*SPPDYTMAWAEYYR.Q
FBP3 FUBP3  FCH and double SH3 domains 2 FCHSD2	S539		<u> </u>	13.8	60.7	K.QSHAASAAPQASS*PPDYTMAWAEYYR.Q  R.EIQISPSPKPHAS*LPPLPLYDQPPSS*PYPS*PDKR.S
FCH domain only 1 FCHO1	\$596\$609\$613 \$523\$529			9.2 59.1	12.9	R.APPLPDS*PQPLAS*SPGPWGLEALAGGDLMPAPADPTAR.E
FCH domain only 1 <sub>FCHO1</sub>	S523S530			43.1	79.8	R.APPLPDS*PQPLASS*PGPWGLEALAGGDLMPAPADPTAR.E
FCH domain only 1 FCHO1	\$583\$585\$587	••••		34.5	19.6	R.S*LS*PS*PLGSSAASTALERPS*FLSQTGHGVSR.G
Ferm, RhoGEF and pleckstrin domain FARP2	S399Y407		• =	19.8	55.8	R.TPAS*PSSANAFY*SLSPSTLVPSGLPEFK.D
Ferm, RhoGEF and pleckstrin domain FARP2	\$399\$408			1.5	33.8	R.TPAS*PSSANAFYS*LSPSTLVPSGLPEFK.D
Ferm, RhoGEF and pleckstrin domain FARP2	\$399\$410			1.7	42.1	R.TPAS*PSSANAFYSLS*PSTLVPSGLPEFK.D
Ferritin heavy chain 1 <sub>FTH1</sub>	<b>S</b> 179			17.9	44.7	K.HTLGDS*DNES
Fetal Alzheimer antigen BPTF	S216			100.0	36.2	R.S*PILEEK.D
Fetal Alzheimer antigen BPTF	T938	Ţ.		38.7	22.6	R.KSLEGT*K.N
FGD1 family member 3 FGD3	S128			34.5	41.2	K.VTPQEEADS*DVGEEPDSENTPQK.A
FGD1 family member 3 FGD3	T121		•	5.9	12.5	K.VT*PQEEADSDVGEEPDSENTPQK.A
FGD1 family, member 2 <sub>FGD2</sub> FGFR1 oncogene partner FGFR1OP	S654			30.9	34.5	R.AASGWSPSWPNDGDLS*D  K.EKGPTTGEGALDLSDVHS*PPKS*PEGK.T
FGFR1 oncogene partner FGFR1OP				35.9	30.6	K.GPTTGEGALDLS*DVHSPPKS*PEGK.T
Fibrillarin FBL	\$1528160 \$124			18.8	67.2	K.RVS*ISEGDDKIEYR.A
Filamin A, alpha <sub>FLNA</sub>	S2144			51.1	41.8	R.RAPS*VANVGSHCDLSLK.I
FIP1 like 1 FIP1L1	T494S500			44.8	42.8	R.ERDHSPT*PSVFNS*DEER.Y
FIP1 like 1 FIP1L1	\$492T494\$500			23.9	37.2	R.ERDHS"PT"PSVFNS"DEER.Y
FIP1 like 1 FIP1L1	<b>S</b> 492	<del>!!!</del>		53.8	87.0	R.DHS*PTPSVFNSDEER.Y
FIP1 like 1 FIP1L1	\$492\$496	-		42.0	78.2	R.DHS*PTPS*VFNSDEER.Y
FIP1 like 1 FIP1L1	T81S87S89			16.9	69.6	K.VTET'EDDSDS'DS'DDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	\$85\$87\$89			39.3	59.8	K.VTETEDDS*DS*DS*DDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	S304			100.0	44.2	R.AES*PDLR.R
FIP1 like 1 FIP1L1	T494			5.0	95.7	R.DHSPT*PSVFNSDEER.Y
FIP1 like 1 FIP1L1 FIP1 like 1 FIP1L1	\$492T494	-		34.3	84.9	R.DHS'PT'PSVFNSDEER.Y  R.DHSPT'PS'VFNS'DEER.Y
FIP1 like 1 FIP1L1	T494S496S500 T81S85S87			10.3	73.9	R.DHSP1"PS"VFNS"DEER.Y  K.VTET"EDDS"DS"DS"DSDDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	S496S500			18.9	73.9	R.DHSPTPS*VFNS*DEER.Y
FIP1 like 1 FIP1L1	T79T81S85S89	<del></del>		7.8	54.0	K.VT*ET*EDDS*DSDS*DDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	T494S496			13.3	48.1	R.DHSPT*PS*VFNSDEER.Y
FIP1 like 1 FIP1L1	T79T81S87S89			16.4	23.1	K.VT*ET*EDDSDS*DS*DDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	T81S85S89	-		8.8	51.5	K.VTET*EDDS*DSDS*DDDEDDVHVTIGDIK.T
FIP1 like 1 FIP1L1	\$492\$500	<u></u>	•	31.4	67.1	R.DHS*PTPSVFNS*DEER.Y
FIP1 like 1 FIP1L1	\$492T494\$496		■.	15.9	47.5	R.DHS*PT*PS*VFNSDEER.Y
FIP1 like 1 FIP1L1	T79T81S85S87	-		12.7	39.6	K.VT*ET*EDDS*DS*DSDDEDDVHVTIGDIK.T

<-10 0 abundance	ts-Significant char e at 5%FDR o with the minimum	ompared to	the			
.3 42 PSM 71 3 86		CarT	RajiB			
>100 Protein Name Gene	Phosphosites	8 m m	5 % B	Ascor	MOWSE	Sequence
FK506 binding protein 15, 133kDa <sub>FKBP15</sub> FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	S1164 S1162S1164		• •	19.8	87.9	R.SSLS*GDEEDELFK.G  R.SS*LS*GDEEDELFK.G
FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	S1102S1104 S1114			9.6	92.1	R.LSLTSDPEEGDPLALGPES*PGEPQPPQLK.K
FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	<b>S</b> 311			27.7	33.9	R.DSAAPS*PIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDa FKBP15	\$307\$311		•••	5.0	25.2	R.DS*AAPS*PIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	S295S297				12.9	R.DS*GS*DGHSVSSRDSAAPSPIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDa <sub>FKBP15</sub> FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	\$320 \$320\$326			3.3	15.9	R.DSAAPSPIPGADNLS*ADPVVSPPTSIPFK.S  R.DSAAPSPIPGADNLS*ADPVVS*PPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	\$939\$940\$941			17.5	22.1	K.MVTLQLLNQQEQEKEES*S*S*EEEEEK.A
FK506 binding protein 15, 133kDa <sub>FKBP15</sub>	S956		•	22.8	64.5	R.RPS*QEQSASASSGQPQAPLNR.E
FK506 binding protein 15, 133kDa FKBP15	S1162			-0.4	60.7	R.SS*LSGDEEDELFK.G
FK506 binding protein 15, 133kDaFKBP15	S1161S1162		<u>.</u>	11.6	51.0	R.S'S'LSGDEEDELFK.G
FK506 binding protein 15, 133kDa <sub>FKBP15</sub> FK506 binding protein 4 <sub>FKBP4</sub>	\$311\$326 \$453		-	13.6	13.1	R.DSAAPS*PIPGADNLSADPVVS*PPTSIPFK.S  K.SNTAGSOS*QVETEA -
FKHR FOXO1	\$298\$301			29.8	75.3	K.WPAS*PGS*HSNDDFDNWSTFRPR.T
FKHR FOXO1	S298S303			6.4	16.1	K.WPAS*PGSHS*NDDFDNWSTFRPR.T
FLI1 <sub>FLI1</sub>	S241			37.6	55.3	R.GAWGNNMNSGLNKS*PPLGGAQTISK.N
FLI1 <sub>FLI1</sub>	S236			18.6	42.8	R.GAWGNNMNS*GLNKSPPLGGAQTISK.N
Flightless 1 <sub>FLII</sub>	\$436			100.0	45.4	R.RKDS*AQDDQAK.Q  R.NAEAVLQS*PGLSGK.V
FLJ10378 LARP1B	\$856 T362	<b>T</b>		11.2	75.5	R.GLST*SLPDLDSEPWIEVK.K
FLJ10378 LARP1B	\$363		•	-0.2	82.5	R.GLSTS*LPDLDSEPWIEVK.K
FLJ10378 LARP1B	\$340\$343		=	100.0	27.4	R.IGS*PLS*PK.K
FLJ12387 KLC2	<b>S</b> 609			14.2	89.4	R.TLSS*SSMDLSR.R
FLJ12387 <sub>KLC2</sub>	S582			30.2	70.1	R.ASS*LNFLNK.S
FLJ12387 KLC2	\$581 \$610			12.1	49.2 84.7	R.AS"SLNFLNK.S  R.TLSSS"SMDLSR.R
FLJ12387 KLC2	S609S611		=	10.5	35.6	R.TLSS'SS'MDLSR.R
FLJ12387 KLC2	S609S610		Ť	2.4	38.4	R.TLSS*S*SMDLSR.R
	S193S194			68.7	95.0	R.VSALEEDMDDVES*S*EEEEEEDEK.L
FLJ14936 PRPF38A				100.0	22.1	R.S'KS'PGHHR.S
FLJ14936 PRPF38A FLJ14936 PRPF38A			•••	100.0	36.2 83.2	R.VPS*PDHR.R  R.VS*ALEEDMDDVESS*EEEEEEDEKLER.V
FLJ14936 PRPF38A				3.6	11.4	R.VS*ALEEDMDDVES*SEEEEEEDEKLER.V
FLJ14936 PRPF38A				100.0	10.8	R.HRS'KS'PR.R
PRPF38A	\$105\$107\$109			100.0	11.2	R.HRS'HS'KS'PER.S
FLJ14936 PRPF38A  FLJ20105 protein ERCC6L				26.0	20.5	R.RS*PTLR.Y
FLJ20105 protein ERCC6L	\$820 \$946			7.4	97.9	K.GFGS*VEELCTNSSLGMEK.S  K.LEEEPSASS*PQYACDFNLFLEDSADNR.Q
FLJ20105 protein ERCC6L	Y949	7		5.6	79.5	K.LEEEPSASSPQY*ACDFNLFLEDSADNR.Q
FLJ20105 protein ERCC6L	S1028	<del>_</del>		24.1	62.0	R.IVS*DGEDEDDSFKDTSSINPFNTSLFQFSSVK.Q
FLJ20105 protein ERCC6L	S1098			100.0	44.5	R.S'LINMVLDHVEDMEER.L
FLJ20514 GEMIN8 FLJ20514 GEMIN8	T124S126	-		34.9	70.5	K.EEEMET'ES'DAEVECDLSNMEITEELR.Q
FLJ20514 GEMIN8  FLJ20514 GEMIN8	T124S135 S126S135			11.2	62.3 46.7	K.EEEMET*ESDAEVECDLS*NMEITEELR.Q  K.EEEMETES*DAEVECDLS*NMEITEELR.Q
FLJ21924 QSER1	S991S992			0.9	31.3	K.NLEHLSSFS*S*DEDDPGYSQDAYK.S
FLJ36874 protein PATL1	S36			13.8	47.0	R.STS*PIIGSPPVRA
FLJ36874 protein PATL1	T35S36	-		2.7	25.1	R.ST*S*PIIGSPPVR.A
FLJ46354 protein MROH7-	Y1166		-		12.0	K.RAY'SR.K
FLN29 protein TRAFD1  FLN29 protein TRAFD1	\$415 \$327			19.1	38.2 66.4	R.LDSQPQETS*PELPR.R  R.ALPSLNTGSSS*PR.G
FLN29 protein TRAFD1	\$327 \$325	•	• • •	13.9	44.6	R.ALPSLNTGS*SSPR.G
FLN29 protein TRAFD1	T323			6.1	24.0	R.ALPSLNT*GSSSPR.G
FLN29 protein TRAFD1	T414			35.7	12.3	R.LDSQPQET*SPELPR.R
FMRP interacting protein, 82-kD NUFIP2	S652			55.8	57.7	R.NDS*WGSFDLR.A
FMRP interacting protein, 82-kD NUFIP2  FMRP interacting protein, 82-kD NUFIP2	\$629 \$572			26.0	99.2	K.DYEIESQNPLAS*PTNTLLGSAK.E  K.RTS*PQVLGSILK.S
FMRP interacting protein, 82-kD NUFIP2	S572 T571			37.7	47.5 38.6	K.RT'SPQVLGSILK.S
FNBP4	\$497\$506			100.0	32.8	K.IDENS'DKEMEVEES'PEKIK.V
FNBP4FNBP4	Y111	•••		36.4	113.5	K.ATGGLCLLGAY*ADSDDDDDDDVSEK.L
FNBP4 FNBP4	<b>S</b> 114			33.4	102.8	K.ATGGLCLLGAYADS*DDDDDDVSEK.L
FNBP4 FNBP4	S462		•	19.9	35.4	R.ATS*PESTSR.S

Peak Area	0 abundano	ts-Significant char se at 5%FDR o with the minimum	ompared to	the .			
0 3 5	71 86 >100		CarT	RajiB			
>10	Protein Name Gene FNBP4 FNBP4	Phosphosites \$429	9 g g	5 g g	Ascor 12.3	MOWSE 33.2	Sequence RALEEGDGSVSGS*SPR.S
	FNBP4 FNBP4	S961S962S963		•••	14.5	25.7	R.ELDEEDNS*S*S*S*EEDRESTAQKR.I
	FNBP4 FNBP4	T461			27.8	28.3	RAT*SPESTSR.S
	FNBP4 FNBP4	S430		•	7.0	32.7	R.ALEEGDGSVSGSS*PR.S
	Fodrin beta SPTBN1	S2160S2161S2	-		4.3	22.6	R.TS*S*KES*SPIPS*PTSDRK.A
	Fodrin beta SPTBN1	S2165S2169			18.0	38.1	K.ESS*PIPS*PTSDR.K
	Fodrin beta SPTBN1	S2138			78.4	68.3	K.GEQVSQNGLPAEQGS*PR.M
	Fodrin beta SPTBN1	S2341			9.1	69.3	R.AQTLPTSVVTITSESS*PGKR.E
	Fodrin beta SPTBN1	S2358			100.0	32.7	K.RFS*LFGK.K
	Fodrin beta SPTBN1	Y17	i i		5.5	60.5	R.TSSISGPLSPAY*TGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S10	•		16.7	72.6	R.TSSIS*GPLSPAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S8			13.4	89.4	R.TSS*ISGPLSPAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S14	•		7.4	88.3	R.TSSISGPLS*PAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S8Y17	•••		8.0	88.0	R.TSS*ISGPLSPAY*TGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S7S8	•		6.2	150.4	R.TS*S*ISGPLSPAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S7Y17	i.		-0.3	60.1	R.TS*SISGPLSPAY*TGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S2160S2164S2			2.5	19.5	R.TS*SKES*S*PIPS*PTSDRK.A
	Fodrin beta SPTBN1	S8S14			9.9	75.1	R.TSS*ISGPLS*PAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S2319			23.0	19.8	K.DDEEMNTWIQAISSAISSDKHEVSASTQS*TPASSR.A
	Fodrin beta SPTBN1	\$2303T2320			13.6	26.3	K.DDEEMNTWIQAIS*SAISSDKHEVSASTQST*PASSR.A
	Fodrin beta SPTBN1	S2307T2317			9.1	15.4	K.DDEEMNTWIQAISSAIS*SDKHEVSAST*QSTPASSR.A
	Fodrin beta SPTBN1	\$2307\$2319			5.4	14.3	K.DDEEMNTWIQAISSAIS*SDKHEVSASTQS*TPASSR.A
	Fodrin beta SPTBN1	S2319T2320			3.4	13.9	K.DDEEMNTWIQAISSAISSDKHEVSASTQS*T*PASSR.A  K.DDEEMNTWIQAISSAISSDKHEVS*ASTQS*T*PASSR.A
	Fodrin beta SPTBN1	S2314S2319T2			13.2	11.3	K.DDEEMNTWIQAISSAISSDKHEVS*ASTQS*T*PASSK.A
	Fodrin beta SPTBN1	T2317S2319T23	=-		4.6	15.1	R.TSS*KES*S*PIPS*PTSDRK.A
	Fodrin beta SPTBN1	S2161S2164S2 S2338	<u> </u>		8.2	19.3	R.AQTLPTSVVTITS*ESSPGKR.E
	Fodrin beta SPTBN1	S8S10			10.8	115.4	R.TSS*IS*GPLSPAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S8T18	• • •		2.9	45.2	R.TSS*ISGPLSPAYT*GQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	S2314T2320	•		5.0	15.2	K.DDEEMNTWIQAISSAISSDKHEVS*ASTQST*PASSR.A
	Fodrin beta SPTBN1	S2303S2319	=		8.7	22.5	K.DDEEMNTWIQAIS*SAISSDKHEVSASTQS*TPASSR.A
	Fodrin beta SPTBN1	S2316S2319	-		7.5	22.0	K.DDEEMNTWIQAISSAISSDKHEVSAS*TQS*TPASSR.A
	Fodrin beta SPTBN1	\$2304\$2307\$2	•		-1.5	12.4	K.DDEEMNTWIQAISS*AIS*S*DKHEVSASTQSTPASSR.A
			-		10.7	21.1	K.DDEEMNTWIQAIS*SAISSDKHEVSASTQS*T*PASSR.A
	Fodrin beta SPTBN1	T2317T2320			11.9	13.1	K.DDEEMNTWIQAISSAISSDKHEVSAST*QST*PASSR.A
	Fodrin beta SPTBN1	S2164S2165			31.0	19.9	K.ES*S*PIPSPTSDRK.A
	Fodrin beta SPTBN1	T2159S2160S2			8.8	13.4	R.T"S"S"KESSPIPS"PTSDRK.A
	Fodrin beta SPTBN1	S2316T2320			9.5	12.8	K.DDEEMNTWIQAISSAISSDKHEVSAS*TQST*PASSR.A
	Fodrin beta SPTBN1	S2303T2317			-1.1	13.2	K.DDEEMNTWIQAIS*SAISSDKHEVSAST*QSTPASSR.A
	Fodrin beta SPTBN1	\$2303\$2314			-0.1	11.3	K.DDEEMNTWIQAIS*SAISSDKHEVS*ASTQSTPASSR.A
	Fodrin beta SPTBN1	S2304T2320			7.5	19.2	K.DDEEMNTWIQAISS*AISSDKHEVSASTQST*PASSR.A
	Fodrin beta SPTBN1	S2160S2161S2			4.5	23.8	R.TS*S*KESS*PIPS*PTSDRK.A
	Fodrin beta SPTBN1	S2102			49.2	46.2	R.RPPS*PEPSTK.V
	Fodrin beta SPTBN1	S2340			11.1	54.2	R.AQTLPTSVVTITSES*SPGKR.E
	Fodrin beta SPTBN1	<b>S</b> 7			2.5	88.0	R.TS*SISGPLSPAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	T2297	••			12.8	K.DDEEMNT*WIQAISSAISSDKHEVSASTQSTPASSR.A
	Fodrin beta SPTBN1	S2160S2161S2			9.1	11.7	R.TS*S*KESSPIPS*PTSDRK.A
	Fodrin beta SPTBN1	T2328S2340			15.6	42.9	R.AQT*LPTSVVTITSES*SPGKR.E
	Fodrin beta SPTBN1	T2320	•		6.8	36.8	K.DDEEMNTWIQAISSAISSDKHEVSASTQST*PASSR.A
	Fodrin beta SPTBN1	Y17T18	••		3.5	12.4	R.TSSISGPLSPAY*T*GQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	T2328S2341			18.2	11.3	R.AQT"LPTSVVTITSESS"PGKR.E
	Fodrin beta SPTBN1	T2328	•		56.8	83.8	R.AQT*LPTSVVTITSESSPGKR.E
	Fodrin beta SPTBN1	S7S14			0.7	106.7	R.TS*SISGPLS*PAYTGQVPYNYNQLEGR.F
	Fodrin beta SPTBN1	T2317			7.3	23.1	K.DDEEMNTWIQAISSAISSDKHEVSAST*QSTPASSR.A
	Fodrin beta SPTBN1	S2164S2169			16.7	15.7	K.ES*SPIPS*PTSDRK.A
	Forkhead box J3 FOXJ3	S223			10.9	29.8	K.VTLYNTDQDGSDS*PR.S
	Forkhead box K1 FOXK1	T436S441	<b></b>	•	32.4	36.4	R.SGGLQT*PECLS*R.E
-	Forkhead box K1 FOXK1	<b>S</b> 445	•		95.6	47.3	R.EGS*PIPHDPEFGSK.L
	Forkhead box K1 FOXK1	\$416\$420\$428		<u></u>	20.8	53.2	R.S*APAS*PTHPGLMS*PR.S
	Forkhead box K1 FOXK1	S213S223			43.0	25.8	K.EEAPAS*PLRPLYPQIS*PLK.I
ı		\$213\$223 \$299	<b></b>		43.0 6.7	25.8 41.2	K.EEAPAS*PLRPLYPQIS*PLK.I  K.AASEQQADTSGGDS*PKDESKPPFSYAQLIVQAISSAQE

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>10 >100 Protein Name Gene	Phosphosites	CarT	RajiB E E E	Ascor	MOWSE	Sequence
Forkhead box K1 FOXK1	\$416\$420T422		.■.	14.0	27.9	R.S*APAS*PT*HPGLMSPR.S
Forkhead box K1 FOXK1	\$416\$420	<u> </u>		47.3	45.0	R.S*APAS*PTHPGLMSPR.S
Forkhead box K1 FOXK1  Forkhead box K1 FOXK1	Y219S223 S295S299			39.4 5.7	18.4 51.0	K.EEAPASPLRPLY*PQIS*PLK.I  K.AASEQQADTS*GGDS*PKDESKPPFSYAQLIVQAISSAQDR.Q
Forkhead box K1 FOXK1	T294S299			7.3	55.4	K.AASEQQADT*SGGDS*PKDESKPPFSYAQLIVQAISSAQDR.Q
Forkhead box K1 FOXK1	\$309 <b>Y</b> 310			9.6	51.8	K.AASEQQADTSGGDSPKDESKPPFS*Y*AQLIVQAISSAQDR.Q
Forkhead box K1 FOXK1	<b>S</b> 213	<del></del>		14.0	27.6	K.EEAPAS*PLRPLYPQISPLK.I
Forkhead box K1 FOXK1	S441			11.1	18.0	R.SGGLQTPECLS*R.E
Forkhead box K1 FOXK1	S416T422		-	17.3	33.1	R.S*APASPT*HPGLMSPR.S
Forkhead box K1 FOXK1  Forkhead box K2 FOXK2	\$420T422\$428		■.■	7.4	30.1	R.SAPAS*PT*HPGLMS*PR.S
Forkhead box K2 <sub>FOXK2</sub>	\$398 \$424\$431			100.0	49.9 65.1	R.EGS*PAPLEPEPGAAQPK.L  R.FAQS*APGSPLS*SQPVLITVQR.Q
Forkhead box K2 FOXK2	S428S431			9.1	38.2	R.FAQSAPGS*PLS*SQPVLITVQR.Q
Forkhead box K2 <sub>FOXK2</sub>	<b>S</b> 428			20.9	45.3	R.FAQSAPGS*PLSSQPVLITVQR.Q
Forkhead box K2 FOXK2	\$424\$428	ij		22.0	39.0	R.FAQS*APGS*PLSSQPVLITVQR.Q
Forkhead box P4FOXP4	<b>S</b> 443			-0.3	45.0	R.SS*DKFCSPISSELAQNHEFYK.N
Forkhead box protein O3A ZNF286B	S7S12	4		18.1	13.8	MAEAPAS*PAPLS*PLEVELDPEFEPQSRPR.S
Formin binding protein 1 FNBP1	<b>S</b> 497	• • •		19.2	61.8	R.RQS*GLYDSQNPPTVNNCAQDR.E
Formin binding protein 1 <sub>FNBP1</sub> Formin binding protein 1 <sub>FNBP1</sub>	T507			-1.4	17.0	R.RQSGLYDSQNPPT*VNNCAQDRESPDGSYTEEQSQESEMK.V  R.RQSGLYDSQNPPTVNNCAQDRESPDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1	\$521 \$497T507			10.0	22.1	R.RQS*GLYDSQNPPT*VNNCAQDRESPDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1	S497Y500			12.9	28.8	R.RQS*GLY*DSQNPPTVNNCAQDRESPDGSYTEEQSQESEMK.V
Formin binding protein 1 FNBP1	S296S299			19.0	40.6	R.TVS*DNS*LSNSR.G
Formin binding protein 1 FNBP1	S296			25.3	63.3	R.TVS*DNSLSNSR.G
Formin binding protein 1 FNBP1	T294			9.8	27.9	R.T*VSDNSLSNSR.G
Formin binding protein 1 FNBP1	S517S521			14.6	95.3	R.ES*PDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1	T507S521			5.3	18.6	R.RQSGLYDSQNPPT*VNNCAQDRESPDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1	S497Y522	<b>L</b>		13.6	21.9	R.RQS*GLYDSQNPPTVNNCAQDRESPDGSY*TEEQSQESEMK.V  R.RQS*GLYDSQNPPTVNNCAQDRESPDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1  Formin binding protein 1 FNBP1	\$497\$521 \$497\$517\$521			13.0	23.3	R.RQS*GLYDSQNPPTVNNCAQDRESPDGS*YTEEQSQESEMK.V  R.RQS*GLYDSQNPPTVNNCAQDRES*PDGS*YTEEQSQESEMK.V
Formin binding protein 1 FNBP1	T507S517			9.1 5.4	42.2	R.QSGLYDSQNPPT*VNNCAQDRES*PDGSYTEEQSQESEMK.V
Formin binding protein 1 FNBP1	T294S296			20.9	34.0	R.T*VS*DNSLSNSR.G
Formin binding protein 1 FNBP1	T294S299			20.1	29.8	R.T"VSDNS"LSNSR.G
Formin binding protein 1 FNBP1	Y500			5.6	31.8	R.RQSGLY*DSQNPPTVNNCAQDR.E
FMNL1	S184			67.8	48.9	K.NKPLEQS*VEDLSK.G
Formin like FMNL1	S624			100.0	56.2	R.RDS*ELGPGVK.A
Formin like 2 <sub>FMNL3</sub> Formin like 3 <sub>FMNL3</sub>	T622			100.0	22.2	K.KPIKT*K.F  R.S*IEDLQPPSALSAPFTNSLAR.S
Formin like 3FMNL3	\$174 \$182		===	38.8	24.0	R.SIEDLQPPS*ALSAPFTNSLAR.S
Formin-like protein 1 FMNL1	S681		•	48.8	85.8	R.RPPGPPLQVTSDLS*L
Formin-like protein 1 FMNL1	T677			2.2	27.8	R.RRPPGPPLQVT*SDLSL
Forty-two-three domain containing 1 FYTTD1	S23	•		78.7	84.0	R.S*NENLDKIDMSLDDIIK.L
FRAS1-related extracellular matrix protein 3 FREM3	Y1044			-0.3	19.6	K.DSY*QWVVGNSIIEK.V
WAPL	S264S269	<u></u>		22.3	34.3	K.RPES*PSEIS*PIKGSVR.T
Friend of EBNA2 WAPL	S120			36.0	82.3	K.VEEESTGDPFGFDS*DDESLPVSSK.N
Friend of EBNA2 WAPL Friend of EBNA2 WAPL	\$502\$504			54.6	79.8	K.IKYFGFDDLS'ES'EDDEDDDCQVER.K  K.VEEES'TGDPFGFDSDDESLPVSSK.N
Friend of EBNA2 WAPL	\$111 \$266\$269			13.1	19.8	K.PESPS'EIS'PIKGSVR.T
Friend of EBNA2 WAPL	S264S266			3.0	47.8	K.RPES*PS*EISPIKGSVR.T
FtsJ homolog 3 <sub>FTSJ3</sub>	\$335\$336		•	40.2	155.7	K.ALDISLS*S*GEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 <sub>FTSJ3</sub>	T467S468S471			13.2	55.1	R.DDIYVSDVEDDGDDT*S*LDS*DLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub>	\$458T467\$468			24.4	94.1	R.DDIYVS*DVEDDGDDT*S*LDS*DLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub>	Y456S458T467		•	11.6	85.1	R.DDIY*VS*DVEDDGDDT*SLDS*DLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub>	\$458T467\$471			2.2	64.3	R.DDIYVS*DVEDDGDDT*SLDS*DLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub> FtsJ homolog 3 <sub>FTSJ3</sub>	\$458T467\$468			6.6	35.3	R.DDIYVS*DVEDDGDDT*S*LDSDLDPEELAGVR.G  R.GHOLLEEVT*QGDMSAADTFLS*DLPR.D
FtsJ homolog 3 <sub>FTSJ3</sub> FtsJ homolog 3 <sub>FTSJ3</sub>	T436S448 S441S448			9.1	64.0 45.4	R.GHQLLEEVT*QGDMSAADTFLS*DLPR.D  R.GHQLLEEVTQGDMS*AADTFLS*DLPR.D
FtsJ homolog 3 <sub>FTSJ3</sub>	\$333\$335\$336			44.1	67.7	K.ALDIS'LS'S'GEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 <sub>FTSJ3</sub>	Y456S458S468			4.4	74.7	R.DDIY*VS*DVEDDGDDTS*LDS*DLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub>	\$333\$335			25.1	52.9	K.ALDIS*LS*SGEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 <sub>FTSJ3</sub>	Y456S458T467		<del>-</del>	11.1	58.3	R.DDIY*VS*DVEDDGDDT*S*LDSDLDPEELAGVR.G
FtsJ homolog 3 <sub>FTSJ3</sub>	\$335\$336\$347	-		7.5	33.3	K.ALDISLS*S*GEEDEGDEEDS*TAGTTK.Q

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3 5 >10	>100		CarT	RajiB			
- 10	Protein Name Gene FUS FUS	Phosphosites \$277	9 m m	5 F B	Ascor 51.8	MOWSE 77.6	Sequence R.HDS*EQDNSDNNTIFVQGLGENVTIESVADYFK.Q
FUS i	nteracting protein 1 SRSF10	T255S256			5.3	16.2	R.SWT*S*PK.S
FUS i	nteracting protein 1 SRSF10	S133		•	28.6	27.8	R.S*FDYNYRR.S
FUS i	nteracting protein 1 SRSF10	S131S133			44.5	38.7	R.S*RS*FDYNYR.R
FUS i	nteracting protein 1 SRSF10	S156S158			24.4	18.1	R.S'RS"HSDNDRPNCSWNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S158			30.0	66.3	R.S*HSDNDRPNCSWNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S158S160			36.2	80.5	R.S*HS*DNDRPNCSWNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	\$156\$158\$160	•••	•	60.5	49.3	R.S*RS*HS*DNDRPNCSWNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S171S173		•••	100.0	12.2	R.NRS*FS*R.S
FUS i	nteracting protein 1 SRSF10	S158S160			100.0	22.1	R.S*HS*DNDRFK.H
FUS i	nteracting protein 1 SRSF10	\$253\$256			16.7	19.9	R.S'WTS'PK.S
FUS i	nteracting protein 1 SRSF10	S168			9.0	26.7	R.SHSDNDRPNCS*WNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S156S158T171			14.5	32.4	R.S*RS*HSDNDRPNCSWNT*QYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S160S168T171	<u> </u>		9.4	24.4	R.SRSHS*DNDRPNCS*WNT*QYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S156S168		ļ.	9.7	41.8	R.S*RSHSDNDRPNCS*WNTQYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S156T171			3.4	27.9	R.S*RSHSDNDRPNCSWNT*QYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	S160			1.4	40.9	R.SHS*DNDRPNCSWNTQYSSAYYTSR.K
	nteracting protein 1 SRSF10	S156S158S160			100.0	17.6	R.S*RS*HS*DNDRFK.H
FUSI	nteracting protein 1 SRSF10	S251S253T255			2.7	11.1	R.S'RS'WT'SPK.S
FUSi	nteracting protein 1 SRSF10	S156S158S168			19.2	29.2	R.S'RS'HSDNDRPNCS'WNTQYSSAYYTSR.K
	nteracting protein 1 CCNL2	S121S123	<u> </u>		10.2	11.2	R.S*RS*YER.T
	nteracting protein 1 SRSF10	<b>S</b> 256	•••		22.5	16.5	R.SWTS*PK.S
FUS i	nteracting protein 1 SRSF10	\$156\$160\$168			7.3	22.9	R.S*RSHS*DNDRPNCS*WNTQYSSAYYTSR.K
	nteracting protein 1 SRSF10	Y136		•	1.9	19.4	R.SFDY*NYRR.S
	nteracting protein 1 SRSF10	S156S168T171			-3.3	41.7	R.S*RSHSDNDRPNCS*WNT*QYSSAYYTSR.K
FUS i	nteracting protein 1 SRSF10	\$160\$168		-	-0.2	20.5	R.SHS*DNDRPNCS*WNTQYSSAYYTSR.K
	FXR1 FXR1	<b>S</b> 409			15.7	32.5	R.RGPNYTSGYGTNSELSNPS*ETESER.K
	FXR1 FXR1	\$406\$409			11.0	14.7	R.RGPNYTSGYGTNSELS'NPS'ETESER.K
	FXR2 FXR2	S601S603			18.7	56.4	R.TDGS*IS*GDRQPVTVADYISR.A
	FXR2 FXR2	S601		·	7.5	25.1	R.TDGS*ISGDRQPVTVADYISR.A
	FYB FYB1	T443			-1.2	39.7	K.SPVNEDNQDGVT*HSDGAGNLDEEQDSEGETYEDIEASK.E
	FYB FYB1	\$432				76.2	K.S*PVNEDNQDGVTHSDGAGNLDEEQDSEGETYEDIEASK.E
	FYB FYB1	\$457			10.8	30.0	K.SPVNEDNQDGVTHSDGAGNLDEEQDS*EGETYEDIEASK.E
G note:	Fyn YES1	Y420			12.1	38.5	R.LIEDNEY*TAR.Q  K.DHS*DS*DDQMLVAK.R
	Iomain containing 2 GPATCH2				100.0	54.0	R.S*QSPHYFR.S
	Iomain containing 8 GPATCH8				14.0	22.8	R.SQS*PHYFR.S
	ergic receptor P2Y8 P2RY8	\$1035 \$324			10.4	30.9	R.RES*LFSAR.T
	ergic receptor P2Y8 P2RY8	\$324 \$324\$327			39.9	44.6	R.RES*LFS*AR.T
	ergic receptor P2Y8 P2RY8	\$324\$327 \$335	•••		100.0 45.6	16.1	R.S*EAGAHPEGMEGATRPGLQR.Q
	ed receptor kinase 6 GRK6	\$484			13.9	50.4	K.DVLDIEQFS*TVK.G
	ed receptor kinase 6 GRK6	S484T485			36.4	46.3	K.DVLDIEQFS*T*VKGVELEPTDQDFYQK.F
	nt receptor kinase 2 <sub>GRK2</sub>	\$670		•	71.9	50.3	R.S*PVVELSK.V
	nalling modulator 3 GPSM3	S59		_	8.1	57.1	R.SASLLS*LQTELLLDLVAEAQSR.R
	nalling modulator 3 GPSM3	S54			10.1	51.7	R.S*ASLLSLQTELLLDLVAEAQSR.R
	nalling modulator 3 GPSM3	S54S59	•	•	12.3	68.9	R.S*ASLLS*LQTELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	S54S56			24.8	31.5	R.S'AS'LLSLQTELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	S54T62		<del></del>	7.2	84.5	R.S*ASLLSLQT*ELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	T62			8.3	73.7	R.SASLLSLQT*ELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	S59T62			6.7	69.4	R.SASLLS*LQT*ELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	S56S59			4.6	64.5	R.SAS*LLS*LQTELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	S56T62			9.1	76.6	R.SAS*LLSLQT*ELLLDLVAEAQSR.R
G protein sig	nalling modulator 3 GPSM3	<b>S</b> 56			-0.1	26.7	R.SAS*LLSLQTELLLDLVAEAQSR.R
G-protein sig	nalling modulator 1 GPSM1	<b>S</b> 469			23.9	84.4	R.APS'SDEECFFDLLTK.F
G-protein sig	nalling modulator 1 GPSM1	<b>S</b> 470			10.2	44.0	R.APSS*DEECFFDLLTK.F
	Ga55 TACC1	S276			9.2	80.4	K.ASYHFSPEELDENTS*PLLGDAR.F
	Gamma synergin SYNRG	\$854\$855			15.5	33.3	K.HVMSDS*S*LDLPTVSGQHPPAADIEDLK.Y
	Gamma synergin SYNRG	\$852\$854			19.0	21.1	K.HVMS*DS*SLDLPTVSGQHPPAADIEDLK.Y
	Gamma synergin SYNRG	S752			12.4	13.6	R.QLS*LEGSGLGVEDLKDNTPSGK.S
	Gamma synergin SYNRG	S935			12.1	56.3	K.ETSFGS*SENITMTSLSK.V
	Gamma synergin SYNRG	\$852\$855			14.7	41.6	K.HVMS*DSS*LDLPTVSGQHPPAADIEDLK.Y
	Gamma synergin SYNRG	S1075		• •	10.6	12.8	R.SLS'LGDK.E

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-3 42 PSM 0 71	1	CarT	RajiB			
>100 >10 Protein Name Gen	e Phosphosites	5 m m	5 m g	Ascor	MOWSE	Sequence
Gamma synergin SYNi			<b></b>	46.8	86.9	K.S'LDLPSIGGSSVGK.E  RLRVS'LGTR.G
Gamma-tubulin complex component 3 <sub>TUB0</sub>				11.9	76.0	R.STS*EGAWPQLPSGLSMMR.C
Gasdermin domain containing 1 GSD				-0.3	75.6	R.ST*SEGAWPQLPSGLSMMR.C
GATA binding protein 3 <sub>GAT</sub>	A3 \$110\$115			13.0	35.9	KALGSHHTAS*PWNLS*PFSK.T
GATA binding protein 3 <sub>GAT</sub>				11.2	18.2	K.ALGS*HHTASPWNLS*PFSK.T
GATA zinc finger domain containing 2B GAT			•	5.0	47.1	R.GRLT*PSPDIIVLSDNEASS*PR.S
GATA zinc finger domain containing 2E <sub>GAT</sub> ,  GATA zinc finger domain containing 2E <sub>GAT</sub> ,		==		67.5	38.9	R.GRLT*PS*PDIIVLS*DNEASS*PR.S  R.GRLT*PS*PDIIVLSDNEASS*PR.S
GATA zinc finger domain containing 28 GATA				50.0	30.2	R.GRLT'PS'PDIIVLS'DNEAS'SPR.S
GATA zinc finger domain containing 2B GATA	AD2B T120S122S134			37.1	10.7	R.GRLT*PS*PDIIVLSDNEAS*SPR.S
GCF GCF				60.6	82.7	R.NEET*S*EES*QEDEKQDTWEQQQMR.K
GCF GCF				10.2	65.9	R.VLSGNCNHQEGTS*S*DDELPSAEMIDFQK.S
GCF GCF		-		0.8	12.2	R.VLS*GNCNHQEGT*SSDDELPSAEMIDFQK.S  R.VLSGNCNHQEGT*SS*DDELPSAEMIDFQK.S
GCF GCF			•	27.0	26.0	R.AADS'S'DS'DGAEESPAEPGAPR.E
GEM interacting protein GMIF				11.3	15.5	R.SLDS*PTS*SPGAGTR.Q
GEM interacting protein GMIF	S19		•	20.1	25.6	R.KRYS*DIFR.S
GEM interacting protein GMIF			<b>.</b>	12.6	65.2	R.SLDS*PTSS*PGAGTR.Q
GEM interacting protein GMIF				12.6	46.4	R.SLDSPT*SS*PGAGTR.Q
GEM interacting protein GMIF  Gemin 5 GEM				14.9	31.0	R.KRY*SDIFR.S  K.ENSGPVENGVS*DQEGEEQAR.E
General transcription factor 2 I GTF			<b></b>	12.2	108.0	R.S'PGSNSKVPEIEVTVEGPNNNNPQTSAVR.T
General transcription factor 21 GTF	2I <b>S</b> 679			2.8	65.1	R.SPGSNS*KVPEIEVTVEGPNNNNPQTSAVR.T
General transcription factor 2 I GTF2	2I <b>S</b> 818				33.4	K.ES*TSSKSPPR.K
General transcription factor 2 I GTF2			₽.	17.4	42.0	K.INS*SPNVNTTASGVEDLNIIQVTIPDDDNER.L
General transcription factor 21 <sub>GTF</sub>				8.7	80.2	R.SPGS*NSKVPEIEVTVEGPNNNNPQTSAVR.T  K.ESTSSKS*PPR.K
General transcription factor 2 I GTF:				22.8	50.8 67.7	R.KINSS*PNYNTTASGVEDLNIIQVTIPDDDNER.L
General transcription factor IIA, 1, 19/37kDa GTF				16.1	80.2	K.DGAEDGQVEEEPLNS*EDDVS*DEEGQELFDTENVVVCQYDK.I
General transcription factor IIIC, GTF;	3C2 <u>\$</u> 892			27.8	56.0	R.AHFNAMFQPS*SPTR.R
General transcription factor IIIC, GTFS	3C2 <u>\$</u> 893			21.2	55.9	R.AHFNAMFQPSS*PTR.R
General transcription factor IIIC, GTFS polypeptide 2. beta 110kDa				32.1	28.7	K.DLDRPESQS*PK.R
General transcription factor IIIC, GTF; polypeptide 2, beta 110kDa			_	7.0	14.4	K.VSS*PTKPK.K
GFAT GFP				17.0	92.6	R.S'SPSLSDSYSHLSGRPIR.K
	C88A S1491T1509		•	8.1	51.4	R.SMS*MNDLVQSMVLAGQWTGST*ENLEVPDDISTGKR.R
- Girdin <sub>CCD</sub>	C88A S1491T1506			15.2	38.7	R.SMS*MNDLVQSMVLAGQWT*GSTENLEVPDDISTGKR.R
- Girdin CCD	C88A \$1489\$1491			3.2	20.3	R.S'MS'MNDLVQSMVLAGQWTGSTENLEVPDDISTGK.R
	C88A \$1491\$1508			4.6	42.6	R.SMS*MNDLVQSMVLAGQWTGS*TENLEVPDDISTGKR.R
GIT1 GIT1	\$385\$388	-		13.4	94.5	R.SQSDLDDQHDYDS*VAS*DEDTDQEPLR.S
GIT1 <sub>GIT1</sub>	\$362 \$361			30.2	93.9	K.SLSS*PTDNLELSLR.S  K.SLS*SPTDNLELSLR.S
GIT1 GIT1	S414			5.8	63.0	R.SMDSS*DLSDGAVTLQEYLELKK.A
GIT1 GIT1	Y383S385			14.7	26.4	R.SQSDLDDQHDY*DS*VASDEDTDQEPLR.S
GIT1 GIT1	<b>S</b> 410		<u>:</u>	37.7	81.5	R.S*MDSSDLSDGAVTLQEYLELKK.A
GIT1 GIT1	<b>S</b> 592	<u> </u>		7.4	13.4	R.HGS*GADSDYENTQSGDPLLGLEGK.R
GIT1 GIT1	\$592\$596	•••		38.4	55.3	R.HGS*GADS*DYENTQSGDPLLGLEGK.R
GIT1 <sub>GIT1</sub>	Y383S388 S413			27.5	92.3 76.0	R.SQSDLDDQHDY*DSVAS*DEDTDQEPLR.S  R.SMDS*SDLSDGAVTLQEYLELK.K
GIT1 GIT1	\$413 \$417		-	-0.3	31.7	R.SMDSSDLS*DGAVTLQEYLELK.A
GL004 protein MFF	S157			35.1	34.6	R.SMS*ENAVR.Q
GL004 protein MFF	S155			9.2	28.3	R.S*MSENAVR.Q
Glucocorticoid induced transcript 1 GLC				7.4	32.9	R.GS*QHSPTRPPVAAAAASLGSLPGPGAAR.G
Glucocorticoid induced transcript 1 GLC	****			3.2	31.8	R.TSSLDTIT*GPYLTGQWPR.D
Glucocorticoid induced transcript 1 GLC				59.9	45.0	K.DRQS*PLHGNHITISHTQATGSR.S  R.TSSLDT*ITGPYLTGQWPR.D
Glucocorticoid induced transcript 1 GLC				41.2	45.9 62.4	R.TSSLDT*ITGPYLTGQWPR.D  R.SAS*WGSADQLK.E
Glucocorticoid induced transcript 1 GLC			• •	3.5	41.8	R.GSQHS*PTRPPVAAAAASLGSLPGPGAAR.G
Glucocorticoid induced transcript 1 GLC	CI1 S171			-0.4	61.2	R.TS*SLDTITGPYLTGQWPR.D
Glucocorticoid induced transcript 1 GLC		Ė		-0.4	57.5	R.TSS*LDTITGPYLTGQWPR.D
Glucocorticoid receptor DNA binding factor ARHO	GAP3 S1150	-		46.9	53.5	R.KVS*IVSKPVLYR.T

Peak Area %	abundani		compared to	the			
.5 29 .3 42 0 71		with the minimum					
3 86 5 >100				_RajiB_			
Pr Glucocorticoid receptor DNA bi	rotein Name Gene	Phosphosites	% # #	F # E	Ascor 32.3	MOWSE 54.4	Sequence R.TSFSVGS*DDELGPIR.K
Glucocorticoid receptor DNA bi	1		==		1.2	30.9	R.AGS*PLCNSNLQDSEEDIEPSYSLFR.E
Glucocorticoid receptor DNA bi	1				19.1	61.0	R.AGSPLCNS*NLQDS*EEDIEPSYSLFR.E
Glucocorticoid receptor DNA bi	1				18.0	78.7	K.S*VSSSPWLPQDGFDPSDYAEPMDAVVKPR.N
Glucocorticoid receptor DNA bi	1				60.6	86.6	K.NIIEATHMYDNAAEACSTTEEVFNS*PR.A
Glucocorticoid receptor DNA bi	1			• •	37.3	64.4	R.AGS*PLCNSNLQDS*EEDIEPSYSLFR.E
Glutamate-rich WD repea	at-containing GRWD1				63.6	73.0	R.MHNLHGTKPPPS*EGS*DEEEEEEDEEDEER.K
Glutamate-rich WD repea	protein 1	T114S122			10.8	64.2	R.MHNLHGT*KPPPSEGS*DEEEEEEDEEDEER.K
Glutamate-rich WD repea	protein 1	T114S119			13.5	74.5	R.MHNLHGT*KPPPS*EGSDEEEEEEDEEDEER.K
	cAD	S1859	-		100.0	49.9	R.AS*DPGLPAEEPK.E
Slutamine dependent carbamoy	yl phosphate CAD	S1406			36.8	13.4	R.RLS*SFVTK.G
GlutaminetRNA ligase	synthase e (Fragment) QARS	T47			100.0	22.5	R.GLT*LAQGGVK.W
Glutamine-fructose-	6-phosphate GFPT2	Y479S494			3.6	12.7	K.AY*TSQFISLVM#FGLM#M#S*EDR.I
tra	nsaminase 2 ich protein 1 QRICH1	T347			2.3	19.9	R.GDPQQQSITHIAIPQEAYNAVHVSGSPT*ALAAVK.L
	ich protein 1 QRICH1	S343	=		-0.5	15.2	R.GDPQQQSITHIAIPQEAYNAVHVS*GSPTALAAVK.L
Glutamyl-prolyl-tRN/		S885	-		16.1	45.6	K.EYIPGQPPLSQSSDS*SPTR.N
Glutamyl-prolyl-tRN/		S883			8.9	36.8	K.EYIPGQPPLSQSS*DSSPTR.N
Glutamyl-prolyl-tRN/		\$882\$885			13.6	31.4	K.EYIPGQPPLSQS'SDS'SPTR.N
Glutamyl-prolyl-tRN/		\$882\$885 \$882			13.6	33.4	K.EYIPGQPPLSQS'SDSSPTR.N
Glutamyl-prolyl-tRN/		\$883\$886		_		11.6	K.EYIPGQPPLSQSS*DSS*PTR.N
Glutamyl-prolyl-tRN/		\$883\$886 \$882\$886			9.9	23.4	K.EYIPGQPPLSQS'SDSS'PTR.N
Glutamyl-prolyl-tRN/		\$882\$886 \$886			15.3	11.9	K.EYIPGQPPLSQSSDSS*PTR.N
Glutamyl-prolyl-tRN/		\$886 \$880\$885			7.0	14.0	K.EYIPGQPPLS'QSSDS'SPTR.N
	3 phosphate GAPDH				7.3		R.GALQNIIPAS'TGAAKA
del	3 phosphate GAPDH	S210 T75			8.9	26.3	K.LVINGNPIT*IFQERDPSK.I
del	3 phosphate GAPDH		•		-4.2		K.VIHDNFGIVEGLMTTVHAIT*ATQK.T
del	3 phosphate GAPDH	T182			17.0	66.3	
del Glycogen phosphorylas	nydrogenase	S83			-3.3	27.0	K.LVINGNPITIFQERDPS*K.I  R.KOIS*VR.G
Glycogen synthase kii		S15			100.0	31.9	R.TSS*FAEPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Glycogen synthase kii		S21			22.2	104.0	R.TS*SFAEPGGGGGGGGGGGGGGGGGGGGGGA
Glycogen synthase kii		S20			-0.4	94.4	R.TS*SFAEPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
		Y216			16.9	43.5	
Glycogen synthase k		<b>S</b> 9			8.7	53.4	R.TTS*FAESCKPVQQPSAFGSMK.V
Golgi autoantigen, golgin si					11.7	93.5	R.TSS*FTEQLDEGTPNRE
Golgi autoantigen, golgin sı		S71			55.8	57.2	R.VPS*VESLFR.S
Golgi autoantigen, golgin si					-0.5	49.8	R.TS*SFTEQLDEGTPNR.E
Golgi autoantigen, golgin si					22.4	46.4	R.LDLDSSTASFDPPS*DMDS*EAEDLVGNSDSLNK.E
Golgi reassembly stacking prot					6.6	15.6	R.VGDSTPVSEKPVSAAVDAN <mark>AS*</mark> ESP
Golgi reassembly stacking prot			-		17.5	37.4	R.VGDSTPVSEKPVSAAVDANASES*P
Golgi specific brefeldin A resis	1	S1298			61.7	79.3	R.ADAPDAGAQS*DSELPSYHQNDVSLDR.G
Golgi specific brefeldin A resis	1	T1337			19.9	98.2	R.SAT*DADVVNSGWLVVGK.D
Golgi specific brefeldin A resis	1	T1317				20.9	R.GYT*SDSEVYTDHGRPGK.I
Golgi specific brefeldin A resis	1	S1318	•		17.7	24.6	R.GYTS*DSEVYTDHGRPGK.I
Golgi specific brefeldin A resis	1	S1320			8.3	19.9	R.GYTSDS*EVYTDHGRPGK.I
Golgi specific brefeldin A resis	1	S1475			25.8	40.1	R.GGQS*DDDEDEGVPASYHTVSLQVSQDLLDLMHTLHTR.A
Golgi specific brefeldin A resis	1	\$349\$352	-		14.4	41.8	K.SQSAS*VES*IPEVLEECTSPADHSDSASVHDMDYVNPR.G
Golgi specific brefeldin A resis	1	\$347 <b>\$</b> 352			12.8	13.4	K.SQS*ASVES*IPEVLEECTSPADHSDSASVHDMDYVNPR.G
	Golgin 84 GOLGA5				134.5	111.8	K.S*EPDDELLFDFLNSSQK.E
GRAM domain	containing 2 GRAMD2/	A \$248		·	100.0	12.2	R.KPPMS*EK.S
	Grb2 GRB2	T159				15.4	R.DIEQVPQQPT*YVQALFDFDPQEDGELGFR.R
GRB2 associated bind		S173			8.5	22.5	R.S*ESELLFLPDYLVLSNCETGR.L
GRB2 associated bind		S175	<b>!</b> •		-0.3	12.3	R.SES*ELLFLPDYLVLSNCETGR.L
GRB2 associated bind		Y183			2.1	15.9	R.SESELLFLPDY*LVLSNCETGR.L
GRB2 associated bind		T191			-3.2	13.7	R.SESELLFLPDYLVLSNCET*GR.L
	Grb4 <sub>NCK2</sub>	Y110	• •		100.0	64.1	R.IY*DLNIPAFVK.F
	GRID GRAP2	Y222			100.0	26.0	R.Y*LQHHHFHQER.R
	GRID GRAP2	T262	-		100.0	54.5	R.RHT*DPVQLQAAGR.V
	GRID GRAP2	S164			59.7	47.8	R.S*QGGPHLSGAVGEEIRPSMNR.K
	GRID GRAP2	S187Y207			7.8	30.9	R.KLS'DHPPTLPLQQHQHQPQPPQY"APAPQQLQQPPQQR.Y
	GRID GRAP2	<b>S</b> 187			15.9	44.4	R.KLS*DHPPTLPLQQHQHQPQPPQYAPAPQQLQQPPQQR.Y
	GRID GRAP2	S236	•		90.3	97.6	R.GGS*LDINDGHCGTGLGSEMNAALMHR.R
	GRID GRAP2	<b>S</b> 159	•		100.0	27.7	R.GNS*LDRR.S
	GRID GRAP2	S181	-		19.9	26.7	R.SQGGPHLSGAVGEEIRPS*MNR.K

Peak Area	0 abundanc		ompared to	the			
-5	timepoint PSM	with the minimum					
>10	>100 Protein Name Gene	Phosphosites	CarT	RajiB E E E	Accor	MOWSE	Sequence
	GRID GRAP2	Y207		0 (4 2)	-0.3	18.5	R.KLSDHPPTLPLQQHQHQPQPPQY*APAPQQLQQPPQQR.Y
	GRID GRAP2	T192Y207	-		2.9	14.0	R.KLSDHPPT*LPLQQHQHQPQPPQY*APAPQQLQQPPQQR.Y
GDINI 14 downstroa	GRID GRAP2	\$187T192	_			11.1	R.KLS*DHPPT*LPLQQHQHQPQPPQYAPAPQQLQQPPQQR.Y  R.VSS*QAEDTSSSFDNLFIDR.L
	m protein Gdown1 GCOM1	\$179 \$178	-		30.1	110.2 54.6	R.VS*SQAEDTSSSFDNLFIDR.L
	m protein Gdown1 GCOM1	\$364\$365	=		100.0	32.1	R.DEDDDWS*S*DEF
GRIP1 as	sociated protein 1 GRIPAP1	<b>S</b> 691			17.7	56.5	R.SLSS*SPQAQPPRPAELSDEEVAELFQR.L
GRIP1 as	sociated protein 1 GRIPAP1	<b>S</b> 655			15.8	45.3	R.SGLEELVLSEMNS*PSR.T
GRIP1 as	sociated protein 1 GRIPAP1	S688S691			17.4	55.8	R.S*LSS*SPQAQPPRPAELSDEEVAELFQR.L
	sociated protein 1 GRIPAP1				13.6	56.5	R.SLS*SS*PQAQPPRPAELSDEEVAELFQR.L
	sociated protein 1 GRIPAP1		<b></b>		5.8	53.5	R.SLSSS*PQAQPPRPAELSDEEVAELFQR.L  R.SLS*S*SPQAQPPRPAELSDEEVAELFQR.L
		\$690\$691 \$688\$692		• • •	16.9	59.1 68.7	R.S'LSSS'PQAQPPRPAELSDEEVAELFQR.L
		\$690\$691\$692	=		-0.4	28.0	R.SLS'S'S'PQAQPPRPAELSDEEVAELFQR.L
GRK-in	teracting protein 2 <sub>GIT2</sub>	Y392S397			26.7	110.6	K.TINNQHSVESQDNDQPDY*DSVAS*DEDTDLETTASK.T
GRK-in	teracting protein 2 <sub>GIT2</sub>	Y392S394			5.4	38.5	K.TINNQHSVESQDNDQPDY*DS*VASDEDTDLETTASK.T
GRK-in	teracting protein 2 <sub>GIT2</sub>	S418S421			7.4	41.7	K.SLDS*DLS*DGPVTVQEFMEVK.N
	teracting protein 2 <sub>GIT2</sub>	S415S418	<u> </u>		12.3	34.5	K.S*LDS*DLSDGPVTVQEFMEVK.N
	teracting protein 2 <sub>GIT2</sub>	S415S421	Ţ.		5.8	41.2	K.S*LDSDLS*DGPVTVQEFMEVK.N
GRK-in	teracting protein 2 <sub>GIT2</sub>	\$397		·	5.9	55.4	K.TINNQHSVESQDNDQPDYDSVAS*DEDTDLETTASK.T
Growth arre	GIT2 est specific 2 like 1 GAS2L1	\$614 \$316			114.6	49.0 15.0	R.S*MVWPGDGLVPDTAEPHVAPSPTLPSTEDVIR.K  R.RGS*RPEMTPVSLR.S
	binding protein 1 GTPBP1	\$44\$47	-		57.2	59.6	R.LHGGFDS*DCS*EDGEALNGEPELDLTSK.L
	P binding protein 1 GTPBP1	S25		• • •	6.5	42.2	R.SAMDSPVPASMFAPEPSS*PGAAR.A
GTF	binding protein 1 GTPBP1	<b>S</b> 24			57.7	30.3	R.SAMDSPVPASMFAPEPS*SPGAAR.A
GTF	P binding protein 4 GTPBP4	\$468\$470\$472	Ħ.		17.5	114.1	R.TAAGEYDS*VS*ES*EDEEMLEIR.Q
GTF	binding protein 4 GTPBP4	Y466S470S472			5.1	81.2	R.TAAGEY"DSVS"ES"EDEEMLEIR.Q
	binding protein 4 GTPBP4	Y466S468S472		■.	6.1	113.8	R.TAAGEY*DS*VSES*EDEEMLEIR.Q
	binding protein 4 GTPBP4	Y466S468S470			5.3	84.5	R.TAAGEY*DS*VS*ESEDEEMLEIR.Q
	iting protein Ran 1 RANGAP1				23.5	38.4	K.ILDPNTGEPAPVLSS*PPPADVSTFLAFPS*PEK.L  K.ILDPNTGEPAPVLS*SPPPADVSTFLAFPS*PEK.L
	ting protein Ran 1 RANGAP1				-0.4	18.2	K.ILDPNTGEPAPVLSS*PPPADVSTFLAFPSPEK.L
	iting protein Ran 1 RANGAP1				10.3	17.1	K.ILDPNTGEPAPVLSSPPPADVS*TFLAFPS*PEK.L
GTPase activa	iting protein Ran 1 RANGAP1	T419S427				31.4	K.ILDPNT*GEPAPVLS*SPPPADVSTFLAFPSPEK.L
GTPase activating Rap/Ra	InGAP domain like RALGAPA	\$860\$861		•	33.1	12.4	R.RGS*S*PGSLEIPK.D
GTPase activating Rap/Ra	nGAP domain like RALGAPA 1	<b>S</b> 773			16.0	87.7	R.HFS*QSEETGNEVFGALNEEQPLPR.S
	inGAP domain like RALGAPA 1				15.0	69.8	R.SSS*TSDILEPFTVER.A
	inGAP domain like <sub>RALGAPA</sub> 1				23.9	46.0	K.LPPLNSDIGGS*SANVPDLMDEFIAER.L
	INGAP domain like RALGAPA 1 INGAP domain like RALGAPA		<u> </u>		3.5	42.2	R.HFSQS*EETGNEVFGALNEEQPLPR.S  R.S*QT*PS*PSTLNIDHMEQK.D
	1 InGAP domain like RALGAPA				-0.4	26.2	R.SSST*SDILEPFTVER.A
	nGAP domain like RAP1GAP		•	-	14.2	51.2	K.SETSS*NPSS*PEICPNK.E
	nGAP domain like RAP1GAP				10.7	13.5	K.SET*S*S*NPSSPEICPNK.E
	RAP1GAP	S45T49	-		34.7	24.4	K.QELANSSDATLPDRPLS*PPLT*APPTMK.S
	inGAP domain like RAP1GAP		•		33.6	75.1	R.SVS*FGGFGWIDK.T
	inGAP domain like RAP1GAP 4				9.1	80.7	K.QEVFVYSPS*PSSES*PSLGAAATPIIMSR.S
	InGAP domain like RAP1GAP				14.5	35.2	K.QEVFVYS*PSPSSES*PSLGAAATPIIMSR.S
	INGAP domain like RAP1GAP 4 INGAP domain like RAP1GAP		i i		8.5	22.3	K.QEVFVY*SPSPS*SESPSLGAAATPIIM#SR.S
	INGAP domain like RAP1GAP				5.6	76.0	K.QEVFVYSPS*PSSESPSLGAAATPIIMSR.S  K.QEVFVYS*PS*PSSESPSLGAAATPIIMSR.S
	InGAP domain like RAP1GAP				4.5	39.2	K.QELANS*SDATLPDRPLSPPLT*APPTMK.S
	4 InGAP domain like RAP1GAP				2.8	80.8	K.QEVFVYSPSPS*SESPSLGAAATPIIMSR.S
GTPase activating Rap/Ra	inGAP domain like RAP1GAP	S680S682			2.0	94.5	K.QEVFVYSPS*PS*SESPSLGAAATPIIMSR.S
GTPase activating Rap/Ra	inGAP domain like RAP1GAP	S678S683T693	ij		12.0	26.8	K.QEVFVYS'PSPSS'ESPSLGAAAT'PIIMSR.S
	InGAP domain like RAP1GAP 4		_		5.1	28.5	K.SETSS'NPS'S'PEICPNK.E
	nGAP domain like RAP1GAP 4				23.4	54.7	K.QEVFVYS*PSPSSESPSLGAAAT*PIIMSR.S
	INGAP domain like RAP1GAP		<u></u>		9.2	22.7	K.QEVFVYSPS*PS*SESPSLGAAAT*PIIMSR.S
	INGAP domain like RAP1GAP 4 INGAP domain like RAP1GAP				18.1	22.3	K.SETS*SNPS*S*PEICPNK.E  K.QELANS*S*DATLPDRPLSPPLTAPPTMK.S
	INGAP domain like RAP1GAP				7.7	17.2	K.QEVFVYS'PSPS'SESPSLGAAATPIIM#SR.S
	InGAP domain like RAP1GAP				5.0	50.2	K.QEVFVYS*PSPSS*ESPSLGAAATPIIMSR.S
GTPase activating Rap/Ra	inGAP domain like RAP1GAP	S608S613			5.8	26.8	K.SETS"SNPSS"PEICPNK.E

Peak Area %CV	abundanc		compared to	the			
-5 25 42 71		with the minimum					
3 88 >100 >100				RajiB			
Protein Na GTPase activating Rap/RanGAP domain	me Gene like RAP1GAP	Phosphosites S683S685	£ £ £	£ £ £	Ascor	MOWSE 29.9	Sequence K.QEVFVYSPSPSS*ES*PSLGAAATPIIMSR.S
GTPase activating Rap/RanGAP domain	4				7.6	20.3	K.QEVFVYSPSPSS*ESPSLGAAAT*PIIMSR.S
Guanine nucleotide binding protein 0	G(S), GNAS	<b>S</b> 572			13.3	11.6	R.ALS'RSR.R
Guanine nucleotide binding protein li		\$580\$581\$582			108.2	61.4	R.DDAEES*S*S*EPEEENVGNDTK.A
Guanine nucleotide binding protein li	ike 2 GNL2	\$580\$581			82.9	45.6	R.DDAEES*S*SEPEEENVGNDTK.A
Guanine nucleotide binding protein	like1 GNL1	T48T50			16.1	71.5	R.EEQT'DT'SDGESVTHHIR.R
Guanine nucleotide binding protein	like1 GNL1	S51S55			8.9	22.4	R.EEQTDTS*DGES*VTHHIR.R
	GNL1	T48T50S51			59.6	65.5	R.EEQT*DT*S*DGESVTHHIR.R
Guanine nucleotide binding protein		S32S33S34S36		<b>.</b> .	100.0	16.7	R.GLQDGLRS*S*S*NS*R.S
Guanine nucleotide binding protein		T50S51	<b></b>		12.7	17.1	R.EEQTDT*S*DGESVTHHIR.R
Guanine nucleotide binding protein		T48S51			6.0	31.0	R.EEQT*DTS*DGESVTHHIR.R
Guanine nucleotide binding protein		\$561\$562\$563			100.0	71.5	R.VGPAGDEEEEEEELS*S*S*CEEEGEEDR.D
Guanine nucleotide binding protein		T50		-	7.9	51.6	R.EEQTDT*SDGESVTHHIR.R  R.EEQTDTS*DGESVTHHIR.R
Guanine nucleotide releasing fact		S51		-	7.8	26.1	K S*DEOLSSLDR D
Guanine nucleotide releasing fact				===	60.6	62.9	R.ATS*GSSLPVGINR.Q
Guanine nucleotide releasing fact					13.9	26.0	R.AT*SGSSLPVGINR.Q
H1 histone family, memb			•		24.1	11.2	RAT*T*PKTVR.S
	tone H2AFX	S140			22.8	30.9	KATQAS*QEY
	H2AFX	T137S140			4.9	12.5	K.AT*QAS*QEY
H2B Histone family, memb	er E <sub>HIST1H2B</sub>	S37			21.2	33.3	R.KES*YSVYVYK.V
H3 Histone, famil	y 3B <sub>H3F3A</sub>	S58			17.0	38.0	K.S'TELLIR.K
H4 Histone family, memb	er A HIST 1H4A	S48			74.6	46.6	K.RIS*GLIYEETR.G
НВ	IS1L HBS1L	Y22			-0.4	38.1	R.GYNYDEDFEDDDLY*GQSVEDDYCISPSTAAQFIYSR.R
HE	IS1L HBS1L	<b>S</b> 33			18.2	76.4	R.GYNYDEDFEDDDLYGQSVEDDYCIS*PSTAAQFIYSR.R
HE	S1L HBS1L	S25			2.3	60.5	R.GYNYDEDFEDDDLYGQS*VEDDYCISPSTAAQFIYSR.R
НВ	XAP RSF1	S604		• • •	100.0	38.9	R.LS*PIPEEVPK.S
	XAP RSF1	S1345			100.0	89.0	R.IES*DEEEDFENVGK.V
	XAP RSF1	S1359S1375			32.2	40.3	K.VGS*PLDYSLVDLPSTNGQS*PGK.A
	XAP RSF1	\$1277T1278\$1			9.5	38.0	R.GRS*T*DEYS*EADEEEEEEGKPSR.K
	XAP RSF1	S1370			8.2	18.1	K.VGSPLDYSLVDLPS*TNGQSPGK.A  K.STLESEKPGS*PEAAET*SPPSNIIDHCEK.L
	XAP RSF1	S622T628 S622S629			25.9	38.4	K.STLESEKPGS*PEAAETS*PSNIIDHCEK.L
HDCMA18P pro		\$258\$261		-	9.8	25.7 39.3	R.SRPTS*EGS*DIESTEPQK.Q
HDCMA18P pro		S337T338	• • •		69.1	57.2	R.DIEIS*T*EEEKDTGDLKDSSLLK.T
HDCMA18P pro	tein LARP7	S261			44.8	70.7	R.SRPTSEGS*DIESTEPQK.Q
HDCMA18P pro	tein LARP7	T257S258			10.7	16.7	R.SRPT*S*EGSDIESTEPQK.Q
HDCMA18P pro	tein LARP7	\$300			-0.4	36.4	R.SSS*EDAESLAPR.S
Headcase protein hom	olog HECA	S264S268		•	38.0	66.6	R.S*PGGS*PGQSPPTGYSILSPAHFSGPR.S
Headcase protein hom	olog HECA	S264S268S272			51.5	73.2	R.S'PGGS'PGQS'PPTGYSILSPAHFSGPR.S
Headcase protein hom	olog HECA	<b>S</b> 272			16.8	17.8	R.SPGGSPGQS*PPTGYSILSPAHFSGPR.S
Headcase protein hom	ologHECA	S268S272	•		12.2	69.7	R.SPGGS*PGQS*PPTGYSILSPAHFSGPR.S
Heat shock 40 kDa prote	ein 3 DNAJB2	S247S250		÷		22.7	R.SGGTQVQQTPASCPLDS*DLS*EDEDLQLAMAYSLSEMEAAGK.K
Heat shock 40 kDa prote		S335			18.4	31.7	K.VNFPENGFLS*PDKLSLLEK.L
Heat shock 60 KD protein 1 (chapero		<b>S</b> 70			55.8	70.3	R.TVIIEQSWGS*PK.V
Heat shock 60 KD protein 1 (chapero		<b>S</b> 67		-	5.0	30.4	R.TVIIEQS*WGSPK.V
Heat shock 70 kDa prote		\$362			10.1	73.3	K.S'INPDEAVAYGAAVQAAILSGDK.S
Heat shock 70kD protein					100.0	15.0	R.RS*RHS*R.T
HECT domain and ankyrin re containing. E3 ubiquitin protein liga Hect domain and RCC1 like doma	ise 1	\$385	-		62.4	54.0	K.NKRDS*TEITSILLK.Q
Helicase with zinc finger dor		\$4857			20.6	13.3	R.NVDNAEGS*DTDY
Hematological and neurological expres		S1614			73.8	48.6	R.S*PPAVPSPPSSTDHSSHFSNFNDNSR.D  R.RNSS*EASSGDFLDLK.G
Hematological and neurological expres	1	\$88 \$87			16.9 27.6	106.7	R.NS*SEASSGDFLDLK.G
Hematological and neurological expres	1	\$87 \$92			10.9	106.7	R.RNSSEASS'GDFLDLK.G
Hematopoietic cell specific LYN substra	1	\$275			100.0	53.3	R.S'PEAPQPVIAM#EEPAVPAPLPK.K
Hepatocyte cell adhesion mole					7.2	15.0	R.T'HS'SPPR.A
Hepatocyte cell adhesion mole				<del></del>	11.1	16.4	R.THS'S'PPR.A
Hepatoma derived growth fa	ictor <sub>HDGF</sub>	S165		-	100.0	38.3	R.RAGDLLEDS*PK.R
Hepatoma derived growth fa	ictor <sub>HDGF</sub>	S132			9.0	21.4	K.GNAEGS*SDEEGKLVIDEPAK.E
Hepatoma derived growth fa	ctor <sub>HDGF</sub>	S132S133		•	100.0	132.7	K.GNAEGS*S*DEEGKLVIDEPAK.E
Hepatoma derived growth fa	ictor <sub>HDGF</sub>	S107S132		<u></u>		15.1	K.S*CVEEPEPEPEAAEGDGDKKGNAEGS*SDEEGK.L
Hepatoma-derived growth factor-rel	ated HDGFL2 ein 2	S232S234S236			7.1	24.3	K.KAPSAS*DS*DS*KADS*DGAKPEPVAMAR.S

Peak Area %CV	White do	ts-Significant cha	nge in pepti ompared to	de the			
<-10 0 -6 29 -3 42		e at 5%FDR o with the minimum					
0 3 85 >100			CarT	RajiB			
	Name Gene	Phosphosites	8 g g	£ 5 5		MOWSE	Sequence
Hepatoma-derived growth factor-r	otein 2	S454			42.5	50.4	R.S*EGFSMDR.K  R.GVMAVTAVTATA&*DR.M
Hepatoma-derived growth factor-	otein 2	\$137 \$652		• • •	9.8	25.8	R.EGPDLDRPGS*DR.Q
pro Hepatoma-derived growth factor-r	otein 2				100.0	20.4	R.GEAERGS*GGS*S*GDELREDDEPVK.K
Hepatoma-derived growth factor-r	otein 2	\$366\$369\$370 \$230\$232\$234			100.0	19.2	K.KAPS*AS*DS*DSKADS*DGAKPEPVAMAR.S
Hepatoma-derived growth factor-r	otein 2	\$671			8.9	19.2	R.GDSEALDEES*
Hepatoma-derived growth factor-r	otein 2	S664			5.4	10.9	R.GDS*EALDEES
Pro-	otein 2	\$395\$396\$397	=		100.0	21.7	R.GRGPPS*S*S*DS*EPEAELER.E
Hepatoma-derived growth factor-r	otein 2	T132	==		18.8	14.0	R.GVM#AVTAVT*ATAASDR.M
Hepatoma-derived growth factor-r	otein 2	T134	•		9.0	48.4	R.GVMAVTAVTA**AASDR.M
Hepatoma-derived growth factor-r	elated HDGFL2	\$230\$232\$234		-	-2.6	24.2	K.KAPS*AS*DS*DS*KADSDGAKPEPVAMAR.S
Heterochromatin protein 1	alpha <sub>CBX5</sub>	S11S12S13S14			44.4	55.2	K.RTADS*S*S*S*EDEEEYVVEK.V
Heterochromatin protein 1	alpha <sub>CBX5</sub>	T8S11S13S14			6.7	14.4	R.T*ADS*SS*S*EDEEEYVVEK.V
Heterogeneous nuclear ribonucleop	rotein HNRNPA2	S259	ij		40.6	129.0	R.GFGDGYNGYGGGPGGGNFGGS*PGYGGGR.G
Heterogeneous nuclear ribonucleop	rotein HNRNPA2	S341			15.8	119.1	R.NMGGPYGGGNYGPGGS*GGSGGYGGR.S
Heterogeneous nuclear ribonucleop	A2 rotein HNRNPA2 A2	Y331		•••	13.3	37.0	R.NMGGPY*GGGNYGPGGSGGSGGYGGR.S
Heterogeneous nuclear ribonucleop	rotein HNRNPA3	S358	•		25.4	158.8	R.SSGS*PYGGGYGSGGGSGGYGSR.R
Heterogeneous nuclear ribonucleop	A3 rotein HNRNPA3 A3	<b>S</b> 356			-0.3	128.8	R.SS*GSPYGGGYGSGGGSGGYGSR.R
Heterogeneous nuclear ribonucleop		Y360	• • •		-0.5	13.6	R.SSGSPY*GGGYGSGGGSGGYGSR.R
Heterogeneous nuclear ribonucleopro		<b>S</b> 253	•	•		68.8	K.MES*EGGADDSAEEGDLLDDDDNEDRGDDQLELIKDDEK.E
	HNRNPC	S253S260	•••		100.0	81.6	K.MES*EGGADDS*AEEGDLLDDDDNEDRGDDQLELIKDDEK.E
	HNRNPC	S260			98.8	107.2	K.M#ESEGGADDS*AEEGDLLDDDDNEDRGDDQLELIK.D
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	<b>S</b> 299			58.5	71.3	K.EAEEGEDDRDS*ANGEDDS
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	<b>S</b> 306			3.2	15.9	K.DDEKEAEEGEDDRDSANGEDDS*
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	S240S241			4.5	29.6	K.SEEEQSSS*S*VKKDETNVK.M
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	S233			56.4	65.6	K.NDKS'EEEQSSSSVKK.D
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	S238S240				13.2	K.SEEEQS*SS*SVKKDETNVK.M
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	S238S241			7.0	38.0	K.SEEEQS*SSS*VKKDETNVK.M
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	<b>S</b> 107		■.	10.9	77.0	R.SAAEMYGS*SFDLDYDFQR.D
Heterogeneous nuclear ribonucleopro	tein C HNRNPC	S238S239		-	18.1	19.5	K.SEEEQS*S*SVKKDETNVK.M
Heterogeneous nuclear ribonucleopro	tein D HNRNPD	\$80\$83	<b>F</b>		12.8	45.6	K.NEEDEGHS*NSS*PR.H
	HNRNPD	S83			23.9	89.0	K.NEEDEGHSNSS*PR.H
Heterogeneous nuclear ribonucleopro	tein D HNRNPD	<b>S</b> 82			19.8	58.6	K.NEEDEGHSNS*SPR.H
	HNRNPD	<b>S</b> 80			62.3	66.4	K.IDASKNEEDEGHS*NSSPR.H
Heterogeneous nuclear ribonucleopro					6.0	41.2	K.NEEDEGHS*NS*SPR.H
Heterogeneous nuclear ribonucleop	H1				44.4	85.2	K.HTGPNS*PDTANDGFVR.L
Heterogeneous nuclear ribonucleop	H1			■.	9.2	31.0	K.HT*GPNSPDTANDGFVR.L
Heterogeneous nuclear ribonucleop	H1		<b>—</b>		42.3	48.8	K.ATENDIYNFFS*PLNPVR.V
Heterogeneous nuclear ribonucleop	H1				12.2	18.0	K.HTGPNSPDT*ANDGFVR.L
Heterogeneous nuclear ribonucleopro					99.9	115.7	R.GS*YGDLGGPIITTQVTIPK.D
Heterogeneous nuclear ribonucleopro		Y380			-0.1	70.1	R.GSY*GDLGGPIITTQVTIPK.D
Heterogeneous nuclear ribonucleopro		T389	==		4.3	55.0	R.GSYGDLGGPIIT*TQVTIPK.D
Heterogeneous nuclear ribonucleopro					26.0	64.4	K.IILDLISES*PIK.G
Heterogeneous nuclear ribonucleopro		T118			3.8	25.7	K.IIPTLEEGLQLPSPT'ATSQLPLESDAVECLNYQHYK.G  K.IIPT'LEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G
Heterogeneous nuclear ribonucleopro		T107				55.8	K.IIPT*LEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G  K.IIPTLEEGLQLPS*PTATSQLPLESDAVECLNYQHYK.G
Heterogeneous nuclear ribonucleopro		S116			28.4	62.6	R.RDYDDMS*PR.R
Heterogeneous nuclear ribonucleopro					32.7	37.5	R.RDYDDMS*PR.R  K.IIPTLEEGLQLPSPTAT*SQLPLESDAVECLNYQHYK.G
Heterogeneous nuclear ribonucleopro					5.0	16.3	K.IIDLIS*ESPIKGR.A
Heterogeneous nuclear ribonucleop					E2 2	21.6 57.8	R.GNFGGS*FAGSFGGAGGHAPGVAR.K
Heterogeneous nuclear ribonucleopro	М				52.3	57.8	R.LQAALDDEEAGGRPAMEPGNGS*LDLGGDSAGR.S
	HNRNPU				7.7	41.5	K.S'PQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I
Heterogeneous nuclear ribonucleopro		T286			0.8	15.2	K.SPQPPVEEEDEHFDDT*VVCLDTYNCDLHFK.I
Heterogeneous nuclear ribonucleopro	tein U HNRNPUL				5.3	21.8	R.APQQQPPPQQPPPPQPPPQQPPPPSY*SPAR.N
Heterogeneous nuclear ribonucleopro	tein U HNRNPUL					26.1	R.APQQQPPPQQPPPPQPPPQQPPPPPS*YSPAR.N
Heterogeneous nuclear ribonucleopro	like 1 tein U HNRNPUL				5.8	19.5	R.APQQQPPPQQPPPPQPPPQQPPPPSYS*PAR.N
Heterogeneous nuclear ribonucleopro	like 1 tein U HNRNPUL				11.9	21.3	R.S*PQPPAEEDEDDFDDTLVAIDTYNCDLHFK.V
Heterogeneous nuclear ribonucleop	rotein HNRNPUL				49.3	75.1	R.S*GDET*PGSEVPGDK.A
Heterogeneous nuclear ribonucleop	-like 2 rotein HNRNPUL				100.0	73.1	R.S'GDET'PGS'EVPGDK.A
Heterogeneous nuclear ribonucleop	-like 2 rotein HNRNPUL			• • •	10.4	27.7	K.SKPAGS*DGER.R
Heterogeneous nuclear ribonucleop	-like 2 rotein HNRNPUL				100.0	58.9	K.AAEEQGDDQDS*EK.S
Heterogeneous nuclear ribonucleop	-like 2				39.8	52.7	R.SKS*PLPPEEEAK.D

Peak Area %CV	abundand		ompared to	the			
.5 25 42 42 71	timepoint PSM	with the minimum	peak area fo	or a given			
88 5 >100			CarT	RajiB			
Protein Name		Phosphosites	9m 2m 2m 2m	5 P B	Ascor	MOWSE	Sequence
Heterogeneous nuclear ribonucleoprotei U-like	2			==	37.7	87.1	R.S*GDET*PGSEVPGDK.A  R.S*GDETPGSEVPGDKAAEEQGDDQDSEK.S
Heterogeneous nuclear ribonucleoprotei	HNRNPUL			-	11.8	21.3	R.S*KSPLPPEEEAK.D
U-like	2				9.2	40.6	R.SGDET*PGS*EVPGDK.A
U-like  Heterogeneous nuclear ribonucleoprotein	2				34.8	57.2	
C1/C	2				40.8	99.3	K.MESEGGADDS*AEEGDLLDDDDNEDRGDDQVK.T
Heterogeneous nuclear ribonucleoprotein C1/C	2				100.0	78.7	K.MES*EGGADDS*AEEGDLLDDDDNEDRGDDQVK.T
Heterogenous nuclear ribonucleoprotein A					100.0	29.7	K.S*ES*PKEPEQLRK.L
Heterogenous nuclear ribonucleoprotein A			<u> </u>		12.0	48.9	K.SES*PKEPEQLR.K
Heterogenous nuclear ribonucleoprotein A					-0.3	91.6	R.SS*GPYGGGGQYFAKPR.N
Heterogenous nuclear ribonucleoprotein A		S4	<u> </u>		8.5	35.0	K.S'ESPKEPEQLR.K
Hexamthylene bis-acetamide inducible		S51S53			100.7	45.7	R.MES*HS*EDEDLAGAVGGLGWNSR.S
	LGCSAM	S102			16.3	36.4	R.VLCTRPSGNS'AEEYYENVPCK.A
	LGCSAM	S120			20.3	34.3	R.ES*LGGTETEYSLLHMPSTDPR.H
	L GCSAM	S69			7.2	56.1	R.MSS*TPIQDNVDQTYSEELCYTLINHR.V
	L GCSAM	S68			9.2	86.1	R.MS*STPIQDNVDQTYSEELCYTLINHR.V
	LGCSAM	T70			5.3	22.1	R.MSST*PIQDNVDQTYSEELCYTLINHR.V
High mobility group 20.		S105			48.9	46.0	K.S*PLTGYVR.F
High mobility group AT hook		S102			42.5	68.9	K.EEEEGISQES"SEEEQ
	HMGA1	S102S103	<u></u>		20.6	82.5	K.EEEEGISQES'S'EEEQ
High mobility group AT hook	1 <sub>HMGA1</sub>	S9			-0.2	54.8	K.SS*QPLASK.Q
High mobility group AT hook	1 <sub>HMGA1</sub>	S99S102			12.6	41.8	K.EEEEGIS*QES*SEEEQ
	HMGA1	S44			51.6	70.1	R.KQPPVSPGTALVGS*QK.E
High mobility group AT hook	1 <sub>HMGA1</sub>	<b>S</b> 36			12.5	18.4	R.KQPPVS*PGTALVGSQK.E
High mobility group AT hook	1 <sub>HMGA1</sub>	T39	Ţ.		1.5	21.0	R.KQPPVSPGT*ALVGSQKEPSEVPTPK.R
High mobility group AT hook	1 <sub>HMGA1</sub>	<b>S</b> 99				13.2	K.EEEEGIS'QESSEEEQ
High mobility group AT hook	1 <sub>HMGA1</sub>	S99S102S103		·	100.0	54.5	K.KLEKEEEEGIS*QES*S*EEEQ
High mobility group AT hook	1 <sub>HMGA1</sub>	S103	<b>—</b>		7.0	14.4	K.EEEEGISQESS*EEEQ
High mobility group AT hook 1 like	4INO80B	S84T87				19.7	K.S'VPT'FTVIPEGPRSPSPLMVVDNEEEPMEGVPLEQYR.A
High mobility group AT hook 1 like	4INO80B	S97S99	Ħ.		4.2	17.5	K.SVPTFTVIPEGPRS*PS*PLMVVDNEEEPMEGVPLEQYR.A
High mobility group protein 2 like	1 <sub>HMGXB4</sub>	\$393\$403	-		25.8	13.3	K.S*PPTTMLLPAS*PAKAPETEPIDVAAHLQLLGESLSLIGHR.L
High mobility group protein 2 like	1 <sub>HMGXB4</sub>	T396S403			11.5	18.8	K.SPPT*TMLLPAS*PAKAPETEPIDVAAHLQLLGESLSLIGHR.L
HIP5	5 DBNL	S275			26.0	34.8	R.AMSTTSIS*SPQPGK.L
HIP5	5 DBNL	S284	<b>.</b>		100.0	17.3	K.LRS*PFLQK.Q
HIRA interacting protein	3 <sub>HIRIP3</sub>	S289S291			100.0	66.8	R.LLGDS*DS*EEEQK.E
HIRA interacting protein	3 <sub>HIRIP3</sub>	T358S359S363			34.3	66.6	R.LGST*S*GEES*DLER.E
HIRA interacting protein	3 <sub>HIRIP3</sub>	S223S227			33.0	59.8	K.SLKES*EQES*EEEILAQK.K
HIRA interacting protein	3 <sub>HIRIP3</sub>	S530			28.3	23.5	R.TLDS*DEERPRPAPPDWSHMR.G
HIRA interacting protein	3 <sub>HIRIP3</sub>	S550S551S555			100.0	41.8	R.GIIS*S*DGES*N
HIRA interacting protein	3 <sub>HIRIP3</sub>	\$357T358\$359			100.0	65.2	R.LGS*T*S*GEES*DLER.E
	HIRIP3	S142S143			100.0	33.1	K.AVEES*S*DEER.Q
HIRA interacting protein	3 <sub>HIRIP3</sub>	<b>S</b> 370			32.2	77.2	R.EVS*DSEAGGGPQGER.K
HIRA interacting protein	3 <sub>HIRIP3</sub>	S370S372	<u> </u>		100.0	68.9	R.EVS*DS*EAGGGPQGER.K
HIRA interacting protein	3 <sub>HIRIP3</sub>	\$330\$332\$333			16.7	25.7	K.RLS*GS*S*EDEEDS*GKGEPTAK.G
HIRA interacting protein	3 <sub>HIRIP3</sub>	\$196\$199			100.0	84.6	R.EES*EES*EAEPVQR.T
HIRA interacting protein	3 <sub>HIRIP3</sub>	T358S363			15.7	25.9	R.LGST*SGEES*DLER.E
HIRA interacting protein	3 <sub>HIRIP3</sub>	S551S555	•		8.6	42.3	R.GIISS*DGES*N
	HIRIP3	\$159\$160			40.9	24.9	R.GEES'S'EEEEKGYK.G
HIRA interacting protein	3 <sub>HIRIP3</sub>	\$289\$291\$300			100.0	16.9	R.LLGDS*DS*EEEQKEAAS*S*GDDS*GRDR.E
	HIRIP3	\$300\$301\$305			100.0	23.4	K.EAAS*S*GDDS*GRDR.E
HIRA interacting protein	3 <sub>HIRIP3</sub>	T84S87			100.0	19.1	K.RPPT*PCS*DPER.K
HIRA interacting protein		\$330\$332\$333			47.9	34.2	K.RLS'GS'S'EDEEDSGKGEPTAK.G
HIRA interacting protein	3 <sub>HIRIP3</sub>	S550S551			4.6	41.9	R.GIIS*S*DGESN
HIRA interacting protein	3 <sub>HIRIP3</sub>	S227			26.5	54.3	K.ESEQES*EEEILAQK.K
HIRA interacting protein		S550S555			5.6	42.4	R.GIIS'SDGES'N
HIRA interacting protein		\$196			28.4	13.9	R.EES*EESEAEPVQR.T
HIRA interacting protein		S219S227			13.0	29.8	K.S*LKESEQES*EEEILAQKK.E
HIRA interacting protein		\$219\$227 \$357\$359\$363			13.0	25.2	R.LGS*TS*GEES*DLER.E
Histamine receptor H		\$396\$398			100.0	12.5	RLRS'HS'R.Q
Histidyl tRNA synthetase		\$396\$398 \$197				77.1	R.SASS*GAEGDVSSEREP
Histidyl tRNA synthetase		\$197 \$196			9.1	77.1	R.SAS*SGAEGDVSSEREP
Histidyl tRNA synthetase		\$196 \$194			5.5		R.S*ASSGAEGDVSSEREP
Histidyl tRNA synthetase lik		\$194 \$67		•	7.0	36.7	R.DLS*PQHMVVR.E
		301		-	100.0	30.1	· =

Peak Area	o abundanc	ts-Significant cha e at 5%FDR c with the minimum	compared to	the			
.3 0 3	42 PSM 71 86		CarT				
>10	Protein Name Gene Histone 1 H1C HIST1H1C	Phosphosites	5 g g	8 g g		MOWSE	Sequence K.KAGGT*PR.K
	Histone 1 H1C HIST1H1C				100.0	24.9 48.1	K.KAAGGAT*PK.K
	Histone 1 H1E HIST1H1E	T146			49.2	49.6	K.KATGAAT*PK.K
	Histone 1 H1E HIST1H1E	S187	• • •		100.0	51.4	K.KAPKS*PAK.A
	Histone 1 H1E HIST1H1E	T142	<u> </u>		7.3	11.3	K.KAT*GAATPK.K
	Histone 1, H1a HIST1H1A		<del></del>		100.0	18.2	R.KS*S*KNPK.K
	Histone 1, H1b HIST1H1B				47.5	47.0	M.SETAPAETATPAPVEK°PAK.K
	Histone 1, H1b HIST1H1B				100.0	40.3	K.KVAKS*PK.K  K.ATKS*PAKPK.A
	HIST1H1B Histone 1, H1b HIST1H1B				100.0	19.0	KAKKPAGAT*PK.K
Histone ace	etyltransferase 1 HAT1	S361		_	10.9	21.1	R.LIS*PYK.K
Histor	ne deacetylase 1 HDAC1	\$421\$423			100.0	88.9	R.IACEEEFS*DS*EEEGEGGR.K
Histor	ne deacetylase 1 HDAC1	<b>S</b> 393			100.0	44.5	R.MLPHAPGVQMQAIPEDAIPEES*GDEDEDDPDKR.
	HDAC2	S516S518			100.0	82.1	R.IACDEEFS*DS*EDEGEGGRR.N
	ne deacetylase 2 HDAC2	S488	<b></b>		100.0	30.3	R.MLPHAPGVQMQAIPEDAVHEDS*GDEDGEDPDKR
	ne deacetylase 3 HDAC3	<b>S</b> 424			49.9	30.1	R.GPEENYSRPEAPNEFYDGDHDNDKES'DVEI
	ne deacetylase 4 HDAC4	\$632			35.8	110.8	R.AQS*SPASATFPVSVQEPPTKPR.F
	ne deacetylase 4 HDAC4	\$467 \$486		_	12.1 56.6	45.6 83.2	R.TQS*APLPQNAQALQHLVIQQQHQQFLEK.H  R.AQS*SPAAPASLSAPEPASQAR.V
	deacetylase 7A HDAC7	\$486 \$487		<u></u>	-0.4	32.8	R.AQSS*PAAPASLSAPEPASQAR.V
	Histone H1x H1FX	S31			29.3	73.1	K.AGGSAALS*PSK.K
	Histone H1x <sub>H1FX</sub>	<b>S</b> 33	<u> </u>		11.0	55.4	K.AGGSAALSPS*KK.R
	nsferase DOT1L DOT1L	<b>S</b> 447			12.6	59.8	K.KNQTALDALHAQTVSQTAAS*SPQDAYR.S
Histone methyltra	nsferase DOT1L DOT1L	S448	·		7.2	61.9	K.KNQTALDALHAQTVSQTAASS*PQDAYR.S
	Histone1, H1D HIST1H1D		<b></b>		100.0	38.7	K.KVAGAAT*PK.K
	binding protein AGFG1	T177S179			9.2	14.7	K.SLLGDSAPTLHLNKGT*PS*QSPVVGR.S  K.GT*PSQSPVVGR.S
	binding protein AGFG1	T177 T177S181			28.8	43.5	K.SLLGDSAPTLHLNKGT*PSQS*PVVGR.S
	binding protein AGFG1	\$162			78.9	54.1	K.S*LLGDSAPTLHLNK.G
HIV 1 REV	binding protein AGFG1	T170S181	•		4.1	14.5	K.SLLGDSAPT*LHLNKGTPSQS*PVVGR.S
HLA class I histocompatibil	ity antigen, B-58 <sub>HLA-B</sub> alpha chain	<b>S</b> 359			12.1	69.6	K.GGSYSQAASSDSAQGSDVS*LTA
HLA class I histocompatibil		\$356			14.0	51.8	K.GGSYSQAASSDSAQGS*DVSLTA
HLA class I histocompatibil	alpha chain	S356S359	<b></b>		16.9	74.7	K.GGSYSQAASSDSAQGS*DVS*LTA-
HLA class I histocompatibil	alpha chain	\$352\$356\$359			11.0	38.4	K.GGSYSQAASSDS*AQGS*DVS*LTA
HLA class I histocompatibil	alpha chain	\$350\$352\$359			10.2	16.6	K.GGSYSQAASS*DS*AQGSDVS*LTA  K.GGSYSQAASS*DS*AQGS*DVSLTA
HLA class I histocompatibil	alpha chain ity antigen, B-58 <sub>HLA-B</sub>	\$350\$352\$356 \$350\$356\$359			-0.5	14.3 35.9	K.GGSYSQAASS*DS*AQGS*DVSLTA
	alpha chain  HLA-A <sub>HLA-A</sub>	\$350\$356\$359 \$359			28.2	114.2	R.KGGSYTQAASSDSAQGSDVS*LTACKV
	HLA-A HLA-A	S352		===	33.2	107.3	R.KGGSYTQAASSDS*AQGSDVSLTACKV
	HLA-A HLA-A	S350			10.9	68.8	R.KGGSYTQAASS*DSAQGSDVSLTACKV
	HLA-A <sub>HLA-A</sub>	\$352\$359	•••		26.1	70.0	R.KGGSYTQAASSDS*AQGSDVS*LTACKV
	HLA-A <sub>HLA-A</sub>	\$352\$356\$359			20.0	70.8	R.KGGSYTQAASSDS*AQGS*DVS*LTACKV
	HLA-A <sub>HLA-A</sub>	Y344	_		17.7	54.7	R.KGGSY*TQAASSDSAQGSDVSLTACKV
	HLA-A HLA-A	\$356			15.9	96.9	R.KGGSYTQAASSDSAQGS*DVSLTACKV
	HLA-A HLA-A	\$356\$359 \$350\$359			19.4	33.8	R.KGGSYTQAASSDSAQGS*DVS*LTACKV  R.KGGSYTQAASS*DSAQGSDVS*LTACKV
	HLA-A HLA-A	T345		-	9.0	27.2	R.KGGSYT*QAASSDSAQGSDVSLTACKV
	HLA-A <sub>HLA-A</sub>	\$352\$356			8.9	39.6	R.KGGSYTQAASSDS*AQGS*DVSLTACKV
HLA-B associa	ated transcript 2 PRRC2A	\$342\$350			100.0	41.3	K.LKFS*DEEDGRDS*DEEGAEGHR.D
HLA-B associa	ated transcript 2 PRRC2A	S456			22.5	81.7	R.KQS*SSEISLAVER.A
	ated transcript 2 PRRC2A	\$1089\$1092			52.2	83.2	R.S'EGS'EYEEIPK.R
	ated transcript 2 PRRC2A	S1014	<b>H</b>		15.8	13.9	R.DYS*YER.V
	ated transcript 2 PRRC2A	T825			-0.9	21.4	R.SET*PPVPPPPPYLASYPGFPENGAPGPPISR.F
	ated transcript 2 PRRC2A	Y1013 S1168			18.1	21.2	R.DY*SYER.V  R.GVPS*RR.G
	ated transcript 2 PRRC2A	\$1168 \$1306\$1310\$1			100.0	11.1	K.S'PDLS'NQNS'DQANEEWET'ASESSDFTSER.R
	ated transcript 2 PRRC2A	\$1306\$1314\$1			17.8	15.8	K.S*PDLSNQNS*DQANEEWETAS*ES*SDFTSER.R
HLA-B associa	ated transcript 2 PRRC2A	\$457		•	8.0	27.8	R.KQSS*SEISLAVER.A
HLA-B associa	ated transcript 2 PRRC2A	S1089			30.0	30.0	R.S*EGSEYEEIPK.R
	ated transcript 3 BAT3	S973			75.8	114.5	R.ENAS*PAPGTTAEEAMSR.G
	ated transcript 3 BAT3	S964S973			36.3	44.8	R.AS*PEPQRENAS*PAPGTTAEEAMSR.G
HLA-B associa	ated transcript 3 BAT3	S964	•		100.0	27.7	R.AS*PEPQR.E

<-10 0 al	bundanc	ts-Significant cha e at 5%FDR o with the minimum	compared to peak area f	the or a given			
>10 Protein Name G	Sene	Phosphosites	E E E	RajiB E E E	Ascor	MOWSE	Sequence
HLA-B associated transcript 3 BA	AT3	S113			7.7	40.4	R.APPQTHLPSGASSGTGSASATHGGGS*PPGTR
HLA-B associated transcript 3 BA		S964T978			5.9	19.9	R.AS*PEPQRENASPAPGT*TAEEAMSR.G  R.APPQT*HLPSGASSGTGSASATHGGGSPPGTF
HLA-B-associated transcript 1 DD		S38			30.0	32.9	K.GS*YVSIHSSGFR.D
HMG CoA reductase HM		S872	•		120.6	84.5	R.S*KINLQDLQGACTK.K
HMG-BOX transcription factor BBX BE		S478S479S481		• •	19.4	35.3	K.KRQS*S*ES*DIESVIYTIEAVAK.G
HMGN1 HM	MGN1	\$86\$89			45.2	78.0	K.TEES*PAS*DEAGEK.E
HMGN1 HM	MGN1	S89			32.3	67.2	K.TEESPAS*DEAGEK.E
HNRPLL HI	NRNPLL	T46		• •	100.0	12.0	R.REAT*PR.G
Host cell factor C1 HC	CFC1	S666	• •		50.0	72.9	K.S*PISVPGGSALISNLGK.V
Host cell factor C1 HC	CFC1	S411			6.5	19.9	K.YDIPATAATAB*PTPNPVPSVPANPPK.S
Host cell factor C1 HO	CFC1	T413			-0.3	31.8	K.YDIPATAATATSF*PNPVPSVPANPPK.S
Host cell factor C1 <sub>HC</sub>	CFC1	S1205	·		113.9	56.1	R.S*PAFVQLAPLSSK.V
HP1 beta CE	BX1	S89			39.0	51.5	R.KADS*DSEDKGEESKPK.K
HP1-BP74 HF	P1BP3	\$441\$442\$446	<b></b>		84.1	40.7	K.KEPDDSRDEDEDEDES*S*EEDS*EDEEPPPK.F
HPK1 <sub>M</sub> /	AP4K1	S376S377Y381		•	6.7	16.9	R.KQLSES*S*DDDY*DDVDIPTPAEDTPPPLPPKP
HPK1 <sub>M</sub> /	AP4K1	\$374\$376\$377		·	10.7	14.8	R.KQLS*ES*S*DDDYDDVDIPTPAEDTPPPLPPKP
HPRP3P PF		S619			100.0	64.2	K.GDDDEES*DEEAVKK.T
HPRP3P PF		T611			5.8	20.1	R.IKWDEQTSNT*KGDDDEESDEEAVK.K
Hsc70 interacting protein ST		<b>S</b> 79		<b>—</b>	16.4	86.4	K.KVEEDLKADEPSSEES*DLEIDK.E
Hsc70 interacting protein ST		<b>S</b> 76			9.1	83.0	K.KVEEDLKADEPSS*EESDLEIDK.E
Hsc70 interacting protein ST		S75S76S79			100.0	71.6	K.KVEEDLKADEPS*S*EES*DLEIDK.E
Hsc70 interacting protein ST		S75S79		•••	28.4	56.5	K.ADEPS*SEES*DLEIDK.E
	Γ13	S75S76				39.6	K.ADEPS*S*EESDLEIDK.E
	Γ13	S76S79	-		19.1	41.8	K.ADEPSS*EES*DLEIDK.E
Hsc70 interacting protein ST		<b>S</b> 75		-	10.9	48.0	K.KVEEDLKADEPS*SEESDLEIDK.E
HSHIN1 OT		S480			15.3	54.8	K.RPEPSTLENITDDKYATVSS*PSK.S
HSHIN1 OT		\$957\$958			103.0	105.1	K.EES*S*EDENEVSNILR.S
HSHIN1 OT		S827		·	33.4	19.1	K.GELDLS*LENLDLSK.D
HSHIN1 OT		\$479			10.7	69.2	K.RPEPSTLENITDDKYATVS*SPSK.S
HSP90A HS					144.9	97.3	K.ESEDKPEIEDVGS*DEEEKK.D
HSP90A HS	SP90AA1				76.3	74.7	K.LGLGIDEDDPTADDTSAAVTEEMPPLEGDDDT*  R.DKEVS*DDEAEEKEDK.E
HSP90A HS					100.0	85.4	K.ES*EDKPEIEDVGSDEEEEKK.D
HSP90B HS			•		400 -	44.4	K.EIS*DDEAEEEKGEK.E
HSP90B HS					100.0	87.7	K.EIS*DDEAEEEKGEK.E  K.IEDVGS*DEEDDSGKDK.K
HSP90B HS					71.8	131.8 47.0	K.IGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDAS*
Hugl protein LL					100.0		R.FS*LSAR.N
Human immunodeficiency virus type1 HI		S936			10.9	12.6	RRDLS*PRR
enhancer-binding protein2  Huntingtin H		\$2130 \$421\$434			100.0	90.1	R.SGS*IVELIAGGGSSCS*PVLSR.K
Huntingtin H		\$421\$434 \$432			9.1	52.0	R.SGSIVELIAGGGSS*CSPVLSR.K
Huntingtin H		\$432 \$419\$434			9.1	70.4	R.S*GSIVELIAGGGSSCS*PVLSR.K
Huntingtin H		\$419\$434 \$421\$432				23.9	R.SGS*IVELIAGGGSS*CSPVLSR.K
Huntingtin interacting protein 1 SE		\$421\$432 \$121			1.4	23.9	R.LNDS*PTLK.K
Huntingtin interacting protein 1 SE		T123			6.0	10.8	R.LNDSPT*LK.K
Hydroxymethylglutaryl-CoA synthase, Hi			انج		6.8	38.5	R.RPT*PNDDTLDEGVGLVHSNIATEHIPSPAKK.V
cytoplasmic	MGCS1				40.7		R.RPTPNDDTLDEGVGLVHSNIATEHIPS*PAKK.V
Hyperpolarization activated cyclic HO		T380	-		49.7	24.6	K.YKQVEQYMSFHKLPADT*R.Q
nucleotide gated potassium channel  Hypothetical protein BC007540 C1		S248S251			8.7	11.1	K.NLDPDPEPPS*PDS*PTETFAAPAEVR.H
Hypothetical protein BC008207 NA		\$248\$251 \$315	-		12.8	18.6	K.NDQEPPPEALDFS*DDEKEK.E
Hypothetical protein DKFZp762E1312 HJ		\$315 \$473			68.0	40.8	R.GGPAS*PGGLQGLETR.R
Hypothetical protein DKFZp762E1312 HJ		T600				20.0	K.SPGQMT*VPLCIGVSTDK.A
Hypothetical protein FLJ10154 AF		S76			-9.4	39.7	R.AS*SPPDRIDIFGR.T
Hypothetical protein FLJ10154 AF		S77			12.2	39.7	R.ASS*PPDRIDIFGR.T
Hypothetical protein FLJ10154 AF		S60			17.0	53.0	R.S*TNTAVSR.R
Hypothetical protein FLJ10154 AF		\$58\$60				18.6	R.S*RS*TNTAVSR.R
Hypothetical protein FLJ10154 AF		T61			16.3		R.ST*NTAVSR.R
Hypothetical protein FLJ20160 MF		S644			-0.1	56.0	R.IPVPSS*PVPIATIDLVQQQTEDVMPR.I
Hypothetical protein FLJ20309 IN					5.3	59.4	K.S*PQPQNTSLPMQGVAPTTHTIAQAR.Q
	ASAL3	S232			29.8	48.9	R.VGS*AS*SEGSIHVAMGNFRDPDRMPGK.T
Hypothetical protein FLJ21438 R.F.		\$164\$166			21.4	22.8	R.VGS*AS*S*EGSIHVAMGNFRDPDRMPGK.1  R.VGSAS*S*EGSIHVAMGNFR.D
Hypothetical protein FLJ21438 RA		\$166\$167	===		2.6	78.4	
	noAL3	S164S167			12.5	80.0	R.VGS*ASS*EGSIHVAMGNFR.D

		ceat 5%FDR o					
	mepoin SM	with the minimum	peak area f	or a given			
5 >100			CarT	RajiB			
>10 Protein Name	Sene	Phosphosites	5 F B	9 J J	Ascor	MOWSE	Sequence
Hypothetical protein FLJ21438 F	ASAL3	S228S231			12.8	75.4	R.DGPPSALGS*RES*LATLSELDLGAER.D
Hypothetical protein FLJ21438 F	ASAL3	<b>S</b> 72			29.9	40.5	R.TQS*VPVR.R
Hypothetical protein FLJ21438 F	ASAL3	S164S166S167			6.7	44.2	R.VGS*AS*S*EGSIHVAMGNFR.D
Hypothetical protein FLJ21438 F	ASAL3	S94			32.1	46.9	K.GS*LSMGPAPR.A
Hypothetical protein FLJ21438 F	ASAL3	T70			12.2	35.7	R.T*QSVPVR.R
Hypothetical protein FLJ21438 F	ASAL3	\$247			-0.2	21.1	R.TRGS*WSQPQPLK.A
Hypothetical protein FLJ21438 F		\$166\$167\$170	=			22.4	R.VGSAS*S*EGS*IHVAMGNFR.D
Hypothetical protein FLJ25476 2					5.5		K.HTVVEHLVSHHS*PQR.T
		S404	•		51.2	62.5	
Hypothetical protein FLJ25476 Z	NF362	S401			7.1	60.8	K.HTVVEHLVS*HHSPQR.T
Hypothetical protein KIAA0084 (HA2022) (Fragment)		<b>S</b> 32			100.0	14.4	R.RPS*PPR.R
Hypothetical protein KIAA0826 F	RYL	T745			-0.2	92.2	K.ST*GQLNLSTSPINSSSYLGYNSNAR.S
Hypothetical protein KIAA0826 F	RYL	T752			5.8	43.7	K.STGQLNLST*SPINSSSYLGYNSNAR.S
Hypothetical protein KIAA0826 F	RYL	T7458751			8.2	76.4	K.ST*GQLNLS*TSPINSSSYLGYNSNAR.S
Hypothetical protein KIAA0826 F	RYL	<b>S</b> 753	ii.		19.1	51.5	K.STGQLNLSTS*PINSSSYLGYNSNAR.S
Hypothetical protein KIAA0826 F	RYL	S744S757			11.9	14.8	K.S*TGQLNLSTSPINS*SSYLGYNSNAR.S
Hypothetical protein KIAA0826 F	RYL	T7458757				55.0	K.ST*GQLNLSTSPINS*SSYLGYNSNAR.S
Hypothetical protein KIAA0826 F			-		4.0		K.S*TGQLNLSTSPINSSSYLGYNSNAR.S
		S744		-	8.0	111.2	
Hypothetical protein KIAA0826 F		T745S753			1.2	52.0	K.ST*GQLNLSTS*PINSSSYLGYNSNAR.S
Hypothetical protein KIAA0889 S	DGA1	S64			11.5	68.9	K.SVSSMSEFES*LLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S57S64			0.6	62.1	R.TKSVS*SMSEFES*LLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S55S60			-0.8	58.0	R.TKS*VSSMS*EFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	\$57\$58			1.8	59.9	K.SVS*S*MSEFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S55S57			6.9	72.6	K.S*VS*SMSEFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 s							R.TKSVSSMS*EFES*LLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S		S60S64			1.1	40.2	
		<b>S</b> 57	•••		15.8	27.6	K.SVS*SMSEFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S55S58			6.8	60.0	K.S*VSS*MSEFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	<b>S</b> 60			1.2	70.5	K.SVSSMS*EFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S58			9.8	19.6	K.SVSS*MSEFESLLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 S	DGA1	S55S64		•	8.0	75.5	R.TKS*VSSMSEFES*LLDCSPYLAGGDAR.G
Hypothetical protein KIAA0889 s	DGA1	S55			16.1	115.2	K.S*VSSMSEFESLLDCSPYLAGGDAR.G
Hypothetical protein LOC137886 L	RYNOR	S17				16.0	K.RSS*GPR.A
				=	10.9		
Hypothetical protein LOC137886		S16		• • •	23.9	27.3	K.RS*SGPR.A
Hypothetical protein LOC137886		S235S242			5.6	54.9	K.LGSLTPEIVSTPSS*PEEEDKS*ILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L	BXN2B	T232S242			2.6	52.0	K.LGSLTPEIVST*PSSPEEEDKS*ILNAVVLIDDSVPTT
Hypothetical protein LOC137886	3XN2B	T232S234			4.3	51.0	K.LGSLTPEIVST*PS*SPEEEDKSILNAVVLIDDSVPTT
Hypothetical protein LOC137886 L	BXN2B	S16S17		•	100.0	21.7	K.RS*S*GPR.A
Hypothetical protein LOC137886 L	3XN2B	S234S235			2.9	31.3	K.LGSLTPEIVSTPS*S*PEEEDKSILNAVVLIDDSVPTT
Hypothetical protein LOC137886 [					2.9		
Hypothetical protein LOC137886 L	3XN2B	S224S234		-	1.6	17.9	K.LGS*LTPEIVSTPS*SPEEEDKSILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L  Hypothetical protein LOC137886 L  Hypothetical protein LOC137886 L	BXN2B BXN2B	\$224\$234 \$234\$242		-			KLGS*LTPEIVSTPS*SPEEEDKSILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L	BXN2B BXN2B BXN2B	\$224\$234 \$234\$242 \$231\$234			1.6	17.9	KLGS*LTPEIVSTPS*SPEEEDKSILNAVVLIDDSVPTTI KLGSLTPEIVS*TPS*SPEEEDKS*ILNAVVLIDDSVPTTI KLGSLTPEIVS*TPS*SPEEEDKSILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L  Hypothetical protein LOC137886 L  Hypothetical protein LOC137886 L	BXN2B BXN2B BXN2B	\$224\$234 \$234\$242 \$231\$234			1.6	17.9	KLGS*LTPEIVSTPS*SPEEEDKSILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L	3XN2B 3XN2B 3XN2B ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260			1.6	17.9 23.4 35.1	KLGS*LTPEIVSTPS*SPEEEDKSILNAVVLIDDSVPTTI KLGSLTPEIVS*TPS*SPEEEDKS*ILNAVVLIDDSVPTTI KLGSLTPEIVS*TPS*SPEEEDKSILNAVVLIDDSVPTTI
Hypothetical protein LOC137886 L	3XN2B 3XN2B 3XN2B ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 T440			1.6 11.4 4.3 171.7	17.9 23.4 35.1 58.0	KLGS*LTPENSTPS*SPEEEDKSILNAVVLIDDSVPTTI  KLGSLTPENS*TPS*SPEEEDKS*ILNAVVLIDDSVPTTI  KLGSLTPENS*TPS*SPEEEDKSILNAVVLIDDSVPTTI  RAMDNHS*DS*EEELAAFCPQLDDSTVAR.E
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 R Hypothetical protein LOC162427 R	3XN2B 3XN2B 3XN2B ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 T440			1.6 11.4 4.3 171.7 31.8	17.9 23.4 35.1 58.0 47.2	KLGS-LTPENSTPS-SPEEEDKSILNAVVLIDDSVPTTI  KLGSLTPENSTPS-SPEEEDKS-LNAVVLIDDSVPTTI  KLGSLTPENS-TPS-SPEEEDKS-LNAVVLIDDSVPTTI  RAMDNHS-TDS-EEELAAFCPQLDDSTVARE  RSPSSDLDT-DAEGDDFELLDQSELSQLDPASSRS
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC152427 F Hypothetical protein LOC162427 F Hypothetical protein LOC162427 F Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 T440 3 \$435\$436 3 \$435\$436			1.6 11.4 4.3 171.7 31.8 8.4 3.9	17.9 23.4 35.1 58.0 47.2 90.0	KLGS*LTPENSTPS*SPEEEDKSILNAVVLIDDSVPTTI  KLGSLTPENSTPS*SPEEEDKS*LNAVVLIDDSVPTTI  KLGSLTPENS*TPS*SPEEEDKSILNAVVLIDDSVPTTI  RAMDNHS*DS*EEELAFCPQLIDDSTVARE  R SPSSDLDT*DAEGDDFELLDQSELSQLDPASSR S  R SPS*S*DLDT*DAEGDDFELLDQSELSQLDPASSR S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 T440 3 \$435\$436 3 \$435\$436 3 \$435\$436			1.6 11.4 4.3 171.7 31.8 8.4 3.9	17.9 23.4 35.1 58.0 47.2 90.0 67.6	KLGS'LTPENSTPS'SPEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEDKS'LNAVVLIDDSVPTTI RAMDNHS'DS'EELAAFCPOLDDSTVAR.E R.SPSSDLDT'DAEGDDFELLDOSELSQLDPASSR.S R.SPSS'DLDT'DAEGDDFELLDOSELSQLDPASSR.S R.S*PSS'DLDT'DAEGDDFELLDOSELSQLDPASSR.S R.S*PSS'DLDT'DAEGDDFELLDOSELSQLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 T440 3 \$435\$436 3 \$435\$436 3 \$435\$436 3 \$435\$436 3 \$435\$436			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDDSVPTTI KLGSLTPENS'TPS'SPEEDKSILNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPOLDDSTVARE R.SPSSDLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.S'PSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 \$ \$2585260 3 \$445 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436			1.6 11.4 4.3 171.7 31.8 8.4 3.9	17.9 23.4 35.1 58.0 47.2 90.0 67.6	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI  KLGSLTPENS'TPS'SPEEEDKSILNAVVLIDDSVPTTI  RAMDNHS'DS'EEELAFCPOLDDSTVARE  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.DLPOFPSINMDPAGLDDEDDTS'IGMPSLMYR.S  R.DLPOFPSINMDPAGLDDEDDTS'IGMPSLMYR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC152427 F Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 \$ \$2585260 3 \$445 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDDSVPTTI KLGSLTPENS'TPS'SPEEDKSILNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPOLDDSTVARE R.SPSSDLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.S'PSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLDT'DAEGDDFELLDQSELSQLDPASSR'S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$2585280 3 \$440 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436			1.6  11.4  4.3  171.7  31.8  8.4  3.9  12.2  12.1  8.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI  KLGSLTPENS'TPS'SPEEEDKSILNAVVLIDDSVPTTI  RAMDNHS'DS'EEELAFCPOLDDSTVARE  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDGSELSQLDPASSR.S  R.DLPOFPSINMDPAGLDDEDDTS'IGMPSLMYR.S  R.DLPOFPSINMDPAGLDDEDDTS'IGMPSLMYR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 \$ \$2585260 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436 3 \$435436			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI RAMDNHS'DS'EELAAFCPOLDDSTVARE R.SPSSDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DLPOFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.DLPOFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.DLPOFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC152427 F Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$231\$234 3 \$258\$260 3 \$435436 3 \$435436 3 \$4355436 3 \$4355436 3 \$4355436 3 \$4355436 3 \$4355436 3 \$4355436 3 \$4355436 3 \$4355436			11.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5	KLGS'LTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPQLDDSTVARE R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DLPDFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.DLPDFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 \$3 \$2585200 \$7 1440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440			11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5	KLGS'LTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT.  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT.  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT.  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT.  RAMDNHS'DS'EEELAFCPPOLDDSTVARE  R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.DPOFPSINMDPAGLDDEDDT'SIGMPSLMYR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.  R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S.
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG ETREG ETREG ETREG ETREG ETREG ETREG ETREG ETREG ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 3 \$2585280 3 7440 3 \$43584367440 3 \$43584367440 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$4354365436 3 \$435436536 3 \$435643666 3 \$4356436666 3 \$435643666666666666666666666666666666666			1.6 11.4 4.3 171.7 31.8 8.4 12.2 12.1 19.3 7.9 8.9	17.9 23.4 35.1 58.0 90.0 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPOLDDSTVARE RSPSSDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.DLPDFPSINMDPAGLDDEDDT'SIGMPSLMYRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SDLDTDAEGDDFELLDQSELSQLDPASSRS
Hypothetical protein LOC137886 L Hypothetical protein LOC152427 F Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$231\$224 \$231\$224 \$3 \$2585280 \$3 \$435438 \$3 \$43554387440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354365 \$3 \$335 \$3 \$335 \$3 \$3357310\$333 \$3 \$3357440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 37.5 11.3	17.9 23.4 35.1 55.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI RAMONHS'DS'EEELAAFCPOLDOSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLPDFPSINMDPAGLDDEDT'SIGMPSLMYR'S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDL
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 \$3 \$2585260 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354363 \$3 \$4357440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 19.3 7.9 8.9	17.9 23.4 35.1 58.0 90.0 67.6 77.7 70.9 36.4 89.5 11.1 22.7 96.6 52.8 40.5	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI RAMDNHS'DS'EELAAFCPQLDDSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DLPDFPSINMDPAGLDDEDTS'IGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.S'PS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 \$3 \$2585260 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354363 \$3 \$4357440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 37.5 11.3	17.9 23.4 35.1 55.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI RAMONHS'DS'EEELAAFCPOLDOSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLPDFPSINMDPAGLDDEDT'SIGMPSLMYR'S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDLDT'DAEGDDFELSQUPASSR'S R.SPS'SDL
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 \$3 \$2585260 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354363 \$3 \$4357440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 37.5 11.3	17.9 23.4 35.1 58.0 90.0 67.6 77.7 70.9 36.4 89.5 11.1 22.7 96.6 52.8 40.5	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'ILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI RAMDNHS'DS'EELAAFCPQLDDSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DLPDFPSINMDPAGLDDEDTS'IGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.S'PS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DPEESFAR.D
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B	\$224\$234 \$224\$242 \$234\$242 \$231\$224 \$3 \$2585260 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440 \$3 \$4354357440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 19.3 7.9 8.9 17.1 37.5 11.3 10.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9 52.8 40.5 21.9	KLGS'LTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPQLIDDSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DLPDFPSINMDPAGLDDEDTS'IGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.GT'PLT'EGS'EDLDGHS'DPEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F	BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$234\$242 \$234\$242 \$231\$234 \$3 \$2585280 \$1 7440 \$3 \$435\$436 \$3 \$435\$4367440 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$3 \$435\$436 \$440 \$3 \$435\$436 \$440 \$4 \$435\$436 \$4 \$456\$440 \$4 \$456\$			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 19.3 7.9 8.9 17.1 10.2 -1.2	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5 111.1 32.7 96.6 24.9 52.8 40.5 21.9	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTTI RAMDNHS'DS'EEELAAFCPOLDDSTVARE R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSR.S R.DPDFPSINMDPAGLDDEDDT'SIGMPSLMYR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDTDAEGDDFELLDQSELSQLDPASSR.S R.SPS'SDLDTDAEGDDFELLDQSELSQLDPASSR.S R.GOT'PLT'EGS'EDLDGHS'DFEESFAR.D R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC137886 L Hypothetical protein LOC132427 F Hypothetical protein LOC162427 F	BXN2B	\$224\$234 \$234\$242 \$231\$234 \$3 \$2585280 \$3 1440 \$3 \$43584361440 \$3 \$43584361440 \$3 \$43584365 \$3 \$43584365 \$3 \$43584365 \$3 \$43584365 \$3 \$43584365 \$3 \$43584365 \$3 \$43584365400 \$3 \$435843600 \$3 \$4358436000 \$3 \$4358436000000000000000000000000000000000000			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 37.5 11.3 10.2 -1.2 7.1	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9 52.8 40.5 21.9 17.0 87.1	KLGS'LTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT  KLGSLTPENSTPS'SPEEEDKS'LNAVVLIDDSVPTT  RAMDNHS'DS'EEELAFCPOLDDSTVARE  R.SPSS'DLDT'DAEGDDFELLDOSELSOLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDOSELSOLDPASSR.S  R.SPSS'DLDT'DAEGDDFELLDOSELSOLDPASSR.S  R.DLPDFPSINMDPAGLDEEDTS'IGMPSLMYR.S  R.DLPDFPSINMDPAGLDEEDTS'IGMPSLMYR.S  R.SPS'SDLDT'DAEGDDFELLDOSELSOLDPASSR.S  R.DLPDFPS'INMDPAGLDEEDTS'IGMPSLMYR.S  R.SPS'SDLDTDAEGDDFELLDOSELSOLDPASSR.S  R.SPS'SSLDTDAEGDDFELLDOSELSOLDPASSR.S
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F Hypothetical protein LOC342826 N Hypothetical protein LOC348262 N	BXN2B	\$224\$234 \$234\$24 \$234\$24 \$231\$224 \$231\$224 \$3 \$2585280 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$3 \$435436740 \$4 \$435436740 \$4 \$435436740 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$5 \$			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 10.2 -1.2 7.1 28.1	17.9 23.4 35.1 58.0 47.2 90.0 67.8 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9 52.8 40.5 21.9 17.0 87.1 55.1 14.2	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI RAMONHS'DS'EEELAAFCPOLDOSTVARE RSPSSIDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.DLDFDFPSINMDPAGLDDEDDT'SIGMPSLMYRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SSLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SSLTTPAHEENVRF
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F Hypothetical protein LOC342828 Hypothetical protein LOC348282 L Hy	BXN2B BXN2B BXN2B ETREG	\$224\$234 \$224\$234 \$234\$242 \$231\$224 \$3 \$2585260 \$3 \$440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$4354367440 \$3 \$43567456 \$5568 \$524 \$525			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 17.1 37.5 11.3 10.2 -1.2 7.1 13.1	17.9 23.4 35.1 58.0 47.2 90.0 67.6 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9 40.5 21.9 17.0 87.1 14.2 40.6	KLGS'LTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'LNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKS'LNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEDKSILNAVVLIDOSVPTTI RAMONHS'DS'EEELAAFCPOLDOSTVARE R.SPSSOLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'S'DLDT'DAEGDDFELLDQSELSQLDPASSR'S R.DLPDFFSINMDPAGLDDEDT'SIGMPSLMYR'S R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSR'S R.SPS'SSEIFTPAHEENVR.F R.SPPS'SSEIFTPAHEENVR.F R.SPPS'SSEIFTPAHEENVR.F R.SPPS'SSEIFTPAHEENVR.F
Hypothetical protein LOC137886 L Hypothetical protein LOC162427 F Hypothetical protein LOC342826 N Hypothetical protein LOC348282 N Hypothetical protein LOC348282 N	BXN2B BXN2B BXN2B BXN2B BXN2B BXN2B BXN2B BXN2B ETREG	\$224\$234 \$224\$234 \$234\$242 \$231\$234 \$3 \$2585260 \$3 \$440 \$3 \$435\$436\$7440 \$3 \$435\$436\$7440 \$3 \$435\$436\$7440 \$3 \$435\$436\$7440 \$3 \$435\$436\$7440 \$3 \$435\$436\$7440 \$5 \$435\$436\$7440 \$5 \$435\$436\$7540 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440 \$5 \$435\$436\$75440			1.6 11.4 4.3 171.7 31.8 8.4 3.9 12.2 12.1 8.2 19.3 7.9 8.9 17.1 10.2 -1.2 7.1 28.1	17.9 23.4 35.1 58.0 47.2 90.0 67.8 77.7 70.9 36.4 89.5 11.1 32.7 96.6 24.9 52.8 40.5 21.9 17.0 87.1 55.1 14.2	KLGS'LTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI KLGSLTPENSTPS'SPEEEDKSILNAVVLIDOSVPTTI RAMONHS'DS'EEELAAFCPOLDOSTVARE RSPSSIDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPSS'DLDT'DAEGDDFELLDQSELSQLDPASSRS R.DLDFDFPSINMDPAGLDDEDDT'SIGMPSLMYRS R.SPS'SDLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SSLDT'DAEGDDFELLDQSELSQLDPASSRS R.SPS'SSLTTPAHEENVRF

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-3 42 PSM	war are million	CarT	RajiB			
>10 >100 Protein Name Gene	Phosphosites	# # # # # #	# # #	Ascor	MOWSE	Sequence
Hypothetical protein LOC55580 CCDC88A			<u> </u>	3.5	44.5	R.DGLHFLPHASS*SAQSPCGSPGMK.R
Hypothetical protein LOC55580 CCDC88A  Hypothetical protein LOC729440 CCDC61	\$158\$162 \$392\$395			37.5 57.5	40.8 86.8	R.DGLHFLPHASSSAQS'PCGS'PGMK.R  R.LGS'GGS'GDGPSVSWSR.Q
Hypothetical protein MGC22014 TET3	T657S666			18.6	18.0	K.AENPLT*PTLSGFLES*PLK.Y
Hypoxia inducible factor 1 alpha subunit HIF3A	S22S28	ij		100.0	14.1	K.S'RDAARS'R.R
Hypoxia inducible factor 1 alpha subunit HIF1A	S687	•	. =	63.9	53.0	R.S*PNVLSVALSQR.T
ig alpha CD79A	S215		-	15.2	30.5	R.GLQGTYQDVGS'LNIGDVQLEKP
IGF II mRNA binding protein 3 <sub>IGF2BP3</sub>	S184			22.0	51.9	R.QGS*PGSVSK.Q  K.ALSSLHGDDQDS*EDEVLTIPEVK.V
IGF II receptor IGF2R	\$2409 \$2479		• • •	25.8	65.3 23.6	K.LVS*FHDDSDEDLLHI
IGF II receptor IGF2R	\$2479\$2484			100.0	45.4	K.LVS*FHDDS*DEDLLHI
IGF II receptor IGF2R	S2484			19.9	22.2	K.LVSFHDDS*DEDLLHI
IK factor <sub>IK</sub>	S460			49.0	76.3	K.QLGDFFGMSNSYAECYPATMDDMAVDS*DEEVDYSK.M
Immediate early response erythropoietin 4 ZC3H15  Immediate early response erythropoietin 4 ZC3H15	\$328			11.1	74.2	R.YTQGTGGDEVDDSVS*VNDIDLSLYIPR.D  R.YTQGTGGDEVDDS*VSVNDIDLSLYIPR.D
Immediate early response erythropoietin 4 ZC3H15	\$326 \$381		-	100.0	42.7 52.3	R.S*DLEEDNER.E
Immediate early response erythropoletin 4 ZC3H15	T315			-0.4	28.5	R.YT*QGTGGDEVDDSVSVNDIDLSLYIPR.D
Immunoglobulin superfamily, member 3 IGSF3	T637	Ė		15.1	16.9	R.TRT*AIEK.A
IMP dehydrogenase 2 IMPDH2	S159			8.9	33.6	R.LVGIIS*SR.D
IMP dehydrogenase 2 IMPDH2  Importin 7 IPO7	S416			100.0	45.4	R.GMGS*LDAMDK.H
Importin 7 IPO7	Y876S886 S886S903			31.9	73.8	R.
Importin 7 IPO7	S886T898			25.2	81.1	R. AMACHAEUENDEDDDEAEDDDETTEL CONDEDDDDEDCOEVI EII
Importin 7 IPO7	S886Y915			15.2	67.6	R. AVACUAEUENING*NDDDEAEDDDETEEI GEDEDDIDEDGOEV*I EII
Importin 7 IPO7	T898S903			12.6	29.7	R. AVACUAEUEAINENNNNEAENNNET*EEI GE*NENNINENGOEVI EII
Influenza virus NS1A binding protein IVNS1ABF				22.5	68.9	K.SLS*FEMQQDELIEKPMSPMQYAR.S
Inner centromere protein INCENP	Y818S824T828 S142T145			13.2	50.5	K.INPDNY*GMDLNS*DDST*DDEAHPR.K  R.AAAAAAAATMALAAPS*SPT*PESPTMLTK.K
Inner centromere protein INCENP	S142S148			25.3	55.2	R.AAAAAAAATMALAAPS*SPTPES*PTMLTK.K
Inner centromere protein INCENP	Y818S827T828			8.2	71.4	K.INPDNY*GMDLNSDDS*T*DDEAHPR.K
Inner centromere protein INCENP	\$302\$312	<b>.</b>		7.2	14.5	R.TDSQS*VRHSPIAPSS*PSPQVLAQK.Y
Inner centromere protein INCENP	S824S827T828			8.9	75.8	K.INPDNYGMDLNS'DDS'T"DDEAHPR.K  R.IAQVS'PGPR.D
Inner centromere protein INCENP	\$263 \$300\$311	==		100.0	12.0	R.TDS*QSVRHSPIAPS*SPSPQVLAQK.Y
Inner centromere protein INCENP	S142T150	•		5.5	21.2	R.AAAAAAAATMALAAPS*SPTPESPT*MLTK.K
Inorganic pyrophosphatase 2 PPA2	<b>S</b> 317		•	14.3	57.4	R.SLVESVSSS*PNKESNEEEQVWHFLGK
Inorganic pyrophosphatase 2 PPA2	S315		-	18.4	24.7	R.SLVESVS*SSPNKESNEEEQVWHFLGK
Inorganic pyrophosphatase 2 ppA2	S316			15.3	44.2	R.SLVESVSS*SPNKESNEEEQVWHFLGK
Inorganic pyrophosphatase 2 PPA2  Inositol 1,4,5-trisphosphate receptor type 3 ITPR3	\$313 \$934	<u> </u>		19.4	79.1	R.SLVES*VSSSPNKESNEEEQVWHFLGK  R.KQS*VFSAPSLSAGASAAEPLDR.S
Inositol 1,4,5-trisphosphate receptor type 3  TPR3	S937			3.2	23.1	R.KQSVFS*APSLSAGASAAEPLDR.S
Inositol 1,4,5-trisphosphate receptor type 3  TPR3	S2670			100.0	52.3	R.LGFVDVQNCIS*R
Inositol polyphosphate 5-phosphatase INPP5J	\$545\$547			31.9	17.9	R.S'PS'PQSR.R
Inositol-trisphosphate 3-kinase B ITPKB	S174S176		₽.₽	100.0	22.0	R.ARS'PS'PCPFR.S
Integrator complex subunit 1  NTS1	\$134 \$166			-0.8	37.2	R.RPSAAAKPS'GHPPPGDFIALGSK.G  K.SS'PEQPIGGGR.I
Integrin alpha 4 ITGA4	S1021			17.8	41.8	R.RDS*WSYINSK.S
Intercellular adhesion molecule 1  CAM1	T530			25.4	35.8	K.GTPMKPNTQAT*PP
Intercellular adhesion molecule 1 ICAM1	T527			-0.4	31.4	K.GTPMKPNT*QATPP
Interferon gamma inducible protein 16  F 16	S153			58.0	90.8	K.VSEEQTQPPS*PAGAGMSTAMGR.S
Interferon gamma inducible protein 16  F 16	T723 S36			5.0	12.2	K.DILNPDSSM#ET*SPDFFF  R.KELGDS*PK.D
Interferon regulatory factor 2 binding IRF2BP2	S71			100.0 54.1	73.3	R.S'PPGAAASAAAKPPPLSAK.D
Interferon regulatory factor 2 binding IRF2BP2 protein 2	\$406			5.1	25.5	K.IPMTPTSSFVSPPPPTAS*PHSNR.T
Interferon regulatory factor 2 binding IRF2BP2 protein 2	S423	<b></b>		27.0	68.8	R.TTPPEAAQNGQS*PMAALILVADNAGGSHASK.D
Interferon regulatory factor 2 binding IRF2BP2 protein 2	T413S423			2.6	36.4	R.TT*PPEAAQNGQS*PMAALILVADNAGGSHASK.D
Interferon regulatory factor 2 binding  RF2BP2 protein 2   Interferon regulatory factor 2 binding  RF2BP2	T413 S175		-	-0.5	21.1	R.TT*PPEAAQNGQSPMAALILVADNAGGSHASK.D  K.LEEPPELNRQS*PNPR.R
Interferon regulatory factor 2 binding IRF2BP2	S175 T404			3.5	23.5	K.IEEPPELNRQS PNPK.R  K.IPMTPTSSFVSPPPPT*ASPHSNR.T
protein 2 Interferon regulatory factor 3 IRF3	S173			31.8	36.7	R.S*PSLDNPTPFPNLGPSENPLKR.L
Interferon regulatory factor 3 IRF3	<b>S</b> 175			26.3	53.9	R.SPS*LDNPTPFPNLGPSENPLKR.L
Interleukin 17 receptor IL17RA	S726S736	<u> </u>		18.1	45.3	R.NSVLFLPVDPEDS*PLGSSTPMAS*PDLLPEDVR.E

Peak Area	0 abundano		ompared to	the			
.5 .3 0	timepoint v 42 PSM	with the minimum	peak area fo	or a given			
3 5 >10	>100 			_RajiB_			
Interleukin enhance	Protein Name Gene er binding factor 3 <sub>ILF3</sub>	Phosphosites S792	8 % &	8 % %	Ascor 33.3	MOWSE 112.9	Sequence K.GYNHGQGSYSYSNSYNS*PGGGGGSDYNYESK.F
Interleukin enhance	er binding factor 3 <sub>ILF3</sub>	S787			9.1	21.9	K.GYNHGQGSYSYS*NSYNSPGGGGGSDYNYESK.F
Interleukin enhance	er binding factor 3 <sub>ILF3</sub>	<b>S</b> 476				51.5	R. DOUVEDBAFFTFAVDALA/ADADA//FAVETBBAAFDBDATAFOCDII
Interleukin enhance	er binding factor 3 ILF3	S482	-	•••		76.2	K.GEDS*AEETEAKPAVVAPAPVVEAVSTPSAAFPSDATAEQGPILTK.
Interleukin enhance	er binding factor 3 ILF3	S382			28.4	73.6	K.RPMEEDGEEKS*PSK.K
Interleukin enhance	er binding factor 3 ILF3	S789			7.8	36.9	K.GYNHGQGSYSYSNS*YNSPGGGGGSDYNYESK.F
Interleukin enhance	er binding factor 3 ILF3	\$476\$477				35.4	R. DOWN CODE AFFET AND ANALADADA OF AN OTTO CA AFFED DATA FOOD
	er binding factor 3 ILF3	T469S476S477				23.9	K. VI ODMGI DTYCAECODOSSIVCEDSAECTEARDANA/ADADIA/EANST
	er binding factor 3 ILF3	S860			7.4	108.9	K.QGGYSQSNYNS'PGSGQNYSGPPSSYQSSQGGYGR.N
	er binding factor 3 <sub>ILF3</sub>	\$868		-	10.2	66.9	K.QGGYSQSNYNSPGSGQNYS*GPPSSYQSSQGGYGR.N
	er binding factor 3 ILF3	\$476\$477\$482	-			39.6	R.  DOLONGED A FETT AND ANALADADIA/FAVIET DE A AFDEDATA FOCE  K. G. GGYSOSNY'NSPGSGONYSGPPSSYGSSGGGYGR. N
	er binding factor 3 ILF3	Y858 \$854		Ξ	0.0	31.0	K.OGGYS'QSNYNSPGSGQNYSGPPSSYQSSQGYGR.N
	er binding factor 3 ILF3	T469S476		•	9.0	15.3	К.
	er binding factor 3 ILF3	Y790	•		-0.3	71.8	K.GYNHGQGSYSYSNSY*NSPGGGGGSDYNYESK.F
	Intersectin 1 ITSN1	S315		• •	-0.3	29.0	R.SGS*GISVISSTSVDQR.L
	Intersectin 2 ITSN2	\$883\$888			14.2	54.0	R.TVS*PGSVS*PIHGQGQVVENLK.A
	Intersectin 2  TSN2	S886S888		• • •	12.6	33.2	R.TVSPGS*VS*PIHGQGQVVENLK.A
	Intersectin 2 ITSN2	\$883\$886			10.1	57.1	R.TVS*PGS*VSPIHGQGQVVENLK.A
	Intersectin 2 ITSN2	S888			0.4	41.6	R.TVSPGSVS*PIHGQGQVVENLK.A
	Intersectin 2  TSN2	T881		• • •	10.1	26.4	R.T*VSPGSVSPIHGQGQVVENLK.A
	Intersectin 2 ITSN2	S886			22.2	28.4	R.TVSPGS*VSPIHGQGQVVENLK.A
	Intersectin 2 ITSN2	S883			7.6	34.5	R.TVS*PGSVSPIHGQGQVVENLK.A
	Intersectin 2  TSN2	T881S888	<u> </u>		6.3	37.9	R.T*VSPGSVS*PIHGQGQVVENLK.A
Intraflagellar trans	port protein IFT20 <sub>IFT20</sub>	S72S76		<b>-</b>	100.0	12.6	K.S'LAVS'PR.L
		S925			9.8	53.1	R.SALSSS*LR.D
		S512			76.7	84.8	R.NS*WDSPAFSNDVIR.K
		S87		■.		19.4	K.LQHS*TSILR.K
	protein 1	S802		<u> </u>	-0.4	16.3	R.SALSS*SLRDLSEAGVHH
	omain-containing IQSEC1 protein 1	S926S940		===	27.5	74.8	R.RSS*AGSLESNVEGSIIS*SPHMR.R  R.RSS*AGSLESNVEGSIISS*PHMR.R
- IQ motir and SEC7 to	protein 1	S926S941			9.9	76.6	R.SSAGS*LESNVEGSIIS*SPHMR.R
IQ motif and SEC7 d		\$929\$940 \$929\$941			9.0	54.3	R.SSAGS*LESNVEGSIISS*PHMR.R
	protein 1	S929S932S941			8.1	12.4	R.RSSAGS*LES*NVEGSIISS*PHMR.R
IQ motif and SEC7 d	protein 1	S932S940		<del>-</del>	-2.2	46.7	R.SSAGSLES*NVEGSIIS*SPHMR.R
	protein 1 IQGAP2 IQGAP2	S16		•	39.3	53.9	R.YGS*IVDDER.L
	IQGAP2 IQGAP2	Y14			20.1	34.0	R.Y'GSIVDDER.L
	MPST	S15			7.3	37.8	R.ARS*PSVAAMASPQLCR.A
Isoform 2 of Armadillo	repeat-containing ARMC10 protein 10	<b>S</b> 45			29.0	80.4	K.S*AEDLTDGSYDDVLNAEQLQK.L
Isoform 2 of Chromatin c	omplexes subunit BAP18 BAP18	<b>S</b> 35			-0.2	26.1	K.LGELTMQLHPVADS*SPAGAQIK.A
Isoform 2 of EF-han domain-con	d calcium-binding CRACR2A taining protein 4B	<b>S</b> 473			120.5	60.6	R.IIS*VEEDPLPQLLDGGFEQPLSK.C
Isoform 2 of Eomes	odermin homolog EOMES	T177S187			4.5	25.2	R.DNYDSMYT*ASENDRLTPS*PTDSPR.S
resistance guanine nu		S1487			11.2	16.4	R.GGQSDDDEDEGVPAS*YHTVSLQLLDLMHTLHTR.A
resistance quanine nu	cleotide exchange	S1476			26.2	55.3	R.GGQS*DDDEDEGVPASYHTVSLQLLDLMHTLHTR.A
	HBS1-like protein HBS1L	S483	<u> </u>		24.5	50.5	R.S*PGIDSNIDLSVLIK.N
	specific protein	T166S167			100.0	13.5	R.RRNT*S*PR.E
	of Protein SOGA1 SOGA1	S141S142			46.7	64.6	R.LLGLELALS'S'DAESAAGGPAGVR.T
е	uanine nucleotide ARHGEF1 xchange factor 18 uanine nucleotide ARHGEF1				8.7	32.5	R.S'RSVPVSFYEIR.S
е	uanine nucleotide ARHGEF1 xchange factor 18 uanine nucleotide ARHGEF1				97.3	75.0	R.RLS*LDASAVDEEPCLPR.T  R.SVPVS*FYEIR.S
е	uanine nucleotide ARHGEF1 xchange factor 18 uanine nucleotide ARHGEF1				13.3	38.3 17.8	R.RLS*CLR.S
lsoform 2 of Rho g	xchange factor 18 uanine nucleotide ARHGEF1				100.0 36.8	63.9	R.DSLFSSLAGS*QDLSR.R
е	xchange factor 18  ARHGEF1				-0.3	28.6	R.SRS*VPVSFYEIR.S
Isoform 2 of Uncha	racterized protein C15orf39	S496S497			100.8	76.2	K.EGARPPS*S*PPMPVIDNVFSLAPYR.D
Isoform 3 of Proli	C15orf39 ne-rich protein 12 PRR12	S651	• •		73.0	34.4	R.TEDEEFLIQHLLQAPS*PPR.T
Isoform 3 of UV excis	sion repair protein RAD23A	Y197				71.6	R.AVEY*LLTGIPGSPEPEHGSVQESQVSEQPATEAGENPLEFLR.D
Isoform 3 of UV excis		S219			3.0	26.2	R.AVEYLLTGIPGSPEPEHGSVQESQVS*EQPATEAGENPLEFLR.D
Isoform 3 of UV excis		S205	ij		2.2	39.8	R.AVEYLLTGIPGS*PEPEHGSVQESQVSEQPATEAGENPLEFLR.D
Isoform 4 of Interleukin		<b>S</b> 476	•			49.6	R. NO-OUTGENEAUETEAUDANA/ADADIA/EANGTDGAAEDGDATAENNA/
Isoform 4 of Interleukin		S482			60.3	70.0	K.GEDS*AEETEAKPAVVAPAPVVEAVSTPSAAFPSDATAENVK.Q
Isoform 4 of Interleukin	enhancer-binding ILF3 factor 3	T486			0.3	37.4	K.GEDSAEET*EAKPAVVAPAPVVEAVSTPSAAFPSDATAENVK.Q
Isoform 4 of Interleukin	enhancer-binding ILF3 factor 3	T469S476S477				21.4	K.  18 ODINGI BTSCAFORDOSON/CEDRAFETEAK/DANA/ADADIA/EAN/ET
<u> </u>							

Peak Area	0 abunda		compared to	the			
.5 -3	timepoir PSM	nt with the minimum	peak area f	or a given			
3 5 >10	86 100			RajiB			
Isoform 4 of Interleukin enl	Protein Name Gene hancer-binding ILF3	Phosphosites T469S476	£ £ £	5 % B	Ascor	MOWSE 18.2	Sequence K.
Isoform 4 of	factor 3 f Protein YIF1B YIF1B	T285S287			100.0	11.3	R.IT'RS'GR.C
Isoform 5 of Mitochondria	I fission factor MFF	S146	•		100.0	24.0	R.NDS*LPVLR.G
	ITK <sub>ITK</sub>	Y512		•	26.0	48.1	R.FVLDDQY*TSSTGTKFPVK.W
	IWS1 homolog IWS1	\$302\$304\$313			8.9	29.6	R.VSDS*ES*EGPQKGPAS*DS*ETEDASR.H
	IWS1 homolog IWS1	S287S289			100.0	46.8	R.NQAS'DS'ENEELPKPR.V
	IWS1 homolog IWS1	\$398\$400			100.0	58.0	K.AAVLS*DS*EDEEK.A
	IWS1 homolog IWS1	\$415\$420\$422			100.0	53.9	R.VVS*DADDS*DS*DAVS*DK.S
	IWS1 homolog IWS1	\$300\$302\$304	<b></b>		17.4	38.3	R.VS'DS'ES'EGPQKGPASDS'ET'EDASR.H  K.TIAS'DS'EEEAGKELSDK.K
	IWS1 homolog IWS1	\$438\$440 \$274\$276\$287		• • •	12.5	13.1	R.IS'DS'ESEDPPRNQAS'DS'ENEELPKPR.V
	IWS1 homolog IWS1	T67S69S80S82			56.4	43.6	K.GHHVT*DS*ENDEPLNLNAS*DS*ESEELHR.Q
	IWS1 homolog IWS1	T67S69S80S82	• • • •		100.0	22.6	K.GHHVT*DS*ENDEPLNLNAS*DS*ES*EELHR.Q
	IWS1 homolog IWS1	S511S513			100.0	89.5	K.EAEDS*DS*DDNIKR.G
	IWS1 homolog IWS1	\$248\$250			28.3	53.4	R.IS*DS*ESEDPPR.H
	IWS1 homolog IWS1	S248S250S261			19.2	13.3	R.IS*DS*ESEDPPRHQAS*DS*ENEELPKPR.I
	IWS1 homolog IWS1	S93S95			5.7	13.3	R.QKDS'DS'ESEER.A
	IWS1 homolog IWS1	\$300\$304\$313			12.6	17.8	R.VS*DSES*EGPQKGPAS*DS*ETEDASR.H
	IWS1 homolog IWS1	S415S420S422	<b></b>		52.3	75.8	R.VVS*DADDS*DS*DAVSDK.S
	IWS1 homolog IWS1	\$300\$302\$304			5.8	11.5	R.VS*DS*ES*EGPQKGPAS*DS*ETEDASR.H
	IWS1 homolog IWS1	S196S198			100.0	26.2	R.HQAS*DS*ENEEPPKPR.M  R.HQAS*DS*ENEELPKPR.I
	IWS1 homolog IWS1	\$261\$263 \$80\$82			100.0	49.8	K.GHHVTDSENDEPLNLNAS*DS*ESEELHR.Q
	IWS1 homolog IWS1	\$69\$80\$82			13.8	34.5	K.GHHVTDS*ENDEPLNLNAS*DS*ESEELHR.Q
	IWS1 homolog IWS1	T67S80S84	•		3.8	14.5	K.GHHVT*DSENDEPLNLNAS*DSES*EELHR.Q
	IWS1 homolog IWS1	\$377			100.0	91.7	K.MDS*DEDEKEGEEEK.V
	IWS1 homolog IWS1	S313S315		•	25.1	33.1	K.GPAS*DS*ETEDASR.H
	IWS1 homolog IWS1	\$400			24.1	32.2	K.AAVLSDS*EDEEK.A
	IWS1 homolog IWS1	T67S69S80S84			14.4	15.0	K.GHHVT*DS*ENDEPLNLNAS*DSES*EELHR.Q
	IWS1 homolog IWS1	\$300\$302\$313	Ŧ.		18.5	22.8	R.VS*DS*ESEGPQKGPAS*DS*ETEDASR.H
	IWS1 homolog IWS1	S276S278S287			3.9	13.0	R.ISDS*ES*EDPPRNQAS*DS*ENEELPKPR.V
	Janus kinase 3 JAK3	\$17\$20	<u> </u>		18.2	79.2	R.SCS'LLS'TEAGALHVILPAR.G
Janus kinase and microtub	protein 1  JAW1 LRMP				30.2	40.0	R.HTS*LNDLSLTR.D  R.S*ASPTIEAQGTSPAHDNIAFQDSTSKDK.T
	JAW1 LRMP	\$73 \$75			13.2	71.0	R. SAS'PTIEAGGTSPAHDNIAFQDSTSK.D
	JAW1 <sub>LRMP</sub>	S75T83			27.7	47.8	R.SAS*PTIEAQGT*SPAHDNIAFQDSTSK.D
	JAW1 <sub>LRMP</sub>	S36			5.1	29.0	R.HTS*STDGTITSSDPGLEILNMASCDLDR.N
	JAW1 <sub>LRMP</sub>	S403		•	10.4	27.6	R.TRKPS*LSEK.K
	JAW1 <sub>LRMP</sub>	\$388\$391			52.2	67.7	K.TKDDS'EPS'GEETVER.T
	JAW1 <sub>LRMP</sub>	S75S84			28.9	49.6	R.SAS*PTIEAQGTS*PAHDNIAFQDSTSK.D
	JAW1 <sub>LRMP</sub>	T319		<b>-</b>	26.4	29.0	R.RVT*IASLPR.N
	JAW1 <sub>LRMP</sub>	S322		•	48.6	55.2	R.VTIAS*LPR.N
	JAW1 LRMP	T41			12.4	56.4	R.HTSSTDGT*ITSSDPGLEILNMASCDLDR.N
	JAW1 LRMP	777			5.0	23.7	R.SASPT*IEAQGT*SPAHDNIAFQDSTSKDK.T  R.S*ASPTIEAQGT*SPAHDNIAFQDSTSK.D
	Jouberin AHI1	S73T83 S267		-	5.4	35.6	K.KES'SVR.S
Jumonji domain	containing 1B KDM3B	S727S743			8.3	21.8	R.SSS'PTSSLTQPIEMPTLSS'SPTEERPTVGPGQQDNPLLK.T
	containing 1B KDM3B	S727S742	• • •		5.9	22.9	R.SSS*PTSSLTQPIEMPTLS*SSPTEERPTVGPGQQDNPLLK.T
Jumonji domain	containing 1B KDM3B	S730S743			7.1	16.5	R.SSSPTS*SLTQPIEMPTLSS*SPTEERPTVGPGQQDNPLLKT
Jumonji domain	containing 18 KDM3B	S731S744			9.8	19.3	R.SSSPTSS*LTQPIEMPTLSSS*PTEERPTVGPGQQDNPLLK.T
Jumonji domain	containing 1B KDM3B	S727S744			7.6	14.7	R.SSS*PTSSLTQPIEMPTLSSS*PTEERPTVGPGQQDNPLLK.T
Jumonji domain	containing 1B KDM3B	S725S726	-			14.9	R.S'S'SPTSSLTQPIEMPTLSSSPTEERPTVGPGQQDNPLLKT
	containing 1B KDM3B	S730S744			7.5	18.5	R.SSSPTS*SLTQPIEMPTLSSS*PTEERPTVGPGQQDNPLLK.T
	containing 1B KDM3B	S725S744			7.6	10.9	R.S*SSPTSSLTQPIEM#PTLSSS*PTEERPTVGPGQQDNPLLK.T
	containing 1B KDM3B	S727T746	Ţ		5.1	13.7	R.SSS*PTSSLTQPIEMPTLSSSPT*EERPTVGPGQQDNPLLKT
	containing 1B KDM3B	S730S742 T733S742			8.2	22.4	R.SSSPTS'SLTQPIEMPTLS'SSPTEERPTVGPGQQDNPLLK.T  R.SSSPTSSLT'QPIEMPTLS'SSPTEERPTVGPGQQDNPLLK.T
	containing 18 KDM3B	T733S742 S632S633			44.2	11.2	K.QEAS*S*DEEASPFSGEEDVSDPDALRPLLSLQWK.N
	JUN-D JUND	S251S259			22.8	10.8	K.DEPQTVPDVPS*FGESPPLS*PIDMDTQER.I
	KAISO ZBTB33					11.6	K.ET*LPSNNTVAQVQSNPGPVAISDVAPSASNNSPPLTNITPTQK.L
	Kanadaptin SLC4A1	AP \$466		·-	26.0	152.3	K.NWEDEDFYDS*DDDTFLDR.T
	Kanadaptin SLC4A1	AP \$258			118.6	115.5	K.MLGEDS*DEEEEMDTSER.K
		_	_	_		_	

Peak Area <-10	o abundano	ts-Significant cha be at 5%FDR of with the minimum	compared to peak area fo	the or a given			
5 >10	>100 Protein Name Gene	Phosphosites	CarT	RajiB E E E	Accor	MOWSE	Sequence
	Kanadaptin SLC4A1AI				10.9	96.5	K.NWEDEDFY*DSDDDTFLDR.T
	CEP170	S356S359			70.4	52.7	K.S*IKS*DVPVYLK.R
	P 1 binding protein CEP170 P 1 binding protein CEP170	S1165		-	13.1	20.1	R.S*DSEATISR.S  K.SIKS*DVPVYLKR.L
	P 1 binding protein PLIN5	S359 S1160	•		11.8	13.6	RLGS*LSAR.S
	P 1 binding protein CEP170	S356	-		4.2	12.7	K.S*IKSDVPVYLKR.L
KARI	P 1 binding protein CEP170	\$838			9.5	15.0	R.QGS*FTIEKPSPNIPIELIPHINK.Q
KARI	P 1 binding protein CEP170	S1167			-0.8	26.4	R.SDS*EATISR.S
•	Caryopherin alpha3 KPNA3	S60			51.5	75.1	R.NVPQEESLEDS*DVDADFK.A
	Caryopherin alpha3 KPNA3	S56			9.4	43.6	R.NVPQEES*LEDSDVDADFK.A
	Karyopherin beta 3 IPO5	<b>S</b> 670			2.5	26.7	K.TASIKPEVALLDTQDMENMS*DDDGWEFVNLGDQQSFGIK.T
	omain containing 4 <sub>KLHDC4</sub>	S413S418			76.0	117.2	R.S'EDEDS'LEEAGSPAPGPCPR.S  R.S'EDEDSI EFAGSPAPGPCPR.S
	omain containing 4 <sub>KLHDC4</sub>	\$413 \$418			-0.5	45.7 58.8	R.SEDEDS*LEEAGSPAPGPCPR.S
	Keratin 13 KRT13	T319	•		12.3	11.4	K.T*EITELR.R
KH type splicing	regulatory protein KHSRP	S181	•	•	25.4	41.1	K.VQIS*PDSGGLPER.S
	KIAA0056 NCAPD3	S1382	<u> </u>	-	18.4	36.1	R.SLGVLPFTLNS*GSPEK.T
	KIAA0056 NCAPD3	S1384			16.1	45.5	R.SLGVLPFTLNSGS*PEK.T
	KIAA0082 CMTR1	T48S49S55		-	6.0	58.7	K.ASTT*S*LSGSDS*ETEGK.Q
	KIAA0082 CMTR1	S51S53S55			7.1	63.1	K.ASTTSLS*GS*DS*ETEGK.Q
	KIAA0082 CMTR1	T47T48S55 S132		=	9.1	47.8 64.3	K.AST*T*SLSGSDS*ETEGK.Q  R.DELQFIDWEIDS*DR.A
	KIAA0153 protein TTLL12	S16		<b>-</b> . <del>.</del>	9.1	99.9	R.SS*PGQTPEEGAQALAEFAALHGPALR.A
	KIAA0153 protein TTLL12	S15			10.5	66.5	R.S*SPGQTPEEGAQALAEFAALHGPALR.A
	KIAA0157 ABRAXAS	S368S372Y377			9.6	46.4	R.AAGDS*GEDS*DDSDY*ENLIDPTEPSNSEYSHSK.D
	KIAA0157 ABRAXAS	S368S372S375			15.2	55.5	R.AAGDS*GEDS*DDS*DYENLIDPTEPSNSEYSHSK.D
	KIAA0157 ABRAXAS	S368S375Y377			4.6	46.6	R.AAGDS*GEDSDDS*DY*ENLIDPTEPSNSEYSHSK.D
	KIAA0179 RRP1B	S732S735			28.4	38.5	K.TPTSS*PAS*SPLVAK.K
	KIAA0179 RRP1B	T7288732			14.5	28.4	R.VAFDPEQKPLHGVLKT*PTSS*PASSPLVAK.K
	KIAA0179 RRP1B	\$731\$732\$736 T728T730			14.1	20.4	R.VAFDPEQKPLHGVLKTPTS*S*PASS*PLVAK.K  R.VAFDPEQKPLHGVLKT*PT*SSPASSPLVAK.K
	KIAA0179 RRP1B	T728S731S736	=		7.1	18.3	R.VAFDPEQKPLHGVLKT*PTS*SPASS*PLVAK.K
	KIAA0179 RRP1B	S731S735			35.5	36.6	K.TPTS*SPAS*SPLVAK.K
	KIAA0179 RRP1B	T728S732S736			10.4	21.2	R.VAFDPEQKPLHGVLKT*PTSS*PASS*PLVAK.K
	KIAA0179 RRP1B	T728T730S736	<del>_</del>		11.9	23.7	R.VAFDPEQKPLHGVLKT*PT*SSPASS*PLVAK.K
	KIAA0179 RRP1B	T728S732S735			11.4	35.3	R.VAFDPEQKPLHGVLKT*PTSS*PAS*SPLVAK.K
	KIAA0179 RRP1B	T728S731	<b>—</b>		18.2	29.6	R.VAFDPEQKPLHGVLKT*PTS*SPASSPLVAK.K
	KIAA0182 <sub>GSE1</sub>	S10	•		44.9	59.5	K.S*PSLGMLSTATR.T
	KIAA0217 protein LARP4B KIAA0217 protein LARP4B	S516T518			14.5	24.7	K.FTSSQTQS*PT*PPKPPSPSFELGLSSFPPLPGAAGNLK.T  K.FTS*S*QTQSPTPPKPPSPSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	S511S512 T514T518S526			7.8	37.7	K.FTSSQT'QSPT'PPKPPSPS'FELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	T510S511S516			5.9	14.2	K.FT*S*SQTQS*PTPPKPPSPSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	S498		•	34.4	37.4	R.KNS*FGYR.K
	KIAA0217 protein LARP4B	T510S511			8.7	18.2	K.FT*S*SQTQSPTPPKPPSPSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	S601			11.4	30.0	R.SPS'PAHLPDDPK.V
	KIAA0217 protein LARP4B	Y501			13.8	25.6	R.KNSFGY*R.K
	KIAA0217 protein LARP4B	T518S532		_	2.9	17.6	K.FTSSQTQSPT*PPKPPSPSFELGLS*SFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B KIAA0217 protein LARP4B	S511T518S526			12.4	25.7	K.FTS*SQTQSPT*PPKPPSPS*FELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	S516S524S526 S516T518S524			6.0	16.5 38.4	K.FTSSQTQS*PTPPKPPS*PS*FELGLSSFPPLPGAAGNLK.T  K.FTSSQTQS*PT*PPKPPS*PSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	T518S524			19.3	16.9	K.FTSSQTQSPT*PPKPPS*PSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	T514T518S524			8.5	16.9	K.FTSSQT*QSPT*PPKPPS*PSFELGLSSFPPLPGAAGNLK.T
	KIAA0217 protein LARP4B	S568			-0.5	14.4	R.TLS*ADASVNTLPVVVSR.E
	KIAA0217 protein LARP4B	S516S524		÷	7.0	12.4	K.FTSSQTQS*PTPPKPPS*PSFELGLSSFPPLPGAAGNLK.T
	KIAA0284 protein CEP170B	S221			100.0	13.1	K.FS*LRQR.R
	KIAA0409 protein RRP8	S104S106		-	100.0	20.7	K.QGPPCS'DS'EEEVER.K
	KIAA0409 protein RRP8	S62S64			17.3	55.4	R.ALEAASLSQHPPSLCIS*DS*EEEEEER.K
	KIAA0409 protein RRP8	\$58\$62 \$58\$64			8.3	11.6	R.ALEAASLSQHPPS*LCIS*DSEEEEEER.K  R.ALEAASLSQHPPS*LCISDS*EEEEEER.K
	KIAA0433 protein PPIP5K2	S58S64 S38	-		100.0	59.1	R.HFFHHADEDDEEEDDS*PPER.Q
	KIAA0433 protein PPIP5K2	S492S493			-0.4	22.1	K.TS*S*EEEDSRR.E
	KIAA0433 protein PPIP5K2	S1151		-	-0.2	26.2	R.SS*PIMR.K
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Peak Area %CV	abundand		compared to	the			
.5 25 42 42 71	timepoint PSM	with the minimum					
3 86 5 5 >100 >100				RajiB			
Protein Nan KIAA04	ne Gene 60 RPRD2	Phosphosites S899S902	2 4 6	9 H H	Ascor	MOWSE 41.9	Sequence R.GNEPGS*DRS*PSPSKNDSFFTPDSNHNSLSQSTTGHLSLPQK.Q
KIAA04	60 RPRD2	S348			71.6	112.6	R.DVEDMELS*DVEDDGSK.I
KIAA04	60 RPRD2	<b>S</b> 459			15.2	20.5	K.NTGVSPASRPSPGTPTS*PSNLTSGLK.T
KIAA04	60 RPRD2	S902S904	-		12.3	24.2	R.GNEPGSDRS*PS*PSKNDSFFTPDSNHNSLSQSTTGHLSLPQK.Q
	60 RPRD2	S902S906			17.4	36.7	R.GNEPGSDRS*PSPS*KNDSFFTPDSNHNSLSQSTTGHLSLPQK.Q
	60 RPRD2 60 RPRD2	T458 8330T332			4.0	26.2	K.S'AT'PEPVTDNR.D
	60 RPRD2	\$3301332 \$902\$910	-		53.2 15.7	20.0	R.GNEPGSDRS*PSPSKNDS*FFTPDSNHNSLSQSTTGHLSLPQK.Q
	67 SZT2	S920S926			23.0	57.6	R.AEGIEGETLTAS*PQAPGS*PEDSEGVPLISLPR.V
KIAA0515 prote	ein PRRC2B	S388			100.0	36.1	K.LKFS*DDEEEEEVVK.D
KIAA0515 prote	in PRRC2B	T225			23.9	91.5	R.HIISATSLST*SPTELGSR.N
KIAA0515 prote	in PRRC2B	S226			17.2	36.0	R.HIISATSLSTS*PTELGSR.N
KIAA0515 prote		S224			0.5	38.1	R.HIISATSLS*TSPTELGSR.N
	28 C2CD5	S260			80.2	40.7	K.LSSPAAFLPACNS*PSK.E
	28 C2CD5	S817			12.2	42.7	R.AS*TDNEELLQFPLELCSDSLPSHPFPPAK.A
	56 KIAA0556		_		5.8	10.8	K.GLFS'WLQPS'PTGK.D  K.GLFS'DEEDSEDLFSSQSASNLK.G
	92 WASHC20				75.8 5.1	173.2 33.2	K.GLFS'DEEDSEDLFSSQSASNLK.G  K.GLFSDEEDS'EDLFSSQSASNLK.G
	92 WASHC2A			•	11.3	32.2	R.VSLLFEDDVDS*GGSLFGS*PPTSVPPATK.K
	92 WASHC2				11.1	16.4	R.S*RPTS*FADELAAR.I
KIAA05	92 WASHC2	\ S352			23.9	62.8	K.LTDEDFS*PFGSGGGLFSGGK.G
KIAA05	92 WASHC2A	A \$284T287	-	•	8.6	12.1	R.S*RPT*SFADELAAR.I
KIAA05	92 WASHC2A	S686S695			2.7	16.9	R.VS*LLFEDDVDS*GGSLFGSPPTSVPPATK.K
KIAA05	92 WASHC2	S695S698S702			13.7	12.0	R.VSLLFEDDVDS*GGS*LFGS*PPTSVPPATK.K
	92 WASHC2A	S698S702			2.4	34.5	R.VSLLFEDDVDSGGS*LFGS*PPTSVPPATK.K
KIAA0652 gene produ		S324			86.0	45.5	R.AS*PHDVLETIFVR.K
	83 TELO2	T632			5.6	48.8	R.T*PQPGSPSPNTPCLPEAAVSQPGSAVASDWR.V
	83 TELO2 83 TELO2	S637			5.0	57.4	R.TPQPGS*PSPNTPCLPEAAVSQPGSAVASDWR.V
	85 PPP6R2	\$639	-		2.3	55.1	K.TPQPGSPS*PNTPGLPEAAVSQPGSAVASDWK.V  KAFS*PASPCAWNVCVTR.K
	92 ANKLE2	\$766 \$662			13.8	19.1	R.NNS*PPTVGAFGHTR.C
KIAA0701 prote					7.6	37.4	K.SPVSES'VS'PVVPDYLPTENGDFLSSK.R
KIAA0701 prote					23.8	46.0	K.SPVS*ES*VSPVVPDYLPTENGDFLSSK.R
KIAA0701 prote	in <sub>UHRF1BP</sub>	S935		•	7.6	27.7	R.SMS*VDLSHIPLKDPLLFK.S
KIAA07	48 TESPA1	S454		•	61.4	77.6	K.S*LDLSITQQK.W
KIAA07	76 UFL1	S458			69.6	98.6	R.KDDDS*DDESQSSHTGK.K
KIAA07	76 UFL1	<b>S</b> 790			12.1	23.7	R.KSS*VTEE
KIAA0912 prote		S717			4.0	16.5	R.THLQLRS*ELDK.L
KIAA0912 prote		S1405			100.0	47.9	R.NVS*PEFVPCEGEGGFGLHK.K
KIAA0999 prote		S568			60.3	51.0	R.RES'DGAASIQAFK.A
KIAA0999 prote		T163			37.8	89.6	K.T*WCGSPPYAAPELFEGK.E  K.TWCGS*PPYAAPELFEGK.E
KIAA1002 prote		\$167 \$10		•	-0.5	47.9 66.6	K.ASS'FSGISILTR.G
KIAA1002 prote		S9			10.2	74.3	KAS*SFSGISILTR.G
KIAA1115 prote		S540S541			12.7	56.0	K.NMVDLVNTHHLHSS*S*DDEDDRLK.E
KIAA1115 prote	ein ppp6R1	S539S540			11.0	38.0	K.NMVDLVNTHHLHS*S*SDDEDDRLK.E
KIAA1115 prote	ein PPP6R1	S541			11.3	41.8	K.NMVDLVNTHHLHSSS*DDEDDRLK.E
KIAA1115 prote	ein PPP6R1	S539S540S541			15.0	30.3	K.NMVDLVNTHHLHS*S*S*DDEDDRLK.E
KIAA1115 prote	ein PPP6R1	T735			11.0	22.1	R.GGATPLSYPSPGPQPPGPSWTATFDPVPTDAPT*SPR.V
KIAA1115 prote		S712T735	•••		18.0	30.5	R.GGATPLSYPS*PGPQPPGPSWTATFDPVPTDAPT*SPR.V
KIAA1115 prote		S540			13.9	48.2	K.NMVDLVNTHHLHSS*SDDEDDRLK.E
KIAA1115 prote		S677T678S680			6.2	68.3	R.SGGS*T*DS*EDEEEEDEEEEDEEGIGCAAR.G
KIAA1115 prote		T534S539S541			3.6	12.5	K.NMVDLVNT*HHLHS*SS*DDEDDRLK.E
KIAA1115 prote		S674S677T678		<b>.</b>	4.3	85.8	R.S'GGS'T'DSEDEEEEDEEEEDEEGIGCAAR.G  K.NM#VDLVNT'HHLHSSSDDEDDRLK.E
KIAA1115 prote		T534 T534S540S541			82	16.7	K.NMWDLVNT*HHLHSS*S*DDEDDR.L.
KIAA1115 prote		T534\$540\$541			4.2	22.7	R.GGATPLSYPSPGPQPPGPSWTATFDPVPT*DAPTSPR.V
KIAA1115 prote		\$736			8.0	38.9	R.GGATPLSYPSPGPQPPGPSWTATFDPVPTDAPTS*PR.V
KIAA1115 prote		S539S541			7.9	16.9	K.NMVDLVNTHHLHS'SS'DDEDDRLK.E
KIAA1115 prote	ein PPP6R1	T706				22.5	R.GGAT*PLSYPSPGPQPPGPSWTATFDPVPTDAPTSPR.V
KIAA1115 prote	ein ppp6R1	T723T735			23.8	15.9	R.GGATPLSYPSPGPQPPGPSWT*ATFDPVPTDAPT*SPR.V
KIAA1115 prote	ein ppp6R1	T534S539			0.1	15.4	K.NMVDLVNT*HHLHS*SSDDEDDRLK.E
					_	_	

Peak Area	%CV White do	ts-Significant cha	inge in pepti compared to	de the			
-5 -3	timepoint PSM	with the minimum	peak area f	or a given			
3 5 >10	>100			RajiB			
	Protein Name Gene KIAA1115 protein PPP6R1	Phosphosites T534S539S540	8 4 5	9 H H	Ascor	MOWSE 16.2	Sequence K.NMVDLVNT*HHLHS*S*SDDEDDRLK.E
	KIAA1115 protein PPP6R1	S887	=		16.7	18.0	K.SPEPLGLPQSQSAQALTPPPIPNGSAPEGPAS*PGSQ
	KIAA1115 protein ppp6R1	S645S648	÷		75.2	101.4	R.IQQFDDDEEEEDEEEAQGS*GES*DGEDGAWQGSQLAR.G
	KIAA1115 protein PPP6R1	<b>S</b> 712			12.2	31.1	R.GGATPLSYPS*PGPQPPGPSWTATFDPVPTDAPTSPR.V
	KIAA1115 protein PPP6R1	S712S736			6.5	22.1	R.GGATPLSYPS*PGPQPPGPSWTATFDPVPTDAPTS*PR.V
	KIAA1115 protein PPP6R1	<b>S</b> 539			-0.3	22.0	K.NMVDLVNTHHLHS*SSDDEDDRLK.E
	KIAA1143 protein KIAA1143	<b>S</b> 50	•		100.0	22.6	R.IQPQPPDEDGDHS*DKEDEQPQVVVLK.K
	KIAA1211 protein KIAA1211	T968S975			5.0	25.6	K.MPLAQKPALAPKPT*SQTPPAS*PLSK.L
	KIAA1211 protein KIAA1211	T968S969			3.1	21.1	K.MPLAQKPALAPKPT*S*QTPPASPLSK.L
	KIAA1211 protein KIAA1211	T971S975			9.4	20.5	K.MPLAQKPALAPKPTSQT*PPAS*PLSK.L
	KIAA1267 KANSL1	S268			31.8	100.3	K.S*PLSSILFSALDSDTR.I
	KIAA1267 KANSL1	S271			-2.8	38.3	K.SPLS*SILFSALDSDTR.I
	KIAA1271 protein MAVS	S222			67.6	24.7	R.GPVS*PSVSFQPLAR.S
	KIAA1370 FAM214A	T32			49.3	10.8	R.T*PECSVKGR.T
	KIAA1429 VIRMA	S1579			9.8	23.9	R.SFLSEPSS*PGR.T
	KIAA1429 <sub>VIRMA</sub>	S1578			42.4	16.6	R.SFLSEPS*SPGR.T
	KIAA1429 <sub>VIRMA</sub>	T184	<b>H</b>		25.5	14.4	R.T*PPGPPPPDDDEDDPVPLPVSGDK.E
	KIAA1432 RIC1	T913S916	Ė		7.0	43.1	K.AIGSGESET*PPS*TPTAQEPSSSGGFEFFR.N
	KIAA1462 protein JCAD	S948S949S951			4.9	19.5	K.EVS*S*VS*RM#RVLSFR.N
	KIAA1467 FAM234B	S16T26S33			16.9	41.5	K.S'PDLGEYDPLT'QADSDES'EDDLVLNLQK.N
	KIAA1467 FAM234B				8.4	16.3	K.S'PDLGEYDPLT'QADS'DESEDDLVLNLQK.N
	KIAA1467 FAM234B		-		7.6	13.6	K.SPDLGEYDPLT*QADS*DESEDDLVLNLQK.N
	KIAA1467 FAM234B	\$30\$33	-		23.1	68.3	K.SPDLGEYDPLTQADS*DES*EDDLVLNLQK.N
	KIAA1468 RELCH	S45S51S54				33.6	R. LGAGS*GLDBGS*AGS*LSBDDBVALGSSABBGLBGEASAAAVALGG
	KIAA1542 Protein PHRF1	S973			51.5	61.3	R.TVTCVTVVEPEAPPS*PDVLQAATHR.V
	KIAA1542 Protein PHRF1	S1032S1034			37.7	38.0	R.S*AS*PSVGEERPR.R
	KIAA1542 Protein PHRF1	S1114S1116	==		100.0	15.8	R.RS*AS*RPR.G
	KIAA1542 Protein PHRF1	S1032S1036			11.8	37.6	R.S'ASPS'VGEERPR.R  K.AFAPS'SPDVAPAGKFDS'PSASGR V
	KIAA1542 Protein PHRF1  KIAA1542 Protein PHRF1	S1359S1371			29.4	13.3	R.SAS'PS'VGEERPR.R
	KIAA1542 Protein PHRF1	\$1034\$1036	=		6.7	39.2	K.SAS*PS*VGEERPR.R  K.LEAAGSFNS*DDDAESCPICLNAFR.D
	KIAA1542 Protein PHRF1	\$101 \$98			20.4	19.6	K.LEAAGS*FNSDDAESCPICLNAFR.D
	KIAA1602 NCKAP5L		☵		10.6	16.5	R.GPS*PEPPPS*PLQVPTYPQLTLEVPQAPEVLR.S
	KIAA1604 protein CWC22	S91S93	=		25.1	13.8	R.SRKS'PS'PGR.R
	KIAA1604 protein CWC22	S831	-		5.2	14.5	R.RNSFS*ENEK.H
	KIAA1604 protein CWC22	S829			13.4	23.0	R.RNS*FSENEK.H
	KIAA1704 protein GPALPP1	S105			100.0	47.3	K.QDDS*PPRPIIGPALPPGFIK.S
	GPALPP1	T138S140S141			100.0	30.1	R.DDPGQQET*DS*S*EDEDIIGPMPAK.G
	KIAA1706 protein EEPD1	S173	·· <del>·</del>		100.0	50.6	R.S*VEDLVR.M
	KIAA1706 protein EEPD1	S25S31			100.0	63.8	R.KFS*AACNFS*NILVNQER.L
	KIAA1826 protein MSANTD4	S152			78.4	37.9	R.DPQS*PEFEIEEEEEMLSSVIPDSR.R
	KIAA1836 protein CC2D1B	T824			100.0	10.8	R.KPT*GGKLEVK.V
	KIAA1949 PPP1R18	S224		•	67.0	50.0	R.LS*PGESAYQK.L
	KIDINS220 KIDINS220	S1411		i ii	-0.4	42.2	R.SS'PHSTYYMGQSSSGGSIHSNLEQEK.G
Kinase	suppressor of ras 1 KSR1	T133T136			50.0	44.9	R.ALHSFIT*PPT*TPQLR.R
Kinase	suppressor of ras 1 KSR1	T133T137			11.6	31.9	R.ALHSFIT*PPTT*PQLR.R
	Kindlin 2 <sub>FERMT2</sub>	T188T190T192	Ļ			24.8	K. THATEDTAYDALIDOSDI SDTSAMISODSAL SECADORI AVSODITSDER
	Kinectin KTN1	<b>S</b> 75			14.4	20.0	K.EIQNGNLHES*DSESVPR.D
	Kinesin 2 <sub>KLC1</sub>	S521			18.7	53.9	R.S'RESLNVDVVK.Y
	Kinesin 2 <sub>KLC1</sub>	S521S524			100.0	37.5	R.S'RES'LNVDVVK.Y
	Kinesin 2 <sub>KLC1</sub>	S524	Ļ		1.3	31.8	R.SRES*LNVDVVK.Y
	family member 13B KIF13B	S1778		•	12.1	17.3	R.RS*TGLR.L
	n family member 1B KIF1B	S1612	-		15.2	52.3	R.AS*SPCPEFEQFQIVPAVETPYLAR.A
	n family member 18 <sub>KIF1B</sub>	S1613			16.9	24.8	R.ASS'PCPEFEQFQIVPAVETPYLAR.A
	n family member 1C KIF1C	S1033		·	100.0	34.3	R.RNS*LDGGGR.S
	n family member 1C KIF1C	S674S676			37.5	65.6	R.LYADS*DS*GDDSDKR.S
	family member 21B KIF21B	S1167	Ţ,		31.4	12.3	K.S*LASLVEIK.E
	n family member 23 KIF23	S684			5.1	73.4	R.SVS*PSPVPLLFQPDQNAPPIR.L
	n family member 23 KIF23	S686			-0.3	44.6	R.SVSPS*PVPLLFQPDQNAPPIR.L
	n family member 23 KIF23	S684S686			-0.4	31.4	R.SVS*PS*PVPLLFQPDQNAPPIR.L
	n family member 23 KIF23	S682S684			6.2	47.2	R.S*VS*PSPVPLLFQPDQNAPPIR.L
Kinesii	n family member 3A KIF3A	T692		<u> </u>	3.3	16.1	R.SAKPET*VIDSLLQ

Peak Area %CV <-10 0	abundano		compared to	the			
-5 29 42 42 71 92 92 92 92 92 92 92 92 92 92 92 92 92	timepoint n	with the minimum					
>10 Protein Na	me Con-	Phosphosites	CarT	RajiB E E E	Asse-	MOWSE	Sequence
Kinesin family member		S933		0 (4 2)	9.1	15.1	R.GHSAQIAKPIRPGQHPAAS*PTHPSAIR.G
Kinesin heavy cha		T78			24.1	13.0	K.EIDLESIFSLNPDLVPDEEIEPSPET*PPPPASSAK.V
Kinesin heavy cha  Kinesin light cha		S75			8.3	21.9	K.EIDLESIFSLNPDLVPDEEIEPS*PETPPPPASSAK.V  R.AS*SLNVLNVGGK.A
Kinesin light cha		\$590 \$591			9.8 25.6	75.4	R.ASS'LNVLNVGGK.A
Kinesin light chain 1 (Fragm	ent) KLC1	S262	•	•••	29.8	73.4	R.ALSAS*HTDLAH
Kinesin light cha	in 4 <sub>KLC4</sub>	S608	<del>iii</del>		44.2	130.8	R.AAS'LNYLNQPSAAPLQVSR.G
Kinesin light cha		T630	ij.		7.0	18.5	R.GLSAST*MDLSSSS
Kinesin light cha		<b>S</b> 629	<u> </u>		16.1	38.2	R.GLSAS*TMDLSSSS
KRI1 home		\$177 \$634\$645			110.9	154.1	R.AFVEDS*EDEDGAGEGGSSLLQK.R  R.QLPALDGSLMGPES*PPAQEEAPVS*PHKKPAPQKR.R
KRI1 homo	log KRI1	S99S100S101S	• •		17.7	61.2	R.TAS*S*S*DS*EEDPEALEK.Q
Kruppel like facto	r 12 KLF12	S202		• • • •	70.9	119.5	R.S*PGNVNNTIVVPLLEDGR.G
Kruppel like facto		S238S240			1.7	52.6	R.QSKS*DS*DDDDLPNVTLDSVNETGSTALSIAR.A
Kruppel like facto		S236S240	<b>!!</b>		12.2	74.0	R.QS*KSDS*DDDDLPNVTLDSVNETGSTALSIAR.A
Kruppel like facto  Kruppel like facto		\$236T249 \$311			11.0	74.5	R.QS*KSDSDDDDLPNVT*LDSVNETGSTALSIAR.A  R.SESPDS*RK.R
Kruppel like fact		T244S248			7.3	11.4 48.7	R.GLLT*PPAS*PLELLEAKPK.R
L3MB	TL2 <sub>L3MBTL2</sub>	T66S73			25.1	22.9	R.EAGELPT'SPLHLLS'PGTPR.S
L3MB	TL2 <sub>L3MBTL2</sub>	S67S73			5.6	21.4	R.EAGELPTS*PLHLLS*PGTPR.S
Lactate dehydrogenas		Y10			100.0	43.4	K.DQLIY*NLLK.E
LAG1 longevity assurance homolo		\$350\$354\$355			15.6	27.6	K.VSKDDRS*DVES*S*S*EEEDVTTCTK.S
LAG1 longevity assurance homolo		\$345\$354\$355 \$86			100.0	20.2	K.VS*KDDRSDVES*S*S*EEEDVTTCTK.S  R.S*PGRPPK.S
Lamin B recep		S84S86			100.0	18.6	R.S'RS'PGRPPK.S
Lamin B recep	otor <sub>LBR</sub>	<b>S</b> 99	Ħ		11.1	76.7	R.SAS*ASHQADIK.E
Lamin B rece	otor <sub>LBR</sub>	S97			23.5	46.2	R.S*ASASHQADIK.E
Lamin B recep		S67T68			6.5	16.4	R.KGGS*T*SSSPSRR.R
	B1 LMNB1	\$391 \$391\$393			22.4	39.2	RLKLS*PSPSSR.V  RLKLS*PS*PSSR.V
	B1 LMNB1	T20S23			15.2	24.0	R.AGGPTT*PLS*PTR.L
Lamir	B1 LMNB1	T575	•		114.9	29.0	K.TTIPEEEEEEEAAGVVVEEELFHQQGT*PR.A
Lamir	B1 <sub>LMNB1</sub>	T19S23			9.0	18.4	R.AGGPT*TPLS*PTR.L
		S156S157		•••	10.4	73.5	R.DSHS*S*EEDEASSQTDLSQTISKK.T
Lamina associated polypeptide			-		9.0	45.4	K.VNFSEEGET*EEDDQDSSHSSVTTVK.A  R.LQQQHSEQPPLQPS*PVMTR.R
Lamina associated polypeptide					24.0 64.6	66.5	R.GLRDS'HS'S'EEDEASSQTDLSQTISK.K
Lamina associated polypeptide	1B TOR1AIP1	S154S157	•••		8.9	41.2	R.DS*HSS*EEDEASSQTDLSQTISK.K
Lamina associated polypeptide	1B TOR1AIP1	S154S156S163	Ţ.	•	9.4	26.5	R.RGLRDS'HS'SEEDEAS'SQTDLSQTISK.K
Lamina associated polypeptide		S154S156			24.1	17.3	R.DS*HS*SEEDEASSQTDLSQTISK.K
	IRP LARP1	S697			25.6	49.9	R.SLPTTVPES*PNYR.N
	RP LARP1	\$689 \$689\$697			30.0	38.2	R.S'LPTTVPESPNYR.N  R.S'LPTTVPES'PNYR.N
	RP LARP1	S770S776			3.4	64.3	R.TAS*ISSSPS*EGTPTVGSYGCTPQSLPK.F
	RP LARP1	<b>S</b> 90	<u> </u>		105.7	139.4	R.ESPRPLQLPGAEGPAIS*DGEEGGGEPGAGGGAAGAAGAGR.R
	RP LARP1	<b>S</b> 75				79.2	R.ES*PRPLQLPGAEGPAISDGEEGGGEPGAGGGAAGAAGAGR.R
	RP LARP1	S747		-	15.3	83.4	R.HSS*NPPLESHVGWVMDSR.E
	IRP LARP1	\$75\$90 \$550\$554			100.0	47.5	R.ES*PRPLQLPGAEGPAIS*DGEEGGGEPGAGGGAAGAAGAGR.R  K.NTFTAWS*DEES*DYEIDDR.D
	RP LARP1	\$550\$554 \$471			23.9	137.9	K.GLSAS*LPDLDSENWIEVK.K
	RP LARP1	S440S444			23.4	52.2	K.ETES*APGS*PR.A
L	IRP LARP1	T449			26.5	40.7	R.AVT*PVPTK.T
	IRP LARP1	T693		<u>.</u> .	23.6	49.7	R.SLPTT*VPESPNYR.N
	RP LARP1	T570			11.4	29.2	K.ILIVT*QTPHYMR.R
	RP LARP1	\$770T779			8.0	56.2 38.8	R.TAS*ISSSPSEGT*PTVGSYGCTPQSLPK.F  R.TASISSS*PS*EGT*PTVGSYGCTPQSLPK.F
	RP LARP1	\$774\$776T779 \$774			2.3	19.3	R.TASISSS*PSEGTPTVGSYGCTPQSLPK.F
	RP LARP1	T545T547		-	10.8	13.0	K.NT*FT*AWSDEESDYEIDDRDVNK.I
L	IRP LARP1	\$550Y556			18.9	76.8	K.NTFTAWS*DEESDY*EIDDR.D
	IRP LARP1	T692	i.		-0.2	16.3	R.SLPT*TVPESPNYR.N
	RP LARP1	S550	•		25.3	54.3	K.NTFTAWS*DEESDYEIDDR.D
	IRP LARP1	S444	÷		19.3	27.3	K.ETESAPGS*PR.A

<-10 0 abundano	ts-Significant cha e at 5%FDR c with the minimum	ompared to	the or a given			
>10 Protein Name Gene	Phosphosites	9 H H	5	Ascor	MOWSE	Sequence
LARP LARP1	S979			18.8	19.3	R.CPS*QSSSRPAAMISQPPTPPTGQPVR.E  R.TASISSSPSEGT*PTVGSYGCTPQSLPK.F
LARP LARP1	T779 S143		===	9.1	73.3	K.NALPPVLTTVNGQS*PPEHSAPAK.V
LARP LARP1	\$746		• • •	69.6	61.3	R.HS*SNPPLESHVGWVMDSR.E
LARP LARP1	\$772\$773\$776	•		6.0	17.3	R.TASIS*S*SPS*EGTPTVGSYGCTPQSLPK.F
LARP LARP1	<b>S</b> 469			37.2	66.9	K.GLS*ASLPDLDSENWIEVK.K
LARP LARP1	<b>S</b> 776		<b>—</b>	-0.2	48.0	R.TASISSSPS'EGTPTVGSYGCTPQSLPK.F
LARP LARP1	S554Y556			10.3	43.7	R.KNTFTAWSDEES*DY*EIDDR.D
LARP LARP1	<b>S</b> 770	•		5.8	49.3	R.TAS*ISSSPSEGTPTVGSYGCTPQSLPK.F
LARP LARP1	\$770\$772\$773		_	8.7	33.3	R.TAS*IS*SPSEGTPTVGSYGCTPQSLPK.F
LARP LARP1	\$772T779			9.4	44.9	R.TASIS*SSPSEGT*PTVGSYGCTPQSLPK.F  R.TAS*ISSS*PSEGTPTVGSYGCTPQSLPK.F
LARP LARP1	S770S774 T693S697			5.1	14.2	R.SLPTT*VPES*PNYR.N
LARP LARP1	S772S776			4.4	21.3	R.TASIS'SSPS'EGTPTVGSYGCTPQSLPK.F
LARP LARP1	S774S776T781			4.6	24.3	R.TASISSS'PS'EGTPT"VGSYGCTPQSLPK.F
LARP LARP1	T438S444			19.3	45.8	K.ET*ESAPGS*PR.A
LARP LARP1	\$770\$773			3.8	48.7	R.TAS*ISS*SPSEGTPTVGSYGCTPQSLPK.F
LARP LARP1	\$770\$772	Ţ.	<u> </u>	0.5	43.1	R.TAS*IS*SSPSEGTPTVGSYGCTPQSLPK.F
LASS2 CERS2	S341T346S348			100.0	59.0	K.LVEDERS'DREET'ES'S'EGEEAAAGGGAK.S
LASS2 CERS2	S341			100.0	51.6	K.LVEDERS*DR.E
LASS2 CERS2	T346S348S349			100.0	112.3	R.EET'ES'S'EGEEAAAGGGAK.S
LATS1 LATS1	S278		•	25.6	53.2	K.RYS*GNMEYVISR.I
LATS1 LATS1	S1111		<u> </u>	15.1	31.0	R.FFDDNGYPYNYPKPIEYEYINSQGSEQQS*DEDDQNTGSEIK.N
LBALRBA	S2064		-	15.2	112.3	R.SQALGNQNSENEILLEGDDDTLS*SVDEK.D
LBA LRBA	\$1787			11.1	80.6	K.LPSVPTVDSVS*QDPVSNMSITER.L  K.SAVSPSTFNTSIPTNAVSVVSSVDSAQASDMGGBS*PGSR.S
LBALRBA	\$1767 \$1785	• • •		17.2 8.0	83.4 45.5	KLPSVPTVDS*VSQDPVSNMSITER.L
LBALRBA	\$1783 \$1733			8.0	38.4	K.S*AVSPSTFNTSIPTNAVSVVSSVDSAQASDMGGESPGSR.S
LBH limb bud and heart development LBH	S63			89.5	31.5	R.LPS*IVVEPTEGEVESGELR.W
homoloa Lck <sub>LCK</sub>	Y192			32.1	58.9	R.NLDNGGFY*ISPR.I
LckLCK	<b>S</b> 42				45.6	R. MCCCC/DDDLATVECCNDDACDLODNILA/ALLIEVEDSUDCDLCEEK
LckLCK	T50				74.5	R.DPLVT*YEGSNPPASPLQDNLVIALHSYEPSHDGDLGFEK.G
Lck_LCK	<b>S</b> 59	•		48.9	53.0	R.DPLVTYEGSNPPAS*PLQDNLVIALHSYEPSHDGDLGFEK.G
Lck <sub>LCK</sub>	Y505			27.9	28.7	R.SVLEDFFTATEGQY*QPQP
Lck <sub>LCK</sub>	T501			13.4	19.1	R.SVLEDFFTAT*EGQYQPQP
Lck_LCK	\$42T50	• •			41.4	R. MIGGIEV/DODI VITIVEGENIDDARDI ODNII VIAI LIEVEDRUDGDI GEEV
Lck-interacting transmembrane adapter 1 LIME1	S86			31.1	51.7	R.AAPGPAQQQGPAACQHGS*PAPTLAGGVQGHHR.T
LEM domain containing 2 <sub>LEMD2</sub> Leucine rich repeat containing 47 <sub>LRRC47</sub>	\$496	•		9.1	42.3	R.WTKPS'SFSDSER
Leucine rich repeat containing 47 LRRC47	S518			12.6	76.9	K.EEGS*LSDTEADAVSGQLPDPTTNPSAGK.D  K.EEGSLS*DTEADAVSGQLPDPTTNPSAGK.D
Leucine rich repeat containing 47 LRRC47	\$520 \$518\$520			18.8	71.3	K.EEGS'LS"DTEADAVSGQLPDPTTNPSAGK.D
Leucine rich repeat containing 47 LRRC47	T522			18.4	73.8	K.EEGSLSDT*EADAVSGQLPDPTTNPSAGK.D
Leucine rich repeat in FLII interacting LRRFIP1	S115			9.8	57.6	R.NMPGLSAATLASLGGTS*SR.R
protein 1  Leucine rich repeat in FLII interacting LRRFIP1 protein 1	T114			29.3	51.3	R.NMPGLSAATLASLGGT*SSR.R
Leucine rich repeat in FLII interacting LRRFIP1	S116	· · · ·		6.8	69.8	R.NMPGLSAATLASLGGTSS*R.R
Leucine rich repeat in FLII interacting LRRFIP1 protein 1	<b>S</b> 110	<b>—</b>		6.2	60.4	R.NMPGLSAATLAS*LGGTSSR.R
Leucine rich repeats and calponin LRCH1 homology domain containing protein 1	\$532\$536			37.0	72.5	R.ENS*PAVS*PTTNSTAPFGLKPR.S
Leucine rich repeats and calponin LRCH1 homology domain containing protein 1	T538T539			17.2	26.4	R.ENSPAVSPT*T*NSTAPFGLKPR.S
Leucine zipper protein 1 LUZP1	<b>S</b> 659	<u></u>		57.5	46.2	R.EKPDS*DDDLDIASLVTAK.L
Leucine-rich repeat flightless-interacting LRRFIP1 protein 1	S124		-	8.5	53.8	R.RGSGDTS*ISIDTEASIR.E
Leucine-rich repeat flightless-interacting LRRFIP1 protein 1	S120		•••	68.1	81.4	R.RGS*GDTSISIDTEASIR.E
Leucine-rich repeat flightless-interacting LRRFIP1 protein 1 Leucine-rich repeats and IO motif CEDO7	\$126		-	6.5	55.0	R.RGSGDTSIS*IDTEASIR.E  K.ESSNNEODNS*ILEOVI TSVOOLEDADER T
Leucine-rich repeats and IQ motif CEP97 containing 2 Leucine-rich repeats and IQ motif CEP97	\$770 T011\$012			21.9	83.2	K.ESSNNEQDNS'LLEQYLTSVQQLEDADER.T  K.LHIACFPVQLDT'LS'DGASVDESHGISPPLQGEISQTQENSK.L
Leucine-rich repeats and IQ motif CEP97	T811S813 S813S817			0.1	28.5	K.LHIACFPVQLDT-LS-DGASVDESHGISPPLQGEISQTQENSK.L  K.LHIACFPVQLDTLS*DGAS*VDESHGISPPLQGEISQTQENSK.L
Leucine-rich repeats and IQ motif CEP97	S762			15.2	58.5	K.ES*SNNEQDNSLLEQYLTSVQQLEDADER.T
Leucine-rich repeats and IQ motif CEP97	S763			-0.4	36.6	K.ESS*NNEQDNSLLEQYLTSVQQLEDADER.T
Containing 2  Leucine-rich repeats and IQ motif CEP97	\$763\$770			4.1	83.8	K.ESS*NNEQDNS*LLEQYLTSVQQLEDADER.T
containing 2  Leupaxin LPXN	<b>S</b> 19	-		7.4	49.2	R.STLQDS*DEYSNPAPLPLDQHSR.K
Leupaxin LPXN	S81		<u>-</u>	58.0	33.3	K.ES*PPPSK.T
LIG1 DNA ligase I LIG1	T195		• • •	32.3	63.0	KAET*PTESVSEPEVATK.Q
LIG1 DNA ligase I LIG1	S911T918			15.2	67.9	R.KQSQIQNQQGEDS*GSDPEDT*Y

<-10 0 abundan	ots-Significant cha ce at 5%FDR of with the minimum	compared to	the			
5 >100		CarT	RajiB			
Protein Name Gene LIG1 DNA ligase I LIG1	Phosphosites T918Y919	9 J J	5 F B	Ascor	MOWSE 18.3	Sequence  R.KQSQIQNQQGEDSGSDPEDT*Y*
LIG1 DNA ligase I LIG1	T195S201	Ξ		10.6	70.4	K.AET*PTESVS*EPEVATK.Q
LIG1	S911S913	<del></del>		33.9	37.5	K.QSQIQNQQGEDS*GS*DPEDTY
LIG1	<b>S</b> 51				49.9	K.EWNGVVSESDS*PVK.R
LIG1 DNA ligase I LIG1	S66S76			100.0	105.0	R.VLGS*EGEEEDEALS*PAK.G
LIG1 DNA ligase I LIG1	S141			134.4	95.6	R.TIQEVLEEQS*EDEDR.E
LIG1 DNA ligase I <sub>LIG1</sub>	S91S109	-		13.1	32.8	K.GQKPALDCSQVS*PPRPATSPENNASLSDTS*PMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	S91T108 S91T97			6.1	30.2	K.GQKPALDCSQVS*PPRPATSPENNASLSDT*SPMDSSPSGIPK.R  K.GQKPALDCSQVS*PPRPAT*SPENNASLSDTSPMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	S91197 S91			2.3	35.8	K.GQKPALDCSQVS*PPRPATSPENNASLSDTSPMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	S91S113			16.2	26.0	K.GQKPALDCSQVS*PPRPATSPENNASLSDTSPMDS*SPSGIPK.R
LIG1 DNA ligase I LIG1	<b>S</b> 76			84.2	99.6	R.VLGSEGEEEDEALS*PAK.G
LIG1 DNA ligase I LIG1	S91S98			3.9	41.8	K.GQKPALDCSQVS*PPRPATS*PENNASLSDTSPMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	S88S91			0.1	20.0	K.GQKPALDCS*QVS*PPRPATSPENNASLSDTSPMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	<b>S4</b> 9			22.4	30.6	K.EWNGVVSES*DSPVK.R
LIG1 DNA ligase I LIG1	T97	<u> </u>		-5.7	38.9	K.GQKPALDCSQVSPPRPAT*SPENNASLSDTSPMDSSPSGIPK.R
LIG1 DNA ligase I <sub>LIG1</sub> LIG1 DNA ligase I <sub>LIG1</sub>	S47			•	17.4	K.EWNGVVS*ESDSPVK.R  R.KQSQIQNQQGEDS*GSDPEDTY*
LIG1 DNA ligase I LIG1	S911Y919 S88S109	=		2.2	23.5	K.GQKPALDCS*QVSPPRPATSPENNASLSDTS*PMDSSPSGIPK.R
LIG1 DNA ligase I LIG1	S91S104			11.4	22.3	K.GQKPALDCSQVS*PPRPATSPENNAS*LSDTSPMDSSPSGIPK.R
Lim and SH3 protein 1 <sub>LASP1</sub>	S146			41.3	50.8	R.DS*QDGSSYR.R
LIM domain containing 2 <sub>LIMD2</sub>	<b>S</b> 29		•••	39.8	43.6	R.SKS*FSLR.A
LIM domain only 7 <sub>LMO7</sub>	S1159			12.0	64.2	R.SAS*VNKEPVSLPGIMR.R
LIM domain only 7 LMO7	<b>S</b> 342			60.7	85.1	R.S*WASPVYTEADGTFSR.L
LIM domain only 7 LMO7	S863			21.8	63.9	R.S*QFFEQGSSDSVVPDLPVPTISAPSR.W
LIM domain only 7 <sub>LMO7</sub> LIM domain only 7 <sub>LMO7</sub>	S531			35.4	51.0	R.VTTEIQLPS*QSPVEEQSPASLSSLR.S  R.S*ASVNKEPVSLPGIMR.R
LIM Contain only 7 Limp1	S1157 S316	==		6.2	73.9	R.S. ASVNKEPVSLPGIMR.R  R.SNS*GLGGEVSGVMSKPNVDPQPWFQDGPK.S
LIMD1 LIMD1	S424	• • •		14.5	144.3	K.EGPLGWSSDGSLGSVLLDSPSS*PR.V
LIMD1 LIMD1	S421	• •		-0.3	82.2	K.EGPLGWSSDGSLGSVLLDS*PSSPR.V
Limkain b1 <sub>MARF1</sub>	S1093	Ï		22.5	62.3	R.SKS*PVGNPQLIQFSR.E
Limkain b1 MARF1	S1091	<del>;;</del>		12.2	71.1	R.S'KSPVGNPQLIQFSR.E
Limkain beta 2 CCDC92	S211			18.6	14.3	K.SLS*APLHPEFEEVYR.F
Lin 9 homolog <sub>LIN9</sub>	\$325\$337			87.5	49.7	R.LHYTPPLQS*PIIDNDPLLGQS*PWR.S
Lin 9 homolog L <sub>IN9</sub>	T320S325S337			52.0	34.7	R.LHYT"PPLQS"PIIDNDPLLGQS"PWR.S
Lin 9 homolog LIN9	Y319S325S337			39.3	32.1	R.LHY*TPPLQS*PIIDNDPLLGQS*PWR.S
Linker for activation of T cells <sub>LAT</sub> Linker for activation of T cells <sub>LAT</sub>	S224 S84			67.0	71.5	R.S*PQPLGGSHR.T
Lipase hormone sensitive LIPE	S950			10.5	27.9	R.RS*SQGATQMPLYSSPIVK.N
Liprin beta 2 PPFIBP2	S387			29.8	33.1	K.KLSCS*LEDLR.S
Liprin beta 2 PPFIBP2	<b>S</b> 512			19.9	108.8	R.TQS*GNFYTDTLGMAEFR.R
Liprin beta 2 PPFIBP2	S414			32.7	21.6	K.DS*PFLAEHKYPTLPGK.L
Liver-specific bHLH-Zip transcription factor LSR	<b>S</b> 530		-	43.4	41.5	R.S'RDDLYDQDDSRDFPR.S
Liver-specific bHLH-Zip transcription factor LSR	S643S646			100.0	15.7	K.NLALS*RES*LVV
Liver-specific bHLH-Zip transcription factor LSR	T336		<u>.</u>	11.4	23.4	K.T*PPPPAMIPMGPAYNGYPGGYPGDVDR.S
LKB1 interacting protein 1 STK11IP	S643			100.0	13.1	K.NLALS*R.E  R.SPRPT*GSDLLPGAPILSLR.F
LKB1 interacting protein 1 STK11 P	T614 S610			4.7	35.8 42.4	R.SPRPT*GSDLLPGAPILSLR.F
LKB1 interacting protein 1STK11IP	S610 S616	•••		21.3	52.5	R.SPRPTGS*DLLPGAPILSLR.F
LKB1 interacting protein 1 <sub>STK11IP</sub>	S415S431			18.2	25.9	R.TLNPS*PAGWFVQQHPELELMS*SFR.E
LNK SH2B3	S121		<del>-</del>	-0.4	15.4	R.SS*EELAPPRPPGPCSFQHFR.R
LNK SH2B3	<b>S</b> 120		=	8.5	14.5	R.S*SEELAPPRPPGPCSFQHFR.R
LOC115294 protein PCMTD1	\$302		<u> </u>	100.4	56.7	R.INTYVFVGNQLIPQPLDS*EEDEK.M
LOC159090 FAM122B			<b>.</b>	100.0	66.7	R.HS*LEEGLDMVNR.E
LOC159090 SPACIA2		<b></b>		36.8	44.6	K.RIDFTPVS*PAPS*PTR.G
LOC159090 SPACIA2			Į	8.9	32.7	R.RNS*TTIMSR.H
LOC159090 SPACIA2				15.5	24.4	R.SSSAPLIHGLS*DLSQVFQPYTLR.T
LOC159090 SPACIA2  LOC388974 RGPD2				6.6	24.7	R.SSS*APLIHGLSDLSQVFQPYTLR.T  R.EDALDDNVSSSSVHDS*PLASS*PVRK.N
LOC388974 RGPD2	\$520\$525 \$990			14.9	17.0 35.4	R.ESLLPVINTMLQLS*PEEK.G
LOC389677 protein RBM12B	S638	• • • •		28.4	47.7	R.S'PTEDFR.Q
LOC389677 protein RBM12B	S710S718			100.0	22.6	R.RPPEEDFRHS*PEEDFRQS*PQEHFR.R

Peak Area %CV <-10 0	abundand		compared to	the			
-5 25 42 0 47 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	timepoint PSM	with the minimum					
5 >100 >100				RajiB E E E		Menne -	Saguanca
Protein Name LOC389677 proteir		Phosphosites S278S280	5 2 8	ลัต์ธ	Ascor 50.8	MOWSE 28.8	Sequence R.S'RS'PLGFYVHLK.N
LOC389677 protein	RBM12B	S250S254	<del>;;;</del>		100.0	29.1	R.S*EEHS*PPR.G
LOC389677 proteir	RBM12B	T640			16.9	50.6	R.SPT*EDFR.Q
LOC389677 protein		S98T100			16.0	42.7	R.GRPGS*GT*SGVDSLSNFIESVK.E
LOC389677 proteir		T100S101			6.4	31.7	R.GRPGSGT*S*GVDSLSNFIESVK.E
LOC389677 protein	RBM12B	T100 S324			1.8	54.0 81.8	R.GRPGSGT*SGVDSLSNFIESVK.E  R.WS*GNEPTDEFSDLPLR.V
	LRRFIP2				29.9	65.1	R.RGS*GDTSSLIDPDTSLSELR.D
	LRRFIP2	S333			4.2	20.2	R.RGSGDTSS*LIDPDTSLSELR.D
LUC7 like	LUC7L	S363		•	100.0	39.8	R.S'EEKEAGEI
LUC7 like 2	LUC7L2	T17				39.0	R.AMLDQLMGT*SR.D
LUC7 like 2	FMC1	\$383\$384			14.2	24.1	R.SEDRRS*S*EER.E
LUC7 like 2		S378S383			6.7	18.3	R.S'EDRRS'SEER.E
LUC7 like 2		S18			6.5	48.3	R.AMLDQLMGTS*R.D
LUC7 like 2		S281S283S285			100.0	10.9	R.S'RS'MS'R.E
Lymphocyte antigen s		S648 T650		•	9.1	24.7	R.KPQVVPPPQQNDLEIPES*PTYENFT  R.KPQVVPPPQQNDLEIPESPT*YENFT
Lymphocyte cytosolic protein		S5		-	13.9	18.9	R.GS*VSDEEMM#ELR.E
Lymphocyte cytosolic protein 1		S7	<del></del>		-0.1	84.6	R.GSVS*DEEMM#ELR.E
Lymphocyte cytosolic protein 1	LCP1	S257			100.0	75.0	R.EGES*LEDLMK.L
Lymphocyte cytosolic protein 1	LCP1	Y28			35.4	71.8	K.VDTDGNGY*ISFNELNDLFK.A
Lymphocyte cytosolic protein 1	LCP1	S406			100.0	45.0	R.NWMNS*LGVNPR.V
Lymphocyte specific protein	LSP1	<b>S</b> 139			5.4	36.3	K.EDSDEVHLEELS*LSK.E
Lymphocyte specific protein	LSP1	S130			99.2	87.5	K.EDS*DEVHLEELSLSK.E
Lymphocyte specific protein	LSP1	S111S130			7.5	33.2	R.S*PEGEQEDRPGLHAYEKEDS*DEVHLEELSLSK.E
Lymphocyte specific protein		S252			60.5	102.9	R.QAS*IELPSMAVASTK.S
Lymphocyte specific protein		S189			9.2	94.0	R.TPSPLVLEGTIEQSS*PPLSPTTK.L
Lymphocyte specific proteir		T184			32.4	74.8	R.TPSPLVLEGT*IEQSSPPLSPTTK.L
Lymphocyte specific protein	2011	S177			21.0	77.5	R.TPS*PLVLEGTIEQSSPPLSPTTK.L
Lymphocyte specific protein	2011	S177S189			26.8	47.7	R.TPS*PLVLEGTIEQSS*PPLSPTTK.L  R.TPSPLVLEGTIEQS*S*PPLSPTTK.L
Lymphocyte specific protein		\$188\$189 \$188\$196		• • •	14.8	41.8	R.TPSPLVLEGTIEQS*SPPLSPTT*K.L
Lymphocyte specific protein		T175S177			30.0	53.2	R.T*PS*PLVLEGTIEQSSPPLSPTTK.L
Lymphocyte specific protein	LSP1	S177S189S193		•••	14.1	21.0	R.TPS*PLVLEGTIEQSS*PPLS*PTTK.L
Lymphocyte specific protein	LSP1	T244			33.1	59.1	K.IDQWLEQYTQAIETAGRT*PK.L
Lymphocyte specific protein	LSP1	T175T184			9.9	36.7	R.T*PSPLVLEGT*IEQSSPPLSPTTK.L
Lymphocyte specific protein	LSP1	T175S177S189			23.1	52.2	R.T*PS*PLVLEGTIEQSS*PPLSPTTK.L
Lymphocyte specific protein	LSP1	S177T184S189			15.1	45.9	R.TPS*PLVLEGT*IEQSS*PPLSPTTK.L
Lymphocyte specific protein	LSP1	T175S177S189			22.3	16.4	R.T*PS*PLVLEGTIEQSS*PPLS*PTTK.L
Lymphocyte specific protein	LSP1	T175S177S188		<u> </u>	19.1	14.2	R.T*PS*PLVLEGTIEQS*SPPLS*PTTK.L
Lymphocyte specific protein		S204			38.1	32.7	R.TES*LNR.S
Lymphocyte specific protein		S188			62.3	88.9	R. TPSPLVLEGTIEQS*SPPLSPTTK.L
Lymphocyte specific protein		T184S189			24.1	40.6	R.TPSPLVLEGT*IEQSS*PPLSPTTK.L  R.T*PS*PLVLEGT*IEQSSPPLS*PTTK.L
Lymphocyte specific protein		T175S177T184 S177T184			13.2	17.4 51.4	R.TPS*PLVLEGT*IEQSSPPLS*PTTK.L
Lymphocyte specific protein		\$1771184 \$188\$193			16.7	41.0	R.TPSPLVLEGTIEQS*SPPLS*PTTK.L
Lymphocyte specific protein		S1111	••••		53.7	24.0	R.S*PEGEQEDRPGLHAYEK.E
Lymphocyte specific protein	LSP1	S24			5.7	56.3	R.EELLGPTAQWS*VEDEEEAVHEQCQHER.D
Lymphocyte specific protein	LSP1	T20			4.3	16.3	R.EELLGPT*AQWSVEDEEEAVHEQCQHER.D
Lymphocyte specific protein	LSP1	T175S177T184			6.6	14.6	R.T*PS*PLVLEGT*IEQSSPPLSPT*TK.L
Lymphocyte specific protein	LSP1	S141			22.5	113.1	K.EDSDEVHLEELSLS*K.E
Lymphocyte specific protein	LSP1	S177T184S188		<b>—</b>	18.5	11.2	R.TPS*PLVLEGT*IEQS*SPPLSPTTK.L
Lymphocyte specific protein		S177S188S189		÷	15.6	21.7	R.TPS*PLVLEGTIEQS*S*PPLSPTTK.L
Lymphocyte specific protein		T184S188			8.0	56.4	R.TPSPLVLEGT*IEQS*SPPLSPTTK.L
Lymphocyte specific protein		T175S177T184		•	5.5	11.5	R.T'PS'PLVLEGT'IEQSSPPLSPTTK.L
Lymphoid enhancer binding factor		S132	·		2.6	21.4	K.GPSYSSYSGYIMMPNMNNDPYMSNGSLS*PPIPR.T
1	LYN	S13		<u> </u>	25.3	80.3	K.DSLS*DDGVDLK.T  K.AEERPTFDYLQSVLDDFY*TATEGQYQQQP
	LYN	Y501 T502		==	7.4	56.2	KAEERPTFDYLQSVLDDFY*1ATEGQYQQQP  KAEERPTFDYLQSVLDDFYT*ATEGQYQQQP
	LYN	T502 S11			13.3	62.9	K.DS*LSDDGVDLK.T
LysM, peptidoglycan-binding, domain	LYSMD2	S33		-	-0.2	77.1	R.SGS*ESEEAELSLSLAR.T
containing 2  Lysosomal trafficking regulator	!	S2105			61.9	80.4	R.S*LPAFPTSSLLTQSQK.L

Peak Area %CV	abundand		compared to	the			
-5 25 25 42 71 0		with the minimum					
3 80 5 >100 >10			CarT	RajiB			
Protein Name M phase phosphoprotein 9		Phosphosites	# # # # # #	8 2 2	Ascor 61.2	MOWSE 19.7	Sequence K.NES*SPIRFDILLDDLDTVPVSTLQR.T
M phase phosphoprotein, mpp8	MPHOSPI	H 851	•-		100.0	112.8	R.GAEAFGDS*EEDGEDVFEVEK.I
M phase phosphoprotein, mpp8	MPHOSPI	1 S188S189		•••	21.0	46.3	K.SKPDLES*S*LESLVFDLR.T
M phase phosphoprotein, mpp8	MPHOSPI	H S188S192			12.8	33.9	K.SKPDLES*SLES*LVFDLR.T
M phase phosphoprotein, mpp8	MPHOSPI	H S136S138		<b>-</b>	10.0	60.3	R.LSLNNDIFEANS*DS*DQQSETK.E
M phase phosphoprotein, mpp8	MPHOSPI	1 S189S192			7.3	60.9	K.SKPDLESS*LES*LVFDLR.T
M phase phosphoprotein, mpp8			Ţ.		100.0	11.2	R.RLS*GEER.G
M phase phosphoprotein, mpp8		HS188S189S192			3.5	28.8	K.SKPDLES*S*LVFDLR.T
Macrophin 1		S2956			100.0	36.1	K.AFLAELEQNS*PK.I
Macrophin 1  Macrophin 1		S5829			7.2	21.5	K.LKRPTPTFHSS*R.T
	ZCRB1	\$5828 \$155			29.8	76.0	KAPEPEEIEEVEES*EDEGEDPALDSLSQAIAFQQAK.I
MADP 1 protein		S210S216	=		12.4	26.2	K.STYFS*DEEELS*D
MADP 1 protein		Y208S216	ⅲ		7.7	18.7	K.STY*FSDEEELS*D
Maestro heat-like repeat-containing protein	MROH6	T506			100.0	11.4	R.HT*GLNPR.L
family member 6 (Fragment)  Major vault protein		S873		•	28.2	75.9	R.VASGPSPGEGIS*PQSAQAPQAPGDNHVVPVLR
Major vault protein	MVP	S876			12.0	29.5	R.VASGPSPGEGISPQS*AQAPQAPGDNHVVPVLR
Major vault protein	MVP	S864		· <del>···</del>	3.5	24.9	R.VAS*GPSPGEGISPQSAQAPQAPGDNHVVPVLR
Major vault protein	MVP	S867		•	5.6	29.6	R.VASGPS*PGEGISPQSAQAPQAPGDNHVVPVLR
Male specific lethal 3 like 1	MSL3	\$400T405		•	6.4	16.1	R.SSS*PIPLT*PSKEGSAVFAGFEGR.R
Male-specific lethal 2-like 1	MSL2	S447			9.5	41.6	K.EKIPSHHFMPGS*PTK.T
Male-specific lethal-1 homolog		<b>S</b> 99	<b>—</b>		121.5	51.5	K.HS*PIKEEPCGSLSETVCK.R
MAN antigen 1	LEMD3	S259S261	Ţ.		6.6	69.8	R.ENYS*DS*EEEDDDDVASSR.Q
MAN antigen 1		Y258S259	<b>-</b>		6.5	102.2	R.ENY*S*DSEEEDDDDVASSR.Q
MAN antigen 1		S144			9.1	45.6	K.VLLGFSSDES*DVEASPR.D
MAN antigen 1		Y258S261			77.7	115.6	R.ENY*SDS*EEEDDDDVASSR.Q
MAP kinase activating death domain protein		S1239			21.2	148.5	R.GTLS*DSEIETNSATSTIFGK.A
MAP kinase activating death domain protein  MAP kinase activating death domain protein		S1241			-0.2	73.9	R.GTLSDS*EIETNSATSTIFGKA
	MAP2K2	T1237		_	9.2	59.6	RUNDPGTPT*R.T
	MAP2K2	T394		• •	25.6	31.7	RLNQPGT*PTR.T
	MAP3K2	S163	==		77.8	93.2	R.DRS*SPPPGYIPDELHQVAR.N
MAP3K2	MAP3K2	S239			10.3	35.8	R.AQS*YPDNHQEFSDYDNPIFEK.F
MAP3K2	MAP3K2	S153			67.4	45.0	K.RLS*IIGPTSR.D
MAP3K2	MAP3K2	S164			5.8	73.6	R.DRSS*PPPGYIPDELHQVAR.N
MAP3K4	MAP3K4	S66S84	•••		17.1	16.9	K.SPES*DLEDFSDETNTENLYGTS*PPSTPR.Q
MAP3K4	MAP3K4	S66T77S84		÷	11.3	13.6	K.SPES*DLEDFSDETNT*ENLYGTS*PPSTPR.Q
MAP3K4	MAP3K4	S66T83		Ī	12.8	26.7	K.SPES*DLEDFSDETNTENLYGT*SPPSTPR.Q
MAP3K4	MAP3K4	<b>S</b> 499			2.0	14.4	R.LES'EDDSLGWGAPDWSTEAGFSR.H
MAP3K4	MAP3K4	<b>S</b> 503		-	2.0	24.6	R.LESEDDS*LGWGAPDWSTEAGFSR.H
MAP3K7		S439	-		39.3	68.8	R.S*IQDLTVTGTEPGQVSSR.S
MAP3K7		S417			-0.9	53.4	K.TAS*FGNILDVPEIVISGNGQPR.R
	MAP4K4	S981	÷		79.5	20.4	R.KGS*VVNVNPTNTRPQSDTPEIR.K
	MAP4K4	S787			-0.2	42.4	R.SS*SKSEGSPSQR.L
MAP4K4	MAP4K4 MAP4K4	T705S708			5.7	15.1	R.TT*SRS*PVLSR.R  K.SS*SSFTPFIDPR.L
MAP4K4		S934			-0.1	71.4	R.NT*FIGTPYWMAPEVIACDENPDATYDYR.S
	MAP4K4	T187			12.7	75.3	K.HKS*SSSFTPFIDPR.L
	MAP4K4	S936T938			4.4	16.9	K.HKSSSS*FT*PFIDPR.L
	MAP4K4	S933S934			9.3	22.0	K.HKS*S*SSFTPFIDPR.L
	MAP4K4	S933S936			14.2	63.6	K.HKS*SSS*FTPFIDPR.L
MAP4K4	MAP4K4	T319S324			3.1	26.7	K.DET*EYEYS*GSEEEEEEVPEQEGEPSSIVNVPGESTLR.R
MAP4K4	MAP4K4	S324S326			9.6	28.8	K.DETEYEYS*GS*EEEEEEVPEQEGEPSSIVNVPGESTLR.R
MAP4K4	MAP4K4	Y323S324			6.8	44.6	K.DETEYEY*S*GSEEEEEEVPEQEGEPSSIVNVPGESTLR.R
MAP4K4	MAP4K4	T705S706			8.6	11.0	R.TT*S*RSPVLSR.R
MAP4K4	MAP4K4	S935S936			6.4	14.5	K.HKSSS'S'FTPFIDPR.L
MAP4K4	MAP4K4	S934S935	-		4.3	11.8	K.HKSS*S*SFTPFIDPR.L
	MAP4K4	T319S326	<b>.</b> .		7.6	14.2	K.DET*EYEYSGS*EEEEEEVPEQEGEPSSIVNVPGESTLR.R
	MAP4K4	Y323S326		•	12.4	31.2	K.DETEYEY*SGS*EEEEEEVPEQEGEPSSIVNVPGESTLR.R
	MAP4K4	S788	-		11.7	28.1	R.SSS*KSEGSPSQR.L
	MAP4K4	T704T705			8.5	14.8	R.T*T*SRSPVLSR.R
MAP7 domain containing 1	MAP7D1	S544S548T554			5.1	22.4	K.ESAAPAS"PAPS"PAPSPT"PAPPQK.E

<	Peak Area	o abundano	s-Significant cha e at 5%FDR o with the minimum	compared to	the			
	-3 0	42 PSM 71		CarT	RajiB			
;	5 >10	>100 Protein Name Gene	Phosphosites	5 E B	5 % B	Ascor	MOWSE	Sequence
			S544S548S552	<b></b>		22.7	26.6	K.ESAAPAS"PAPS"PAPS"PTPAPPQK.E
		domain containing 1 <sub>MAP7D1</sub>	T813			26.8	65.8	R.T*PETILIPFAEAEAFLK.K
		domain containing 1 <sub>MAP7D1</sub>			• • •	13.9	15.0	R.TPET*LLPFAEAEAFLK.K  K.RQS*LPASPRAR.L
		domain containing 1 <sub>MAP7D1</sub>		-		7.3	12.3	K.ES*AAPAS*PAPSPAPSPT*PAPPQK.E
		MAPK14 MAPK14			•	17.8	72.3	R.HTDDEMTGY*VATR.W
		MAPK14 MAPK14	T180			10.2	54.9	R.HTDDEMT*GYVATR.W
	N.	MARCKS like protein MARCKSL	T122	-		8.1	87.3	K.EGGGDSSASSPT*EEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL	<b>S</b> 119		•••	3.0	55.2	K.EGGGDSSAS*SPTEEEQEQGEIGACSDEGTAQEGK.A
	ħ.	MARCKS like protein MARCKSL	S116S119			10.7	126.3	K.EGGGDS*SAS*SPTEEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL				46.0	119.7	K.EGGGDS*S*ASSPTEEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL				29.8	124.9	K.GAEASAASEEEAGPQATEPS*TPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL				6.8	90.7	K.GAEASAASEEEAGPQATEPST*PSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL  MARCKS like protein MARCKSL				6.6	116.6	K.GAEASAASEEEAGPQAT*EPSTPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL				100.0	92.4	K.GAEASAAS*EEEAGPQATEPSTPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL				19.1	61.7	K.GAEAS'AAS'EEEAGPQATEPSTPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL		•••		-0.2	33.5	K.GAEASAASEEEAGPQATEPS*T*PSGPESGPTPASAEQNE
	N.	MARCKS like protein MARCKSL	S104	•		67.4	33.0	KLSGLS*FK.R
	h.	MARCKS like protein MARCKSL	S101			14.9	36.2	K.KPFKLS*GLSFK.R
	h	MARCKS like protein MARCKSL	S101S104			100.0	44.6	K.KPFKLS*GLS*FK.R
	N.	MARCKS like protein MARCKSL	S36	-		78.3	78.3	K.S*NGDLSPK.G
	N	MARCKS like protein MARCKSL	<b>S</b> 22			146.6	73.1	R.GDVTAEEAAGAS*PAK.A
		MARCKS like protein MARCKSL				2.2	73.2	K.GAEASAASEEEAGPQAT*EPS*TPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL			•	7.2	60.5	K.EGGGDS*S*ASS*PTEEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL		·			57.4	K.GAEAS*AASEEEAGPQATEPSTPSGPESGPTPASAEQNE
		MARCKS like protein MARCKSL  MARCKS like protein MARCKSL				4.5	126.3	K.EGGGDS'SAS'SPT'EEEQEQGEIGACSDEGTAQEGK.A  K.GAEASAASEEEAGPQATEPS'TPSGPES'GPTPASAEQNE
		MARCKS like protein MARCKSL		•		-0.2	45.5 107.4	K EGGOSS*AS*SPTEFFOFOGEIGACSDEGTADEGK A
		MARCKS like protein MARCKSL			-	11.1	45.5	K.EGGGDS*SASSPTEEEQEQGEIGACS*DEGTAQEGK.A
		MARCKS like protein MARCKSL				16.3	33.2	K.GAEASAASEEEAGPQATEPSTPSGPESGPTPAS*AEQNE
	h	MARCKS like protein MARCKSL	S116S119S120			12.5	72.0	K.EGGGDS'SAS'S'PTEEEQEQGEIGACSDEGTAQEGKA
	N.	MARCKS like protein MARCKSL	S116S117T122			6.7	76.2	K.EGGGDS*S*ASSPT*EEEQEQGEIGACSDEGTAQEGK.A
	N.	MARCKS like protein MARCKSL	S135			13.6	40.4	K.EGGGDSSASSPTEEEQEQGEIGACS*DEGTAQEGK.A
	N.	MARCKS like protein MARCKSL	S116S120			7.3	75.2	K.EGGGDS'SASS'PTEEEQEQGEIGACSDEGTAQEGKA
		MARCKS like protein MARCKSL				2.4	82.5	K.GAEASAASEEEAGPQATEPSTPS*GPESGPTPASAEQNE
		MARCKS like protein MARCKSL				17.4	107.5	K.EGGGDS*SASSPT*EEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL			-	4.3	59.7	K.EGGGDSS*ASSPTEEEQEQGEIGACSDEGTAQEGK.A
		MARCKS like protein MARCKSL  Mastermind like 1 MAML1	\$119\$120 \$1015			2.8	32.0	K.EGGGDSSAS*S*PTEEEQEQGEIGACSDEGTAQEGK.A  R.TSEEWMSDLDDLLGS*Q
		MASTL MASTL	\$370			17.0 43.9	28.8	K.DLELALS*PIHNSSALPTTGR.S
Maternal	embryonic le	oucine zipper kinase MELK	S505			135.8	109.0	R.S*VELDLNQAHMEETPK.R
		Matrin 3 <sub>MATR3</sub>	T741				25.6	K. MEENT*EDGAESSEMADDDNIZDTSEMADGGSDENIZDDYTIDDEVD I
		MATR3	<b>S</b> 598			30.2	38.6	R.SYS*PDGK.E
		Matrin 3 <sub>MATR3</sub>	S596S598	<b>—</b>		9.8	29.7	R.KRS*YS*PDGK.E
		Matrin 3 <sub>MATR3</sub>	S598S604			16.7	47.5	R.SYS*PDGKES*PSDKK.S
		Matrin 3 <sub>MATR3</sub>	Y597S604	<b></b>		7.1	21.8	R.SY*SPDGKES*PSDKK.S
		Matrin 3 <sub>MATR3</sub>	S195	·		10.5	33.9	R.DSFDDRGPS*LNPVLDYDHGSR.S
		Matrin 3 <sub>MATR3</sub>	S188	÷		100.0	29.1	R.RDS*FDDR.G
		Matrin 3 <sub>MATR3</sub>	T644S654S671				27.1	K.
		Matrin 3 <sub>MATR3</sub>	\$654\$673\$674 \$596¥597			6.1	24.4	R.KRS'Y'SPDGK.E
		MBC2 <sub>ESYT1</sub>	Y822			3.5	42.9	K.HLSPY*ATLTVGDSSHK.T
		MBC2 <sub>ESYT1</sub>	\$820			7.3	53.3	K.HLS*PYATLTVGDSSHK.T
		MBD5 <sub>MBD5</sub>	S1493			100.0	19.7	R.RKIS*R
		MCM2	T39S40S41			35.6	27.8	R.TDALT*S*S*PGR.D
мсма	2 minichrom	osome maintenance MCM2 deficient 2. mitotin	<b>S</b> 27			12.1	53.5	R.GNDPLTSS*PGR.S
мсма	2 minichrom	osome maintenance MCM2 deficient 2. mitotin	Y137				24.5	R.GLLY*DSDEEDEERPARK.R
		osome maintenance MCM2 deficient 2, mitotin	<b>S</b> 139	<b></b> :		32.7	65.2	R.GLLYDS*DEEDEERPAR.K
		osome maintenance MCM2 deficient 2. mitotin	S108			20.7	98.9	R.AIPELDAYEAEGLALDDEDVEELTAS*QR.E
		osome maintenance MCM2 deficient 2. mitotin	T106			14.0	44.4	R.AIPELDAYEAEGLALDDEDVEELT*ASQR.E
MCM	4 minichrom	osome maintenance MCM2 deficient 2, mitotin	S53			20.0	93.7	R.DLPPFEDES*EGLLGTEGPLEEEEDGEELIGDGMER.D

<-10 0 abundan		compared to	the			
25 timepoint 23 42 PSM	with the minimum					
3 5 >100 >10		CarT				
Protein Name Gene MCM2 minichromosome maintenance MCM2 deficient 2. mitotin	Phosphosites T59	9 2 2	5 F E	Ascor 24.1	MOWSE 93.5	Sequence R.DLPPFEDESEGLLGT*EGPLEEEEDGEELIGDGMER.D
MCM2 minichromosome maintenance MCM2 deficient 2. mitotin	S53T59	<u> </u>		100.0	81.9	R.DLPPFEDES*EGLLGT*EGPLEEEEDGEELIGDGMER.D
MCM2 minichromosome maintenance MCM2 deficient 2, mitotin	S41			20.1	56.7	R.RTDALTSS*PGR.D
MCM2	<b>S</b> 40			20.1	59.0	R.TDALTS*SPGR.D
MCM2 minichromosome maintenance MCM2 deficient 2. mitotin	S40S41			35.8	35.5	R.TDALTS'S'PGR.D
MCM2 minichromosome maintenance MCM2 deficient 2. mitotin	T39S40			25.9	20.3	R.TDALT*S*SPGR.D
MCM2 minichromosome maintenance MCM2 deficient 2, mitotin	Y90			12.9	15.4	R.AIPELDAY*EAEGLALDDEDVEELTASQR.E
MCM2 minichromosome maintenance MCM2 deficient 2. mitotin  MCM2 minichromosome maintenance MCM2	S26S27	=		12.5	11.9	R.GNDPLTS'S'PGR.S
deficient 2. mitotin  MCM3 MCM3	S26			10.8	11.6	R.RGNDPLTS*SPGR.S  K.DGDSYDPY*DFSDTEEEM#PQVHT*PK.T
MCM3 MCM3	Y708T722 S711T722	• • •		23.3	17.0	K.DGDSYDPYDFS*DTEEEM#PQVHT*PK.T
MCM3 <sub>MCM3</sub>	S711			14.5	64.4	K.DGDSYDPYDFS*DTEEEMPQVHTPK.T
MCM3 <sub>MCM3</sub>	Y708S711T722		• • •	47.3	17.3	K.DGDSYDPY*DFS*DTEEEMPQVHT*PK.T
MCM3 <sub>MCM3</sub>	S160			7.2	64.0	R.RYS*DLTTLVAFPSSSVYPTK.D
MCM3	S672T674			34.8	63.3	R.SEDES*ET*EDEEEKSQEDQEQKR.K
MCM3 <sub>MCM3</sub>	S711T713T722			15.2	11.0	K.DGDSYDPYDFS*DT*EEEM#PQVHT*PK.T
MCM3 <sub>MCM3</sub>	Y708			26.8	55.7	K.DGDSYDPY*DFSDTEEEMPQVHTPK.T
MCM3 <sub>MCM3</sub>	Y708S711			8.6	26.1	K.DGDSYDPY*DFS*DTEEEMPQVHTPK.T
MCM3 <sub>MCM3</sub>	Y705T713T722			11.6	12.1	K.DGDSY*DPYDFSDT*EEEMPQVHT*PK.T
мсмз	S711T713		-	3.2	11.3	K.DGDSYDPYDFS*DT*EEEM#PQVHTPK.T
MCM3 <sub>MCM3</sub>	Y708T713			9.4	38.2	K.DGDSYDPY*DFSDT*EEEMPQVHTPK.T
MCM3 <sub>MCM3</sub>	Y708T713T722	-		24.3	13.7	K.DGDSYDPY*DFSDT*EEEMPQVHT*PK.T
MCM6 MCM6	S804	•		4.6	25.4	K.GSTEGSES*YEEDPYLVVNPNYLLED  R.SOPPGEDS*DT*DVDDDSRPPGRPAEVHLER.A
Mediator of DNA damage checkpoint 1 MDC1  Mediator of DNA damage checkpoint 1 MDC1	S299T301			16.1	11.0	R.SQTTTERDS*DT*DVEEEELPVENR.E
Mediator of DNA damage checkpoint 1 MDC1	\$453T455 \$376			35.4	19.8	R.GPGAPGLAHLQESQAGS*DTDVEEGKAPQAVPLEK.S
Mediator of DNA damage checkpoint 1 <sub>MDC1</sub>	\$376T378			19.6	33.9	R.GPGAPGLAHLQESQAGS*DT*DVEEGKAPQAVPLEK.S
Mediator of DNA damage checkpoint 1 <sub>MDC1</sub>	S329T331			79.3	24.3	R.AQPFGFIDS*DT*DAEEERIPATPVVIPMK.K
Mediator of DNA damage checkpoint 1 MDC1	\$402 <b>T</b> 404	=		44.0	140.5	K.SQASMVINS*DT*DDEEEVSAALTLAHLK.E
Mediator of DNA damage checkpoint 1 MDC1	S168			121.5	125.9	R.LLLAEDS'EEEVDFLSER.R
Mediator of DNA damage checkpoint 1 MDC1	S1775			72.7	54.8	R.AAESLTAIPEPAS*PQLLETPIHASQIQK.V
Mediator of DNA damage checkpoint 1 MDC1	<b>S</b> 329			6.3	16.2	R.AQPFGFIDS*DTDAEEERIPATPVVIPMK.K
Mediator of DNA damage checkpoint 1 MDC1	S372S376				18.0	R.GPGAPGLAHLQES*QAGS*DTDVEEGKAPQAVPLEK.S
Mediator of DNA damage checkpoint 1 MDC1	S397T404	•		6.0	62.6	K.SQAS*MVINSDT*DDEEEVSAALTLAHLK.E
Mediator of DNA damage checkpoint 1 MDC1	S372T378		-	8.6	16.9	R.GPGAPGLAHLQES*QAGSDT*DVEEGKAPQAVPLEK.S
Mediator of DNA damage checkpoint 1 MDC1	S329T341			13.2	11.4	R.AQPFGFIDS*DTDAEEERIPAT*PVVIPM#KK.R
Mediator of DNA damage checkpoint 1 MDC1	T448S453		•	3.4	13.3	R.SQTT*TERDS*DTDVEEEELPVENR.E
Mediator of RNA polymerase II transcription MED19 subunit 19	S226	=		58.0	26.6	K.NRHS*PDHPGMGSSQASSSSSLR
MEK1 MAP2K2  MEK1 MAP2K1	S218S222			53.9	81.4	K.LCDFGVSGQLIDS*MANS*FVGTR.S  R.T*PGRPLSSYGMDS*RPPMAIFELLDYIVNEPPPK.L
MEK1 MAP2K1	T292S304 T292S298			8.6	36.5 21.3	R.T*PGRPLS*SYGMDS*RPPMAIFELLDYIVNEPPPK.L
Melanoma antigen family F 1 MAGEF1	S95			28.2	28.0	K.KS*PITR.S
Melanoma differentiation associated protein IFIH1	S301			78.5	50.3	R.AS*PEPELQLRPYQMEVAQPALEGK.N
Melanoma inhibitory activity family, member MIA3	S1739			62.9	46.6	R.WSAEASGKPSPSDPGSGTATMMNS*SSR.G
Melanoma inhibitory activity family, member MIA3	S1741			9.1	53.3	R.WSAEASGKPSPSDPGSGTATMMNSSS*R.G
Melanoma inhibitory activity family, member MIA3	S1740			9.0	43.7	R.WSAEASGKPSPSDPGSGTATMMNSS*SR.G
Melanoma inhibitory activity family, member MIA3	S1721			12.9	12.9	R.WSAEAS*GKPSPSDPGSGTATMMNSSSR.G
Melanoregulin MREG	S213			75.8	34.4	K.ELHYLPFPS*P
Membrane component, chromosome 11, CAPRIN1 surface marker 1	T317		-		12.4	K. EOV/DEWIT*VETVEVA/NSI OOODOAASDEV/DEDUSI TDVAOADDI V/D
Meningioma expressed antigen 5 <sub>MGEA5</sub>	S364			119.8	91.7	K.LENEGS*DEDIETDVLYSPQMALK.L
Mesoderm induction early response 1 MIER1	S507S512			22.0	78.1	R.VNS*NGKES*PGSSEFFQEAVSHGK.F
Mesoderm induction early response 1 MIER1	T182S190			12.9	60.4	K.YFDT*NSEVEEES*EEDEDYIPSEDWK.K
Mesoderm induction early response 1 MIER1  Mesoderm induction early response 1 MIER1	S184S190	-		23.7	55.0	K.Y*FDTNS*EVEEES*EEDEDYIPSEDWK.K  K.Y*FDTNSEVEEES*EEDEDYIPSEDWK.K
Mesoderm induction early response 1 MIER1  Mesoderm induction early response 1 MIER1	Y179S190			10.1	46.5	K.Y*FDTNSEVEEES*EEDEDYIPSEDWK.K  K.YFDT*NS*EVEEESEEDEDYIPSEDWK.K
Metadherin MTDH	T182S184 S426			79.4	29.3 52.0	K.SQEPIPDDQKVS*DDDKEK.G
Metadherin MTDH	\$426 \$344\$347			79.4	79.0	R.SWSDRS*IFS*GIGSTAEPVSQSTTSDYQWDVSR.N
Metastasis associated protein MTA1 <sub>MTA1</sub>	S562		•	20.1	31.2	K.SVSSVLSS*LTPAK.V
Metastasis associated protein MTA1 MTA1	T564			19.8	54.6	K.SVSSVLSSLT*PAK.V
Metastasis associated protein MTA1 MTA1	<b>S</b> 449			3.9	19.4	R.SNMS*PHGLPAR.S
Metastasis associated protein MTA2 <sub>MTA2</sub>	S435	<u> </u>		33.2	79.7	R.GHLSRPEAQSLS*PYTTSANR.A
Metastasis associated protein MTA2 <sub>MTA2</sub>	T505			100.0	35.7	K.T*PLKIHPLVR.L

Peak Area	o abundano		compared to	the			
-5 -3 0	timepoint PSM	with the minimum	peak area fo	or a given			
3 5 >10	>100		CarT	RajiB			
Metastasis asso	Protein Name Gene ciated protein MTA2 <sub>MTA2</sub>	Phosphosites Y437	£ 5, 5	5 F B	Ascor 25.6	MOWSE 27.9	Sequence R.GHLSRPEAQSLSPY*TTSANR.A
Methio	nyl tRNA synthetase MARS	S825	••		13.6	66.0	K.TS*PKPAVVETVTTAKPQQIQALMDEVTK.Q
Methio	nyl tRNA synthetase MARS	T824			7.4	49.4	K.T*SPKPAVVETVTTAKPQQIQALMDEVTK.Q
	ing domain protein 1 <sub>MBD1</sub>	S408			20.2	18.2	R.EGAS*SPVQVPGPVAASTEALLQAVDPGLPSVK.Q
	ing domain protein 2 <sub>MBD2</sub>	<b>S</b> 407			93.2	25.2	R.AADTEEMDIEMDS*GDEA
	0 domain containing METTL16 hyltransferase like 6 METTL6	\$329 \$53T54			31.7	21.1	K.ELSLKAS'PLR.S  K.RNS'T'NFFK.D
	MGC13125 BUD13	T159S163			100.0	24.5	R.HDT*PDPS*PLR.G
	MGC13125 BUD13	S271	===		139.2	59.5	R.ARHDS*PDLAPNVTYSLPR.T
	MGC13125 BUD13	S248			32.3	11.1	R.VHNNS*PDTSR.R
	MGC13125 BUD13	T135S139	<del>-</del>		100.0	34.4	R.HGT*PDPS*PR.K
	MGC13125 BUD13	S364S370S372			100.0	13.7	R.HKQS*PGHQDS*DS*DLS*PPR.N
	MGC13125 BUD13	T147S151	<b>—</b>		100.0	29.4	R.HDT*PDPS*PR.R
	MGC13125 BUD13	T352S354S357			17.3	22.2	KAT*DS*DLS*SPR.H
	MGC20460 RBM33	S293S295		_	11.5	13.2	R.LAQQQQQLYAPPPPAEQEEQALS*PS*PTNGNPLLPFPGAQVR.Q
	MGC20460 RBM33	\$293T297			4.1	17.9	R.LAQQQQQLYAPPPPAEQEEQALS*PSPT*NGNPLLPFPGAQVR.Q  R.LAQQQQQLY*APPPPAEQEEQALSPSPTNGNPLLPFPGAQVR.Q
	MGC20460 RBM33	Y279 S293			12.7	25.1	R.LAQQQQQLYAPPPPAEQEEQALSPSPTNGNPLLPFPGAQVR.Q  R.LAQQQQQLYAPPPPAEQEEQALS*PSPTNGNPLLPFPGAQVR.Q
	MGC51029 FUNDC1	\$13			12.7	48.1	R.NPPPQDYES*DDDSYEVLDLTEYAR.R
	MGC51029 FUNDC1	Y11				26.0	R.NPPPQDY*ESDDDSYEVLDLTEYAR.R
	MGC51029 FUNDC1	S17			0.5	40.4	R.NPPPQDYESDDDS*YEVLDLTEYAR.R
	MGC874 PBDC1	S181		•	49.5	19.2	K.RADS*GEEENTK.N
	MGC874 PBDC1	<b>S</b> 197			100.0	23.4	K.GADS*GEEKEEGINR.E
	MGEA6 CTAGE4	S139			8.6	63.1	R.SNS*ELEDEILCLEK.D
	MICA like 1 MICALL1	T469			32.3	25.5	K.SLHPWYGITPT*SSPK.T
	MICA like 1 MICALL1	S471			8.2	36.7	K.SLHPWYGITPTSS*PK.T
	MICA like 1 MICALL1	S470			9.8	25.3	K.SLHPWYGITPTS*SPK.T
	MICA like 1 MICALL1	T467S471		==	23.8	18.9	K.SLHPWYGIT*PTS*SPK.T
	MFAP1	S132S133		•	100.0	145.3	R.EDS'S'EEEEEEIDDEEIER.R
Microfibrillar	associated protein 1 <sub>MFAP1</sub>	S52S53			65.4	86.4	K.RPDYAPMES*S*DEEDEEFQFIKK.A
Microfibrillar	associated protein 1 MFAP1	S116S118			100.0	68.0	K.IVEPEVVGES*DS*EVEGDAWR.M
Microfibrillar	associated protein 1 MFAP1	T267			105.2	114.8	R.SLAALDALNT'DDENDEEEYEAWK.V
Mic	rospherule protein 1 <sub>MCRS1</sub>	S354			84.8	66.4	K.GDQVLNFS*DAEDLIDDSKLK.D
	ssociated protein 1A MAP1A	S2019S2022			13.5	23.8	K.ELSS'PIS'PK.S
	ssociated protein 1A MAP1A	S2108			22.4	32.7	R.SHWDDSTSDS*ELEK.G
	ssociated protein 1A <sub>MAP1A</sub>	\$2104T2105 \$1172	•••		14.5 53.9	55.3 63.7	R.SHWDDS'T'SDSELEK.G  K.S'PCGLTEQYLHK.D
	ssociated protein 1A MAP1A	S667			24.7	24.2	K.AELEEMEEVHPS*DEEEEDATK.A
Microtubule as	ssociated protein 1A MAP1A	S1654			13.9	64.1	R.GQDVVQEWQETS*PTR.E
Microtubule as	ssociated protein 1A MAP1A	S1675			10.8	63.8	K.ELAPAWEDTS*PEQDNR.Y
Microtubule as	ssociated protein 1A MAP1A	S1069			124.2	91.3	K.VPPPRS*PQAQEAPVNIDEGLTGCTIQLLPAQDK.A
Microtubule as	ssociated protein 1A MAP1A	S2449			15.2	72.8	R.GELS'PSFLNPPLPPSIDDR.D
	ssociated protein 1A MAP1A	S526S527			100.4	93.8	R.ELVLS'S'PEDLTQDFEEMKR.E
	ssociated protein 1A MAP1A	S1218			48.8	98.8	K.QLS*PESLGTLQFGELNLGK.E
	ssociated protein 1A MAP1A	S2617			100.0	13.6	KAKPAS*PAR.R
	ssociated protein 1A <sub>MAP1A</sub>	T1834	<del></del>		22.0	31.4	K.NEPT*TPSWLADIPPWVPK.D  K.ELAPAWEDT*SPEQDNR.Y
	ssociated protein 1A MAP1A	T1674 S612T616			36.2	51.8	R.GLDS*GAET*EEEKDTWEEK.K
	ssociated protein 1A MAP1A	T1653			7.6	29.7	R.GQDVVQEWQET*SPTR.E
Microtubule as	ssociated protein 1A MAP1A	S2629T2631			100.0	29.4	R.S*PT*PGKGPADR.A
Microtubule as	ssociated protein 1A MAP1A	S1797S1801			36.1	22.4	R.SPFEIIS*PPAS*PPEMVGQR.V
Microtubule as	ssociated protein 1A MAP1A	S2018S2019	·		9.4	14.9	K.ELS*S*PISPK.S
	ssociated protein 1A MAP1A	T2105			8.2	39.0	R.SHWDDST*SDSELEK.G
	ssociated protein 1A MAP1A	S1203	<b>—</b>		3.2	33.0	K.DRWPEVSPEDTQSLSLSEES*PSK.E
	ssociated protein 1A MAP1A	T1835			9.1	36.5	K.NEPTT*PSWLADIPPWVPK.D
	ssociated protein 1A MAP1A	S2104S2106			8.6	52.1	R.SHWDDS*TS*DSELEK.G
	ssociated protein 1A MAP1A	S2451			-0.4	48.2	R.GELSPS*FLNPPLPPSIDDR.D
	associated protein 18 <sub>MAP1B</sub>	T1270			100.0	12.3	K.T*PLGER.S  R.RS*S*LPR.R
	associated protein 4 MAP4	\$1539\$1540 \$928			100.0	18.5 75.5	R.LATNTS*APDLK.N
	associated protein 4 MAP4	\$825			13.9	62.9	R.S'PSTLLPK.K
						-	

<-10 0 abundanc -29 timepoint	ts-Significant change in p e at 5%FDR compare with the minimum peak ar	to the			
3 42 PSM 0 71 3 86 5 >100		RajiB			
>10 Protein Name Gene Microtubule associated protein 4 <sub>MAP4</sub>	Phosphosites & K		Ascor 33.9	MOWSE	Sequence RAS*PIRMDLAPSK.D
Microtubule associated protein 4 <sub>MAP4</sub>	S1073		100.0	109.3	K.VGS*LDNVGHLPAGGAVK.T
Microtubule associated protein 4 <sub>MAP4</sub>	\$280		22.4	88.4	K.DMES'PTKLDVTLAK.D
Microtubule associated protein 4 <sub>MAP4</sub>	T521	1	56.6	38.9	K.DVT*PPPETEVVLIKN
Microtubule associated protein 4 <sub>MAP4</sub>	<b>S</b> 507		68.1	73.0	K.DMS*PLSETEMALGK.D
Microtubule associated protein 4 <sub>MAP4</sub>	S507S510		46.4	83.2	K.DMS*PLS*ETEMALGK.D
Microtubule associated protein 4 <sub>MAP4</sub>	S941		25.6	56.5	R.SKVGS*TENIKH  K.VGS*TENIKH
Microtubule associated protein $4_{MAP4}$ Microtubule associated protein $4_{MAP4}$	T942		8.9	52.0	K.VGST*ENIK.H  K.MAYQEY*PNSQNWPEDTNFCFQPEQVVDPIQTDPFKM
Microtubule associated protein 4 <sub>MAP4</sub>	Y113 S68		27.3	32.7 42.6	K.KKPCS'ETSQIEDTPSSKPTLLANGGHGVEGSDTTGSPTEFLEEK.
Microtubule associated protein 4 <sub>MAP4</sub>	S116		8.8	24.1	K.MAYQEYPNS"QNWPEDTNFCFQPEQVVDPIQTDPFKM
Microtubule associated protein 4 <sub>MAP4</sub>	T123		0.1	22.7	K.MAYQEYPNSQNWPEDT*NFCFQPEQVVDPIQTDPFK.M
Microtubule associated protein 4 <sub>MAP4</sub>	T925	<del></del>	4.0	10.7	RLAT'NTSAPDLK.N
Microtubule associated protein 4 <sub>MAP4</sub>	\$827		2.6	50.2	R.SPS*TLLPK.K
Microtubule associated protein 4 <sub>MAP4</sub>	T927			29.2	RLATNT*SAPDLK.N
Microtubule associated protein 4 <sub>MAP4</sub>	S68T70			14.1	K. WURDCO-ET-SOIENTROSCURTI I ANDOLLOVEOSONTTOSOTESI ESU M
Microtubule associated protein 4 <sub>MAP4</sub>	\$507\$510T521	<u> </u>	14.2	12.0	K.DMS*PLS*ETEMALGKDVT*PPPETEVVLIK.N
Microtubule associated protein tau MAPT  Microtubule associated protein tau MAPT	\$713\$717T720	<u> </u>	15.8	39.8	K.TDHGAEIVYKS'PVVS'GDT'SPR.H  R.HLSNVS'S'TGSIDMVDSPQLATLADEVSASLAK.Q
Microtubule associated protein tau MAPT	\$729\$730 \$726\$729\$730		0.4	22.6	R.H.LS.NVS*S*TGSIDMVDS*PQLATLADEVSASLAK.Q  R.H.LS*NVS*S*TGSIDMVDS*PQLATLADEVSASLAK.Q
Microtubule associated protein tau MAPT	S726S729		13.9	45.0	R.HLS*NVS*STGSIDMVDSPQLATLADEVSASLAK.Q
Microtubule associated protein tau MAPT	S717T720S721		15.4	22.0	K.TDHGAEIVYKSPVVS'GDT'S'PR.H
Microtubule associated protein tau MAPT	\$733\$739	<u> </u>	5.3	24.5	R.HLSNVSSTGS*IDMVDS*PQLATLADEVSASLAK.Q
Microtubule associated serine/threonine MAST2 kinase 2	S148	-	37.7	44.7	R.NQSLGQS'APSLTAGLK.E
Microtubule associated serine/threonine MAST3 kinase 3	S88S100		11.3	40.8	R.RWSLAS*LPSSGYGTNTPS*STLSSSSSSR.E
Microtubule associated serine/threonine MAST3 kinase 3	S85S106		7.4	39.3	RRWS*LASLPSSGYGTNTPSSTLSSS*SSSR.E
Microtubule associated serine/threonine MAST3 kinase 3	\$85\$100		11.6	58.8	R.RWS*LASLPSSGYGTNTPS*STLSSSSSR.E
Microtubule associated serine/threonine MAST3 kinase 3  Microtubule associated serine/threonine MAST3	S85T98		9.1	36.9	RRWS*LASLPSSGYGTNT*PSSTLSSSSSSRE  K.YYS*S*SEFLAVQPTPTFAERS
Microtubule associated serine/threonine MAST3	\$709\$710 \$85\$105		16.7	72.2 51.8	R.WS*LASLPSSGYGTNTPSSTLSS*SSSSR.E
Microtubule associated serine/threonine MAST3	Y708S709	• •	61.2	20.5	K.VY*S*SSEFLAVQPTPTFAER.S
kinase 3  Microtubule associated serine/threonine MAST3 kinase 3	S85S108		5.2	11.9	RRWS*LASLPSSGYGTNTPSSTLSSSSS*SR.E
Microtubule associated serine/threonine MAST3 kinase 3	S92S106		10.8	26.4	R RWSLASLPSS*GYGTNTPSSTLSSS*SSSR.E
Microtubule associated serine/threonine MAST3 kinase 3	S774	÷	14.0	20.6	R.GPS*PSLLNTISLDTMPK.F
Microtubule associated serine/threonine MAST3 kinase 3	S88Y94		7.6	12.8	R.RWSLAS*LPSSGY*GTNTPSSTLSSSSSSRE
Microtubule associated serine/threonine MAST3 kinase 3	Y708S711	_	12.0	23.5	K.VY*SSS'EFLAVQPTPTFAER.S
Microtubule-associated protein 1A <sub>MAP1A</sub>	S25		100.0	63.3	R.S'PGAPLAQNPAELLCEAGAAVAAAR.W
Microtubule-associated protein 9 <sub>MAP9</sub> Midasin MDN1	\$175 \$4762\$4764		100.0	22.3	MPS'PRPR.G  KMHDGELEEQEEDDEKS'DS'EGGDLDK.H
Midasin MDN1	\$4752\$4754 \$4538		100.0	98.2	KAEENTDQAS*PQEDYAGFER.L
Midasin <sub>MDN1</sub>	T5017	• • •	-0.2	32.8	REDSDT*EEQVPEALER.K
Midasin <sub>MDN1</sub>	S5015	• • •	15.2	71.8	REDS*DTEEQVPEALER K
Minichromosome maintenance protein 10 MCM10	T85		60.8	63.1	K.ENLATLFGDMEDLT*DEEEVPASQSTENR.V
Minor histocompatibility antigen HA1 ARHGAP4	S23		32.1	58.5	RAGS*PSPQPSGELPRK
Minor histocompatibility antigen HA1 ARHGAP4			18.6	66.7	R.KSS'FNVSDVARPEAAGSPPEEGGCTEGTPAK.D
Minor histocompatibility antigen HA1 ARHGAP4			8.2	60.7	R.DQEPDVHYDFEPHVS'ANAWSPVMRA
Minor histocompatibility antigen HA1 ARHGAP4	-		19.8	57.9	R.DQEPDVHYDFEPHVSANAWS'PVMR.A  K.TPS'ISKK.N
Minor histocompatibility antigen HA1 ARHGAP4  Minor histocompatibility antigen HA1 ARHGAP4			7.8	14.1	K.FYSYISKK.N  K.SYWPLSISDSDSGLDPGPGAGDFKK.F
Misshapen-like kinase 1 (zebrafish) MINK1	S701		36.8	78.8	R.SNS'AWQIYLQR.R
Misshapen-like kinase 1 (zebrafish) MINK1	S674	===	8.7	28.8	R.TSS*IATALNTSGAGGSRPAQAVRA
Misshapen-like kinase 1 (zebrafish) <sub>MINK1</sub>	S763	<del>.</del> .	46.1	41.4	R.SDSVLPASHGHLPQAGS*LER.N
Misshapen-like kinase 1 (zebrafish) MINK1	T681		-5.9	12.6	R.TSSIATALNT*SGAGGSRPAQAVR.A
Misshapen-like kinase 1 (zebrafish) <sub>MINK1</sub>	T860		-0.8	44.6	R.SDGDT*DSVSTMVVHDVEEITGTQPPYGGGTMVVQR.T
Mitochondrial fission factor MFF	<b>Y</b> 19		13.9	114.6	R.NDSLY*GISNIDTTIEGTSDDLTVVDAASLR.R
Mitochondrial fission factor MFF	T26	-	8.0	73.4	R.NDSLYGISNIDT*TIEGTSDDLTVVDAASLR.R
Mitochondrial isolaucina tRNA synthetasa is pos	S17		12.1	100.1	R.NDS*LYGISNIDTTIEGTSDDLTVVDAASLR.R
Mitochondrial isoleucine tRNA synthetase IARS2  Mitochondrial ribosomal protein \$16 MRPS16	S186	•	100.0	25.0 65.0	K.TDAEAT*DTEATET-
Mitogen activated protein kinase 8 MAPK8IP3	•		25.6	65.0	K.SNTPTS*SVPSAAVTPLNESLQPLGDYGVGSK.N
interacting protein 3 Mitogen activated protein kinase 8 MAPK8IP3			12.2	58.1	K.SNTPT*SSVPSAAVTPLNESLQPLGDYGVGSK.N
interacting protein 3  Mitogen activated protein kinase 8 MAPK8IP3 interacting protein 3	S365	•	9.1	55.7	R.TGSS'PTQGIVNK.A

Peak Area %CV	White do	ts-Significant cha	nge in pepti	de the			
-5 29 42 42 71	timepoint PSM	with the minimum	peak area f	or a given			
3 86 5 >100			CarT	RajiB			
	Name Gene	Phosphosites	£ £ £	5 2 B	Ascor	MOWSE	Sequence K.S'NTPTSSVPSAAVTPLNESLQPLGDYGVGSK.N
interacting o	rotein 3			_	7.5	66.7	K.S*NTPTSS*VPSAAVTPLNESLQPLGDYGVGSK.N  K.SNTPTSS*VPSAAVTPLNESLQPLGDYGVGSK.N
interacting o	rotein 3			-	10.7	46.0	
associated p	rotein 1				12.3	14.1	R.RTS*FSFQK.E
associated p	rotein 1				3.5	20.4	R.RT*SFSFQK.E
Mitogen-activated protein kinase	rotein 1				8.9	13.4	R.S*LLQSEQQPSWTDDLPLCHLSGVGSASNR.S
kinase 7 interacting p	rotein 1	S7 S238			34.5	39.0	R.LAIQGPEDS*PSR.Q
	MLL <sub>KMT2A</sub>	S1114S1115S11	<del></del>		6.8	43.2	K.ILSSMGNDDKS*S*IAGS*EDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S2869			6.5	83.0	K.NTPSMQALGESPES*SSSELLNLGEGLGLDSNR.E
	MLL <sub>KMT2A</sub>	S1114S1119			9.4	33.7	K.ILSSMGNDDKS*SIAGS*EDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S2866			6.4	49.6	K.NTPSMQALGES*PESSSSELLNLGEGLGLDSNR.E
	MLL <sub>KMT2A</sub>	S2872			8.0	53.4	K.NTPSMQALGESPESSSS*ELLNLGEGLGLDSNR.E
	MLL <sub>KMT2A</sub>	S1107S1119			1.1	23.7	K.ILSS*MGNDDKSSIAGS*EDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S2870			5.3	72.3	K.NTPSMQALGESPESS*SSELLNLGEGLGLDSNR.E
	MLL <sub>KMT2A</sub>	\$3036			25.4	30.2	R.NSSTPGLQVPVS*PTVPIQNQK.Y
	MLL <sub>KMT2A</sub>	S2866S2871			10.4	34.2	K.NTPSMQALGES*PESSS*SELLNLGEGLGLDSNR.E
	MLL <sub>KMT2A</sub>	S1115S1119		•	8.4	27.8	K.ILSSMGNDDKSS*IAGS*EDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S1107S1114S11			6.7	25.5	K.ILSS*MGNDDKS*S*IAGSEDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S153			43.3	53.2	R.AVFGESGGGGSGEDEQFLGFGS*DEEVR.V
	MLL <sub>KMT2A</sub>	S1106S1107S11		·		27.3	K.ILS*S*MGNDDKS*SIAGSEDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S1114S1115			1.9	20.0	K.ILSSMGNDDKS*S*IAGSEDAEPLAPPIKPIKPVTR.N
	MLL <sub>KMT2A</sub>	S1107S1114S11			9.2	15.2	K.ILSS*MGNDDKS*SIAGS*EDAEPLAPPIKPIKPVTR.N
	MLL2 <sub>KMT2D</sub>	<b>S</b> 4738			100.0	42.7	R.ALS'PVIPLIPR.A
-	MLL3 <sub>KMT2C</sub>	S2937S2946			15.0	30.3	K.SDNSDIRPSGS*PPPPTLPAS*PSNHVSSLPPFIAPPGR.V
	MLL3 <sub>KMT2C</sub>	S2927S2930				28.6	K.S'DNS'DIRPSGSPPPPTLPASPSNHVSSLPPFIAPPGR.V
	MLLT2 <sub>AFF1</sub>	\$203\$206\$212	•		20.0	28.7	R.ELSPLIS*LPS*PVPPLS*PIHSNQQTLPR.T
	MLLT2 <sub>AFF1</sub>	\$199\$206\$212			21.3	12.4	R.ELS*PLISLPS*PVPPLS*PIHSNQQTLPR.T
	MLLT2 <sub>AFF1</sub>	S206S212			27.6	16.0	R.ELSPLISLPS*PVPPLS*PIHSNQQTLPR.T
	IMRP19 APIP	<b>S</b> 87	•	•	13.9	34.7	K.DISGPS*PSKK.L
	IMRP19 APIP	<b>S</b> 89			13.9	20.4	K.DISGPSPS*KK.L
	MPP10 MPHOSPI	H S120S139			100.0	128.0	R.EEDGS*EIEADDKEDLEDLEEEEVS*DMGNDDPEMGER.A
	MPP10 MPHOSPI	H S163S167S171			78.7	94.3	K.S*PVFS*DEDS*DLDFDISK.L
	MPP10 MPHOSPI	H S242			92.1	122.5	R.KDDNDEEEEDIDFFEDIDS*DEDEGGLFGSK.K
	MPP10 MPHOSPI	H S163S171			24.0	45.9	K.S*PVFSDEDS*DLDFDISK.L
	MPP10 MPHOSPI	1 S167S171			39.5	55.5	K.SPVFS*DEDS*DLDFDISK.L
	MSH6 MSH6	S219S227			100.0	95.1	K.S'EEDNEIES'EEEVQPK.T
	MSH6 MSH6	\$252\$254\$256			41.0	50.2	R.VIS*DS*ES*DIGGS*DVEFKPDTK.E
	MSH6 <sub>MSH6</sub>	S137		•	17.8	47.9	R.VHVQFFDDS*PTR.G
mSin3A-associated pro		T853S855			12.8	56.7	R.KQQHVISTEEGDMMET*NS*TDDEKSTAK.S
mSin3A-associated pro		S855T856			19.7	52.6	R.KQQHVISTEEGDMMETNS*T*DDEK.S
	MST4 <sub>STK26</sub>	\$300\$304\$306	•••		45.4	48.6	R.WKAEGHS*DDES*DS*EGS*DSESTSR.E
	MST4 <sub>STK26</sub>	T178			32.5	67.4	R.NT*FVGTPFWMAPEVIQQSAYDSK.A
	MST4 <sub>STK26</sub>	T182	<u>.</u>		-0.2	17.8	R.NTFVGT*PFWMAPEVIQQSAYDSK.A
	mTOR <sub>MTOR</sub>	S1261			12.1	24.3	K.LHVS*TINLQK.A
Muccopidermoid carcinoma transle		Y60		<u> </u>	1.9	54.9	R.GQY*YGGSLPNVNQIGSGTMDLPFQTPFQSSGLDTSR.T
Muccopidermoid carcinoma transle		S73		-	-0.2	44.3	R.GQYYGGSLPNVNQIGS*GTMDLPFQTPFQSSGLDTSR.T
Muccepidermoid carcinoma transle		T75			-0.1	51.8	R.GQYYGGSLPNVNQIGSGT*MDLPFQTPFQSSGLDTSR.T
Mucoepidermoid carcinoma translo  Mucoepidermoid carcinoma translo		S64			1.7	55.2	R.GQYYGGS*LPNVNQIGSGTMDLPFQTPFQSSGLDTSR.T
	merin 2 <sub>MMRN2</sub>	Y61		<u> </u>	8.2	38.0	R.GQYY*GGSLPNVNQIGSGTMDLPFQTPFQSSGLDTSR.T  R.AAT*S*RLR.S
	MMKN2	T561S562			100.0	12.9 53.7	NAME OF TAXABLE
ascie-derived pr	otein 77 TVI ND	ecco.			6.2		R DS ESPI PPI TPOAEAEGGSDAEDDSV A
Muscle-derived or	otein 77 TXLNB	S552		-	2.1		R DS*ESPLPPLTPQAEAEGGSDAEPPSK.A  R DSES*PLPPLTPQAEAEGGSDAEPPSK.A
Muscle-derived pr	otein 77 TXLNB	S554			3.1	39.7	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A
MYC binding p	rotein 2 MYCBP2	\$554 \$2749			20.2	39.7 66.3	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A
MYC binding p	rotein 2 <sub>MYCBP2</sub>	\$554 \$2749 \$2749\$2751			20.2 44.0	39.7 66.3 46.8	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A
MYC binding p MYC binding p	rotein 2 MYCBP2 rotein 2 MYCBP2 rotein 2 MYCBP2 rotein 2 MYCBP2	\$2749 \$2749\$2751 \$2833			20.2 44.0 39.9	39.7 66.3 46.8 65.7	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A  R.S*LS*PNHNTLQTLK.S  R.S*LS*PNHNTLQTLK.S
MYC binding p MYC binding p MYC binding p	rotein 2 <sub>MYCBP2</sub> rotein 2 <sub>MYCBP2</sub> rotein 2 <sub>MYCBP2</sub> rotein 2 <sub>MYCBP2</sub>	\$2749 \$2749\$2751 \$2833 \$3467			20.2 44.0 39.9 67.4	39.7 66.3 46.8 65.7 80.3	R DSES*PLPPLTPQAEAEGGSDAEPPSKA R.S*LSPNHNTLQTLK.S R.S*LS*PNHNTLQTLK.S R.S*LS*PNHNTLQTLK.S
MYC binding p	rotein 2 <sub>MYCBP2</sub>	\$2749 \$2749\$2751 \$2833 \$3467			20.2 44.0 39.9 67.4 71.7	39.7 66.3 46.8 65.7 80.3	R DSES*PLPPLTPQAEAEGGSDAEPPSKA  R.S*LSPNHNTLOTLK.S  R.S*LS*PNHNTLOTLK.S  R.SKS*DSYTLDPDTLRK  R.VNS*GDTEVGSSLLR.H
MYC binding p	rotein 2MYCBP2	\$2749 \$2749\$2751 \$2833 \$3467 T2645			20.2 44.0 39.9 67.4 71.7	39.7 66.3 46.8 65.7 80.3 95.6	R.DSES*PLPPLTPQAEAEGGSDAEPPSKA R.S*LS*PNHNTLQTLK.S R.S*LS*PNHNTLQTLK.S R.SKS*DSYTLDPDTLR.K R.VNS*GDTEVGSSLLR.H R.HEDEQALLDQNSQT*PPPSPFSVQAFNK.G
MYC binding p	rotein 2 <sub>MYCBP2</sub>	\$2749 \$2749\$2751 \$2833 \$3467 \$72645 \$2882			20.2 44.0 39.9 67.4 71.7 22.2 68.5	39.7 66.3 46.8 65.7 80.3 95.6 93.8	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A R.S*LS*PNHNTLOTLK.S R.S*LS*PNHNTLOTLK.S R.SKS*DSYTLDPDTLR.K R.VNS*GDTEVGSSLLR.H R.HEDEGALLDONSQT*PPPS*PSVQAFNK.G R.HEDEGALLDQNSQT*PPPS*PFSVQAFNK.G R.APS*PHVVQENLHSEVVEVCTSSTLK.T
MYC binding p	rotein 2 <sub>MYCBP2</sub>	\$2749 \$2749\$2751 \$2833 \$3467 \$72645 \$2882 \$2882			20.2 44.0 39.9 67.4 71.7 22.2 68.5	39.7 66.3 46.8 65.7 80.3 95.6 93.8 33.8	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A  R.S*LS*PNHNTLQTLK.S  R.S*LS*PNHNTLQTLK.S  R.SKS*DSYTLDPDTLR.K  R.VNS*GDTEVGSSLLR.H  R.HEDEGALLDONSQT*PPPS*PFSVQAFNK.G  R.HEDEGALLDONSQT*PPPS*PFSVQAFNK.G  R.APS*PHVVQENLHSEVVEVCTSSTLK.T
MYC binding p	ortein 77 TXLNB rotein 2 MYCBP2	\$2749 \$2749\$2751 \$2833 \$3467 \$2845 \$2845 \$2882 \$2882			20.2 44.0 39.9 67.4 71.7 22.2 68.5 10.5	39.7 66.3 46.8 65.7 80.3 95.6 93.8 33.8 40.9	R DSES*PLPPLTPQAEAEGGSDAEPPSKA  R.S*LS*PNHNTLQTLK.S  R.S*LS*PNHNTLQTLK.S  R.SKS*DSYTLDPDTLR.K  R.VNS*GDTEVGSSLLR.H  R.HEDEQALLDQNSQT*PPPS*PSVQAFNK.G  R.HEDEQALLDQNSQT*PPPS*PSVQAFNK.G  R.APS*PHVVQENLHSEVVEVCTSSTLK.T  R.S*KSDSYTLDPDTLR.K  R.AES*PGPGSRL
MYC binding p	rotein 2 <sub>MYCBP2</sub>	\$2749 \$2749\$2751 \$2833 \$3467 \$72645 \$2882 \$2882			20.2 44.0 39.9 67.4 71.7 22.2 68.5	39.7 66.3 46.8 65.7 80.3 95.6 93.8 33.8	R.DSES*PLPPLTPQAEAEGGSDAEPPSK.A  R.S*LS*PNHNTLOTLK.S  R.S*LS*PNHNTLOTLK.S  R.SKS*DSYTLDPDTLR.K  R.VNS*GDTEVGSSLLR.H  R.HEDEGALLDONSQT*PPPS*PSVQAFNK.G  R.HEDEGALLDONSQT*PPPS*PSVQAFNK.G  R.APS*PHVVQENLHSEWEVCTSSTLK.T

<-10 0		compared to	the			
.5 42 F	imepoint with the minimum PSM	CarT	RajiB			
5 >100 >10 Protein Name(			E E E	Ascor	MOWSE	Sequence
Myc Promoter binding protein				10.9	84.2	R.SIS'TSGPLDKEDTGR.Q
Myc Promoter binding protein D			<u> </u>	20.8	38.5	K.SSPST*ENMHFPSSISSQTR.Q
Myc Promoter binding protein D				22.4	59.9	K.VDSPVIFDLEDLDS*ETDVSK.A  K.SSPS*TENMHFPSSISSQTR.Q
Myc Promoter binding protein D				13.3	52.2 27.8	R.RDLAEEIVMYMNNMSSPLT*S*R.T
	ENND4A \$1216T1220			12.3	15.4	R.DLAEEIVMYMNNMS*SPLT*SR.T
Myc Promoter binding protein D				21.7	66.2	R.RDLAEEIVMYMNNMS*SPLTSR.T
Myc Promoter binding protein D	ENND4A S1216S1221			13.6	32.2	R.RDLAEEIVMYMNNMS*SPLTS*R.T
Myc Promoter binding protein D	ENND4A \$1217\$1221			8.5	17.3	R.DLAEEIVMYMNNMSS*PLTS*R.T
Myc Promoter binding protein D	ENND4A S1099			4.3	52.2	K.ESS*DDDTPFDGSNYLADKVDSPVIFDLEDLDSETDVSK.A
Myc Promoter binding protein D	ENND4A S1015	-		22.0	63.6	R.HKS*DNETNLQQQVVWGNR.N
Myc Promoter binding protein D				12.3	56.5	R.DLAEEIVMYMNNMSS*PLTSR.T
Myc Promoter binding protein			•		28.2	R.DS*LEKES*S*DDDTPFDGSNYLADKVDSPVIFDLEDLDSETDVSK.
Myc Promoter binding protein		ı	-	-1.4	19.2	R.DSLEKESSDDDTPFDGS*NY*LADKVDS*PVIFDLEDLDSETDVSK.
Myc Promoter binding protein D			•	-0.3	31.7	K.SS*PSTENMHFPSSISSQTR.Q  R.HKSDNET*NLQQQVVWGNR.N
Myc proto-oncogene protein M				1.2	20.6	M.PLNVS*FTNR.N
Myelin basic protein M		==		9.6	40.3 82.5	R.TTS*EDNEVFGEADANQNNGTSSQDTAVTDSKR.T
Myelin basic protein M		=		8.3	107.1	K.DRPS*ESDELQTIQEDSAATSESLDVMASQK.R
				100.0	17.2	R.NLGELS*R.T
Myelin expression factor 2 M				15.5	29.8	K.AEVPGATGGDS*PHLQPAEPPGEPR.R
Myelin expression factor 2 <sub>M</sub>	YEF2 T13			9.2	11.3	K.AEVPGAT*GGDSPHLQPAEPPGEPR.R
Myeloid/lymphoid or mixed-lineage M	ILLT1 \$359\$361\$366		•	100.0	30.3	K.ALEVEES*NS*EDEAS*FK.S
Myeloid/lymphoid or mixed-lineage M	ILLT1 S475			46.9	34.4	R.S*PESCSKPEK.I
Myocardin related protein M	IKL1 \$446\$454			9.0	13.4	K.FGS*TGSTPPVS*PTPSER.S
Myocardin related protein M	IKL1 T447S449		•	8.5	20.4	K.FGST*GS*TPPVSPTPSER.S
Myocardin related protein M			-		14.5	K.
Myocardin related transcription factor B M		<b>#</b>		6.7	18.0	K.VSESPS*PVTTNTPAQFASVSPTVPEFLK.T
Myocardin related transcription factor B M		=		5.1	14.1	K.VSESPS*PVTTNTPAQFASVS*PTVPEFLK.T
Myocardin related transcription factor B M  Myocyte specific enhancer factor 2A M		-		7.0	22.7	K.VSESPSPVTTNT*PAQFAS*VSPTVPEFLK.T  R.ES*PSVKR.M
Myocyte specific enhancer factor 2C M				16.1	35.7	K.S'PPPMNLGMNNR.K
Myocyte specific enhancer factor 2C <sub>M</sub>	0240		• • •	90.1	72.1	R.NS*PGLLVSPGNLNK.N
Myosin 5A M	YO5A S1115S1119		•••	7.1	71.8	R.TDS*THSS*NESEYIFSSEIAEMEDIPSR.T
Myosin 5A M	YO5A \$1115T1116		•	8.2	95.2	R.TDS*T*HSSNESEYIFSSEIAEMEDIPSR.T
Myosin 5A M	YO5A S1652	•	• • •	11.9	85.6	R.TSS*IADEGTYTLDSILR.Q
Myosin 5A M	YO5A \$1115\$1118			5.7	74.3	K.RTDS*THS*SNESEYIFSSEIAEMEDIPSR.T
Myosin 5A M	YO5A T1116S1119			11.0	39.1	R.TDST*HSS*NESEYIFSSEIAEMEDIPSR.T
Myosin heavy chain 9, nonmuscle M	YH9 S1943			100.0	72.7	R.KGAGDGS*DEEVDGKADGAEAKPAE
Myosin heavy chain, nonmuscle type B M		i i		20.9	25.2	R.RQLHLEGASLELSDDDT*ESK.T
Myosin heavy chain, nonmuscle type B M		•		33.6	72.8	R.RQLHLEGAS*LELS*DDDTESK.T
Myosin heavy chain, nonmuscle type B M				29.7	97.6	R.QLHLEGASLELS*DDDTESK.T
Myosin IF <sub>M</sub> Myosin IG <sub>M</sub>			-	8.9	12.9	R.RSS*QAPTR.A  K.NS*MVALVENLASK.E
Myosin IG M				85.6 32.1	36.0 62.6	R.GS*FTLLWPSR-
Myosin phosphatase target subunit 1 p				12.1	52.0	R.LAS*TSDIEEK.E
Myosin phosphatase target subunit 1 p				0.1	58.7	R.STGVSFWTQDS*DENEQEQQSDTEEGSNKK.E
Myosin phosphatase target subunit 1 p	PP1R12A S871	•••		19.2	71.9	R.STGVSFWTQDSDENEQEQQS*DTEEGSNKK.E
Myosin phosphatase target subunit 1 p	PP1R12A T859	<b>—</b>	•••	5.9	15.1	R.STGVSFWT*QDSDENEQEQQSDTEEGSNKK.E
Myosin phosphatase target subunit 1 <sub>P</sub>	PP1R12A S445			23.9	93.7	K.TGS*YGALAEITASK.E
Myosin phosphatase target subunit 1 p	PP1R12A Y446	-		6.8	50.5	R.KTGSY*GALAEITASK.E
Myosin phosphatase target subunit 1 p		-		4.0	42.6	R.STGVSFWTQDS*DENEQEQQS*DTEEGSNKK.E
Myosin phosphatase target subunit 1 p			Ţ	6.0	23.6	R.KT*GSYGALAEITASK.E
	YL12A \$20		••••	16.9	127.5	R.ATS*NVFAM#FDQSQIQEFK.E
Myosin regulatory light chain MRLC2 $_{ m M}$				58.1	86.9	R.AT*S*NVFAMFDQSQIQEFK.E  R.AT*SNVFAMFDQSQIQEFK.E
Myosin regulatory light chain MRLC2 <sub>M</sub> Myosin XVIIIA <sub>M</sub>				15.7	100.4	R.AT*SNVFAMFDQSQIQEFK.E  R.YSHSYLS*DS*DTEAK.L
Myosin XVIIIA		• • • •		32.2	56.2	R.RVS*SSSELDLPSGDHCEAGLLQLDVPLLR.T
Myosin XVIIIA <sub>M</sub>				100.0	30.0	R.IGDLQAAIEDEMES'DENEDLINS'EGDS'DVDS'ELEDRVDGVK.S
Myosin XVIIIA M				10.0	21.7	R.YSHSY'LS'DSDTEAK.L
Myosin XVIIIA M				5.8	49.3	R.YSHSY*LSDS*DTEAK.L
Myosin XVIIIA M	YO18A \$1942			79.0	105.1	R.IGDLQAAIEDEMES*DENEDLINSLQDMVTK.Y
			•			

Peak Area	o abundano		ompared to	the			
-5 -3 0	timepoint of PSM	with the minimum	peak area f	or a given			
3 5 >10	>100		CarT	RajiB			
_	Protein Name Gene Myosin XVIIIA MYO18A	Phosphosites \$1069	9 # # 5 # #	5 2 8	Ascor 35.1	MOWSE 43.0	Sequence R.RVSSS*SELDLPSGDHCEAGLLQLDVPLLR.T
		S1068	=		6.5	18.5	R.RVSS*SSELDLPSGDHCEAGLLQLDVPLLR.T
	Myosin XVIIIA MYO18A	S2007	i		27.6	44.3	K.SSS*PTSYWK.S
	Myosin XVIIIA <sub>MYO18A</sub>	S140			24.1	15.2	K.RFS*FSQR.S
	Myosin XVIIIA MYO18A	Y2039S2041S2	Ļ	•••	-0.2	31.0	R.YSHSY"LS"DS"DTEAK.L
	Myosin XVIIIA MYO18A	S2041S2043T2	Ė		9.0	21.7	R.YSHSYLS*DS*DT*EAK.L
	Myosin XVIIIA MYO18A	S2038S2043			8.3	14.1	R.YSHS*YLSDS*DTEAK.L
	Myosin XVIIIB <sub>MYO18B</sub>	T2549		₽.	100.0	19.6	R.REPGT*GR.K
	Myotubularin MTM1	S588S591			2.7	11.8	K.LSDPPTS'PSS'PSQMMPHVQTHF
	Myotubularin MTM1	\$590\$591	<b>L</b>		6.5	23.8	K.LSDPPTSPS'S'PSQMMPHVQTHF
	Myotubularin MTM1	T587S591	٠.		8.0	19.9	K.LSDPPT*SPSS*PSQMMPHVQTHF
	Myotubularin MTM1	S591S593	<u> </u>		4.6	30.6	K.LSDPPTSPSS*PS*QMMPHVQTHF
	related protein 1 <sub>MTMR1</sub>	S652	<u> </u>		13.8	14.8	R.GS*SPSHSATSVHTSV
	related protein 3 <sub>MTMR3</sub>	S647			43.2	107.0	R.S*LELSSLAGPGEDPLSADSLGKPTR.V  K.NT*ADHDES*PPRTPTGNAPSSESDIDISSPNVSHDESIAK.D
	cetyltransferase 2 KAT7	T118S124				30.9	R.S*S*GS*ETEQVVDFSDR.E
	cetyltransferase 2 KAT7	\$99\$100\$102 \$124T128	=		13.6	93.1	K.NTADHDES*PPRT*PTGNAPSSESDIDISSPNVSHDESIAK.D
	cetyltransferase 2 KAT7	S56			9.8	51.7	R.LSQSSQDS*SPVR.N
	cetyltransferase 2 KAT7	\$100\$102T104			9.8	14.3	R.SS*GS*ET*EQVVDFSDR.E
MYST histone ac	cetyltransferase 2 KAT7	<b>S</b> 57			7.6	58.2	R.LSQSSQDSS*PVR.N
N-acetylglu	cosamine kinase NAGK	S76			10.9	82.5	R.SLGLSLS*GGDQEDAGR.I
N-myrist	toyl transferase 1 <sub>NMT1</sub>	<b>S</b> 47	•	•	59.6	82.9	R.GGLS*PANDTGAK.K
NACHT and WD repeat do	omain-containing NWD2	T695S698			100.0	11.7	K.ENT*RPS*NPLR.V
	NACSIN EHBP1	S335			21.0	14.6	K.EVQTPQYLNPFDEPEAFVTIKDS*PPQSTK.R
	NACSIN EHBP1	T165S171			20.2	20.9	K.AT*DEDMQS*LASLMSMK.Q
	NACSIN EHBP1	S171S174			8.5	16.4	K.ATDEDMQS*LAS*LMSMK.Q
	NACSIN EHBP1	T165S174			8.4	41.7	K.AT*DEDMQSLAS*LMSMK.Q
1	NAD synthetase 1 NADSYN1	S280Y281	<del>ب</del>		18.1	12.3	R.S"Y"RAEISSR.N
	flavoprotein 3	\$159\$160\$164			6.3	111.8	R.KVTSPSSSSSSSS'S'DSES'DDEADVSEVTPR.V
	e oxidoreductase NDUFV3 flavoprotein 3	S162			6.0	58.1	R.KVTSPSSSSSSSSSDS*ESDDEADVSEVTPR.V
	e oxidoreductase NDUFV3 flavoprotein 3	S159S162S164			10.6	116.7	R.KVTSPSSSSSSS*SDS*ES*DDEADVSEVTPR.V
	flavoprotein 3	\$158\$159\$160			7.6	74.7	K.VTSPSSSSSSS*S*S*DSESDDEADVSEVTPR.V
	flavoprotein 3	\$160\$162			1.3	66.0	R.KVTSPSSSSSSSSSSSS*DS*ESDDEADVSEVTPR.V
	flavoprotein 3	\$160\$162\$164			11.2	102.1	R.KVTSPSSSSSSSSS*DS*ES*DDEADVSEVTPR.V  R.KVTSPSSSSSSSS*S*S*DSESDDEADVSEVTPR.V
	flavoprotein 3	\$159\$160 \$159\$160\$162			16.2	69.4	R.KVTSPSSSSSSS'S'DS'ESDDEADVSEVTPR.V
	flavoprotein 3 e oxidoreductase NDUFV3	\$158\$159\$162			5.4	62.5	K.VTSPSSSSSS*S*S*SDS*ESDDEADVSEVTPR.V
	flavoprotein 3	\$473			13.9	91.2	R.AGEEDEGEEDS*DSDYEISAK.A
	NAG NBAS	\$473\$475			28.8	29.7	R.AGEEDEGEEDS*DS*DYEISAK.A
	NaGLT1 <sub>MFSD4B</sub>	S474			10.2	22.7	R.SS*LTEPTAEVYNQYPSNALVFESSPFNTGSAHVK.H
	NaGLT1 <sub>MFSD4B</sub>	T476			-0.8	26.2	R.SSLT*EPTAEVYNQYPSNALVFESSPFNTGSAHVK.H
	Nardilysin NRDC	S94	•	•	17.8	40.8	R.RGS*LSNAGDPEIVK.S
Nascent polypeptide ass	ociated complex, NACA	S166	<del>-</del>		11.5	129.6	K.VQGEAVSNIQENTQTPTVQEES*EEEEVDETGVEVK.D
Nascent polypeptide ass		T161			44.9	83.9	K.VQGEAVSNIQENTQTPT*VQEESEEEEVDETGVEVK.D
Nascent polypeptide ass		T159			5.1	44.0	K.VQGEAVSNIQENTQT*PTVQEESEEEEVDETGVEVK.D
Nascent polypeptide ass	ociated complex, NACA	S151				76.4	K.VQGEAVS*NIQENTQTPTVQEESEEEEVDETGVEVK.D
Nascent polypeptide ass	ociated complex, NACA alpha polypeptide	T157S166		-	13.3	74.5	K.VQGEAVSNIQENT*QTPTVQEES*EEEEVDETGVEVK.D
	NATH <sub>NAA15</sub>	\$855	÷.		22.0	11.3	K.ITVNGDS*SAEAEELANEI
	NATH NAA15	S855S856			45.1	26.3	K.ITVNGDS*S*AEAEELANEI
	TRA2B	S225Y226			17.5	17.8	R.SRS'Y"SPR.R
Natural killer tumor reco		S699S701			17.4	23.1	R.S*RS*YSR.D
Natural killer tumor reco		S613			9.1	44.0	R.ATMAQNENVVVQPVVAENIPVIPLSDS*PPPSR.W
Natural killer tumor reco		\$701Y702			9.6	13.5	R.SRS*Y*SR.D
Natural killer tumor reco	NCK1 NCK1	S611			15.6	21.8	R.ATMAQNENVVVQPVVAENIPVIPLS*DSPPPSR.W  R.LY*DLNMPAYVK.F
NDRG	family member 2 NDRG2	Y105			190.9	66.4	R.LY*DENMPAYVK.F
	family member 2 NDRG2	\$332 \$331			12.3	73.1	R.THS*TSSSLGSGESPFSR.S
	family member 3 NDRG3	T332			-0.3	73.1	R.THST*SSSLGSGESPFSR.S
	family member 3 NDRG3	S335		. –	18.0	44.0	R.THSTSSS*LGSGESPFSR.S
	family member 3 NDRG3	T329S333			2.6	66.1	R.SRT"HSTS"SSLGSGESPFSR.S
	family member 3 NDRG3	T329T332		• • •	16.7	86.8	R.SRT"HST"SSSLGSGESPFSR.S
	NDRG3	S331T332		• • •	3.3	54.6	R.SRTHS*T*SSSLGSGESPFSR.S

Peak Area %CV	abundand		compared to	the			
.5 29 42 42 0 71	timepoint PSM	with the minimum	peak area f	or a given			
3 5 >100 >10			CarT	RajiB E E E			_
Protein Name NDRG family member		Phosphosites T329S331	5 H B	5 4 8	Ascor 16.9	MOWSE 66.8	Sequence R.SRT"HS"TSSSLGSGESPFSR.S
	NDRG3	S331S334		-	19.5	60.5	R.THS*TSS*SLGSGESPFSR.S
NDRG family member		T332S333		-	1.8	40.4	R.THST*S*SSLGSGESPFSR.S
NECAP endocytosis associated		T182			25.4	39.5	R.VRPAST*GGLSLLPPPPGGK.T  K.AGIPQHHPPMAQNLQYPDDS*DDEKK.A
	1 NECTIN1	\$422 \$508\$511		•	31.5 5.2	48.7	R.TLGYQYDPEQLDLAENMVSQNDGS*FIS*KK.E
	NECTIN1				14.6	40.2	R.TLGYQYDPEQLDLAENMVSQNDGS*FISKK.E
Nectin	1 NECTIN1	S503S511			10.4	57.3	R.TLGYQYDPEQLDLAENMVS*QNDGSFIS*KK.E
	NECTIN1	S434S435		• • •	17.2	74.8	K.AGPLGGS'S'YEEEEEEEGGGGGERK.V
Nectin	1 NECTIN1	<b>S</b> 435		·	8.2	16.1	K.AGPLGGSS*YEEEEEEEGGGGGER.K
		S434Y436			15.6	35.6	K.AGPLGGS*SY*EEEEEEEGGGGGER.K
		\$435Y436 \$503\$508			10.4	80.2	K.AGPLGGSS*Y*EEEEEEEGGGGGER.K  R.TLGYQYDPEQLDLAENMVS*QNDGS*FISK.K
	4 NEDD4	\$503\$508 \$675		•	18.6	47.6	R.RGS*LQAYTFEEQPTLPVLLPTSSGLPPGWEEK.Q
NEDD	4 NEDD4	Y679	▔			45.5	R.RGSLQAY*TFEEQPTLPVLLPTSSGLPPGWEEK.Q
Negative elongation factor protein	B <sub>NELFB</sub>	<b>S</b> 557			46.6	46.9	R.KPS*PAQAAETPALELPLPSVPAPAPL
NELF	ENELFE	S115			26.9	75.8	R.SIS*ADDDLQESSR.R
NELF	ENELFE	S113		•	10.5	62.4	R.S*ISADDDLQESSR.R
	ENELFE	S353			44.2	60.8	K.SVWGSLAVQNS*PK.G
Nesprin		S4108			85.4	28.6	R.RGS*MSYLAAVEEEVEESSVK.S
Nesprin Nesprin		T6422S6428 S4110			9.6 5.8	18.2 48.2	R. eccetavevinoidi evinutranvicas soueeneeabvvoni sav s
Nesprin		Y4111			-0.2	31.6	R.RGSMSY*LAAVEEEVEESSVK.S
Neurobeachin-like	2 NBEAL2	<b>S</b> 770			4.3	94.3	R.SQSVPASTGLGWGS*GLVAPLQEGSIDSTLAGTQDTR.W
Neurobeachin-like	2 NBEAL2	<b>S</b> 763			12.0	118.6	R.SQSVPAS*TGLGWGSGLVAPLQEGSIDSTLAGTQDTR.W
Neurobeachin-like	2 NBEAL2	T764			8.2	124.8	R.SQSVPAST*GLGWGSGLVAPLQEGSIDSTLAGTQDTR.W
Neurobeachin-like		S1364S1367			1.5	85.8	R.SS*VGS*GNTAGGGGSSGTLTPASQPGTPSPLDGPRPFPAAPGR.
Neurobeachin-like		S1363S1364				12.7	R.S*S*VGSGNTAGGGGSSGTLTPASQPGTPSPLDGPRPFPAAPGR.
Neurobeachin-like Neurobeachin-like		\$1367T1370			2.3	24.5	R.SSVGS*GNT*AGGGGSSGTLTPASQPGTPSPLDGPRPFPAAPGR.  R.SQS*VPASTGLGWGSGLVAPLQEGSIDSTLAGTQDTR.W
Neurobeachin-like		\$759 \$757			3.2	74.9	R.S*QSVPASTGLGWGSGLVAPLQEGSIDSTLAGTQDTR.W
Neurofibromatosis type	I <sub>NF1</sub>	S2515			9.5	21.1	K.GSEGYLAATYPTVGQTS*PR.A
Neurofibromatosis type	I <sub>NF1</sub>	S1140	Ė		100.0	23.8	R.RLAS*LR.H
Neurofibromatosis type	I <sub>NF1</sub>	T2514	<u> </u>		6.0	12.1	K.GSEGYLAATYPTVGQT*SPR.A
Neurofibromin		S518			100.0	29.7	K.RLS*MEIEK.E
Neutrophil cytosolic factor  NF kappaB activating protei		T233	<u> </u>		100.0	18.3	K.T*PEIFR.A  R.IGELGAPEVWGLS*PK.N
NF kappaB activating protein		S149 S15			100.0	71.9	R.SPDREAS*GSGGR.R
	1 <sub>NFATC2</sub>	T216S221			20.6	18.9	R.T'SPIMS'PR.T
NFAT	1NFATC2	S268			142.1	38.9	R.HSCAEALVALPPGAS*PQR.S
NFAT	1 <sub>NFATC2</sub>	S755S757		•••	4.0	79.5	R.S*KS*LSPSLLGYQQPALMAAPLSLADAHR.S
	1NFATC2	S56			7.8	30.6	K.VASPPS*GPAYPDDVLDYGLKPYSPLASLSGEPPGR.F
	1NFATC2	S757S759			14.0	72.4	K.S"LS"PSLLGYQQPALMAAPLSLADAHR.S
	1NFATC2	S326		• • • •	-0.3	52.3	K.TS*PDPSPVSAAPSK.A  R.LSPGS*YPTVIQQONATSQR.A
	1NFATC2	S859 T803Y813			7.8	101.4	R.SVLVHAGSQGQSSALLHPSPT*NQQASPVIHY*SPTNQQLR.C
	1NFATC2	S808Y813			6.7	22.3	R.SVLVHAGSQGQSSALLHPSPTNQQAS*PVIHY*SPTNQQLR.C
NFAT	1 <sub>NFATC2</sub>	<b>S</b> 53		•	14.6	32.1	K.VAS*PPSGPAYPDDVLDYGLKPYSPLASLSGEPPGR.F
NFAT	1NFATC2	S272S274S276				34.3	R.  C'DC'DC'DCDCCUL/ADADAGCACACACACACACACACACACACACACACACACA
	1 <sub>NFATC2</sub>	Y294S300S309			5.0	13.9	R. edependential deliaced a chieffica challiment at per
	1NFATC2	S272S274S276				34.9	R.  CHDCHDCHDODCHCHAADODLICCDACVDDL/ACCAVINDALNCLATDCD
	1NFATC2	\$272\$290Y294 \$56Y72			5.3	34.8	R.  C*DEDEDIGECUL/ADODUGE*BAGY*BDI/AGC*AV/IMDALMSLATINED  K.VASPPS*GPAYPDDVLDYGLKPY*SPLASLSGEPPGR.F
	1 <sub>NFATC2</sub>	\$56Y/2 \$856			7.5	20.6 88.1	R.LS*PGSYPTVIQQQNATSQRA
	1 <sub>NFATC2</sub>	S274S276Y294			1.0	11.4	R. CODE DODGE LIVADODILOS DAGYODIVAGE ANJIMDAI NEI ATDEDOGI
NFAT	1NFATC2	S274S276S280				15.6	R.  CHOCHDODGESULVADODUGSDAGVEDVAGSAVIMDALNISI ATRODOGI
NFAT	1NFATC2	S53S73	•		30.5	17.2	K.VAS*PPSGPAYPDDVLDYGLKPYS*PLASLSGEPPGR.F
	1NFATC2	S53Y72			10.7	17.2	K.VAS*PPSGPAYPDDVLDYGLKPY*SPLASLSGEPPGR.F
	1NFATC2	S236S243			15.1	24.1	R.TSLAEDSCLGRHS'PVPRPAS'R.S
	1NFATC2	S255S268		•••	100.0	31.0	K.RRHS*CAEALVALPPGAS*PQR.S
	1NFATC2	\$759\$761 \$217\$221			14.3	91.1	R.SKSLS*PS*LLGYQQPALMAAPLSLADAHR.S  R.TS*PIMS*PR.T
	02	JE UEE !			14.3	1711	

Peak Area	o abundano		compared to	the			
-5	timepoint PSM	with the minimum					
3 5 >10	86 >100			RajiB E E E			
	Protein Name Gene NFAT1 NFATC2	Phosphosites S757S761	5 2 9	9 H H	Ascor 6.6	MOWSE 75.3	Sequence R.SKS'LSPS'LLGYQQPALMAAPLSLADAHR.S
	NFAT1 <sub>NFATC2</sub>	T862			20.5	76.0	R.LSPGSYPT*VIQQQNATSQRA
	NFAT1 <sub>NFATC2</sub>	S759Y765		. •	1.6	57.3	K.SLS*PSLLGY*QQPALMAAPLSLADAHR.S
	NFAT1 <sub>NFATC2</sub>	S761Y765		. •	0.0	31.7	K.SLSPS*LLGY*QQPALMAAPLSLADAHR.S
	NFAT1 <sub>NFATC2</sub>	\$230\$243		•	6.5	27.7	R.TSLAEDS*CLGRHSPVPRPAS*R.S
	NFAT1 <sub>NFATC2</sub>	\$274\$280\$309 \$221T226			6.6	43.1	R. coc-bedodescul/adodulgedacyddi/acea//imfai ac-i atoed R.AS-PRPWT-PEDPWSLYGPSPGGR.G
	NFKB1 NFKB1	S893		•	55.4 85.0	56.2	R.QMGYTEAIEVIQAAS*SPVK.T
	NFKB1 NFKB1	S894			7.2	52.0	R.QMGYTEAIEVIQAASS*PVK.T
	NHS GALR1	S836			13.9	26.3	R.RSSS*LR.V
	NHS GALR1	S834				17.0	R.RS*SSLR.V
	Nibrin <sub>NBN</sub>	\$432			25.4	87.5	R.IPNYQLS'PTKLPSINK.S
	Nibrin NBN	Y429			9.2	60.3	R.IPNY*QLSPTKLPSINK.S
	NICE 4 protein UBAP2L	\$453	=		19.8	38.7	K.SPAVATSTAAPPP®*SPLPSK.S  R.RYPS*SISSS*POKDLTQAK.N
	NICE 4 protein UBAP2L	\$604\$609 \$609			13.9	40.2 35.2	R.RYPSSISSS*PQK.D
	NICE 4 protein UBAP2L	S454			7.0	27.4	K.SPAVATSTAAPPPPS*PLPSK.S
	NICE 4 protein UBAP2L	\$605\$608			11.1	13.3	R.RYPSS*ISS*SPQK.D
	NICE 4 protein UBAP2L	Y602S608	<u> </u>		14.0	40.4	R.RY*PSSISS*SPQKDLTQAK.N
	NICE 4 protein UBAP2L	\$604\$608			12.6	34.5	R.RYPS*SISS*SPQKDLTQAK.N
	NICE 4 protein UBAP2L	\$605\$607	<u> </u>		6.5	15.8	R.RYPSS*IS*SSPQKDLTQAK.N
	NICE 4 protein UBAP2L	\$608			29.7	18.2	R.RYPSSISS*SPQKDLTQAK.N
NifU-like N-terminal	NICE 4 protein UBAP2L	\$458 \$14	-	_	7.9	50.1	K.SPAVATSTAAPPPPSSPLIC*K.S  R.AAS*ALLLR.S
	I domain containing ISCU	S29			100.0	23.3	RELS*APAR.L
Nin	one binding protein NOB1	S184			100.0	98.3	R.GEDVPS*EEEEEEENGFEDR.K
Nin	one binding protein NOB1	S201		•	144.2	124.3	R.KDDS*DDDGGGWITPSNIK.Q
	NIP2 BNIP2	S114			19.8	55.3	R.KGS*ITEYTAAEEK.E
	ZC3HC1	\$354\$370	•		24.3	21.4	R.S'WDSSSPVDRPEPEAAS'PTTR.T
	NIPA ZC3HC1	S62		•	1.9	62.6	K.DTSATSQSVNGS*PQAEQPSLESTSK.E
AUDA III.a	NIPAZC3HC1	S58		-	8.9	32.2	K.DTSATSQS*VNGSPQAEQPSLESTSK.E
	domain containing 3NIPAL3	\$372Y375 \$359\$361		•	1.2	17.0	K.ASFSYGALENNDNIS'EIY'APATLPVMQEEHGSR.S  K.AS'FS'YGALENNDNISEIYAPATLPVMQEEHGSR.S
	NIR2 PITPNM1	\$593\$600			9.1	27.5	R.RGS*MNNELLS*PEFGPVRDPLADGVEGLGR.G
	NIR2 PITPNM1				46.8	76.3	K.WNS*NDFIDAFASPVEAEGTPEPGAEAAK.G
	NIR2 PITPNM1	S593			29.7	14.8	R.RGS*MNNELLSPEFGPVRDPLADGVEGLGR.G
	NIR3 PITPNM2	S1277	• •	•	100.0	48.5	R.KGS*FGLPGQGDFLR.S
	NIX BNIP3L	S168	•		14.7	22.2	R.SVSLS*MR.K
	NIX BNIP3L	S164	ı.		9.2	21.9	R.S*VSLSMR.K
	NIX BNIP3L	S166			17.4	27.0	R.SVS'LSMR.K  K.NGGLEHVPSS'S'SIHNGDMEK.I
NmrA-like family domain	nix BNIP3L n-containing protein NMRAL1	S63S64 S218		•	-0.3	15.9	R.REGVS*R.A
	1 (Fragment) am regulated gene 1 NDRG1	\$218 \$330			-0.1	30.4	R.TAS*GSSVTSLDGTR.S
NMYC downstrea	am regulated gene 1 NDRG1	T366			6.5	39.7	R.SHT*SEGAHLDITPNSGAAGNSAGPK.S
NMYC downstrea	am regulated gene 1 NDRG1	T346			16.9	19.0	R.SHT*SEGTR.S
NMYC downstrea	am regulated gene 1 NDRG1	\$330\$333\$336			9.7	33.3	R.TAS*GSS*VTS*LDGTR.S
	am regulated gene 1 NDRG1	\$330\$332\$336	<b>!</b>		8.1	15.8	R.TAS'GS'SVTS'LDGTR.S
	in family, member 2 <sub>NSUN2</sub>	S743	-		80.9	75.3	R.AGEPNS*PDAEEANSPDVTAGCDPAGVHPPR-
	containing octamer NONO	\$743\$751			67.4	57.0	R.AGEPNS'PDAEEANS'PDVTAGCDPAGVHPPR
	binding protein  containing octamer NONO	T15			79.9	83.5	K.QNHT*PR.K  R.FGQAATMEGIGAIGGT*PPAFNR.A
	bindina protein complex, subunit H2 <sub>NCAPH2</sub>	\$232\$246			79.9	35.5	R.
	complex, subunit H2 <sub>NCAPH2</sub>	S284			69.9	76.9	R.S'PQQSAALPR.R
Non-SMC condensin II o	complex, subunit H2 <sub>NCAPH2</sub>	\$232\$240				21.1	R. SUDVIDAL OF SUDED DED CODED DATE AVEL DE ASADY A
Non-SMC condensin II c	complex, subunit H2 <sub>NCAPH2</sub>	S240S246	<del> </del>		0.1	13.3	R. SDIVIDAL GESTOEDGDS*DEGDMDLGGGEDEDAEEAVELDEASADV A
	NOP56 NOP56	<b>S</b> 569			15.0	75.0	K.EEPVS*SGPEEAVGK.S
	NOP56 NOP56	S569S570			100.0	39.2	K.EEPVS'S'GPEEAVGK.S
	NOP56 NOP56	\$467T468	<u></u>		3.4	32.6	R.LAALALASSENSSS*T*PEECEEMSEKPK.K
	NOP56 NOP56	\$520			4.8	54.1	K.EELMS*DLEETAGSTSIPK.R  K.EELMS*SDLEETAGSTSIPK.R
	NOP56 NOP56	\$519 \$519\$520			73.8	70.1	K.EELMS SPLEETAGSTSIPK.R
	NOT2 CNOT2	S161S169			2.7	27.7	R.TNSMSSS*GLGSPNRS*SPSIICMPK.Q

Peak Area <-10 -5 -3 -3	o abundano	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
>10	Protein Name Gene	Phosphosites	5 E B		Ascor	MOWSE	Sequence
	NOT2 CNOT2	S165S169			4.0	26.3	R.TNSMSSSGLGS*PNRS*SPSIICMPK.Q
	NOT2 CNOT2	S165	·		27.8	78.2	R.TNSMSSSGLGS*PNR.S
	NOT2 CNOT2	S101S120	·		2.8	12.8	R.SLS'QGTQLPSHVTPTTGVPTMS'LHTPPSPSR.G
	NOT2 CNOT2	\$160\$161			6.8	12.6	R.TNSMSS*S*GLGSPNRSSPSIICMPK.Q
	NOT4 CNOT4	T328			18.4	60.5	R.SPFEGAVT*ESQSLFSDNFR.H
	NOT4 CNOT4  Notch2 NOTCH2	\$321 \$1841			3.6	73.7	R.S*PFEGAVTESQSLFSDNFR.H  R.GGS*SDLSDEDEDAEDSSANIITDLVYQGASLQAQTDR.T
	NPATNPAT	\$1841 \$775\$779			5.5 8.8	36.0	K.VIISDDPFVSSDTELTSAVSSINGENLPTIILSS*PTKS*PTK.N
	NPATNPAT	\$774\$779			13.9	31.9	K.VIISDDPFVSSDTELTSAVSSINGENLPTIILS*SPTKS*PTK.N
	NPATNPAT	S774T781			10.1	17.5	K.VIISDDPFVSSDTELTSAVSSINGENLPTIILS*SPTKSPT*K.N
	NPATNPAT	S762T770			5.1	16.4	K.VIISDDPFVSSDTELTSAVSS*INGENLPT*IILSSPTKSPTK.N
	NSFL1C NSFL1C	S140		•	80.8	23.6	K.S*PGETSKPRPFAGGGYR.L
	NSFL1C NSFL1C	S114			100.0	100.6	K.S*PNELVDDLFK.G
	NTBA SLAMF6	S277			12.1	64.6	R.NLEYVSVS*PTNNTVYASVTHSNR.E
	NTBA SLAMF6	<b>S</b> 275		•		40.8	R.NLEYVS*VSPTNNTVYASVTHSNR.E
Nuclear autoanti	genic sperm protein NASP	T479S482			52.2	52.8	K.EGEET*EGS*EEDDKENDKTEEMPNDSVLENK.S
Nuclear autoanti	genic sperm protein NASP	S728			100.0	45.9	R.KPEEES*PR.K
Nuclear autoanti	genic sperm protein NASP	S505			100.0	81.1	K.S*LQENEEEEIGNLELAWDMLDLAK.I
	NASP	S141			34.5	57.5	K.TEDESLVENNDNIDETEGS*EEDDKENDK.T
Nuclear autoanti	genic sperm protein NASP	S127			12.8	41.4	K.TEDES*LVENNDNIDETEGSEEDDKENDK.T
	NASP	T138S141			9.5	42.5	K.TEDESLVENNDNIDET*EGS*EEDDKENDK.T
Nuclear autoanti	genic sperm protein <sub>NASP</sub>	T123S127		<u> </u>		49.5	K.T'EDES'LVENNDNIDETEGSEEDDKENDKTEEMPNDSVLENK.S
Nuclear autoanti	genic sperm protein NASP	S127T138		·	11.1	42.1	K.TEDES*LVENNDNIDET*EGSEEDDKENDKTEEMPNDSVLENK.S
	NASP	T138			6.8	56.4	K.TEDESLVENNDNIDET*EGSEEDDKENDK.T
	NASP	\$127\$141	·		10.0	47.2	K.TEDES*LVENNDNIDETEGS*EEDDKENDK.T
	genic sperm protein NASP e membrane protein POM121	T123		-		16.7	K.T*EDESLVENNDNIDETEGSEEDDKENDKTEEMPNDSVLENK.S
	POM 121 e membrane protein POM121	S127			-0.2	96.6	R.SS*SMSSLTGAYASGIPSSSR.N  R.SSSMS*SLTGAYASGIPSSSR.N
	POM 121 e membrane protein POM121	\$130 \$127\$131			16.1	75.2	R.SS*SMSS*LTGAYASGIPSSSR.N
	POM 121 e membrane protein POM121	S131			0.3	41.5 58.7	R SSSMSS*LTGAYASGIPSSSR N
	POM 121 Nuclear factor I/A NFIA	\$300			49.3	66.6	R.S*PGSGSQSSGWHEVEPGMPSPTTLKK.S
	Nuclear factor I/A NFIA	S258			23.9	47.6	R.VSQTPIAAGTGPNFSLSDLESSSYYSMS*PGAMR.R
Nuclear factor	of activated T-cells, NFATC1	S233			54.3	66.3	R.GLGACTLLGS*PR.H
	ineurin-dependent 1 I to kappa B binding NFRKB	\$372\$376			52.1	40.7	K.SEAEDLAEPLSSTEGVAPLS*QAPS*PLAIPAIK.E
Nuclear factor related	I to kappa B binding NFRKB	S376			27.2	51.1	K.SEAEDLAEPLSSTEGVAPLSQAPS*PLAIPAIK.E
Nuclear factor related	I to kappa B binding NFRKB	T365 <b>S</b> 376		••	8.3	16.5	K.SEAEDLAEPLSST*EGVAPLSQAPS*PLAIPAIK.E
Nuclear FMRP	interacting protein 1 NUFIP1	S338S342S351	÷		13.3	31.5	K.LEGPPEANADPLGVLINS*DSES*DKEEKPQHS*VIPK.E
Nuclear FMRP	interacting protein 1 NUFIP1	\$338\$340\$342			28.7	24.6	K.LEGPPEANADPLGVLINS*DS*ES*DKEEKPQHSVIPK.E
Nuclear mitotic	apparatus protein 1 NUMA1	<b>S</b> 1757	<b></b> :		42.5	64.1	R.TQPDGTSVPGEPAS*PISQR.L
Nuclear mitotic	apparatus protein 1 NUMA1	T2055			41.9	89.9	R.QSMAFSILNT*PK.K
Nuclear mitotic	apparatus protein 1 NUMA1	S1862			82.2	78.1	R.LGS*PDYGNSALLSLPGYRPTTR.S
	apparatus protein 1 NUMA1	S1721S1724			30.5	51.4	K.SREPQAKPQLDLS*IDS*LDLSCEEGTPLSITSK.L
	apparatus protein 1 NUMA1	S1225	-		9.3	54.9	R.KNS*LISSLEEEVSILNR.Q
	apparatus protein 1 NUMA1	S1760			-9.8	21.2	R.TQPDGTSVPGEPASPIS*QR.L
	apparatus protein 1 NUMA1	\$1721\$1724\$1			21.4	36.0	K.SREPQAKPQLDLS*IDS*LDLS*CEEGTPLSITSK.L
	apparatus protein 1 NUMA1	\$200\$203T211		•	16.8	41.1	K.VASSSSGNNFLSGS*PAS*PMGDILQT*PQFQMR.R
	apparatus protein 1 NUMA1 apparatus protein 1 NUMA1	S1228			6.9	41.4	R.KNSLIS*SLEEEVSILNR.Q  K.VES*LESLYFT*PIPAR.S
	apparatus protein 1 NUMA1	\$1769T1776			26.1	54.4	R.SQAPLESSLDS*LGDVFLDS*GRK.T
	apparatus protein 1 NUMA1	\$1792\$1800 \$1788\$1789			0.0	11.2	R.SQAPLESSLDS*LGDVFLDS*GRK.T
	clear protein UKp68 ZC3H14	\$1788\$1789 \$515	-			43.9	R.DLVQPDKPAS*PK.F
	clear protein UKp68 ZC3H14	\$515 \$274			9.0	57.0	R.LCEPEVLNSLEETYS*PFFR.N
	clear protein UKp68 ZC3H14	S527S533			33.0	32.3	K.FIVTLDGVPS'PPGYMS'DQEEDMCFEGMKPVNQTAASNK.G
	clear protein UKp68 ZC3H14	Y531S533	• • •		10.1	11.4	K.FIVTLDGVPSPPGY*MS*DQEEDMCFEGMKPVNQTAASNK.G
	clear protein UKp68 ZC3H14	T521S527		•		21.1	K.FIVT*LDGVPS*PPGYMSDQEEDMCFEGMKPVNQTAASNK.G
	ceptor coactivator 5 NCOA5	S126			16.9	29.9	R.EGS*YDR.Y
	ceptor coactivator 5 NCOA5	S29S34			100.0	15.5	R.DRS*PIRGS*PR.R
Nuclear re-	ceptor coactivator 5 NCOA5	<b>S</b> 29	• • •		100.0	14.9	R.DRS*PIR.G
Nuclear re	ceptor coactivator 5 NCOA5	\$378 <b>T</b> 379		•	-0.4	38.8	R.SS*T*DSLPGPISR.Q
Nuclear receptor coac	ctivator 6 interacting TGS1	<b>S</b> 89			41.9	95.1	K.GIGLDESELDS*EAELMR.S
Nuclear receptor coac	ctivator 6 interacting TGS1	\$85\$89			100.0	90.8	K.GIGLDES'ELDS'EAELMR.S
Nuclear re-	ceptor coactivator 7 NCOA7	<b>S</b> 376			12.1	13.1	K.KLDS*SR.E

<-10 0 abu	ite dots- Significant chi ndance at 5%FDR	compared to	the .			
.5 29 time .3 42 PSM	point with the minimum	n peak area	for a given			
3 86 5 5 >100 >100			_RajiB_			
Protein Name Ger Nuclear receptor corepressor 1 NCO		£ £ £	£ £ £	Ascor 100.0	MOWSE 36.8	Sequence R.VS*PENLVDK.S
Nuclear receptor corepressor 1 NCO				69.6	21.1	K.S*PIPGQGYLGTERPSSVSSVHSEGDYHR.Q
Nuclear receptor corepressor 1 NCO	R1 \$2151			50.4	60.5	R.SHVSSEPYEPIS*PPQVPVVHEK.Q
Nuclear receptor corepressor 1 NCO	R1 \$992T996			11.8	30.3	R.SSTS*PCGT*SKSPNREWEVLQPAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1 NCO	R1 \$999			104.6	59.7	K.S*PNREWEVLQPAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1 NCO	R1 S2436S2438			11.5	18.7	R.EPAPLLSAQYETLS*DS*DD
Nuclear receptor corepressor 1 NCO				48.4	98.7	R.S'PGSISYLPSFFTK.L
Nuclear receptor corepressor 1 NCO	R1 \$992\$999			-0.3	26.3	R.SSTS*PCGTSKS*PNREWEVLQPAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1 NCO	R1 S1977S1981			14.5	34.2	R.YETPSDAIEVIS*PASS*PAPPQEK.L
Nuclear receptor corepressor 1 NCO	R1 S2395T2399			20.6	68.9	R.MLSS*TPPT*PIACAPSAVNQAAPHQQNR.I
Nuclear receptor corepressor 2 NCO	R2 \$149\$152			102.2	53.9	K.LEPVS*PPS*PPHTDPELELVPPR.L
Nuclear receptor corepressor 2 NCO	R2 \$2056\$2064	•••		20.9	16.9	R.SLGYHGSSYS*PEGVEPVS*PVSSPSLTHDK.G
Nuclear receptor corepressor 2 NCO	R2 S2056S2064S2		• •	12.3	20.6	R.SLGYHGSSYS*PEGVEPVS*PVS*SPSLTHDK.G
Nuclear receptor corepressor 2 NCO	R2 \$2268			33.2	54.0	K.S*PGNTSQPPAFFSK.L
Nuclear receptor corepressor 2 NCO	R2 \$2056\$2067			10.7	28.4	R.SLGYHGSSYS*PEGVEPVSPVS*SPSLTHDK.G
Nuclear receptor corepressor 2 NCO	R2 \$2054\$2064\$2			10.6	11.0	R.SLGYHGSS*YSPEGVEPVS*PVS*SPSLTHDK.G
Nuclear receptor corepressor 2 NCO	R2 Y2055S2064S2			14.0	14.1	R.SLGYHGSSY*SPEGVEPVS*PVSS*PSLTHDK.G
Nuclear ubiquitous casein kinase and NUC	KS1 S181			35.4	80.3	R.LKATVTPS*PVK.G
Nuclear ubiquitous casein kinase and NUC	KS1 T179S181		•	32.2	27.3	R.LKATVT*PS*PVK.G
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC cyclin dependent kinase substrate	KS1 S19		• • • •	83.0	114.9	K.VVDYSQFQES*DDADEDYGR.D
Nuclear ubiquitous casein kinase and NUC	KS1 Y13			15.9	76.8	K.VVDY*SQFQESDDADEDYGR.D
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 T202S204		•	100.0	26.2	K.EKT*PS*PK.E
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 T222		• • •	27.6	23.9	K.TST*SPPPEK.S
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S75S79	•		28.0	55.5	K.DDSHS*AEDS*EDEKEDHK.N
Cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC			• • • •	42.5	96.6	K.NSQEDS*EDSEDKDVK.T
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S54S58S61			19.2	46.1	R.SGKNS*QEDS*EDS*EDKDVK.T
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S73S75S79		• • • •	100.0	40.4	K.DDS*HS*AEDS*EDEKEDHKNVR.Q
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S58S61	• • • •		70.3	78.7	K.NSQEDS*EDS*EDKDVK.T
Cvclin dependent kinase substrate Nuclear ubiquitous casein kinase and NUC			• • •	100.0	59.7	K.EEDEEPES*PPEKK.T
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 T177T179			10.3	11.8	K.AT"VT"PSPVKGK.G
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S234S240		•	46.1	41.6	K.SGDEGS*EDEAPS*GED
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 T179			13.9	76.1	R.LKATVT*PSPVKGK.G
Cvclin dependent kinase substrate Nuclear ubiquitous casein kinase and NUC	KS1 S229S234S240			100.0	47.2	K.S*GDEGS*EDEAPS*GED
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S130S132S144			75.7	97.3	K.DS*GS*DEDFLM#EDDDDS*DYGSSK.K
Cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S130S132			91.1	100.2	K.DS*GS*DEDFLMEDDDDSDYGSSK.K
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S223	•	• • • •	10.8	42.2	K.TSTS*PPPEK.S
Nuclear ubiquitous casein kinase and NUC	KS1 854858			7.6	28.4	K.NS*QEDS*EDSEDKDVK.T
vcclin dependent kinase substrate Nuclear ubiquitous casein kinase and NUC			• •	14.3	89.9	R.KVVDYS*QFQESDDADEDYGR.D
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 Y13S14			6.9	22.2	R.KVVDY*S*QFQESDDADEDYGR.D
cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC				14.7	27.4	K.EKTPS*PK.E
Cvclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC	KS1 S54S61			7.5	28.8	K.NS*QEDSEDS*EDKDVK.T
cvclin dependent kinase substrate NUC					39.6	R.
Nuclear ubiquitous casein kinase and NUC				8.7	15.2	R.S'GKNS'QEDS'EDSEDKDVK.T
cyclin dependent kinase substrate  Nuclear ubiquitous casein kinase and NUC			•	23.0	17.1	R.LKAT"VTPS"PVKGK.G
cvclin dependent kinase substrate  Nucleolar phosphoprotein p130 NOL-					55.3	K.KKAS*S*S*DS*EDS*S*EEEEEVQGPPAK.K
Nucleolar phosphoprotein p130 NOL	C1 <b>S</b> 699			78.2	69.9	R.GGSISVQVNSIKFDS*E
Nucleolar phosphoprotein p130 NOL	C1 <b>S</b> 539			100.0	40.4	K.GKGS*PRPQAPK.A
Nucleolar phosphoprotein p130 NOL				25.6	43.5	R.ASS'PFR.R
Nucleolar phosphoprotein p130 NOL	C1 <b>S</b> 644		<del></del>	100.0	23.1	R.VADNS*FDAK.R
Nucleolar phosphoprotein p130 NOL	C1 T608T611			100.0	42.7	K.LQT*PNT*FPK.R
NOL	C1 S564	•••		100.0	22.0	K.NS*EEEEEEKKK.A
Nucleolar phosphoprotein p130 NOL			•	10.4	20.5	R.GGSISVQVNS*IKFDSE
Nucleolar protein 1 NOP				108.6	77.4	R.EAAAGIQWS*EEET*EDEEEEKEVTPESGPPK.V
Nucleolar protein 1 NOP				6.9	64.0	K.GTDTQTPAVLS*PSK.T
Nucleolar protein 1 NOP			•	14.7	24.8	K.GPQPPTVS*PIR.S
Nucleolar protein 8 NOL				100.0	39.3	K.KRNS*IS*DDDT*DS*EDELR.M
Nucleolar protein 8 NOL:				100.0	41.4	R.FLET*DS*EEEQEEVNEKK.T
Nucleolar protein 8 NOL:				79.6	123.4	R.LQDS*S*S*EEEDVTEETDHR.N
Nucleolar protein 8 NOL				48.2	66.2	R.NSIS*DDDT*DS*EDELR.M
Nucleolar protein 8 NOL			• • •	40.8	51.5	K.LFDS*S*DDDES*DS*EDDSNRFK.I
NOL				6.0	13.3	R.EY*DS*GDTDEIIAMKK.N
Nucleolar protein NOP5 NOP			•	29.1	53.1	K.EEPLS*EEEPCTSTAIAS*PEKK.K
	•					

Peak Area <-10 -6 -3 0	%CV 0 29 42 71	White dots-Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a PSM						
3 5 >10	>100			CarT	Ra			
	Protein Name	Gene	Phosphosites	£ # #	Ę.,			
		NOP58	S502					
Nucleolar protein wit	th MIF4G domain 1	NOM1	S317S320S321					
		NCL	S145S153					
	Nucleolin	NCL	S184S206	·				
	Nucleolin	NCL	S153					
	Nucleolin	NCL	S145					
	Nucleolin	NCL	S41S42					
	Nucleolin	NCL	S34S41					
		NCL	\$28\$34\$41\$42	•				
	Nucleolin	NCL	S28S34S41					
	Nucleolin	NCL	<b>S</b> 67					
	Nucleolin	NCL	T69					

.3 42 PSM						
5 >100			RajiB			
Protein Name Gene NOP58	Phosphosites \$502	5 5 5	e # #	Ascor 101.3	MOWSE 101.5	Sequence K.EEPLS*EEEPCTSTAIASPEK.K
Nucleolar protein with MIF4G domain 1 NOM1	S317S320S321			40.0	36.3	R.FAEDEEKS'ENS'S'EDGDITDK.S
NCL	S145S153	•••		100.0	101.1	K.KEDS*DEEEDDDS*EEDEEDDEDEDEDEDEEPAAM#K.A
Nucleolin NCL			• • •			KAAAAPAS'EDEDDEDDEDDDDDEEDDS'EEEAMETTPAK G
Nucleolin NCL	S184S206			70.9	77.0	K.KEDSDEEDDDS*EEDEEDDEDEDEDEDEEPAAMK.A
Nucleolin NCI	S153			26.3	146.8	K.KEDS'DEEEDDDS EEDEEDDEDEDEDEDEDEFAANK.A
	S145		• • •	53.4	135.0	K EVERDS DEEDDDSSEDEDDDEDEDEDEDEDEDEDEDEDEDEDE
Nucleolin <sub>NCL</sub>	S41S42			17.0	33.2	
Nucleolin <sub>NCL</sub>	S34S41			27.0	35.3	K.EVEEDSEDEEMS*EDEEDDS*SGEEVVIPQKK.G
NCL	S28S34S41S42	•		100.0	38.4	K.EVEEDS*EDEEM#S*EDEEDDS*S*GEEVVIPQKK.G
Nucleolin <sub>NCL</sub>	S28S34S41			19.0	41.3	K.EVEEDS*EDEEMS*EDEEDDS*SGEEVVIPQKK.G
Nucleolin <sub>NCL</sub>	S67	•		25.8	44.5	K.VVVS*PTKK.V
Nucleolin <sub>NCL</sub>	T69		•	22.5	41.3	K.VVVSPT*KK.V
Nucleolin <sub>NCL</sub>	Y495			-0.2	39.5	K.TLVLSNLSY*SATEETLQEVFEK.A
Nucleolin <sub>NCL</sub>	S184			4.3	42.6	K.AAAAAPAS*EDEDDEDDEDDDDDDEEDDSEEEAMETTPAK.G
Nucleolin <sub>NCL</sub>	S28S41			8.2	20.0	K.EVEEDS*EDEEMSEDEEDDS*SGEEVVIPQKK.G
Nucleolin <sub>NCL</sub>	S206			18.7	45.9	K.AAAAAPASEDEDDEDDEDDEDDDDDEEDDS*EEEAMETTPAK.G
Nucleolin <sub>NCL</sub>	S28S34S42			-2.0	16.8	K.EVEEDS*EDEEMS*EDEEDDSS*GEEVVIPQKK.G
Nucleolin <sub>NCL</sub>	S34S41S42			5.6	11.0	K.EVEEDSEDEEMS*EDEEDDS*S*GEEVVIPQK.K
Nucleolin <sub>NCL</sub>	S34S42			7.5	18.8	K.EVEEDSEDEEM#S*EDEEDDSS*GEEVVIPQKK.G
Nucleolin <sub>NCL</sub>	S491				22.3	K.TLVLS*NLSYSATEETLQEVFEK.A
NCL	S28S41S42			13.1	31.1	K.EVEEDS*EDEEMSEDEEDDS*S*GEEVVIPQK.K
Nucleolin <sub>NCL</sub>	S28S34			4.6	16.2	K.EVEEDS*EDEEMS*EDEEDDSSGEEVVIPQKK.G
Nucleophosmin 1 NPM1	<b>S</b> 243			23.9	36.5	K.GPSS*VEDIK.A
Nucleophosmin 1 <sub>NPM1</sub>	S125			118.9	75.9	K.CGSGPVHISGQHLVAVEEDABS*EDEEEEDVK.L
Nucleophosmin 1 <sub>NPM1</sub>	S70		•	14.6	69.3	K.DELHIVEAEAM#NYEGS*PIK.V
Nucleophosmin 1 <sub>NPM1</sub>	S218			15.5	20.6	K.DSKPSS*TPR.S
Nucleophosmin 1 NPM1	S214	•			12.9	K.DS*KPSSTPR.S
Nucleophosmin 1 NPM1				8.1		K.MQAS*IEK.G
	S254		<u></u>	100.0	28.3	
NPM1	Y67			3.6	32.3	K.DELHIVEAEAM#NY*EGSPIKVTLATLK.M
Nucleophosmin 1 NPM1	S106		•		51.3	K.CGS*GPVHISGQHLVAVEEDAESEDEEEEDVK.L
Nucleophosmin 1 NPM1	S137			27.7	41.7	K.LLS*ISGKR.S
Nucleophosmin 1 NPM1	S217			7.6	11.1	K.DSKPS*STPR.S
Nucleoporin 160kDa NUP160	Y1151			12.7	35.1	R.LIRPEYAWIVQPVSGAW*DRPGASPK.R
Nucleoporin 160kDa <sub>NUP160</sub>	S1157			37.3	28.9	R.LIRPEYAWIVQPVSGAVYDRPGAS*PK.R
Nucleoporin 205kDa NUP205	S1165			20.0	83.8	R.S*VSGFLHFDTATK.V
Nucleoporin 205kDa NUP205	S1167			-0.4	105.3	R.SVS*GFLHFDTATK.V
Nucleoporin 50kDa <sub>NUP50</sub>	T219	Ţ.		10.9	38.1	R.NSESESNKVAAET*QSPSLFGSTK.L
Nucleoporin 50kDa <sub>NUP50</sub>	S221			26.0	100.4	K.VAAETQS*PSLFGSTK.L
Nucleosome assembly protein 1 like 1 NAP1L1	<b>S</b> 10			100.3	68.3	K.EQS*ELDQDLDDVEEVEEEETGEETK.L
Nucleosome assembly protein 1 like 1 NAP1L1	T62			14.0	62.0	R.LDGLVET*PTGYIESLPR.V
Nucleosome assembly protein 1 like 1 NAP1L1	<b>S</b> 143			1.8	30.9	R.FEIINAIYEPTEEECEWKPDEEDEIS*EELK.E
Nucleosome assembly protein 1 like 4 NAP1L4	S125			38.9	71.4	R.EFITGDVEPTDAESEWHS'ENEEEEK.L
Nucleosome assembly protein 1 like 4 NAP1L4	S304			21.1	114.9	KASGDGES*LDEDSEFTLASDFEIGHFFR.E
Nucleosome assembly protein 1 like 4 NAP1L4	\$304\$309		<u> </u>	5.5	60.4	K.ASGDGES*LDEDS*EFTLASDFEIGHFFR.E
Nucleosome assembly protein 1 like 4 NAP1L4	S299S309		<u>:</u>	4.7	44.7	K.AS*GDGESLDEDS*EFTLASDFEIGHFFR.E
Nucleosome assembly protein 1 like 4 NAP1L4	S299		•	15.0	65.2	K.AS*GDGESLDEDSEFTLASDFEIGHFFR.E
Nucleosome assembly protein 1 like 4 NAP1L4	S121				30.7	R.EFITGDVEPTDAES*EWHSENEEEEK.L
Numb homolog NUMB	\$228 <b>\$</b> 229				22.6	K.IVVGS*S*VAPGNTAPSPSSPTSPTSDATTSLEMNNPHAIPR.R
NUP107 NUP107	S86		•	24.7	38.0	R.QPDISCILGTGGKS*PR.L
NUP107 NUP107				31.7		K.GLPLGSAVSS*PVLFS*PVGR.R
NUP133 NUP133	S45S50			43.2	49.1	
	S44S50			53.6	15.7	K.GLPLGSAVS*SPVLFS*PVGR.R
NUP133 NUP133	<b>S</b> 57			31.9	19.0	R.RSS*LSSR.G
NUP153 NUP153	S192		<del></del>	41.4	51.4	R.AS*DKDITVSK.N
NUP153 <sub>NUP153</sub>	T102			9.1	37.4	R.IT*PEPAVSNTEEPSTTSTASNYPDVLTRPSLHR.S
NUP153 NUP153	S333			76.7	101.0	R.IPSIVS*SPLNSPLDR.S
NUP153 NUP153	S334S338		-	11.9	18.1	K.RIPSIVSS*PLNS*PLDR.S
NUP210 NUP210	S1852			3.2	51.4	R.ASPGHS*PHYFAASSPTSPNALPPAR.K
NUP210 NUP210	S1848	<b></b>		6.2	75.8	R.AS*PGHSPHYFAASSPTSPNALPPAR.K
NUP210 NUP210	S1874			14.9	48.8	R.KAS*PPSGLWSPAYASH
NUP210 NUP210	S1877			4.6	43.9	R.KASPPS*GLWSPAYASH
NUP210 NUP210	Y1855			0.7	58.9	R.ASPGHSPHY*FAASSPTSPNALPPAR.K
NUP210 NUP210	S1859	••		13.9	16.0	R.ASPGHSPHYFAAS*SPTSPNALPPAR.K
			•			

<-10 0 abundance	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
42 PSM			RajiB			
>10 Protein Name Gene	Phosphosites	E # #	E E E	Ascor	MOWSE	Sequence
NUP214 <sub>NUP214</sub>	\$433T436			14.6	43.5	K.SPGS*TPT*TPTSSQAPQK.L  R.TPS*IQPSLLPHAAPFAK.S
NUP214 NUP214	\$1023 \$433T437			15.7	81.0 47.0	K.SPGS*TPTT*PTSSQAPQK.L
NUP214 NUP214	S1081			2.8	33.0	K.HGAPS*PSHPISAPQAAAAAALR.R
NUP88 NUP88	<b>S</b> 35	•		39.9	43.2	K.NQS*PTEAEKPASSSLPSSPPPQLLTR.N
NUP98 NUP98	S871			64.3	45.6	K.YGLQDS*DEEEEEHPSK.T
NUP98 NUP98	S606			32.1	78.7	R.DSENLAS*PSEYPENGER.F
NUP98 NUP98	<b>S</b> 595			67.0	83.3	K.NLNNSNLFS*PVNR.D
NUP98 NUP98	S591	<b></b>		61.4	70.2	K.NLNNS*NLFSPVNR.D
NUP98 NUP98	\$608	÷		10.9	27.8	R.DSENLASPS*EYPENGER.F
Odin <sub>ANKS1A</sub>	S620	•		100.0	28.7	K.AELKLS*R.S  K.SPS*FASEWDEIEK.I
Odin ANKS1A	\$663 \$647			9.9	70.5	R.SES*LSNCSIGK.K
OIP106 TRAK1	S919		=	30.0	101.3	R.S*FPTMVGSSMQMK.A
Opa interacting protein 5 OIP5	S48			-0.2	70.3	K.GSS*PLGPAGLGAEEPAAGPQLPSWLQPER.C
Opioid growth factor receptor OGFR	<b>S</b> 315	•••		52.0	64.6	R.KVEEEGS*PGDPDHEASTQGR.T
Opioid growth factor receptor OGFR	<b>S</b> 378			55.8	41.9	R.SQGDEAGGHGEDRPEPLS*PK.E
OSBP related protein 10 OSBPL10				26.0	45.4	R.SLTLLPHGTPNS*ASPCSQR.H
OSBP related protein 10 OSBPL10			-	6.7	55.7	R.SLTLLPHGTPNSAS*PCSQR.H
OSBP related protein 11 OSBPL11		<u>:</u>		75.4	76.6	R.RPS*QNAISFFNVGHSK.L
OSBP related protein 11 <sub>OSBPL11</sub> OSBP related protein 11 <sub>OSBPL11</sub>				12.9	73.1	R.SFSLASSSNS*PISQR.R  R.SFSLASSS*NSPISQR.R
OSBP related protein 9 OSBPL9	\$334			17.6	33.5	R.LIDSSGSASVLTHS*SSGNSLK.R
OSBP related protein 9 OSBPL9	S329		•••	6.4	24.3	R.LIDSSGSAS*VLTHSSSGNSLK.R
OSBP related protein 9 OSBPL9	<b>S</b> 335			9.1	20.6	R.LIDSSGSASVLTHSS*SGNSLK.R
Osmosis responsive factor TTC33	S197	Ė		15.6	52.2	K.SEAPAEVTHFS*PK.S
Osteoclast stimulating factor 1 OSTF1	S213			53.5	94.1	R.TLSNAEDYLDDEDS*D
Osteoclast stimulating factor 1 OSTF1	S202S213			26.9	84.2	R.TLS*NAEDYLDDEDS*D
Osteoclast stimulating factor 1 OSTF1	Y207	<u>:</u> -		21.7	17.6	R.TLSNAEDY*LDDEDSD
Osteoclast stimulating factor 1 OSTF1  Osteoclast stimulating factor 1 OSTF1	\$202Y207			9.9	34.3	R.TLS*NAEDY*LDDEDSD  R.TLSNAEDY*LDDEDS*D
Osteoclast stimulating factor 1 OSTF1	Y207S213 T200S202			6.9	38.2 43.8	R.T*LS*NAEDYLDDEDSD
Osteoclast stimulating factor 1 OSTF1	T200S213	=		6.1	14.1	R.T*LSNAEDYLDDEDS*D
Osteopetrosis associated transmembrane OSTM1 protein 1	T324			21.2	21.9	K.SST*SFANIQENSN
Osteopetrosis associated transmembrane OSTM1 protein 1	<b>S</b> 325			-0.3	23.5	K.SSTS*FANIQENSN
OTUBAIN 1 OTUB1	S18		•	13.8	87.1	K.QEPLGSDS*EGVNCLAYDEAIMAQQDR.I
OTUBAIN 1 OTUB1	S16			16.2	82.7	K.QEPLGS*DSEGVNCLAYDEAIMAQQDR.I
Oxidative stress responsive 1 OXSR1	<b>S</b> 339		• • •	92.5	98.5	K.TEDGGWEWS*DDEFDEESEEGK.A
Oxidative stress responsive 1 OXSR1	S325			20.1	29.8	R.RVPGSS*GR.L
Oxysterol binding protein OSBP  Oxysterol binding protein OSBP	S379 T377S382S385			10.9	88.4	R.TGS*NISGASSDISLDEQYK.H  R.T*GSNIS*GAS*SDISLDEQYKHQLEETKK.E
Oxysterol binding protein OSBP	\$190\$193		<del>-</del>	17.2	76.2 98.5	K.MLAES*DES*GDEESVSQTDKTELQNTLR.T
Oxysterol binding protein OSBP	S351			91.6	82.3	K.GDMS*DEDDENEFFDAPEIITMPENLGHK.R
Oxysterol binding protein OSBP	\$379\$382\$385			21.1	124.5	R.TGS*NIS*GAS*SDISLDEQYK.H
Oxysterol binding protein OSBP	T367		• • •	13.6	25.7	K.GDMSDEDDENEFFDAPEIIT*MPENLGHK.R
Oxysterol binding protein OSBP	\$382\$386		-	11.9	47.8	R.TGSNIS*GASS*DISLDEQYKHQLEETKK.E
Oxysterol binding protein OSBP	T377S382		-	9.5	51.1	R.T*GSNIS*GASSDISLDEQYK.H
Oxysterol binding protein OSBP	T377S379S389		_	16.0	20.0	R.T'GS'NISGASSDIS'LDEQYKHQLEETKK.E
Oxysterol binding protein OSBP	\$379\$382		÷	3.4	51.8	R.TGS*NIS*GASSDISLDEQYK.H
Oxysterol binding protein like 8 OSBPL8  Oxysterol binding protein like 8 OSBPL8	\$328\$331\$342 \$807\$808\$810			19.2	35.2	K.DQDMYS'DKS'DKENDQEHDES'DNEVMGK.S  K.GYSSPEPDIQDS'S'GS'EAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	\$807\$808\$810 \$799\$807\$810	• • •		39.3	30.3	K.GYSS*PEPDIQDS*SGS*EAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	S798S799S810			10.8	35.8	K.GYS*S*PEPDIQDSSGS*EAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	\$799\$810\$814			15.3	20.6	K.GYSS*PEPDIQDSSGS*EAQS*VKPSTR.R
Oxysterol binding protein like 8 OSBPL8	\$799\$808\$810			9.4	27.6	K.GYSS*PEPDIQDSS*GS*EAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	Y327S328S342		=	13.3	27.2	K.DQDMY*S*DKSDKENDQEHDES*DNEVMGK.S
Oxysterol binding protein like 8 OSBPL8	\$798\$799\$807			8.9	24.7	K.GYS*S*PEPDIQDS*SGSEAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	\$798\$799\$807	<b>—</b>		25.8	20.9	K.GYS*S*PEPDIQDS*S*GS*EAQSVKPSTR.R
Oxysterol binding protein like 8 OSBPL8	\$807\$810\$814			16.2	24.0	K.GYSSPEPDIQDS*SGS*EAQS*VKPSTR.R
Oxysterol binding protein like 8 OSBPL8  Oxysterol binding protein like 8 OSBPL8	Y327S328S331 S799S807S808		•	4.9	18.1	K.DQDMY*S*DKS*DKENDQEHDESDNEVMGK.S  K.GYSS*PEPDIQDS*S*GSEAQSVKPSTR.R
Oxysterol binding protein-like 3 OSBPL3	\$799\$807\$808 \$304			7.2	27.5 54.5	R.LHSS*NPNLSTLDFGEEK.N
				_	-	

Peak Area %CV Wi	hite dots- Significant cha undance at 5%FDR (	ange in pept	ide the			
.5 25 tim	epoint with the minimum SM	peak area t	or a given			
3 86 5100 5100 510		CarT	_RajiB_			
Protein Name Ge Oxysterol binding protein-like 3 <sub>OSI</sub>		8 2 2	8 % %	Ascor 56.7	MOWSE 42.9	Sequence R.LHS*SNPNLSTLDFGEEK.N
Oxysterol binding protein-like 3 OSI	BPL3 S251			12.1	71.0	R.TYS*APAINAIQGGSFESPKK.E
P160 MY	BBP1A S1163		• •	5.2	40.0	K.EIPSATQS*PISK.K
P160 MY	BBP1A S1267			25.1	43.0	K.NQKPSQVNGAPGS*PTEPAGQK.Q
P160 MY	BBP1A S11			59.4	23.2	R.DPAQPMS*PGEATQSGARPADR.Y
P160 MY1	BBP1A \$731\$732\$734	-		17.7	11.0	K.SEEGEDNRS*S*ES*EEES*EGEES*EEEER.D
	BBP1A T1161	÷.		8.1	28.1	K.EIPSAT*QSPISK.K
p21 activated kinase 3 PAF		<u>.</u>		-0.3	68.5	R.ST*MVGTPYWMAPEVVTR.K
p21 activated kinase 4 PAP				48.7	76.9	K.S*LVGTPYWMAPELISR.L
p21 activated kinase 4 PAI				5.3	19.9 39.2	K.SLVGT*PYWMAPELISR.L  R.DKRPLS*GPDVGTPQPAGLASGAK.L
p21 activated kinase 4 PA				28.9	40.0	K.SLVGTPY*WMAPELISR.L
p53 induced gene 8 E12				100.0	39.5	R.AQS*IER.K
p53 induced gene 8 E12			<del>.</del>	-0.2	23.3	K.TVYLQSALSSSTS*AEKFPSPHPSPAK.L
p53 induced gene 8 E12	4 S316			-0.0	14.6	K.TVYLQSALS*SSTSAEKFPSPHPSPAK.L
PA2G4PA2	2G4 <b>T</b> 386		•	39.9	56.1	K.TAENATSGET*LEENEAGD
Paf1, RNA polymerase II associated factor, PAF	F1 \$456\$460\$466			100.0	43.8	R.DKEEIFGS*DADS*EDDADS*DDEDR.G
PAG PAG	31 <b>S</b> 296		·	9.1	30.9	R.FSS*LSYK.S
PAG PAG	31 <b>S</b> 295			9.8	23.5	K.RFS*SLSYK.S
PAG PAG	G1 S295S296			5.4	19.8	K.RFS*S*LSYK.S
PAG PAG			•	35.4	92.8	R.S*PSSCNDLYATVK.D
PAG PAG				23.9	55.3	K.AEFAEYAS*VDR.N
PAG PAG				4.7	16.0	K.EGGEAEESATDTTS"ETNKRFS"SLS"YK.S  K.SGQSLTVPESTYTSIQGDPQRS"PSS"CNDLYATVK.D
PAG PAG				25.4	19.7	K.DSS*SQENMVEDCLYETVK.E
PAGPAG				19.7	78.0	K.S*REEDPTLTEEEISAMYSSVNKPGQLVNK.S
PAG PAG				18.4	59.1	K.EGGEAEESATDTTS'ETNKR.F
PAG PAG				-0.3	38.3	K.EGGEAEESATDT*TSETNKR.F
PAG PAG	G1 S295S298			12.6	21.4	K.RFS*SLS*YK.S
PAG PAG	G1 S354			33.6	81.4	R.SPSS*CNDLYATVK.D
PAG PAG	G1 S351S353			6.0	15.2	K.SGQSLTVPESTYTSIQGDPQRS*PS*SCNDLYATVK.D
PAG PAG	31 S169			67.8	53.4	K.DS*SSQENMVEDCLYETVK.E
PAG PAG				11.7	82.3	R.SPS*SCNDLYATVK.D
PAG PAG			<u></u>	38.2	69.2	K.ENDY*ESISDLQQGR.D
PAG PAG				-0.2	99.6	K.DSSS*QENMVEDCLYETVK.E  R.S*VDGDQGLGMEGPYEVLK.D
PAGPAG				51.7	38.0	R.FSSLS*YK.S
PAG PAG			•	7.8 -5.9	13.0	K.SGQSLTVPESTYTSIQGDPQRSPS*S*CNDLYATVK.D
PAK2 <sub>PAF</sub>				81.1	41.1	R.S*VIDPVPAPVGDSHVDGAAK.S
PAK2 <sub>PA</sub>	K2 S141			25.3	56.3	K.YLS*FTPPEK.D
PAK2 <sub>PAF</sub>	<2 S141S152			18.6	36.2	K.YLS*FTPPEKDGFPS*GTPALNAK.G
PAK2 <sub>PAP</sub>	C2 S141T154			4.9	22.2	K.YLS*FTPPEKDGFPSGT*PALNAK.G
PAK2 <sub>PAF</sub>	C2 T143S152	•		14.9	21.3	K.YLSFT*PPEKDGFPS*GTPALNAK.G
PAK2 <sub>PAF</sub>	<2 T143				50.1	K.YLSFT*PPEKDGFPSGTPALNAK.G
PAK2 <sub>PA</sub>		•		6.2	18.2	K.YLS'FT'PPEKDGFPSGTPALNAK.G
PAK2 <sub>PAF</sub>			•	13.9	35.1	K.Y*LSFTPPEK.D
PAK2 <sub>PA</sub>				28.4	45.3	K.IIS*IFSGTEK.G  R.S*RS*RDS*GDENEPIQER.F
Palladin PAL				100.0	21.9	R.IAS*DEEIQGTK.D
Palladin <sub>PAL</sub>		-		37.6 14.3	35.7	K.QFIAAQNLGPASGHGTPASSPSSSSLPS*PMS*PTPR.Q
Pannexin 1 PAP				3.5	28.6	R.DGACSVPGVTENLGQS*LWEVSESHFK.Y
Pantothenate kinase 4 PAN		•		18.4	93.1	K.GAEQDNPNQYSWGENYAGSSGLMSAS*PELGPAQR.A
Pantothenate kinase 4 PAN	NK4 \$404			16.7	58.1	R.S*GTFDLLEMDR.L
Pantothenate kinase 4 PAN	NK4 Y383		<u> </u>	12.4	22.4	K.GAEQDNPNQYSWGENY*AGSSGLMSASPELGPAQR.A
Pantothenate kinase 4 PAN	NK4 T406			-0.8	36.3	R.SGT*FDLLEMDR.L
PARD3 PAR	RD3 <b>S</b> 174		•	12.1	25.8	R.WS*TTAGFLK.Q
PARN PAR		•		42.4	59.6	K.ELS*PAGSISK.N
PARN PAR				16.4	36.3	K.NS*PATLFEVPDTW
PARNPAR			.■.	8.4	112.3	R.NLS*PSQEEAGLEDGVSGEISDT*ELEQTDSCAEPLSEGR.K
PARN PAR				7.8	72.4	R.NLS*PSQEEAGLEDGVS*GEISDTELEQTDSCAEPLSEGR.K
PARN PAR				8.3	41.3	R.NLS*PSQEEAGLEDGVSGEIS*DTELEQTDSCAEPLSEGR.K R.SPT*PRPR.R
	RVB T9		•	14.8	22.6	

Peak Area %CV	abundano	ts-Significant cha e at 5%FDR o	compared to	the			
-6 29 -3 42	timepoint PSM	with the minimum	peak area fo	or a given			
3 86 5 >100			CarT	RajiB			
	in Name Gene	Phosphosites	9 m g	9 % E	Ascor	MOWSE	Sequence
Pa	arvin beta PARVB	<b>S</b> 7		•	-4.7	18.2	R.S*PTPRPR.R
	AS kinase PASK	S119			-0.4	24.5	R.GLSSGWS*SPLLPAPVCNPNK.A
Patatin like phospholipas cor	e domain <sub>PNPLA2</sub> ntaining 2	S404			55.8	58.3	R.VQS*LPSVPLSCAAYR.E
Patatin like phospholipas	e domain PNPLA2	S428			100.0	37.6	R.NNLS*LGDALAK.W
Patatin like phospholipas	e domain PNPLA2	<b>S</b> 407			15.8	43.7	R.VQSLPS*VPLSCAAYR.E
	Paxillin PXN	S336	• • •		8.0	61.7	K.TGSSS*PPGGPPKPGSQLDSMLGSLQSDLNK.L
	Paxillin <sub>PXN</sub>	S346		• • •	6.8	45.0	K.TGSSSPPGGPPKPGS*QLDSMLGSLQSDLNK.L
	Paxillin PXN	T332			6.7	12.4	K.T*GSSSPPGGPPKPGSQLDSMLGSLQSDLNK.L
	PC2 CBX4	\$432\$434		-		50.4	R.S*IS*TPTCLGGSPAAERPADLPPAAALPQPEVILLDSDLDEPIDLR.
	PC2 CBX4	\$432\$434T435	=			34.7	R.S*IS*T*PTCLGGSPAAERPADLPPAAALPQPEVILLDSDLDEPIDLR.
	PC2 CBX4		<u>=</u>				R.SIS*T*PTCLGGSPAAERPADLPPAAALPQPEVILLDSDLDEPIDLR.
	PC2 CBX4	\$434T435			-0.8	12.7	R.SISTPT*CLGGS*PAAERPADLPPAAALPQPEVILLDSDLDEPIDLR.
		T437S442		-	0.3	26.4	
PC4 and SFRS1 interacting		T272S273S275			16.8	95.9	K.TGVTST*S*DS*EEEGDDQEGEK.K
PC4 and SFRS1 interacting		S177			10.9	50.3	K.QVETEEAGVVTTATASVNLKV6*PK.R
PC4 and SFRS1 interacting	protein 1 PSIP1	S106			16.9	96.5	K.QSNASS*DVEVEEK.E
PC4 and SFRS1 interacting	protein 1 PSIP1	S273S275			22.9	105.8	K.TGVTSTS*DS*EEEGDDQEGEK.K
PC4 and SFRS1 interacting	protein 1 PSIP1	T272S275			17.3	75.4	K.TGVTST*SDS*EEEGDDQEGEK.K
	PSIP1	T272S273		•	9.9	125.6	K.TGVTST*S*DSEEEGDDQEGEK.K
PC4 and SFRS1 interacting	protein 1 PSIP1	T270S275		• •	6.7	26.3	K.TGVT*STSDS*EEEGDDQEGEK.K
PC4 and SFRS1 interacting	protein 1 PSIP1	T270S271			13.9	13.6	K.TGVT*S*TSDSEEEGDDQEGEK.K
PC4 and SFRS1 interacting	protein 1 PSIP1	S118S129	_		7.0	17.0	K.ETSVS*KEDTDHEEKAS*NEDVTK.A
PC4 and SFRS1 interacting		S271S275	=		3.5	31.9	K.TGVTS*TSDS*EEEGDDQEGEKKR.K
PC4 and SFRS1 interacting			-				
		S271T272			7.5	42.0	K.TGVTS*T*SDSEEEGDDQEGEK.K
PC4 and SFRS1 interacting		S271T272S273	-		7.7	52.6	K.TGVTS*T*S*DSEEEGDDQEGEK.K
PC4 and SFRS1 interacting	protein 1 PSIP1	S271T272S275	-		9.8	44.7	K.TGVTS*T*SDS*EEEGDDQEGEK.K
PCTAIRE protein	kinase 1 <sub>CDK16</sub>	S119	•		100.0	43.7	K.RLS*LPADIR.I
PCTAIRE protein	kinase 1 <sub>CDK16</sub>	S153	-		32.3	44.9	R.RVS*LSEIGFGK.L
PCTAIRE protein	kinase 2 <sub>CDK17</sub>	<b>S</b> 9			19.8	30.6	R.RLS*LTLR.G
PCTAIRE protein	kinase 2 <sub>CDK17</sub>	S180			40.2	58.8	R.RAS*LSEIGFGK.M
PCTAIRE protein	kinase 2 <sub>CDK17</sub>	S182			10.9	33.4	R.RASLS*EIGFGK.M
PCTAIRE protein	kinases 3 <sub>CDK18</sub>	S132			38.2	61.1	R.RAS*LSDIGFGK.L
PCTAIRE protein	kinases 3 CDK18	S98			100.0	48.1	K.RLS*LPMDIR.L
PCTAIRE protein		S14				37.7	R.RFS*LSVPR.T
				•	19.8		
	PDAP1	\$60\$63			45.3	83.5	K.KSLDS*DES*EDEEDDYQQK.R
PDGF alpha associated		S63			0.7	32.9	K.SLDSDES*EDEEDDYQQK.R
PDGF alpha associated	protein 1 PDAP1	<b>S</b> 60			23.6	44.0	K.SLDS*DESEDEEDDYQQK.R
PDGF alpha associated	protein 1 PDAP1	S57S60			8.3	20.6	K.KS*LDS*DESEDEEDDYQQKR.K
PDGF alpha associated	protein 1 PDAP1	S57S63			6.8	40.3	K.KS*LDSDES*EDEEDDYQQK.R
PDZ and LIM	domain 5 PDLIM5	<b>S</b> 360			24.0	33.0	K.S*PSWQRPNQGVPSTGR.I
PDZ bindi	ng kinase PBK	S23S32			25.1	30.8	K.SVLCS*TPTINIPAS*PFMQK.L
PDZ bindi	ng kinase PBK	T26S32			13.9	13.8	K.SVLCSTPT*INIPAS*PFMQK.L
PDZ bindi	ng kinase PBK	T24S32	=		17.9	19.3	K.SVLCST*PTINIPAS*PFMQK.L
	PEPP2 PLEKHA5		-		65.4	27.2	R.S*AVEQLCLAESTRPR.M
	PEPP2 PLEKHA5			•			R.AKSPT*PESSTIASYVTLR.K
					5.0	64.3	
	PLEKHA5				28.9	76.3	R.TNS*M#QQLEQWIK.I
	PEPP2 PLEKHA5				100.0	60.1	K.IVNVS*LADLR.G
	PEPP2 PLEKHA5				9.6	23.8	K.LNSLPSEYES*GSACPAQTVHYRPINLSSSENK.I
	PEPP2 PLEKHA5	S855		•	10.1	55.5	K.S*PTPESSTIASYVTLR.K
	PEPP2 PLEKHA5	S933		•	15.5	35.5	K.GLNVIGASDQS*PLQSPSNLR.D
	PEPP2 PLEKHA5	T408			9.2	67.4	R.T*NSMQQLEQWIK.I
	PEPP2 PLEKHA5	<b>S</b> 372		•	4.7	18.5	K.LNSLPSEYESGSACPAQTVHYRPINLS*SSENK.I
	PEPP2 PLEKHA5	Y366				14.3	K.LNSLPSEYESGSACPAQTVHY*RPINLSSSENK.I
	PEPP2 PLEKHA5	S861			0.8	15.2	R.AKSPTPESS*TIASYVTLR.K
	PEPP2 PLEKHA5				6.4	48.8	K.S*EPELTTVAEVDESNGEEK.S
Peptidyl prolyl iso		S356T358		-	100.0	53.6	R.S'ET'PPHWRQ
Peptidyl prolyl iso							R.NVS*ES*PNRK.N
reptiayi proiyl iso		\$413\$415			100.0	30.5	
	PPIG	S290			100.0	26.9	R.KS*PPKADEK.E
Peptidyl prolyl iso		S687	<u></u>		27.6	29.8	K.ADRDQS*PFSK.I
Peptidyl prolyl iso	merase G PPIG	S744S745T748			100.0	18.8	K.FDHES*S*PGT*DEDKS*G
Peptidyl prolyl iso	merase G PPIG	S587			30.0	21.7	R.S*KEYHR.Y
Peptidyl prolyl iso	merase G PPIG	S254S256S257			69.1	44.6	K.S*AS*S*ES*EAENLEAQPQSTVRPEEIPPIPENR.F
Peptidyl prolyl iso	merase G PPIG	S546		• •	37.5	25.2	R.S'RECDITK.G

<-10 0 abund		compared to	the			
.5 25 timepo .3 42 PSM	int with the minimum					
5 >100 >100 >100			RajiB E E E		MOWSE	Sequence
Protein Name Gene Peptidyl prolyl isomerase G PPIG	Phosphosites S415	5 2 0	0 4 5	13.4	15.5	R.NVSES*PNRK.N
Peptidyl prolyl isomerase like 4 pp <sub>IL4</sub>	S178			11.3	40.0	R.INHTVILDDPFDDPPDLLIPDRS*PEPTR.E
Peptidyl prolyl isomerase like 4 ppiL4	T182	•		-0.1	22.1	R.INHTVILDDPFDDPPDLLIPDRSPEPT*R.E
Pericentrin 2 PCNT  Pericentriolar material 1 PCM1	\$2177 \$65			91.9	16.6	K.NWDSLIPDEMPDS*PIQEK.S  R.VTNDIS*PESSPGVGR.R
Pericentriolar material 1 PCM1	S1958			100.0	95.3	K.S*DEEDFVK.V
Pericentriolar material 1 PCM1	T531Y536S538	≕		5.0	81.0	R.KDEET*EESEY*DS*EHENSEPVTNIR.N
Pericentriolar material 1 PCM1	S1765S1768			32.8	50.9	K.NVRS*DIS*DQEEDEESEGCPVSINLSK.A
Pericentriolar material 1 PCM1	S1765S1768S1			53.3	44.5	K.NVRS*DIS*DQEEDEES*EGCPVSINLSK.A
Pericentriolar material 1 PCM1	S1257S1260S1	-		52.3	48.6	R.RQFDEES*LES*FS*SMPDPVDPTTVTK.T
Pericentriolar material 1 PCM1	\$1257\$1260\$1			7.2	18.1	R.QFDEES*LES*FSS*MPDPVDPTTVTK.T
Pericentriolar material 1 PCM1  Pericentriolar material 1 PCM1	\$1485\$1494				83.4	K.IS*EQNDADNAS*VLSVSSNFEPFATDDLGNTVIHLDQALAR.M  R.RQFDEES*LESFS*S*MPDPVDPTTVTK.T
Pericentriolar material 1 PCM1	\$1257\$1262\$1 T531\$534\$538			5.0	50.4	R.KDEET*EES*EYDS*EHENSEPVTNIR.N
Pericentriolar material 1 PCM1	\$1494\$1497\$1			15.8 8.2	70.4 59.3	K.ISEQNDADNAS*VLS*VS*SNFEPFATDDLGNTVIHLDQALAR.M
Pericentriolar material 1 PCM1	S65S69			22.4	28.5	R.VTNDIS*PESS*PGVGR.R
Pericentriolar material 1 PCM1	S65S68S69			35.3	53.0	R.VTNDIS*PES*S*PGVGR.R
Pericentriolar material 1 PCM1	T531S534Y536			5.9	17.6	R.KDEET*EES*EY*DSEHENS*EPVTNIR.N
Pericentriolar material 1 PCM1	S777S780			15.8	16.2	K.IQALQTACPDLQLS*AAS*VGNCPTKK.Y
Pericentriolar material 1 PCM1	T1481S1485S1				20.9	R. ET*UKIQ*EONIDADNIAQ*V/I Q*V/QQNEEDEATRDI QNTVIIUI DOALAD
Pericentriolar material 1 PCM1	S862S867	-		19.7	41.8	R.RQGLAETAS*PVAVS*LR.S
Pericentriolar material 1 PCM1	\$534Y536\$538	-		-2.4	16.1	R.KDEETEES*EY*DS*EHENS*EPVTNIR.N
Pericentriolar material 1 PCM1  Pericentriolar material 1 PCM1	\$1494\$1499 \$65\$68			0.3	29.7	K.ISEQNDADNAS*VLSVS*SNFEPFATDDLGNTVIHLDQALAR.M  R.VTNDIS*PES*SPGVGR.R
Pericentriolar material 1 PCM1	T531S534Y536			7.8	38.7 61.7	K.DEET*EES*EY*DSEHENSEPVTNIR.N
Pericentriolar material 1 PCM1	T860S867			26.9	27.5	R.RQGLAET*ASPVAVS*LR.S
Pericentriolar material 1 PCM1	\$1485\$1494\$1			2.5	33.8	R.
Pericentriolar material 1 PCM1	S1485S1494S1				60.1	K.IS*EQNDADNAS*VLS*VSSNFEPFATDDLGNTVIHLDQALAR.M
Pericentriolar material 1 PCM1	S1497S1499		<b>—</b>	2.2	61.4	K.ISEQNDADNASVLS"VS"SNFEPFATDDLGNTVIHLDQALAR.M
Pericentriolar material 1 PCM1	S534Y536S538			8.9	50.7	K.DEETEES'EY'DS'EHENSEPVTNIR.N
Pericentriolar material 1 PCM1	S1185S1187S11			12.4	15.9	K.TEYMAFPKPFES*SS*S*IGAEKPR.N
Pericentriolar material 1 PCM1  Periodic tryptophan protein 1 homolog PWP1	S1260S1262S1			0.5	18.9	R.QFDEESLES*FS*S*MPDPVDPTTVTK.T  K.EKLQEEGGGS*DEEETGSPSEDGMQSAR.T
Periodic tryptophan protein 1 homolog pWP1	\$50 \$50\$57			<b>42.7</b> <b>8.7</b>	60.9	K.EKLQEEGGGS*DEEE1GSPSEDGMQSAR.1  K.EKLQEEGGGS*DEEETGS*PSEDGMQSAR.1
Periodic tryptophan protein 1 homolog PWP1	S50T55	==		5.4	34.5	K.EKLQEEGGGS*DEEET*GSPSEDGMQSAR.T
Periphilin 1 PPHLN	1 <b>S</b> 133			49.5	32.1	R.DNTFFRES*PVGR.K
Periphilin 1 PPHLN	1 T204			36.0	101.6	R.DT*SPSSGSAVSSSK.V
Periphilin 1 PPHLN	1 <b>S</b> 205			30.2	100.0	R.DTS*PSSGSAVSSSK.V
Periphilin 1 PPHLN		-		2.1	35.6	R.DNT*FFRESPVGR.K
Peroxisomal acyl-coenzyme A oxidase 1 ACOX1	S217			-0.2	14.3	R.SS'FSTVLL
Pescadillo homolog 1 PES1	S457S488			100.0	56.5	R.  GENDONI MEC*EEEEEENNMEGNONEEGEMEEEEENAEAGC*EV
PEST containing nuclear protein PCNP  PEST containing nuclear protein PCNP	S108		•	15.1	66.1	K.TLS*VAAAFNEDEDSEPEEMPPEAK.M  K.TLSVAAAFNEDEDS*EPEEM#PPEAK.M
PEST containing nuclear protein PCNP	S119 T106			29.2	13.9	K.T*LSVAAAFNEDEDSEPEEMPPEAK.M
PH domain containing protein PLEKH				15.3	56.3	K.VLGSEPAPVS*AETLLSQAVEQLR.Q
PHC2 polyhomeotic homolog 2 <sub>PHC2</sub>	T619S621			9.3	52.8	K.LPQQDHTTTT*DS*EMEEPYLQESK.E
PHD finger protein 10 PHF10	<b>S</b> 56	诫		14.7	68.2	R.S*CETSSQDLGFSYYPAENLIEYK.W
PHD finger protein 10 PHF10	\$50\$53			15.3	24.9	R.MGS*GDS*SR.S
PHD finger protein 14 PHF14	S208			39.4	90.7	R.NRPLLDFVSMEELNDMDDYDS*EDDNDWRPTVVK.R
PHD finger protein 14 PHF14	\$25\$26\$29	•		3.7	13.5	R.RQVKPLAASLLEALDYDS*S*DDS*DFK.V
PHD finger protein 14 PHF14	Y23S25S29			49.3	21.4	R.RQVKPLAASLLEALDY*DS*SDDS*DFK.V
PHD finger protein 14 PHF14  PHD finger protein 14 PHF14	Y23S26S29 S25S26			7.7	14.8	R.QVKPLAASLLEALDY*DSS*DDS*DFK.V  R.QVKPLAASLLEALDYDS*S*DDSDFK.V
PHD finger protein 14 PHF14	\$25\$26 \$25\$29			7.1	27.7	R.QVKPLAASLLEALDYDS*SDDS*DFK.V
PHD finger protein 14 PHF14	Y23S25S26			56.0	36.4	R.RQVKPLAASLLEALDY*DS*S*DDSDFK.V
PHD finger protein 14 PHF14	Y206			2.4	34.8	R.NRPLLDFVSMEELNDMDD Y*DSEDDNDWRPTVVK.R
PHD finger protein 14 PHF14	S835	ij		100.0	32.2	R.S'FVPEEEKHEER.V
PHD finger protein 14 PHF14	T287S290			18.5	75.7	R.NSADDEELT"NDS"LTLSQSK.S
PHD finger protein 14 PHF14	T217	-		7.0	16.9	R.NRPLLDFVSMEELNDMDDYDSEDDNDWRPT*VVK.R
PHD finger protein 2 PHF2	T541			2.8	64.5	R.ESASPT*IPNLDLLEAHTK.E
PHD finger protein 2 <sub>PHF2</sub> PHD finger protein 2 <sub>PHF2</sub>	S879			16.4	23.8	K.DSDYVYPS*LESDEDNPIFK.S
	<b>S</b> 537	-		3.8	64.3	R.ES*ASPTIPNLDLLEAHTK.E

Peak Area	%CV	abundance	ts-Significant cha e at 5%FDR o with the minimum	ompared to	the			
-5 -3 0	42 71 86	PSM	with the minimum		RajiB			
>10	Protein Name PHD finger protein 2		Phosphosites		# # #		MOWSE	Sequence
	PHD finger protein 2		\$882 \$539			12.9	52.6 75.1	K.DSDYVYPSLES*DEDNPIFK.S  R.ESAS*PTIPNLDLLEAHTK.E
	PHD finger protein 3		S682	==		10.9	80.9	K.SFS*LDEPPLFIPDNIATIR.R
	PHD finger protein 3	PHF3	S680			17.0	65.4	K.S*FSLDEPPLFIPDNIATIR.R
	PHD finger protein 3	PHF3	\$680\$682			11.2	34.0	R.SSKS*FS*LDEPPLFIPDNIATIR.R
	PHD finger protein 3	PHF3	S678S680	<u> </u>		4.8	21.6	R.RSS*KS*FSLDEPPLFIPDNIATIR.R
	PHD finger protein 6		S145S154			27.6	36.0	K.TAHNSEADLEES*FNEHELEPS*SPK.S
	PHD finger protein 6		S154			61.4	48.0	K.TAHNSEADLEESFNEHELEPS*SPK.S
	PHD finger protein 6 PHD finger protein 6		\$146\$155			33.8	30.9	K.TAHNSEAADLEES*FNEHELEPS*SPK.S  K.TAHNSEAADLEESFNEHELEPS*SPK.S
	PHD finger protein 6		\$155 \$145\$155			16.9	41.3	K.TAHNSEADLEES*FNEHELEPS*PK.S
	PHD finger protein 6		S199S203			22.2	20.2	R.S*PHRS*SPSDTRPK.C
	PHD finger protein 6	PHF6	S138S154			39.6	14.7	K.TAHNS*EADLEESFNEHELEPS*SPK.S
	PHD finger protein 6	PHF6	S199S204			11.4	17.9	R.S*PHRSS*PSDTRPK.C
	Phosducin like	PDCL	S296			39.4	28.8	R.NSATCHSEDS*DLEID
	Phosducin like		Y16Y17S19S25			11.8	20.3	K.LQYY"Y"SS"SEDEDS"DHEDKDR.G
	Phosducin like		S293S296	<u></u>		21.8	37.0	R.NSATCHS*EDS*DLEID
	Phosducin like		T290S296			17.2	12.8	R.NSAT*CHSEDS*DLEID
	Phosducin like		Y16Y17S18S19 Y17S18S19S25			5.5	19.6	K.LQYYYYS'S'SEDEDSDHEDKDR.G  K.LQYYYYS'S'SEDEDS'DHEDKDR.G
Phosophatidylino	ositol 3 kinase, class 2		S338			33.6	46.6	R.SQS*LNIR.T
Phosphata	alpha se and actin regulator	PHACTR2	<b>S</b> 70				22.8	R.VHIS*GSVDGLDK.A
Phosphatase	and actin regulator 4	PHACTR4	<b>S</b> 127			-0.3	54.3	R.SS*SPVQVEEEPVR.L
Phosphatase	e and actin regulator 4	PHACTR4	S638			31.2	48.3	R.KLS*QRPTVAELLAR.K
	e and actin regulator 4					61.5	59.2	R.S*LPITIEMLK.V
	e and actin regulator 4					22.2	14.3	R.SPS*PPLPTHIPPEPPRT*PPFPAK.T
	e and actin regulator 4 e and actin regulator 4			•••		32.4	37.4	R.IQQALT SPLPMT PILEGSHR.A  R.SSS*PVQVEEEPVR.L
	e and actin regulator 4				-	10.2	18.4	R IOOAI T'S'PI PMTPII EGSHR A
	Itransferase 1 choline		\$343\$347	•		5.0	14.0	K.TS*PPCS*PANLSR.H
	alpha isoform dtransferase 1 choline alpha isoform		<b>S</b> 315		-	100.0	14.3	R.MLQAIS*PK.Q
Phosphate cytidyly	Itransferase 1 choline alpha isoform	PCYT1A	S362		•	31.9	41.4	K.AAAYDIS*EDEED
	Itransferase 1 choline alpha isoform		S329S331			22.7	15.9	R.ERS'PS'PSFR.W
	ltransferase 1 choline alpha isoform		S319S321			10.0	12.4	K.QS*PS*SSPTR.E
	Itransferase 1 choline, beta		S335		<u> </u>	10.6	66.3	R.SPS*PTFSWLPLK.T
phosph	inositol 3 phosphate 3 atase adaptor subunit 3-kinase, regulatory 4		S716			20.0	62.4	R.HSS*KPVLPTSGWK.A  R.SESSAGICVPLS*TSSQVPEVTTVQNK.K
	4 kinase catalytic beta		\$903 \$440			-1.5 92.3	37.9 56.6	R.S*VENLPECGITHEQRA
	polypeptide 4 kinase catalytic beta		S523			37.4	19.6	R.RLS*EQLAHTPTAFK.R
Phosphatidylir	polypeptide nositol 4 kinase type II	PI4K2A	<b>\$4</b> 62	•		11.7	69.5	R.SSS'ESYTQSFQSR.K
Phosphatidylin	nositol 4 kinase type II	PI4K2A	S47S51			12.9	34.0	R.VAAAAGSGPS*PPGS*PGHDR.E
Phosphatidyli	nositol 4-kinase alpha	PI4KA	S172	-		100.0	24.6	R.S*FNDFR.S
	l transfer protein, beta		S262			100.0	14.6	R.KRGS*VR.G
	ositol transfer protein, cvtoplasmic 1		<b>S</b> 270			5.1	26.6	R.S*APSSAPSTPLSTDAPEFLSVPK.D
	ositol transfer protein, cvtoplasmic 1 hosphatidylinositol-3-		S274			8.0	49.2	R.SAPSS*APSTPLSTDAPEFLSVPK.D  R.SPT*S*PSHLTHFKPLTPDODEPPFK.S
phosphate/phosph	atidylinositol 5-kinase hosphatidylinositol-3-		T22S23 S307			18.9	44.0 56.6	R.SAS*ITNLSLDR.S
phosphate/phosph P	atidylinositol 5-kinase hosphatidylinositol-3-					6.4	45.1	R.S'PTSPS"HLTHFKPLTPDQDEPPFK.S
phosphate/phosph	atidvlinositol 5-kinase -4-phosphate 5-kinase type II beta		T322S326			50.5	63.0	R.AEDEECENDGVGGNLLCSYGT*PPDS*PGNLLSFPR.F
Phosphatidylinositol	-4-phosphate 5-kinase type II beta	PIP4K2B	Y320			6.6	49.9	R.AEDEECENDGVGGNLLCSY*GTPPDSPGNLLSFPR.F
Phosphatidylinositol	-4-phosphate 5-kinase tvoe II beta	PIP4K2B	\$319\$326			22.3	28.8	R.AEDEECENDGVGGNLLCS*YGTPPDS*PGNLLSFPR.F
	-4-phosphate 5-kinase tvpe II beta		Y320S326			20.2	17.1	R.AEDEECENDGVGGNLLCSY*GTPPDS*PGNLLSFPR.F
	4-phosphate 5-kinase type II beta		T322			2.2	53.0	R.AEDEECENDGVGGNLLCSYGT*PPDSPGNLLSFPR.F
	tidylserine synthase 1		\$417			28.6	61.1	K.TYS'ECEDGTYSPEISWHHR.K  K.TY'SECEDGTYSPEISWHHR.K
	tidylserine synthase 1		Y416 T423			-0.5	10.9	K.TYSECEDGT'YSPEISWHHR.K
	Phosphodiesterase 7A		Y61	-		19.7	34.5	R.RGSHPY*IDFR.I
	hosphofructokinase 1		S775			100.0	19.0	R.KRS*GEAAV
		PFKP	S386			89.8	73.8	R.S'FAGNLNTYKR.L
Phosphofurin acidic	cluster sorting protein 1	PACS1	<b>S</b> 779		•••	29.0	29.0	K.VGLVEDSPSTAGDGDDSPVVSLTVF6*TSPPSSSGLSR.D
	cluster sorting protein 1		<b>S</b> 379			19.3	78.8	R.EVEEDLDELYDSLEMYNPS*DSGPEMEETESILSTPKPK.L
Phosphofurin acidic	cluster sorting protein 1	PACS1	\$379\$381			42.7	84.6	R.EVEEDLDELYDSLEMYNPS*DS*GPEMEETESILSTPKPK.

Peak Area	%CV White do	ts-Significant cha	inge in pepti	de the			
<-10 -5 -3		with the minimum					
0 3 5	86 >100		CarT	RajiB			
>10	Protein Name Gene	Phosphosites	8 8 5	5 g g	Ascor	MOWSE	Sequence
Phosphofurin acidic clus	1	S529S531		•••	11.0	45.2	R.TNSS'DS'ERSPDLGHSTQIPR.K
Phosphofurin acidic clus	1	Y370S372				50.0	R.EVEEDLDELY*DS*LEMYNPSDSGPEMEETESILSTPKPK.L
Phosphofurin acidic clus	1	S410		•	6.8	12.6	K.LKPFFEGMSQSS*SQTEIGSLNSK.G
Phosphofurin acidic clus	1	S781		-	9.0	35.5	K.VGLVEDSPSTAGDGDDSPVVSLTVPSTS*PPSSSGLSR.D
Phosphofurin acidic clus	1	S529S534		•	3.1	45.2	R.TNSS'DSERS'PDLGHSTQIPR.K
	phoglucomutase 1 PGM1	S117			6.1	68.0	K.AIGGIILTAS*HNPGGPNGDFGIK.F
	phoglucomutase 1 PGM1	T115				76.2	K.AIGGIILT*ASHNPGGPNGDFGIK.F
	ucomutase 2 like 1 PGM2L1	T173			10.9	61.8	K.AVAGVMIT*ASHNR.K
	ucomutase 2 like 1 PGM2L1	S175			6.7	39.0	K.AVAGVMITAS*HNR.K
	phoglucomutase 3 PGM3	T62			9.1	118.8	K.STIGVMVT*ASHNPEEDNGVK.L
	phoglucomutase 3 PGM3	S64			13.0	119.7	K.STIGVMVTAS*HNPEEDNGVK.L
	glycerate kinase 1 PGK1	S203			100.0	71.2	K.ALES*PERPFLAILGGAK.V
	lycerate mutase 1 PGAM1	S14			100.0	67.3	R.HGES*AWNLENR.F
	llycerate mutase 1 PGAM1	S23		• • •	45.2	57.0	R.FS*GWYDADLSPAGHEEAK.R
	lycerate mutase 1 PGAM1	Y119			-0.2	47.8	R.SY*DVPPPPMEPDHPFYSNISK.D
	se adaptor protein PIK3AP1 1	<b>S</b> 759		•••	19.6	25.0	R.SRS*PGPPQVDGTPTMSLERPPR.V
Phosphoinositide 3 kinas	se adaptor protein PIK3AP1 1	S757			16.5	20.7	R.S*RSPGPPQVDGTPTMSLERPPR.V
	AGAP2	S312	-		13.9	23.2	R.RTS*LFANR.R
	3 kinase enhancer AGAP2	Y272S278			6.3	14.8	K.SLPSSPSHSAASTPVAGQASNGGHTSDY*SSSLPS*SPNVGHR.E
	3 kinase enhancer AGAP2	S245S248				18.5	K.S*LPS*SPSHSAASTPVAGQASNGGHTSDYSSSLPSSPNVGHR.E
	3 kinase enhancer AGAP2	T311			8.2	39.1	K.RRT*SLFANR.R
	3 kinase enhancer AGAP2	T269S279	-		8.2	11.7	K.SLPSSPSHSAASTPVAGQASNGGHT*SDYSSSLPSS*PNVGHR.E
	3 kinase enhancer AGAP2	S274S279	-		7.1	15.2	K.SLPSSPSHSAASTPVAGQASNGGHTSDYSS*SLPSS*PNVGHR.E
	pholipase C like 1 PLCL1	S762S764			100.0	20.8	K.RS*LS*VR.M
	holipase C, beta 3 PLCB3	<b>S</b> 537			100.0	13.9	K.S*LGDEGLNR.G
	lipase C, gamma 1 PLCG1	Y783			158.2	71.6	R.NPGFY*VEANPMPTFK.C
Phosphol	lipase C, gamma 1 PLCG1	Y775Y783			59.8	41.9	K.IGTAEPDYGALY*EGRNPGFY*VEANPMPTFK.C
	PLCG1	S1248	÷		9.8	21.0	R.AREGS*FESR.Y
	lipase C, gamma 1 PLCG1	Y771Y775Y783			48.0	15.4	K.IGTAEPDY*GALY*EGRNPGFY*VEANPMPTFK.C
Phosphoribosylfor	rmylglycinamidine PFAS synthase	<b>S</b> 569			93.9	35.3	R.S*PNRDFLTHVSAR.E
Phosphorybos	sylaminoimidazole PAICS carboxylase	S27		• •	112.3	58.9	K.TKEVYELLDS*PGK.V
Phosphoryla	ase B kinase, beta PHKB	S700S701			4.3	46.0	K.RQS*S*TPSAPELGQQPDVNISEWK.D
Phosphorylase kinase liv	er alpha 2 subunit PHKA2	T1041S1044			3.4	24.2	R.SST*PSS*PTGTSSSDSGGHHIGWGER.Q
Phosphorylase kinase liv	er alpha 2 subunit <sub>PHKA2</sub>	T1041S1043		•	6.0	11.4	R.SST*PS*SPTGTSSSDSGGHHIGWGER.Q
Phosphorylated CTD in	nteracting factor 1 PCIF1	S144			12.1	27.0	K.IEIPVTPTGQSVPSS*PSIPGTPTLK.M
Phosphorylated CTD in	nteracting factor 1 PCIF1	T137S144			5.5	10.8	K.IEIPVTPT*GQSVPSS*PSIPGTPTLK.M
Phosphorylated CTD is	nteracting factor 1 PCIF1	S144T150			13.1	12.1	K.IEIPVTPTGQSVPSS*PSIPGT*PTLK.M
Phosphorylated CTD in	nteracting factor 1 PCIF1	S140S144			6.2	21.5	K.IEIPVTPTGQS*VPSS*PSIPGTPTLK.M
Phosphorylated CTD is	nteracting factor 1 PCIF1	T137S143			6.5	19.6	K.IEIPVTPT*GQSVPS*SPSIPGTPTLK.M
Phosphorylated CTD is	nteracting factor 1 PCIF1	S143T150	Ļ		9.5	11.6	K.IEIPVTPTGQSVPS*SPSIPGT*PTLK.M
Phosphorylated CTD is	nteracting factor 1 PCIF1	S143S146			8.4	11.0	K.IEIPVTPTGQSVPS*SPS*IPGTPTLK.M
PI3 kinase rel	ated kinase SMG1 SMG1	T3569S3570		-	26.2	22.7	K.NLAT*S*ADTPPSTVPGTGK.S
	Pinin PNN	S347			100.0	55.5	K.EIAIVHS*DAEK.E
	Pinin PNN	<b>S</b> 99			122.4	67.1	R.QES*DPEDDDVKKPALQSSVVATSK.E
	Pinin PNN	S442			18.6	81.4	K.SLS*PGKENVSALDMEK.E
	Pinin PNN	S718S720			27.7	36.1	R.SIS*ES*SR.S
	Pinin PNN	S684	-		15.8	19.6	R.DTS*GLER.S
	Pinin PNN	S720S721			8.0	16.9	R.SISES*S*R.S
	Pinin PNN	<b>S</b> 380			34.9	80.4	R.ESEKQQDS*QPEEVMDVLEMVENVK.H
	Pinin <sub>PNN</sub>	S718S721			16.4	28.0	R.SIS*ESS*R.S
	Pinin PNN	\$440\$442			30.5	10.8	K.S*LS*PGKENVSALDMEK.E
	Pinin PNN	<b>S</b> 449			-18.5	30.9	K.SLSPGKENVS*ALDMEK.E
	Pinin PNN	S716S718			7.6	16.3	R.S*IS*ESSR.S
	PKD1like KIAA0319	- \$998\$1003\$10	•		6.4	28.8	K.GLLLSS*SLMHS*ES*ELDSDDAIFTWPDR.E
	PKD1like KIAA0319	- \$998\$1003\$10			8.8	16.2	K.GLLLSS*SLM#HS*ESELDS*DDAIFTWPDR.E
PKF	R protein activator PRKRA	S18		•	39.3	75.2	R.EDS*GTFSLGK.M
Plasma membrane Ca(	2+) ATPase type 4 ATP2B4	S328			47.3	41.5	K.TQDGVALEIQPLNS*QEGIDNEEK.D
Plasma membrane Ca(	2+) ATPase type 4 ATP2B4	T1145	•		100.0	65.0	R.T*PLLDEEEEENPDK.A
Plasma membrane Ca(2	2+) ATPase, type 1 ATP2B1	S1140	•••	•	9.6	59.6	R.SS'IHNFMTHPEFR.I
Plasma pro	tease C1 inhibitor SERPING	1 <sub>T47</sub>				13.3	K.VAT*TVISK.M
Platelet-activati	ng factor receptor PTAFR	<b>S</b> 339			50.2	22.3	R.ATTDTVTEVVVPFNQIPGNS*LKN
	PLC, gamma 2 PLCG2	S677			32.1	50.6	R.EGS*DSYAITFR.A
•							

Peak Area <-10 -5 -3 0 3	o abunda	lots-Significant cha nce at 5%FDR on t with the minimum	compared to peak area f	the			
>10	Protein Name Gene	Phosphosites	£ 5 5	8 £ £	Ascor	MOWSE	Sequence
	Pleckstrin PLEK	\$199T204 \$222\$231		•••	5.3	41.0 32.6	K.S'AVDGT'AENPFLDNPDAFYYFPDSGFFCEENSSDDDVILK.E  K.SAVDGTAENPFLDNPDAFYYFPDS'GFFCEENSS'DDDVILK.E
	Pleckstrin <sub>PLEK</sub>	\$230\$231		=	4.8	27.0	K.SAVDGTAENPFLDNPDAFYYFPDSGFFCEENS'S'DDDVILK.E
	Pleckstrin PLEK	\$222\$230		=	4.8	11.1	K.SAVDGTAENPFLDNPDAFYYFPDS*GFFCEENS*SDDDVILK.E
Pleckstrin and Sec7 do	omain containing 4 PSD4	S118			11.5	46.4	R.QDAPPWGSGVELTHLGS*PSAQR.E
Pleckstrin and Sec7 do	omain containing 4 PSD4	T114			17.8	21.5	R.QDAPPWGSGVELT*HLGSPSAQR.E
Pleckstrin and Sec7 do	omain containing 4 PSD4	\$461\$464\$465			41.7	10.7	R.GPGPRPS*PAS*S*QEGS*PQLQHHSSGILPK.W
Pleckstrin homology of family F (with FYVE	domain containing, PLEKHF domain) member 2	2 \$239\$248			36.6	100.6	K.SPLNDMS*DDDDDDDSS*D
Pleckstrin homology of family F (with FYVE	domain containing, PLEKHF domain) member 2	2 \$239\$247 <b>\$</b> 248	•		81.6	107.8	K.SPLNDMS*DDDDDDDS*S*D
family F (with FYVE			÷		23.9	38.2	R.SDS*YSQSLK.S
family F (with FYVE	domain containing, PLEKHF domain) member 2 domain containing, PLEKHN				46.6	50.7	K.SPLNDMS*DDDDDDS*SD  R.TGS*PGDAPERPPLCDFSEGLSAPMDFYRF
family M (with RUN	domain) member 2 domain containing, PLEKHN		_		3.0	29.2	R.T'GSPGDAPERPPLODFSEGLSAPMDFTR.F
family M (with RUN	domain interacting PHIP	S1783	•		10.1	55.4 87.4	R.TAFYNEDDS*EEEQR.Q
	protein domain interacting PHIP	S911	==		100.0	45.6	K.DGPIS*PK.K
Pleckstrin homology	protein  domain interacting PHIP	S674			8.9	55.8	R.GS*ISSTSEVHSPPNVGLR.R
	protein	S1315			16.9	12.6	R.AQS"YDIQAWKK.Q
Pleckstrin homology	domain-containing PLEKHA family A member 2	2 <b>S1</b> 34	<u> </u>		15.1	20.7	R.SQS*YIPTSQCR.A
Pleckstrin homology	domain-containing PLEKHA family A member 2	2 <b>S</b> 351	•••		100.0	20.9	R.S*EPQHPK.E
Pleckstrin homology	domain-containing PLEKHA family A member 2	2 <b>S</b> 299		•	24.3	24.3	K.APS*VASSWQPWTPVPQAGEK.L
Pleckstrin homology	domain-containing PLEKHA family A member 2	2 S132	•		12.3	18.4	R.S'QSYIPTSGCR.A
	Plectin 1 PLEC	T4623			27.6	78.6	K.GYYSPYSVSGSGST*AGSR.T
	Plectin 1 PLEC	\$4626	-		19.1	64.7	K.GYYSPYSVSGSGSTAGS*R.T
	Plectin 1 PLEC	S4386			11.7	79.4	R.SSS*VGSSSSYPISPAVSR.T
	Plectin 1 PLEC	\$4620\$4622 \$21	-		3.7	97.8	K.GYYSPYSVSGS*GS*TAGSR.T  R.TSS*EDNLYLAVLR.A
	Plectin 1 PLEC	S4385			-0.2	82.2	R.SS*SVGSSSSYPISPAVSR.T
	Plectin 1 PLEC	S20			10.8	90.3	R.TS*SEDNLYLAVLR.A
	Plectin 1 PLEC	S4620			9.1	33.6	K.GYYSPYSVSGS'GSTAGSR.T
	Plectin 1 PLEC	S4622			7.8	22.1	K.GYYSPYSVSGSGS*TAGSR.T
	Plectin 1 PLEC	\$4622T4623		• •	1.5	53.5	K.GYYSPYSVSGSGS*T*AGSR.T
	Plectin 1 PLEC	S4618			10.9	29.1	K.GYYSPYSVS*GSGSTAGSR.T
	Plectin 1 PLEC	S4618T4623			0.6	43.7	K.GYYSPYSVS*GSGST*AGSR.T
	PLEKHA7 PLEKHA				8.3	107.4	R.SYVSEPELAT*LSGDMAQPSLGLVGPESR.Y
	PLEKHA7 PLEKHA				4.2	88.5	R.SYVSEPELATLS*GDMAQPSLGLVGPESR.Y
	PLEKHA7 PLEKHA		-		7.1	98.5	R.SYVS'EPELATLSGDMAQPSLGLVGPESR.Y  KAVS'PPHLDGPPS'PR.S
	PMLPML	\$518\$527 \$530			100.0	76.0	R.S'PVIGSEVFLPNSNHVASGAGEAGR.E
	PMLPML	\$530 \$530			108.4	76.0	R.S*PVIGSEVFLPNSNHVASGAGEAEER.V
	PML PML	\$505			-0.3	39.0	R.SS*PEQPRPSTSK.A
	PMLPML	S518S527S530			18.4	20.5	KAVS*PPHLDGPPS*PRS*PVIGSEVFLPNSNHVASGAGEAEER.V
	PMLPML	\$518\$527\$530			12.5	25.2	KAVS*PPHLDGPPS*PRS*PVIGSEVFLPNSNHVASGAGEAGRE
	PML PML	S504			12.4	33.6	R.S'SPEQPRPSTSKA
Poly A	A polymerase alpha PAPOLA	S24	•		23.9	58.0	K.HYGITS'PISLAAPK.E
	e binding protein 2 PABPN1	<b>S</b> 150		-	74.7	36.4	K.QMNMS*PPPGNAGPVIMSIEEK.M
	binding protein 1 PCBP1	S189			29.8	57.9	R.VMTIPYQPMPAS'SPVICAGGQDR.C
	binding protein 1 PCBP1	S262			53.2	42.0	R.QQSHFAMMHGGTGFAGIDS*SSPEVK.G
	b) binding protein 1 PCBP1	S190		•	4.6	68.5	R.VMTIPYQPMPASS*PVICAGGQDR.C
	binding protein 1 PCBP1	Y183 S264			21.2	72.0	R.VMTIPY*OPMPASSPVICAGGODR.C  R.QQSHFAMMHGGTGFAGIDSSS*PEVK.G
	b) binding protein 2 <sub>PCBP2</sub>	S264 S189			9.1	40.1	K.GVTIPYRPKPSSS*PVIFAGGODR.Y
	) binding protein 2 <sub>PCBP2</sub>	Y182			13.1	28.3	K.GVTIPY*RPKPSSSPVIFAGGQDR.Y
Poly(rC	b) binding protein 2 PCBP2	S187			12.2	21.1	K.GVTIPYRPKPS*SSPVIFAGGQDR.Y
Poly(rC	binding protein 2 <sub>PCBP2</sub>	<b>S</b> 270			-1.4	16.0	K.LHQLAMQQSHFPMTHGNTGFSGIES*SSPEVK.G
Poly(rC	b) binding protein 2 PCBP2	<b>S</b> 272			3.6	21.2	K.LHQLAMQQSHFPMTHGNTGFSGIESSS*PEVK.G
Poly(rC	b) binding protein 2 PCBP2	S188			16.9	39.3	K.GVTIPYRPKPSS*SPVIFAGGQDR.Y
Polyco	omb protein SUZ12 SUZ12	<b>S</b> 546			89.9	131.8	K.ASMSEFLES'EDGEVEQQR.T
	omb protein SUZ12 SUZ12	<b>S</b> 539	-		12.2	78.6	K.AS*MSEFLESEDGEVEQOR.T
	omb protein SUZ12 SUZ12	S583			15.5	20.4	R.LYFHSDTCLPLRPQEMEVDS'EDEKDPEWLR.E
	Polyhomeotic like 3 PHC3	<b>S773</b>	-		32.7	22.1	K.HADNS*SDTEMEDMIAEETLEEMDSELLK.C
	Polyhomeotic like 3 PHC3	S774	Ļ		7.8	71.4	K.HADNSS*DTEMEDMIAEETLEEMDSELLK.C
r oryanyosius/scierode	erma autoantigen 1 EXOSCS	S306			25.6	61.8	K.APIDTS'DVEEK.A

Peak Area %CV White do	ts-Significant cha e at 5%FDR c	nge in peption	de the			
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3 86 86 86 810 810 810 810 810 810 810 810 810 810		CarT	_RajiB_			
Protein Name Gene Polymyositis/scleroderma autoantigen 1 EXOSC9	Phosphosites	9 m g	F F E	Ascor	MOWSE	Sequence K.MDTGVEVSDIGSQDAPIILS*DS*EEEEMIILEPDKNPK.K
Polymyositis/scleroderma autoantigen 1 EXOSC9	\$392\$394 \$384\$392		-	11.5	30.5	K.MDTGVEVSDIGS*QDAPIILS*DS*EEEEMIILEPDKNPK.K  K.MDTGVEVSDIGS*QDAPIILS*DSEEEEMIILEPDKNPK.K
Polynucleotide kinase 3 prime phosphatase PNKP				16.9	14.5	
	T118T122			31.4	34.7	R.TPESQPDT*PPGT*PLVSQDEKR.D
Polypyrimidine tract binding protein 1 PTBP1	S141			23.9	54.5	K.TDSS'PNQAR.A
Polypyrimidine tract binding protein 1 PTBP1	S140			16.9	55.8	K.TDS*SPNQAR.A
POM121 membrane glycoprotein-like POM121C  POM121 membrane glycoprotein-like POM121C					15.7	R.RHDS*S*GS*GHSAFEPLVASGVPASFVPKPGSLK.R
POM121 membrane glycoprotein-like POM121C				-0.5	92.6	R.SS*SMSSLTGAYTSGIPSSSR.N  R.RHDSS*GS*GHS*AFEPLVASGVPASFVPKPGSLK.R
POM121 membrane glycoprotein-like POM121C				4.5	24.2	R.SSS*MS*SLTGAYTSGIPSSSR.N
POM121 membrane glycoprotein-like POM121C				13.5	85.7	R.SS*SMS*SLTGAYTSGIPSSSR.N
POM121 membrane glycoprotein-like POM121C				5.9	93.0	R.SS*SMSS*LTGAYTSGIPSSSR.N
POM121 membrane glycoprotein-like POM121C				10.3		R.SS*MSS*LTGAYTSGIPSSSR.N
POM121 membrane glycoprotein-like POM121C				11.8	116.6	R.SSSMS*SLTGAYTSGIPSSSR.N
POM121 membrane glycoprotein-like POM121C		=		7.6	54.9	R.SSS*MSSLTGAYTSGIPSSSR.N
POP1 POP1				9.6	57.8	R.VQAYEEPSVAS*SPNGK.E
Positive cofactor 2 glutamine MED15	S729		=	28.4	20.5	R.TPQNFSVPS*PGPLNT*PVNPSSVMSPAGSSQAEEQQYLDK.L
Positive cofactor 2 glutamine MED15	S505T511		-	9.3	52.7	R.TPQNFSVPS*PGPLNTPVNPSS*VMSPAGSSQAEEQQYLDK.L
	\$505\$517	<del></del>		7.7	27.6	R.S*PVSPLAAQGIPLPAQLTK.S
Potassium channel tetramerisation domain KCTD15 containing 15  Potassium channel tetramerisation domain KCTD15	S35		===	24.0	62.8	
Potassium channel tetramerisation domain KCTD15 containing 15  Potassium channel tetramerisation domain KCTD15	S38			0.3	14.3	R.SPVS*PLAAQGIPLPAQLTK.S  R.S*PVS*PLAAQGIPLPAQLTK.S
containing 15	S35S38		_	43.6	12.8	
Potassium channel, calcium activated, KCNN3 intermediate/small conductance subfamily	S128			57.2	16.8	R.QGS*QLNLNDHLLGHSPSSTATSGPGGGSR.H
Potassium channel, voltage gated, KQT like KCNQ5 subfamily, member 4	S484		_ · <u>=</u>	17.3	18.0	K.SWS*FNDR.T
Potassium channel, voltage gated, KQT like KCNQ5 subfamily, member 4	S482			12.2	17.5	K.S*WSFNDR.T
Potassium voltage gated channel, shaker KCNAB1 related subfamily. beta member 1	S153			7.6	16.0	R.RSS*LVITTK.I
Potassium voltage gated channel, shaker KCNAB1 related subfamilv. beta member 1	S152			39.1	11.6	R.RS*SLVITTK.I
Potassium voltage-gated channel, KQT-like KCNQ5 subfamilv. member 5	S831			2.7	62.8	K.SLS*VQNLIR.S
Potassium voltage-gated channel, KQT-like KCNQ5 subfamily, member 5	S829			9.3	51.0	K.S*LSVQNLIR.S
Pre mRNA cleavage complex II protein PCF11 Pcf11	S705			100.0	52.9	R.S*PFNDRFPLK.R
Pre mRNA cleavage complex II protein PCF11 Pcf11	\$489\$494			29.1	16.6	K.SRS*PIIHS*PK.R
Pre mRNA splicing factor PRP17 CDC40	S46			15.9	100.2	K.SPSS*KPSLAVAVDSAPEVAVK.E
Pre mRNA splicing factor PRP17 CDC40	S43		-	8.4	50.2	K.S*PSSKPSLAVAVDSAPEVAVK.E
Pre mRNA splicing factor PRP17 CDC40	S45		==	11.5	68.8	K.SPS*SKPSLAVAVDSAPEVAVK.E
Pre mRNA splicing factor PRP17 CDC40	S49			8.0	35.0	K.SPSSKPS*LAVAVDSAPEVAVK.E
Pre-B-cell leukemia transcription factor PBXIP1 interacting protein 1	S146S147S148			100.0	13.5	R.EEGRCS'S'S'DDDT'DVDMEGLRR.R
PREDICTED: lateral signaling target protein 2 homolog isoform X5 [Homo sapiens]	S921	<u> </u>		-0.9	16.0	K.SS*ARAAPR.S
PREDICTED: paired box protein Pax-2 isoform X8 [Homo sapiens]	S337				19.1	K.RS"YPR.N
Prefoldin 4 PFDN4	S125	<u> </u>		16.4	36.0	K.FGS*NINLEADES
PRO1770 PELO	\$374\$380\$381			100.0	44.0	R.FPVPELS*DQEGDS*S*S*EED
Probable ATP-dependent RNA helicase DDX27	S23S25			26.3	69.5	M.LADLGLIGTIGEDDEVPVEPES*DS*GDEEEEGPIVLGR.R
Processing of precursor 5, ribonuclease POP5 P/MRP subunit	S154			108.1	112.0	R.SCLLEEEEES*GEEAAEAME
Profilin 1 PFN1	T93			-0.3	72.7	K.ST*GGAPTFNVTVTK.T
Progesterone receptor membrane PGRMC1 component 1		•••		19.8	74.7	K.EGEEPTVYS*DEEEPKDESAR.K
Progesterone receptor membrane PGRMC1 component 1	Y180			5.8	42.5	K.EGEEPTVY*SDEEEPKDESAR.K
Progesterone receptor membrane PGRMC1 component 1	T178				22.2	K.EGEEPT*VYSDEEEPK.D
Progesterone receptor membrane PGRMC2 component 2	S208			15.7	43.0	R.LLKPGEEPS*EYTDEEDTKDHNKQD
Progesterone receptor membrane PGRMC2 component 2			===	12.2	55.5	R.LLKPGEEPSEY*TDEEDTKDHNKQD
Programmed cell death 4 PDCD4	S94			8.2	44.5	R.SGLTVPTS*PK.G
Programmed cell death 4 PDCD4	T93	•		32.3	44.2	R.SGLTVPT*SPK.G
Programmed cell death 4 PDCD4	S457	÷		100.0	23.6	R.FVS*EGDGGR.L
Programmed cell death 5 PDCD5	S119		•••	63.8	53.0	R.KVM#DS*DEDDDY
Programmed cell death 5 PDCD5	Y125			21.6	67.3	R.RKVMDSDEDDDY*
Programmed cell death 8 AIFM1	S266		•	10.5	42.4	R.S'LSAIDR.A
Programmed cell death 8 AIFM1	S268		•	15.1	32.6	R.SLS*AIDR.A
Proline glutamic acid leucine-rich protein 1 PELP1	S481			35.4	70.2	R.GS*PDGSLQTGKPSAPK.K
Proline-rich transmembrane protein 3 PRRT3	S924S928			15.9	35.3	R.HGLS*SVDS*LPLDELPSTVQLLPAPTPAPDSTAAR.Q
Proline-rich transmembrane protein 3 PRRT3	S798S808		-	21.1	18.6	R.NGVGPAPS*LSELDLRPPS*PINLSR.S
Proline-rich transmembrane protein 3 PRRT3	\$925\$928			5.1	38.9	R.HGLSS*VDS*LPLDELPSTVQLLPAPTPAPDSTAAR.Q
Proline-rich transmembrane protein 3 PRRT3	S924S925			7.7	25.6	R.HGLS'S'VDSLPLDELPSTVQLLPAPTPAPDSTAAR.Q
Proline-rich transmembrane protein 3 PRRT3	\$798\$800\$808		-	38.3	13.8	R.NGVGPAPS*LS*ELDLRPPS*PINLSR.S
Proline-rich transmembrane protein 3 PRRT3	S815	-	<b>-</b> .	100.0	37.7	R.S*IDAALFR.E
Proline/serine-rich coiled-coil 1 PSRC1	\$65\$70	<b>—</b>		100.0	17.6	R.LS*LGPLS*PEKLEEILDEANR.L
Proteasome 26S subunit ATPase 4 PSMC4	S19S21T25				28.1	K.AQDEIPALS*VS*RPQT*GLSFLGPEPEDLEDLYSR.Y

Peak Area	o ab	undance	s-Significant cha	ompared to	the			
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	S subunit ATPase 4 PSI		S19T25S28		-	29.6	37.2	KAQDEIPALS*VSRPQT*GLS*FLGPEPEDLEDLYSR.Y  KAQDEIPALSVS*RPQT*GLS*FLGPEPEDLEDLYSR.Y
	S subunit ATPase 4 <sub>PSI</sub>		\$21T25\$28 \$19\$21			13.6	52.8 25.9	KAQDEIPALS*VS*RPQTGLSFLGPEPEDLEDLYSR.Y
	S subunit ATPase 4PS		S19S28			4.7	15.7	K.AQDEIPALS*VSRPQTGLS*FLGPEPEDLEDLYSR.Y
Proteasome 26S sub	unit, non ATPase, 2 <sub>PSI</sub>	MD2	S16			92.8	68.3	R.DKAPVQPQQS*PAAAPGGTDEKPSGK.E
Proteasome si	ubunit alpha type 2 PSI	MA2	<b>S</b> 7			10.8	77.3	R.GYS*FSLTTFSPSGK.L
			S250	ı.		100.0	10.8	K.EEDES'DDDNM
	ABHD11 (Fragment) ABH		S106			44.9	14.6	K.TAM#ILALORIS'AQWKA  R.GAVENEEDLPELS'DS'GDEAAWEDEDDADLPHGK.Q
	ulfide isomerase P5 PDI		\$25\$27 \$428			100.0	86.9	R.DGELPVEDDIDLS*DVELDDLGKDEL-
	Protein FAM117BFAN	M117B	S220		• • •	24.4	88.9	R.TSS*LDTLAAPYLAGHWPR.D
	Protein FAM117BFAN	M117B	S219			-0.4	51.2	R.TS*SLDTLAAPYLAGHWPR.D
	Protein FAM117BFAN					25.1	62.2	R.GSPPRPPPPPLLGT"VSS"PSSSPT"HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN					25.3	52.8	R.GSPPRPPPPPLLGT"VS"SPSSSPT"HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN				•	11.9	17.6	R.GS*PPRPPPPPLLGT*VSSPSSS*PTHLWTGEVSAAPPPAR.V  R.GS*PPRPPPPPPLLGT*VSSPS*SSPTHLWTGEVSAAPPPAR.V
	Protein FAM117BFAN			•		27.1	40.3 26.0	R.GS'PPRPPPPPLIGT'VSSPSSSPT'HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN					34.5	54.9	R.GS*PPRPPPPPLLGTVSSPS*SSPT*HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN	M117B	S136S151S156			27.4	40.6	R.GS'PPRPPPPPLLGTVS"SPSSS'PTHLWTGEVSAAPPPAR.V
	Protein FAM117BFAN	M117B	S151S154			2.6	17.7	R.GSPPRPPPPPLLGTVS*SPS*SSPTHLWTGEVSAAPPPAR.V
	Protein FAM117B <sub>FAM</sub>			ļ.		10.5	22.1	R.GS*PPRPPPPPLLGTVS*SPS*SSPTHLWTGEVSAAPPPAR.V
	Protein FAM117B <sub>FAM</sub>						36.9	R.GS*PPRPPPPPLLGT*VS*SPSSSPTHLWTGEVSAAPPPAR.V
	Protein FAM117BFAN				•	7.4	20.6	R.TSSLDT*LAAPYLAGHWPR.D  R.GS*PPRPPPPPPLLGTVSSPS*SPT*HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN					17.2	18.9	R.GS*PPRPPPPPLIGTVSSPS*SS*PTHLWTGEVSAAPPPAR.V
	Protein FAM117BFAN			▔		39.3	129.0	R.NGS*PTPAGSLGGGAVATAGGPGSR.L
	Protein FAM117BFAN	M117B	S151S152T158			14.4	27.5	R.GSPPRPPPPPLLGTVS"S"PSSSPT"HLWTGEVSAAPPPAR.V
	Protein FAM117BFAN	M117B	S136T158T162			27.6	39.9	R.GS*PPRPPPPPLLGTVSSPSSSPT*HLWT*GEVSAAPPPAR.V
	Protein FAM189A1 FAM		S18S20			100.0	22.2	R.S'LS'RLR.E
Protein inhibitor	Protein HSPC148 CW		T110S121			45.3	78.3	R.LDQIPAANLDADDPLT*DEEDEDFEEES*DDDDTAALLAELEK.I  R.TPS*LPAVDTSYINTSLIODYR.H
	of activated STAT, 1PIA		S510 T508			12.2	46.6 86.3	R.T-PSLPAVDTSYINTSLIQDYR.H
Protein inhibitor of	of activated STAT, 1PIA		S503			18.8	66.7	K.GILSLPHQAS*PVSR.T
Protein inhibitor of	of activated STAT, 1 <sub>PIA</sub>	S1	S517			-2.9	51.1	R.TPSLPAVDTS*YINTSLIQDYR.H
Pro	tein kinase B, beta AKT	T2	S447T449			14.8	15.5	R.YFDDEFTAQS*IT*ITPPDRYDSLGLLELDQR.T
Prof	tein kinase C alpha PRI	KCA	S226	<b></b>		48.5	75.7	R.STLNPQWNES'FTFK.L
	tein kinase C alpha PRI		T497			19.5	92.0	R.T*FCGTPDYIAPEIIAYQPYGK.S
	tein kinase C alpha <sub>PRI</sub> and casein kinase <sub>PA</sub> (		T321T325	•••		1.8	12.3	R.TFCGT*PDYIAPEIIAYQPYGK.S
sub	strate in neurons 2 C binding protein 1 <sub>ZM</sub>		\$445	•	-	22.4	45.0	R.RIS*LSDMPR.S
Protein kinase	C binding protein 1 <sub>ZM</sub>	YND8	S426	•••		35.4	60.2	KLNFDMTAS*PK.I
Protein kinase	C binding protein 1 <sub>ZM</sub>	YND8	S510		<del></del>	20.7	65.8	K.TGQAGSLSGS*PKPFSPQLSAPITTK.T
	C binding protein 1 <sub>ZM</sub>		S508			14.9	58.1	K.TGQAGSLS*GSPKPFSPQLSAPITTK.T
	C binding protein 1 ZM		S506S515			9.2	24.4	K.TGQAGS*LSGSPKPFS*PQLSAPITTK.T
	C binding protein 1 <sub>ZM</sub>		\$506\$510 \$510\$515			8.4	50.7 35.6	K.TGQAGS'LSGS'PKPFSPQLSAPITTK.T  K.TGQAGSLSGS'PKPFS'PQLSAPITTK.T
	C binding protein 1 <sub>ZM</sub>		S510S515 S506			4.2	35.6	KTGQAGS*LSGSPKPFSPQLSAPITIKT
Protein kinase	C binding protein 1 <sub>ZM</sub>		S506S508			18.7	52.7	K.TGQAGS'LS'GSPKPFSPQLSAPITTK.T
Protein kinase	C binding protein 1 <sub>ZM</sub>	YND8	S515	<del></del>		20.4	30.8	K.TGQAGSLSGSPKPFS*PQLSAPITTK.T
	C binding protein 1 <sub>ZM</sub>		S508S515		<u>.</u>	13.6	24.8	K.TGQAGSLS*GSPKPFS*PQLSAPITTK.T
	tein kinase C delta PRI		S506			9.2	60.4	R.AS*TFCGTPDYIAPEILQGLK.Y
Pro	otein kinase C delta PRI		T507 S654			11.2	94.2	RAST'FCGTPDYIAPEILQGLK.Y  RLSYSDKNLIDS'MDQSAFAGFSFVNPK.F
Pro	otein kinase C delta PRI		Y646			15.5 5.3	73.8	RLSY*SDKNLIDSMDQSAFAGFSFVNPK.F
	otein kinase C delta PRI		Y646S664			54.2	82.2	RLSY'SDKNLIDSMDQSAFAGFS'FVNPK.F
Pro	otein kinase C delta PRI	KCD	S645S664			33.4	79.9	R.LS*YSDKNLIDSMDQSAFAGFS*FVNPK.F
Pro	otein kinase C delta PRI	KCD	S645			23.9	44.7	RLS*YSDK.N
	tein kinase C delta PRI		T511		-	0.1	21.6	R.ASTFCGT*PDYIAPEILOGLK.Y
	otein kinase C delta PRI		S647			5.8	44.8	RLSYS*DKNLIDSMDQSAFAGFSFVNPK.F  KNLIDSMDQSAFAGFS*FVNPK.F
	otein kinase C delta PRI		\$664 \$506T507			62.3	85.1 48.3	K.NLIDSMDQSAFAGFS*FVNPK.F  RAS*T*FCGTPDYIAPEILQGLK.Y
	otein kinase C delta PRI		S654S664			25.7	69.6	KARLSYSDKNLIDS*MDQSAFAGFS*FVNPK.F

Peak Area	abundani	ets-Significant cha be at 5%FDR of with the minimum	compared to	the			
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5 >10 >10 F	Protein Name Gene	Phosphosites		# # # #	Ascor	MOWSE	Sequence
	kinase C delta PRKCD	S506Y514			6.7	27.6	R.AS*TFCGTPDY*IAPEILQGLK.Y
	cinase C delta PRKCD	\$658\$664 Y514		==	26.1	17.7	R.LSYSDKNLIDSMDQS"AFAGFS"FVNPK.F  R.ASTFCGTPDY"IAPEILQGLK.Y
	ase C epsilon PRKCE	S729			-0.6	59.1	K.GFS*YFGEDLMP
Protein k	inase C like 2 PKN2	S583	•••		10.2	76.3	R.ASS*LGEIDESSELR.V
Protein k	inase C like 2 PKN2	T814			7.2	83.9	R.T*STFCGTPEFLAPEVLTETSYTR.A
Protein k	inase C like 2 PKN2	T816			6.1	72.7	R.TST*FCGTPEFLAPEVLTETSYTRA
	nase C, beta 1 PRKCB	<b>S</b> 654			10.2	78.2	R.NIDQS*EFEGFSFVNSEFLKPEVK.S
	nase C, beta 1 PRKCB	<b>S</b> 660			32.2	68.4	R.NIDQSEFEGFS*FVNSEFLKPEVK.S
	nase C, beta 1 PRKCB	\$660\$664 \$654\$660			12.1	64.0	R.NIDQSEFEGFS*FVNS*EFLKPEVK.S  R.NIDQS*EFEGFS*FVNSEFLKPEVK.S
	nase C, beta 1 PRKCB	S654S660S664			100.0	15.1	R.NIDQS*EFEGFS*FVNS*EFLKPEVK.S
Protein kir	nase C, beta 1 PRKCB	S654S664	•	-	11.2	24.2	R.NIDQS*EFEGFSFVNS*EFLKPEVK.S
Protein	kinase C, eta PRKCH	S28S32	•		100.0	20.5	R.WS*LRHS*LFK.K
Protein	kinase C, eta PRKCH	<b>S</b> 317			13.9	65.3	K.TLAGMGLQPGNIS*PTSK.L
Protein	kinase C, eta PRKCH	<b>S</b> 675	-		21.2	37.1	R.NFS"YVSPELQP
	e C, iota type PRKCI	T412			10.3	60.1	K.EGLRPGDTTST*FCGTPNYIAPEILR.G
	e C, iota type PRKCI	T416		<u> </u>	-2.0	12.6	K.EGLRPGDTTSTFCGT*PNYIAPEILR.G
	kinase C, mu PRKD1	\$411T412 \$742		■.	6.5	38.2 53.5	K.EGLRPGDTTS'T'FCGTPNYIAPEILR.G  R.S'VVGTPAYLAPEVLR.S
	kinase C, nu PRKD3	\$27\$30	•••		43.6 35.1	18.8	K.SVLPTAIPAVLPAAS*PCS*SPK.T
Proteir	kinase C, nu <sub>PRKD3</sub>	S27S31			9.0	14.8	K.SVLPTAIPAVLPAAS*PCSS*PK.T
Protein k	inase C, theta PRKCQ	<b>S</b> 676		•••	100.0	29.2	R.LS*FADR.A
Protein k	inase C, theta PRKCQ	<b>S</b> 695			100.0	51.5	R.NFS*FMNPGMER.L
Protein k	inase C, theta PRKCQ	<b>S</b> 685			100.0	69.0	R.ALINS*MDQNMFR.N
	inase C, theta PRKCQ	T538			10.1	73.3	K.TNT*FCGTPDYIAPEILLGQK.Y
	inase C, theta PRKCQ	S323	÷		100.0	34.0	R.EGPVEIGLPCS*IK.N
	inase C, theta PRKCQ	Y545			11.3	16.5	K.TNTFCGTPDY*IAPEILLGQK.Y  K.TNTFCGT*PDYIAPEILLGQK.Y
Protein kinase cAMP depend		T542 T245			19.9	95.7	R.TWT*LCGTPEYLAPEILLSK.G
	beta ein kinase D2 PRKD2	S710	•••		19.6	105.5	R.S*VVGTPAYLAPEVLLNQGYNR.S
Prot	ein kinase D2 PRKD2	S396			10.9	19.1	R.KSS*TTLR.E
Prot	ein kinase D2 PRKD2	<b>S</b> 197			31.1	53.5	R.RLS*STSLASGHSVR.L
Prot	ein kinase D2 PRKD2	<b>S</b> 375	•		15.0	38.7	K.AQSS*LGYIPLMR.V
	ein kinase D2 PRKD2	S200			3.0	27.9	R.RLSSTS*LASGHSVR.L
Protein kinase serine/argin		S505T509	=		18.4	36.5	R.TVS*ASST*GDLPK.A
Protein kinase serine/argin		T52 S391				32.1	K. ADI VIDDODDODDODDODDI DIDT*DDEDECEII GENNECICENDANVOV  K.DEDDVDQELANIDPTWIES*PK.T
Protein kinase serine/argin		\$505\$507	=		6.3	18.4	R.TVS'AS'STGDLPK.A
Protein kinase serine/argin	ine specific 2 SRPK2	T503S508			8.1	41.7	R.T*VSASS*TGDLPK.A
Protein kinase serine/argin	ine specific 2 SRPK2	\$505\$508			12.0	45.7	R.TVS*ASS*TGDLPK.A
Protein kinase serine/argin	ine specific 2 SRPK2	\$507 <b>T</b> 509			8.3	22.5	R.TVSAS*ST*GDLPK.A
	strate MK2S4 RCSD1	S268		•••	11.9	70.9	R.SS*EEVDGQHPAQEEVPESPQTSGPEAENR.C
	strate MK2S4 RCSD1	S216			56.2	95.4	K.APGS*PLSSEGAAGEGVR.T
	strate MK2S4 RCSD1	S179			35.1	85.6	R.SQS*DCGELGDFR.A  K.AMVSPFHS*PPSTPSS*PGVR.S
	strate MK2S4 RCSD1	\$120\$127 \$83			-0.5	28.6	K.SS*PLIEK.L
	strate MK2S4 RCSD1	S120		-	14.4	20.8	K.AMVSPFHS*PPSTPSSPGVR.S
Protein kinase sub	strate MK2S4 RCSD1	S116S120			43.5	45.3	K.AM#VS*PFHS*PPSTPSSPGVR.S
Protein kinase sub	strate MK2S4 RCSD1	S284	•		40.6	65.5	R.SSEEVDGQHPAQEEVPES*PQTSGPEAENR.C
Protein kinase sub	strate MK2S4 RCSD1	S116S126	-		17.2	38.7	K.AMVS*PFHSPPSTPS*SPGVR.S
	strate MK2S4 RCSD1	\$177\$179			100.0	60.3	R.S'QS'DCGELGDFR.A
	strate MK2S4 RCSD1	S116S120T124			7.9	20.8	K.AMVS*PFHS*PPST*PS*SPGVR.S
	strate MK2S4 RCSD1	\$120\$123			34.0	25.5	K.AMVSPFHS'PPS'TPSSPGVR.S  K.AMVS'PFHS'PPS'TPSS'PGVR.S
	strate MK2S4 RCSD1	\$116\$120\$123 \$268\$284			10.3	37.4	R.SS*EEVDGQHPAQEEVPES*PQTSGPEAENR.C
	strate MK2S4 RCSD1	\$208\$284 \$120\$126		•	1.3	39.5	KAMVSPFHS*PPSTPS*SPGVR.S
	strate MK2S4 RCSD1	S116S123T124			4.6	11.7	K.AMVS*PFHSPPS*T*PSS*PGVR.S
Protein kinase sub	strate MK2S4 RCSD1	S116S120S123	ij.		16.3	17.9	K.AMVS*PFHS*PPS*TPS*SPGVR.S
Protein kinase sub	strate MK2S4 RCSD1	<b>S</b> 177			11.0	10.8	R.S'QSDCGELGDFR.A
	strate MK2S4 RCSD1	S126			22.6	22.4	K.AMVSPFHSPPSTPS*SPGVR.S
Protein kinase sub	strate MK2S4 RCSD1	S116T124		·	5.5	22.1	K.AMVS*PFHSPPST*PSSPGVR.S
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.5 25 timepoint -3 42 PSM 71	are ininimum j					
5 >100		CarT				
Protein Name Gene Protein kinase substrate MK2S4 RCSD1	Phosphosites S116S127	8 8 8	2 4 5	Ascor 14.2	MOWSE 30.1	Sequence K.AMVS*PFHSPPSTPSS*PGVR.S
Protein kinase, cAMP dependent, regulatory PRKAR2A type II. alpha	<b>S</b> 99			40.7	55.9	R.RVS*VCAETYNPDEEEEDTDPR.V
PRKAR2A	\$78\$80			85.8	51.4	R.VADAKGDS*ES*EEDEDLEVPVPSR.F
PRKAR1A	<b>S</b> 83			100.0	20.2	R.EDEIS*PPPPNPVVK.G
Protein kinase, cAMP dependent, PRKAR2B regulatory. type II. beta	S83S85	ļ		100.0	50.4	K.GVNFAEEPMQS*DS*EDGEEEEAAPADAGAFNAPVINR.F
Protein kinase, cAMP dependent, PRKAR2B regulatory. type II. beta	S114	-		49.8	73.6	R.RAS*VCAEAYNPDEEEDDAESR.I
Protein kinase, lysine deficient 1 WNK1	S2011			26.0	21.3	K.KEKPELSEPSHLNGPS*SDPEAAFLSR.D
Protein kinase, lysine deficient 1 WNK1	\$2027\$2029\$2	ļ		49.9	24.4	R.DVDDGS*GS*PHS*PHQLSSK.S
Protein kinase, lysine deficient 1 WNK1	S1978			100.0	50.3	K.EGPVAS*PPFMDLEQAVLPAVIPK.K
Protein kinase, lysine deficient 1 WNK1  Protein kinase, lysine deficient 4 WNK1	S2011S2012			6.8	34.4	K.RAS'FAK.S
Protein phosphatase 1 regulatory subunit ppp1R10	S331		_	100.0	21.8	K.GPQGPGGGINVQEILTS*IMGSPNSHPSEELLK.Q
10  Protein phosphatase 1 regulatory subunit ppp1R10			=	4.4	41.8 37.1	K.GPQGPGGGINVQEILTSIMGS*PNSHPSEELLK.Q
10 Protein phosphatase 1 regulatory subunit 7 PPP1R7	S27		-	18.2	33.4	R.VESEES*GDEEGKKHSSGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7 ppp1R7	S24S36		• •	9.8	66.4	R.VES*EESGDEEGKKHS*SGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7 PPP1R7	\$27 <b>\$</b> 36			6.0	55.2	R.VESEES*GDEEGKKHS*SGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7 ppp1R7	S24S27		•	100.0	70.2	R.VES*EES*GDEEGKK.H
Protein phosphatase 1 regulatory subunit 7 PPP1R7	S27S37			-0.2	20.8	R.VESEES*GDEEGKKHSS*GIVADLSEQSLK.D
Protein phosphatase 1, regulatory subunit PPP1R11	S73S74T75S77			125.5	68.4	R.AFGES*S*T*ES*DEEEEEGCGHTHCVR.G
Protein phosphatase 1, regulatory subunit PPP1R9B	S192			32.0	67.1	R.FNGS*TEALDKLDADAVSPTVSQLSAVFEK.A
Protein phosphatase 1, regulatory subunit PPP1R9B	T193S205	i		17.1	28.3	R.FNGST*EALDKLDADAVS*PTVSQLSAVFEK.A
Protein phosphatase 1, regulatory subunit PPP1R9B	S205			3.7	23.3	R.FNGSTEALDKLDADAVS*PTVSQLSAVFEK.A
Protein phosphatase 4, regulatory subunit 2 PPP4R2	S226			12.1	46.0	K.NHSDSSTSESEVSSVS*PLK.N
Protein phosphatase 4, regulatory subunit 2 PPP4R2	S223	·		11.2	16.9	K.NHSDSSTSESEVS*SVSPLK.N
Protein phosphatase inhibitor 2 ppp1R2	S121			55.5	151.5	R.IQEQES*SGEEDSDLSPEER.E
Protein phosphatase inhibitor 2 PPP1R2	S121S122	:		73.3	155.0	R.IQEQES*S*GEEDSDLSPEER.E
Protein phosphatase inhibitor 2 PPP1R2	Y75	ļ		2.3	54.0	K.IDEPSTPY*HSMM#GDDEDACSDTEATEAMAPDILAR.K
PPP1R2	S87	ļ		22.0	99.3	K.IDEPSTPYHSMMGDDEDACS*DTEATEAMAPDILAR.K
Protein phosphatase inhibitor 2 ppp1R2	S72			15.8	17.6	K.IDEPS*TPYHSMMGDDEDACSDTEATEAM#APDILAR.K
PPP1R2	T89			18.7	79.6	K.IDEPSTPYHSMM#GDDEDACSDT*EATEAMAPDILAR.K
Protein phosphatase inhibitor 2 ppp1R2  Protein phosphatase methylesterase 1 ppME1	S77			-2.2	31.9	K.IDEPSTPYHS*MMGDDEDACSDTEATEAMAPDILAR.K  R.DFS*PVPWSQYFESMEDVEVENETGKDTFR.V
Protein phosphatase methylesterase 1 PPME1	\$42 \$47	•		80.2	99.6	R.DFSPVPWS*QYFESMEDVEVENETGKDTFR.V
Protein phosphatase methylesterase 1 PPME1	S52			11.1	30.6	R.DFSPVPWSQYFES*MEDVEVENETGK.D
Protein phosphatase methylesterase 1 PPME1	Y49	-	•	2.3	14.0	R.DFSPVPWSQY*FESMEDVEVENETGK.D
Protein RUFY3 (Fragment) RUFY3	\$50\$55				24.9	R. EGEAGDDAS*DAGOS*EDDSD//AADEELLVDGDGGAGEGV/DDDDO
Protein SET SET	<b>S</b> 7	•••		100.0	36.7	K.RQS*PLPPQK.K
Protein strawberry notch homolog 1 SBNO1	S754S755			52.6	84.3	K.NMS*S*GDDDDFNPFLDESNEDDENDPWLIR.K
Protein strawberry notch homolog 1 SBNO1	S754S768			4.8	22.7	K.NMS*SGDDDDFNPFLDES*NEDDENDPWLIR.K
Protein transport protein SEC61 beta SEC61B subunit	<b>S</b> 17			7.4	41.9	M.PGPTPSGTNVGSSGRS*PSK.A
Protein tyrosine phosphatase nonreceptor PTPN7	<b>S</b> 83			100.0	13.4	R.RGS*NVALMLDVR.S
Protein tyrosine phosphatase nonreceptor PTPN7	S398	<b>-</b>		52.7	20.9	R.GGMIQTAEQYQFLHHTLALYAGQLPEERS*P
Protein tyrosine phosphatase nonreceptor PTPN12 type 12	<b>S</b> 435			100.0	22.9	R.NLS*FEIK.K
Protein tyrosine phosphatase receptor type PTPRC	<b>S</b> 992			100.0	66.9	R.VPLKHELEMS*K.E
Protein tyrosine phosphatase receptor type PTPRC	S1297			16.8	23.5	K.EQAEGSEPTSGTEGPEHSVNGPAS*PALNQGS
Protein tyrosine phosphatase receptor type PTPRC	S973			95.6	55.3	R.NS*NVIPYDYNR.V
Protein tyrosine phosphatase receptor type PTPRC	S1291	ı.		7.4	11.4	K.EQAEGSEPTSGTEGPEHS"VNGPASPALNQGS
Protein tyrosine phosphatase receptor type PTPRC C	\$992\$995\$999				26.9	K.HELEMS'KES'EHDS'DES'S'DDDS'DSEEPSK.Y
Protein tyrosine phosphatase receptor type PTPRC C  Protein tyrosine phosphatase, non receptor PTPN2	\$999\$1002\$10		•	16.2	26.3	K.ESEHDS*DES*S*DDDS*DSEEPSK.Y  K.EDLSPAFDHS*PNK.I
type 2  PRP38 pre-mRNA processing factor 38 PRPF38B	S304			39.1	54.2	R.RS*LS*PR.R
domain containing B  PRP38 pre-mRNA processing factor 38 PRPF38B				100.0	16.0	R.RSLS*PR.R
domain containing B	\$268 \$527\$529	===		73.3	31.1 60.9	R.S'QS'IEQESQEK.Q
			• • •	17.8	28.5	R.RS*LSPR.R
PRP38 pre-mRNA processing factor 38 PRPF38B	S266					
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B PRP38 pre-mRNA processing factor 38 PRPF38B				100.0	21.9	R.S'RS'IDR.G
PRP38 pre-mRNA processing factor 38 pRPP388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 39 pRPF388	S318S320			100.0	21.9	
PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 PRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 PRPF388	\$318\$320 \$529					R.S'RS'IDR.G
PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B	\$318\$320 \$529		•	19.9	47.9	R.SYRS'IDR.G R.SQS'IEQESQEK.Q
PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP4 pre-mRNA processing factor 4 pRPF48 homolog B PRP4 pre-mRNA processing factor 4 pRPF48	\$318\$320 \$529 \$527		•	19.9	47.9 49.8	R.S'RS'IDR.G R.SQS'IEOESQEK.Q R.S'QSIEQESQEK.Q
PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 34 pRPF388 domain containing B	\$318\$320 \$529 \$527 \$431\$437		•	19.9 9.2 21.0	47.9 49.8 21.1	R SYRS'IDR.G  R SQS'IEQESQEK.Q  R SYQSIEQESQEK.Q  K DAS'PINRWS'PTR.R
PRP38 pre-mRNA processing factor 38 pRP538B domain containing B PRP38 pre-mRNA processing factor 38 pRP538B domain containing B PRP38 pre-mRNA processing factor 38 pRP538B domain containing B PRP38 pre-mRNA processing factor 38 pRP538B domain containing B PRP4 pre-mRNA processing factor 4 pRP54B homolog B PRP4 pre-mRNA processing factor 4 pRP54B homolog B PRP4 pre-mRNA processing factor 4 pRP54B homolog B	\$318\$320 \$529 \$527 \$431\$437 Y849		•	19.9 9.2 21.0 52.3	47.9 49.8 21.1 76.6	R S'RS'IDR.G  R SOS'IEOESOEK.Q  R S'OSIEOESOEK.Q  K.DAS'PINRWS'PTR.R  K.LCDFGSASHVADNDITPY'LVSR.F
PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP38 pre-mRNA processing factor 38 pRPF388 domain containing B PRP4 pre-mRNA processing factor 4 pRPF48 domain containing B PRP4 pre-mRNA processing factor 4 pRPF48 homolog B PRP4 pre-mRNA processing factor 4 pRPF48 homolog B PRP4 pre-mRNA processing factor 4 pRPF48 homolog B	\$318\$320 \$529 \$527 \$431\$437 Y849		•	19.9 9.2 21.0 52.3	47.9 49.8 21.1 76.6 68.5	R.SYRS'IDR.G  R.SYS'IEOESQEK.Q  R.S'QSIEQESQEK.Q  K.DAS'PINRWS'PTR R  K.LCDFGSASHVADNDITPY'LVSR.F  K.LCDFGSASHVADNDITPYLVSR.F

Peak Area	%CV White do	ts-Significant cha	nge in pepti	de			
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-3 0 3	42 PSM 71						
5 >10	>100			RajiB			
PRP4 pre-mRNA	Protein Name Gene processing factor 4 PRPF4B	Phosphosites	9 H H	9 H H		MOWSE	Sequence R.S*LS*PKPR.D
	homoloa B	S354S356			100.0	38.0	
	processing factor 4 PRPF4B homolog B	S277			91.7	54.5	R.KKS'PIINESR.S
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S294			100.0	35.0	R.S*PVDLR.G
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S292S294			100.0	26.1	K.S*RS*PVDLR.G
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	T576S578S580		•	100.0	27.1	R.T*RS*PS*PDDILER.V
PRP4 pre-mRNA	processing factor 4 PRPF4B	\$239\$241		• • •	29.0	24.7	K.S*KS*PTLR.R
PRP4 pre-mRNA	homolog B processing factor 4 PRPF4B	\$427\$431\$437			18.5	14.4	R.S*KDAS*PINRWS*PTR.R
	homolog B processing factor 4 PRPF4B						K.LLAPDMFTES*DDMFAAYFDSAR.L
	homoloa B	S636			5.4	24.8	
	processing factor 4 PRPF4B homolog B	S20S23S32			47.4	19.7	R.EQPEMEDANS*EKS*INEENGEVS*EDQSQNK.H
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	\$427\$431T439			14.6	13.9	R.S*KDAS*PINRWSPT*R.R
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S427S431			100.0	27.7	R.S*KDAS*PINR.W
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S131Y140			6.4	13.1	K.VQS*GMGLILQGY*ESGSEEEGEIHEK.A
PRP4 pre-mRNA	processing factor 4 PRPF4B	S131S144		•	5.3	14.2	K.VQS*GMGLILQGYESGS*EEEGEIHEK.A
	homolog B processing factor 4 PRPF4B		•				K.VQSGMGLILQGY"ES"GSEEEGEIHEK.A
	homoloa B	Y140S142		<u> </u>	4.8	27.0	
	processing factor 4 PRPF4B homolog B	T259	<u> </u>		16.6	12.3	R.SPT*DDKVK.I
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S431			100.0	18.9	K.DAS*PINR.W
	PRPF4B	S87S93			100.0	38.6	K.EIIDAS*DKEGMS*PAKR.T
PRP4 pre-mRNA	processing factor 4 PRPF4B	S578S580	•		31.8	28.3	R.TRS*PS*PDDILER.V
PRP4 pre-mRNA	homolog B processing factor 4 PRPF4B	\$20\$23			34.5	21.5	R.EQPEMEDANS*EKS*INEENGEVSEDQSQNK.H
	homolog B						K.VQSGM#GLILQGY*ESGS*EEEGEIHEK.A
	homoloa B	Y140S144		•	4.5	21.8	
	processing factor 4 PRPF4B homolog B	T634			45.0	44.5	K.LLAPDMFT*ESDDMFAAYFDSAR.L
PRP4 pre-mRNA	processing factor 4 PRPF4B homolog B	S142S144			9.4	11.3	K.VQSGMGLILQGYES*GS*EEEGEIHEK.A
	PRPF40A	T190S191S193			35.1	83.3	K.DSGNWDT*S*GS*ELS*EGELEK.R
PRP40 pre-mRNA	processing factor 40 PRPF40A	S141S143S146			100.0	26.0	R.HKS*DS*PES*DAEREK.D
PRP40 pre-mRNA p	homolog A processing factor 40 PRPF40A	\$143\$146			5.7	13.9	R.HKSDS*PES*DAER.E
	homolog A  PRPF31 PRPF31		=				
		T455			17.6	67.0	R.SSGTASSVAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	T448T455			12.2	92.9	R.SSGT*ASSVAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	T448			-0.5	24.8	R.SSGT'ASSVAFTPLQGLEIVNPQAAEKK.V
	PRPF31 PRPF31	S450T455			14.6	77.7	R.SSGTAS*SVAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	S445T448		• • • •	4.9	37.4	R.S*SGT*ASSVAFTPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	<b>S</b> 450	-	_		77.6	R.SSGTAS*SVAFTPLQGLEIVNPQAAEKK.V
					7.3		
	PRPF31 PRPF31	\$445T455			3.6	40.1	R.S*SGTASSVAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	S451T455			11.9	51.1	R.SSGTASS*VAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	\$450\$451			11.5	65.9	R.SSGTAS*S*VAFTPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	S446T455			-0.7	27.6	R.SS*GTASSVAFT*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	T448S450			3.1	45.7	R.SSGT*AS*SVAFTPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	T448\$451T455					R.SSGT*ASS*VAFT*PLQGLEIVNPQAAEK.K
					-2.3	12.0	
	PRPF31 PRPF31	S445S446T448		-	-6.1	12.7	R.S*S*GT*ASSVAFTPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	T448S450S451			5.0	20.6	R.SSGT*AS*S*VAFTPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31	S445S446			3.4	55.4	R.S'S'GTASSVAFTPLQGLEIVNPQAAEK.K
PRPP synthetase	associated protein 2 PRPSAP2	S227	•		16.4	61.6	R.LGIAVIHGEAQDAESDLVDGRHS*PPMVR.S
PRPP synthetase	associated protein 2 PRPSAP2	\$219		• • •	4.6	15.7	R.LGIAVIHGEAQDAES*DLVDGRHSPPMVR.S
	PSD3 PSD3						K.ES*SKVPR.H
		S337			23.9	23.8	
	PSD3 PSD3	S338			8.9	22.7	K.ESS*KVPR.H
Pseudoa	autosomal gene XE7 AKAP17A	T639S640			-0.2	13.1	R.ST*S*PDHTR.S
Pseud	louridine synthase 1 PUS1	T426			47.1	72.7	K.VPSPLEGSEGDGDT*D
Pseud	louridine synthase 1 PUS1	S420T426			22.7	46.7	K.VPSPLEGS*EGDGDT*D
	PSPC1 PSPC1	S409			100.0	58.0	R.GAINMGDAFS*PAPAGNQGPPPMMGMNMNR.A
PTK2R protoin for	rosine kinase 2 beta PTK2B						K.RNS*LPQIPMLNLEAR.R
		S375			100.0	58.6	
PTK2B protein ty	rosine kinase 2 beta <sub>PTK2B</sub>	S839T842			10.2	54.5	K.SLDPMVYMNDKS*PLT*PEKEVGYLEFTGPPQKPPR.L
PTK2B protein ty	rosine kinase 2 beta PTK2B	Y834T842			20.1	60.8	K.SLDPMVY*MNDKSPLT*PEKEVGYLEFTGPPQKPPR.L
PTK2B protein ty	rosine kinase 2 beta PTK2B	S746T765			18.7	18.7	K.LQFQVPEGLCAS*SPTLTSPMEYPSPVNSLHT*PPLHR.H
PTK2B protein ty	rosine kinase 2 beta PTK2B	S778			100.0	18.8	K.RHS*MR.E
PTK2B protein tv	rosine kinase 2 beta <sub>PTK2B</sub>	S746S762			10.0	12.1	K.LQFQVPEGLCAS*SPTLTSPM#EYPSPVNS*LHTPPLHR.H
	rosine kinase 2 beta PTK2B						KLQFQVPEGLCAS*SPTLTSPMEYPSPVNSLHTPPLHR.H
		S746			13.6	42.2	
PTPRO	C-associated protein PTPRCAP	<b>S</b> 99			22.5	91.0	R.AELGS*TDNDLER.Q
PTPRO	C-associated protein PTPRCAP	S153				57.8	R. AEEADDS*DTECDI VI GSDGDASAGGSAEAI I SDI HAEAGSAAWDD
PTPRO	C-associated protein PTPRCAP	S153T155				58.7	R.
PTPRO	C-associated protein PTPRCAP	S163S172			6.1	39.9	R.
	C-associated protein PTPRCAP					90.4	R.DSDT*EGDLVLGSPGPASAGGSAEALLSDLHAFAGSAAWDDSAR
			===		-0.3		A
	C-associated protein PTPRCAP					42.7	R. AEEADDO*DT*EGDI VI GO*DODASAGGSAEALI SDI UAEAGSAAWIF
PTPRO	C-associated protein PTPRCAP	T155S172	•		1.4	28.8	R.
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3 86 5 >100 >10			CarT				
Protein Name PTPRC-associated protein		Phosphosites T155S168	£ 5 8	5 2 8	Ascor 2.9	MOWSE 88.7	Sequence  R.  RDT**CCDLV// CSDCDAS**ACCSAEALLSDLHAEACSAAW/DDSADA
PTPRC-associated protein	PTPRCAP	S163	<del>!</del>		45.8	80.4	R.DSDTEGDLVLGS*PGPASAGGSAEALLSDLHAFAGSAAWDDSAR.
PTPRC-associated protein	PTPRCAP	S163S168			2.9	33.3	R. DEDTECTION CONDEDACA CONSERVINO DI MACA CON AMPODO ADIA
PTPRF interacting protein alpha 1		S239S242		-	1.1	37.7	R.SS*DGS*LSHEEDLAK.V
PTPRF interacting protein alpha 1		S238S239			9.3	15.4	R.S*S*DGSLSHEEDLAK.V
PTPRF interacting protein binding protein 1  PTPRF interacting protein binding protein 1		\$448 \$346\$347		=	-0.6	25.3	K.SS*SLGNLKK.E  K.GKDGEYEELLNSSSIS*S*LLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1		\$340\$347 \$342\$347			0.2	45.9	K.GKDGEYEELLNS*SSISS*LLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1		S343S347			10.1	78.5	K.DGEYEELLNSS*SISS*LLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1	PPFIBP1	S342S346			9.3	68.2	K.GKDGEYEELLNS*SSIS*SLLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1	PPFIBP1	S342S343			-0.0	55.1	K.GKDGEYEELLNS*S*SISSLLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1	PPFIBP1	\$344 <b>\$</b> 347			4.5	17.9	K.GKDGEYEELLNSSS*ISS*LLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1		S37S40			7.3	13.3	K.ALEYSNGIFDCQS*PTS*PFMGSLR.A
PTPRF interacting protein binding protein 1		\$344 <b>\$</b> 346		-	4.7	67.1	K.DGEYEELLNSS <mark>S'IS'</mark> SLLDAQGFSDLEK.S
PTPRF interacting protein binding protein 1		\$343\$344		-	10.7	68.2	K.DGEYEELLNSS'S'ISSLLDAQGFSDLEK.S  R.RDS'LTGSSDLYKR.T
Pumilio homolog 1		\$709 \$228	=		12.8 8.0	30.3	R.SESGGLGVSMVEYVLSS*SPGDSCLR.K
Pumilio homolog 1		S229			9.0	57.8	R.SESGGLGVSMVEYVLSSS*PGDSCLR.K
Pumilio homolog 1	PUM1	S220S228			5.8	21.6	R.SESGGLGVS*MVEYVLSS*SPGDSCLR.K
Pumilio homolog 1	PUM1	T112		•	100.0	27.5	K.HRWPT*GDNIHAEHQVR.S
Pumilio homolog 1	PUM1	S214S229		نب	2.9	23.4	R.SES'GGLGVSMVEYVLSSS'PGDSCLR.K
Pumilio homolog 1	PUM1	S209				55.6	R.RPGQSFHVNSEVNSVLS*PR.S
Pumilio homolog 1		S227			10.3	21.9	R.SESGGLGVSMVEYVLS*SSPGDSCLR.K
Pumilio homolog 1		S124			100.0	52.2	R.S'MDELNHDFQALALEGR.A  R.SGOGFHGNSEVNAILS'PR.S
Pumilio2		S82 S136	•		59.9	32.3 50.6	K.GKAS*PFEEDQNR.D
PUR alpha		S182	==		16.3	61.8	R.GPGLGS*TQGQTIALPAQGLIEFR.D
Purine rich element binding protein B	PURB	S101			22.4	79.6	R.DSLGDFIEHYAQLGPSS*PEQLAAGAEEGGGPR.R
Purine rich element binding protein B	PURB	S298S304			100.0	53.7	R.RGGGS*GGGEES*EGEEVDED
ı	PURB	S304			25.8	60.7	R.GGGSGGGEES*EGEEVDED
Purine rich element binding protein B	PURB	S100			6.9	57.0	R.DSLGDFIEHYAQLGPS*SPEQLAAGAEEGGGPR.R
Purine rich element binding protein B		S86				56.8	R.DS*LGDFIEHYAQLGPSSPEQLAAGAEEGGGPR.R
PWP2	PWP2	Y613S614S619		•	3.5	13.9	K.GKAFTALCY"S"ADGHS"ILAGGMS"K.F  R.SLDPLGS"EEEAEAS"EDDS"LHLLGGGGRDS"EEEMLA-
Pyruvate dehydrogenase complex, E1-alpha		\$891\$898\$902 \$232			37.9 8.9	13.9	R.YGMGTS*VER.A
polypeptide 1  Pyruvate dehydrogenase E1 alpha subunit,		S291			10.9	16.2	R.YHGHS*MSDPGVSYR.T
Pyruvate dehydrogenase E1 alpha subunit,	PDHA1	S291S298			20.5	51.3	R.YHGHS*MSDPGVS*YR.T
testis specific form	PDHA1	S293S298			3.8	28.1	R.YHGHSM#S*DPGVS*YR.T
Pyruvate dehydrogenase E1 alpha subunit,   testis specific form	PDHA1	S291Y299			9.1	28.3	R.YHGHS*MSDPGVSY*R.T
Pyruvate dehydrogenase E1 alpha subunit, testis specific form		S298		. =	16.4	25.1	R.YHGHSMSDPGVS"YR.T
Pyruvate dehydrogenase E1 alpha subunit, testis specific form		S293			-1.0	38.5	R.YHGHSMS*DPGVSYR.T
R Ras2		S186			27.8	52.8	K.FQEQECPPS'PEPTR.K  K.ASS'FSGISVLTR.G
R3H domain protein 1		\$381 \$141			-0.3	27.8 38.3	R.DS*SQEYTDSTGIDLHEFLVNTLK.N
R3H domain protein 1		S141			10.5	82.0	R.DSS'QEYTDSTGIDLHEFLVNTLK.N
R3H domain protein 1		S380	• • •		26.4	44.7	KAS*SFSGISVLTR.G
RA regulated nuclear matrix associated protein	DTL	S655			5.8	52.5	K.ENS*SPENKNWLLAMAAK.R
RA regulated nuclear matrix associated protein	DTL	S623S626			87.7	38.9	K.IEGAGTSISEPPS'PIS'PYASESCGTLPLPLRPCGEGSEMVGK.E
RA regulated nuclear matrix associated protein		T616S617				21.4	K.IEGAGT*S*ISEPPSPISPYASESCGTLPLPLRPCGEGSEMVGK.E
RA regulated nuclear matrix associated protein	DTL	S619S623S626			21.5	41.5	K.IEGAGTSIS*EPPS*PIS*PYASESCGTLPLPLRPCGEGSEMVGK.E
RA regulated nuclear matrix associated protein		T616S617S619	-			46.7	K.IEGAGT*S*IS*EPPSPISPYASESCGTLPLPLRPCGEGSEMVGK.E
RA regulated nuclear matrix associated protein		S656	•••		-0.3	82.4	K.ENSS*PENKNWLLAMAAK.R
RA regulated nuclear matrix associated protein  RA regulated nuclear matrix associated		\$485\$487 \$679			12.2	25.2 59.2	R.RGS*VS*SVSPKPPSSFK.M  R.S*PSSQTPNSR.R
RA regulated nuclear matrix associated		\$443			10.7	35.5	K.CNPSNS*SPSSAACAPSCAGDLPLPSNTPTFSIK.T
RA regulated nuclear matrix associated		S441			9.1	16.4	K.CNPS*NSSPSSAACAPSCAGDLPLPSNTPTFSIK.T
RAB GTPase activating protein 1 like	RABGAP1	S464		<u>.</u>		71.6	R.ES*DKEEPVTPTSGGGPMSPQDDEAEEESDNELSSGTGDVSK.D
RAB GTPase activating protein 1 like	RABGAP1	<b>S</b> 490			4.5	43.0	R.ESDKEEPVTPTSGGGPMSPQDDEAEEES*DNELSSGTGDVSK.D
RAB GTPase activating protein 1 like		S480		•	-4.8	34.0	R.ESDKEEPVTPTSGGGPMS*PQDDEAEEESDNELSSGTGDVSK.D
Rab GTPase binding effector protein 2		S193		<u> </u>	28.7	61.0	R.HAPSLHGS*TELLPLSR.D
Rab GTPase binding effector protein 2		S193T194			11.4	45.5	R.HAPSLHGS*T*ELLPLSR.D
311 use billullig ellector protein 2	MDEP2	T194		• .	9.1	41.1	R.HAPSLHGST*ELLPLSR.D

Peak Area	o abundano		compared to	the			
-5 -3	timepoint PSM	with the minimum					
5 >10	>100	Dharri	CarT	RajiB E E E		MOWSE	Sequence
Rab GTPase b	Protein Name Gene inding effector protein 2 RABEP2	Phosphosites S200	000	. 2 2	Ascor 12.8	59.4	R.HAPSLHGSTELLPLS'R.D
	inding effector protein 2 RABEP2	T194S200			11.4	60.6	R.HAPSLHGST*ELLPLS*R.D
Rab GTPase b	inding effector protein 2 RABEP2	S193S200	-		12.3	15.7	R.HAPSLHGS*TELLPLS*R.D
	Rab-coupling protein RAB11FIP  Rab-coupling protein RAB11FIP				73.8	50.0 49.4	R.S*NVCINGNHVYLEQPEAK.G  K.NKDSGSDTASAIIPSTTPSVDS*DDESVVK.D
	RAB11FIP			-	64.0	76.3	R.NNMT*ASMFDLSMKDK.S
	Rab-coupling protein RAB11FIP	S356			9.5	119.0	K.HLFS*STENLAAGSWK.E
	Rab-coupling protein RAB11FIP	T358			25.4	62.7	K.HLFSST*ENLAAGSWK.E
	Rab-coupling protein RAB11FIP				20.1	102.1	K.HLFSS*TENLAAGSWK.E
	Rab-coupling protein RAB11FIP				27.6	79.7	R.NNMTAS*MFDLSMK.D  K.SPIMADLNLSLPSIPEVAS*DDER.I
	Rab-coupling protein RAB11FIP		• • • •		6.7	38.6	K.TPLSQS*MSVLPTSKPEK.V
	Rab-coupling protein RAB11FIP				12.9	69.5	K.SPIMADLNLS*LPSIPEVASDDER.I
	Rab-coupling protein RAB11FIP	S290		•	5.3	43.1	K.SPIMADLNLSLPS*IPEVASDDER.I
	Rab-coupling protein RAB11FIP			•	12.2	15.4	R.TAS*TDLK.Q
	Rab-coupling protein RAB11FIP			·	13.3	21.9	K.NKDSGSDTAS*AIIPSTTPSVDS*DDESVVK.D  R.RSS*LLSLMTGK.K
	Rab-coupling protein RAB11FIP  Rab-coupling protein RAB11FIP				9.8	38.7	R.RSS*LLS*LMTGK.K
R	AB11 interacting protein RAB11FIP				41.9	34.6	R.NNLS*ASMFDLSMK.D
R.	AB11 interacting protein RAB11FIP	S176			7.8	46.0	R.NNLSAS*MFDLSMK.D
	RAB14 RAB14	<b>Y</b> 99	•	_	-0.4	17.8	R.STY*NHLSSWLTDAR.N
	AB3A interacting protein RAB3IP	T289			15.2	44.7	R.NKST*SSAMSGSHQDLSVIQPIVK.D
R/	RAB7 RAB7A	S288	<b>!!!</b>		15.3	14.0	R.NKS*TSSAMSGSHQDLSVIQPIVK.D  R.FQS*LGVAFYR.G
	Rabaptin 5 RABEP1	\$72 T486			75.4	47.9	K.AMTPEQEET*ASLLSSVTQGMESAYVSPSGYR.L
	Rabaptin 5 RABEP1	S374S377		• • •	41.0	25.7	R.GS*VHS*LDAGLLLPSGDPFSK.S
	Rabaptin 5 RABEP1	\$407\$410			22.6	54.5	R.AQS*TDS*LGTSGSLQSK.A
	Rabaptin 5 RABEP1	T480			2.7	19.4	K.AMT*PEQEETASLLSSVTQGMESAYVSPSGYR.L
	Rabaptin 5 RABEP1	\$437T454\$456			1.4	27.4	K.SAGNLDES*DFGPLVGADSVSENFDT*AS*LGS*LQMPSGFMLTK.
	Rabaptin 5 RABEP1	\$488 \$430\$437\$447			5.7	24.0	K.S'AGNLDES'DFGPLVGADS'VSENFDT'ASLGSLQMPSGFMLTK.
	Rabconnectin-3 DMXL2	S1857		•	49.2	78.9	R.NLAS*PEGTLATLGLK.T
	Rabconnectin-3 beta WDR7	S1153			-0.4	52.3	R.SS*SQIPEGFGLTSGGSNYSLAR.H
	Rabconnectin-3 beta WDR7	S1154	<del></del>		7.2	32.4	R.SSS*QIPEGFGLTSGGSNYSLAR.H
	Rabphilin 3A RPH3A	S259	-		100.0	17.0	R.S'PAGLRR.A  R.NHLLQFALES'PAKS'PASSSSK.N
	RAD18 RAD18	\$99\$103 \$99			15.8	45.3 64.6	R.NHLLQFALES*PAK.S
	RAD18 RAD18	S471			39.7	55.9	R.DLLEEEEAWEASHKNDLQDTEIS*PR.Q
	RAD21 RAD21	S153			100.0	62.2	R.EEVGNIS*ILQENDFGDFGMDDR.E
	RAD21 RAD21	Y105				21.4	R.EAAY"NAITLPEEFHDFDQPLPDLDDIDVAQQFSLNQSR.V
	RAD23A RAD23A	Y197				72.7	R.AVEY*LLTGIPGSPEPEHGSVQESQVSEQPATEAAGENPLEFLR.D
	RAD23A RAD23A	\$295 \$128				46.1	R. HOEOFICHI NEDDOEL ADISIDVECE VOALOEEA DOMINYOVEDOEK  R EDKSPSEES APTISPESVSGSVPSSGSSGR E
	RAD23A RAD23A	\$128 \$123			-2.8	17.8 34.2	R.EDKS'PSEESAPTTSPESVSGSVPSSGSSGRE
	RAD23A RAD23A	S205			7.4	28.6	R.AVEYLLTGIPGS*PEPEHGSVQESQVSEQPATEAAGENPLEFLR.D
	RAD23A RAD23A	Y313			2.7	14.6	R. HOPOPIONI NECEDICE ADISDIFICATION AND TRANSPORTED FOR
	RAD23B RAD23B	S160			11.3	59.0	K.QEKPAEKPAETPVA®*PTATDSTSGDSSR.S
		T155			45-	22.0	K.QEKPAEKPAET*PVAT*SPTATDSTSGDSSR.S  K.QEKPAEKPAETPVAT*SPTATDSTSGDSSR.S
R	AD51 interacting protein RAD51AP	T159 1 S21S27			7.1	25.2	R.HKKPVNYSQFDHSDS*DDDFVS*ATVPLNK.K
	AD51 interacting protein RAD51AP				9.5	13.9	R.HKKPVNYS*QFDHS*DSDDDFVSATVPLNKK.S
	RAD51AP	<sup>1</sup> S19S21			27.2	28.7	K.KPVNYSQFDHS'DS'DDDFVSATVPLNKK.S
	AD51 interacting protein RAD51AP				4.6	13.8	R.HKKPVNY*SQFDHS*DSDDDFVSATVPLNKK.S
	AD51 interacting protein RAD51AP		-		3.0	27.8	R.HKKPVNY*SQFDHSDS*DDDFVSATVPLNKK.S
R	AD51 interacting protein RAD51AP  RAD54-like 2 RAD54L2				6.7	16.4	R.HKKPVNYSQFDHS*DSDDDFVS*ATVPLNK.K  K.APDPEGLARPVS*PDS*PEIISELQQYADVAAAR.E
	RAD54-like 2 RAD54L2				12.2	116.5 45.5	R.QSSPS*TNAALPGPPAQLMDSSAVPGTALGTEPR.L
	RAD9 RAD9A	\$375\$387			19.6	56.0	R.S'PQGPSPVLAEDS'EGEG
	RAD9 RAD9A	S277		-	25.0	90.1	K.DSLLDGHFVLATLSDTDSHSQDLGS*PER.H
	RAD9 RAD9A	S272		•		67.8	K.DSLLDGHFVLATLSDTDSHS*QDLGSPER.H
	RAD9 RAD9A	S387			66.8	48.6	R.SPQGPSPVLAEDS*EGEG  K.DSLLDGHFVLATLS*DTDSHSQDLGSPER.H
	KADYA	S266			4.3	15.7	NOOSEDONN VENTED DYDOROGUEGOFERCH

Peak Area %CV <-10 0 29	abundanc	ts-Significant cha e at 5%FDR c with the minimum	ompared to	the	
>10 Protein Name	C	Phosphosites	2 J J	2 2 5	Ascor
Radial spokehead like 2		S530	0 14 45		15.0
Raf kinase inhibitor protein	DCDD1	S52		•	
		552			22.4
Raf kinase inhibitor protein	PEBP1	T51	•		2.8
RAF1	RAF1	S259			9.6
RAF1	RAF1	<b>S</b> 29			6.5
RAF1	RAF1	S25			5.3
RAF1	ARAF	S621	<b>—</b>		16.6
RAF1	RAF1	T258			8.2
RAF1	RAF1	S296			6.8
RAF1	RAF1	S295			17.4
RAF1	RAF1	S26	• •		10.3
RAF1	RAF1	T260			7.4
RAF1	RAF1	S295S301	ı,		18.6
RAF1	ARAF	S619		Ţ.	7.2
Raft linking protein	RFTN1	S199			80.7
Raft linking protein	RFTN1	S220		•••	76.1
Ral guanine nucleotide dissociation stimulator-like 3	RGL3	\$361\$366	Ţ.		100.0
RalA binding protein 1	RALBP1	S92S93		•••	70.9
RalA binding protein 1	RALBP1	<b>S</b> 30			17.7
RalA binding protein 1	RALBP1	S29S34			17.3
RalA binding protein 1	RALBP1	S29			13.4
RalA binding protein 1	RALBP1	S29S30			6.1
RalA binding protein 1	RALBP1	\$30\$34	-		13.4
RalA binding protein 1	RALBP1	Y85S92			13.1
RalA binding protein 1	RALBP1	T27S29			6.6

RALBP1 REPS1 S656

RALBP1 REPS1 \$220

RALBP1 REPS1 \$340

RALBP1 REPS1 S508

RALBP1 REPS1 \$378

RALBP1 REPS1 \$484\$505

RALBP1 REPS1 S484T491

RALBP1 REPS1 \$378\$379

RALBP1 REPS1 \$376

RALBP1 REPS1 T358

RALBP1 REPS1 \$349

RALBP1 REPS1 T486S487

RALBP1 REPS1 S484T486

RALBP1 REPS1 \$484\$487\$505

RALBP1 REPS1 \$484T486\$505

RALBP1 REPS1 \$110S118S122

RALBP1 REPS1 \$110\$114\$118T

RALBP1 REPS1 \$378\$387

RALBP1 REPS1 \$354

RALBP1 REPS1 S387

RALBP1 REPS1 S68

RALBP1 REPS1 Y223

RALBP1 REPS1 S66

RALBP1 REPS1 S430

RALBP1 REPS1 S509

RAM2 CDCA7L S21

RAM2 CDCA7L T77T81

RAM2 CDCA7L S79T81

RAM2 CDCA7L T77S79

Ran binding protein 1 RANBP1 T13S14

RAM2 CDCA7L \$195T196\$197

RALBP1 REPS1 \$114\$118T121

RALBP1 REPS1 S487S505

RALBP1 REPS1 \$110S118T121

S378T383

RALBP1 REPS1

RALBP1 REPS1

RALBP1 REPS1 \$110\$114\$118\$

Ascor MOWSE 15.0 22.6

9.6 71.2

6.5 104.1

8.2 76.0

7.4 25.8 18.6 21.8

75.4

58.1 16.6 35.6

91.1

62.8 10.3 38.3

45.3 80.7 59.6

122.0 17.7 57.3

43.7 13.4 56.9

33.3

22.6

50.0

35.5

15.6 13.1

54.6

13.4 7.2

15.7 5.1

10.9 13.2

22.0

57.7 21.6

15.2 15.4

76.1 35.5 100.0 11.7

17.3 59.5

13.4 31.1

13.1 29.4

30.0 18.5

6.1 43.3

51.2 26.3

-0.3

19.7 54.6

8.9 28.9

13.2 25.2

7.6 63.0

6.1 62.2

27.6 23.2

8.3 11.8

12.5 15.8

26.2

2.0 23.4

8.4 27.9

10.7 13.0

-5.2 48.5

5.9 18.4

9.5 25.4

7.2 29.9

15.6 12.8

9.1 19.9

10.1 31.7

9.4

31.4 50.5

11.2 20.9

100.0 95.2

57.1

42.3

28.4

R.RSS\*QER.K

K.NRPTS\*ISWDGLDSGK.L

K.NRPT\*SISWDGLDSGK.L R.STS\*TPNVHMVSTTLPVDSR.M

R.SAS\*EPSLHR.T

R.S\*ASEPSLHR.T

K.RS\*WGAVS\*R.E R.TEGYAAFQEDS\*S\*GDEAESPSK.M

R.TPSS\*EEISPTKFPGLYR.T R.TPS\*SEEIS\*PTKFPGLYR.T

R.TPS\*SEEISPTKFPGLYR.T

R.TPS\*S\*EEISPTKFPGLYR.T

R.TPSS\*EEIS\*PTKFPGLYR.T R.TEGY\*AAFQEDS\*SGDEAESPSK.M

R.T\*PS\*SEEISPTKFPGLYR.T

R.LKS\*EDELRPEVDEHTQK.T

R.TSADAQEPAS\*PVVS\*PQQS\*PPTS\*PHTWR.K

K.LIDLEDSADVGDQPGEVGYSGS\*PAEAPPSK.S

R.SSS\*SQTLTQFDSNIAPADPDTAIVHPVPIR.M

R.SSS\*SQTLT\*QFDSNIAPADPDTAIVHPVPIR.M

R.SHS\*GTSPDNTAPPPPPPRPQPSHS\*R.S

R.SHS\*GTSPDNT\*APPPPPPRPQPSHSR.S

R.S\*SSSQTLTQFDSNIAPADPDTAIVHPVPIR.M

R.SSS\*S\*QTLTQFDSNIAPADPDTAIVHPVPIR.M

K.SPSMPSLNQT\*WPELNQSSEQWETFSER.S

K.S\*PSMPSLNQTWPELNQSSEQWETFSER.S

R.SHSGT\*S\*PDNTAPPPPPPRPQPSHSR.S

R.SHS\*GT\*SPDNTAPPPPPPRPQPSHSR.S

R.SHS\*GTS\*PDNTAPPPPPPRPQPSHS\*R.S

R.SHS\*GT\*SPDNTAPPPPPPRPQPSHS\*R.S

R.TSADAQEPAS\*PVVSPQQS\*PPTS\*PHTWR.K

R.TSADAQEPAS\*PVVS\*PQQS\*PPT\*SPHTWR.K

R.SSS\*SQTLTQFDS\*NIAPADPDTAIVHPVPIR.M

K.SPSMPS\*LNQTWPELNQSSEQWETFSER.S

R.SSSSQTLTQFDS\*NIAPADPDTAIVHPVPIR.M

R.SHSGTS\*PDNTAPPPPPPRPQPSHS\*R.S

R.HAASYSSDS\*ENQGSYSGVIPPPPGR.G

R.HAASYSS\*DSENQGSYSGVIPPPPGR.G

R.TSADAQEPASPVVS\*PQQS\*PPT\*SPHTWR.K

R.TGSDHTNPTS\*PLLVKPSDLLEENK.I

K.EVADIFNAPS\*DDEEFVGFR.D

R.IFIEDT\*DSET\*EDFAGFTQSDLNGK.T R.EDS\*T\*S\*ES\*EDDSRDESQESSDALLKR.T

R.IFIEDTDS\*ET\*EDFAGFTQSDLNGK.T

R.IFIEDT\*DS\*ETEDFAGFTQSDLNGK.T

K.DTHEDHDT\*S\*TENTDESNHDPQFEPIVSLPEQEIK.T

R.RQSSSY\*DDPWK.I

R.SSS\*LDMNR.T

R.TSADAQEPAS\*PVVSPQQS\*PPT\*SPHTWR.K

R.TGSDHTNPT\*SPLLVKPSDLLEENK.I

R.RQS\*SSYDDPWK.I

R.SS\*SLDMNR.T

K.DAVFDGSSCIS\*PTIVQQFGYQR.R K.DAVFDGS\*SCISPTIVQQFGYQR.R

R.ST\*STPNVHMVSTTLPVDSR.M

K.DAVFDGSS\*CISPTIVQQFGYQR.R R.STST\*PNVHMVSTTLPVDSR.M

R.SHSESASPSALSSS\*PNNLSPTGWSQPK.T

R.SHSESASPSALSS\*SPNNLSPTGWSQPK.T

R.SHSESASPSALSS\*SPNNLS\*PTGWSQPK.T

R.GDHAS\*LENEKPGTGDVCSAPAGR.N R.NQS\*PEPSSGPR.G

<-10 0 abundanc		ompared to	the			
-5 25 timepoint:	with the minimum	peak area f	or a given			
3 86 86 86 81 81 81 81 81 81 81 81 81 81 81 81 81		CarT	RajiB			
Protein Name Gene Ran binding protein 1 RANBP1	Phosphosites T18	9 # g	5 t d	Ascor 8.4	MOWSE	Sequence K.DTHEDHDTSTENT*DESNHDPQFEPIVSLPEQEIK.T
Ran binding protein 1 RANBP1	T18S21	•		-1.7	10.8	K.DTHEDHDTSTENT*DES*NHDPQFEPIVSLPEQEIK.T
Ran binding protein 1 RANBP1	S14T15			5.6	21.8	K.DTHEDHDTS*T*ENTDESNHDPQFEPIVSLPEQEIK.T
Ran binding protein 1 RANBP1	T15S21			7.1	14.3	K.DTHEDHDTST*ENTDES*NHDPQFEPIVSLPEQEIK.T
Ran binding protein 2 RANBP2	T1156			4.0	20.1	K.NHET*DGGSAHGDDDDDGPHFEPVVPLPDKIEVK.T
Ran binding protein 2 RANBP2	S2900		•	64.1	38.3	K.VGEDEDGS*DEEVVHNEDIHFEPIVSLPEVEVK.S
Ran binding protein 2 RANBP2	S1509	•••		13.8	24.9	R.KQS*LPATSIPTPASFK.F
Ran binding protein 2 <sub>RANBP2</sub>	S788	•	•	16.1	21.3	K.YSLS*PSK.S
Ran binding protein 2 <sub>RANBP2</sub>	S1400			-0.2	47.2	K.TS*PENVQDR.F
Ran binding protein 3 RANBP3	S539	•	•	24.2	49.8	K.
Ran binding protein 3 RANBP3	S548	•••		9.6	40.8	K.
Ran binding protein 3 RANBP3	S211	•••		18.2	15.5	K.ALSQTVPSSGTNGVSLPADCTGAVPAAS*PDTAAWR.S
Ran binding protein 3 RANBP3	\$101\$108	•		4.5	22.1	R.SAGGSS*PEGGEDS*DREDGNYCPPVKR.E
Ran binding protein 3 RANBP3	S333	-		62.7	51.6	R.VLS*PPKLNEVSSDANR.E
Ran binding protein 3 RANBP3	S96S101S108			3.7	13.3	R.S'AGGSS'PEGGEDS'DREDGNYCPPVK.R
Ran binding protein 3 RANBP3	S533S539			15.5	12.9	K. MDADEDGAADS*NEEDDS*DDDDU// ADSGATAAGAGDEGDGGTTG
Ran binding protein 3 RANBP3	S100S108			16.2	12.0	R.SAGGS*SPEGGEDS*DREDGNYCPPVKR.E
Ran binding protein 3 RANBP3	\$100\$101\$108	Ţ		13.8	12.1	R.SAGGS*S*PEGGEDS*DREDGNYCPPVK.R
Ran binding protein 3 RANBP3	<b>S</b> 533	<u>.</u> .			35.5	K.
Ran binding protein 3 RANBP3	S96S100S108			10.2	11.1	R.S*AGGS*SPEGGEDS*DREDGNYCPPVK.R
RAN binding protein 3-like RANBP3L	T142		<u> </u>	100.0	14.2	R.KT*FGHK.A
RAN binding protein 9 RANBP9	\$470\$485			-0.7	15.3	K.S*QDSYPVSPRPFSSPS*MSPSHGMNIHNLASGK.G
RANBP9	\$477\$482\$487			19.0	11.3	K.SQDSYPVS*PRPFS*SPSM#S*PSHGMNIHNLASGK.G
RANBP9	\$477\$482\$485			23.4	21.2	K.SQDSYPVS*PRPFS*SPS*M#SPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$487			26.2	26.5	K.SQDSYPVS*PRPFSSPSMS*PSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$483\$487			27.8	37.2	K.SQDSYPVS*PRPFSS*PSMS*PSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$487\$489			15.1	11.9	K.SQDSYPVS*PRPFSSPSM#S*PS*HGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$482\$483\$485			12.6	18.0	K.SQDSYPVSPRPFS*S*PS*M#SPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$482			15.6	15.4	K.SQDSYPVS*PRPFS*SPSMSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$482\$483			16.8	18.6	K.SQDSYPVS*PRPFS*S*PSMSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	Y474S487	<u> </u>		9.8	16.9	K.SQDSY*PVSPRPFSSPSMS*PSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	S477S485			22.1	25.6	K.SQDSYPVS*PRPFSSPS*MSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$485\$487			19.2	18.5	K.SQDSYPVS*PRPFSSPS*MS*PSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	Y474S485	<b></b> :		11.1	23.2	K.SQDSY*PVSPRPFSSPS*MSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$482\$485	Ħ.		-1.1	13.2	K.SQDSYPVSPRPFS*SPS*MSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$483\$485			4.1	11.9	K.SQDSYPVSPRPFSS*PS*MSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$483			18.5	12.0	K.SQDSYPVS*PRPFSS*PSMSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$482\$483	<u> </u>		3.1	10.9	K.SQDSYPVSPRPFS*S*PSMSPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$470\$473¥474				22.2	K.S'QDS'Y'PVSPRPFSSPSM#SPSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$485\$487	÷.		6.0	11.6	K.SQDSYPVSPRPFSSPS*MS*PSHGMNIHNLASGK.G
RAN binding protein 9 RANBP9	\$477\$483\$489			13.4	23.7	K.SQDSYPVS*PRPFSS*PSMSPS*HGMNIHNLASGK.G
RANBP9  RAN, member RAS oncogene family RAN	\$477\$482\$489			9.9	15.1	K.SQDSYPVS*PRPFS*SPSM#SPS*HGMNIHNLASGK.G
	S135	<u> </u>		100.0	27.4	K.S*IVFHR.K
Rap guanine nucleotide exchange factor 6RAPGEF6  Rap guanine nucleotide exchange factor RAPGEF6		-		8.4	19.9	K.LGDVTDADS*EADENEQVSAV  R.RSS*LLNAK.K
Rap guanine nucleotide exchange factor RAPGEF6  GEF 6  Rap guanine nucleotide exchange factor RAPGEF6				9.8	22.4	R.RSS*LLNAK.K  K.GLIVYCVTS*PK.K
GEF 6  RAP1 GTPase activating protein 1 RAP1GAP		==		16.9	27.9	K.AGISLIVPGKS*PTR.K
Rap1 interacting factor 1 RIF1				13.9	35.1	K.AAGISLIVPGKS*PTR.K  K.SNES*VDIQDQEEK.V
Rap1 interacting factor 1 RIF1	\$1579 \$2196			6.9	39.9	R.SQEDEISS*PVNK.V
Rap1 interacting factor 1 RIF1	\$2196 \$2144			12.1	76.6	K.VEEPSQCLASGTAISELIIEDNNAS*PQK.L
Rap1 interacting factor 1 RIF1	\$2144 \$2195			47.7	19.7	R.SQEDEIS*SPVNK.V
Rap1 interacting factor 1 RIF1	\$2195 \$1454			100.0	60.5	K.S*PLHIKDDVLPK.Q
APBB1IP	\$1454 \$526			-0.4	59.6	R.SS*DTSGSPATPLK.A
RAP80 UIMC1	S677			100.0	23.1	R.DLNES*PVK.S
RAP80 UIMC1	S463			18.8	17.6	R.EVS'PGSR.D
RaptorRPTOR	S722	-		15.0	35.5	R.SVSS'YGNIR.A
RaptorRPTOR	S877		• • •	62.5	108.0	K.GVHIHQAGGS*PPASSTSSSSLTNDVAK.Q
RaptorRPTOR	T857S863			15.6	56.6	R.VLDTSSLT*QSAPAS*PTNK.G
RaptorRPTOR	\$859\$863			24.3	72.4	R.VLDTSSLTQS*APAS*PTNK.G
RaptorRPTOR	S863	•	• • •	19.3	71.8	R.VLDTSSLTQSAPAS*PTNK.G
RaptorRPTOR	S721			10.6	12.3	R.SVS*SYGNIR.A
Ras association (RaIGDS/AF-6) domain RASSF4	<b>S</b> 91		•	15.1	34.3	R.RPS*CPLKEPSPQNGNITAQGPSIQPVHK.A
family 4						

Peak Area %CV	White dot abundano	ts-Significant cha	nge in peptic compared to	the				
.5 25 -3 42 71	timepoint o	with the minimum	peak area fo	or a given				
3 86 5 >100			CarT	_RajiB_				
>10 Protein Name		Phosphosites	9 H H	9 H H	Ascor	MOWSE	Sequence	
RAS family, member RAB11B F	RAB11A	S42	·		17.0	64.5	K.S*TIGVEFATR.S	
RAS guanyl nucleotide releasing protein 1 p	RASGRP1	T710S715			19.6	18.6	K.TAQDTLYVLPSPT*SPCPS*PVLVR.K	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S616S625S627			16.7	21.2	R.AQS*VSLEGSAPS*PS*PMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S616S625			25.4	65.3	R.AQS*VSLEGSAPS*PSPMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S616			43.4	92.5	R.AQS*VSLEGSAPSPSPMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S178			45.4	45.8	R.RHS*SLIDIDSVPTYK.W	
RAS guanyl nucleotide releasing protein 2 p							R.AFS*FSLPRPGR.R	
					26.0	32.1		
RAS guanyl nucleotide releasing protein 2 p			•		5.4	34.1	R.AQSVS*LEGSAPSPS*PMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S618			5.3	60.9	R.AQSVS*LEGSAPSPSPMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S178S179			39.0	14.6	R.RHS*S*LIDIDSVPTYK.W	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S616S627			8.0	45.4	R.AQS*VSLEGSAPSPS*PMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	S622S625			16.0	33.2	R.AQSVSLEGS*APS*PSPMHSHHHR.A	
RAS guanyl nucleotide releasing protein 2 p	RASGRP2	C622C627			13.9	20.1	R.AQSVSLEGS*APSPS*PMHSHHHR.A	
								ACUD D
RAS guanyl releasing protein 3 F				-	10.8	10.8	R.APSLSSGHGS*LPGSPSLPPAQDEVFEFPGVT	лопк.В
Ras-GTPase activating protein binding of protein 2		T227			18.6	68.3	K.STT*PPPAEPVSLPQEPPKPR.V	
Ras-GTPase activating protein binding of protein 2	G3BP2	S141S149			64.3	122.5	R.YEDEVFGDS*EPELDEES*EDEVEEEQEER.Q	
Ras-GTPase activating protein binding or protein 2	G3BP2	S149			23.5	34.9	R.YEDEVFGDSEPELDEES*EDEVEEEQEER.Q	
Ras-GTPase activating protein binding	G3BP2	S141			13.8	32.8	R.YEDEVFGDS*EPELDEESEDEVEEEQEER.Q	
protein 2  Ras-GTPase activating protein binding of	33BP2	S225			8.4	23.9	K.S*TTPPPAEPVSLPQEPPKPR.V	
protein 2  Ras-GTPase-activating protein SH3-							K.SSS*PAPADIAQTVQEDLR.T	
domain-binding protein		S232			22.2	130.8		
Ras-GTPase-activating protein SH3- o domain-binding protein		S149			62.9	84.4	R.YQDEVFGGFVTEPQEES*EEEVEEPEER.Q	
Ras-GTPase-activating protein SH3- of domain-binding protein	G3BP1	S231			-0.3	117.9	K.SS*SPAPADIAQTVQEDLR.T	
Ras-GTPase-activating protein SH3-o	33BP1	S230			5.5	12.7	K.S*SSPAPADIAQTVQEDLR.T	
RB1 inducible coiled coil 1 <sub>F</sub>	RB1CC1	T238	-		-0.2	94.1	R.ST*ELVLSPDMPR.T	
RBM15B F	RBM15R	S552		. ===	12.1	37.3	R.TFLEGDWTS*PSK.S	
RBM15B F							R.RSSS'S'SAAASTPPPGPPAPADPLGYLPLHG	GVOVY C
		S231S232S233	_		12.6	12.3		JIWIK.U
RBM15B F		S265S267			100.0	18.8	R.S*LS*PVAAPPLREPR.A	
RBMX	RBMX	S208			39.3	26.3	R.DVYLS*PR.D	
RCAS1 E	BAG9	<b>S</b> 36			84.9	120.9	R.KLS*GDQITLPTTVDYSSVPK.Q	
RCAS1 E	BAG9	T41			8.7	39.3	R.KLSGDQIT*LPTTVDYSSVPK.Q	
RE repeats encoding gene	RERE	T144		=	-5.5	11.4	R.SPT*PALCDPPACSLPVASQPPQHLSEAGR.G	
							R.TS*PINEDIR.S	
RE repeats encoding gene F		\$600		-	-0.4	23.1		
RE repeats encoding gene F		S1106S1113S11		·	27.1	18.5	K.EEALDDAEEPES*PPPPPRS*PS*PEPTVVDTP:	SHASQSAF
Receptor expressed in lymphoid tissues Filike 1	RELL1	S109			9.5	47.2	K.IELNDS"VNENSDTVGQIVHYIMK.N	
Receptor expressed in lymphoid tissues Filike 1	RELL1	S109T116			4.4	20.3	K.IELNDS"VNENSDT"VGQIVHYIMK.N	
Receptor expressed in lymphoid tissues F	RELL1	S109S114			15.4	34.2	K.IELNDS*VNENS*DTVGQIVHYIMK.N	
like 1  Receptor expressed in lymphoid tissues F		S114T116			5.4	17.1	K.IELNDSVNENS*DT*VGQIVHYIMK.N	
like 1  Receptor TNFRSF-interacting serine-								
threonine kinase 1		\$320			117.6	101.9	R.MQS*LQLDCVAVPSSR.S	
RecQ protein like 3 p	BLM	S147	•		1.7	43.4	K.KLEFSSSPDS*LSTINDWDDMDDFDTSETSK.S	
Regulating synaptic membrane exocytosis p	RIMS3	S295S298			19.7	18.5	R.RLS*QSS*LESATSPSCS	
Regulating synaptic membrane exocytosis F	RIMS4	S6		-	10.9	15.1	M.ERSQS*R.L	
Regulator of G protein signaling 14 p	RGS14	S218			100.0	38.5	K.S*LPLGVEELGQLPPVEGPGGRPLRK.S	
Regulator of G protein signaling 14 p		\$40\$45				48.0	R.GSS*LSIHS*LPSGPSSPFPTEEQPVASWALSF	ER.I
					1.5			
Regulator of G protein signaling 14 F		\$40\$48			3.7	41.2	R.GSS*LSIHSLPS*GPSSPFPTEEQPVASWALSF	
Regulator of G protein signaling 14 F	RGS14	S48S51S52			1.6	31.7	R.GSSLSIHSLPS*GPS*S*PFPTEEQPVASWALS	FER.L
Regulator of G protein signaling 14 F	RGS14	S39S40S42			11.1	49.5	R.GS*S*LS*IHSLPSGPSSPFPTEEQPVASWALSI	ER.L
Regulator of G protein signaling 14 F	RGS14	S39S40S48			4.0	29.7	R.GS*S*LSIHSLPS*GPSSPFPTEEQPVASWALSI	FER.L
Regulator of G protein signaling 14 p	RGS14	\$39\$42\$48			7.1	40.5	R.GS*SLS*IHSLPS*GPSSPFPTEEQPVASWALS	FER.L
Regulator of G protein signaling 3 p			-				R.THS*EGSLLQEPR.G	
		S943		-	33.7	21.7		
Regulator of G protein signaling 3 p		S943S946		•	45.4	28.1	R.THS*EGS*LLQEPR.G	
Regulator of G protein signaling 3 p	RGS3	S916		•	3.1	27.4	K.RS*SMIETGQGAEGGLSLR.V	
Regulator of nonsense transcripts 1 L	JPF1	S1107			37.7	124.5	K.SQIDVALS*QDSTYQGER.A	
Regulator of nonsense transcripts 1 L	JPF1	S1127		•••	28.2	72.4	R.AYQHGGVTGLS*QY	
Regulator of nonsense transcripts 1	JPF1	S1107S1110			20.4	98.5	K.SQIDVALS*QDS*TYQGER.A	
Regulator of nonsense transcripts 1 (							R.AYQHGGVTGLSQY*	
		Y1129			12.1	71.6		
Regulatory factor X 1 p		S117		-	20.7	55.9	R.ASETVS*EASPGSTASQTGVPTQVVQQVQGT0	QQR.L
Regulatory factor X 1 F	RFX1	S120		<u> </u>	4.6	36.8	R.ASETVSEAS*PGSTASQTGVPTQVVQQVQGT	QQR.L
Regulatory factor X 3 influences HLA class F	RFX3	S664		-	54.3	85.6	R.VAQATGETPIAVMGEFGDLNAVS*PGNLDK.D	
Regulatory factor X domain containing 2 <sub>F</sub>	RFX7	S1178			35.4	76.4	R.NLS*GSTLYPVSNIPR.S	
Renal cell carcinoma, papillary 1 p		\$157\$159				43.8	K.IAAPELHKGDS*DS*EEDEPTK.K	
					45.9			
Renal cell carcinoma, papillary 1 p		S267			43.5	77.0	K.QITQEEDDS*DEEVAPENFFSLPEK.A	
Replication factor C1 F	RFC1	S108T110			-0.1	47.8	R.QDPVTYIS*ET*DEEDDFMCKK.A	

Peak Area	o abuni	e dots-Significant cha dance at 5%FDR o oint with the minimum	compared to	the			
3	42 PSM	one was all single	pour arou i	or a giron			
5 >10	>100			RajiB			
Rep	Protein Name Gene		8 4 5	5 g g	Ascor 10.2	MOWSE 37.5	Sequence K.NKPLS*PIKLTPTS*VLDYFGT*GSVQR.S
	lication factor C1 RFC1				15.6	23.5	R.S*YS*PR.S
	lication factor C1 RFC1	S368				52.1	K.ESVS*PEDSEK.K
	lication factor C1 RFC1		=		28.9		R.IIYDS*DS*ESEETLQVK.N
					43.7	84.3	
	lication factor C1 RFC1			•	19.1	85.2	R.IIY*DSDS*ESEETLQVK.N
	lication factor C1 RFC1				14.5	32.3	K.NKPLS*PIKLTPT*SVLDYFGTGSVQR.S
	lication factor C1 RFC1				26.8	65.7	K.NKPLS*PIKLT*PTSVLDYFGTGSVQR.S
	lication factor C1 RFC1				14.3	40.4	K.NKPLS*PIKLT*PTSVLDYFGT*GSVQR.S
Rep	lication factor C1 RFC1	S281Y282			14.0	17.3	R.S"Y"SPR.S
Rep	lication factor C1 RFC1	Y282S283			10.6	26.2	R.SY*S*PR.S
Rep	lication factor C1 RFC1	T161T171			18.2	40.7	K.LT*PTSVLDYFGT*GSVQR.S
Rep	lication factor C1 RFC1	T163T171			9.0	44.1	K.LTPT*SVLDYFGT*GSVQR.S
Rep	lication factor C1 RFC1	S156S164S173			6.3	51.9	K.NKPLS*PIKLTPTS*VLDYFGTGS*VQR.S
Rep	lication factor C1 RFC1	T163S164T171			5.3	41.8	K.NKPLSPIKLTPT*S*VLDYFGT*GSVQR.S
R	REST corepressor RCOR	R1 <b>S</b> 457	•		24.1	16.1	K.S*PDNSIK.M
R	REST corepressor RCOR	R1 S257			100.0	46.8	R.EREES*EDELEEANGNNPIDIEVDQNK.E
	ST corepressor 3 RCOR				24.5	31.1	R.HNQGDS*DDDVEETHPMDGNDS*DYDPKK.E
	Reticulon 2 <sub>RTN2</sub>				10.6	12.1	R.SVS*EPR.D
	RTN4						K.RRGSS*GSVDETLFALPAASEPVIR.S
					10.3	41.3	
	RTN4				12.2	48.5	K.RRGSSGS*VDETLFALPAASEPVIR.S
	Reticulon 4 RTN4				10.5	17.3	R.RGSSGSVDET*LFALPAASEPVIR.S
	Reticulon 4 RTN4	S181S182			16.4	48.9	R.RGS*S*GSVDETLFALPAASEPVIR.S
	RTN4	S181			9.1	43.8	K.RRGS*SGSVDETLFALPAASEPVIR.S
	Reticulon 4 RTN4	S184T188			5.5	12.5	R.RGSSGS*VDET*LFALPAASEPVIR.S
	Reticulon 4 <sub>RTN4</sub>	S181S184	,		10.6	41.2	R.RGS*SGS*VDETLFALPAASEPVIR.S
	RTN4	S182S184			3.1	21.9	R.GSS*GS*VDETLFALPAASEPVIR.S
	Reticulon 4 RTN4	S181T188			21.8	13.6	K.RRGS*SGSVDET*LFALPAASEPVIR.S
ļ	Retinoblastoma 1 RB1	S249			82.7	50.4	K.TAVIPINGS*PR.T
ļ	Retinoblastoma 1 RB1	T823T826			21.5	34.6	K.ISEGLPTPT*KMT*PR.S
1	Retinoblastoma 1 RB1	T373			124.8	44.3	R.KSNLDEEVNVIPPHT*PVR.T
	Retinoblastoma 1 RB1	T821T826				20.0	K.ISEGLPT*PTKMT*PR.S
	Retinoblastoma 1 RB1				18.9		K.TLQTDSIDSFET*QRTPR.K
		T353			17.2	24.3	
	Retinoblastoma 1 RB1	S788			18.0	51.7	R.S'PYKFPSSPLR.I
	Retinoblastoma 1 <sub>RB1</sub>	S788S794			26.8	36.3	R.S*PYKFPS*SPLR.I
	Retinoblastoma 1 RB1	S788S795			10.0	25.2	R.S*PYKFPSS*PLR.I
-	Retinoblastoma 1 RB1	Y790S794			24.3	39.9	R.SPY*KFPS*SPLR.I
	RB1	Т9				58.4	R.KT*AATAAAAAAEPPAPPPPPPEEDPEQDSG
	Retinoblastoma 1 <sub>RB1</sub>	S807S811			55.8	55.3	R.IPGGNIYIS*PLKS*PYK.I
	RB1	S37			80.2	47.6	R.KTAATAAAAAAEPPAPPPPPPEEDPEQID*G
	Retinoblastoma 1 RB1	Y606S612			7.3	17.9	K.DREGPTDHLESACPLNLPLQNNHTAADMY*LS
I	Retinoblastoma 1 RB1	S608S612			20.9	31.7	K.DREGPTDHLESACPLNLPLQNNHTAADMYLS*
	Retinoblastoma 1 RB1	T601			8.2	38.4	K.DREGPTDHLESACPLNLPLQNNHT*AADMYLS
	Retinoblastoma 1 RB1		==				R.S*PYKFPS*SPLRIPGGNIYIS*PLK.S
		\$788\$794\$807			37.8	23.9	
	Retinoblastoma 1 RB1	S838			33.2	34.1	R.ILVSIGES*FGTSEK.F
	Retinoblastoma 1 RB1	S855			100.0	58.7	K.INQMVCNS*DR.V
	Retinoblastoma 1 RB1	S807S811T821			13.1	29.3	R.IPGGNIYIS*PLKS*PYKISEGLPT*PTK.M
ı	Retinoblastoma 1 RB1	S807			44.9	65.7	R.IPGGNIYIS*PLK.S
I	Retinoblastoma 1 RB1	T583S588	جعة			16.1	K.DREGPT*DHLES*ACPLNLPLQNNHTAADMYL
I	Retinoblastoma 1 RB1	S794			71.6	30.4	R.SPYKFPS*SPLR.I
I	Retinoblastoma 1 <sub>RB1</sub>	S811Y813			5.9	13.4	R.IPGGNIYISPLKS*PY*K.I
-	Retinoblastoma 1 RB1	T601S612		•	5.9	14.9	R.EGPTDHLESACPLNLPLQNNHT*AADM#YLSP
	Retinoblastoma 1 RB1	\$807Y813	•		8.9	12.7	R.IPGGNIYIS*PLKSPY*K.I
	Retinoblastoma 1 RB1	S608		•		12.7	R.EGPTDHLESACPLNLPLQNNHTAADMYLS*PV
	Retinoblastoma 1 RB1				3.8		
		S624	=		6.5	19.6	R.VNS*TANAETQATSAFQTQKPLK.S
	Retinoblastoma 1 RB1	S350			28.3	15.3	K.TLQTDSIDS*FETQRTPR.K
	Retinoblastoma 1 RB1	Y790			9.2	47.2	R.SPY*KFPSSPLR.I
	Retinoblastoma 1 RB1	Y606S608S612			1.1	16.0	R.EGPTDHLESACPLNLPLQNNHTAADMY*LS*P
I	Retinoblastoma 1 RB1	T841	<b>—</b>		13.8	21.1	R.ILVSIGESFGT*SEK.F
I	Retinoblastoma 1 RB1	Y790S795			5.8	32.3	R.SPY*KFPSS*PLR.I
	Retinoblastoma 1 RB1	Y606S608			21.5	10.7	K.DREGPTDHLESACPLNLPLQNNHTAADMY*LS
I	Retinoblastoma 1 RB1	S788S795S807			9.6	11.6	R.S*PYKFPSS*PLRIPGGNIYIS*PLK.S
Retinoblastoma asso	ociated factor 600 UBR4				40.2	30.8	R.HVTLPS*SPR.S

Peak Area %CV	abundano		compared to	the			
.5 29 -3 42 0 71	timepoint v PSM	with the minimum					
5 >100 >10	tein Name Gene	Phosphosites		RajiB E E E	Accor	MOWSE	Sequence
Retinoblastoma associated		S2719			8.2	26.3	R.HVTLPSS*PR.S
Retinoblastoma binding		S1111			109.0	101.6	K.DLDLEPLS*DLEEGLEETR.D
Retinoblastoma binding		\$350 \$525		•••	100.0	28.2	R.ES*EFDIEDEDK.S  K.VQAELS*QPLTAGGAISELL
Retinoblastoma binding		\$1277			29.3	33.1	K.VTGTEGSSSTLVDYTSTSSTGGS*PVRK.S
Retinoblastoma binding	g protein 6 RBBP6	<b>S</b> 1179	•		65.5	71.4	K.LEVTEIVKPS*PK.R
Retinoblastoma binding	g protein 6 RBBP6	S1328	•		100.0	79.5	K.WDKDDFES'EEEDVK.S
Retinoblastoma binding	g protein 6 RBBP6	S873			46.9	34.3	R.NS*PFTR.G
Retinoblastoma binding	g protein 6 RBBP6	S770S772			100.0	33.4	R.S'RS'PQAFR.G
Retinoblastoma binding		S861			100.0	21.3	R.ENFS*PER.F
	oma like 1 <sub>RBL1</sub>	\$988 <b>T</b> 997			16.2	14.9	R.ISQQHSIYIS*PHKNGSGLT*PR.S  K.VKS*PVSLTAHSLIGAS*PK.Q
	oma like 2 RBL2	S749S762 T1065S1068			25.7	36.6	R.IQLSQNHPVYISPHKNET*MLS*PR.E
	oma like 2 RBL2	\$1059\$1068			9.8	21.2	R.IQLSQNHPVYIS*PHKNETMLS*PR.E
Retinoblast	oma like 2 RBL2	\$1059T1065	=		13.9	32.9	R.IQLSQNHPVYIS*PHKNET*MLSPR.E
RFFL ring finger and FYVE-li	ke domain hCG_2039	S240	• •		19.2	75.9	R.RAS*LSDLTDLEDIEGLTVR.Q
	hCG_2039	S242			6.1	137.1	R.ASLS*DLTDLEDIEGLTVR.Q
	ontaining 1	\$226\$229\$232			18.2	42.3	R.VPAEDETQS*IDS*EDS*FVPGR.R
	ontaining 1			-	-0.2	15.2	R.ASLSDLT*DLEDIEGLTVR.Q
RGD, leucine-rich repeat, tropomo proline-rich containi Rho family-interacting cell po	na protein		<del>-</del> -		100.0	23.2	R.AVS*VHEDQLQAPAERPLR.L
RHO GDP dissociation inh	regulator 1	\$20 \$146			9.0	19.8	R.THS*MMSLSVRPQR.R  K.ATFMVGS*YGPRPEEYEFLTPVEEAPK.G
Rho GTPase activating p					60.5	42.7	R.RQS*VGDFVSGALNK.F
Rho GTPase activating					19.1	33.5	R.ATT*PPNQGRPDS*PVYANLQELK.I
Rho GTPase activating	protein 15 ARHGAP1	<b>S</b> 43	•		61.5	58.7	K.S*MILTDVGK.V
Rho GTPase activating	protein 15 ARHGAP1	S212			12.0	51.1	R.SSS*TELLSHYDSDIK.E
Rho GTPase activating					100.0	21.5	R.NHS*QHILK.D
Rho GTPase activating				•	12.6	39.8	R.SSST*ELLSHYDSDIK.E
Rho GTPase activating				<u></u>	18.6	61.1	R.SPS*PPTQHTGQPPGQPSAPSQLSAPR.R  R.NNS*GIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLR.R
Rho GTPase activating					40.0	32.7 46.0	R.S'PS'PPTOHTGQPPGQPSAPSQLSAPR.R
Rho GTPase activating					11.6	33.7	R.S*PSPPT*QHTGQPPGQPSAPSQLSAPR.R
Rho GTPase activating					15.6	31.0	R.NNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPS*PHTLR.R
Rho GTPase activating	protein 17 ARHGAP1	S598T601			16.7	44.4	R.SPS*PPT*QHTGQPPGQPSAPSQLSAPR.R
Rho GTPase activating	protein 17 ARHGAP1	\$598 <b>T</b> 604	-		3.4	39.2	R.SPS*PPTQHT*GQPPGQPSAPSQLSAPR.R
Rho GTPase activating	protein 17 ARHGAP1	T604			24.1	35.2	R.SPSPPTQHT*GQPPGQPSAPSQLSAPR.R
Rho GTPase activating			<b>—</b>		-1.9	16.7	R.S'PSPPTQHT'GQPPGQPSAPSQLSAPR.R
Rho GTPase activating				_	13.8	28.8	R.TMS*QDLR.Q
Rho GTPase activating  Rho GTPase activating					26.0	71.4	K.GS*GSLEGEAAGCGR.Q  K.GS*GS*LEGEAAGCGR.Q
Rho GTPase activating			• • •		17.0	76.9	R.S*YAFETQANPGK.G
Rho GTPase activating			-		-0.1	86.0	K.GSGS*LEGEAAGCGR.Q
Rho GTPase activating	protein 30 ARHGAP3	Y876			-0.3	79.5	R.SY*AFETQANPGK.G
Rho GTPase activating	protein 30 ARHGAP3	<b>S</b> 785			13.9	68.6	R.NGGSLS*FDAAVALAR.D
Rho GTPase activating					100.0	33.6	R.S*IFNLGR.S
Rho GTPase activating					54.2	65.9	R.LSGSGPAELS*AGEDEEEESELVSKPLLR.L
Rho guanine nucleotide exchangement of the second of the s					27.4	35.9	R.SES'LRVS'DR.R
Rho guanine nucleotide exchange					0.4	102.6 62.3	R.SRS'DVDMDPSSATAVLGPAR.R
Rho guanine nucleotide exchan					-0.4	26.5	R.
Rho guanine nucleotide exchange					32.1	82.2	R.ILSQS*TDSLNMR.N
Rho guanine nucleotide exchan	ge factor 2 <sub>ARHGEF2</sub>	S172			13.4	98.4	R.ILS*QSTDSLNMR.N
Rho guanine nucleotide exchan	ge factor 2 ARHGEF2	S122		•••	25.6	52.2	R.ERPSS*AIYPSDSFR.Q
Rho guanine nucleotide exchang	ge factor 2 <sub>ARHGEF2</sub>	S151			12.6	155.4	K.SVS*TTNIAGHFNDESPLGLR.R
	ARHGEF2				33.2	56.4	K.SVS*TTNIAGHFNDES*PLGLR.R
Rho guanine nucleotide exchang					66.7	125.0	R.S'LPAGDALYLSFNPPQPSR.G
Rho guanine nucleotide exchang			<u> </u>		100.0	22.4	R.LS'PPHS'PR.D  R.ILSQS'TDS'LNMR.N
Rho guanine nucleotide exchang					16.9	21.9	R.ILSQS*IDS*LNMR.N  K.SVSTTNIAGHFNDES*PLGLR.R
Rho guanine nucleotide exchang					25.4	66.2	R.SLPAGDALY*LSFNPPQPSR.G
Rho guanine nucleotide exchange					13.0	48.2	R.ILSQS'T'DSLNMR.N
Rho guanine nucleotide exchang	ge factor 2 <sub>ARHGEF2</sub>	<b>S</b> 695			6.8	30.7	R.EPALPLEPDSGGNTS*PGVTANGEAR.T

Peak Area %	abundano		compared to	the			
-6 29 -3 42 0 71		with the minimum					
3 86 5 >100 >10			CarT				
P Rho guanine nucleotide excha	rotein Name Gene ange factor 2 <sub>ARHGEF2</sub>	Phosphosites \$690	F 2 E	9 g	Ascor 4.8	MOWSE 25.3	Sequence R.EPALPLEPDS*GGNTSPGVTANGEAR.T
Rho guanine nucleotide excha	ange factor 2 <sub>ARHGEF2</sub>	S151T153			9.4	15.9	K.SVS*TT*NIAGHFNDESPLGLRR.I
Rho guanine nucleotide excha	ange factor 2 <sub>ARHGEF2</sub>	T678			100.0	48.5	K.DLLVGPGVELLLT*PR.E
Rho guanine nucleotide excha					4.1	11.3	R.ILS*QST*DSLNMR.N
Rho guanine nucleotide excha			•		100.0	48.0	R.QELGS*PEERL
Rho guanine nucleotide excha				<u> </u>	5.9	18.3	K.SVS*T*TNIAGHFNDESPLGLRR.I
Rho guanine nucleotide excha					18.9	11.2 88.2	R.ERPSS*AIYPS*DSFRQSLLGSR.R  K.SVST*TNIAGHFNDESPLGLR.R
Rho guanine nucleotide excha					14.3	43.8	K.SVSTT*NIAGHFNDES*PLGLR.R
Rho guanine nucleotide excha					41.9	18.6	R.ERPS*SAIYPSDSFR.Q
Rho guanine nucleotide excha	ange factor 2 <sub>ARHGEF2</sub>	S172S177			10.0	21.2	R.ILS*QSTDS*LNMR.N
Rho guanine nucleotide excha					100.0	17.6	R.KLS*FEKK.K
Rho guanine nucleotide excha			Ļ		49.2	25.6	R.KPS*EEEYVIR.K
Rho guanine nucleotide exchi					45.8	46.7	R.MS*GFIYQGK.I
Rho guanine nucleotide excha					45.7	105.0	R.SSSLSAANTSQT*NPQGAVSSTVSGLQR.Q  R.KDS*IPQVLLPEEEK.L
Rho guanine nucleotide excha					100.0	85.0 54.4	K.S*TAALEEDAQILK.V
Rho guanine nucleotide excha					5.3	76.4	R.SS*SLSAANTSQTNPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha					7.9	47.1	R.SSS*LSAANTSQTNPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha	ange factor 6 ARHGEF6	S124S126	•		8.4	87.9	R.SSS*LS*AANTSQTNPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha					4.2	72.0	R.SSS*LSAANTSQT*NPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha			<del></del>		-0.4	34.9	K.ST*AALEEDAQILK.V
Rho guanine nucleotide exchi			•		14.9	205.3	R.SSSLS*AANTSQTNPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha					7.7	84.1	R.SSS*LSAANT*SQTNPQGAVSSTVSGLQR.Q  R.SSSLS*AANTSQT*NPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha		\$126T133 \$739\$740\$742	لتبه		1.0	71.8	R.RS*S*LS*AANTSQT*NPQGAVSSTVSGLQR.Q
Rho guanine nucleotide excha		\$739\$740\$742 \$739\$740			28.6	15.5	R.RS*S*LSR.L
Rho guanine nucleotide excha		S739			14.9	24.9	R.RS*SLSR.L
Rho guanine nucleotide excha	ange factor 7 <sub>HIVEP3</sub>	\$739\$742		<u> </u>	10.3	13.3	R.RS*SLS*R.L
Rho specific guanine nucleoti	factor p114		•	-	18.6	26.1	K.AGGTALLPGPPAPS*PLPATPLS*AK.E
Rho specific guanine nucleoti	factor p114					21.8	R.S*LS*PILPGRHSPAPPPDPGFPAPSPPPADSPSEGFSLK.A
Rho specific guanine nucleoti	tactor b114					15.3	R.S'LS'PILPGRHS'PAPPPDPGFPAPSPPPADSPSEGFSLK
Rho specific guanine nucleoti	factor p114				6.9	43.9	K.AGGTALLPGPPAPSPLPATPIS*AK.E  K.AGGTALLPGPPAPSPLPAT*PLS*AK.E
Rho specific guanine nucleoti	de exchange ARHGEF1				16.9	26.7	R.SLS*PILPGR.H
Rho specific guanine nucleoti	de exchange ARHGEF1				31.1	21.9	KAGGTALLPGPPAPSPLPAT*PLSAK.E
	RhoGAP1 ARHGAP1				12.6	51.0	K.SSS*PELVTHLK.W
Ribonucle	ase P, 29 KD <sub>POP4</sub>	S38T39		<u> </u>	100.0	30.9	R.RS*T*PR.S
Ribonucleotide reductase	e M2 subunit RRM2	S20		•••	137.3	71.7	R.VPLAPITDPQQLQLS*PLK.G
Ribosomal L1 domain		S361			25.8	80.4	K.ATNES*EDEIPQLVPIGK.K
Ribosomal L1 domain		T358			6.1	31.3	K.AT*NESEDEIPQLVPIGK.K
Ribosomal phosphopro		\$102\$105			100.0	68.8	K.DEKKEES*EES*DDDMGFGLFD  R.YVASYLLAALGGNSS*PSAK.D
Ribosomal phosphopro		S17 S16			7.6	70.5	R.YVASYLLAALGGNS*PSAK.D
	I protein L14 RPL14	S139			100.0	47.3	K.AALLKAS'PK.K
Ribosoma	I protein L17 RPL17-	S142			14.9	45.1	R.INPYMSS*PCHIEMILTEK.E
Ribosoma	I protein L17 RPL17-	S141			8.5	40.2	R.INPYMS*SPCHIEMILTEK.E
Ribosomal	protein L23a RPL23A	T42		•••	8.0	18.4	K.IRT*SPTFR.R
	protein L23a RPL23A	S43			8.9	22.0	K.IRTS*PTFR.R
	I protein L31 RPL31	S98			15.5	55.1	R.NEDEDS'PNKLYTLVTYVPVTTFK.N
	I protein L31 RPL31	Y103			5.5	33.7	R.NEDEDSPNKLY*TLVTYVPVTTFK.N
	I protein S17 RPS17	S115 S113		-	-0.3 9.1	71.7	K.LLDFGSLS*NLQVTQPTVGMNFK.T  K.LLDFGS*LSNLQVTQPTVGMNFK.T
	al protein \$2 <sub>RPS2</sub>	S264			17.2	50.7	K.S'PYQEFTDHLVK.T
	al protein \$3 <sub>RPS3</sub>	T221			13.9	41.8	K.DEILPTT*PISEQK.G
Ribosom	al protein \$3 <sub>RPS3</sub>	T220		<del></del>	25.4	31.3	K.DEILPT*TPISEQK.G
Ribosoma	I protein S3a RPS3A	S263			102.5	36.0	R.ADGYEPPVQES*V
	I protein S3a RPS3A	S237		<b>.</b>	12.1	28.8	K.LMELHGEGSS*SGK.A
Ribosoma	I protein S3a RPS3A	S238		·	9.8	44.4	K.LMELHGEGSSS*GK.A
Pile	RPS6	S236S240			17.7	43.2	R.RLSS*LRAS*TSK.S
	al protein \$6 <sub>RPS6</sub>	\$235\$236 \$235			100.0	25.2	R.RRLS'S'LR.A  R.RRLS'SLR.A
	-14 30		-		0.9	23.0	

Peak Area %CV	abundand		compared to	the			
.5 29 .3 42	timepoint PSM	with the minimum	peak area f	or a given			
3 86 5 >100 >10			CarT				
Protein Ribosomal prot	Name Gene ein S6 <sub>RPS6</sub>	Phosphosites S236S240T241	£ 5, 5	9 # E	Ascor 0.7	MOWSE 12.3	Sequence R.RLSS*LRAS*T*SK.S
Ribosomal prot	ein S6 <sub>RPS6</sub>	S236T241			11.0	41.1	R.LSS*LRAST*SK.S
Ribosomal prot	ein S6 <sub>RPS6</sub>	\$235\$236\$240			1.1	12.6	R.RLS*S*LRAS*TSK.S
Ribosomal prot		S236			9.8	26.7	R.RRLSS*LR.A
Ribosomal protein S6 kinase a					8.8	66.2	K.AY*SFCGTVEYMAPEVVNR.Q
Ribosomal protein S6 kinase a  Ribosomal protein S6 kinase a					-0.2	25.6	K.AYSFCGT*VEYMAPEVVNR.Q  K.DS*PGIPPSANAHQLFR.G
Ribosomal protein S6 kinase a				•	43.9 5.8	31.8	K.AYS'FCGTVEYMAPEVVNR.Q
Ribosomal protein S6 kinase a					19.9	34.4	K.LFQGY*S*FVAPSILFK.R
Ribosomal protein S6 kinase a	lpha 5 RPS6KA5	Y375S381			12.6	55.7	K.LFQGY*SFVAPS*ILFK.R
Ribosomal protein S6 kinase, 7	'0kDa, RPS6KB1	T444S447	•		75.3	79.5	R.T'PVS'PVKFSPGDFWGR.G
Ribosomal protein S6 kinase, 7	'0kDa, RPS6KB1	\$447\$452			30.3	11.0	R.TPVS*PVKFS*PGDFWGR.G
Ribosomal protein, lar	ge, P0 RPLP0	S307	•		28.1	49.7	K.EESEES*DEDMGFGLFD
Ribosomal protein, lar	ge, P0 RPLP0	S304			16.1	41.8	K.EES*EESDEDMGFGLFD
Ribosomal protein, lar	ge, P0 RPLP0	\$304\$307	<u></u>		100.0	53.2	K.EES*EES*DEDM#GFGLFD
	RPLP1	S101			24.6	74.8	K.KEES*EESDDDMGFGLFD
	RPLP1	S101S104	•		100.0	69.2	K.KEES*EES*DDDMGFGLFD
Ribosomal RNA processing 12 hou	RPLP1	S104	-		22.8	27.1	K.EESEES'DDDMGFGLFD
Ribosomal RNA processing 12 ho		\$1080 \$1072			40.6	91.3	K.GDSIEEILADS*EDEEDNEEEER.S  K.GDS*IEEILADSEDEEDNEEEER.S
	RictorRICTOR	\$1072 \$1385Y1386	•	•	5.2 21.8	72.1	K.ALS'Y'ASLDKEDLLSPINQNTLQR.S
	Rictor RICTOR	\$1385\$1388			16.2	43.5	K.ALS*YAS*LDKEDLLSPINQNTLQR.S
	RictorRICTOR	S1282			13.1	56.1	K.S*NSVSLVPPGSSHTLPR.R
	RIMS1 RIMS1	S989T991			21.6	17.0	R.RSRS*PT*R.H
Ring Finger Pro	otein 1 RING1	S163T166T167				94.3	R. VEDDIDGS*DOT*T*TMSCGEGEDGEGEGGGEDVSSDSADDSADGD
Ring Finger Pro	otein 1 RING1	T238T243				24.2	R.GGT*LGGGT*LGPPSPPGAPSPPEPGGEIELVFRPHPLLVEK.G
Ring Finger Pro	otein 1 RING1	\$170\$187\$188			12.9	40.1	R. VEDDIDGEDOTTTME COECEDERCE DE COECED VE COECED NA DE LA DELA DELA DELA DELA DELA DELA DE
Ring Finger Pro	otein 1 RING1	S248S254			69.3	12.1	R.GGTLGGGTLGPPS*PPGAPS*PPEPGGEIELVFRPHPLLVEK.G
Ring Finger Pro	otein 1 RING1	S163T166T167	Ţ			16.8	R. VEDDIDGE*DOT*T*T*MSCGEGEGEGEGEGEGEGN/SSDSADDSADG
Ring finger prote		S301			12.2	42.0	K.SLTGQNTATNPPGLTGVSFSSSSSSSSSSS*PSNENATSNS
Ring finger prote		S297			3.7	22.9	K.SLTGQNTATNPPGLTGVSFSSSSSS*SSSSPSNENATSNS
Ring finger prote		S303			8.0	19.9	K.SLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSP8*NENATSNS
Ring finger prote		S298	<u></u>		5.9	23.8	K.SLTGQNTATNPPGLTGVSFSSSSSSS*SSPSNENATSNS  R.VPAPDTSIEET*ES*DAS*SDSEDVSAVVAQHSLTQQR.L
Ring finger prote		T288S290S293 S403			100.0	49.4	R.VLS'PLIIK.S
Ring finger pro		T197T199		•	100.0	10.9	R.T'KT'SDDSGLELDNNNAAMAIDPVMDGASEIELVFRPHPTLMEK.
RING finger prot	ein 20 RNF20	S138	_		7.8	17.6	K.ALVVPEPEPDSDS*NQER.K
RING finger prot	ein 29 <sub>TRIM55</sub>	S292			37.7	40.8	K.KISEAS*K.A
Ring finger pro	otein 4 <sub>RNF4</sub>	S94S95			36.1	50.3	R.RLPQDHADSCVVS*S*DDEELSR.D
RIO kir	nase 1 RIOK1	<b>S</b> 22	••		7.0	71.6	R.VVPGQFDDADSS*DSENR.D
RIO kii	nase 1 RIOK1	S21			22.0	42.0	R.VVPGQFDDADS*SDSENR.D
RIO kir	nase 2 RIOK2	\$380\$382\$385			22.3	58.5	R.SSGDPEQIKEDS*LS*EES*ADAR.S
	nase 2 RIOK2	S337	i i		10.2	43.8	K.EGSEFSFS*DGEVAEK.A
	nase 2 RIOK2	S442			52.5	50.8	R.VQGGVPAGS*DEYEDECPHLIALSSLNR.E
	nase 2 RIOK2	\$332\$335\$337	===		100.0	80.6	K.EGS*EFS*FS*DGEVAEK.A
	nase 2 RIOK2	\$390	===		71.4	99.8	R.S*FEMTEFNQALEEIK.G
	nase 2 RIOK2	\$370\$382\$385			13.8	24.2	R.SS*GDPEQIKEDSLS*EES*ADAR.S  K.EGSEFS*FSDGEVAEK.A
	nase 2 RIOK2	\$335 \$380\$382			13.4	52.7 24.0	R.SSGDPEQIKEDS*LS*EESADAR.S
	nase 2 <sub>RIOK2</sub>	Y445			13.2	15.1	R.VQGGVPAGSDEY*EDECPHLIALSSLNR.E
	RIP2 RIPK2	S393	-		24.5	65.9	K.LHHCPGNHS*WDSTISGSQR.A
	RIP2 RIPK2	<b>S</b> 527			29.8	56.0	K.QMGLQPYPEILVVS*R.S
	RIP2 RIPK2	S363			56.8	28.2	R.S*LPAPQDNDFLSR.K
	RIP2 RIPK2	S176		-	35.4	20.8	R.MMSLS*QSR.S
	RIP2 RIPK2	S531			1.4	56.9	R.SPS*LNLLQNK.S
	RIP2 RIPK2	<b>S</b> 396			13.7	61.8	K.LHHCPGNHSWDS*TISGSQR.A
RNA binding motif prot	ein 10 <sub>RBM10</sub>	S89			42.3	42.2	R.HRHS*PTGPPGFPR.D
RNA binding motif prof		S736S738			36.7	88.9	R.GLVAAYSGES*DS*EEEQER.G
RNA binding motif prot		S733S736S738			35.1	89.3	R.GLVAAYS*GES*DS*EEEQER.G
RNA binding motif prof		S661		-	100.0	13.0	R.S'LNKQK.E
RNA binding motif prof		\$733\$738		■.	22.1	30.5	R.GLVAAYS*GESDS*EEEQER.G
RNA binding motif prot	en iURBM10	Y732S736S738			17.6	62.0	R.GLVAAY*SGES*DS*EEEQER.G

<-10 0 abundan	ts-Significant cha ce at 5%FDR of with the minimum	compared to	the			
.s 23 timepoint	with the minimum	реак агеа п	or a given			
5 >100 ==================================		CarT				
Protein Name Gene RNA binding motif protein 10 <sub>RBM10</sub>	Phosphosites T91	£ 5 g	2 2 2	Ascor 10.9	MOWSE 19.0	Sequence R.HRHSPT*GPPGFPR.D
RNA binding motif protein 10 RBM10	Y732S733S738	=	• •	5.6	26.7	R.GLVAAY*S*GESDS*EEEQER.G
RNA binding motif protein 12 <sub>RBM12</sub>	S411			12.2	20.1	R.S*KSPSGQKR.S
RNA binding motif protein 12 <sub>RBM12</sub>	<b>S</b> 413			39.8	32.1	R.SKS*PSGQKR.S
RNA binding motif protein 13 <sub>MAK16</sub>	S199S200			1.9	80.6	K.ALEQQEAESDS*S*DTEEKDDDDDDEEDVGKR.E
RNA binding motif protein 13 <sub>MAK16</sub>	S197S199			22.9	57.0	K.ALEQQEAES*DS*SDTEEKDDDDDDEEDVGKR.E
RNA binding motif protein 13 <sub>MAK16</sub>	\$197\$199\$200	<b></b>		20.1	55.9	K.ALEQQEAES*DS*S*DTEEKDDDDDDEEDVGKR.E
RNA binding motif protein 13 <sub>MAK16</sub>	S229S232			100.0	82.9	R.EFVEDGEVDES*DIS*DFEDMDK.L
RNA binding motif protein 13 <sub>MAK16</sub>	\$197\$199\$200	<u> </u>		100.0	58.1	K.ALEQQEAES*DS*S*DT*EEKDDDDDDEEDVGKR.E
RNA binding motif protein 13 <sub>MAK16</sub> RNA binding motif protein 13 <sub>MAK16</sub>	S197S200	=		8.3	53.5	K.ALEQQEAES*DSS*DTEEKDDDDDDEEDVGKR.E
RNA binding motif protein 13 <sub>MAK16</sub>	S199T202	-		7.8	19.8	K.ALEQQEAESDS*SDT*EEKDDDDDDEEDVGKR.E  K.ALEQQEAESDS*S*DT*EEKDDDDDDEEDVGKR.E
RNA binding motif protein 14 <sub>RBM14</sub>	\$199\$200T202 \$520	•		-0.2	93.7	R.TQS*SASLAASYAAQQHPQAAASYR.G
RNA binding motif protein 14 RBM14	T572			19.1	92.0	R.GQPGNAYDGAGQPSAAYLSMSQGAVANANST*PPPYER.T
RNA binding motif protein 14 RBM14	S555		• • •	5.3	18.5	R.GQPGNAYDGAGQPS*AAYLSMSQGAVANANSTPPPYER.T
RNA binding motif protein 14 RBM14	S291				78.9	R.
RNA binding motif protein 14 RBM14	S582			32.3	28.0	R.TRLS*PPR.A
RNA binding motif protein 14 RBM14	S520S521			10.6	90.7	R.TQS*S*ASLAASYAAQQHPQAAASYR.G
RNA binding motif protein 14 RBM14	T206		•	100.0	30.4	R.QPT*PPFFGR.D
RNA binding motif protein 14 <sub>RBM14</sub>	<b>S</b> 571	· <del>· ·</del>		33.7	62.4	R.GQPGNAYDGAGQPSAAYLSMSQGAVANANS*TPPPYER.T
RNA binding motif protein 14 RBM14	S618		• • •	17.0	21.9	R.RLS*ESQLSFR.R
RNA binding motif protein 14 RBM14	Y548				39.5	R.GQPGNAY*DGAGQPSAAYLSMSQGAVANANSTPPPYER.T
RNA binding motif protein 14 RBM14	T579			14.9	20.9	R.T*RLSPPR.A
RNA binding motif protein 15 <sub>RBM15</sub>	T568	•		56.6	29.9	R.DRT*PPLLYR.D
RNA binding motif protein 15 RBM15	T265Y266			16.2	61.5	R.SRSPLDKDT"Y"PPSASVVGASVGGHR.H
RNA binding motif protein 15 RBM15	S257Y266			5.1	59.4	R.S*RSPLDKDTY*PPSASVVGASVGGHR.H
RNA binding motif protein 15 <sub>RBM15</sub>	S259T265	<u> </u>		4.9	59.9	R.SRS*PLDKDT*YPPSASVVGASVGGHR.H
RNA binding motif protein 15 RBM15	S292			10.6	60.5	R.S*LSPGGAALGYR.D
RNA binding motif protein 15 RBM15	S51			100.0	13.3	K.ERS*PVK.A
RNA binding motif protein 15 <sub>RBM15</sub>	S708	<u> </u>		100.0	16.4	R.RGS*LEK.S
RNA binding motif protein 15 <sub>RBM15</sub>	S259Y266			6.8	45.7	R.SRS*PLDKDTY*PPSASVVGASVGGHR.H  R.SLS*PGGAALGYR.D
RNA binding motif protein 15 <sub>RBM15</sub> RNA binding motif protein 15 <sub>RBM15</sub>	S294	=		16.7	69.7	R.HCAPS*PDRS*PELSSSR.D
RNA binding motif protein 15 <sub>RBM15</sub>	\$670\$674 \$257\$259			39.0	18.1	R.S*RS*PLDKDTYPPSASVVGASVGGHR.H
RNA binding motif protein 15 <sub>RBM15</sub>	\$257\$259 \$259	•		2.8	36.7 60.7	R.S*PLDKDTYPPSASVVGASVGGHR.H
RNA binding motif protein 15 <sub>RBM15</sub>	T265			2.0	18.9	R.SPLDKDT*YPPSASVVGASVGGHR.H
RNA binding motif protein 15 <sub>RBM15</sub>	\$700	=		100.0	17.3	R.LLLERPS*PIRDR.R
RNA binding motif protein 15 <sub>RBM15</sub>	S622			100.0	19.0	R.DGWS*LDR.D
RNA binding motif protein 15 <sub>RBM15</sub>	S257T265		• •	7.0	42.4	R.S*RSPLDKDT*YPPSASVVGASVGGHR.H
RNA binding motif protein 15 RBM15	S656	•		12.2	31.0	R.S*PESDRPR.K
RNA binding motif protein 19 RBM19	S949T957		•	9.9	29.1	R.SVVLDEILEQLEGS*DSDSEEQT*LQL-
RNA binding motif protein 19 RBM19	S953T957			13.4	19.2	R.SVVLDEILEQLEGSDSDS'EEQT'LQL
RNA binding motif protein 19 RBM19	S949S951			6.2	20.1	R.SVVLDEILEQLEGS*DS*DSEEQTLQL
RNA binding motif protein 19 RBM19	S949S953T957			19.5	17.3	R.SVVLDEILEQLEGS*DSDS*EEQT*LQL
RNA binding motif protein 25 <sub>RBM25</sub>	S677			55.2	101.9	K.LGASNS*PGQPNSVK.R
RNA binding motif protein 25 RBM25	<b>S</b> 703			100.0	60.8	K.FEDEDS*DDVPR.K
RBM33	S41			206.3	153.6	R.AADEDWDS*ELEDDLLGEDLLSGK.K
RNA binding motif protein 33 RBM33	S205			119.4	79.0	K.EES*DEEEEDDEESGR.L
RNA binding motif protein 34 <sub>RBM34</sub>	<b>S</b> 9	Ţ.		100.0	57.4	R.S*VQEGENPDDGVR.G
RNA binding motif protein 5 <sub>RBM5</sub>	S624			39.4	130.0	R.GLVAAYSGDS*DNEEELVER.L
RNA binding motif protein 6 <sub>RBM6</sub>	S362			20.3	73.6	R.EGETQGVAFEHESPADFQNSQS*PVQDQDK.S
RNA binding motif protein 6 RBM6	Y908			17.6	66.7	K.VVNPLIGLLGEY*GGDSDYEEEEEEEQTPPPQPR.T
RNA binding motif protein 6 <sub>RBM6</sub>	Y914			5.5	48.4	K.VVNPLIGLLGEYGGDSDY*EEEEEEQTPPPQPR.T  R.EGETQGVAFEHESPADFQNS*QSPVQDQDK.S
RNA binding motif protein 6 RBM6	\$360 T923			7.3	19.4	K.EGE I QGVAFEHESPADFQNS*QSPVQDQDK.S  K.VVNPLIGLLGEYGGDSDYEEEEEEEQT*PPPQPR.T
RNA binding motif protein 6 <sub>RBM6</sub>	T923 S912			-0.0	19.4	K.VVNPLIGLLGEYGGDS*DYEEEEEEEQTPPPQPR.T
RNA binding motif protein 7 RBM7	S912 S136			7.0	14.9	R.SFS*SPENFQR.Q
RNA binding motif protein 8A RBM8A	S42			41.9	30.3	R.GFGS*EEGSR.A
RNA binding motif protein 8A RBM8A	S166S168			100.0	15.6	R.S'RS'PDRR.R
RNA binding protein 4 <sub>RBM4</sub>	S309			100.0	16.6	R.DRS*PLRR.S
RNA binding protein 4 <sub>RBM4</sub>	S86			10.9	38.8	K.LHVGNIS*PTCTNK.E
RNA binding protein S1, serine-rich domain RNPS1	S27			22.6	28.3	R.APS'PTKR.K

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7	mepoint with th SM	ne minimum	<sub>P</sub> eak area fo	or a given			
3 86 5 >100			CarT	RajiB			
Protein Name		sphosites	9 J J	£ £ £	Ascor	MOWSE	Sequence
RNA binding protein S1, serine-rich domain R	NPS1 S139	9 <b>S</b> 141	-		100.0	15.0	R.S*KS*KPPKR.D
RNA binding protein S1, serine-rich domain R	NPS1 \$14	1	_		100.0	20.4	K.S*KPPKRDEK.E
R	NPS1 \$155	5 <mark>S</mark> 157	-		20.9	11.0	K.RRS*PS*PKPTK.V
RNA polymerase I transcription factor RRN3 R	RN3 S170	DS172			76.4	41.9	K.EGDVDVS*DS*DDEDDNLPANFDTCHR.A
RNA polymerase II associated protein 3 R	PAP3 \$116	6S119S121			21.7	34.3	R.ILDELDKDDSTHESLS*QES*ES*EEDGIHVDSQK.A
RNA polymerase II elongation factor ELLE	L <b>S</b> 437	7		• • •	0.6	21.3	R.LGLPLLTDCAQPS*RPHGSPSR.S
RNA polymerase II elongation factor ELLE					12.2	14.0	R.LGLPLLTDCAQPSRPHGS*PSR.S
RNA polymerase IIA 220 kd subunit p	-						K.YSPTS*PTYSPT*SPK.Y
		13 <b>T</b> 1919			14.1	19.9	
RNA polymerase IIA 220 kd subunit p	DLR2A S196	62			19.7	27.4	K.GSTYSPTSPGYSPTSPTYSLTSPAB*PDDSDEEN
RNA polymerase IIA 220 kd subunit p	DLR2A S19	13 <mark>S</mark> 1920			15.2	15.9	K.YSPTS*PTYSPTS*PK.Y
RNA polymerase IIA 220 kd subunit p	DLR2A Y190	09 <b>T</b> 1919			5.5	21.1	K.Y*SPTSPTYSPT*SPK.Y
RNA polymerase III subunit 5 p	DLR3E S16	1 <mark>S</mark> 162		•	100.0	92.7	R.EAANEAGDS*S*QDEAEDDVK.Q
RNA polymerase-associated protein RTF1 R	F1 \$53	S58S60		• • • •	14.6	36.1	R.VVIDS*DTEDS*GS*DENLDQELLSLAK.R
homoloα  RNA polymerase-associated protein RTF1 R			=				R.VVIDS*DT*EDS*GS*DENLDQELLSLAK.R
homoloa		T55858860	===		74.9	80.5	
RNA polymerase-associated protein RTF1 R homolog	TF1 T555	S58S60			1.7	29.4	R.VVIDSDT*EDS*GS*DENLDQELLSLAK.R
RNA polymerase-associated protein RTF1 R homolog	F1 S53	T55 <b>S</b> 58			10.2	72.7	R.VVIDS*DT*EDS*GSDENLDQELLSLAK.R
RNA U3 small nucleolar interacting protein R	RP9 <b>S</b> 508	S51S53			37.1	108.6	K.MNEEIS*S*DS*ESESLAPR.K
RNA U3 small nucleolar interacting protein R	RP9 \$508	S51S53S55			14.0	46.0	K.MNEEIS'S'DS'ES'ESLAPR.K
2 RNA U3 small nucleolar interacting protein R		S51S53S57		•	15.8	58.1	K.MNEEIS'S'DS'ESES'LAPR.K
2 RNA-binding protein 7 R				-			R.SGSSHAPQDVSLSYPOHHVGNS*SPTSTSPSSR.Y
			_=		12.2	22.8	
RNA-binding protein Raly R		В	<u> </u>		29.3	52.6	R.TRDDGDEEGLLTHS*EEELEHSQDTDADDGALQ
RNA-binding protein Raly R	ALY S288	BS295			22.8	40.0	R.TRDDGDEEGLLTHS*EEELEHS*QDTDADDGALQ
RNA-binding protein Raly R	ALY T286	SS295T298			28.3	39.7	R.TRDDGDEEGLLT*HSEEELEHS*QDT*DADDGALQ
RNA-binding protein Raly R	ALY T298	3			27.8	52.0	R.TRDDGDEEGLLTHSEEELEHSQDT*DADDGALQ
RNA-binding protein Raly R	AIY TOOK	SS288S295			55.5	34.1	R.TRDDGDEEGLLT*HS*EEELEHS*QDT*DADDGALQ
RNA-binding protein Raly R							R.TRDDGDEEGLLTHSEEELEHS*QDT*DADDGALQ
		5T298			10.5	37.8	
RNA-binding protein Raly R	ALY T286	SS288			20.3	33.2	R.TRDDGDEEGLLT*HS*EEELEHSQDTDADDGALQ
RNA-binding protein Raly R	ALY T286	3 <b>T</b> 298			13.5	38.6	R.TRDDGDEEGLLT*HSEEELEHSQDT*DADDGALQ
R	ALY S135	5	•		100.0	20.9	R.LS*PVPVPR.A
RNA-binding protein Raly R	ALY S288	8S295T298			7.9	18.3	R.TRDDGDEEGLLTHS*EEELEHS*QDT*DADDGALQ
RNA-binding protein Raly R	ALY \$288	BT298	•		15.6	34.6	R.TRDDGDEEGLLTHS*EEELEHSQDT*DADDGALQ
RNA-binding protein Raly R	0200						R.AAS*AIYSGYIFDYDYYR.D
		5			28.6	69.6	
RNA-binding protein Raly R		5	÷		2.5	11.5	R.TRDDGDEEGLLTHSEEELEHS*QDTDADDGALQ
RNA-binding protein Raly R	ALY T286	SS295	÷.		9.3	17.1	R.TRDDGDEEGLLT*HSEEELEHS*QDTDADDGALQ
Round spermatid basic protein 1-like R	SBN1L Y80	S96	Ļ		15.7	25.9	R.QLQPPAAPSPQSY*GSPASWSFAPLSAAPS*PSSSR.S
RUN domain containing 2A S	1X29 <b>S</b> 344	4			114.7	97.4	K.S*IDDEDVDENEDDVYGNSSGR.K
RY1 <sub>S</sub>	NRNP27 \$59	T60S61		• •	5.9	16.0	R.S*T*S*PSPSR.L
					3.3		
Ryanodine recentor 4 -	/P1	,	•			21.9	K KT*KI PK T
Ryanodine receptor 1 <sub>R</sub>		2		<u>.</u>	100.0		K.KT*KLPK.T
S phase kinase associated protein 2 S	(P2 S64	2	· •	<u>.</u>	100.0 30.2	28.9	K.EEPDSENIPQELLSNLGHPES*PPR.K
	(P2 S64		· · · · · · · · · · · · · · · · · · ·	·			
S phase kinase associated protein 2 S	(P2 S64 .TM S553		· ••••		30.2	28.9	K.EEPDSENIPQELLSNLGHPES*PPR.K
S phase kinase associated protein 2 S SAFB-like, transcription modulator S	TM \$55:	3		<u></u>	30.2 116.5	28.9	K.EPDSENIPGELLSNLGHPES*PPR.K K.S*PGHMVILDQTK.G
S phase kinase associated protein 2 s  SAFB-like, transcription modulator s  SAFB-like, transcription modulator s	TM S550 TM S550 TM S550	3 18553 08553			30.2 116.5 17.8 61.8	28.9 94.6 130.8 64.1	K.EEPDSENIPQELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.ISS*KS*PGHMVILDQTK.G
S phase kinase associated protein 2 S SAFB-like, transcription modulator S SAFB-like, transcription modulator S SAFB-like, transcription modulator S SAFB-like, transcription modulator S	TM S55: TM S55: TM S55: TM S55: TM S550:	3 18553 08553			30.2 116.5 17.8 61.8 39.1	28.9 94.6 130.8 64.1 34.2	K.EEPDSENIPGELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DQQQAIAQS*PEKESK.D
S phase kinase associated protein 2 s SAFB-like, transcription modulator s	(P2 S64  TM S55: TM S55: TM S55: TM S550  TM S289	3 18553 08553 9			30.2 116.5 17.8 61.8	28.9 94.6 130.8 64.1	K.ESPDENIPQELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.IS*KS*PGHMVILDQTK.G  K.DGQDAIAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G
S phase kinase associated protein 2 S SAFB-like, transcription modulator S SAFB-like, transcription modulator S SAFB-like, transcription modulator S SAFB-like, transcription modulator S	CP2 S64  TM S55:  TM S55:  TM S55:  TM S55:  TM S28:  TM S55:	3 18553 08553 9			30.2 116.5 17.8 61.8 39.1	28.9 94.6 130.8 64.1 34.2	K.EEPDSENIPQELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DQQQAIAQS*PEKESK.D
S phase kinase associated protein 2 s SAFB-like, transcription modulator s	CP2 S64  TM S553  TM S555  TM S556  TM S556  TM S556  TM S556  TM S286  TM S556  TM S100	3 18553 9 9 9 95551			30.2 116.5 17.8 61.8 39.1 68.5	28.9 94.6 130.8 64.1 34.2	K.ESPDENIPQELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.IS*S*KS*PGHMVILDQTK.G  K.DGQDAIAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G
S phase kinase associated protein 2 s SAFB-like, transcription modulator s	KP2         \$64           .TM         \$555           .TM         \$555           .TM         \$556           .TM         \$556           .TM         \$286           .TM         \$556           .TM         \$556           .TM         \$556           .TM         \$556           .TM         \$556           .TM         \$556	3 18553 08553 9 9 08551			30.2 116.5 17.8 61.8 39.1 68.5	28.9 94.6 130.8 64.1 34.2 53.4 36.9	K.S*PGHMVILDQTK.G  R.IS*KS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DGQDAIAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G
S phase kinase associated protein 2 s SAFB-like, transcription modulator s Saft inducible kinase 2 s Salt inducible kinase 2 s Salt inducible kinase 2 s	(P2 S64 .TM S55: .TM S55: .TM S56: .TM S28: .TM S28: .TM S56: .TM S56	3 18553 08553 9 9 08551			30.2 116.5 17.8 61.8 39.1 68.5 -0.2	28.9 94.6 130.8 64.1 34.2 53.4 36.9	K.EPPDSENIPGELLSNLGHPES*PPR.K  K.S*PGHMVILDQTK.G  R.IS*KS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DQQDAIAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G  R.AGAGMITQHSSNAS*PINR.I  R.RAS*DTSLTQGIVAFR.Q
S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	(P2 S64 .TM S55: .TM S55: .TM S55: .TM S28( .TM S55: .TM S10( .TM	3 18553 08553 9 9 08551			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9	K.EPPDSENIPGELLSNLGHPES*PPR.K K.S*PGHMVILDQTK.G R.ISS*KS*PGHMVILDQTK.G R.ISS*SKS*PGHMVILDQTK.G K.DQQDAIAQS*PEKESK.D R.ISS*KSSPGHMVILDQTK.G R.AGAGMITOHSSNAS*PINR.I R.RAS*DTSLTQGIVAFR.Q R.DLINFLEDNPS*LKDIMLANQPSPR.M
S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	KP2 S64  TM S55: TM S55: TM S55: TM S55: TM S55: TM S28: TM S55: TM S28: TM S56: TM S28: TM S56: TM S100  TM S1	3 18553 9 9 08561 02 7			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4 16.7	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 58.2 63.0	K.ESPDENIPQELLSNLGHPES*PPR.K  K.S*PGHMVILDOTK.G  R.IS*SKS*PGHMVILDOTK.G  K.DGODAIAGS*PEKESK.D  R.IS*SKSPGHMVILDOTK.G  R.AGAGMITOHSSNAS*PINR.I  R.RAS*DTSLTQGIVAFR.Q  R.DLNFLEDNPS*LKDIMLANQPSPR.M  R.TPSNTPSAEADWS*PGLELHPDYK.T
S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	KP2 S84  TM S55: TM S55: TM S55: TM S56: TM S28: TM S28: TM S10: TM S1	3 18553 9 9 08561 02 7			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 58.2 63.0 61.9	K.S*PGHMVILDQTK.G  R.IS*KS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DGQDAJAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G  R.AGAGMITGHSSNAS*PINR.I  R.RAS*DTSLTOGIVAFR.Q  R.DLNFLEDNPS*LKDMLANQPSPR.M  R.TPSNT*PSAEADWS*PGLELHPDYK.T  R.TPSNT*PSAEADWS*PGLELHPDYK.T
S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	KP2         S64           TM         S55:           TM         S55:           TM         S55:           TM         S56:           TM         S28:           TM         S10:           S50:         TM           S10:         S58:           K2         S58:           K2         S58:           MMHD1         T25:           MMHD1         T21:           MMHD1         S27:	3 18553 9 9 9 9 9 7 7 4			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4 16.7	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 58.2 63.0	K.EPDSENIPGELLSNLGHPES*PPR.K K.S*PGHMVILDOTK.G  R.IS*SKS*PGHMVILDOTK.G  K.DGODAIAGS*PEKESK.D  R.IS*S*KSPGHMVILDOTK.G  R.AGAGMITOHSSNAS*PINR.I  R.RAS*DTSLTQGIVAFR.Q  R.DLNFLEDNPS*LKDIMLANQPSPR.M  R.TPSNTPSAEADWS*PGLELHPDYK.T
S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	KP2         S64           TM         S55:           TM         S55:           TM         S55:           TM         S56:           TM         S28:           TM         S10:           S50:         TM           S10:         S58:           K2         S58:           K2         S58:           MMHD1         T25:           MMHD1         T21:           MMHD1         S27:	3 18553 9 9 9 9 9 7 7 4			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4 16.7 1.8	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 58.2 63.0 61.9	K.S*PGHMVILDQTK.G  R.IS*KS*PGHMVILDQTK.G  R.IS*SKS*PGHMVILDQTK.G  K.DGQDAJAQS*PEKESK.D  R.IS*S*KSPGHMVILDQTK.G  R.AGAGMITGHSSNAS*PINR.I  R.RAS*DTSLTOGIVAFR.Q  R.DLNFLEDNPS*LKDMLANQPSPR.M  R.TPSNT*PSAEADWS*PGLELHPDYK.T  R.TPSNT*PSAEADWS*PGLELHPDYK.T
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S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	CP2 S64  CP2 S64  CP2 S65  CP3 S65  CP4 S65  CP5 CP5 CP5 CP5  CP5 CP5 CP5  CP5 CP5 CP5 CP5  CP5 CP5 C	3 18553 9 9 9 9 9 9 7 7 4			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4 16.7 1.8 16.3 -0.5	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 58.2 63.0 61.9 55.3 23.0	K.EPPDSENIPGELLSNLGHPES*PPR.K K.S*PGHMVILDOTK.G R.IS*KS*PGHMVILDOTK.G R.IS*SKS*PGHMVILDOTK.G K.DGQDAIAQS*PEKESK.D R.IS*SKSPGHMVILDOTK.G R.AGAGMITGHSSNAS*PINR.I R.RAS*DTSLTQGIVAFR.Q R.U.NFLEDNPS*LKDIMLANOPSPR.M R.TPSNTPSAEADWS*PGLELHPDYK.T R.TPSNT*PSAEADWS*PGLELHPDYK.T R.TPSNT*PSAEADWS*PGLELHPDYK.T R.TPSNT*PSAEADWS*PGLELHPDYK.T
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S phase kinase associated protein 2 s SAFB-like, transcription modulator s SAFB-like,	(P)2 S64  TM S65: TM S65: TM S56: TM S56: TM S56: TM S10: TM S	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3			30.2 116.5 17.8 61.8 39.1 68.5 -0.2 44.7 95.4 16.7 1.8 16.3 -0.5 5.4	28.9 94.6 130.8 64.1 34.2 53.4 36.9 56.0 56.9 56.2 63.0 61.9 55.3 23.0 55.3	K.S*PGHMVILDQTK.G  RIS*S*KS*PGHMVILDQTK.G  RIS*S*KS*PGHMVILDQTK.G  K.DGQDAIAQS*PEKESK.D  RIS*S*KS*PGHMVILDQTK.G  K.DGQDAIAQS*PEKESK.D  R.AGAGMITQHSSNAS*PINR.I  R.RAS*DTSLTQGIVAFR.Q  R.DLNFLEDNPS*LKDIMLANQPSPR.M  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPSNTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.TPS*NTPSAEADWS*PGLELHPDYK.T  R.SSS*FGNFDR.F
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SAM	Protein Name Gene domain protein SAMSN1 SAMSN1	Phosphosites S123S125	2 2 2	<b>ជំ</b> ភ	Ascor 3.3	MOWSE 44.9	Sequence KAS*DS*MDSLYSGQSSSSGITSCSDGTSNR.D
SAM	domain protein SAMSN1 SAMSN1	S134S136		■.	6.3	66.8	K.ASDSMDSLYSGQS*SS*SGITSCSDGTSNR.D
SAM	domain protein SAMSN1 SAMSN1			•	10.0	44.6	K.ASDSMDSLYS*GQSSSSGITSCSDGTSNR.D
	Sam68 KHDRBS1					30.2	R.AS <sup>-</sup> PATQPPPLLPPSATGPDATVGGPAPTPLLPPSATASVKM
	Sam68 KHDRBS1			<u>.</u>	9.1	36.5	R.SGS*MDPSGAHPSVR.Q
	Sam68 KHDRBS1				5.9	15.7	RASPAT'OPPPLLPPSATGPDATVGGPAPTPLLPPSATASVK.M  R.S'GSMDPSGAHPSVR.Q
	SAP30-like SAP30L	S93S99			22.0	72.0	R.KTS'DDGGDS'PEHDTDIPEVDLFQLQVNTLR.R
	SAP30-like SAP30L	S93T104			7.1	31.5	R.KTS*DDGGDSPEHDT*DIPEVDLFQLQVNTLR.R
	SAP30-like SAP30L	T92T104			2.4	39.1	R.KT*SDDGGDSPEHDT*DIPEVDLFQLQVNTLR.R
	SAP30-like SAP30L	T92S99			4.8	22.6	R.KT*SDDGGDS*PEHDTDIPEVDLFQLQVNTLR.R
	SAPK substrate protein 1 UBXN1	S200	<b>-</b>		9.2	13.0	K.YGGSVGSQPPPVAPEPGPVPSS'PSQEPPTKR.E
	rcoma antigen NY-SAR-91 MEAF6	S118T120S122				12.8	K.REPGS*GT*ES*DTSPDFHNQENEPSQEDPEDLDGSVQGVKPQK.
	rcoma antigen NY-SAR-91 MEAF6	S118T120T124	=		3.3	20.7	K.REPGS*GT*ESDT*SPDFHNQENEPSQEDPEDLDGSVQGVKPQK.
	rcoma antigen NY-SAR-91 MEAF6	\$118\$122			2.2	18.4	KREPGS*GTES*DTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKA  REPGS*GTESDTS*PDFHNQENEPSQEDPEDLDGSVQGVKPQKA
	rcoma antigen NY-SAR-91 MEAF6	S118S125 S122T124S125			-1.0	13.4	K.REPGSGTES*DT*S*PDFHNQENEPSQEDPEDLDGSVQGVKPQK.
	rcoma antigen NY-SAR-91 MEAF6	S118T120S125			0.0	27.9	A  K.REPGS*GT*ESDTS*PDFHNQENEPSQEDPEDLDGSVQGVKPQK.
	SART1 SART1	S448			112.6	30.1	* R.RVS*EVEEKEPVPQPLPSDDTR.V
	SART1 SART1	\$474\$486			100.0	72.2	R.VENMDIS'DEEEGGAPPPGS'PQVLEEDEAELELQK.Q
	SART1 SART1	S596S607T608			11.8	25.0	R.SANGGS'ESDGEENIGWS'T'VNLDEEK.Q
	SART1 SART1	\$596\$598\$607			17.2	33.3	R.SANGGS*ES*DGEENIGWS*TVNLDEEK.Q
	SART1 SART1	S591S596S598		•••	26.3	37.7	R.S'ANGGS'ES'DGEENIGWSTVNLDEEK.Q
	SART1 SART1	\$598\$607 <b>T</b> 608			8.8	12.6	R.SANGGSES'DGEENIGWS'T'VNLDEEK.Q
	ffold Attachment Factor B SAFB	S604	<u></u>		44.5	32.5	R.SWS*FDK.V
	ffold Attachment Factor B SAFB2	T307	==		40.0	97.7	RTDCEPVGLEPAVEGSSAASELAEASSELAEAPTEAPSPEAR D  RTDCEPVGLEPAVEGSSAASELAEASSEELAEAPTEAPS PEAR D
	ffold Attachment Factor B SAFB	S197			18.0	69.4	K.ETINILDTSS: DFTILQEIEEPSLEPENEK.1
	ffold Attachment Factor B SAFB	S195			29.0	79.0	K.ETINNLDTS*SSDFTILQEIEEPSLEPENEK.I
Sca	ffold Attachment Factor B SAFB	S195S196			10.6	46.4	K.ETINNLDTS*S*SDFTILQEIEEPSLEPENEK.I
Sca	ffold Attachment Factor B SAFB	T194S195S197		• • • •	13.2	42.5	K.ETINNLDT'S'SS'DFTILQEIEEPSLEPENEK.I
Sca	ffold Attachment Factor B SAFB	S195S196S197			9.5	36.1	K.ETINNLDTS'S'S'DFTILQEIEEPSLEPENEK.I
	ffold Attachment Factor B SAFB	S373S384	•		14.1	58.1	K.ESS'TSEGADQKMSS'PEDDSDTKR.L
	ffold Attachment Factor B <sub>SAFB2</sub>	T340	•		6.8	35.3	R.TDCEPVGLEPAVEQSSAASELAEASSEELAEAPT 'EAPSPEAR.D
	ffold Attachment Factor B SAFB	S196		•••	8.0	69.1	KETINILDTSS'SDFTILQEIEEPSLEPENEKI
	ffold Attachment Factor B SAFB	T374S383			0.4	16.9	K.ESST'SEGADOKMS'SPEDDSDTKR.L  K.ELPEGLGEHAIEDKETINNLDT'SSSDFTILGEIEEPSLEPENEK.I
	ffold Attachment Factor B SAFB	S373S383			13.7	47.9	KESS*TSEGADQKMS*SPEDDSDTKR.L
Scar	ffold Attachment Factor B SAFB	T194S195			7.5	49.1	K.ETINNLDT'S'SSDFTILQEIEEPSLEPENEK.I
Scar	ffold Attachment Factor B SAFB	T374S384			10.8	52.8	K.ESST'SEGADQKMSS'PEDDSDTKR.L
Scar	ffold Attachment Factor B SAFB	S375S383	<b>!!!</b>		4.5	25.5	K.ESSTS'EGADQKMS'SPEDDSDTKRL
	ffold Attachment Factor B SAFB	T194S195S196			-1.1	27.8	K.ETINNLDT'S'S'SDFTILQEIEEPSLEPENEK.I
	ffold Attachment Factor B SAFB	\$373\$375			0.7	31.4	K.ESS*TS*EGADQKMSSPEDDSDTKR.L
	ffold Attachment Factor B SAFB	S195T200			11.3	23.0	K.ETINNLDTS'SSDFT*ILQEIEEPSLEPENEK.I
	Fold Attachment Factor B SAFB	S375S384	_		7.1	21.1	K.ESSTS*EGADQKMSS*PEDDSDTKRL
	ffold Attachment Factor B SAFB2	T245			31.6	16.7	K.SEPVKEESSELEOPFADOT'SSVGPDRKL  R.TDCEPVGLEPAVEGS'SAASELAEASSEELAEAPTEAPS'PEAR.D
	ffold Attachment Factor B SAFB	S321S344 S195S197			10.2	43.4	KETINLDTS'SS'DFTILQEIEEPSLEPENEK.
	ffold Attachment Factor B SAFB	S197T200	-		7.5	46.8	K.ETINNLDTSSS*DFT*ILQEIEEPSLEPENEK.I
Scar	ffold Attachment Factor B SAFB	T188		-		32.8	K.ET'INNLDTSSSDFTILQEIEEPSLEPENEK I
Sca	ffold Attachment Factor B SAFB	T200	•		1.2	12.4	K.ETINNLDTSSSDFT*ILQEIEEPSLEPENEK.I
Scar	ffold Attachment Factor B SAFB	T194S195T200		•	3.7	33.4	K.ETINNLDT'S'SSDFT'ILQEIEEPSLEPENEK.I
	ffold Attachment Factor B SAFB	T188S195S197			8.7	11.1	K.ET'INNLDTS'SS'DFTILQEIEEPSLEPENEK.I
	fold attachment factor B2 <sub>SAFB2</sub>	S109			59.8	45.9	K.MEEEGTEDNGLEDDS'R.D
Scat	fold attachment factor B2 SAFB2	S832			100.0	15.9	K.RLS*EGR.G
	SCC112 protein PDS5A Scribble SCRIB	S1265 S688T689			100.0	73.9	R.AAVGOES'PGGLEAGNAK.A  R.AEEEEAS'T'EEEDKEGAVVSAPSVK.G
	Scribble SCRIB	\$6881689 \$1220			96.4 57.3	90.1 52.2	RNS*LESISSIDRE
	Scribble SCRIB	\$1559\$1566			13.2	32.7	RLAEAPSPAPTPSPTPVEDLGPQTS*TSPGRLS*PDFAEELR.S
	Scribble SCRIB	T1558S1566			6.0	31.9	R.LAEAPSPAPTPSPTPVEDLGPQT*STSPGRLS*PDFAEELR.S
	Scribble SCRIB	T1342S1348			30.4	37.3	R.AFAAVPTSHPPEDAPAQPPT*PGPAAS*PEQLSFR.E
	Scribble SCRIB	T1560S1566	<b>—</b>		17.9	32.0	RLAEAPSPAPTPSPTPVEDLGPQTST*SPGRLS*PDFAEELR.S

Peak Area	0 abundan	ots-Significant cha ce at 5%FDR of with the minimum	compared to	the			
3 5 >10	>100			RajiB_			
	Protein Name Gene Scribble SCRIB	Phosphosites T1549S1566	5 t g	9 H H	Ascor 7.2	MOWSE 11.4	Sequence RLAEAPSPAPTPSPT*PVEDLGPQTSTSPGRLS*PDFAEELR.S
	Scribble SCRIB	S1547S1566			8.0	21.0	R.LAEAPSPAPTPS*PTPVEDLGPQTSTSPGRLS*PDFAEELR.S
	SCY1 like 1 SCYL1	S651	-		7.2	87.5	R.WDDEDWGS'LEQEAESVLAQQDDWSTGGQVSR.A
	SCY1-like 2 SCYL2	T679	-		10.9	28.4	K.RASLT*LEEK.Q
	SCY1-like 2 SCYL2	S677	-		20.1	35.3	K.RAS*LTLEEK.Q
	SDAD1 SDAD1  SDS3 SUDS3	\$525 \$234\$236			84.9 47.5	73.3	K.YIEIDS'DEEPR.G  K.RPAS'PS'SPEHLPATPAESPAOR.F
	SDS3 SUDS3	S236S237			8.2	30.6	K.RPASPS'S'PEHLPATPAESPAQR.F
	SDS3 SUDS3	S45T49T55			19.0	24.7	R.GRES'DEDT'EDASET'DLAKHDEEDYVEMK.E
	SDS3 SUDS3	S45T49S53	Ė		24.3	31.4	R.GRES*DEDT*EDAS*ETDLAK.H
	SEC16 homolog A SEC16A	\$587\$595 <b>T</b> 600			13.3	35.4	R.GS'VSQPSTPS'PPKPT'GIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	\$587T593			5.8	36.5	R.GS*VSQPST*PSPPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A SEC16 homolog A SEC16A	\$587T593\$595		_	9.1	20.6	R.GS*VSQPST*PS*PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	\$342 \$589\$592		-	100.0	18.3 74.3	R.GSVS*OPS*TPSPPKPTGIFQTSANSSFEPVKS
	SEC16 homolog A SEC16A	T197S201				36.1	R.  ANDURCHATEDANSEDSI DODGI ANDGOWACDIAGGEDOSCOMO S
	SEC16 homolog A SEC16A	S592T593S595			18.7	44.0	R.GSVSQPS'T'PS'PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	S589S592T593	••	_	13.4	36.0	R.GSVS'QPS'T'PS'PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	S592T593			19.7	55.2	R.GSVSQPS*T*PSPPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	S589T593S595			16.0	43.6	R.GSVS*QPST*PS*PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A  SEC16 homolog A SEC16A	\$589\$592\$595			14.0	77.2	R.GSVS'QPS'TPS'PPKPTGIFQTSANSSFEPVK.S  R.GS'VSQPS'TPS'PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	\$587\$592\$595 \$587\$592T600		===	12.2	41.6 29.3	R.GS*VSQPS*TPSPPKPT*GIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	S2022			68.3	61.2	R.S'PDPGIVPQEAPVGNSLSELSEENFDGK.F
	SEC16 homolog A SEC16A	\$587\$592 <b>T</b> 593			13.9	35.8	R.GS*VSQPS*T*PS*PPKPTGIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	S587T593T600		Ė	10.3	44.2	R.GS*VSQPST*PSPPKPT*GIFQTSANSSFEPVK.S
	SEC16 homolog A SEC16A	\$587\$589T593		Ė	11.3	33.4	R.GS*VS*QPST*PS*PPKPTGIFQTSANSSFEPVK.S
	SEC22B SEC22B	S137			46.9	104.7	RNLGS'INTELQDVQR.I
	SEC31 like 1 SEC31A	T1161			30.5	64.9	R.EQT*LSPTITSGLHNIAR.S
	SEC31 like 1 SEC31A	S527			17.1	54.9	K.DSDQVAQS*DGEESPAAEEQLLGEHIK.E  REOTLS*PTITSGLHNIAR.S
	SEC31 like 1 SEC31A	S1163 S527S532			10.7	13.9	K.DSDQVAQS*DGEES*PAAEEQLLGEHIK.E
	SEC63 SEC63	S593S597		•	100.0	39.7	K.DDGS*DRDS*DREQDEK.Q
Second	step splicing factor 1 PPAN-	<b>S</b> 359			79.1	121.0	R.VGGS*DEEASGIPSR.T
Second	step splicing factor 1 PPAN-	S238S240			4.8	78.9	RLQDISELLATGAGLS'ES'EAEPDGDHNITELPQAVAGR.G
	step splicing factor 1 PPAN-	S228T233			15.0	96.9	RLQDIS'ELLAT'GAGLSESEAEPDGDHNITELPQAVAGR.G
	step splicing factor 1 PPAN-	S238			17.2	64.0	RLQDISELLATGAGLS'ESEAEPDGDHNITELPQAVAGR.G
	step splicing factor 1 PPAN-	T233 T233S240			5.4	69.1	RLQDISELLAT'GAGLSESEAEPDGDHNITELPQAVAGR.G  RLQDISELLAT'GAGLSES'EAEPDGDHNITELPQAVAGR.G
	step splicing factor 1 PPAN-	T233S238		• • •	26.1	49.8	RLQDISELLAT'GAGLS'ESEAEPDGDHNITELPQAVAGR.G
Secreted friz	zled related protein 2 SFRP2	S287S289	•	• • •	100.0	16.9	K.RIS'RS'IR.K
Secreted friz	zled related protein 2 SFRP2	S289	ij		29.8	23.4	K.RISRS*IR.K
Secretory carrier	r membrane protein 2 SCAMP2	S320			-0.2	59.5	R.AASS*AAQGAFQGN
	r membrane protein 2 <sub>SCAMP2</sub>					53.6	R.AAS*SAAQGAFQGN-
	r membrane protein 3 SCAMP3		• •		111.4	36.7	R.DGGNPFAEPSELDNPFQDPAVIQHRRS'R.Q
Secretory carrier	r membrane protein 3 <sub>SCAMP3</sub> Selectin P ligand <sub>SELPLG</sub>		_		25.8	36.3	R.KLS'PTEPK.N  R.NYS'PTEMVCISSLLPDGGEGPSATANGGLSK.A
	Selectin P ligand SELPLG				5.7	70.9	R.NY'SPTEMVCISSLIPDGGEGPSATANGGLSK.A
	Selectin P ligand SELPLG				9.1	31.2	R.NYSPT*EMVCISSLLPDGGEGPSATANGGLSK.A
	Senataxin <sub>SETX</sub>	S1017S1019			100.0	82.5	R.GQVIIIS'DS'DDDDDER.I
Senescence do	wnregulated leo1 like LEO1	T188S197	-	• •	100.0	31.5	K.MQNT*DDEERPQLS*DDER.Q
Senescence do	wnregulated leo1 like LEO1	S212S220S229	<b></b>		100.0	35.1	KANS'DDERPVAS'DNDDEKQNS'DDEEQPQLS'DEEK.M
	wnregulated leo1 like LEO1	S294S296S300			47.4	77.9	K.NAIAS*DS*EADS*DTEVPK.D
	wnregulated leo1 like LEO1	S658	<u></u>		12.3	44.8	K.YVIS*DEEEEDD
	wnregulated leo1 like LEO1	\$171\$179 \$151\$154\$162			100.0	90.0	R.AQGS'DEDKLQNS'DDDEK.M  R.EDKS'DQS'DDEKIQNS'DDEERA
	wnregulated leo1 like LEO1	\$151\$154\$162 \$171\$179T188			100.0	21.7	RAQGS'DEDKLQNS'DDDEKMQNT'DDEERPQLS'DDER.Q
	wnregulated leo1 like LEO1	S271S273S277			100.0	15.1	K.S'ES'ARGS'DS'EDEVLR.M
Senescence do	wnregulated leo1 like LEO1	S162			100.0	40.2	K.IONS'DDEER.A
Senescence do	wnregulated leo1 like LEO1	S205			100.0	40.4	R.QQLS*EEEK.A
Senescence do	wnregulated leo1 like LEO1	S66S72S75S77			100.0	13.9	K.ELFGDDS'EDEGAS'HHS'GS'DNHS'ER.S
Senescence do	wnregulated leo1 like LEO1	S84S88S91	<b></b>		100.0	17.5	R.S'DNRS'EAS'ER.S

<-10 0	abundano		ompared to	the			
-5 25 42 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PSM	with the minimum					
5 >100 >100 Protein Name	Gene	Phosphosites	CarT	RajiB E E E	Ascor	MOWSE	Sequence
Sentrin specific protease 3 g		S232			14.8	60.2	K.S*PLDPDSGLLSCTLPNGFGGQSGPEGER.S
Sentrin specific protease 3 s		S169		•••	67.4	51.4	K.NHLS*PQQGGATPQVPSPCCR.F
Sentrin specific protease 7 S		\$443\$444			87.9	85.2	R.GHNEGNQSLISAEPIVVS*S*DEEGPVEHK.S  K.EEEIHIYQFPECDS*DEDEDFKRQDAEMK.E
septin 1 S		\$206 \$248	-:-		19.2	63.8	R.YS*WGTVEVENPHHCDFLNLR.R
septin 1 s		S315			84.3	75.4	R.QS*ATEIPLPMLPLADTEK.L
septin 1 S	EPT1	T251			15.4	43.3	R.RYSWGT*VEVENPHHCDFLNLR.R
septin 1 S	EPT1	T317			21.2	40.9	R.QSAT*EIPLPMLPLADTEK.L
septin 1 S	EPT1	Y247	•		7.8	33.1	R.RY*SWGTVEVENPHHCDFLNLR.R
Septin 2 <sub>S</sub>	EPT2	S218			63.9	109.8	K.IYHLPDAES*DEDEDFKEQTR.L
Septin 5 <sub>S</sub>		S225	-		72.9	72.1	K.FGIHVYQFPECDS*DEDEDFKQQDR.E
Sequestosome 1 S		S365			16.5	35.6	K.EVDPSTGELQSLQMPESEGPS*SLDPSQEGPTGLK.E
Sequestosome 1 S  Serine arginine repetitive matrix protein 1 S		S366		-	9.0	33.8	K.EVDPSTGELQSLQMPESEGPSS*LDPSQEGPTGLK.E
Serine arginine repetitive matrix protein 1 s		S597 T220			27.6	31.3	K.EKT*PELPEPSVK.V
Serine arginine repetitive matrix protein 1 s		S874		•	40.7 35.4	149.9	K.KETES*EAEDNLDDLEK.H
		S769S775			45.6	60.2	K.KPPAPPS*PVQSQS*PSTNWSPAVPVKK.A
s		S769S777			52.8	65.9	K.KPPAPPS*PVQSQSPS*TNWSPAVPVKK.A
Serine arginine repetitive matrix protein 1 S	RRM1	S769S775S781			22.4	29.2	K.KPPAPPS*PVQSQS*PSTNWS*PAVPVKK.A
Serine arginine repetitive matrix protein 1 S	RRM1	S769S777S781	• • •		14.3	53.6	K.KPPAPPS*PVQSQSPS*TNWS*PAVPVKK.A
Serine arginine repetitive matrix protein 1 S	RRM1	T872S874			100.0	108.3	K.KET*ES*EAEDNLDDLEK.H
Serine arginine repetitive matrix protein 1 S	RRM1	\$769\$777T778			8.2	13.9	K.KPPAPPS*PVQSQSPS*T*NWSPAVPVKK.A
Serine arginine repetitive matrix protein 1 s	RRM1	S769S773S781			25.4	29.1	K.KPPAPPS*PVQS*QSPSTNWS*PAVPVKK.A
Serine arginine repetitive matrix protein 1 S	RRM1	\$769\$773\$775			31.7	36.1	K.KPPAPPS*PVQS*QS*PSTNWSPAVPVKK.A
Serine arginine repetitive matrix protein 1 s		\$769\$773\$775			53.6	33.5	K.KPPAPPS*PVQS*QS*PSTNWS*PAVPVKK.A
Serine arginine repetitive matrix protein 1 S		\$705\$707	<u> </u>		13.4	19.6	R.RGAS*SS*PQR.R
Serine arginine repetitive matrix protein 1 S		S524S526	===		100.0	27.1	R.RHS*PS*R.S
Serine arginine repetitive matrix protein 1 S  Serine arginine repetitive matrix protein 1 S		S748			9.8	26.4	R.RVS*SSR.S
Serine arginine repetitive matrix protein 1 s		S541 T540			7.6	31.5	R.QKET'SPR.G
Serine arginine repetitive matrix protein 1 <sub>S</sub>		\$260			100.0	44.9	K.EPS*PEK.N
Serine arginine repetitive matrix protein 1 s		S292S294			30.2	29.7	R.S*PS*HTRPR.R
Serine arginine repetitive matrix protein 1 s	RRM1	S209S211			100.0	34.2	R.S*PS*PAPEKK.E
Serine arginine repetitive matrix protein 1 S	RRM1	\$207\$209\$211			100.0	21.0	K.S*RS*PS*PAPEKK.E
s	RRM1	S626S628	<del></del>		100.0	31.1	R.AS*PS*PPPKR.R
Serine arginine repetitive matrix protein 1 S	RRM1	T411T416			14.2	15.1	K.T*RHSPT*PQQSNR.T
s	RRM1	S186S187			100.0	20.8	R.RS*S*PVRR.E
Serine arginine repetitive matrix protein 1 S	RRM1	S683S685		•••	100.0	19.2	R.HS*PS*PRPR.A
Serine arginine repetitive matrix protein 1 s	RRM1	S904			16.0	40.8	R.KAQVSPQS*
Serine arginine repetitive matrix protein 1 g		S414			17.9	21.8	K.TRHS*PTPQQSNR.T
Serine arginine repetitive matrix protein 1 s		S316			100.0	23.1	R.RRPS*PR.R
Serine arginine repetitive matrix protein 1 s  Serine arginine repetitive matrix protein 1 s		\$450\$452	==		100.0	35.4	K.RES'PS'PAPKPR.K  R RVS'RT'PEPK K
Serine arginine repetitive matrix protein 1 s		\$725T727 \$369			100.0	22.5	R.S*PPKKPPKR.T
Serine arginine repetitive matrix protein 1 s		\$369 \$549T555			17.4	20.7	R.RRS*PSPPPT*R.R
Serine arginine repetitive matrix protein 1 U		S653			26.1	54.4	R.S*PSLSSK.H
Serine arginine repetitive matrix protein 1 s	RRM1	T572T574		• • •	100.0	37.0	R.T'PT'PPPR.R
Serine arginine repetitive matrix protein 1 S	RRM1	<b>S</b> 450			18.6	39.3	K.RES*PSPAPKPR.K
s	RRM1	T581S583	<b></b>		100.0	28.7	R.RRT*PS*PPPR.R
s	RRM1	\$560\$562	<b></b>		100.0	13.7	R.RRS*PS*PAPPPR.R
Serine arginine repetitive matrix protein 1 S		\$653 <b>\$</b> 655	<b></b>		14.2	20.3	K.RRS*PS*LSSK.H
Serine arginine repetitive matrix protein 1 s		S653S657			14.1	17.5	K.RRS*PSLS*SK.H
		T614S616			100.0	38.1	R.T*AS*PPPPPKR.R
Serine arginine repetitive matrix protein 1 S		S616	-		8.7	13.2	R.TAS*PPPPPKR.R
Serine arginine repetitive matrix protein 1 S  Serine arginine repetitive matrix protein 1 S		\$752\$754\$756		===	100.0	43.9	R.S*VS*GS*PEPAAK.K  R.VSVS*PGR.T
Serine arginine repetitive matrix protein 1 S		\$431 \$738\$740\$743			26.0	47.4	K.VSVS*PGR.1
Serine arginine repetitive matrix protein 1 s		\$738\$740\$743 \$695		===	-0.3	26.2	R.APQTSS*SPPPVRR.G
Serine arginine repetitive matrix protein 1 s		\$426\$431			9.1	28.4	R.KS'RVSVS'PGR.T
Serine arginine repetitive matrix protein 1 s		\$4205431 \$402T406			100.0	44.2	R.HRPS*PPAT*PPPK.T
Serine arginine repetitive matrix protein 1 S		S713S717			29.1	27.0	R.RQS*PSPS*TRPIR.R
Serine arginine repetitive matrix protein 1 S	RRM1	S713T718			23.2	21.6	R.RQS*PSPST*RPIR.R
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Peak Area	o at		compared to	the .			
3		nepoint with the minimu SM					
5 >10	>100 Protein Name G	ene Phosphosites	CarT_	RajiB E E E	Ascor	MOWSE	Sequence
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$463\$465			100.0	66.7	R.KVELS*ES*EEDKGGK.M
Serine arginine repetitiv				• • •	19.3	39.6	R.RLS*PS*ASPPR.R
Serine arginine repetitiv			3		100.0	24.9 42.9	R.RLS*PS*AS*PPR.R  K.KET*ESEAEDNLDDLEK.H
Serine arginine repetitiv					9.5	13.0	K.KPPAPPSPVQSQSPSTNWS*PAVPVKK.A
Serine arginine repetitiv			в	•	13.3	26.6	K.KPPAPPS*PVQS*QSPST*NWSPAVPVKK.A
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$901	• • •	•	12.2	46.1	R.KAQVS*PQS
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 <b>T</b> 416		• • •	18.4	12.6	K.TRHSPT*PQQSNR.T
Serine arginine repetitiv	re matrix protein 1 US	SP24 S655			2.7	54.2	R.SPS*LSSK.H
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$738			32.1	31.9	K.AAS*PSPQSVR.R
Serine arginine repetitiv			•		16.5	16.7	K.KPPAPPS*PVQSQSPSTNWSPAVPVKK.A
Serine arginine repetitiv					36.6	33.1	K.KPPAPPS*PVQSQSPST*NWSPAVPVKK.A
Serine arginine repetitiv				• • •	44.7	28.0	R.RRS*PS*PPPTR.R
Serine arginine repetitiv					10.5	25.4	R.KS*RVS*VSPGR.T  R.RQS*PS*PSTRPIR.R
Serine arginine repetitiv					18.1	18.2	R.RY*S*PSPPPK.R
Serine arginine repetitiv		1004000			11.6	18.2	R.RYS*PS*PPPK.R
Serine arginine repetitiv					21.7	53.8	K.KPPAPPS*PVQSQSPSTNWS*PAVPVK.K
Serine arginine repetitiv					7.0	43.8	K.KPPAPPS*PVQS*QSPSTNWSPAVPVK.K
Serine arginine repetitiv	re matrix protein 1 SR	RRM1 \$290\$292			11.2	10.8	R.S'RS'PSHTRPR.R
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 S715T718		• •	16.0	17.4	R.RQSPS*PST*RPIR.R
Serine arginine repetitiv	re matrix protein 1 SR	RRM1 \$528\$530\$53	2		100.0	18.1	R.S*AS*PS*PR.K
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 8675			100.0	21.7	R.S*PQPNKR.H
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$754\$756			17.3	32.4	R.SVS*GS*PEPAAK.K
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$773\$775\$78	1		17.6	34.2	K.KPPAPPSPVQS*QS*PSTNWS*PAVPVKK.A
Serine arginine repetitiv			7	-	16.0	29.8	K.KPPAPPS*PVQSQS*PS*TNWSPAVPVKK.A
Serine arginine repetitiv			-		3.9	31.0	R.SPS'HTRPR.R
Serine arginine repetitiv					7.2	22.9	R.APQT*SSSPPPVRR.G  R.KVFLS*ESFEDKGGK M
Serine arginine repetitiv				-	9.6	29.3 15.5	K KPPAPPS*PVOSOS*PST*NWSPAVPVKK A
Serine arginine repetitiv			•		-0.4	27.9	R.APQTSSS*PPPVRR.G
Serine arginine repetitiv	re matrix protein 1 SR			•	10.5	12.4	K.KAAS'PS'PQSVR.R
Serine arginine repetitiv	re matrix protein 1 SR	RRM1 \$429\$431			0.4	24.3	R.KSRVS*VS*PGR.T
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 S694			20.1	11.4	R.APQTS*SSPPPVR.R
Serine arginine repetitiv	re matrix protein 1 SR	RRM1 \$713			12.2	24.2	R.RQS*PSPSTRPIR.R
Serine arginine repetitiv	e matrix protein 1 SR	RRM1 \$769\$773\$77	7		14.0	36.1	K.KPPAPPS*PVQS*QSPS*TNWSPAVPVKK.A
Serine arginine repetitiv			-		9.3	26.5	R.RY*SPS*PPPK.R
Serine arginine repetitiv			-		3.0	13.0	K.KPPAPPSPVQ <mark>S*</mark> QSPSTNWSPAVPVKK.A
Serine arginine repetitiv		01100111		<u>-</u>	0.4	11.2	K.KPPAPPSPVQSQS*PS*TNWSPAVPVKK.A
Serine arginine repetitiv					12.8	21.1	K.KPPAPPS*PVQS*QS*PS*TNWSPAVPVKK.A  R.RGAS*S*SPQR.R
Serine arginine repetitiv					3.3	17.0	R.GASS*S*PQRR.Q
		RRM1 S414T416			20.6	23.5	K.TRHS*PT*PQQSNR.T
Serine arginine repetitiv	e matrix protein 1 SR		•••			14.5	R.RVS*S*SR.S
Serine arginine repetitiv	re matrix protein 1 SP	PCS1 S177S179S18	1		100.0	12.8	R.S'RS'PS'PR.R
Serine arginine repetitiv	re matrix protein 1 SR	RRM1 \$389\$393		•	11.3	37.4	R.RLS*PSAS*PPR.R
Serine arginine rich p	re-mRNA splicing SC factor SR-A1	CAF1 \$874	-	-	100.0	41.7	R.S*PFLKPDER.A
Serine arginine rich p	re-mRNA splicing SC factor SR-A1	CAF1 \$498\$500	-		76.4	62.8	R.S*PS*PAPAPAPAAAAGPPTR.K
		CAF1 \$734\$738			29.1	60.9	R.EVLYDS*EGLS*GEER.G
Serine arginine rich p	factor SR-A1				-0.3	14.1	R.FDIYDPFHPTDEAY*SPPPAPEQK.Y
Serine arginine rich p	factor SR-A1				14.2	46.0	R.EVLY*DSEGLS*GEER.G
Serine arginine rich p	factor SR-A1			•	20.2	13.3	R.FDIYDPFHPT*DEAYSPPPAPEQK.Y  R.FDIYDPFHPTDEAYS*PPPAPEQK.Y
	factor SR-A1				25.1	17.0	R.FS*ILGHSFALLS*PR.W
	Serine protease 23 PR				100.0	22.0	R.FS*IFGK.D
Serine threoning	e protein kinase N PK				8.9	62.8	K.LNLGTDSDSS*PQK.S
Serine threonine	e protein kinase N PK	N1 S916			15.7	69.4	R.TDVSNFDEEFTGEAPTLS*PPR.D
Serine threoning	e protein kinase N PK	N1 T774			7.2	88.1	R.TST*FCGTPEFLAPEVLTDTSYTR.A
Serine threonine	e protein kinase N PK	N1 8773			-0.3	61.3	R.TS*TFCGTPEFLAPEVLTDTSYTR.A
Serine threoning	e protein kinase N PK	N1 S578			5.8	43.9	R.DPPSSPSSLS*SPIQESTAPELPSETQETPGPALCSPLR.K
	e protein kinase N PK				19.1	65.5	R.DPPSS*PSSLSSPIQESTAPELPSETQETPGPALCSPLR.K
Serine threoning	e protein kinase N PK	N1 <b>S</b> 575			7.3	36.6	R.DPPSSPS*SLSSPIQESTAPELPSETQETPGPALCSPLR.K

Peak Area	%CV	White dot	s-Significant char	nge in pepti ompared to	de the			
<-10 -5 -3	0 29 42		e at 5% FDR o with the minimum					
0 3 5	71 86 >100			CarT	RajiB_			
>10	Protein Name	Gene	Phosphosites	8 m m	5 H B	Ascor	MOWSE	Sequence
Serine threonine	protein kinase N	PKN1	T778	•		-0.8	20.0	R.TSTFCGT*PEFLAPEVLTDTSYTR.A
Serine threonine			S561	<b>.</b>		17.8	37.3	K.LNLGTDSDS*SPQK.S
Serine threonine			<b>S</b> 572				18.5	R.DPPS*SPSSLSSPIQESTAPELPSETQETPGPALCSPLR.K
Serine/arginine repetitive			<b>S</b> 547		•	30.7	20.9	R.WQS*PVTK.S
Serine/threonine i	homoloa)		S315S316S317			6.8	32.2	K.AEQSHDDS*S*S*EDSDAET*DGQASGGSDSGDWIFTIR.E
Serine/threonine i	homoloa)		S316S317S320		■	12.3	87.9	K.AEQSHDDSS*S*EDS*DAET*DGQASGGSDSGDWIFTIR.E
Serine/threonine i	homolog)		T190			12.7	18.0	R.NT*FVGTPFWMAPEVIKQSAYDSK.A
Serine/threonine i	homoloa)		S315S316S317			4.4	38.5	K.AEQSHDDS*S*S*EDS*DAETDGQASGGSDSGDWIFTIR.E
Serine/thr	eonine kinase 35	STK35	S281Y288		-	15.6	43.0	K.YWLSS*ACGSDFY*MAPEVWEGHYTAK.A
Serine/thr	eonine kinase 35	STK35	S280S281			14.1	60.3	K.YWLS*S*ACGSDFYMAPEVWEGHYTAK.A
Serine/thr	eonine kinase 35	STK35	S280S285			4.5	58.5	K.YWLS*SACGS*DFYMAPEVWEGHYTAK.A
Serine/thr	eonine kinase 35	STK35	S285Y288			20.4	56.4	K.YWLSSACGS*DFY*MAPEVWEGHYTAK.A
Serine/thr	eonine kinase 35	STK35	S281S285			1.8	34.4	K.YWLSS'ACGS'DFYMAPEVWEGHYTAK.A
Serine/thr	eonine kinase 35	STK35	S280Y288	Ļ		5.1	32.7	K.YWLS*SACGSDFY*MAPEVWEGHYTAK.A
Serine/threoni	ne kinase 38 like	STK38L	Y281			70.1	66.3	R.QLAY*STVGTPDYIAPEVFMQTGYNK.L
Serine/threoni	ne kinase 38 like	STK38L	Y289			0.7	53.1	R.QLAYSTVGTPDY*IAPEVFMQTGYNK.L
Serine/threoni	ne kinase 38 like	STK38L	T286		_	1.0	54.9	R.QLAYSTVGT*PDYIAPEVFMQTGYNK.L
Serine/threoni	ne kinase 38 like	STK38L	S282			6.5	56.1	R.QLAYS*TVGTPDYIAPEVFMQTGYNK.L
serine/threonine kinase rec	eptor associated protein	STRAP	S335			14.8	37.7	K.IGFPETTEEELEEIAS*ENSDCIFPSAPDVK.A
serine/threonine kinase rec	eptor associated protein	STRAP	S335S338			58.8	68.5	K.IGFPETTEEELEEIAS*ENS*DCIFPSAPDVK.A
Serine/Threonine	orotein kinase 10	STK10	S438			100.0	63.7	K.QVAEQGGDLS*PAANR.S
Serine/Threonine	orotein kinase 10	STK10	S514			17.8	36.0	K.EMGS*LSIKDPK.L
Serine/Threonine	orotein kinase 10	STK10	Y197			18.4	56.8	R.DSFIGTPY*WMAPEVVMCETMK.D
Serine/Threonine	rotein kinase 10	STK10	T185		•	100.0	28.5	K.NLKT*LQK.R
		STK10	S191			1.3	13.9	R.DS*FIGTPYWMAPEVVMCETMK.D
Serine/Threonine	rotein kinase 10	STK10	\$450\$454	•••		4.8	48.0	K.ASQS*RPNS*SALETLGGEK.L
Serine/Threonine	rotein kinase 10	STK10	T195			2.8	34.9	R.DSFIGT*PYWMAPEVVMCETMK.D
Serine/Threonine p	orotein kinase 10	STK10	S448S454	•		13.8	19.9	K.AS*QSRPNS*SALETLGGEK.L
Serine/Threonine	rotein kinase 10	STK10	S13	• •		8.9	13.2	R.ILRLS*TFEK.R
Serine/threonine p	orotein kinase 25	STK24	T174			80.7	58.8	R.NT*FVGTPFWMAPEVIK.Q
Serine/threonine	protein kinase 3	STK3	S316			75.5	61.8	R.ELEEEENS*DEDELDSHTMVK.T
Serine/threonine	protein kinase 3	STK3	T384			81.0	24.9	R.NAT*SPQVQRPSFMDYFDK.Q
Serine/threonine	protein kinase 3	STK3	S385			19.1	28.8	R.NATS*PQVQRPSFMDYFDKQDFK.N
Serine/threonine	orotein kinase 38	STK38	S281			9.0	37.2	R.QLAFS*TVGTPDYIAPEVFMQTGYNK.L
Serine/threonine p	protein kinase 38	STK38	T285	•••		-0.7	57.8	R.QLAFSTVGT*PDYIAPEVFMQTGYNK.L
Serine/threonine pro	tein kinase Nek6	NEK6	T201S206		<u> </u>	3.7	37.4	R.FFSSET*TAAHS*LVGTPYYMSPER.I
Serine/threonine pro	tein kinase Nek6	NEK6	S199S206			9.8	69.5	R.FFSS'ETTAAHS'LVGTPYYMSPER.I
Serine/threonine pro	tein kinase Nek6	NEK6	S199T202			5.6	57.7	R.FFSS*ETT*AAHSLVGTPYYMSPER.I
Serine/threonine pro	tein kinase Nek6	NEK6	S199T201T202			10.3	48.5	R.FFSS*ET*T*AAHSLVGTPYYMSPER.I
Serine/threonine pro	tein kinase Nek6	NEK6	S199T201			1.8	14.9	R.FFSS*ET*TAAHSLVGTPYYMSPER.I
Serine/threonine pro	tein kinase Nek6	NEK6	T202S206			8.2	18.5	R.FFSSETT*AAHS*LVGTPYYMSPER.I
Serine/threonine-pro			T793			73.5	115.0	K.T*PIQAGGYGEFAAFK
Serine/threonine-pro			S350			10.9	28.9	K.AEVYGS*ENESER.N
Serine/threonine-pro	tein kinase Sgk1					12.2	12.4	K.ILGLCFSCIS'AR.V
Serine/threonine-protei	n phosphatase 6		T285S291S292			15.8	22.2	R.NTVDLVT*TCHIHS*S*SDDEIDFK.E
Serine/threonine-protei	ulatorv subunit 3 n phosphatase 6		T286S292S293			7.5	22.6	R.NTVDLVTT*CHIHSS*S*DDEIDFK.E
Serine/threonine-protei	n phosphatase 6	PPP6R3	\$291\$292\$293			2.4	19.5	R.NTVDLVTTCHIHS"S"S"DDEIDFK.E
Serine/threonine-protei	ulatory subunit 3 n phosphatase 6		T286S291S292			0.4	15.7	R.NTVDLVTT*CHIHS*S*SDDEIDFK.E
Serologically defined colo	ulatorv subunit 3		S747S748		•	47.5	62.3	R.DELNEELIQEES*S*EDEGEYEEVRK.D
Serologically defined colo	1			• • •		12.2	72.1	R.VS*PASPAGS*PSADFAVHGESLGDR.H
Serologically defined colo	3				. : :	12.2	42.2	R.VSPAS*PAGS*PSADFAVHGESLGDR.H
SERPINE1 mRNA I	3		S203		<u> </u>	-0.2	65.8	R.SS*FSHYSGLK.H
SERPINE1 mRNA I			S330			11.8	61.8	K.SKS*EEAHAEDSVMDHHFR.K
SERPINE1 mRNA I			S328			4.6	30.4	K.S*KSEEAHAEDSVMDHHFR.K
SERPINE1 mRNA I			S25			100.0	45.7	R.FDQLFDDES*DPFEVLK.A
			S234				29.1	K.DELTES*PK.Y
SERPINE1 mRNA I			S234 S237			14.5	13.0	K.DELTDLDQS*NVTEETPEGEEHHPVADTENK.E
SERPINE1 mRNA I			T232			14.0	13.0	K.DELT*ESPK.Y
	amyloid A-like 1					25.		K.SSS*DDEEQLTELDEEMENEICR.V
	amyloid A-like 1		S56			25.4	119.3	K.SS*SDDEEQLTELDEEMENEICR.V
	amyloid A-like 1		S55		_	-0.2	88.0	K.SSSDDEEQLT*ELDEEMENEICR.V
	response factor		T63		. =		58.2	R.EAAAAAAT*T*PAPTAGALYS*GSEGDSES*GEEEELGAER.R
Jei UIII	,		T66T67S77S85	-		5.6	29.1	

<-10 0 abund		compared to	the			
.5 29 timepo .3 42 PSM	int with the minimum	peak area f	or a given			
3 80 5 >100 >10			RajiB			
Protein Name Gene Serum response factor binding protein 1 SRFBF	Phosphosites 1 S264	£ £ £	8 % 6	Ascor 16.8	MOWSE 41.9	Sequence K.EYFDDS*TEER.F
SET binding factor 1 SBF1	T1747			-0.3	72.3	R.ST*STLYSQFQTAESENR.S
SET binding factor 1 SBF1	S1141			7.0	74.3	R.LGLGTLSSS'LSR.A
SET binding factor 1 SBF1	S1140			10.8	54.8	RLGLGTLSS*SLSRA
SET binding factor 1 SBF1	<b>S</b> 1139	•		9.5	29.3	RLGLGTLS*SSLSR.A
SET domain containing 1A SETD1	A \$468\$470			34.2	52.6	R.S'GS'PAPETTNESVPFAQHSSLDSR.I
SET domain-containing protein 5 SETDS	T70S74			33.3	18.4	R.GLPYADHNYGAPPPPT*PPAS*PPVQTIIPR.S
SET protein SET	T23			6.0	50.5	K.ELNSNHDGADET*SEKEQQEAIEHIDEVQNEIDR.L
Sex comb on midleg like 2 SCML2	\$499\$511			43.5	50.9	R.S*PQQTVPYVVPLS*PK.L
Sex comb on midleg like 2 <sub>SCML2</sub>	S511	==		17.6	11.8	K.RSPQQTVPYVVPLS*PK.L  R.S*PQQTVPYVVPLSPK.L
Sex comb on midleg like 2 SCML2				43.6 36.2	94.9	R.SPQQT*VPYVVPLS*PK.L
SFRS protein kinase 1 SRPK1	S51			76.1	95.7	R.GSAPHSESDLPEQEEEILGS*DDDEQEDPNDYCK.G
SFRS15 SCAF4	T138	• • • •			65.0	K.IEIIQPLLDMAAGT*SNAAPVAENVTNNEGSPPPPVK.V
SFRS15 SCAF4	<b>S</b> 139			3.6	41.1	K.IEIIQPLLDMAAGTS*NAAPVAENVTNNEGSPPPPVK.V
SFRS15 SCAF4	S154			19.5	29.0	K.IEIIQPLLDMAAGTSNAAPVAENVTNNEGS*PPPPVK.V
SGEFARHGI	F2 <b>S</b> 222			62.9	22.8	R.LPS*QENELLENPSVVLSTNSPAALK.V
SGT <sub>SGTA</sub>	S305			10.9	71.2	R.SRTPS*ASNDDQQE
SGT <sub>SGTA</sub>	S77T81		-	40.9	33.8	R.S*PART*PPSEEDSAEAER.L
SGT <sub>SGTA</sub>	T303			13.9	46.7	R.SRT*PSASNDDQQE
SGT <sub>SGTA</sub>	T81S84			0.9	16.4	R.SPART*PPS*EEDSAEAER.L
SGT1 protein ECD	\$503\$505\$518			66.4	32.9	K.ILGPRPNES*DS*DDLDDEDFECLDS*DDDLDFETHEPGEEASLK.G
SGTB SGTB	S297	÷		13.9	27.2	R.SFS*SSAEEHS
SH2 B homolog SH2B1	S88S96	•		19.4	42.0	R.ASGSLS*PPILAPLS*PGAEISPHDLSLESCR.V
SH2 domain binding protein 1 <sub>CTR9</sub> SH2 domain binding protein 1 <sub>CTR9</sub>	T925		•••	67.7	89.8	K.KGGEFDEFVNDDT*DDDLPISK.K
SH2D3C SH2D3C	\$1015\$1016\$1		-	100.0	15.0	K.AIIS'S'S'DDS'S'DEDKLK.I  R.YLEASYGLGQGSSKPAS'PVS'PSGPK.G
SH3 domain binding protein 1 BARGI			• • •	17.4	50.4	R.S'PPETAAPVEDMAR.R
SH3 domain binding protein 1 BARGI				15.6	61.3	R.ENHGQADHS*PSMTATHFPR.V
SH3 domain kinase binding protein 1 SH3KE			• •	11.6	23.0	R.RPPSQSLTSSSLSSPDIFDSPS*PEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KE	P1 \$509\$511			40.7	43.4	R.RPPSQSLTSSSLSSPDIFDS*PS*PEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KE	P1 <b>S</b> 493			9.4	45.6	R.RPPS*QSLTSSSLSSPDIFDSPSPEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KE	P1 <b>S</b> 79			40.7	90.4	K.APEKPLHEVPS*GNSLLSSETILR.T
SH3 domain kinase binding protein 1 SH3KE	P1 S230	•		100.0	97.6	R.S*IEVENDFLPVEK.T
SH3 domain kinase binding protein 1 SH3KE	P1 T179	-		7.9	93.7	R.ETT*GSESDGGDSSSTK.S
SH3 domain kinase binding protein 1 SH3KB	P1 S183			14.7	113.6	R.ETTGSES*DGGDSSSTK.S
SH3 domain kinase binding protein 1 SH3KE				25.0	36.1	R.RPPSQSLTSSSLSS*PDIFDSPS*PEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KE				7.4	84.9	R.ET*TGSESDGGDSSSTK.S
SH3 domain kinase binding protein 1 <sub>SH3KE</sub> SH3 domain kinase binding protein 1 <sub>SH3KE</sub>					31.4	R.RPPS'QS'LTSSSLSSPDIFDSPSPEEDKEEHISLAHR.G  R.RPPSQS'LTSSSLSSPDIFDSPSPEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KB				-0.3	43.9	R.RPPSQSLT*SSSLSS*PDIFDSPSPEEDKEEHISLAHR.G
SH3 domain kinase binding protein 1 SH3KB				10.9	107.6	R.ETTGS*ESDGGDSSSTK.S
SH3 multiple domains 2 <sub>SH3RF</sub>				15.1	33.2	R.VS*PPAS*PTLEVELGSAELPLQGAVGPELPPGGGHGR.A
SH3 protein expressed in lymphocytes SASH3	S27	•		21.2	59.8	R.SSS*FKDFAK.S
SH3 protein expressed in lymphocytes SASH3	S26S27	•	• • • •	6.7	48.1	R.SS'S'FKDFAK.S
SH3 protein expressed in lymphocytes SASH3	S108	•••		14.4	88.3	K.ALSEEMADTLEEGS*ASPTSPDYSLDSPGPEK.M
SH3 protein expressed in lymphocytes SASH3	S120		•••	23.9	63.2	K.ALSEEMADTLEEGSASPTSPDYSLDS*PGPEK.M
SH3 protein expressed in lymphocytes SASH3	T103	-		9.2	83.3	K.ALSEEMADT*LEEGSASPTSPDYSLDSPGPEK.M
SH3 protein expressed in lymphocytes SASH3	S97	-		4.3	13.4	K.ALS*EEMADTLEEGSASPTSPDYSLDSPGPEK.M
SH3 protein expressed in lymphocytes SASH3	S108S113			15.9	30.6	K.ALSEEMADTLEEGS*ASPTS*PDYSLDSPGPEK.M
SH3 protein expressed in lymphocytes SASH3	T112S120	-		20.8	38.4	K.ALSEEMADTLEEGSASPT*SPDYSLDS*PGPEK.M
SH3 protein expressed in lymphocytes SASH3	\$113\$120			16.6	48.5	K.ALSEEMADTLEEGSASPTS*PDYSLDS*PGPEK.M
SH3 protein expressed in lymphocytes SASH3  SH3 protein expressed in lymphocytes SASH3	\$108\$120			18.9	46.3	K.ALSEEMADTLEEGS*ASPTSPDYSLDS*PGPEK.M
SH3 protein expressed in lymphocytes SASH3  SH3 protein expressed in lymphocytes SASH3	T318S320			14.5	74.3	K.LLTAAELLLDYDT*GS*EEAEEGAESSQEPVAHTVSEPK.V  K.LLT*AAELLLDYDT*GSEEAEEGAESSQEPVAHTVSEPK.V
SH3 protein expressed in lymphocytes SASH3	T308T318 Y316S320			12.0	70.7	K.LLTAAELLLDY*DTGS*EEAEEGAESSQEPVAHTVSEPK.V
SH3 protein expressed in lymphocytes SASH3	¥3165320 87			24.6	32.3	R.RKPS*NASEKEPTQK.K
SH3 protein expressed in lymphocytes SASH3	\$38\$42			16.9	28.6	K.SKPSS*PVVS*EK.E
SH3 protein expressed in lymphocytes SASH3				11.5	13.9	K.SKPS*SPVVS*EK.E
SH3 protein expressed in lymphocytes SASH3	Y316T318		•	25.3	79.7	K.LLTAAELLLDY'DT'GSEEAEEGAESSQEPVAHTVSEPK.V
SH3 protein expressed in lymphocytes SASH3	S26			-0.6	58.4	R.SS*SFKDFAK.S
SH3 protein expressed in lymphocytes SASH3	S110S120			21.1	56.5	K.ALSEEMADTLEEGSAS*PTSPDYSLDS*PGPEK.M

Peak Area	o ab		compared to	the			
-5 -3 0	29 tin 42 PS 71	nepoint with the minimum SM	ı peak area f	or a given			
3 5 >10	>100		CarT	RajiB			
SH3 protein expresse	Protein Name Ge ad in lymphocytes SA		9 2 6	£ 5 g	Ascor 12.4	MOWSE 20.0	Sequence K.ALSEEMADTLEEGSAS*PT*SPDYSLDSPGPEK.M
SH3 protein expresse	ed in lymphocytes SA	SH3 S108T112			6.7	42.9	K.ALSEEMADTLEEGS*ASPT*SPDYSLDSPGPEK.M
SH3 protein expresse	ed in lymphocytes <sub>SA</sub>	SH3 T308Y316		•		36.9	K.LLT*AAELLLDY*DTGSEEAEEGAESSQEPVAHTVSEPK.V
SH3 protein expresse	ed in lymphocytes SA	SH3 T103S120	i i		13.7	73.8	K.ALSEEMADT*LEEGSASPTSPDYSLDS*PGPEK.M
SH3 protein expresse	ed in lymphocytes SA	SH3 S97S113S120	-		6.7	16.6	K.ALS*EEMADTLEEGSASPTS*PDYSLDS*PGPEK.M
SH3 protein expresse	ed in lymphocytes SA	SH3 S97S120			15.8	66.0	K.ALS*EEMADTLEEGSASPTSPDYSLDS*PGPEK.M
SH3-do	omain GRB2-like 1 SH	3GL1 \$288	• •		8.9	37.7	K.IAASSS*FR.S
	omain GRB2-like 1 SH		•		8.2	34.2	K.IAASS*SFR.S
	omain GRB2-like 1 SH		• •			22.7	K.IAAS*SSFR.S
	binding protein 1 <sub>SH</sub>		•		1.7	19.4	R.ISLTS*LHSAS*SNTSLSGHR.G
SH3KBP1	binding protein 1 <sub>SH</sub>				0.6	16.9	R.ISLTSLHSAS*S*NTSLSGHR.G
	SHARP SP		-		13.7	24.4	R.ESGVVAVS*PEKS*ESPQKEDGLSSQLK.S
	SHARP SP			•	4.9	61.2	R.S'VQS'AAVPAPTSQLLSSLEK.D  R.S'VQSAAVPAPTSQLLSSLEK.D
	SHARP SP				22.2	40.4	R.S'OS'PVHLR.R
Shaw related voltage	gated potassium KC			-	100.0	17.5	R.RS*T*TRDR.N
	channel protein 4				19.2	51.9	R.TLEEVVMAEEEDEGTDRPGS*PA-
	SHIP1 INF				39.2	32.7	R.GESPPTPPGQPPIS*PK.K
	SHIP1 INF				47.7	15.1	R.GESPPT*PPGQPPIS*PK.K
	SHIP1 INF	PP5D Y864			100.0	37.5	R.EKLY*DFVK.T
	SHIP1 INF	PP5D \$959T962			44.7	20.4	R.GES*PPT*PPGQPPISPK.K
	SHIP1 INF	PP5D Y1021			11.1	12.2	K.NAGDTLPQEDLPLTKPEMFENPLY*GSLSSFPKPAPR.K
	SHIP1 INF	PP5D \$959\$970			12.5	17.9	R.GES*PPTPPGQPPIS*PK.K
	Sialophorin SP	N \$336	• •	•	27.5	33.1	K.GSGFPDGEGS*SR.R
	Sialophorin SP	N S291			99.3	49.0	R.TGALVLS*R.G
	Sialophorin SP	N \$351\$355	• •		100.0	45.8	K.S*RQGS*LAMEELK.S
	Sialophorin SP	N \$355	• •		100.0	64.8	R.QGS*LAMEELK.S
-	Sialophorin SP	N T341	•		32.3	54.6	R.RPT"LTTFFGR.R
	Sialophorin SP	N \$368			25.4	58.3	K.SGSGPS*LK.G
	Sialophorin SP		•		35.9	52.1	K.S*RQGSLAMEELK.S
	Sialophorin SP		·		20.6	28.8	K.SGS*GPSLK.G
SID1 transmembrane					33.1	44.9	R.VDS*MS*S*VEEDDYDTLTDIDSDKNVIR.T
	SIGLEC2 CD			_	19.0	34.0	R.TQSQQGLQENS*SGQSFFVR.N
Signal induced prolife	SIGLEC2 CD				8.9	35.1	R.TQS*QQGLQENSSGQSFFVR.N  R.TEFLHSQNSLS*PR.S
Signal induced prolife	protein 1			==	7.7	32.7	R.TEFLHS*QNSLSPR.S
	protein 1	0004		=	35.2 44.1	87.6	R.GTGSGGQLQDLDCS*S*S*DDEGAAQNSTKPSATK.G
	ice receptor alpha SS			===	14.3	31.0	K.VEMGTS*SQNDVDMSWIPQETLNQINK.A
Signal sequer	ice receptor alpha SS	R1 S247			14.3	30.0	K.VEMGTSS*QNDVDMSWIPQETLNQINK.A
Signal sequer	ice receptor alpha SS	R1 T245			28.1	19.9	K.VEMGT*SSQNDVDMSWIPQETLNQINK.A
Signal sequer	ice receptor alpha SS	R1 S268		•	31.5	16.9	K.VEM#GTSSQNDVDMSWIPQETLNQINKAS*PR.R
Signal sequer	ice receptor alpha SS	R1 S247S268			19.0	20.7	K.VEMGTSS*QNDVDMSWIPQETLNQINKAS*PR.R
Signaling lymphocytic ac	ctivation molecule SL	AMF1 Y281			42.9	31.8	K.SLTIY*AQVQKPGPLQK.K
Similar to BMP	2 inducible kinase AA	K1 \$36		••	21.6	104.0	K.S*MEELTVIQCTSQELPAQTGLLSQTGDVPLPAGR.E
Similar to BMP	2 inducible kinase AA	K1 T46			2.3	54.9	K.SM#EELTVIQCT*SQELPAQTGLLSQTGDVPLPAGR.E
Similar to	KIAA0592 protein W.	ASHC2A \$250\$265			20.8	22.3	R.HTTQMS*DEEEDDDGCDLFADS*EKEEEDIEDIEENTRPK.R
	KIAA0592 protein W.F				75.8	142.8	K.GLFS*DEEDSEDLFSSQSASK.L
	KIAA0592 protein W.A				47.0	85.3	K.ASALLFS*S*DEEDQWNIPASQTHLASDSR.S
	KIAA0592 protein W.		•		35.8	61.5	K.ASALLFS*SDEEDQWNIPASQTHLASDSR.S
	KIAA0592 protein W.F				100.0	32.3	K.EEEES'DEDFAHHS'DNEQNR.H
	KIAA0592 protein WA		·		5.8	32.2	K.ASALLFSS*DEEDQWNIPASQTHLASDSR.S
	CDNA 4933437K13 SN				27.1	66.2	R.YSVEAS*SPGHGS*PLSSLLPSASVPESMTISELR.Q
	CDNA 4933437K13 <sub>SN</sub>				12.5	52.2	R.YSVEAS*S*PGHGSPLSSLLPSASVPESMTISELR.Q
	CDNA 4933437K13 <sub>SN</sub>				0.1	34.9	R.YSVEASSPGHGS*PLSS*LLPSASVPESMTISELR.Q  R.YSVEAS*SPGHGSPLSSLLPSASVPESMTISELR.Q
	CDNA 4933437K13 SN				9.8	25.5	R.YSVEAS*SPGHGSPLSSLLPSASVPESMTISELR.Q
	DNA 4933437K13 SN			-	2.2	17.1	R.YSVEASSPGHGS*PLSSLLPS*ASVPESMTISELR.Q
	otein, alpha chain SN		•		12.3	20.2	K.RIS*ISK.Q
	milar to TSG118.1 <sub>KN</sub>				12.3	12.9	R.YSVLNNDDYFADVS*PLR.A
	polypeptide 30KD SA				25.9	78.0	R.KGS*DDDGGDSPVQDIDTPEVDLYQLQVNTLR.R
	polypeptide 30KD SA				10.6	28.1	R.KGSDDDGGDS*PVQDIDTPEVDLYQLQVNTLR.R
Sin3 associated	polypeptide 30KD SA	P30 S131S138			101.4	89.3	R.KGS*DDDGGDS*PVQDIDTPEVDLYQLQVNTLR.R

Peak Area %CV	White dots- Significant change in peptide abundance at 5 %FDR compared to the						
-5 25 42 0 71 3 86 5 >100	PSM				CarTRajiB		
>10 Protein Na		Phosphosites	£ £ £	8 g g		MOWSE	Sequence
Sin3 associated polypeptide 30	SAP30	\$131T145 \$138T145			-0.1	37.6	R.KGS*DDDGGDSPVQDIDT*PEVDLYQLQVNTLR.R  R.KGSDDDGGDS*PVQDIDT*PEVDLYQLQVNTLR.R
SIN	3A SIN3A	T284	==		13.6	57.2	R.SPPVQPHT*PVTISLGTAPSLQNNQPVEFNHAINYVNK.I
	3A SIN3A	S277			1.5	53.9	R.S*PPVQPHTPVTISLGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	S277T284	•		3.4	59.1	R.S*PPVQPHT*PVTISLGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	S832	•		157.7	120.2	R.GDLS*DVEEEEEEEMDVDEATGAVK.K
SIN	3A SIN3A	T287			1.0	39.2	R.SPPVQPHTPVT*ISLGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	S277S289	• •	• •	6.3	39.6	R.S*PPVQPHTPVTIS*LGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	T287S289	•		17.4	43.3	R.SPPVQPHTPVT*IS*LGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	S277T287	•		7.3	54.7	R.S*PPVQPHTPVT*ISLGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	S289T292	•		-0.5	12.9	R.SPPVQPHTPVTIS*LGT*APSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	T284T287	•		7.0	46.4	R.SPPVQPHT*PVT*ISLGTAPSLQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	T292S295	•		14.8	37.8	R.SPPVQPHTPVTISLGT*APS*LQNNQPVEFNHAINYVNK.I
SIN	3A SIN3A	T287T292	•		2.0	26.4	R.SPPVQPHTPVT*ISLGT*APSLQNNQPVEFNHAINYVNK.I
	3A SIN3A	Y272	-		6.0	20.4	K.VSKPSQLQAHTPASQQTPPLPPY*ASPR.S
	3A SIN3A	T292			4.5	41.5	R.SPPVQPHTPVTISLGT*APSLQNNQPVEFNHAINYVNK.I
Single Ig IL 1R related molec		S383	·		-0.3	20.0	R.SS'EVDVSDLGSR.N
Single stranded DNA binding protei		S354			7.6	37.4	R.DDGEMGGNFLNPFQSESYS*PSMTMSV
Single stranded DNA binding protein		S350			-0.3	26.1	R.DDGEMGGNFLNPFQS*ESYSPSMTMSV
Single stranded DNA binding protei		Y353			5.3	13.1	R.DDGEM#GGNFLNPFQSESY*SPSMTMSV
Single stranded DNA binding protei		\$360 \$352			27.6	37.6	R.DDGEMGGNFLNPFQSESYSPSMTMS*V  R.DDGEMGGNFLNPFQSES*YSPSMTMSV
Single stranded DNA binding protei		\$352 \$356	==		12.8	16.4	R.DDGEMGGNFLNPFQSESYSPS*MTMSV
Single stranded DNA binding protei		S387	_		18.6	46.8	R.DDGELGGNFLHSFQNDNYSPSMTMS*V
Single stranded DNA binding protei		S381	=		14.0	56.1	R.DDGELGGNFLHSFQNDNYS*PSMTMSV
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	S381S387			12.9	49.5	R.DDGELGGNFLHSFQNDNYS*PSMTMS*V
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	\$374\$387	=		3.7	15.0	R.DDGELGGNFLHS*FQNDNYSPSMTMS*V
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	Y380S387			19.5	49.7	R.DDGELGGNFLHSFQNDNY*SPSMTMS*V
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	Y380			10.3	16.1	R.DDGELGGNFLHSFQNDNY*SPSM#TMSV
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	S383S387			7.4	37.7	R.DDGELGGNFLHSFQNDNYSPS*MTMS*V
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	S383			7.3	19.8	R.DDGELGGNFLHSFQNDNYSPS*MTMSV
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	T360			7.7	72.5	K.NSPNNISGISNPPGT*PR.D
Single stranded DNA binding protein	n 3 <sub>SSBP3</sub>	S347T360			43.3	58.5	K.NS'PNNISGISNPPGT'PR.D
Sirtui	n 1 <sub>SIRT1</sub>	S47	Ļ		100.0	75.3	R.S*PGEPGGAAPER.E
Sirtui	n 2 SIRT2	T365	Ţ.		8.0	58.6	R.EHASIDAQSGAGVPNPST*SASPK.K
	SIT SIT1	S182	•		25.1	33.2	R.ARAS*FPDQAYANSQPAAS
	SIT <sub>SIT1</sub>	Y188			15.4	58.7	R.ASFPDQAY*ANSQPAAS
	SIT <sub>SIT1</sub>	S191	•		3.5	38.2	R.ASFPDQAYANS*QPAAS
	SIT <sub>SIT1</sub>	S83			22.3	73.3	R.SGES*VEEVPLYGNLHYLQTGR.L  R.S*GES*VEEVPLYGNLHYLQTGR.L
	SIT <sub>SIT1</sub>	S80S83			84.0	63.3	R.S*GESVEEVPLY*GNLHYLQTGR.L
	SIT <sub>SIT1</sub>	\$80Y90 \$80			7.5	41.6	R.S*GESVEEVPLYGNLHYLQTGR.L
	SIT <sub>SIT1</sub>	S102	-		122.6	81.7	R.LS*QDPEPDQQDPTLGGPAR.A
	2W SKIV2L	S256			33.8	64.9	R.ASS*LEDLVLK.E
SKI	2W SKIV2L	S270T271			13.3	47.3	K.EASTAVS*T*PEAPEPPSQEQWAIPVDATSPVGDFYR.L
s	kip SNW1	S224S232		•••	36.1	28.1	R.GPPS*PPAPVMHS*PSRK.M
SLAIN motif family, member	er 2 SLAIN2	S349S353			100.0	18.8	R.NS*PRPS*PK.Q
Si	it 3 <sub>SLIT3</sub>	S685			100.0	28.1	R.IVS*GNPR.C
SLIT-ROBO Rho GTPase activating prof	ein SRGAP2	S1013			4.9	64.9	R.SAS*TAGDIACAFRPVK.S
Smad nuclear-interacting protein	n 1 <sub>SNIP1</sub>	<b>S</b> 35	•		100.0	32.4	R.LS*PEVAPPAHR.R
	SNIP1	S394			9.2	79.7	K.DDEDEEEEEEVS*DS
Smad nuclear-interacting protein		S74S76	<b></b>		100.0	14.0	R.GVS*RS*PPK.K
SMAD4 interacting transcription fac		S315S319	<b></b>		33.6	70.4	K.HAPTYTIPLS*PVLS*PTLPAEAPTAQVPPSLPR.N
SMAD4 interacting transcription fac		S319T321			3.2	28.4	K.HAPTYTIPLSPVLS*PT*LPAEAPTAQVPPSLPR.N
SMAD4 interacting transcription fac		S144			10.0	27.7	R.DKQSPS*QANGCSDHRPIDILEMLSR.A
SMAD4 interacting transcription fac		T309Y310				40.5	K.HAPT*Y*TIPLSPVLSPTLPAEAPTAQVPPSLPR.N
SMAD4 interacting transcription fac		S62	==		8.6	34.1	R.SAS*PYHGFTIVNR.L
SMAD4 interacting transcription fac		S176				40.5	R.NQMGDS*NISSPGLQPSTQLSNLGSTETLEEMPSGSQDK.S  R.NQMGDSNISS*PGLQPSTQLSNLGSTETLEEMPSGSQDK.S
SMAD4 interacting transcription fac		S180	-			108.9	R.NQMGDSNISS*PGLQPSTQLSNLGSTETLEEMPSGSQDK.S  K.HAPTY*T*IPLSPVLSPTLPAEAPTAQVPPSLPR.N
SMAD4 interacting transcription fac		Y310T311 S353		•	72.1	29.6 32.1	R.S*PLLNQPVPELSHASLIANQSPFR.A
SMAD4 interacting transcription fac		S315T321			72.1 4.8	16.2	K.HAPTYTIPLS*PVLSPT*LPAEAPTAQVPPSLPR.N
					-		

Peak Area %CV	abundance	- Significant cha at 5%FDR c ith the minimum	compared to	the			
.5 .3 .3 .42 .71	PSM	un die minimum	CarT				
>10 Protein Na		Phosphosites		8 g g		MOWSE	Sequence
Small integral membrane protei  Small integral membrane protei		650S60 660T62		• •	-0.4	16.2	R.ELVGDTGS*QEGDHEPSGS*ETEEDTSSSPHR.I  R.ELVGDTGSQEGDHEPSGS*ET*EEDTSSSPHR.I
Small integral membrane protei		T48T62			12.0	27.9	R.ELVGDT*GSQEGDHEPSGSET*EEDTSSSPHR.I
Small integral membrane protei	n 13 SMIM13	F48S60		<del>!</del>	20.3	53.9	R.ELVGDT*GSQEGDHEPSGS*ETEEDTSSSPHR.I
Small integral membrane protei		T48S50			1.0	27.7	R.ELVGDT*GS*QEGDHEPSGSETEEDTSSSPHR.I
Small integral membrane protei		F48S58			8.1	24.1	R.ELVGDT*GSQEGDHEPS*GSETEEDTSSSPHR.I
Small integral membrane protei  Small nuclear ribonucleoprotein 7		558 <b>S</b> 60		=	5.8 35.9	31.2	R.ELVGDTGSQEGDHEPS*GS*ETEEDTSSSPHR.I
Small nuclear ribonucleoprotein 7					100.0	17.3	R.S*RDKEER.R
Small nuclear ribonucleoprotein 7	kD SNRNP70	5410			100.0	101.8	R.GGGGGQDNGLEGLGNDS*R.D
Small nuclear ribonucleoprotein 7		320	-		100.0	18.9	R.GGGGDMAEPS'EAGDAPPDDGPPGELGPDGPDGPEEK.G
		517	•		16.8	110.5	R.SAS*PDDDLGSSNWEAADLGNEER.K  K.EES*AEELQAAEHPDEVEDPK.N
		S147 S17S24			1.8	36.1 24.9	R.SAS*PDDDLGS*SNWEAADLGNEERK
		S17 <b>S</b> 25			8.9	52.3	R.SAS*PDDDLGSS*NWEAADLGNEER.K
SI	MAP SMAP	S15S17			6.5	16.8	R.S'AS'PDDDLGSSNWEAADLGNEER.K
		S24		<u></u>	6.2	76.6	R.SASPDDDLGS*SNWEAADLGNEER.K
		S25		-	3.2	52.8	R.SASPDDDLGSS*NWEAADLGNEER.K
	CA2 SMARCA2 S				41.2 100.0	53.1	K.AKPVVS'DFDS'DEEQDER.E
	CA2 SMARCA2				49.2	54.9	K.AKPVVSDFDS*DEEQDER.E
SMAR	CA4 SMARCA4 S	S1627S1631			100.0	74.8	R.AKPVVS*DDDS*EEEQEEDR.S
SMAR	CA4 SMARCA4 §	S1570S1575S1			33.2	74.3	K.EDDS*EGEES*EEEEGEEGGS*ESESR.S
	CA4 SMARCA4 S				100.0	28.6	R.AKPVVS'DDDS'EEEQEEDRS'GS'GS'EED.
	CA4 SMARCA4 T				12.7	32.6	KAENAEGQTPAIGPDGEPLDET'S'QMSDLPVK.V  R.S'DS'EES'GS'EEEEEEEEEEQPQAAQPPTLPVEEK.K
	CA4 SMARCA4				10.8	53.3	K.KAENAEGQTPAIGPDGEPLDETS'QMS'DLPVK.V
	CA4 SMARCA4 §				19.8	37.7	K.EVDYSDS*LTEK.Q
SMAR	CA4 SMARCA4 §	S1380	<b>-</b>	•	13.9	25.1	K.EVDYS*DSLTEK.Q
SMAR	CA4 SMARCA4 S			•	8.2	35.6	R.DSDAGSS'TPTTSTR.S
SMAD	SMARCA4 7		·		8.4	16.4	K.AENAEGQTPAIGPDGEPLDET'SQMS'DLPVK.V  K.QTELFAHFIQPAAQKT'PT'SPLK.M
	CA5 SMARCAS 1				9.0	52.3 36.0	K.QTELFAHFIQPAAQKT*PTS*PLK.M
SMAR	CA5 SMARCA5	5116			12.1	28.7	K.TPTS*PLK.M
SMAR	CA5 SMARCA5	Γ115 <mark>S</mark> 116		<del>ii</del>	8.0	23.4	K.QTELFAHFIQPAAQKTPT*S*PLK.M
	AD1 SMARCAD §				12.5	54.8	R.KLS"SSS"EPYEEDEFNDDQSIKK.T
	AD1 SMARCAD S				15.2	64.6	R.KLS'S'SS'EPYEEDEFNDDQSIKK.T  R.GIQYIDLSS'DSEDVVSPNCSNTVQEK.T
	SMARCAD		==		10.3	105.8	K.TFNKDTVIIVS*EPS*EDEESQGLPTMAR.R
SMARC	AD1 SMARCAD				41.9	53.4	R.GIQYIDLS*S*DSEDVVSPNCSNTVQEK.T
SMARC	AD1 SMARCAD S	5152			58.1	64.2	R.RNDDISELEDLS*ELEDLKDAK.L
	AD1 SMARCAD §				100.0	80.4	R.RNDDIS*ELEDLS*ELEDLKDAK.L
	AD1 SMARCAD		-		40.8	62.4	K.DTVIIVS*EPS*EDEES*QGLPTMAR.R
	AD1 SMARCAD S				14.8	65.2 43.5	R.KLS'S'S'SEPYEEDEFNDDQSIKK.T  K.DT'VIIVS'EPSEDEESQGLPTMAR.R
	AD1 SMARCAD				29.5	32.0	RANT'PDS'DITEK.T
SMARC	AD1 SMARCAD §	S211S212			12.8	29.4	R.KLS*S*SSEPYEEDEFNDDQSIKK.T
	AD1 SMARCAD 1				24.5	25.6	R.ANT'PDS'DIT'EKTEDS'S'VPETPDNER.K
	AD1 SMARCAD S		•		16.1	38.1	R.KAS*ISYFK.N
	AD1 SMARCAD S				32.8	18.4	K.DTVIIVSEPS'EDEESQGLPTMAR.R  R.GIQYIDLS'SDS'EDVVS'PNCSNTVQEK.T
	AD1 SMARCAD				19.2	25.3	R.GIQYIDLS*SDS*EDVVSPNCSNTVQEK.T
	CC1 SMARCC1				1.0	18.3	K.DSENTPVKGGT*VADLDEQDEETVTAGGK.E
SMAR	CC1 SMARCC1	S310			100.0	18.4	K.NEEPVRS*PERR.D
	CC1 SMARCC1 §				132.3	59.5	R.KHS"PS"PPPPTPTESR.K
	CC1 SMARCC1				32.3	37.0	K.DSENT*PVK.G
	CC1 SMARCC1 S				100.0	19.8	R.KHS'PS'PPPPT'PTESR.K  R.S'PQVPAAQQMLNFPEK.N
	CC2 SMARCC2 §				71.0	51.3	K.DMDEPS*PVPNVEEVTLPK.T
	CC2 SMARCC2 §			•	22.8	30.3	R.KRS*PS*PSPTPEAK.K
	CC2 SMARCC2 §	302T308	_		8.7	12.6	R.KRS*PSPSPT*PEAK.K
SMC4 structural maintenanc chromosom	e of SMC4	S22S28			40.3	35.7	R.RREEGPPPPS*PDGASS*DAEPEPPSGR.T

<-10 0 abundano	s-Significant char e at 5%FDR o with the minimum	ompared to the				
3 71 86 5100		CarT	RajiB			
>10 Protein Name Gene	Phosphosites	B 25 B		Ascor	MOWSE	Sequence
SMC4 structural maintenance of SMC4 chromosomes 4	S28			10.3	19.7	R.RREEGPPPPSPDGASS*DAEPEPPSGR.T
SMC4 structural maintenance of SMC4 chromosomes 4	S22S27		:	33.0	38.9	R.EEGPPPPS'PDGAS'SDAEPEPPSGR.T
SMC4 structural maintenance of SMC4 chromosomes 4	S27S28				33.6	R.EEGPPPPSPDGAS*S*DAEPEPPSGR.T
SMC4 structural maintenance of SMC4 chromosomes 4  SMC4 structural maintenance of SMC4	S41				121.3	R.TES'PATAAETASEELDNR.S  R.TESPAT'AAETASEELDNR.S
chromosomes 4  SMC4 structural maintenance of SMC4	T44 S27			19.1	24.4	R.REEGPPPSDGAS*SDAEPEPPSGR.T
chromosomes 4  SMCR7L MIEF1	S94			33.4	52.6	R.S'LOTLPIDSSTFDTDTFCPPRPKPVAR.K
SMCR7L MIEF1	T97	• • •		-0.4	60.5	R.SLQT*LPTDSSTFDTDTFCPPRPKPVAR.K
SMEK homolog 1, suppressor of mek1 PPP4R3A	S771S777			16.9	15.5	K.TNLTSQSSTTNLPGSPGS*PGSPGS*PGSPGSVPK.N
SMEK homolog 1, suppressor of mek1 ppp4R3A	S774S780			16.3	10.8	K.TNLTSQSSTTNLPGSPGSPGS'PGSPGS'PGSVPK.N
SMEK homolog 1, suppressor of mek1 ppp4R3A	S117S126			18.3	19.7	K.DPSVDITQDLVDES*EEERFDDMS*SPGLELPSCELSR.L
SMEK homolog 2, suppressor of mek1 ppp4R3B	S117			82.1	78.1	K.DPSVEVTQDLIDES*EEER.F
Smith Magenis syndrome chromosome SMCR8 region candidate 8 protein	<b>S</b> 417	ļ		13.9	36.5	K.VLISVGS"YK.S
SNAP190 SNAPC4		-		46.1	41.7	R.VGS*ES*EDEDLLSELELADR.D
SNAP190 SNAPC4	S1398S1400S1		-	100.0	121.9	R.VGS*ES*EDEDLLS*ELELADR.D
SLK	S189	-		9.8	67.3	R.RDS*FIGTPYWMAPEVVMCETSK.D
SNF1 sucrose nonfermenting like kinase SLK  SNF1 sucrose nonfermenting like kinase SLK	Y195				61.3	R.DSFIGTPY*WMAPEVVMCETSK.D
SNF1 sucrose nonfermenting like kinase SLK  Sno SBNO1	\$779 \$688\$692		·	4.0	28.9	K_DSGS*ISLQETR.R  K_LYSLLGIDLTAFS*INNS*IPR.D
Sno SBNO1	\$688\$692 \$793	-	•	42.4	135.6	K.S'IDPDSIQSALLASGLGSK.R
Sno SBNO1	\$793 \$798		• •	2.8	14.5	K.SIDPDS*IQSALLASGLGSK.R
SNX17 <sub>SNX17</sub>	\$437\$440		•		33.8	KLSSKLS*AVS*LR.G
SNX5 SNX5	<b>S</b> 22			4.5	46.1	R.SVS*VDLNVDPSLQIDIPDALSER.D
SODD BAG4	Y255S259				26.2	R.Y'PWPS'SAPSAPPGNLYMTESTSPWPSSGSPQSPPSPPVQQPK.
Soluble lamin-associated protein of 75 kDa FAM169A	\$575 <b>\$</b> 576			13.0	60.3	K.AVDS*S*SEEIEVEVPVVDRR.N
Soluble scavenger receptor cysteine-rich SSC5D domain-containing protein SSC5D	S174			100.0	26.3	K.KS*PRPK.Q
acid transporters), member 1	\$461\$467			9.4	53.0	K.KES*KEEETS*IDVAGKPNEVTK.A
Solute carrier family 16 (monocarboxylic SLC16A1 acid transporters). member 1				68.5	65.6	K.KES*KEEETSIDVAGKPNEVTK.A
Solute carrier family 16 (monocarboxylic SLC16A1 acid transporters), member 1		-		5.9	20.1	K.EEETS*IDVAGKPNEVTK.A
Solute carrier family 16 (monocarboxylic SLC16A1 acid transporters). member 1					34.8	K.KES*KEEET*SIDVAGKPNEVTK.A
Solute carrier family 16 (monocarboxylic SLC16A1 acid transporters), member 1  Solute carrier family 16 (monocarboxylic SLC16A1			•••		41.0	K.EES'KEEET'SIDVAGKPNEVTK.A
acid transporters). member 1  Solute carrier family 16 (monocarboxylic SLC16A1					38.8	K.SKAS*LEKA
acid transporters). member 1 Solute carrier family 20 member 1 <sub>SLC20A1</sub>					64.9	R.NNSYTSY*TMAICGMPLDSFR.A
Solute carrier family 20 member 1 SLC20A1	T419			9.1	80.5	R.NNSYT*SYTMAICGMPLDSFR.A
Solute carrier family 20 member 1 SLC20A1	Y418			-0.3	17.5	R.NNSY*TSYTMAICGMPLDSFR.A
Solute carrier family 20 member 1 SLC20A1	T422			0.8	76.4	R.NNSYTSYT*MAICGMPLDSFR.A
Solute carrier family 20 member 1 SLC20A1	<b>S</b> 417			5.2	22.7	R.NNS*YTSYTMAICGMPLDSFR.A
Solute carrier family 20, member 2 SLC20A2	S385				68.5	R.NNS*YTCYTAAICGLPVHATFRA
Solute carrier family 20, member 2 SLC20A2		-		5.5	10.7	R.NNSYTCY*TAAICGLPVHATFR.A
Solute carrier family 20, member 2 SLC20A2				28.8	11.0	K.S*PISNGTFGFDGHTR.S
Solute carrier family 25, member 46 SLC25A46				12.2	61.8	R.SFST*GSDLGHWVTTPPDIPGSR.N
Solute carrier family 25, member 46 SLC25A46  Solute carrier family 25, member 46 SLC25A46				10.9	60.9	R SFS'T'GSDLGHWYTTPPDIPGSRN  R SFS'TGS'DLGHWYTTPPDIPGSRN
Solute carrier family 25, member 46 SLC25A46  Solute carrier family 25, member 46 SLC25A46				9.4	54.3 63.0	R.SFS*1GS*DLGHWV11PPDIPGSRN  R.SFSTGS*DLGHWV1TPPDIPGSRN
Solute carrier family 25, member 46 SLC25A46				14.7	59.3	R.SFS*TGSDLGHWVTTPPDIPGSRN
Solute carrier family 26 (Sulfate SLC26A2				70.4	49.6	R.DS'AEGNDSYPSGIHLELQR.E
transporter), member 2  Solute carrier family 35 member C2 SLC35C2					86.4	K.GLGS*SPDLELLLRS
Solute carrier family 35, member F2 SLC35F2	S371			17.8	38.0	K.LEENLQETHS*AVL-
Solute carrier family 38 member 1 <sub>SLC38A1</sub>	<b>S</b> 52			9.2	16.0	R.S*LTNSHLEK.K
Solute carrier family 38 member 1 SLC38A1	S52T54			9.6	31.1	R.S'LT'NSHLEK.K
Solute carrier family 38 member 1 SLC38A1				10.6	40.9	R.SLT'NS"HLEK.K
Solute carrier family 38 member 1 SLC38A1				17.5	39.2	R.S'LTNS'HLEK.K
Solute carrier family 38 member 1 SLC38A1					41.9	K.SGLELTELQNMT*VPEDDNISNDS*NDFTEVENGQINSK.F
Solute carrier family 38 member 1 SLC38A1					60.4	R.SLT'NSHLEKK
Solute carrier family 38 member 1 <sub>SLC38A1</sub> Solute carrier family 38 member 1 <sub>SLC38A1</sub>			-		30.5	K.S'GLELT'ELQNMTVPEDDNISNDSNDFTEVENGQINSK.F  K.SGLELTELQNMTVPEDDNIS'NDS'NDFTEVENGQINSK.F
Solute carrier family 39 (zinc transporter), SLC39A3					70.4	K.SGLELTELQNMTVPEDDNIS*NDS*NDFTEVENGQINSK.F  K.EKPSFIDLET*FNAGSDVGS*DSEYESPFMGGAR.G
Solute carrier family 39 (zinc transporter), SLC39A3					103.0	K.EKPSFIDLETFNAGS*DVGS*DSEYESPFMGGAR.G
Solute carrier family 39 (zinc transporter), SLC39A3					98.3	K.EKPSFIDLETFNAGS*DVGS*DS*EYESPFMGGAR.G
Solute carrier family 39 (zinc transporter), SLC39A3					72.6	K.EKPSFIDLETFNAGS'DVGS'DSEY'ESPFMGGAR.G
Solute carrier family 39 (zinc transporter), SLC39A3 member 3					22.0	K.EKPSFIDLET'FNAGSDVGS'DS'EYESPFMGGAR.G
- member 3		•				

Peak Area	%CV White	dots-Significant cha	ange in pept	ide the			
-5 -3	timepo 42 PSM	nt with the minimum					
3 5 >10	>100		CarT	RajiB			
Solute carrier family :	Protein Name Gene 39 (zinc transporter), SLC39/	Phosphosites 3 T120S125	9 2 5 4	£ £ £	Ascor	MOWSE 65.5	Sequence K.EKPSFIDLET*FNAGS*DVGSDSEYESPFMGGAR.G
	member 3 39 (zinc transporter), SLC39A		• • •		7.5	45.9	K.EKPSFIDLET*FNAGS*DVGS*DSEYESPFMGGAR.G
	member 3 39 (zinc transporter), SLC39A				2.9	27.7	K.EKPSFIDLET*FNAGSDVGS*DSEY*ESPFMGGAR.G
	member 3 39 (zinc transporter), SLC39A		•		8.0	43.2	K.EKPSFIDLETFNAGS*DVGSDS*EYESPFMGGAR.G
Solute carrier family	member 3 39 (zinc transporter), SLC39A member 3	3 S125Y133			5.8	62.0	K.EKPSFIDLETFNAGS*DVGSDSEY*ESPFMGGAR.G
Solute carrier family	39 (zinc transporter), SLC39/	3 S129S131Y133			5.5	41.9	K.EKPSFIDLETFNAGSDVGS*DS*EY*ESPFMGGAR.G
Solute carrier family	39 (zinc transporter), SLC39A member 3	3 S131Y133			1.9	37.5	K.EKPSFIDLETFNAGSDVGSDS*EY*ESPFMGGAR.G
Solute carrier	r family 39 member 7 SLC39A	7 S275S276			72.8	42.2	K.EKQS*S*EEEEKETR.G
Solute carrie	r family 4, member 7 SLC4A7	S407			16.9	61.4	R.ENS*TVDFSK.G
Solute carrie	r family 4, member 7 SLC4A	S242			100.0	36.5	K.KHS'DPHLLER.N
Solute carrie	r family 4, member 7 SLC4A	0 S233			100.0	46.5	R.S*FADIGK.K
	r family 4, member 7 SLC4A7				61.7	33.0	R.MLQDDDDTVHLPFEGGS*LLQIPVK.A
	r family 4, member 7 SLC4A7				100.0	24.7	R.MLQDDDDT*VHLPFEGGS*LLQIPVK.A
	r family 4, member 7 SLC4A7			•	12.1	43.3	R.KKYVDAETS*L
	er family 4, member 7 SLC4A7			<u> </u>	13.9	31.3	R.KIPVFHNGS*TPTLGETPK.E
cotr	ansporter, member 4				20.2	54.8	R.ISENYS'DKS'DIENADESSSSILKPLISPAAER.I
cotr	sodium bicarbonate SLC4A4 ansporter, member 4				9.8	12.5	R.ISENY*S*DKSDIENADESSSSILKPLISPAAER.I
	r family 43 member 2 <sub>SLC43</sub> , r family 43 member 2 <sub>SLC43</sub> ,				28.4	37.1	R.RLS*VGSSMR.S  K.LCLS*TVDLEVK.C
	er family 5 member 1					47.5	-MDSS*T*WSPK.T
	, member 6 opposite SLC7A6	S4T5 IO Y300S302		•••	12.5	16.1 36.7	K.EFGY*DS*PHDLDSD
	strand , member 6 opposite SLC7A6				12.0	32.1	K.EFGY*DSPHDLDSD
	strand , member 6 opposite SLC7A6				2.7	12.8	K.EFGYDS*PHDLDS*D
	strand r family 9 isoform A3 SLC9A3				100.0	18.8	R.KRLES*FK.S
	family 9, isoform A1 SLC9A1				15.6	45.8	K.IPS*AVSTVSMQNIHPK.S
Solute carrier	family 9, isoform A1 SLC9A	S602			4.1	44.0	K.IPSAVS*TVSMQNIHPK.S
Solute carrier	family 9, isoform A1 SLC9A	Y683T685	•		6.7	13.7	K.INNY*LT*VPAHKLDSPTMSR.A
Solute carrier	family 9, isoform A1 SLC9A1	T695S697			10.0	18.8	K.INNYLTVPAHKLDSPT*MS*R.A
Solute carrier	family 9, isoform A1 SLC9A1	\$602\$605			10.6	50.8	K.IPSAVS*TVS*MQNIHPK.S
Solute carrier	family 9, isoform A1 SLC9A1	Y649T653		• • •	-0.3	42.9	R.SY*NRHT*LVADPYEEAWNQMLLR.R
Solute carrier	family 9, isoform A1 SLC9A	T603S605	•		11.4	32.1	K.IPSAVST*VS*MQNIHPK.S
Solute carrier	family 9, isoform A3, SLC9A3	IR1 \$290	•	•	16.9	138.0	R.SAS*SDTSEELNSQDSPPK.Q
Solute carrier	family 9, isoform A3, SLC9A3	IR1 S280			100.0	61.9	R.EALAEAALES*PRPALVR.S
Solute carrier	family 9, isoform A3, SLC9A3 regulatory factor 1	IR1 S288S291T309			8.0	41.5	R.
Solute carrier	family 9, isoform A3, SLC9A3 regulatory factor 1	IR1 S290T293S302			0.8	55.2	R.SAS*SDT*SEELNSQDS*PPKQDSTAPSSTSSSDPILDFNISLAMAK.
Solute carrier	family 9, isoform A3, SLC9A3 regulatory factor 1	R1 S288T293S308			6.3	22.4	R.S'ASSDT'SEELNSQDSPPKQDS'TAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1					41.5	R.S*AS*SDTSEELNSQDSPPKQDSTAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1		•		15.3	18.4	R.SASSDTS'EELNSQDS'PPKQDSTAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1				4.2	28.8	R.
	family 9, isoform A3, SLC9A3 regulatory factor 1		-		8.2	34.8	R.S*ASSDT*SEELNS*QDSPPKQDSTAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1		<u>.</u>		7.0	22.2	R.S'ASSDT'SEELNSQDSPPKQDSTAPSSTSSS'DPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1		-		2.1	10.9	R.SASSDTSEELNS*QDS*PPKQDSTAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1					20.3	R.S'AS'S'DTSEELNSQDSPPKQDSTAPSSTSSSDPILDFNISLAMAK.
	family 9, isoform A3, SLC9A3 regulatory factor 1 family 9, isoform A3, SLC9A3					20.4	R.S*ASSDTSEELNSQDSPPKQDSTAPSSTSSSDPILDFNISLAMAK.E
	regulatory factor 1 rier family, member 6 SLC2A6		-		0.7	20.2	R.SASSDTSEELNSQDSPPKQDSTAPS*STSSS*DPILDFNISLAMAK.
	DNA binding protein SON	\$496 \$1769		-	70.5	44.5 52.6	R.SAAS*PVVSSMPER.A
	DNA binding protein SON	\$1769 \$1556			7.6 5.2	58.9	K.EMEHNTVCAAGTS*PVGEIGEEK.I
	SON	\$1948\$1950\$1			35.6	25.7	R.S*FS*IS*PSR.R
SON	DNA binding protein SON	\$2129			50.8	38.2	K.EDDDVIVNKPHVS*DEEEEEPPFYHHPFK.L
	DNA binding protein SON	S1774S1780S1		-	4.3	14.6	R.SAASPVVSS*MPERAS*ESS*SEEKDDYEIFVK.V
	DNA binding protein SON	S1697	-		72.2	58.8	K.ESDQTLAALLS'PK.E
SON	DNA binding protein SON	S1769S1780S1		• •	7.0	24.9	R.SAAS*PVVSSMPERAS*ES*S*SEEKDDYEIFVK.V
SON	DNA binding protein SON	S1766S1769S1			6.0	11.1	R.S*AAS*PVVS*S*MPERASESSSEEKDDYEIFVK.V
SON	DNA binding protein SON	S1769S1780S1			1.4	20.3	R.SAAS*PVVSSMPERAS*ES*SS*EEKDDYEIFVK.V
SON	DNA binding protein SON	S1922T1924			12.7	14.5	R.S*RT*PSRR.S
SON	DNA binding protein SON	S1929S1931T1			8.6	12.0	R.S'RS'HT'PSRR.R
SON	DNA binding protein SON	S910			42.4	40.7	K.S'PDPYR.L
SON	DNA binding protein SON	\$2001\$2003			100.0	16.5	R.S*RS*VVR.R
SON	DNA binding protein SON	T1924S1926			13.9	15.5	R.RSRT*PS*R.R
SON	DNA binding protein SON	T1555			40.4	60.0	K.EMEHNTVCAAGT*SPVGEIGEEK.I
SON	DNA binding protein SON	S1780S1782		•	10.6	47.3	R.AS'ES'SSEEKDDYEIFVK.V

Peak Area %CV	abundand		compared to	the			
.5 29 42 42 71	timepoint PSM	with the minimum	peak area f	or a given			
3 86 5 5 >100 >100			CarT	RajiB			
Protein Na SON DNA binding pro		Phosphosites S1782S1783	9 E E	5 % B	Ascor	MOWSE 40.7	Sequence R.ASES'S'SEEKDDYEIFVK.V
SON DNA binding pro	teinSON	S1774S1782S1		•	4.4	19.1	R.SAASPVVSS*MPERASES*S*SEEKDDYEIFVK.V
SON DNA binding pro	tein <sub>SON</sub>	S1769S1782S1			3.3	24.9	R.SAAS*PVVSSMPERASES*S*S*EEKDDYEIFVK.V
SON DNA binding pro	tein <sub>SON</sub>	S1769S1773S1			-4.0	19.1	R.SAAS*PVVS*S*MPERAS*ESSSEEKDDYEIFVK.V
SON DNA binding pro	tein <sub>SON</sub>	S2020T2022			100.0	16.0	R.S*RT*PLRR.R
SON DNA binding pro	tein <sub>SON</sub>	S1766S1769S1			5.7	12.4	R.S*AAS*PVVSS*MPERASESSS*EEKDDYEIFVK.V
SON DNA binding pro		S1766S1769S1			6.4	19.7	R.S*AAS*PVVS*SMPERASESSS*EEKDDYEIFVK.V
SON DNA binding pro		S1769S1773S1			6.7	21.9	R.SAAS*PVVS*S*MPERASESSS*EEKDDYEIFVK.V
SON DNA binding pro		S1769S1773S1			1.7	23.5	R.SAAS*PVVS*SMPERAS*ES*SSEEKDDYEIFVK.V
Sorting nex	tilin SORT1	S825			27.8	41.3	K.SGYHDDS*DEDLLE
Sorting nex		S32S39			34.4	93.0	R.LPPPFPGLEPESEGAAGGS*EPEAGDS*DTEGEDIFTGAAVVSK.H  R.LPPPFPGLEPESEGAAGGSEPEAGDS*DT*EGEDIFTGAAVVSK.H
Sorting nex		S39T41	•		3.1	31.7	R.LPPPFPGLEPES'EGAAGGS'EPEAGDS'DTEGEDIFTGAAVVSK.
Sorting nex		\$25\$32\$39 \$25\$39T41			6.4	91.2	R.LPPPFPGLEPES*EGAAGGSEPEAGDS*DT*EGEDIFTGAAVVSK.
Sorting nex		S32S39T41		=	29.5	47.0	R.LPPPFPGLEPESEGAAGGS*EPEAGDS*DT*EGEDIFTGAAVVSK.
Sorting nex	in 1 <sub>SNX1</sub>	S25S32		•		81.8	R.LPPPFPGLEPES*EGAAGGS*EPEAGDSDTEGEDIFTGAAVVSK.H
Sorting nex	in 1 <sub>SNX1</sub>	S32T41			5.2	56.5	R.LPPPFPGLEPESEGAAGGS*EPEAGDSDT*EGEDIFTGAAVVSK.H
Sorting nexis	11 SNX11	S191S192		•		14.7	R. Described decerring examadra/neer/deg egoti ddi egot cone
Sorting nexis	15 <sub>SNX15</sub>	S179S180				20.3	R.RGLEELEVPVDPPPS'S'PAQEALDLLFNCESTEEASGSPAR.G
Sorting nexis	15 <sub>SNX15</sub>	\$179\$201			6.5	14.4	R.RGLEELEVPVDPPPS*SPAQEALDLLFNCESTEEASGS*PAR.G
Sorting nex	in 2 <sub>SNX2</sub>	S185	•		55.8	32.6	R.RFS*DFLGLHSK.L
Sorting nex	in 2 <sub>SNX2</sub>	S119		. =	33.7	58.4	K.SMS*APVIFDR.S
Sorting nex	in 3 <sub>SNX3</sub>	<b>Y</b> 71			8.9	39.7	R.RY*SDFEWLR.S
Sorting nex		<b>S</b> 72			27.6	46.7	R.RYS*DFEWLR.S
Source of immunodominant N associated pepti	IHC <sub>STT3B</sub> des	\$498\$499			77.9	32.0	R.ENPPVEDS*S*DEDDKRNQGNLYDK.A
	100 SP100	\$407\$409\$410	<b></b> :		101.6	43.9	R.VIGQDHDFS*ES*S*EEEAPAEASSGALR.S
	100 SP100	S157			100.0	45.8	K.GFENVIHDKLPLQES*EEEER.E
	100 SP100	S451S452	_=		25.5	41.9	R.RFS*S*SDFSDLSNGEELQETCSSSLR.R
	100 SP100 100 SP100	S18	•		72.0	47.0	R.LNECIS*PVANEMNHLPAHSHDLQR.M
SP110 nuclear body pro		\$327\$328\$331		•	27.4	41.7	R.THHNQASDIIVIS'S'EDS'EGS'T'DVDEPLEVFISAPR.S  R.DNS'PEPNDPEFPQEVSSTPSDKK G
SP110 nuclear body pro		\$256 \$244			103.8 39.1	37.5	R.DKEDPQEMPHS*PLGSMPEIR.D
	AK STK39	S385	•		161.4	104.7	K.TEDGDWEWS*DDEMDEK.S
Si	PAK STK39	<b>S</b> 370			17.8	36.5	R.RVPGS*SGHLHK.T
Spatao	sin SPG11	T1956S1969S1			3.9	53.9	R.VHST*SSLDSQKFVTVPS*S*NEVVTNLEVLTSK.C
Spatao	sin SPG11	S1955T1966S1			9.6	51.5	R.VHS*TSSLDSQKFVT*VPS*SNEVVTNLEVLTSK.C
Spatao	sin SPG11	S1955S1958S1			9.6	96.7	R.VHS*TSS*LDS*QKFVTVPSSNEVVTNLEVLTSK.C
Spatao	sin SPG11	T1956S1958S1			3.6	35.3	R.VHST*SS*LDS*QKFVTVPSSNEVVTNLEVLTSK.C
Spatao	sin SPG11	T1956S1957S1			0.4	24.5	R.VHST*S*SLDS*QKFVTVPSSNEVVTNLEVLTSK.C
Spatao	sin SPG11	S1969S1970T1			-0.2	23.6	R.VHSTSSLDSQKFVTVPS*S*NEVVT*NLEVLTSK.C
Spatao	sin SPG11	S1955S1958S1		·	6.4	64.4	R.VHS*TSS*LDSQKFVTVPS*SNEVVTNLEVLTSK.C
	sin SPG11	S1955T1956T19	1	•	0.1	14.7	R.VHS*T*SSLDSQKFVT*VPSSNEVVTNLEVLTSK.C
	like SPECC1L				33.8	22.4	R.KGS*SGNASEVSVACLTER.I
	like SPECC1L				9.1	58.9	R.KGSSGNAS'EVSVACLTER.I
	like SPECC1L			<u>.</u>	6.9	24.7	R.DISAQEGASPASLMAMGTTS*PQLSLSSS*PTASVTPTTR.S  R.HS*ISGPISTSKPLTALSDK.R
Spectrin, alpha, non-erythrocytic 1 (alp		\$887 \$1031		•	20.7	32.9	K.HS*ISGPISTSKPLTALSDK.R
Spectrin, alpha, non-erythrocytic 1 (alp	rin) ha-SPTAN1	\$1031 \$1190			10.9 45.2	32.9	K.TAS*PWK.S
Spectrin, alpha, non-erythrocytic 1 (alp	rin) ha-SPTAN1	S1190 S1217			100.0	53.3	R.S*LQQLAEER.S
Spectrin, alpha, non-erythrocytic 1 (alp	rin) ha- <sub>SPTAN1</sub>	S1029			.50.0	18.1	K.KLDPAQS*ASR.E
Spectrin, beta, non erythrocyt		S766S767			100.0	36.4	R.RS*S*LER.A
Sperm associated antige	n 9 SPAG9	S716S719			17.2	87.2	R.SAS'QSS'LDKLDQELK.E
Sperm associated antige	n 9 SPAG9	S203T217	• •	· · <del>· ·</del>	100.0	49.7	K.ERPIS*LGIFPLPAGDGLLT*PDAQK.G
Sperm associated antige	n 9 <sub>SPAG9</sub>	T217	- •		82.2	30.2	K.ERPISLGIFPLPAGDGLLT*PDAQK.G
Sperm associated antige	n 9 SPAG9	S718S719		-	6.1	22.1	R.SASQS'S'LDKLDQELK.E
Sperm associated antige	n 9 SPAG9	S718			20.1	51.8	R.SASQS*SLDKLDQELK.E
Sperm associated antige		S716S718	Ţ.		3.2	22.6	R.SAS'QS'SLDKLDQELK.E
Sperm associated antige		S536S537	<b>—</b>		19.4	11.6	K.RS*S*IWQFFSR.L
Sperm associated antige		S203	÷.		100.5	53.1	K.ERPIS*LGIFPLPAGDGLLTPDAQK.G
Sperm associated antige		S537S543	<b>—</b>		15.0	13.0	K.RSS*IWQFFS*R.L
Sperm specific antige		S739		-	28.9	82.2	R.SQS*LPTTLLSPVR.V
Sperm specific antige	## 2 SSFA2	S737		•	12.2	69.2	R.S*QSLPTTLLSPVR.V
I							

<-10 0 abuno		compared to	the			
.s timep	oint with the minimum					
>10 >10 Protein Name Gene	Phosphosites	CarT_	RajiB E E E	Ascor	MOWSE	Sequence
Sperm specific antigen 2 SSFA2		0 61 60	0 7 5	8.4	18.9	R.S*ADNLSCPSPLNVMEPVTELMQEQSYLK.S
Spermatid perinuclear RNA binding protein STRBI			•	4.6	36.0	K.VLQAMGYPTGFDADIECMS*S*DEKSDNESK.N
Spermatid perinuclear RNA binding protein STRBI		_		11.8	11.1	K.VLQAMGYPT*GFDADIECMSSDEKS*DNESK.N
Spermatid perinuclear RNA binding protein STRBI  Spermatogenesis associated 5 like 1 SPATA		=		4.8	26.3	K.VLQAMGY*PT*GFDADIECMSSDEKSDNESK.N  R.RS*LS*LNR.L
Sphingosine kinase 2 SPHK				41.7	29.0	R.AKSELT*LTPDPAPPMAHS*PLHR.S
Sphingosine kinase 2 SPHK	2 \$399\$414			48.4	12.2	R.AKS'ELTLTPDPAPPMAHS'PLHR.S
Sphingosine-1-phosphate phosphatase 1 SGPP	1 S112	•		35.4	80.2	R.NS*LTGEEGQLAR.V
Spliceosome associated protein 145 SF3B2	S307S309			12.8	50.7	R.SSLGQS*AS*ETEEDTVSVSK.K
Spliceosome associated protein 145 SF3B2				5.9	75.2	K.IEEAMDGSET*PQLFTVLPEKR.T
Spliceosome associated protein 145 SF382  Spliceosome associated protein 145 SF382				13.1	74.7	R.GS*DSPAADVEIEYVTEEPEIYEPNFIFFK.R  K.GFEEEHKDS*DDDS*S*DDEQEKKPEAPK.L
Spliceosome associated protein 145 SF3B2				100.0	31.3	R.SRGS*DS*PAADVEIEYVTEEPEIYEPNFIFFK.R
Spliceosome associated protein 145 SF3B2				5.5	26.1	R.S*RGSDS*PAADVEIEYVTEEPEIYEPNFIFFK.R
Spliceosome associated protein 145 SF3B2	T706S714S718				15.8	R.
Spliceosome associated protein 145 SF3B2	! T706S714S718	÷			17.9	R. THOMASS EDGENESCES CESSES AND A PROPERTY OF THE PROPERTY OF
Spliceosome associated protein 145 SF3B2	! \$302\$309		·	8.5	18.4	R.S'SLGQSAS'ETEEDTVSVSKK.E
Spliceosome associated protein 145 SF3B2		·		10.9	47.1	R.SSLGQSAS'ETEEDTVSVSK.K
Spliceosome associated protein 145 SF3B2				64.0	96.9	K.IEEAMDGS'ETPQLFTVLPEKR.T
Spliceosome associated protein 145 SF3B2  Splicing factor 1 SF1			-	-0.1	11.3	R.GSDS*PAADVEIEYVTEEPEIYEPNFIFFK.R  R.TGDLGIPPNPEDRS*PS*PEPIYNSEGK.R
SF3A1	\$80\$82 \$329			7.8	15.7 49.5	K.FGESEEVEM#EVES*DEEDDKQEK.A
Splicing factor 3 subunit 1 SF3A1				7.0	25.5	К.
Splicing factor 3 subunit 1 SF3A1	<b>S</b> 359	•		57.0	68.0	K.AEEPPSQLDQDTQVQDMDEGS*DDEEEGQK.V
Splicing factor 3A, subunit 3 SF3A3	\$365\$367\$369			102.2	76.2	R.EEEEEEQIS'ES'ES'EDEENEIJYNPK.N
Splicing factor 3B subunit 1 SF3B1	\$308T313			20.8	52.4	R.DTPGHGS*GWAET*PR.T
Splicing factor 3B subunit 1 SF3B1			• •	19.1	53.3	K.GSET*PGAT*PGSK.I
Splicing factor 3B subunit 1 SF3B1			·	100.0	20.3	R.WDET*PGR.A
Splicing factor 3B subunit 1 SF3B1  Splicing factor 3B subunit 1 SF3B1				27.5	106.6	R.KLTAT"PT"PLGGMTGFHMQTEDR.T  R.DT"PGHGSGWAET"PR.T
Splicing factor 3B subunit 1 SF3B1		•••		12.6	16.4	R.TMIIS*PERLDPFADGGKT*PDPK.M
Splicing factor 3B subunit 1 SF3B1				12.7	23.6	R.WDQTADQTPGAT*PK.K
Splicing factor 3B subunit 1 SF3B1	T267T273			17.3	16.2	K.IWDPTPSHTPAGAAT*PGRGDT*PGHATPGHGGATSSAR.K
Splicing factor 3B subunit 1 SF3B1	T257S259	-	•		12.0	K.IWDPT*PS*HTPAGAATPGRGDTPGHATPGHGGATSSAR.K
Splicing factor 3B subunit 1 SF3B1	T223S229			9.3	16.3	K.KLSSWDQAET*PGHTPS*LR.W
Splicing factor 3B subunit 1 SF3B1				7.8	10.8	R.DT*PGHGS*GWAETPR.T
Splicing factor 3B subunit 1 SF3B1		<u> </u>		10.6	17.3	K.LSSWDQAET*PGHT*PSLR.W
Splicing factor 4 <sub>SUGP</sub> Splicing factor 4 <sub>SUGP</sub>				31.5	99.4	KAVQQHQHGYDS*DEEVDS*ELGTWEHQLRR  KAVQQHQHGYDSDEEVDS*ELGTWEHQLRR
Splicing factor arginine/serine rich 5 SRSFS				100.0	34.7	R.S*KS*PAS*VDR.Q
Splicing factor arginine/serine rich 5 SRSF				100.0	21.8	K.S'PAS'VDR.Q
Splicing factor arginine/serine rich 5 SRSF	5 <b>S248S25</b> 0			18.5	36.4	R.S*KS*PASVDR.Q
Splicing factor arginine/serine rich 5 SRSFS	5 <b>S</b> 116				20.9	R.LIVENLS*SR.C
Splicing factor HCC1 RBM3				212.6	64.8	K.DKS*PVREPIDNLTPEER.D
Splicing factor HCC1 RBM3		<u>.</u> .		42.3	19.9	R.Y*RSPYSGPK.F
Splicing factor HCC1 RBM3				100.0	17.6	R.S'KS'PFRK.D  R.S'RS'KS'PFRK
Splicing factor HCC1 RBM3				-10.2	11.9	R.YRS'PYSGPK.F
Splicing factor YT521-B YTHD				7.7	54.5	R.LSSESHHGGS*PIHWVLPAGMSAK.M
Splicing factor YT521-B YTHD	C1 <b>S</b> 308			100.0	40.9	R.GIS*PIVFDR.S
Splicing factor YT521-B YTHD	C1 S146T148			24.6	21.1	R.AKS*PT*PDGSER.I
Splicing factor YT521-B YTHD	C1 <b>S</b> 119		-	2.8	16.2	R.LSS*SASR.E
Splicing factor YT521-B YTHD			•	-0.4	33.4	R.LSSES*HHGGSPIHWVLPAGMSAK.M
Splicing factor YT521-B YTHD		<u>_</u>		3.0	35.2	R.LSS'ESHHGGSPIHWVLPAGMSAK.M
Splicing factor, 45 kd RBM1  Splicing factor, 45 kd RBM1				10.1	119.7	R.S'PTGPSNSFLANMGGTVAHK.I  R.RPDPDS'DEDEDYER.E
Splicing factor, 45 KG RBM1		<u> </u>		76.7 4.3	77.7 68.3	R.SPTGPSNS*FLANM#GGTVAHK.I
Splicing factor, 45 kd RBM1		•		0.5	74.4	R.SPTGPS'NSFLANMGGTVAHK.I
Splicing factor, 45 kd RBM1				-0.0	16.3	R.SPT*GPSNSFLANMGGTVAHK.I
Splicing factor, arginine/serine rich 1 SRSF	1 Y237S238		•	6.1	15.6	R.Y'S'PRHSR.S
Splicing factor, arginine/serine rich 1 SRSF	1 <b>S</b> 199			14.0	42.8	R.S'PSYGR.S
Splicing factor, arginine/serine rich 1 <sub>TRA26</sub>	3 Y226S227			15.0	15.9	R.SY"S"PRR.S

Peak Area <-10 -5	%CV 0 29	abundano timepoint	ts-Significant cha se at 5%FDR o with the minimum	ompared to	the		
-3 0 3 5	71 86 >100	PSM		CarT	RajiB		
>10	Protein Name	Gene	Phosphosites	5 F B	5 P B	Ascor	MOW
Splicing factor, arg	jinine/serine rich 1	TRA2B	S225Y226S227			9.7	16.7
Splicing factor, arg	jinine/serine rich 1	SRSF1	S199S201			14.5	14.1
Splicing factor, arg	jinine/serine rich 1	SRSF1	S231S234			100.0	18.0
Splicing factor, arg	jinine/serine rich 1	SRSF1	Y237S242			10.8	12.5
Splicing factor, arg	jinine/serine rich 1	TRA2B	S223S225Y226			8.3	13.4
Splicing factor, arg	jinine/serine rich 1	SRSF1	S201Y202			5.5	14.8
Splicing factor, arg	jinine/serine rich 1	TRA2B	S223S225S227	<b>.</b>		9.0	17.7
Splicing factor, argi	nine/serine rich 11	SRSF11	S483			100.0	30.4
Splicing factor, argi	nine/serine rich 11	SRSF11	S207			27.7	71.5
Splicing factor, argi	nine/serine rich 11	SRSF11	S323T325	<b>—</b>		100.0	17.9
Splicing factor, argi	nine/serine rich 11	SRSF11	S449	·		29.8	36.8
Splicing factor, argi	nine/serine rich 11	SRSF11	T260S262	•••		13.1	25.0
Splicing factor, argi	nine/serine rich 11	SRSF11	Y432		•	9.1	34.2
Splicing factor, argi			S434			9.7	31.6
Splicing factor, argi			T260S263		■ .	4.0	11.2
Splicing factor, argi			T447			-19.1	40.0
Splicing factor, argi			S263S264	٠.		6.3	15.0
Splicing factor, arg			S119S121			100.0	19.0
Splicing factor, arg			S145			19.1	21.7
Splicing factor, arg			S191			45.2	47.3
Splicing factor, arg			S189S191			61.7	31.0
Splicing factor, arg	jinine/serine rich 2	SRSF2	S187S189S191			70.4	21.7
		SRSF2	S26	••••		15.0	35.2
Splicing factor, arg			S206S208			45.0	28.6
Splicing factor, arg			\$206\$208\$220	Ţ.		14.3	38.8
Splicing factor, arg			S206S208S212			41.8	12.1
Splicing factor, arg			S206S212S220		•	4.7	22.1
	interacting protein	1	S796S802	<b></b>		18.3	32.2
	interacting protein		S796S798			33.6	44.6
	interacting protein		S338	<u></u> :		11.0	46.4
	interacting protein	1	S901	•			44.5
	interacting protein		S816S818			100.0	13.8
	interacting protein		\$878\$880\$882	<del></del> -		100.0	12.4
	interacting protein		S796T800			18.9	33.2
	interacting protein	1	S341	<u></u>		7.9	27.4
Splicing factor, arg			\$364\$366			24.4	20.1
Splicing factor, arg			S316			10.2	32.1
Splicing factor, arg			\$330			16.0	21.2
Splicing factor, arg			S318			9.1	26.8
Splicing factor, arg			S267S269			100.0	36.4
Splicing factor, arg			\$410\$412	<b>—</b>		100.0	16.9
Splicing factor, arg	jinine/serine-rich 4	SRSF4	S456	·		12.8	20.0

Splicing factor, arginine/serine-rich 4 SRSF4 S458

Splicing factor, arginine/serine-rich 6 SRSF6 8303

Splicing factor, arginine/serine-rich 6 SRSF6 S218S220S222

Splicing factor, arginine/serine-rich 6 SRSF6 8314S316

Splicing factor, arginine/serine-rich 6SRSF6 \$263S265

Splicing factor, arginine/serine-rich 6 SRSF6 \$301S303

Splicing factor, arginine/serine-rich 6 SRSF6 S265Y269

Splicing factor, arginine/serine-rich 6 SRSF6 \$265\$272

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 S163S165S167

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 S165S167

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 Y189S192

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 S215S217

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 S181S183

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 8179S181S183

Splicing factor, arginine/serine-rich 7,35kDa SRSF7 S223S225S227

SRSF7 S231S233

Splicing factor, arginine/serine-rich 6 SRSF6 S295S297S299

Splicing factor, arginine/serine-rich 6 SRSF6 845

Splicing factor, arginine/serine-rich 6 SRSF6 S257S259S261

Splicing factor, arginine/serine-rich 6 SRSF6 S265

R.SRS\*Y\*S\*PR.R R.VKVDGPRS\*PS\*YGR.S R.RS\*RGS\*PR.Y R.Y\*SPRHS\*R.S R.S\*RS\*Y\*SPR.R R.VKVDGPRSPS\*Y\*GR.S R.S\*RS\*YS\*PR.R K.VNGDDHHEEDMDMS\*D.-K.LNHVAAGLVS\*PSLK.S R.S\*KT\*PPK.S K.KPIETGS\*PK.T R.RRT\*PS\*SSR.H R.DYDEEEQGY\*DSEKEK.K R.DYDEEEQGYDS\*EKEK.K R.RRT\*PSS\*SR.H K.KPIET\*GSPK.T R.RRTPSS\*S\*R.H R.RS\*RS\*PR.R R.SRYS\*R.S R.S\*PPPVSK.R R.S'RS'PPPVSK.R R.S'RS'RS'PPPVSK.R R.TS\*PDTLR.R R.S\*KS\*PPKSPEEEGAVSS.-R.S\*KS\*PPKSPEEEGAVS\*S.-R.S\*KS\*PPKS\*PEEEGAVSS.-R.S\*KSPPKS\*PEEEGAVS\*S.-R.FHS\*PSTTWS\*PNKDTPQEK.K R.FHS\*PS\*TTWSPNKDTPQEK.K R.S\*PISDNSGCDAPGNSNPSLSVPSSAESEK.Q

RVKDS\*SPGEKS

KKRPQS\*PS\*PRR

RRS\*ES\*LS\*PRR

RFHS\*PSTT\*WSPNKDTPQEKK

R SPIS\*DNSQCDAPGNSNPSLSVPSSAESEKQ

R.SREES'RS'R.S

K.RGS'VSR.G

K.SLRQS'R.S

K.RGSVS'R.G

R.S'KS'KDQAEEK.I

K.SKPNLPS\*ESR.S

K.SKPNLPSES\*R.S

R.SNS\*PLPVPPSK.A

R.S\*IS\*KS\*R.S

R.S\*VS\*PPPKR.A

R.S\*RS\*KDEYEK.S

K.SDRGS\*HS\*HS\*R.S

R.S\*NS\*PLPVPPSK.A

K.NGYGFVEFEDS\*R.D

R.S\*RS\*QS\*RS\*NS\*PLPVPPSK.A

R.S\*KDEY\*EKSR.S

R.S\*KDEYEKS\*R.S

R.S\*RS\*IS\*LR.R

R.Y\*FQS\*PSR.S

R.S\*PS\*GS\*PRR.S

R.RS\*AS\*PER.M

R.S\*GS\*IKGSR.Y

R.S\*RS\*GS\*IKGSR.Y

5.9 30.9

33.6 63.0

100.0 17.5

100.0 29.5

49.2 47.4

18.5 28.4

50.0 18.8

36.9 49.3

22.5 10.9

14.1 26.4

100.0 19.4

100.0 13.3

12.0 22.9

100.0 27.0

100.0 16.2

34.8 31.7

34.7 16.6

39.9 18.3

<-10 o abundano	ts-Significant char e at 5%FDR o with the minimum	ompared to	the			
3 42 PSM						
>10 >10 Protein Name Gene	Phosphosites	E E E	RajiB E E E	Ascor	MOWSE	Sequence
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	S173S175	<b></b>		100.0	18.4	R.S*AS*LRR.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	\$202\$204			100.0	19.7	R.S*IS*RPR.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7  Splicing factor, arginine/serine-rich 7,35kDa SRSF7	Y189S192S196 Y189S194			10.8	32.4	R.Y*FQS*PSRS*R.S  R.Y*FQSPS*R.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	\$192\$194			11.0 42.3	32.4	R.YFQS'PS'R.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	S155S157S159	• • •		100.0	11.1	R.S*RS*AS*PR.R
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	Y189S192S194			6.8	11.8	R.Y"FQS"PS"RSR.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	S213S215S217	<b>.</b>		100.0	12.9	K.S'RS'PS'PKR.S
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	\$181\$183\$187			100.0	19.9	R.S*GS*IKGS*R.Y
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	S165			11.0	19.4	R.S*ISLRR.S
Splicing factor, arginine/serine-rich 7,35kDa <sub>SRSF7</sub> Splicing factor, arginine/serine-rich 7,35kDa <sub>SRSF7</sub>	\$192\$194\$196 \$171\$173\$175		• • •	10.8	12.5	R.YFQS'PS'RS'R.S  R.RS'RS'AS'LR.R
Splicing factor, arginine/serine-rich 7,35kDa SRSF7	Y189S194S196			8.9	11.3	R.Y"FQSPS"RS"R.S
Splicing factor, arginine/serine-rich 8 <sub>SFSWAP</sub>	S604			8.1	12.7	R.VKLDDDS*DDDEESKEGQESSSSAANTNPAVAPPCVVVEEK.K
Splicing factor, arginine/serine-rich 8 SFSWAP	S283			12.1	76.8	K.SGVSS*DNEDDDDEEDGNYLHPSLFASK.K
Splicing factor, arginine/serine-rich 8 SFSWAP	S282	• • • •		24.9	72.3	K.SGVS*SDNEDDDDEEDGNYLHPSLFASK.K
Splicing factor, arginine/serine-rich 8 SFSWAP	S815			100.0	40.3	R.AHS*PER.R
SPT2, Suppressor of Ty, domain containing SPTY2D1		•		52.0	51.0	R.EYEEEDDDDDEY*DSEMEDFIEDEGEPQEEISK.H
SPT2, Suppressor of Ty, domain containing SPTY2D1		•		13.0	69.3	R.EYEEEDDDDDEYDS*EMEDFIEDEGEPQEEISK.H
SPT6 SUPT6H SPT6 SUPT6H	\$73\$75\$78 \$1703\$1712			100.0	26.0	K.GFINDDDDEDEGEEDEGS*DS*GDS*EDDVGHKK.R  R.LTPRPSPS*PMIESTPMS*IAGDATPLLDEMDR
SPT6 SUPT6H	T1532S1535			20.9	29.3	R.TRT*PAS*INATPANINLADLTR.A
SPT6 SUPT6H	\$1703T1718			20.1	48.8	R.LTPRPSPS*PMIESTPMSIAGDAT*PLLDEMDR
SPT6 SUPT6H	S1701T1718			15.0	36.8	R.LTPRPS*PSPMIESTPMSIAGDAT*PLLDEMDR
SPT6 SUPT6H	\$1701\$1712			6.5	32.4	R.LTPRPS*PSPMIESTPMS*IAGDATPLLDEMDR
SPT6 SUPT6H	S1535			6.1	25.0	R.TPAS*INATPANINLADLTR.A
SPT6 SUPT6H	T1532S1535T15			11.6	38.5	R.TRT*PAS*INAT*PANINLADLTR.A
SPT6 SUPT6H	T1530S1535T15	-		13.1	13.8	R.T*RTPAS*INAT*PANINLADLTR.A
SPT6 SUPT6H  Src like adapter protein 2 SLA2	T1530S1535			12.6	46.4	R.T*RTPAS*INATPANINLADLTR.A  R.RGS*YSLSVR.L
SRP20 SRSF3	S129 S148			16.9	31.6	R.NHKPS*R.S
SRP20 SRSF3	\$128\$130			100.0	14.4	R.S'LS'RDR.R
SRP20 TXLNG	<b>S</b> 115			100.0	21.7	R.RRS*PR.R
SRP20 SRSF3	S126S128S130	<del></del>		100.0	12.8	R.S'RS'LS'RDR.R
SRP20 SRSF3	S138S140			100.0	16.6	R.ERS*LS*RER.N
SRP20 KMT2E	\$120\$122\$124			100.0	16.6	K.S'FS'RS'R.T
SRp30c SRSF9	S211			21.8	63.1	R.GS*PHYFSPFRPY
SRp30c SRSF9 SRp30c SRSF9	S204S208S211	<u></u>		10.5	22.0	R.GRDS'PYQS'RGS'PHYFSPFRPY  R.GS'PHYFS'PFRPY
SRp30c SRSF9	S211S216 S204	• • •		25.3	35.7 43.9	R.GRDS*PYQSR.G
SRp30c SRSF9	\$189Y190			10.3	17.2	R.STS*Y*GYSR.S
SRp30c SRSF9	\$187T188			24.7	21.9	R.S*T*SYGYSR.S
SRp30c SRSF9	Y214	<del></del>		7.7	46.3	R.GSPHY*FSPFRPY,-
SRp30c SRSF9	T188			-0.1	31.4	R.ST*SYGYSR.S
SRp30c SRSF9	S189Y192			15.4	23.9	R.STS*YGY*SR.S
SRp30c SRSF9	S204Y206S211			8.0	12.6	R.GRDS*PY*QSRGS*PHYFSPFRPY
SRp30c SRSF9 SRp30c SRSF9	S216Y221		• •	26.6	22.6	R.GSPHYFS'PFRPY'  R.GS'PHY'FSPFRPY
SRp30c SRSF9	S211Y214 S189	•		16.9	33.0	R.STS*YGYSR.S
SRp30c SRSF9	Y192		-	11.5	12.0	R.STSYGY*SR.S
SRp30c SRSF9	Y214S216			-2.6	28.9	R.GSPHY'FS'PFRPY
SRp46 SRSF8	<b>S</b> 100	<u> </u>		100.0	21.2	R.RDLPRS*R.Q
SRP72 SRP72	S620			22.5	63.2	K.TVS*SPPTSPRPGSAATVSASTSNIIPPR.H
SRP72 SRP72	S621T624			16.6	92.1	K.TVSS*PPT*SPRPGSAATVSASTSNIIPPR.H
SRP72 SRP72	S621S625			13.7	92.5	K.TVSS*PPTS*PRPGSAATVSASTSNIIPPR.H
\$RP72 SRP72 SRP72 SRP72	S621	-		8.0	69.6	K.TVSS*PPTSPRPGSAATVSASTSNIIPPR.H  K.TVS*SPPTS*PRPGSAATVSASTSNIIPPR.H
SRP72 SRP72	\$620\$625 \$621\$630			13.8	77.6 89.5	K.TVS*SPPTS*PRPGSAATVSASTSNIIPPR.H
SRP72 SRP72	\$621\$630 \$620\$630			1.9	28.4	K.TVS*SPPTSPRPGS*AATVSASTSNIIPPR.H
SRP72 SRP72	T618S620	•		8.1	49.6	K.T*VS*SPPTSPRPGSAATVSASTSNIIPPR.H
SRP72 SRP72	S621S635		•	4.5	48.5	K.TVSS*PPTSPRPGSAATVS*ASTSNIIPPR.H
SRP72 SRP72	S630T633			8.0	31.4	K.TVSSPPTSPRPGS*AAT*VSASTSNIIPPR.H

PRIMAL SCRIEGE PROTECTION OF PROSPECTION OF PROSPEC	Peak Area 9	More do abundano timepoint	ts-Significant cha be at 5%FDR of with the minimum	inge in pepti compared to peak area f	ide the for a given			
Part   Dec	-3 0 71	PSM						
SEPTIZ AUTO   SECTION	5 >100 >10							
MATT COPTS   DESIGNATION	P			5 4 5	9 2 2			
### 17 SERVICE OF THE PROPERTY PROCESSES OF THE PROCESSES		SRP72 SRP72	S625S630			7.9	36.6	K.TVSSPPTS*PRPGS*AATVSASTSNIIPPR.H
SERVES SERVEY   TOLLINGS		SRP72 SRP72	T624			4.5	12.1	K.TVSSPPT*SPRPGSAATVSASTSNIIPPR.H
SEMEND GROUND   SEMEND STOREST   S. 20   13   S. SEMENT FOR ARCHIVE   SEMEND GROUND   SEMEND		SRP72 SRP72	S620S621		•	-0.3	30.6	K.TVS*S*PPTSPRPGSAATVSASTSNIIPPR.H
		SRP72 SRP72	T624S625			1.6	13.7	K.TVSSPPT*S*PRPGSAATVSASTSNIIPPR.H
######################################		SRRM2 SRRM2	S1876S1878T1			35.3	11.3	R.S*RS*RT*PLISR.R
#### #################################		SRRM2 SRRM2	S2100S2102			23.8	13.8	R.NHS*GS*RTPPVALNSSR.M
SERVED_SIGNED   11000		SRRM2 SRRM2	<b>S</b> 771	•		8.2	36.4	K.S*RLSLR.R
1988   1990		SRRM2 SRRM2	S1727S1729S1			100.0	36.0	R.S*PS*VS*S*PEPAEK.S
### 14		SRRM2	S1320			29.8	42.5	K.ELSNS*PLR.E
### SRMM_CERROR 12004		SRRM2 SRRM2	T1003		• •	75.8	40.6	K.AQT*PPGPSLSGSK.S
SRRWI_DERMIN_   1906-1006		SRRM2	T1003S1014		•	29.4	31.6	K.VKAQT*PPGPSLSGSKS*PCPQEK.S
######################################		SRRM2 SRRM2	T2104	•••		66.3	53.5	R.T*PPVALNSSR.M
### SHAMA SIRRAC 18575864  ### SHAMA SIRRAC 18575866  ### SHAMA SIRRAC 18575866  ### SHAMA SIRRAC 18575866  ### SHAMA SIRRAC 185758666  ### SHAMA SIRRAC 1857586666  ### SHAMA SIRRAC 18575866666  ### SHAMA SIRRAC 185758666666  ### SHAMA SIRRAC 1857586666666666666666666666666666666666			T856S864			10.3	30.1	
1972   14.4   R. SETTE PARWICK			T856T866			11.6	29.2	
### SAMMA SCRIPTO \$1987   10.00   3.40   K.E.DYROPARE   ### SAMMA SCRIPTO \$1988   10.00   3.40   K.E.DYROPARE   ### SAMMA SCRIPTO \$1988   10.00   3.40   K.E.DYROPARE   ### SAMMA SCRIPTO \$100077004   10.00   3.01   K.S.DYROPARE   ### SAMMA SCRIPTO \$100077004   10.00   3.01   K.S.DYROPARE   ### SAMMA SCRIPTO \$100077004   10.00   2.00   K.S.DYROPARE   ### SAMMA SCRIPTO \$100077004   10.00   10.00   K.S.DYROPARE   ### SAMMA SCRIPTO \$100077004   10.00   10.00   K.S.DYROPARE   ### SAMMA SCRIPTO \$100077004   K.S.DYROPARE   ### SAMMA SCRIPTO \$10						26.8	51.6	
						10.2	21.4	
SARRAW 2					• •			
SARRAW SARRAW   SARRAW SARRAW   SARRAW SAR								
SARRAY SERVICE   SOUTH   SOU				<u> </u>				
100.0   22.0   R.SETPLIPEK								
SIRRIA SIRRIA   SISSING								
SRRMAZ SRRMAZ   S15205154251   12.4   51.7   REFOSSOCIAL DAYPPAS PROCES								
SRRMZ_SRRM								
SRMM2 SRRM2   S2208								
SRRM2 GRRM2 0 2023333								
SRRM2_GRRM2   S000250004   12.3   43.3   R.S.FYSTPVERR								
SRRM2_GRRM2   S376								
SRRM2 SERM2   12269								
17.8   32.2   R.SRSST-VIELASR.S								
SRRMZ SRRMZ   STUDEN   STUDEN   SRRMZ SRRMZ   STUDEN   SRRMZ SRRMZ   SRRMZ   SRRMZ   SRRMZ   SRRMZ   SRRMZ   SRRMZ   SRRMZ   SRRMZ SRRMZ   S								
SRRM2   SCHM2   S2272   171.2   119.7   R.TPAAAAANNASPRIT								
SRRM2   SRRM2   S8758976				•••				
SRRMZ SRRMZ   S2132								
SRRM2 SRRM2   S21182121   10.3   23.5   R.MSCFS*RPS*MSPTPLDRC		SRRM2 SRRM2						
SRRM2 SRRM2   S218S2121			S2132				56.3	R.S*PGMLEPLGSSR.T
SRRM2 SRRM2   S2118S2123   9.3   25.4   RMSCFS*RPSMS*PTPLDR.C							23.5	R.MSCFS*RPS*MSPTPLDR.C
SRRM2 SRRM2   S3715398   27.2   44.4   R.HGGS-PQPLATTPLSQEPUNPPSEAS-PTR.D			S2118S2123			9.3	25.4	R.MSCFS*RPSMS*PTPLDR.C
SRRM2 SRRM2   S3515353537   32.9   42.2   K.SATRPS*PS*PERS*STGPEPPAPTPLLAER.H     SRRM2 SRRM2   S2449   18.0   28.5   R.MGQAPSQSLLPPAQDQPRS*PVPSAFSDQSR     SRRM2 SRRM2 SRRM2   S1404   9.1   82.5   K.AGMSSNQSISS*PVLDAVPR.T     SRRM2 SRRM2 SRRM2   S1403   45.8   70.7   K.AGMSSNQSISS*PVLDAVPR.T     SRRM2 SRRM2 S1329   37.7   66.0   R.ENSFGS*PLEFR.N     SRRM2 SRRM2   S1329   37.7   66.0   R.ENSFGS*PLEFR.N     SRRM2 SRRM2   S1401S1404   23.0   103.6   K.AGMSSNQSISS*PVLDAVPR.T     SRRM2 SRRM2   S1401S1404   23.0   103.6   K.AGMSSNQSISS*PVLDAVPR.T     SRRM2 SRRM2   S1318S1329   8.5   53.5   K.ELS*NSPLRENSFGS*PLEFR.N     SRRM2 SRRM2   S1318S1329   8.5   53.5   K.ELS*NSPLRENSFGS*PLEFR.N     SRRM2 SRRM2   S1042   90.1   K.SS*TPPGESYFGVSSLQLK.G     SRRM2 SRRM2   S1042   40.2   90.1   K.SS*TPPGESYFGVSSLQLK.G     SRRM2 SRRM2   S4845486   16.6   15.0   R.S*RS*S*SPPPK.O     SRRM2 SRRM2   S1318S1819   5.0   19.6   R.S*RS*S*S*PPPK.O     SRRM2 SRRM2   S1219   30.7   R.SGAGSS*PETK.E     SRRM2 SRRM2   S1219   30.7   R.SGAGS*PETK.E     SRRM2 SRRM2   S1219   34.7   72.1   K.EONSALPT*SGDEELMEVVEK.S     SRRM2 SRRM2   S1232   5.2   55.7   K.EONSALPT*SGDEELMEVVEK.S     SRRM2 SRRM2   S1318S1320S1   46.6   53.8   K.ELS*NS*PLRENS*FGSPLEFR.N		SRRM2 SRRM2	S377T384S395			23.4	22.2	R.HGGS*PQPLATT*PLSQEPVNPPS*EASPTR.D
SRRM2   S2449		SRRM2 SRRM2	S377S398			27.2	44.4	R.HGGS*PQPLATTPLSQEPVNPPSEAS*PTR.D
SRRM2 SRRM2   S1404   9.1   82.5   K.AGMSSNQSISS*PVLDAVPR.T		SRRM2 SRRM2	\$351\$353\$357			32.9	42.2	K.SATRPS*PS*PERS*STGPEPPAPTPLLAER.H
SRRM2 SRRM2   S1403		SRRM2	<b>S</b> 2449			18.0	28.5	R.MGQAPSQSLLPPAQDQPRS*PVPSAFSDQSR.
SRRM2 SRRM2   S1329   37.7   66.0   R.ENSFGS*PLEFRN		SRRM2 SRRM2	S1404			9.1	82.5	K.AGMSSNQSISS*PVLDAVPR.T
SRRM2 SRRM2   S1398S1401   13.8 62.7   K.AGMSS*NQS*ISSPVLDAVPR.T		SRRM2 SRRM2	S1403			45.8	70.7	K.AGMSSNQSIS*SPVLDAVPR.T
SRRM2 SRRM2   S1401S1404   23.0   103.6   K.AGMSSNQS:ISS*PVLDAVPR.T		SRRM2 SRRM2	S1329			37.7	66.0	R.ENSFGS*PLEFR.N
SRRM2 SRRM2   S1318S1329   8.5   S3.5   K.ELS*NSPLRENSFGS*PLEFR N		SRRM2 SRRM2	S1398S1401			13.8	62.7	K.AGMSS*NQS*ISSPVLDAVPR.T
SRRM2 SRRM2   S1042   -0.2   90.1   K.SSTPPGESYFGVSSLOLK.G		SRRM2 SRRM2	S1401S1404	جبية	••	23.0	103.6	K.AGMSSNQS*ISS*PVLDAVPR.T
SRRM2 SRRM2   S1042   90.1   K.SS*TPPGESYFGVSSLQLK.G		SRRM2 SRRM2	S1318S1329			8.5	53.5	K.ELS*NSPLRENSFGS*PLEFR.N
SRRM2 SRRM2   S4845486   16.6   15.0   R.S'RS'PATAKR		SRRM2 SRRM2	T1043			11.9	99.0	K.SST*PPGESYFGVSSLQLK.G
SRRM2 SRRM2   S818S819   5.0   19.6   R.SRSS'S'SPPPK.Q		SRRM2 SRRM2	S1042			-0.2	90.1	K.SS*TPPGESYFGVSSLQLK.G
SRRM2 SRRM2   S71357157177   100.0   13.0   R.S'HS'RT'PQR.R		SRRM2 SRRM2	S484S486			16.6	15.0	R.S*RS*PATAK.R
SRRM2 SRRM2   S1219   23.9 36.7   R.SGAGSS'PETKE		SRRM2 SRRM2	S818S819			5.0	19.6	R.SRSS*S*SPPPK.Q
SRRM2 SRRM2         S562564S566         47.7         20.8         R.S'HS'RS'PATR.G           SRRM2 SRRM2         T1231         34.7         72.1         K.EQNSALPT'SSQDEELMEVVEK.S           SRRM2 SRRM2         S1818Y1820         6.4         46.7         R.GGS'GY'HSR.S           SRRM2 SRRM2         S1232         5.2         55.7         K.EQNSALPTS'SQDEELMEVVEK.S           SRRM2 SRRM2         S1318S1320S1         46.6         53.8         K.ELS'NS'PLRENS'FGSPLEFR.N           SRRM2 SRRM2         S1318S1320S1         18.2         46.7         K.ELS'NS'PLRENSFGS'PLEFR.N		SRRM2 SRRM2	S713S715T717			100.0	13.0	R.S*HS*RT*PQR.R
\$RRM2 \$RRM2 \$1818Y1820		SRRM2 SRRM2	<b>S</b> 1219			23.9	36.7	R.SGAGSS*PETK.E
SRRM2 S1818Y1820 6.4 46.7 R.GGS'GY'HSR.S  SRRM2 SRRM2 S1232 55.7 K.EQNSALPTS'SQDEELMEVVEK.S  SRRM2 SRRM2 S1318S1320S1 46.6 53.8 K.ELS'NS'PLRENS'FGSPLEFR.N  SRRM2 SRRM2 S1318S1320S1 18.2 46.7 K.ELS'NS'PLRENSFGS'PLEFR.N		SRRM2 SRRM2	\$562\$564\$566			47.7	20.8	R.S*HS*RS*PATR.G
\$RRM2 SRRM2 \$1232		SRRM2 SRRM2	T1231	<del></del>		34.7	72.1	K.EQNSALPT*SSQDEELMEVVEK.S
\$RRM2 SRRM2 \$1318\$1320\$1 46.6 53.8 K.ELS'NS'PLRENS'FGSPLEFR.N  \$RRM2 SRRM2 \$1318\$1320\$1 18.2 46.7 K.ELS'NS'PLRENSFGS'PLEFR.N		SRRM2	S1818Y1820			6.4	46.7	R.GGS*GY*HSR.S
\$RRM2 \$1318\$1320\$1 18.2 46.7 K.ELS*NS*PLRENSFGS*PLEFR.N		SRRM2 SRRM2	S1232		·	5.2	55.7	K.EQNSALPTS*SQDEELMEVVEK.S
00000		SRRM2 SRRM2	S1318S1320S1			46.6	53.8	K.ELS*NS*PLRENS*FGSPLEFR.N
SRRM2 SRRM2 S1014 100.0 25.3 K.S*PCPQEK.S		SRRM2 SRRM2	S1318S1320S1		=	18.2	46.7	K.ELS*NS*PLRENSFGS*PLEFR.N
		SRRM2 SRRM2	S1014			100.0	25.3	K.S*PCPQEK.S

Peak Area %CV	abundan	kts-Significant cha ce at 5%FDR of with the minimum	compared to	the .			
3 86 5 >100 >10			CarT				
Prot	ein Name Gene SRRM2 SRRM2	Phosphosites T627S629	5 P B	9m 5m 5m	Ascor 100.0	MOWSE 12.1	Sequence R.T*RS*PVR.R
	SRRM2 SRRM2	S1937T1939			9.8	18.6	R.S*RT*PTTR.R
	SRRM2 SRRM2	S2426			39.3	31.5	R.APS*PSSR.M
	SRRM2 SRRM2	\$836\$839		==	24.9	15.1	R.QSHS*SSS*PHPK.V
	SRRM2 SRRM2 SRRM2 SRRM2	\$1064 \$295\$297		•	9.8	27.5	K.GQSQTS*PDHR.S  R.S*PS*PASGRR.G
	SRRM2 SRRM2	\$2958297 \$1866\$1869	•		34.5	20.3	R.S*RAS*PATHR.R
	SRRM2 SRRM2	T1986	•••		12.8	22.4	R.SRT*SPVTR.R
	SRRM2 SRRM2	S970S973	•••		5.9	13.5	R.YSHS*GSS*SPDTK.V
	SRRM2 SRRM2	S902S908			8.7	24.9	K.SS*TPPRQS*PSR.S
	SRRM2 SRRM2	S1842S1848	-		13.1	15.5	R.S*RTPPTS*R.K
	SRRM2 SRRM2 SRRM2 SRRM2	S1682T1684			16.4	18.3	K.TKS*RT*PPR.R  R.GDS*RS*PSHKR.R
	SRRM2 SRRM2	\$2727\$2729 \$1913\$1916			19.9	27.9 32.0	R.S*RAS*PVSR.R
	SRRM2 SRRM2	T1892S1893			20.5	26.4	R.SRT*S*PVSR.R
	SRRM2 SRRM2	S1112			100.0	21.4	R.S*PIRQDR.G
	SRRM2 SRRM2	S1984S1987			16.6	19.5	R.S*RTS*PVTR.R
	SRRM2 SRRM2	S1600S1601			20.0	55.9	R.SGS*S*PEVK.D
	SRRM2 SRRM2	S454S456			19.9	36.6	R.EIS*SS*PTSK.N
	SRRM2	S1987	•••		9.8	22.8	R.SRTS*PVTR.R
	SRRM2 SRRM2 SRRM2 SRRM2	\$454\$455 \$2702\$2706		•••	13.0	29.2	R.EIS'S'SPTSK.N  R.RRPS'PQPS'PR.D
	SRRM2 SRRM2	S351S353			30.2	21.0	K.SATRPS*PS*PER.S
	SRRM2 SRRM2	<b>S</b> 1975	•••		-0.1	30.4	R.TS*PITR.R
	SRRM2 SRRM2	S454S455S456			24.0	34.5	R.EIS*S*S*PTSK.N
	SRRM2 SRRM2	T1531			100.0	29.6	R.T*PLGQR.S
	SRRM2 SRRM2	S1598S1600S1			100.0	27.5	R.S*GS*S*PEVK.D
	SRRM2 SRRM2	S1577S1579S1			62.5	24.1	R.S'RS'GS'S'PEVDSK.S
	SRRM2 SRRM2 SRRM2 SRRM2	\$1923\$1925T1 \$1132	•••		31.1	13.8 55.2	R.S*RS*RT*PPVTR.R  K.SGMS*PEQSR.F
	SRRM2 SRRM2	S1925T1927			24.3	19.0	R.S*RT*PPVTR.R
	SRRM2 SRRM2	S2407T2409	•••		22.2	41.6	R.S'RT'PPSAPSQSR.M
	SRRM2 SRRM2	S2407S2412		•••	20.9	39.1	R.S*RTPPS*APSQSR.M
	SRRM2 SRRM2	S1444	<b></b>		19.1	52.0	R.SGSS*PGLR.D
	SRRM2 SRRM2	S759S761S763			100.0	17.4	R.S'RS'LS'S'PR.S
	SRRM2 SRRM2 SRRM2 SRRM2	S1616S1618S1			100.0	23.6	R.AQS*GS*DS*S*PEPK.A  R.QSHSES*PSLQSK.S
	SRRM2 SRRM2	\$1083 \$435\$436\$437			103.8	33.0	R.HAS*S*S*PES*PKPAPAPGSHR.E
	SRRM2 SRRM2	\$435\$436\$437			100.0	18.6	R.HAS*S*S*PES*PKPAPAPGS*HR.E
	SRRM2 SRRM2	S1443S1444			27.9	43.3	R.SGS*S*PGLR.D
	SRRM2 SRRM2	S1694			-0.1	34.4	R.SS*PELTR.K
	SRRM2 SRRM2	S2581	<b></b> :		19.8	41.7	K.RVPS*PTPAPK.E
	SRRM2 SRRM2 SRRM2 SRRM2	S1064S1069T1			8.5	11.5	K.GQSQTS*PDHRS*DT*SS*PEVR.Q
	SRRM2 SRRM2 SRRM2 SRRM2	\$1691\$1693 \$1497\$1499\$1			7.4	20.6	R.SS'RS'SPELTR.K  R.S'RS'PSS'PELNNK.C
	SRRM2 SRRM2	\$1497\$1499\$1 \$778\$783			13.7	38.3	R.S'LSGSS'PCPK.Q
	SRRM2 SRRM2	S1064T1071S1			2.9	10.8	K.GQSQTS*PDHRSDT*S*S*PEVR.Q
	SRRM2 SRRM2	S778S780S783	. –		20.9	40.0	R.S*LS*GSS*PCPK.Q
	SRRM2 SRRM2	T289S297	<del></del>		3.4	13.6	K.THTT*ALAGRSPS*PASGR.R
	SRRM2 SRRM2	S2018S2020T2			100.0	15.5	R.S*RS*RT*PPAIR.R
	SRRM2 SRRM2	S2020T2022			100.0	19.0	R.S*RT*PPAIR.R
	SRRM2 SRRM2 SRRM2 SRRM2	T1453S1458S1 S2688			10.8	21.8	R.DGSGT*PSRHS*LSGS*SPGMK.D  R.KPIDSLRDS*R.S
	SRRM2 SRRM2	\$2684			5.1	27.6	R.KPIDS*LRDSR.S
	SRRM2 SRRM2	S508S510			100.0	18.0	R.S'RS'PQWR.R
	SRRM2 SRRM2	\$950\$952\$954			33.6	18.7	R.S*RS*VS*PCSNVESR.L
	SRRM2 SRRM2	S536			16.3	22.5	R.S*PQRPGWSR.S
	SRRM2 SRRM2	\$534\$536			42.1	18.4	R.S*RS*PQRPGWSR.S
	SRRM2 SRRM2	S952S954	<b></b>		46.7	48.6	R.S*VS*PCSNVESR.L
	SRRM2 SRRM2 SRRM2 SRRM2	S1854T1856			24.3	16.0	R.S*RT*SPAPWKR.S
	SRRM2 SRRM2	T2397			10.2	37.1 18.1	R.GEGDAPFSEPGT*TSTQRPS*SPETATK.Q
		.0.00022			41.0	10.1	

Peak Area <-10	o abundani	ots-Significant cha ce at 5%FDR of with the minimum	compared to	the			
-3 0 3 5	71 86		CarT	RajiB			
>10	Protein Name Gene SRRM2 SRRM2	Phosphosites	9 H J	8 % g		MOWSE	Sequence R.S*RS*S*SPVTELASR.S
	SRRM2 SRRM2	\$1099\$1101\$11 \$1188			10.2 87.4	27.7	K.DKFS*PFPVQDRPESSLVFK.D
	SRRM2 SRRM2	S817S818			6.8	11.1	R.SRS*S*SSPPPK.Q
	SRRM2 SRRM2	S2310S2314			11.5	57.7	R.TPAALAALS*LTGS*GTPPTAANYPSSSR.T
	SRRM2 SRRM2	S525S527		<b></b>	100.0	15.7	R.S*RS*PQRR.G
	SRRM2 SRRM2	S1866T1872			21.5	34.8	R.S*RASPAT*HR.R
	SRRM2 SRRM2 SRRM2 SRRM2	S1762S1764			100.0	17.7	R.GRS'PS'PKPR.G  R.DKS'HS'HT'PSRR.M
	SRRM2 SRRM2	\$472\$474T476 \$1984T1986\$1			34.3	19.3	R.S'RT'S'PVTR.R
	SRRM2 SRRM2	T2409S2412			17.3	40.3	R.SRT"PPS"APSQSR.M
	SRRM2 SRRM2	S1972T1974S1			57.6	19.2	R.S*RT*S*PITR.R
	SRRM2 SRRM2	T1974S1975		•••	12.8	18.9	R.SRT*S*PITR.R
	SRRM2 SRRM2	\$1499\$1501\$1			17.7	26.0	R.SRS*PS*S*PELNNK.C
	SRRM2 SRRM2	S1497S1499S1			100.0	12.6	R.S*RS*PS*S*PELNNK.C
	SRRM2 SRRM2 SRRM2 SRRM2	\$1690\$1693\$1 \$774			9.9	24.0	R.S*SRS*S*PELTR.K  K.SRLS*LR.R
	SRRM2 SRRM2	\$2100\$2102T2		•	49.0	35.8	R.NHS*GS*RT*PPVALNSSR.M
	SRRM2 SRRM2	\$2067T2069\$2			100.0	22.7	R.S'LT'RS'PPAIR.R
	SRRM2 SRRM2	S1101S1102	<del></del>		10.0	45.9	R.S*S*SPVTELASR.S
	SRRM2 SRRM2	\$377T383\$398		<u>.</u> •.	20.3	24.0	R.HGGS*PQPLAT*TPLSQEPVNPPSEAS*PTR.D
	SRRM2 SRRM2	S351S353S358			21.1	29.5	K.SATRPS*PS*PERSS*TGPEPPAPTPLLAER.H
	SRRM2 SRRM2	Y1049			-0.3	52.1	K.SSTPPGESY*FGVSSLQLK.G  R.T*PAALAALSLT*GSGTPPTAANYPSSSR.T
	SRRM2 SRRM2	T2302T2312 S817S819			8.1	16.8	R.SRS*SS*SPPPK.Q
	SRRM2 SRRM2	T1680T1684	_		5.1	18.5	K.T*KSRT*PPR.R
	SRRM2 SRRM2	T1844S1848			12.9	18.8	R.SRT*PPTS*R.K
	SRRM2 SRRM2	T1847S1848	•		23.1	29.2	R.SRTPPT*S*R.K
	SRRM2 SRRM2	T1986S1987			18.2	22.3	R.SRT*S*PVTR.R
	SRRM2 SRRM2	S1982S1984T1	<u> </u>		6.5	19.1	R.S*RS*RT*SPVTR.R
	SRRM2 SRRM2	\$1972T1974			16.0	15.5	R.S*RT*SPITR.R  R.HAS*S*S*PESPKPAPAPGSHR.E
	SRRM2 SRRM2	\$435\$436\$437 \$1691\$1694			4.1	12.5	R.SS*RSS*PELTR.K
	SRRM2 SRRM2	T288T289	-		7.8	14.4	K.THT*T*ALAGRSPSPASGR.R
	SRRM2 SRRM2	S2102T2104		• -	8.8	16.4	R.NHSGS*RT*PPVALNSSR.M
	SRRM2 SRRM2	S1541S1550	-		9.3	14.0	R.SGS*SQELDVKPS*ASPQER.S
	SRRM2 SRRM2	\$1539\$1541\$1	<b></b>		8.3	13.1	R.SRS*GS*S*QELDVKPSAS*PQER.S
	SRRM2 SRRM2 SRRM2 SRRM2	S351S353T359			19.7	18.5	K.SATRPS'PS'PERSST'GPEPPAPTPLLAER.H  KELSNS'PLRENSFGS'PLEFR.N
	SRRM2 SRRM2	\$1320\$1329 \$2314T2316	•	-	9.3	29.3	R.TPAALAALSLTGS*GT*PPTAANYPSSSR.T
	SRRM2 SRRM2	S837S838			15.2	16.2	R.QSHSS'S"SPHPK.V
	SRRM2 SRRM2	S1890T1892			14.6	24.5	R.S*RT*SPVSR.R
	SRRM2 SRRM2	S2090T2092			47.1	23.3	R.S*AT*PPATR.N
	SRRM2 SRRM2	S455S456	<b></b>		16.2	32.7	R.EISS*S*PTSK.N
	SRRM2 SRRM2	S1972S1975	<b>—</b>		7.7	22.1	R.S'RTS'PITR.R
	SRRM2 SRRM2 SRRM2 SRRM2	S1970T1974S1 T2738S2740			5.1	15.7	R.S*RSRT*S*PITR.R  R.RET*PS*PRPMR.H
	SRRM2 SRRM2	S778S780	• • •	•	38.3	73.0	R.S'LS'GSSPCPK.Q
	SRRM2 SRRM2	S1441S1443S1			100.0	34.7	R.S'GS'S'PGLR.D
	SRRM2 SRRM2	T1453S1458S1		• • •	13.5	13.8	R.DGSGT*PSRHS*LS*GSSPGMK.D
	SRRM2 SRRM2	S1878T1880			45.0	13.6	R.S'RT'PLISR.R
	SRRM2 SRRM2	S1542S1550			14.7	11.5	R.SGSS*QELDVKPS*ASPQER.S
	SRRM2 SRRM2 SRRM2 SRRM2	\$323 \$2729\$2731			7.7	28.7	R.GEGDAPFSEPGTTSTQRPSS*PETATK.Q  R.GDSRS*PS*HKR.R
	SRRM2 SRRM2	T318S322			4.4	17.0	R.GEGDAPFSEPGTTST'QRPS'SPETATK.Q
	SRRM2 SRRM2	S1101S1102S11			5.0	32.1	R.SRS*S*S*PVTELASR.S
	SRRM2 SRRM2	\$377\$387T400			13.9	12.8	R.HGGS*PQPLATTPLS*QEPVNPPSEASPT*R.D
	SRRM2 SRRM2	S377S387S398			24.2	14.9	R.HGGS*PQPLATTPLS*QEPVNPPSEAS*PTR.D
	SRRM2 SRRM2	S1403T1413	<u> </u>		10.8	22.8	K.AGMSSNQSIS*SPVLDAVPRT*PSR.E
	SRRM2 SRRM2	S1318S1326			12.1	48.2	K.ELS*NSPLRENS*FGSPLEFR.N
	SRRM2 SRRM2 SRRM2 SRRM2	T2302T2316 S1320S1326S1			9.5	61.9 34.3	R.T*PAALAALSLTGSGT*PPTAANYPSSSR.T  K.ELSNS*PLRENS*FGS*PLEFR.N
	SRRM2 SRRM2	\$1320\$1326\$1 \$837\$839			11.2	12.2	R.QSHSS'SS'PHPK.V
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Peak Area %CV <-10 0 25 -3 42	abundano	ts-Significant cha be at 5%FDR of with the minimum	compared to	the			
3 86 >100			CarT	_RajiB_			
	Name Gene	Phosphosites	£ £ £	8 # B	7,0001	MOWSE	Sequence
	SRRM2 SRRM2 SRRM2 SRRM2	S248S250T251			6.8	11.1	R.S*RS*T*TPAPK.S  R.S*RTSPVTR.R
	SRRM2 SRRM2	\$1984 \$2749\$2751		<del></del>	25.6	17.3	R.HRSS*RS*P
	SRRM2 SRRM2	S1069T1071S1	• • •		10.5	12.9	K.GQSQTSPDHRS*DT*S*S*PEVR.Q
-	SRRM2 SRRM2	T315		•	0.7	16.9	R.GEGDAPFSEPGT*TSTQRPSSPETATK.Q
	SRRM2 SRRM2	S1403S1404			2.1	52.3	K.AGMSSNQSIS*S*PVLDAVPR.T
	SRRM2 SRRM2	S1320S1326			13.8	64.2	K.ELSNS*PLRENS*FGSPLEFR.N
	SRRM2 SRRM2	S1233			1.0	67.8	K.EQNSALPTSS*QDEELMEVVEK.S
	SRRM2 SRRM2	Y1820S1822			1.2	36.7	R.GGSGY*HS*R.S
	SRRM2 SRRM2	Y1820			-0.3	15.7	R.GGSGY*HSR.S
	SRRM2	S790T792			100.0	14.0	K.QKS*QT*PPRR.S
:	SRRM2 SRRM2	S1672S1675			25.6	25.8	R.RGS*RSS*PEPK.T
	SRRM2	S1818S1822			16.1	38.9	R.RGGS*GYHS*R.S
	SRRM2 SRRM2	\$472\$474\$478			15.7	13.5	R.DKS*HS*HTPS*RR.M
	SRRM2 SRRM2	S972S973		-	8.0	16.7	R.YSHSGS*S*SPDTK.V
	SRRM2 SRRM2 SRRM2 SRRM2	T1892			-0.4	14.4	R.SRT*SPVSR.R R.T*PPVTR.R
	SRRM2 SRRM2	T1927 S759S761S763			-0.1	12.1	R.S*RS*LS*SPR.S
	SRRM2 SRRM2	\$759\$761\$763 \$780\$783			-0.1	41.4	R.SLS*GSS*PCPK.Q
	SRRM2 SRRM2	\$1451\$1458\$1			10.2	16.6	R.DGS*GTPSRHS*LS*GSSPGMK.D
	SRRM2 SRRM2	S543			18.5	18.4	R.SPQRPGWS'R.S
	SRRM2 SRRM2	T1856			5.4	13.7	R.SRT*SPAPWKR.S
:	SRRM2 SRRM2	T2034			100.0	37.5	R.T*PLLPR.K
	SRRM2 SRRM2	S317S322		•	0.8	18.6	R.GEGDAPFSEPGTTS*TQRPS*SPETATK.Q
-	SRRM2 SRRM2	S2123			14.0	26.2	R.MSCFSRPSMS*PTPLDR.C
:	SRRM2 SRRM2	S377T384T400			21.5	15.6	R.HGGS*PQPLATT*PLSQEPVNPPSEASPT*R.D
	SRRM2 SRRM2	S819S820			4.6	22.4	R.SRSSS*S*PPPK.Q
:	SRRM2 SRRM2	S486T489	-		3.2	14.4	R.SRS*PAT*AKR.G
	SRRM2 SRRM2	S970S974		<u>.</u>	6.8	12.7	R.YSHS*GSSS*PDTK.V
	SRRM2 SRRM2	S1497S1499			15.4	33.5	R.S*RS*PSSPELNNK.C
	SRRM2 SRRM2 SRRM2 SRRM2	S2100T2104	=		7.7	21.5	R.NHS*GSRT*PPVALNSSR.M  R.SSS*PVTELASR.S
	SRRM2 SRRM2	\$1103 \$875			12.6	55.9	R.SCFES*SPDPELK.S
	SRRM2 SRRM2	S1124	•	-	7.8	13.7	R.GEFSAS*PMLK.S
	SRRM2 SRRM2	S1401S1403			15.5	58.8	K.AGMSSNQS*IS*SPVLDAVPR.T
	SRRM2 SRRM2	T1063			22.4	31.7	K.GQSQT*SPDHR.S
	SRRM2 SRRM2	S1916		• •	10.4	28.7	R.SRAS*PVSR.R
	SRRM2 SRRM2	S1690S1691S1	•		13.5	16.4	R.S*S*RSS*PELTR.K
	SRRM2 SRRM2	S1397			-0.0	17.1	K.AGMS*SNQSISSPVLDAVPR.T
	SRRM2 SRRM2	S2310			13.6	61.9	R.TPAALAALS*LTGSGTPPTAANYPSSSR.T
	SRRM2 SRRM2	T1844T1847			7.1	14.3	R.SRT*PPT*SR.K
	SRRM2 SRRM2	S895			6.0	15.8	R.HSCSGSS*PPR.V
	SRRM2 SRRM2	S1923S1925T1	Ţ		13.8	13.3	R.S*RS*RTPPVT*R.R
	SRRM2 SRRM2 SRRM2 SRRM2	T1974		•	8.2	12.6	R.SRT*SPITR.R  R.SGS*SQELDVKPSAS*PQER.S
	SRRM2 SRRM2 SRRM2 SRRM2	S1541S1552	<u> </u>		4.4	19.5	R.SGS*SQELDVKPSAS*PQER.S  R.HGGS*PQPLATT*PLSQEPVNPPSEAS*PTR.D
	SRRM2 SRRM2	\$377T384\$398 \$377\$395			11.7	19.5	R.HGGS*PQPLATTPLSQEPVNPPS*EASPTR.D
	SRRM2 SRRM2	S1691S1693S1			7.5	13.5	R.SS*RS*S*PELTR.K
	SRRM2 SRRM2	S1537S1539S1			25.7	11.1	R.S*RS*GS*SQELDVKPS*ASPQER.S
	SRRM2 SRRM2	S1541S1542S1			7.7	44.8	R.SGS*S*QELDVKPS*ASPQER.S
-	SRRM2 SRRM2	S2115S2118			3.7	10.7	R.MS*CFS*RPSM#SPTPLDR.C
	SRRM2 SRRM2	T2312S2314			9.9	36.7	R.TPAALAALSLT*GS*GTPPTAANYPSSSR.T
	SRRM2 SRRM2	S596T598	Ļ.		8.8	10.8	R.S*RT*PTR.R
	SRRM2 SRRM2	\$295\$300	-		8.6	12.8	R.S*PSPAS*GRR.G
	SRRM2 SRRM2	T903S908	<b>—</b>		18.1	21.7	K.SST*PPRQS*PSR.S
	SRRM2 SRRM2	S1674S1675	<u> </u>		5.0	11.1	R.RGSRS*S*PEPK.T
	SRRM2 SRRM2	S1890S1893	-		9.1	20.5	R.S'RTS'PVSR.R
	SRRM2 SRRM2	S1984T1986			10.8	17.0	R.S'RT'SPVTR.R
	SRRM2 SRRM2 SRRM2 SRRM2	\$857T866			13.1	45.0	R.QGSITS*PQANEQSVT*PQRR.S  R.SRS*GS*S*QELDVKPS*ASPQER.S
	SRRM2 SRRM2	S1539S1541S1 S1404T1413			7.6	13.3	K.SRS*GS*S*QELDVKPS*ASPQER.S  K.AGMSSNQSISS*PVLDAVPRT*PSR.E
	SRRM2 SRRM2	\$1404T1413 \$815\$817			3.6	12.2	R.S*RS*SSSPPPK.Q
		20100017	•		J.0		

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5 >100			RajiB E E E			S
Protein Name Gene SRRM2 SRRM2	Phosphosites S1218S1219	ăĸŏ	6 4 6	Ascor 22.5	MOWSE 23.1	Sequence R.SGAGS'S'PETK.E
SRRM2 SRRM2	S1061		-		15.7	K.GQS*QTSPDHR.S
SRRM2 SRRM2		<u> </u>		8.9	24.5	R.SGS*SPGLR.D
SRRM2 SRRM2				14.4	11.2	R.HGGS*PQPLATTPLSQEPVNPPS*EAS*PTR.D  K.SSTPPGES*YFGVSSLQLK.G
SRRM2 SRRM2 SRRM2 SRRM2		-		8.2	10.8	R.YSHSGS*SS*PDTK.V
SRRM2 SRRM2				5.1	35.0	R.SRAS*PAT*HR.R
SRRM2 SRRM2	S902T903			-0.1	15.3	K.SS*T*PPRQSPSR.S
SRRM2 SRRM2	S1842T1844			13.9	19.3	R.S'RT'PPTSR.K
SRRM2 SRRM2	S1598S1600	Ė		13.5	41.2	R.S*GS*SPEVK.D
SRRM2 SRRM2	S1982S1984S1	-		2.3	11.4	R.S*RS*RTS*PVTR.R
SRRM2 SRRM2		-		0.6	11.5	R.SLS'GS'S'PCPK.Q
SRRM2 SRRM2 SRRM2 SRRM2			-	4.7	48.2	K.AGMSS*NQSIS*SPVLDAVPR.T  K.ELS*NSPLRENSFGSPLEFR.N
SRRM2 SRRM2	\$1318 \$575T577			10.2	14.6	R.S*RT*PAR.T
SRRM2 SRRM2	S818S820	•		3.0	15.7	R.SRSS'SS'PPPK.Q
SRRM2 SRRM2	T1939T1941			3.5	12.7	R.SRT*PT*TR.R
SRRM2 SRRM2	T348S353			13.3	15.6	K.SAT*RPSPS*PER.S
SRRM2 SRRM2	S377T383T400			18.2	16.4	R.HGGS*PQPLAT*TPLSQEPVNPPSEASPT*R.D
SRRM2 SRRM2	S1318S1326S1		•	9.4	21.5	K.ELS*NSPLRENS*FGS*PLEFR.N
SRRM2 SRRM2	S836S838			29.7	13.6	R.QSHS*SS*SPHPK.V
SRRM2 SRRM2 SRRM2 SRRM2	S817S820			-0.5	12.3	R.SRS*SSS*PPPKQK.S
SRRM2 SRRM2	\$1902\$1905 \$1818\$1822\$1	-		7.6	15.2	R.S'RTS"VTR.R  R.GGS"GYHS"RS"PAR.Q
SRRM2 SRRM2	\$892			19.8	18.9	R.HSCS*GSSPPR.V
SRRM2 SRRM2	S761S763S764		•	-0.1	16.5	R.SRS*LS*S*PR.S
SRRM2 SRRM2	S1081	•	•	13.4	14.9	R.QSHS*ESPSLQSK.S
SRRM2 SRRM2	S1690S1691		<u>.                                    </u>	11.5	32.9	R.S'S'RSSPELTR.K
SRRM2 SRRM2	S1854S1857			14.2	16.1	R.S*RTS*PAPWKR.S
STAM binding protein STAMBI					14.5	K.AELLKRY*TK.E
STARD3 N terminal like STARD: START domain containing 10 STARD				100.0	24.4	R.LLIVQDAS*ER.A  R.MGGAGGEGS*DDDTSLT
START domain containing to STARD	T716S727	• •		27.8	37.2 29.7	K.FICVTPT*TCSNTIDLPMS*PR.T
STAT3 <sub>STAT3</sub>	S719S727	•		25.1	40.3	K.FICVTPTTCS*NTIDLPMS*PR.T
STAT3 <sub>STAT3</sub>	T714S727	•		34.2	50.4	K.FICVT*PTTCSNTIDLPMS*PR.T
STAT3 <sub>STAT3</sub>	<b>S7</b> 27			31.6	21.0	K.FICVTPTTCSNTIDLPMS*PR.T
STAT3 <sub>STAT3</sub>	T721S727			19.0	19.6	K.FICVTPTTCSNT*IDLPMS*PR.T
STAT4 <sub>STAT4</sub>	S708S721			23.2	21.6	R.SDS*TEPHSPSDLLPMS*PSVYAVLR.E
STAT4 <sub>STAT4</sub>	S713S721	•		21.3	40.8	R.SDSTEPHS*PSDLLPMS*PSVYAVLR.E
STAT5B <sub>STAT5B</sub>				100.0	11.0	R.IQAQFGPLAQLS*PQER.L
Stathmin 1 STMN1  Stathmin 1 STMN1	S38			38.8	38.3	R.ASGQAFELILS*PR.S
Stathmin 1 STMN1	\$25 \$16			72.0	72.1	R.AS*GQAFELILSPR.S
Stathmin 1 STMN1	S16S25			100.0	65.8	R.AS*GQAFELILS*PR.S
Stathmin 1 STMN1	S31			25.0	20.8	R.SKES*VPEFPLSPPK.K
Stathmin 1 STMN2	S46			100.0	19.5	K.DLS*LEEIQK.K
Stathmin 1 STMN1	S63		•	100.0	30.4	K.S*HEAEVLK.Q
Staufen STAU1	T277			19.1	22.5	K.TKPIVKPQT*SPEYGQGINPISR.L
Staufen RNA binding protein homolog 2 <sub>STAU2</sub>	S416			6.5	53.1	K.DMNQPS*SSFFSISPTSNSSATIAR.E
Staufen RNA binding protein homolog 2 <sub>STAU2</sub> Staufen RNA binding protein homolog 2 <sub>STAU2</sub>	\$453\$460			16.7	13.8	K.GS*SPTPPCS*PVQPSK.Q  K.DMNQPSSSFFSIS*PTSNSSATIAR.E
STE20 like kinase MST1 STK4	\$423 \$320		•	99.3	90.1	R.EVDQDDEENS*EEDEMDSGTMVR.A
STE20 like kinase MST1 STK4	\$320 \$320T329			32.6	50.6	R.EVDQDDEENS'EEDEMDSGT'MVR.A
Step II splicing factor SLU7 <sub>SLU7</sub>	S235			19.5	53.6	K.DHNS*EDEDEDKYADDIDMPGQNFDSK.R
Stress induced phosphoprotein 1 <sub>STIP1</sub>	S16		•	113.5	105.8	K.ALS*VGNIDDALQCYSEAIK.L
Striatin calmodulin binding protein STRN	S134			0.1	32.9	K.YGTELNQGDMKPPS*YDSDEGNETEVQPQQNSQLMWK.Q
Striatin calmodulin binding protein STRN	T143		•	5.9	30.8	K.YGTELNQGDMKPPSYDSDEGNET*EVQPQQNSQLMWK.Q
Striatin calmodulin binding protein STRN	S137		_	16.2	35.3	K.YGTELNQGDMKPPSYDS'DEGNETEVQPQQNSQLMWK.Q
Striatin calmodulin binding protein STRN  Striatin calmodulin binding protein 4 STRN4	S245		<u> </u>	71.3	150.2	K.FLESAAADFS*DEDEDDDVDGR.E  RLGGSVLGQIPFLQNCEDEDS*DEDDELDSVQHKK.Q
Striatin, calmodulin binding protein 4 STRN4  Striatin, calmodulin binding protein 3 STRN3	\$276 \$229			28.8	18.6 51.2	R.LGGSVLGQIPFLQNCEDEDS*DEDDELDSVQHKK.Q  K.NLEQILNGGES*PK.Q
Striatin, calmodulin binding protein 3 STRN3	\$229 \$257			36.8	108.3	R.SSGDVLETFNFLENADDS*DEDEENDMIEGIPEGK.D

Peak Area	o abundano		compared to	the			
-5 -3	timepoint PSM	with the minimum					
3 5 >10	>100		CarT	RajiB			
	Protein Name Gene Stromal antigen 2 <sub>STAG2</sub>	Phosphosites S1058S1061S1	8 4 5	2	Ascor 10.7	MOWSE 69.4	Sequence R.NSLLAGGDDDTMS*VIS*GIS*SR.G
	Stromal antigen 2 <sub>STAG2</sub>	S1061S1064			7.1	26.5	R.NSLLAGGDDDTMSVIS*GIS*SR.G
	Stromal antigen 2 <sub>STAG2</sub>	S1047S1061S1	• •		11.9	26.3	R.NS*LLAGGDDDTMSVIS*GIS*SR.G
	Stromal antigen 2 STAG2	T1056S1061S1	بكا	•	12.6	80.1	R.NSLLAGGDDDT*MSVIS*GIS*SR.G
	Stromal antigen 2 <sub>STAG2</sub>	S1058			16.1	34.7	R.NSLLAGGDDDTMS*VISGISSR.G
	Stromal antigen 2 <sub>STAG2</sub>	S1058S1061		•	13.1	57.5	R.NSLLAGGDDDTMS*VIS*GISSR.G
	Stromal antigen 2 <sub>STAG2</sub>	T1056S1058S1			13.5	37.4	R.NSLLAGGDDDT*MS*VIS*GISSR.G  R.NSLLAGGDDDT*MS*VISGIS*SR.G
	Stromal antigen 2 <sub>STAG2</sub>	T1056S1058S1			11.7	32.7	R.NSLLAGGDDDT*MS*VISGISSR.G
	Stromal antigen 2 <sub>STAG2</sub>	S1047S1064			10.9	28.0	R.NS*LLAGGDDDTMSVISGIS*SR.G
Stromal in	steraction molecule 1 STIM1	S618	•		7.3	62.4	R.SHS*PSSPDPDTPSPVGDSR.A
Stromal in	steraction molecule 1 STIM1	S521			18.7	65.4	R.DLTHSDS*ESSLHMSDR.Q
Stromal in	teraction molecule 1 STIM1	<b>S</b> 575			82.3	28.4	R.LIEGVHPGSLVEKLPDS*PALAK.K
	teraction molecule 1 STIM1	S519		<del></del>	17.2	54.7	R.DLTHS*DSESSLHMSDR.Q
	teraction molecule 1 STIM1	S521S523			6.5	26.7	R.DLTHSDS*ES*SLHMSDR.Q
	steraction molecule 1 STIM1	S621		•	5.8	24.8	R.SHSPSS*PDPDTPSPVGDSR.A
	steraction molecule 1 STIM1	\$519\$521\$524 \$257			5.3	71.8	R.DLTHS'DS'ESS'LHMSDR.Q  R.AEQS'LHDLQER.L
	steraction molecule 1 STIM1	S519S521			0.6	17.1	R.DLTHS'DS'ESSLHMSDR.Q
	steraction molecule 1 STIM1	S512			4.4	11.9	R.LTEPQHGLGS*QR.D
Stromal in	steraction molecule 1 STIM1	T504			5.1	30.7	R.LT*EPQHGLGSQR.D
Stromal in	teraction molecule 1 STIM1	S519S521S523		•	14.4	16.8	R.DLTHS*DS*ES*SLHMSDR.Q
Stromal in	steraction molecule 1 STIM1	S519S523S524	.=		2.3	15.4	R.DLTHS*DSES*S*LHMSDR.Q
	steraction molecule 1 STIM1	S620		·	5.8	43.3	R.SHSPS*SPDPDTPSPVGDSR.A
	steraction molecule 2 STIM2	S767			35.2	67.0	K.SCS*MNQLSSGIPVPKPR.H
	associated protein 1 SMAP1	\$152 \$151		• • •	15.3	97.2	K.NAIAITNISSSDAPLQPLVSS*PSLQAAVDK.N  K.NAIAITNISSSDAPLQPLVS*SPSLQAAVDK.N
	associated protein 1- SMAP2	\$151 \$240	•		43.7	69.5	R.KVVGSMPTAGSAGS*VPENLNLFPEPGSK.S
	like associated protein 1- SMAP2	S219		• • •	12.2	41.7	K.DLDLLASVPS*PSSSGSR.K
	like SSRP1	\$667\$668\$671		•	16.7	68.3	K.SKEFVS*S*DES*S*SGENK.S
Structure specific i	recognition protein 1 SSRP1	S667S668S671			29.3	24.1	K.EFVS'S'DES'S'S'GENKSK.K
Structure specific	recognition protein 1 SSRP1	<b>S</b> 444			62.9	82.2	K.EGMNPSYDEYADS*DEDQHDAYLER.M
	recognition protein 1 SSRP1	\$437\$444			25.4	47.1	K.EGMNPS*YDEYADS*DEDQHDAYLER.M
	recognition protein 1 <sub>SSRP1</sub>	Y441			3.5	61.3	K.EGM#NPSYDEY*ADSDEDQHDAYLER.M
Structure specific i	sudd RIOK3	\$667\$668\$671		<u> </u>	7.9	33.3	K.EFVS*S*DES*SS*GENK.S  R.KVHPYEDS*DS*S*EDEVDWQDTR.D
	SUDD RIOK3	\$125\$127\$128 Y122\$127\$128	•		6.3	40.7 15.3	R.KVHPY*EDSDS*S*EDEVDWQDTR.D
SUMO	1 specific protease 1 SENP6	\$335\$336			64.7	66.8	R.KTSLSDLNDPIILS*S*DDDDDDR.T
SUMO1 activation	ng enzyme subunit 2 <sub>UBA2</sub>	S565				70.5	K.S*ITNGSDDGAQPSTSTAQEQDDVLIVDSDEEDSSNNADVSEEER.
	Supervillin SVIL	S1000			100.0	20.6	R.RGS*LER.A
	SUPT5H SUPT5H	S32S36		•	37.8	57.3	R.S*AAGS*EKEEEPEDEEEEEEEEEVDEEEEEEDDDRPPKKPR.H
	SUPT5H	S666			76.7	57.8	R.DVTNFTVGGFAPMS*PR.I
	Surfeit 2 SURF2	S155S156S163			14.1	45.0	R.EAFWEPTS'S'DEGGAAS'DDS'MTDLYPPELFTR.K
	Surfeit 2 SURF2	S155S163S166			8.6	27.1	R.EAFWEPTS'SDEGGAAS'DDS'MT'DLYPPELFTR.K  R.EAFWEPTSSDEGGAAS'DDS'MTDLYPPELFTR.K
	Surfeit 2 SURF2	\$163\$166 \$155\$156	:::		14.6	58.5 37.6	R.EAFWEPTSSDEGGAAS*DDS*MTDLYPPELFTR.K  R.EAFWEPTS*S*DEGGAASDDSMTDLYPPELFTR.K
	Surfeit 2 SURF2	T154S155			10.6	24.7	R.EAFWEPT'S'SDEGGAASDDSMTDLYPPELFTR.K
	Surfeit 2 SURF2	S155S166			6.3	22.5	R.EAFWEPTS*SDEGGAASDDS*MTDLYPPELFTR.K
	Surfeit 2 SURF2	T154S155S156		-	5.9	35.7	R.EAFWEPT*S*DEGGAAS*DDSMTDLYPPELFTR.K
	Surfeit 2 SURF2	T154S155S156	-		-0.8	21.7	R.EAFWEPT'S'S'DEGGAASDDSMT'DLYPPELFTR.K
	Surfeit 2 SURF2	S155S156S166		•	1.5	13.2	R.EAFWEPTS'S'DEGGAASDDS'MT'DLYPPELFTR.K
	Surfeit 2 SURF2	S166T168		-	2.9	13.4	R.EAFWEPTSSDEGGAASDDS*MT*DLYPPELFTR.K
	Surfeit 2 SURF2	T190T195			23.9	62.5	R.KDLGSTEDGDGT*DDFLT*DKEDEK.A
	Surfeit 2 SURF2	S156S166		-	7.2	20.3	R.EAFWEPTSS*DEGGAASDDS*MTDLYPPELFTR.K
	Surfeit 2 SURF2	S156S163			5.7	14.1	R.EAFWEPTSS*DEGGAAS*DDSMTDLYPPELFTR.K
	Surfeit 2 SURF2	S155S156S163 T154S155S163	•	_	5.8	32.8	R.EAFWEPTS*S*DEGGAAS*DDSMT*DLYPPELFTR.K  R.EAFWEPT*S*SDEGGAAS*DDS*MTDLYPPELFTR.K
Survival of motor	r neuron 1, telomeric SMN2	T25		•	7.4	38.1	R.RGT'GQSDDSDIWDDTALIK.A
	r neuron 1, telomeric SMN2	T25S31			28.5	53.4	R.RGT*GQSDDS*DIWDDTALIK.A
Survival of motor	r neuron 1, telomeric SMN2	S28			19.8	150.8	R.GTGQS'DDSDIWDDTALIKA
Survival of motor	r neuron 1, telomeric SMN2	T25S28S31	<u> </u>		38.7	19.8	R.RGT*GQS*DDS*DIWDDTALIK.A
Survival of motor	r neuron 1, telomeric SMN2	S28S31	•••		47.3	166.2	R.GTGQS'DDS'DIWDDTALIK.A
				•			

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3 42 PSM	with the minimum p					
>100 >10	Dhambasitas	CarT E E E	RajiB E E E	Ascor	MOWSE	Sequence
Protein Name Gene Survival of motor neuron 1, telomeric SMN2	Phosphosites \$166	0 7 45		12.0	48.1	R.EEQNLSDLLSPICEVANNIEQNAQENENESQVS*TDESENSR.S
Survival of motor neuron 1, telomeric SMN2	S139				22.5	R.EEQNLS*DLLSPICEVANNIEQNAQENENESQVSTDESENSR.S
Survival of motor neuron 1, telomeric SMN2	S163S166T167		-	34.7	30.7	R.EEQNLSDLLSPICEVANNIEQNAQENENES'QVS'T'DES'ENSR.S
Survival of motor neuron 1, telomeric SMN2	S139S143S163		_		23.8	R.EEQNLS*DLLS*PICEVANNIEQNAQENENES*QVS*TDESENSR.S
Survival of motor neuron 1, telomeric SMN2  Survival of motor neuron 1, telomeric SMN2	T167			•	33.6	R.EEQNLSDLLSPICEVANNIEQNAQENENESQVST*DESENSR.S  R.GT*GQS*DDSDIWDDTALIKA
Survival of motor neuron 1, telomeric SMN2	\$139\$143\$163		=	3.0	13.6	R.EEQNLS*DLLS*PICEVANNIEQNAQENENES*QVS*T*DESENSR.S
SVH protein ARMC10	<b>S</b> 45		=	74.9	82.6	K.S'AGALEEGTSEGQLCGR.S
SWI/SNF related matrix associated actin HLTF	\$398\$400T405			10.3	38.3	K.TAVQYIESS*DS*EEIET*SELPQK.M
SWI/SNF related matrix associated actin HLTF dependent regulator of chromatin subfamily	\$397\$398\$400			20.8	26.2	K.TAVQYIES*S*DS*EEIETSELPQK.M
SWI/SNF-related matrix-associated actin-SMARCAS dependent regulator of chromatin subfamily	<b>S</b> 47				66.5	K.GGPEGVAAQAVAS*AASAGPADAEMEEIFDDASPGKQK.E
SWI/SNF-related matrix-associated actin-SMARCAS dependent regulator of chromatin subfamily	S66			134.8	128.0	K.GGPEGVAAQAVASAASAGPADAEMEEIFDDA <mark>S*</mark> PGK.Q
SWI/SNF-related matrix-associated actin-SMARCAS dependent regulator of chromatin subfamily	<b>S</b> 50		-	6.9	27.6	K.GGPEGVAAQAVASAAS*AGPADAEMEEIFDDASPGKQK.E
SYK SYK	S307			-0.1	11.5	R.KSS*PAQGNR.Q
Symplekin SYMPK	S1243	<u></u>		25.6	79.2	R.S*PQTLAPVGEDAMK.T
Symplekin SYMPK	\$494			53.1	98.9	R.RLS*AQGQAISVVGSLSSMSPLEEEAPQAK.R
Synapse associated protein 1 SYAP1  Synapse associated protein 1 SYAP1	T248			100.0	49.4	K.T*PPVVIK.S  K.TQEDEEEISTSPGVS*EFVSDAFDACNLNQEDLR.K
Synapse associated protein 1 SYAP1	\$273			6.5	93.4	K.TQEDEEEIST*SPGVSEFVSDAFDACNLINGEDLR.K
Synaptojanin 1 SYNJ1	T268 S1049S1053		••	12.1	113.6 42.5	R.TS*PCQS*PTISEGPVPSLPIRPSR.A
Synaptojanin 2 SYNJ2	S1124			15.7	47.3	K.SAS*DASISSGTHGQYSILQTAR.L
Synaptosomal associated protein, 23 kd <sub>SNAP23</sub>	S110	•	•	73.1	82.8	K.TTWGDGGENS*PCNVVSK.Q
Synaptosomal associated protein, 23 kd SNAP23	S161			58.0	107.1	R.EDEMEENLTQVGS*ILGNLK.D
Synaptotagmin like 3 SYTL3	S452	•		100.0	15.9	K.S*PVLRK.Q
Synembryn RIC8A	Y441T447			32.4	76.9	R.GLMAGGRPEGQY*SEDEDT*DTDEYKEAK.A
Synembryn RIC8A	Y441S442			3.9	66.9	R.GLMAGGRPEGQY*S*EDEDTDTDEYKEAK.A
Synembryn RIC8A	S442T447			29.0	56.9	R.GLMAGGRPEGQYS'EDEDT"DTDEYK.E
Synembryn RIC8A	\$529\$530\$534			68.2	109.9	R.GHLTSLQDAMCETMEQQLS*S*DPDS*DPD
Synembryn RIC8A	\$530\$534			16.9	49.7	R.GHLTSLQDAMCETMEQQLSS*DPDS*DPD
Synembryn RIC8A  Synembryn RIC8A	S529S534			24.3	37.1	R.GHLTSLQDAMCETMEQQLS*SDPDS*DPD  R.GHLTSLQDAMCET*MEQQLS*SDPDS*DPD
Synembryn RIC8A	T523S529S534 S529S530			15.6	28.2	R.GHLTSLQDAMCET/MEQQLS*S/PDS*DPD
Syntaxin 4A STX4	\$14\$15			100.0	26.5	R.QGDDS*S*DEEDKER.V
Syntaxin 7 STX7	S205			65.7	59.4	K.DLGMMIHEQGDVIDS*IEANVENAEVHVQQANQQLSR.A
Syntrophin beta 2 SNTB2	S393			44.8	75.5	R.S*PSLGSDLTFATR.T
Syntrophin beta 2 SNTB2	S233	•••		13.9	44.1	K.KPSLVSDLPWEGAAPQSPSFSGSEDSGS*PK.H
Syntrophin beta 2 SNTB2	S231			12.6	58.0	K.KPSLVSDLPWEGAAPQSPSFSGSEDS*GSPK.H
Syntrophin beta 2 <sub>SNTB2</sub>	S228			7.3	20.9	K.KPSLVSDLPWEGAAPQSPSFSGS*EDSGSPK.H
Syntrophin beta 2 SNTB2	S222S231		÷	12.4	22.4	K.KPSLVSDLPWEGAAPQS*PSFSGSEDS*GSPK.H
Syntrophin beta 2 SNTB2	S222S233			17.1	24.0	K.KPSLVSDLPWEGAAPQS*PSFSGSEDSGS*PK.H
T box brain 2 <sub>EOMES</sub>	S596			-0.3	40.8	R.TS*PTVFSEDQLSK.E
T box brain 2 EOMES	S107			65.4	90.4	R.KGS*PCGEEELPSAAAAAAAAAAAAAAAATAR.Y
T cell antigen receptor, zeta  T cell lymphoma invasion and metastasis 2 TIAM2	Y72	_		33.9	50.9	R.SADAPAYQQQQNQLY*NELNLGR.R  K.QGS*PTKDIEIQFQR.L
T Complex 1 TCP1	\$1583 \$544			12.1	38.0	K.HGS*YEDAVHSGALND
T Complex 1 TCP1	S551			42.0	14.5	K.HGSYEDAVHS*GALND
T Complex 1 TCP1	Y545			9.8	14.0	K.HGSY*EDAVHSGALND
TAB2 <sub>TAB2</sub>	S524			-0.0	20.3	R.KLS*MGSDDAAYTQALLVHQK.A
TAB2 <sub>TAB2</sub>	<b>S</b> 527			2.6	15.7	R.KLSMGS*DDAAYTQALLVHQK.A
TACC3 <sub>TACC3</sub>	<b>S</b> 402	<b>I</b>	•		36.5	R.GS*YHLDWDK.M
TAF15 TAF15	S226			24.0	76.1	R.TDADS*ESDNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
<b>TAF15</b> TAF15	T235			6.1	119.2	R.TDADSESDNSDNNT*IFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	T222				55.7	R.T*DADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	S231			19.8	110.0	R.TDADSESDNS*DNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF15 <sub>TAF15</sub>	S228			2.0	68.6	R.TDADSES*DNSDNNTIFVQGLGEGVSTDQVGEFFK.Q  R.TDADS*ESDNSDNNT*IFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	S226T235 S231T235			1.0	15.7 53.6	R.TDADS*ESDNSDNNT*IFVQGLGEGVSTDQVGEFFK.Q  R.TDADSESDNS*DNNT*IFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	\$2311235 \$226\$231T235			-0.5	60.1	R.TDADS*ESDNS*DNNT*IFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	T222S226S228			3.3	60.5	R.T*DADS*ES*DNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	T222S226			2.2	25.9	R.T*DADS*ESDNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF15 <sub>TAF15</sub>	S226S231			4.4	47.1	R.TDADS'ESDNS'DNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF15 TAF15	S226S228S231	• •		0.7	29.5	R.TDADS'ES'DNS'DNNTIFVQGLGEGVSTDQVGEFFK.Q
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5 >100 >100 Protein Name	Gene	Phosphosites	CarT_	E E E	Ascor	MOWSE	Sequence
TAF15	TAF15	S226S228T235			1.5	13.5	R.TDADS*ES*DNSDNNT*IFVQGLGEGVSTDQVGEFFK.Q
TAF15		S226S228	<u> </u>		0.7	24.7	R.TDADS*ES*DNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa		S236S243	-		53.0	11.6	K.IPPMLSPVHVQDS*TDLAPPS*PEPPMLAPVAK.S
TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor. 140kDa TAF6 like RNA polymerase II		T237S243 S495S501			24.8	19.3	K.IPPMLSPVHVQDST*DLAPPS*PEPPMLAPVAK.S  R.KMPQLTASAIVS*PHGDES*PR.G
TAF9 RNA polymerase II		T154S158			7.6	61.7	R.LSVGSVT*SRPS*TPTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S152T154			14.8	52.6	R.LSVGS*VT*SRPSTPTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	\$152T159			7.0	75.1	R.LSVGS*VTSRPST*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S155T159			10.1	74.7	R.LSVGSVTS*RPST*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	T154S155	•		-5.2	31.3	R.LSVGSVT*S*RPSTPTLGTPTPQTM#SVSTK.V
TAF9 RNA polymerase II		T154T159	•		12.8	77.6	R.LSVGSVT*SRPST*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II		S152T161			13.1	50.7	R.LSVGS*VTSRPSTPT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II  TAF9 RNA polymerase II		S152T159T164			11.9	36.7	R.LSVGS*VTSRPST*PTLGT*PTPQTMSVSTK.V  R.LSVGS*VTSRPS*TPTLGT*PTPQTMSVSTK.V
TAF9 RNA polymerase II		\$152\$158T164 \$152\$158T161			7.7	31.3	R.LSVGS*VTSRPS*TPT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S158T159T161			4.7	18.0	R.LSVGSVTSRPS*T*PT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	\$149\$152T154			7.5	58.5	R.LS*VGS*VT*S*RPSTPTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	T154T161	•		3.5	70.8	R.LSVGSVT*SRPSTPT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S152S158			4.0	54.8	R.LSVGS*VTSRPS*TPTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S149T161	-		5.7	45.6	R.LS*VGSVTSRPSTPT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II		S149T154S155	<b>-</b> -		6.3	44.3	R.LS*VGSVT*S*RPSTPTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II  TAF9 RNA polymerase II		S155T161	<u> </u>		18.8	47.2	R.LSVGSVTS*RPSTPT*LGTPTPQTMSVSTK.V
TAF9 RNA polymerase II		\$149\$158 \$158T159	<u> </u>		6.3	33.7 54.8	R.LS*VGSVTSRPS*TPTLGTPTPQTMSVSTK.V  R.LSVGSVTSRPS*T*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II		\$158T159T164	•		10.3	32.8	R.LSVGSVTSRPS*T*PTLGT*PTPQTMSVSTK.V
TAF9 RNA polymerase II		S149S158T159			5.7	45.9	R.LS*VGSVTSRPS*T*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S155S158T159			9.0	23.2	R.LSVGSVTS*RPS*T*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	T154S155S158	•		9.5	31.2	R.LSVGSVT*S*RPS*T*PTLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II	TAF9	S155S158			13.6	52.6	R.LSVGSVTS*RPS*TPTLGTPTPQTMSVSTK.V
TAF9L:	TAF9B	S152S153			9.6	33.5	R.LSVGAVS*S*KPTTPTIATPQTVSVPNK.V
TAF9L		S152T156	-		9.6	51.3	R.LSVGAVS*SKPT*TPTIATPQTVSVPNK.V
Talin		S425	-		9.1	55.4	K.SKDHFGLEGDEESTMLEDSVS*PK.K
TANC		\$63\$66 \$63\$67		•	29.7	67.3 52.0	K.GVSMS*LPS*SPLLPR.Q  K.GVSMS*LPSS*PLLPR.Q
Tankyrase 1 binding protein 182KD			-		151.0	76.3	R.VPS*S*DEEVVEEPQSR.R
Tankyrase 1 binding protein 182KD					20.1	81.2	R.LDS*PPPS*PITEASEAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD	TNKS1BP1	S1554			17.1	75.2	R.SPS*QDFSFIEDTEILDSAMYR.S
Tankyrase 1 binding protein 182KD	TNKS1BP1	S672		•••	79.7	39.7	R.AS*PEPPGPESSSR.W
Tankyrase 1 binding protein 182KD	TNKS1BP1	S1024			31.2	36.7	R.GS*GGLFSPSTAHVPDGALGQR.D
Tankyrase 1 binding protein 182KD				■.	-0.1	17.2	R.LDSPPPSPIT*EASEAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD				•	5.5	18.8	R.LDSPPPSPIT*EAS*EAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD  Tankyrase 1 binding protein 182KD				_=	43.4	11.6	R.DS*LGTYSSR.D  R.S*PSQDFSFIEDTEILDSAMYR.S
TAO kinase 1		\$1552 \$965			-2.7	44.9 25.6	R.NS*PQALR.R
TAO kinase 1		S9			100.0	30.9	R.AGS*LKDPEIAELFFK.E
	PLEKHA1		- -		35.1	74.9	R.SNS*LVSTFTMEK.R
TAPP1	PLEKHA1	<b>S</b> 330			12.2	66.8	R.S*NSLVSTFTMEK.R
TAR (HIV) RNA binding protein 2	TARBP2	S156	•••		-0.2	48.6	R.SPPMELQPPVSPQQS*ECNPVGALQELVVQK.G
TAR (HIV) RNA binding protein 2		S142S156			6.4	36.9	R.S'PPMELQPPVSPQQS'ECNPVGALQELVVQK.G
TAR (HIV) RNA binding protein 2		S152S156	<b></b>		2.6	38.5	R.SPPMELQPPVS*PQQS*ECNPVGALQELVVQK.G
TAR (HIV) RNA binding protein 2		S142S152		-	6.5	38.9	R.S'PPMELQPPVS'PQQSECNPVGALQELVVQK.G
TAR (HIV) RNA binding protein 2  Tara like protein		S152			6.0	59.4	R.SPPMELQPPVS*PQQSECNPVGALQELVVQK.G  R.ART*PAR.T
Tara like protein		T248 S5			100.0 46.0	13.6 79.8	R.ART*PAR.T  M.AADS*DDGAVSAPAASDGGVSK.S
Target of myb1 like 2		\$378			77.6	52.3	R.KQS*SEGIPVAQPSVMDDIEVWLR.T
		<b>S</b> 5			100.0	13.5	M.RRPS*VR.A
Taste receptor type 2 member 7	TAS2R7	<b>S</b> 305			100.0	10.9	K.VM#S*ILK.G
TATA element modulatory factor 1	TMF1	<b>S</b> 344	•		51.5	69.0	R.SVSEINS*DDELSGK.G
TatD DNase domain containing 2		\$328\$329\$331			57.4	35.7	R.EVVMEHPS*S*GS*DWS*DVEEISTVR.F
	HTATSF1				-0.2	17.4	K.ESS*PEKEAEEGCPEKESEEGCPK.R
	HTATSF1				100.0	52.8	K.LFEDDDS*NEK.L
TATSF1	HTATSF1	8721			100.0	62.5	K.LFDDS*DER.G

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TABASH   CASE	5 >100 >100						Carriage .
MATE   CAPT			2 2 2	0 4 10			
Manual	TATSF1 <sub>HTATSF1</sub>	\$452\$453	Ţ.		8.1	34.5	K.TEDGGEFEEGASENNAKES*S*PEKEAEEGCPEK.E
MATERIAL					83.7	62.0	
MARTH-CASTER   SECONOMIC   100			==				
MARTHURANTS   SPENSONS							
MARPHANCISCO   CONSTITUTION   100							
NATIFY HANDERS   STORT CONTINUES	TATSF1 <sub>HTATSF1</sub>	\$597\$600\$607			100.0	70.5	K.ELEENDS*ENS*EFEDDGS*EKVLDEEGS*ER.E
TATE   PACTURE   DESCRIPTION	TATSF1HTATSF1	S713S714			63.7	75.6	K.LFDEEEDS*S*EKLFDDSDER.G
MARTHURARIES   STOCK   100	TATSF1 <sub>HTATSF1</sub>	S713S714S721			100.0	57.7	K.LFDEEEDS*S*EKLFDDS*DER.G
MARTHURY NATION   1987   1988   1989   198			• • • •		65.6	59.2	
TABSPHYLATER   000   1							
TABS							
TART FLOATER SAME  ANTE FLOATER							
TATE FINANCIAL DE LEUR						23.3	R.GSEEDS*PKK.E
TATEF HIT AT STATES 2065287  TATEF HIT HIT HIT HIT AT STATES 2065287  TATEF HIT HIT HIT HIT HIT HIT HIT	TATSF1HTATSF1	S385			9.2	30.1	R.S*DSVSASER.A
TATEST HATEST 1788/53807 322 116 REPORTAGEN A  TAMERITALIA 515 212 060 REPORTAGENERA TODOS PLAN TODOS PROVIDED TO TAMERITALIA 515 212 060 REPORTAGENERA TODOS PLAN TODOS PROVIDED TO TAMERITALIA 515 212 060 REPORTAGENERA TODOS PLAN TODOS PROVIDED TO TAMERITALIA 515 212 060 REPORTAGENERA TODOS PROVIDED TO THE TAMERITALIA 515 212 060 REPORTAGENERA TODOS PROVIDED TO THE TAMERITALIA 515 112 060 REPORTAGENERA TODOS PROVIDED TO THE TAMERITALIA 515 112 060 REPORTAGENERA TODOS PROVIDED TO THE TAMERITALIA 515 112 060 REPORTAGENERA TODOS PROVIDED TO THE TAMERITALIA SEA SEA SEA SEA SEA SEA SEA SEA SEA SE	TATSF1 <sub>HTATSF1</sub>	T408			8.9	16.4	R.HFSEHPST*SK.M
TATEP HIGH TEST TYPEST 227214			<b>I</b>		6.8	16.2	K.LFDEEEDSS'EKLFDDS'DER.G
Tabliff TAUM. \$15   212   66.0 R. REFECRALARSSER V  TECT domain family number 19 (Progress) 19 (10 (10 (10 (10 (10 (10 (10 (10 (10 (10			<u> </u>		30.2	12.6	
Table   Tabl							
16.2   23.5					21.2		
15.1   11.6.1   11.					16.2		
TBC1 domain family member 15 [Pragment] TBC1D15 5102			•			53.3	K.SLS'QSFENLLDEPAYGLIQK.I
TBC1 domain family member 22A TBC1022A 5187  TBC1 domain family member 22A TBC1022A 5180  TBC1 domain family member 22A TBC1022A 5180  TBC1 domain family member 22A TBC1022A 5180  TBC1 domain family member 23 TBC1023 533  TBC1 domain family member 23 TBC1023 535  TBC1 domain family member 23 TBC1023 535  TBC1 domain family member 23 TBC1023 535  TBC1 domain family member 4 TBC104 5070  TBC1 domain family member 4 TBC104 5070  TBC1 domain family member 4 TBC104 5088 5091  TBC1 domain family member 4 TBC104 5088 5091  TBC1 domain family member 5 TBC105 5482  TBC1 domain family member 5 TBC105 5483  TBC1 domain family, member 5 TBC105 5483  TBC1 domain family member 5 TBC105 5483  TBC1 domain f	TBC1 domain family member 15 (Fragment) TBC1D15	S106			19.1	115.1	K.SLSQS*FENLLDEPAYGLIQK.I
18.1   12.1.5   R.509*LPHSATVTLOGTSCPSTLSSALSERE	TBC1 domain family member 15 (Fragment) TBC1D15	S102			8.4	51.0	K.S*LSQSFENLLDEPAYGLIQK.I
### 1902 R SOBLPHSATYVILGGTSDPSTLSSSALSERE    TBC1 domain family member 22A TDC1022A 5171   10.3 121.5 R SOBLPHSATYVILGGTSDPSTLSSSALSERE     TBC1 domain family member 22A TDC1022A 5180   2.9 38.4 R SOBLPHSATYVILGGTSDPSTLSSSALSERE     TBC1 domain family member 22A TDC1022A 5180   2.9 38.4 R SOBLPHSATYVILGGTSDPSTLSSSALSERE     TBC1 domain family member 22A TDC1022A 5180   2.9 38.4 R SOBLPHSATYVILGGTSDPSTLSSSALSERE     TBC1 domain family member 22A TDC102B 5987   34.0 47.8 RDTSPTACKELV9*CEEDT -     TBC1 domain family member 24 TDC102B 5987   34.0 47.8 RDTSPTACKELV9*CEEDT -     TBC1 domain family member 24 TDC102B 5987   34.0 47.8 RDTSPTACKELV9*CEEDT -     TBC1 domain family member 25 TDC102B 5987   34.0 47.8 RDTSPTACKELV9*CEEDT -     TBC1 domain family member 27 TDC104 5989591   100.0 39.8 RLSS*VDS*FERS       TBC1 domain family member 27 TDC105 598291   100.0 39.8 RLSS*VDS*FERS       TBC1 domain family member 27 TDC105 5982   39.8 RLSS*VDS*FERS       TBC1 domain family member 27 TDC105 5982   39.8 RLSS*VDS*FERS       TBC1 domain family member 27 TDC105 5982   39.8 RLSS*VDS*FERS       TBC1 domain family, member 19 TDC1015 5983   4.5 24.0 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1015 5983   15.2 41.0 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1015 5983   15.2 41.0 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1015 5983   15.2 41.0 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 59835045008   29.2 15.4 RGS*TSFLDTEF.       TBC1 domain family, member 19 TDC1017 5983504   29.2 15.4 RGS*TSFLDTEF.					14.5	23.8	K.S'LS'QSFENLLDEPAYGLIQK.I
TBC1 domain family member 22A TBC102A 5171  10.3 121.5 R SOSLPHE ATVILOGISOPSTISSSALSERE  TBC1 domain family member 23A TBC102A 5180  2.0 35.4 R SOSLPHEATVILOGISOPSTISSSALSERE  TBC1 domain family member 23 TBC102B 5883  100.0 22.5 R MST PALPWPORS  TBC1 domain family member 25 TBC10B 5967  34.9 47.8 R STST-LENERR G  TBC1 domain family member 4 TBC10B 5970  11.9 57.0 R SLTST-LENERR G  TBC1 domain family member 4 TBC10B 5980  12.0 34.9 R SLTST-LENERR G  TBC1 domain family member 4 TBC10B 5988  17.7 22.8 R SLTST-LENERR G  TBC1 domain family member 4 TBC10B 5988  17.7 22.8 R SLTST-LENERR G  TBC1 domain family member 4 TBC10B 5988  17.7 22.8 R SLTST-LENERR G  TBC1 domain family member 4 TBC10B 5988  18.0 37.7 22.8 R SLTST-LENERR G  TBC1 domain family member 5 TBC10B 5922  28.9 51.4 K SSSS-MPVQUMK.G  TBC1 domain family member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.2 41.9 R GSTTSR-LITEF-  TBC1 domain family, member 4 TBC10B 5943  18.0 R R R R R R R R R R R R R R R R R R R				. ==	15.1	121.5	
TBC1 domain family member 23 TBC1022 S180  2.0 34.4 R. SOSLPHSATVILOGISCOPSILSSSALSERE  TBC1 domain family member 23 TBC1020 S383  100.0 28.5 RAMS*PRAPMYPORS  TBC1 domain family member 28 TBC1020 S067  34.0 47.8 R.DTSPDKCELVS*DEEEDT.  TBC1 domain family member 4 TBC1014 S70  13.9 97.0 R.S.TSS*LENFSR.G  TBC1 domain family member 4 TBC1014 S088S901  100.0 38.0 R.LGS*VOSFERS  TBC1 domain family member 4 TBC1014 S088S901  100.0 38.0 R.LGS*VOSFERS  TBC1 domain family member 4 TBC1015 S082S901  100.0 38.0 R.LGS*VOSFERS  TBC1 domain family member 5 TBC1015 S43  -0.5 12.4 R.TS*STLDBEGTFNSYR.K  TBC1 domain family member 5 TBC1015 S44  -0.3 66.7 R.TSS*LDBEGTFNSYR.K  TBC1 domain family, member 4 TBC10104 S383  112.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10104 S383  112.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1802 15.4 R.RG*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1803 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1803 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1804 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1804 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1805 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1804 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1804 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1804 15.2 41.0 R.GS*TSRLDITEF.  1801 domain family, member 4 TBC10105 S083  1805 15.2 41.0 R.GS*TSRLDITEFSRLDI							
TBC1 domain family member 28 TBC1D23 S833							
TBC1 domain family member 4 TBC1D2   5670   13.9   87.0   R. SLTSSTLENESR.G							
TBC1 domain family member 4 TBC104   \$570   \$13   \$7.0   R.S.T.SSYLENFER.G	TBC1 domain family member 2B TBC1D2B	S957					R.DTSPDKGELVS*DEEEDT
### 1801 domain family member # TBC:104   \$5885991   190.0   36.9   RLGSVDS*FERS    ### 1801 domain family member # TBC:105   \$43   4.5   82.4   RTS*TLDSEGTFNSYR K    ### 1801 domain family member ### 1801   \$622   28.3   \$1.4   K.SES*MPVQLNN.G    ### 1801 domain family, member ### 1801   \$644   4.3   \$6.7   R.GS*TSLDTRF.    ### 1801 domain family, member ### 1801   \$675   4.1   8.0   8.5   8.0   8.	TBC1 domain family member 4 TBC1D4	<b>S</b> 570		•••	13.9	87.0	R.SLTSS*LENIFSR.G
### T8C1 domain family member \$ T8C1DIS S43  -0.5 82.4 R.TS-STLDSEGTRNSYR K  #### T8C1 domain family member \$ T8C1DIS S52  -0.3 66.7 R.TSS-TLDSEGTRNSYR K  #### T8C1 domain family member \$ T8C1DIS S44  -0.3 66.7 R.TSS-TLDSEGTRNSYR K  #### T8C1 domain family, member 10 CT8C1DIOC S438  -0.4 10. R.GSTSR-DTRF-  #### T8C1 domain family, member 15 T8C1DIS S675  -0.4 10. R.GSTSR-DTRF-  #### T8C1 domain family, member 15 T8C1DIS S675  -0.5 14.0 36.3 R.NDS-TTOPVSSDVCR L  #### T8C1 domain family, member 15 T8C1DIS S633  -0.5 15.2 41.0 R.GSTSR-DTRF-  #### T8C1 domain family, member 16 T8C1DIS S633  -0.5 15.1 30.3 R.SSTS-DGLE GLAPPAEPHS-PS-PTAS-PLPLS-PTRA-  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.CLTACPELPINNOCELGLAPPAEPHS-PS-PTAS-PLPLS-PTRA-  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.CLTACPELPINNOCELGLAPPAEPHS-PS-PTAS-PLPLS-PTRA-  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.CLTACPELPINNOCELGLAPPAEPHS-PS-PTAS-PLPLS-PTRA-  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.4 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  #### T8C1DI T8C1DI S605S850  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAFR R  -0.5 16.5 R.SLT-SSLESSLSR SEBLESESSESH-PEEPAPLS-PQQAF	TBC1 domain family member 4 TBC1D4	S588	ij		37.7	32.8	RLGS*VDSFER.S
TBC1 domain family member 5 TBC1DS		S588S591	-		100.0	36.9	
TBC1 domain family, member 10C TBC1D10C S438  15.2 41.0 R.GSTSFLDTRF.  TBC1 domain family, member 10C TBC1D10C S438  15.2 41.0 R.GSTSFLDTRF.  TBC1 domain family, member 15 TBC1D15 8675  14.0 36.3 R.NOS*PTOIPVSSDVCRL  TBC1 domain family, member 15 TBC1D15 8633  53.2 K. SIDANUSERIAL DISSENSITIONS FOR PLANT PROPERTY TRANSPORT PLANT PROPERTY TRANSPORT PLANT PLAN							
TBC1 domain family, member 19CTBC1D10C \$438			÷				
TBC1 domain family, member 15 TBC1D15				•			
TBC1 domain family, member 17 TBC1D17							R.NDS*PTQIPVSSDVCR.L
TBC1 domain family, member 17 TBC1D17 S60258045608 20.2 15.4 R.QLTACPELPHNYOEILGLAPPAEPHS'PS'PTAS'PLPLS'PTRA TBC1 domain family, member 9 (with GRAMTBC1D9 1008 66.6 11.6 RNYLRLWTPENKSK.S  TBC1D1 TBC1D1 S237 35.1 30.3 K.SFS'QPGLR.S  TBC1D1 TBC1D1 T505 18.2 23.7 K.LLGS'SEDLSSDSESHLPEEPAPLS'PQQAFRR  TBC1D1 TBC1D1 T505 19.0 4.1 51.2 R.SLT'ESLESILSR.G  TBC1D1 TBC1D1 S6655870 5.0 23.8 K.LLGS'SEDLS'SDSESHLPEEPAPLS'PQQAFRR  TBP-Interacting protein CAND1 Y304T306 43.9 K.  TCR Interacting molecule TRAT1 S116 18.0 21.5 K.MQEATPSAQATNETOMCYASLDHS'VK.G  Telomeric repeat binding factor 2 TERF2 3323 47.1 67.4 K.DLV.LPTQALPAS'PALK.N  Tensin 3 TNS3 S332 16.9 63.0 R.WDS'YENLSADGEVLHTQPVDGSLYAK.V  Tensin 3 TNS3 S361 27.9 K.S'SSDPGIPGGPQAIPATNSPDHSDHTLSVSSDSGHSTASAR.T  Tensin 3 TNS3 S890 20.0 50.7 R.FPGDQVWQAGQPLISTGPSPGS'PTLDIDQSIEQLNRL  TERF2IP TERF2IP S36 38.7 64.3 R.DDGSSMSFYVRPS'PAKR  TERF2IP TERF2IP S203 44.0 63.8 K.YLLGDAPVS'PSSQKL  TERF2IP TERF2IP S154 39.4 39.7 R.S'PSSVTGNALWKA  TERF2IP TERF2IP S154 39.4 39.7 R.S'PSSVTGNALWKA	TBC1 domain family, member 15 <sub>TBC1D15</sub>	S633				53.2	K. EI DOAMCEII GI OGEFENTTODERIMGEDEMINAMTDODTEAEOEMIAI D
TBC1D1   S237   35.1   30.3   K.SFS*OPGIR.S	TBC1 domain family, member 17 TBC1D17	\$602\$604\$608			20.2	15.4	
TBC1D1 TBC1D1 S665S855		T1008	<u> </u>		86.6	11.6	
TBC1D1 TBC1D1 T505							
TBC1D1 TBC1D1 S656SS70							
18.0   21.5   K.MQEATPSAQATNETQMCYASLDHSVK.G							
TCR Interacting molecule TRAT1 S116 18.0 21.5 KMQEATPSAQATNETOMCYASLDHS*VK.G  Telomerase subunit EST1ASMG6 T479S484 20.8 71.3 K.TQTPQLHFLDT*DDEVS*PTSWGDSR.Q  Telomeric repeat binding factor 2 TERF2 S323 47.1 67.4 K.DLVLPTQALPAS*PALK.N  Tensin 3 TNS3 S332 16.9 63.0 R.WDS*YENLSADGEVLHTQGPVDGSLYAK.V  Tensin 3 TNS3 S776 61.3 120.6 R.KLS*LGQYDNDAGGQLPFSK.C  Tensin 3 TNS3 S361 27.9 K.S*SSDPGIPGGPQAIPATNSPDHSDHTLSVSSDSGHSTASAR.T  Tensin 3 TNS3 S690 20.0 50.7 R.FPGDQVVNGAGPELSTGPSPGS*PTLDIDQSIEQLIN.L  TERF2IP TERF2IP S36 38.7 54.3 R.DGGSSMSFVVRPS*PAK.R  TERF2IP TERF2IP S203 44.0 63.8 K.YLLGDAPVS*PSSQKLL  TERF2IP TERF2IP S154 39.4 39.7 R.S*PSSVTGNALWKA  Testin TERF2IP TERF2IP S154 17.7 12.5 K.NVS*INTVTYEWAPPVQNQALAR.Q							K.
Telomeric repeat binding factor 2   TERF2    S323	TCR interacting molecule TRAT1				18.0		
Tensin 3 TNS3   S332   16.9   63.0   R.W.DS'YENLSADGEVLHTQGPVDGSLYAK.V	Telomerase subunit EST1A SMG6	T479S484			20.8	71.3	K.TQTPQLHFLDT*DDEVS*PTSWGDSR.Q
Tensin 3 TNS3   S776   E1.3   120.6   R.KLS*LGQYDNDAGGQLPFSK.C	Telomeric repeat binding factor 2 <sub>TERF2</sub>	<b>S</b> 323	<b></b>		47.1	67.4	K.DLVLPTQALPAS*PALK.N
27.9   K.S'SSDPGIPGGPQAIPATNSPDHSDHTLSVSSDSGHSTASAR.T		S332			16.9	63.0	
Tensin 3 This 3 Sego 20.0 50.7 R FPGDQVVNGAGPELSTGPSPGS*PTLDIDQSiEQLNR L  TERF2IP TERF2IP S36 38.7 54.3 R.DDGSSMSFVVRPS*PAK.R  TERF2IP TERF2IP S203 44.0 63.8 K.YLLGDAPVS*PSSQKL  TERF2IP TERF2IP S154 39.4 39.7 R.S*PSSVTGNALWKA  Testin TES S105 1.7 12.5 K.NVS*INTVTYEWAPPVQNQALAR.Q					61.3		
TERF2IP TERF2IP S36 38.7 54.3 R.DDGSSMSFYVRPS*PAK.R  TERF2IP TERF2IP S203 44.0 63.8 K.YLLGDAPVS*PSSOKL  TERF2IP TERF2IP S154 39.4 39.7 R.S*PSSVTGNALWKA  Testin TES S105 11.7 12.5 K.NVS*INTVTYEWAPPVQNQALAR.Q					20.2		
TERF2IP TERF2IP S203         44.0         63.8         KYLLGDAPVS*PSSQKL           TERF2IP TERF2IP S154         39.4         39.7         R.S*PSSVTGNALWKA           Testin TES         1.7         12.5         K.NVS*INTVTYEWAPPVQNQALARQ				-			
TERF2IP TERF2IP S154   39.4 39.7   R.S*PSSVTGNALWKA							
	TERF2IP TERF2IP						R.S*PSSVTGNALWK.A
Testin TES T108 9.5 15.6 K.NVSINT"VTYEWAPPVONQALAR.O	TestinTES	S105			1.7	12.5	K.NVS*INTVTYEWAPPVQNQALAR.Q
	TestinŢES	T108			9.5	15.6	K.NVSINT*VTYEWAPPVQNQALAR.Q

Peak Area	%CV White do	ts-Significant cha	nge in pepti compared to	de the			
<-10 -5 -3		with the minimum					
0 3 5	86 >100		CarT	RajiB			
>10	Protein Name Gene	Phosphosites	£ £ £	5 g g	Ascor	MOWSE	Sequence
	ific histone H2B HIST1H2E			<u>.</u>		11.1	K.RS*T*ISSR.E
	ific histone H2B <sub>HIST1H2E</sub>	\$ \$89\$92			7.6	17.5	K.RS*TIS*SR.E
	protein kinase 2 <sub>TESK2</sub>	S456			56.5	48.5	R.S*LPGSPEFLHQEACPFVGR.E
Tetratricopeptide r	repeat protein 16 TTC16	T7658767		•	6.9	17.0	K.TT*RS*PR.Q
Thiorodovin doma	TFIIF beta GTF2F2 in containing 13 TMX4	S248			52.9	22.8	R.HYQGEEKS*D
Thioredoxin domain cont		S251S259		=	100.0	29.4	R.AEQLQDAEEEKDDS*NEEENKDS*LVDDEEEK.E  K.VEEEQEADEEDVS*EEEAESK.E
	eracting protein TXNIP	\$247 \$314\$315\$318			57.3	143.7	R.TS'S'EMS'WVDLNIPDTPEAPPCYMDVIPEDHR.L
	eracting protein TXNIP	T348S358		-	-0.1	17.4	R.LESPT*TPLLDDMDGS*QDSPIFMYAPEFK.F
	eracting protein TXNIP	S361			-0.2	26.4	R.LESPTTPLLDDMDGSQDS*PIFMYAPEFK.F
	THRAP2 MED13L	S806S826			26.4	61.7	R.AGSSSLTQVTDLAPS*LHDLDNIFDNSDDDELGAVS*PALR.S
	THRAP2 MED13L	S796T798	•••		11.3	31.3	R.AGSSS*LT*QVTDLAPSLHDLDNIFDNSDDDELGAVSPALR.S
	THRAP2 MED13L	T801S806			5.6	41.1	R.AGSSSLTQVT*DLAPS*LHDLDNIFDNSDDDELGAVSPALR.S
	THRAP2 MED13L	S817S826		•••	19.5	53.3	R.AGSSSLTQVTDLAPSLHDLDNIFDNS*DDDELGAVS*PALR.S
	THRAP2 MED13L	S817			7.6	24.2	R.AGSSSLTQVTDLAPSLHDLDNIFDNS*DDDELGAVSPALR.S
	THRAP2 MED13L	\$806			1.1	39.6	R.AGSSSLTQVTDLAPS*LHDLDNIFDNSDDDELGAVSPALR.S
	THRAP2 MED13L	<b>S</b> 794	•			26.1	R.AGS*SSLTQVTDLAPSLHDLDNIFDNSDDDELGAVSPALR.S
	THRAP2 MED13L	S794S795		•-		40.3	R.AGS*S*SLTQVTDLAPSLHDLDNIFDNSDDDELGAVSPALR.S
Thryoid hormone recep	tor interactor 11 TRIP11	T1846S1854			7.6	21.8	K.SVPNT*PLRPNQQS*VVNSSFSELFVK.F
Thryoid hormone recep	tor interactor 11 TRIP11	S1842T1846			46.5	37.2	K.S*VPNT*PLRPNQQSVVNSSFSELFVK.F
Thryoid hormone recep	tor interactor 11 TRIP11	S1891			46.8	32.3	K.LSVHDMKPLDS*PGRR.K
	THUMPD:	S86S88			100.0	54.2	K.DQQPS*GS*EGEDDDAEAALKK.E
Thymidin	e kinase soluble TK1	S231			100.0	15.3	K.LFAPQQILQCS*PAN
	Thymopoletin TMPO	Y183			5.6	36.9	R.QNGSNDSDRY*SDNEEDSKIELK.L
	Thymopoletin TMPO	S177S180			25.9	42.3	R.QNGS*NDS*DRYSDNEEDSKIELK.L
	Thymopoletin TMPO	S177Y183			15.0	34.7	R.QNGS*NDSDRY*SDNEEDSKIELK.L
	Thymopoletin TMPO	S159			-0.3	70.7	R.SS*TPLPTISSSAENTR.Q
	Thymopoletin TMPO	S158S159T160			30.7	37.9	R.EQGTESRS*S*T*PLPTISSSAENTR.Q
	Thymopoletin TMPO	<b>S</b> 66	÷.		5.8	22.2	K.GPPDFS*SDEEREPTPVLGSGAAAAGR.S
	Thymopoletin TMPO	S310			12.2	48.9	K.SSSSSQPEHSAMLVSTAAS*PSLIK.E
	Thymopoletin TMPO	S66S67			42.6	92.3	K.GPPDFS*S*DEEREPTPVLGSGAAAAGR.S
	Thymopoletin TMPO	S306			112.4	69.8	K.HAS*PILPITEFSDIPR.R
	Thymopoletin TMPO	S156			26.0	28.7	K.LREQGTES'R.S
	Thymopoletin <sub>TMPO</sub>	T160			10.2	70.6	R.SST*PLPTISSSAENTR.Q
	Thymopoletin TMPO	S159T160			-0.2	52.8	R.SS*T*PLPTISSSAENTR.Q
	Thymopoletin TMPO	S66T74			10.4	22.3	K.GPPDFS*SDEEREPT*PVLGSGAAAAGR.S
	Thymopoletin TMPO	S444	• • •		-0.4	62.5	R.DSGS*FVAFQNIPGSELMSSFAK.T  R.EQGT*ES*RS*STPLPTISSSAENTR.Q
	Thymopoletin TMPO	T154S156S158			24.9	38.3	R.QNGSNDSDRYS*DNEEDSKIELK.L
	Thymopoletin TMPO	S184	-		16.4	35.7	KLREQGTES'RS'S'TPLPTISSSAENTR.Q
	Thymopoletin TMPO	\$156\$158\$159 \$312			6.5	14.7	K.SSSSSQPEHSAMLVSTAASPS*LIK.E
	Thymopoletin TMPO	\$312 \$177\$184			10.7	17.2	R. QNGS*NDSDRYS*DNEEDSKIELK.L
	Thymopoletin TMPO	\$177\$184 \$180Y183			5.1	17.2	R.QNGSNDS*DRY*SDNEEDSKIELK.L
	Thymopoletin TMPO	S67T74	_		6.9	30.6	K.GPPDFSS*DEEREPT*PVLGSGAAAAGR.S
	Thymopoletin TMPO	T154S156T160			4.3	35.9	R.EQGT*ES*RSST*PLPTISSSAENTR.Q
Thyroid hormone recep		S1317S1322		•	22.1	64.3	R.VREDDEDS*DDDGS*DEEIDESLAAQFLNSGNVR.H
Thyroid hormone recep	tor interactor 12 TRIP12	S1322S1329			23.9	47.5	R.VREDDEDSDDDGS*DEEIDES*LAAQFLNSGNVR.H
Thyroid hormone recep	tor interactor 12 TRIP12	S1317S1329			10.6	45.7	R.VREDDEDS*DDDGSDEEIDES*LAAQFLNSGNVR.H
Thyroid hormone rece	ptor interactor 3 ZNHIT3	S80	-		46.3	60.0	K.TVKPVENKDDDDSIADFLNS*DEEEDR.V
Thyroid hormone rece	ptor interactor 8 JMJD1C	S966			9.2	21.4	R.S*PTHLTVSSTNTLR.S
	TIF2 <sub>NCOA2</sub>	S493			34.0	11.1	R.MS*PGVAGSPR.I
Tight ju	nction protein 2 <sub>TJP2</sub>	S1159		•	32.3	78.6	R.GSYGS*DAEEEEYR.Q
Tight ju	nction protein 2 <sub>TJP2</sub>	S398S400		• •	8.1	61.7	R.DSQQTLINIPSLNDS*DS*EIEDISEIESNR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S394S398	•••		28.0	78.4	R.DSQQTLINIPS*LNDS*DSEIEDISEIESNR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S920Y932T933			13.3	82.3	R.LIS*DFEDTDGEGGAY*T*DNELDEPAEEPLVSSITR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S920T925Y932			42.0	73.3	R.LIS*DFEDT*DGEGGAY*TDNELDEPAEEPLVSSITR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S244			56.7	29.7	R.S*IDQDYER.A
Tight ju	nction protein 2 <sub>TJP2</sub>	S394S400		•	10.6	50.9	R.DSQQTLINIPS*LNDSDS*EIEDISEIESNR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S170S174			30.2	19.6	R.SRS*WEDS*PER.G
Tight ju	nction protein 2 <sub>TJP2</sub>	S1156			5.0	48.6	R.GS*YGSDAEEEEYR.Q
Tight ju	nction protein 2 <sub>TJP2</sub>	T925Y932T933		-	0.1	41.1	R.LISDFEDT*DGEGGAY*T*DNELDEPAEEPLVSSITR.S
Tight ju	nction protein 2 <sub>TJP2</sub>	S920T925T933			6.2	76.1	R.LIS*DFEDT*DGEGGAYT*DNELDEPAEEPLVSSITR.S

<-10 0 abundanc	ts-Significant cha e at 5%FDR o with the minimum	compared to	the			
.3 42 PSM 71 3 86			RajiB			
>100 >100 Protein Name Gene	Phosphosites	- E E E	# # # #	Ascor	MOWSE	Sequence
Tight junction protein 2 <sub>TJP2</sub>	S400	0 (12)		11.5	25.1	R.DSQQTLINIPSLNDSDS*EIEDISEIESNR.S
Tight junction protein 2 <sub>TJP2</sub>	T925Y932			6.5	44.7	R.LISDFEDT*DGEGGAY*TDNELDEPAEEPLVSSITR.S
Tight junction protein 2 <sub>TJP2</sub>	S394			2.4	54.6	R.DSQQTLINIPS*LNDSDSEIEDISEIESNR.S
Tight junction protein 3 <sub>TJP3</sub>	S183		·	34.4	58.5	R.S*PGGGSEANGLALVSGFK.R
Tight junction protein 3 <sub>TJP3</sub> Tight junction protein 4, peripheral <sub>TJAP1</sub>	S371S375	<del></del>		12.2	11.3	R.RES*SVDS*R.T  R.KDS*LTQAQEQGNLLN
TIM1 TIMELESS	S535			100.0	86.7	R.QLLDS*DEEQEEDEGR.N
Titin TTN	Y15335S15339			17.6	13.6	K.IRIY*AM#NS*EGLGEPALVPGTPKAEDR.M
TLOC1 SEC62	T375			98.5	101.5	K.EELEQQT*DGDCEEDEEEENDGETPK.S
TLOC1 SEC62	S117			100.0	33.5	K.AES*GKEEDKK.S
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	T431S434			32.7	73.9	K.ALEEALSIQT*PPS*SPPTAFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S434S435			6.6	43.1	K.ALEEALSIQTPPS*S*PPTAFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	\$428\$434			14.5	55.3	K.ALEEALS*IQTPPS*SPPTAFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	T431S435S442			18.3	59.2	K.ALEEALSIQT"PPSS"PPTAFGS"PEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S428S435S442			9.6	49.7	K.ALEEALS*IQTPPSS*PPTAFGS*PEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	<b>S</b> 77			16.2	49.5	K.DNELLPPPS*PSLGSFDPLAELTGK.D
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	T431S434S442	•		11.2	30.4	K.ALEEALSIQT*PPS*SPPTAFGS*PEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	T431S435			7.8	60.7	K.ALEEALSIQT*PPSS*PPTAFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S428S435			1.0	38.4	K.ALEEALS*IQTPPSS*PPTAFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub> TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S79		·	7.9	30.8	K.DNELLPPPSPS*LGSFDPLAELTGK.D  K.ALEEALSIQT*PPSS*PPT*AFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	T431S435T438 S82			3.9	29.6	K.DNELLPPPSPSLGS*FDPLAELTGK.D
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S428S435T438	=		4.2	20.6	K.ALEEALS*IQTPPSS*PPT*AFGSPEGAGALLR.K
TNFAIP3 interacting protein 1 <sub>TNIP1</sub>	S428S434S442			5.6	18.6	K.ALEEALS*IQTPPS*SPPTAFGS*PEGAGALLR.K
TNFAIP3 interacting protein 2 <sub>TNIP2</sub>	S333S339			100.0	59.2	K.VAS*LLHQVS*WR.Q
TOCA1 FNBP1L	S443		•	42.4	83.5	R.ES*PEGSYTDDANQEVR.G
TOCA1 FNBP1L	<b>S</b> 430			48.7	39.6	R.RHS*SDINHLVTQGR.E
TOM1 <sub>TOM1</sub>	T154T164			25.6	19.0	K.GLEFPMT*DLDMLSPIHT*PQR.T
TOM1 TOM1	S160T164			41.7	24.9	R.KGLEFPMTDLDMLS*PIHT*PQR.T
TOM1 <sub>TOM1</sub>	S160	<b>-</b>		9.4	18.2	K.GLEFPMTDLDMLS*PIHTPQR.T
TOM20 TOMM20	S135	<u> </u>		9.5	20.0	R.IVS*AQSLAEDDVE
TOMM70A TOMM70	S91			64.4	59.0	R.AS*PAPGSGHPEGPGAHLDMNSLDR.A
TOMM70A TOMM70	S96			7.8	51.6	R.ASPAPGS*GHPEGPGAHLDMNSLDR.A
Tomosyn <sub>STXBP5</sub> Topoisomerase DNA II, beta <sub>TOP2B</sub>	S723	-		12.9	52.9	R.KLS*LPTDLKPDLDVK.D  K.VVEAVNS*DS*DSEFGIPK.K
Topoisomerase DNA II, beta TOP2B	S1517S1519 S1395S1419			40.2	72.0	K.VKAS*PITNDGEDEFVPSDGLDKDEYTFS*PGK.S
Topoisomerase DNA II, beta TOP2B	\$1395\$1419 \$1395\$1408			38.1	50.2	K.VKAS*PITNDGEDEFVPS*DGLDKDEYTFSPGK.S
Topoisomerase DNA II, beta <sub>TOP2B</sub>	S1395			39.0	63.7	K.AS*PITNDGEDEFVPSDGLDKDEYTFSPGK.S
Topoisomerase DNA II, beta TOP2B	\$1395\$1408\$1		•••	29.5	39.4	K.VKAS*PITNDGEDEFVPS*DGLDKDEYTFS*PGK.S
TOP2B	S1461			32.2	91.5	K.SEDDSAKFDS*NEEDSASVFSPSFGLK.Q
TOP2B	\$1517\$1519\$1			100.0	58.7	K.VVEAVNS*DS*DS*EFGIPK.K
TOP2B	T1398S1408			14.9	35.0	K.ASPIT*NDGEDEFVPS*DGLDKDEYTFSPGK.S
Topoisomerase DNA II, beta TOP2B	T1366			-0.2	48.7	K.YT*FDFSEEEDDDADDDDDDDNNDLEELK.V
Topoisomerase DNA II, beta TOP2B	S1370			17.5	142.9	K.YTFDFS*EEEDDDADDDDDDDNNDLEELK.V
Topoisomerase DNA II, beta TOP2B	S1456S1461		-	18.3	61.4	K.SEDDS*AKFDS*NEEDSASVFSPSFGLK.Q
Topoisomerase DNA II, beta TOP2B	S1461S1466		-	4.3	22.4	K.SEDDSAKFDS*NEEDS*ASVFSPSFGLK.Q
Topoisomerase DNA II, beta TOPOR	S1331S1335S1			67.3	105.5	R.NPWS*DDES*KS*ES*DLEETEPVVIPR.D
Topoisomerase DNA II, beta TOP2B  Topoisomerase DNA II, beta TOP2B	\$1456\$1461\$1			3.1	55.2	K.SEDDS*AKFDS*NEEDS*ASVFSPSFGLK.Q  K.KT*SFDQDS*DVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	T1570S1576 S1449			16.8	44.5 87.6	K.SQDFGNLFSFPSYS*QK.S
Topoisomerase DNA II, beta TOP2B	S1576S1591			21.9	49.0	K.KTSFDQDS*DVDIFPSDFPTEPPS*LPR.T
Topoisomerase DNA II, beta TOP2B	S1576			11.5	65.5	K.TSFDQDS*DVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	S1436S1449	• • •		39.9	100.5	K.S*QDFGNLFSFPSYS*QK.S
Topoisomerase DNA II, beta <sub>TOP2B</sub>	S1608			26.0	48.5	K.YFAES*DEEEDDVDFAMFN
Topoisomerase DNA II, beta TOP2B	S1517S1521			30.3	72.6	K.VVEAVNS*DSDS*EFGIPK.K
TOP2B	S1395T1398			2.4	24.4	K.AS*PIT*NDGEDEFVPSDGLDKDEYTFSPGK.S
Topoisomerase DNA II, beta TOP2B	T1570S1571		-	15.4	25.1	K.KT*S*FDQDSDVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	S1571			-0.2	68.9	K.TS*FDQDSDVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	S1571S1576			11.2	25.1	K.KTS*FDQDS*DVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	T1570S1591	-		21.7	16.6	K.KT*SFDQDSDVDIFPSDFPTEPPS*LPR.T
Topoisomerase DNA II, beta TOP2B	S1436S1444S1			18.6	42.2	K.S'QDFGNLFS'FPSYS'QK.S
Topoisomerase DNA II, beta TOP2B	S1519S1521		-	7.6	26.2	K.KVVEAVNSDS*DS*EFGIPK.K

<-10 0 abundano	ts-Significant cha ce at 5%FDR c with the minimum	compared to	the			
42 PSM 71 3 85			RajiB			
>10 Protein Name Gene Topoisomerase DNA II, beta TOP2B	Phosphosites T1570	9 J J	9 K K	Ascor	MOWSE 30.0	Sequence K.KT*SFDQDSDVDIFPSDFPTEPPSLPR.T
Topoisomerase DNA II, beta TOP2B	\$1452\$1461	•		4.1	12.3	K.S*EDDSAKFDS*NEEDSASVFSPSFGLK.Q
Topoisomerase DNA II, beta <sub>TOP2B</sub>	Y1365		-	7.6	68.0	K.Y*TFDFSEEEDDDADDDDDDDDDDDDLEELK.V
Topoisomerase DNA II, beta TOP2B	T1398S1408T14			8.5	13.5	K.ASPIT*NDGEDEFVPS*DGLDKDEYT*FSPGK.S
Topoisomerase DNA II, beta TOP2B	S1444			14.9	40.4	K.SQDFGNLFS*FPSYSQK.S
Topoisomerase DNA II, beta TOP2B	S1436			21.5	51.3	K.S*QDFGNLFSFPSYSQK.S
Topoisomerase DNA II, beta TOP2B	S1447		•	14.9	13.7	K.SQDFGNLFSFPS*YSQK.S
Topoisomerase DNA II, beta TOP2B	\$1337\$1339	•		61.9	48.1	K.S*ES*DLEETEPVVIPR.D
Topoisomerase DNA II, beta TOP2B	S1331S1335S1			12.0	44.4	R.NPWS*DDES*KSES*DLEET*EPVVIPR.D
TORC3 CRTC3	<b>S</b> 62			53.0	64.6	R.LTQYHGGS*LPNVSQLR.S
TORC3 CRTC3	<b>S</b> 329			31.8	55.3	R.S*NPSIQATLNK.T
TORC3 CRTC3	S391S396			22.6	38.8	R.RQPPVS*PLTLS*PGPEAHQGFSR.Q
TORC3 CRTC3	S391T394	•		32.0	37.9	R.RQPPVS*PLT*LSPGPEAHQGFSR.Q
TORC3 <sub>CRTC3</sub>	S443	<u> </u>		14.0	44.1	R.SQLSFLPTEAQAQVS*PPPPYPAPQELTQPLLQQPR.A
Tousled like kinase 1 <sub>TLK1</sub>	S204T213	=		0.1	13.2	R.SPQNSHSHSTPSSS*VRPNSPSPT*ALAFGDHPIVQPK.Q  K.ISDYFEYQGGNGSS*PVR.G
Tousled like kinase 1 <sub>TLK1</sub> Tousled like kinase 1 <sub>TLK1</sub>	S180	-		8.2	41.6	
Tousled like kinase 1 TLK1	S209S211			13.0	19.1	R.SPQNSHSHSTPSSSVRPNS*PS*PTALAFGDHPIVQPK.Q  R.S*PQNS*HSHSTPSSSVRPNSPSPTALAFGDHPIVQPK.Q
Tousled like kinase 1 <sub>TLK1</sub>	\$191\$195 \$179				42.6	K.ISDYFEYQGGNGS*SPVR.G
Tousled like kinase 1 <sub>TLK1</sub>	S199S209	_		-14.8	13.5	R.SPQNSHSHS*TPSSSVRPNS*PSPTALAFGDHPIVQPK.Q
Tousled like kinase 1 <sub>TLK1</sub>	S199S202	•		7.1	16.0	R.SPQNSHSHS*TPS*SSVRPNSPSPTALAFGDHPIVQPK.Q
Tousled like kinase 1 <sub>TLK1</sub>	S204S211			10.8	14.0	R.SPQNSHSHSTPSSS*VRPNSPS*PTALAFGDHPIVQPK.Q
Tousled like kinase 2 <sub>TLK2</sub>	S98			9.2	20.5	K.ISDYFEFAGGSAPGTS*PGR.S
Tousled like kinase 2 <sub>TLK2</sub>	<b>T</b> 97			-0.4	35.1	K.ISDYFEFAGGSAPGT*SPGR.S
TRA2A TRA2A	S84S86T88			12.2	26.2	R.S'RS"YT"PEYR.R
TRA2A TRA2A	T202			50.5	79.1	R.AHT*PTPGIYMGRPTHSGGGGGGGGGGGGGGGGGR.R
TRA2A TRA2A	Y87T88			15.1	32.5	R.SY*T*PEYR.R
TRA2A TRA2A	\$16\$18\$20T24			28.1	26.6	R.S*QS*KS*PTGT*PAR.V
TRA2A TRA2A	S98S100			29.0	19.5	R.S"HS"PMSNR.R
TRA2A TRA2A	\$96\$98\$100			40.2	42.1	R.S*RS*HS*PMSNR.R
TRA2A TRA2B	S260S262			30.0	31.9	R.RRS*PS*PYYSR.Y
TRA2A TRA2B	S260Y264	-		16.6	29.4	R.RRS*PSPY*YSR.Y
TRA2A TRA2A	S84S86Y87			25.7	25.8	R.S*RS*Y*TPEYR.R
TRA2A TRA2A	S86Y87	-		15.8	15.7	R.S'Y"TPEYR.R
TRA2A TRA2A	S16S18S20	-		28.1	23.4	R.S'QS'KS'PTGTPAR.V
TRA2A TRA2A	S86T88			20.2	27.6	R.S*YT*PEYR.R
TRA2A TRA2A TRA2A TRA2B	\$86Y87T88 \$260			10.9	29.5	R.S°PSPYYSR.Y
TRA2A TRA2A	S98S103			17.5	15.4	R.S*HSPMS*NR.R
TRA2A	T204			56.5	81.4	R.AHTPT*PGIYMGRPTHSGGGGGGGGGGGGGGGGGRR
TRAF1 TRAF1	S66		Ξ	23.9	44.4	R.GEDLQSIS*PGSR.L
TRAF1 TRAF1	<b>S</b> 172		• • •	7.3	81.0	R.APCSES*QEELALQHFMK.E
TRAF1 TRAF1	<b>S</b> 170			20.7	76.3	R.APCS*ESQEELALQHFMK.E
TRAF1 TRAF1	<b>S</b> 64		•	10.9	40.5	R.GEDLQS*ISPGSR.L
TRAF3-interacting JNK-activating TRAF3IP3	S111			19.1	28.2	R.RISS*PR.E
TRAF3-interacting JNK-activating TRAF3IP3 modulator	S110S111	•		100.0	20.2	R.RIS*S*PR.E
Transcription elongation factor A protein-TCEAL1 like 1	S41S42			100.0	17.2	R.RS*S*PRR.R
Transcription elongation factor A, 1 <sub>TCEA1</sub>	S100			80.1	69.8	K.KKEPAITSQNS*PEAR.E
Transcription elongation factor B, 3 <sub>ELOA</sub>	T164S167			4.2	16.3	R.MSPT*YSS*DPESSDYGHVQSPPSCTSPHQMYVDHYR.S
Transcription elongation factor B, 3 <sub>ELOA</sub>	S125			13.6	16.2	R.SYS*PDHR.Q
Transcription elongation factor B, 3 <sub>ELOA</sub>	S162S167			2.7	16.4	R.MS*PTYSS*DPESSDYGHVQSPPSCTSPHQMYVDHYR.S
Transcription elongation factor B, 3 <sub>ELOA</sub>	S162T164				13.0	R.MS*PT*YSSDPESSDYGHVQSPPSCTSPHQMYVDHYR.S
Transcription factor 12 TCF12	S559			15.0	95.2	R.TSS*TNEDEDLNPEQK.I
Transcription factor 12 TCF12	T560			-0.3	91.4	R.TSST*NEDEDLNPEQK.I  R.LGAHEGLS*PTPFMNSNLMGK.T
Transcription factor 12 <sub>TCF12</sub> Transcription factor 12 <sub>TCF12</sub>	S98			13.1	51.0	R.LGAHEGLS*PTPFMNSNLMGK.T  R.LGAHEGLSPT*PFMNSNLMGK.T
Transcription factor 12 <sub>TCF12</sub> Transcription factor 12 <sub>TCF12</sub>	T100			4.2	50.8	R.GGTTSWGTSGQPS*PSYDSSR.G
Transcription factor 2B related factor BRF2	\$67 \$385	<del></del>		14.7	79.3	RICPVPPVSTVTGDENIS*DSEIEQYLR.T
Transcription factor 3 <sub>TCF3</sub>	\$354\$359			19.3	78.8	K.ALASIYSPDHSSNNFSSSPS*TPVGS*PQGLAGTSQWPR.A
Transcription factor 3 <sub>TCF3</sub>	\$354\$359 \$338Y340			JJ.5	73.5	K.ALAS*IY*SPDHSSNNFSSSPSTPVGSPQGLAGTSQWPR.A
Transcription factor 3 <sub>TCF3</sub>	S351T355S359			12.5	78.4	K.ALASIYSPDHSSNNFSS*SPST*PVGS*PQGLAGTSQWPRA
Transcription factor 3 <sub>TCF3</sub>	S346T355S359			9.3	74.4	KALASIYSPDHSS*NNFSSSPST*PVGS*PQGLAGTSQWPRJ

Peak Area	%CV	White do	ots-Significant cha	nge in pepti	ide			
<-10 -5	0 29 42	abundan timepoint PSM	ce at 5%FDR of t with the minimum	ompared to peak area f				
0	71 86			CarT	_RajiB_			
>10	>100		B1 1 1	# # # #	# # # #		MOWSE	Sequence
	Protein N Transcription fac	lame Gene ctor 3 <sub>TCF3</sub>	Phosphosites S352T355S359	0 0 0	0 61 15	Ascor 10.4	80.4	KALASIYSPDHSSNNFSSS*PST*PVGS*PQGLAGTSQWPRA
	Transcription fac	ctor 3 <sub>TCF3</sub>	Y340S350S359	•••		10.6	38.5	K.ALASIY*SPDHSSNNFS*SSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	S346S359		•	6.2	29.6	K.ALASIYSPDHSS*NNFSSSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	T355S359			24.1	94.4	K.ALASIYSPDHSSNNFSSSPST*PVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	\$338Y340\$341				61.2	K.ALAS*IY*S*PDHSSNNFSSSPSTPVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	\$352\$354\$359	-		5.7	76.4	K.ALASIYSPDHSSNNFSSS*PS*TPVGS*PQGLAGTSQWPR.A
	Transcription fac		S341S350S359			9.2	47.6	K.ALASIYS*PDHSSNNFS*SSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac		Y340S350S354		•		34.0	K.ALASIY*SPDHSSNNFS*SSPS*TPVGS*PQGLAGTSQWPR.A
	Transcription fac			-		2.2		KALASIYSPDHSSNNFS*SSPS*TPVGS*PQGLAGTSQWPRA
	Transcription fa		\$350\$354\$359		-	7.9	55.7	
	Transcription fa		S346S351S359			3.5	74.9	K.ALASIYSPDHSS*NNFSS*SPSTPVGS*PQGLAGTSQWPR.A
			\$350\$351\$359		-	5.8	49.1	K.ALASIYSPDHSSNNFS*S*SPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac		\$351\$354\$359			5.3	62.8	K.ALASIYSPDHSSNNFSS*SPS*TPVGS*PQGLAGTSQWPR.A
	Transcription fac		\$345\$350\$354			1.0	56.1	K.ALASIYSPDHS*SNNFS*SSPS*TPVGS*PQGLAGTSQWPR.A
	Transcription fac		S346S351S354			4.2	62.0	K.ALASIYSPDHSS*NNFSS*SPS*TPVGS*PQGLAGTSQWPR.A
	Transcription fa		Y340S351S354			12.9	53.0	K.ALASIY"SPDHSSNNFSS"SPS"TPVGS"PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	S345S351T355			5.1	70.0	K.ALASIYSPDHS*SNNFSS*SPST*PVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	Y340S345S354			2.3	46.1	K.ALASIY*SPDHS*SNNFSSSPS*TPVGS*PQGLAGTSQWPRA
	Transcription fac	ctor 3 <sub>TCF3</sub>	S379			46.2	61.7	R.AGAPGALS*PSYDGGLHGLQSK.I
	Transcription fac	ctor 3 <sub>TCF3</sub>	S350S354	ا بنه		13.5	49.6	K.ALASIYSPDHSSNNFS*SSPS*TPVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	S351T355			4.4	84.0	K.ALASIYSPDHSSNNFSS*SPST*PVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	\$345\$350\$359			-3.4	26.6	K.ALASIYSPDHS*SNNFS*SSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	S346S352	-		1.9	42.7	K.ALASIYSPDHSS*NNFSSS*PSTPVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	S346S354			5.5	38.5	K.ALASIYSPDHSS*NNFSSSPS*TPVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	\$350T355\$359			10.3	69.4	K.ALASIYSPDHSSNNFS*SSPST*PVGS*PQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	\$350\$351\$352			4.5	29.8	K.ALASIYSPDHSSNNFS*S*S*PSTPVGSPQGLAGTSQWPR.A
	Transcription fac	ctor 3 <sub>TCF3</sub>	Y340T355S359			3.0	33.4	K.ALASIY*SPDHSSNNFSSSPST*PVGS*PQGLAGTSQWPR.A
	Transcription fac		\$345 <b>\$</b> 359	=		-4.0	23.2	K.ALASIYSPDHS*SNNFSSSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac		S351S354				56.5	K.ALASIYSPDHSSNNFSS*SPS*TPVGSPQGLAGTSQWPR.A
	Transcription fac					7.2		K.ALASIYSPDHSSNNFS*SSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fa		S350S359			2.5	27.1	K.ALASIYSPDHSSNNFSSS*PS*TPVGSPQGLAGTSQWPR.A
	Transcription fac		S352S354			9.8	54.1	R DAGVGGI TOAGFI S'GFI AI NSPGPI S'PSGMK G
			S127S139	-		6.5	39.5	
	Transcription fac		S134S139	<u></u>		10.5	60.1	R.DAGVGGLTQAGFLSGELALNS*PGPLS*PSGMK.G
	Transcription fac		S346S354S359	-		5.0	57.0	K.ALASIYSPDHSS*NNFSSSPS*TPVGS*PQGLAGTSQWPR.A
	Transcription fa		S354T355	_ب		1.2	31.5	K.ALASIYSPDHSSNNFSSSPS*T*PVGSPQGLAGTSQWPR.A
	Transcription fa		Y340S345S359		<b>.</b>	6.2	50.0	K.ALASIY*SPDHS*SNNFSSSPSTPVGS*PQGLAGTSQWPR.A
	Transcription fac		S346S350S354			3.3	25.6	K.ALASIYSPDHSS*NNFS*SSPS*TPVGSPQGLAGTSQWPR.A
	oindina protein 2 a	aloha)	S181			15.1	21.6	K.KGPVS*LSK.S
Tr	anscription factor	r Dp-2 <sub>TFDP2</sub>	T40			3.5	43.9	K.GNISFVAFPVSNT*NSPTK.I
Tr	anscription factor	r Dp-2 <sub>TFDP2</sub>	S31T40	·		11.8	12.3	R.GFIDQNLSPTKGNIS*FVAFPVSNT*NSPTK.I
Tr	anscription factor	r Dp-2 <sub>TFDP2</sub>	S31T44			6.0	14.7	R.GFIDQNLSPTKGNIS*FVAFPVSNTNSPT*K.I
Transc	cription factor E2-	alpha <sub>TCF3</sub>	<b>S</b> 479			13.6	90.7	R.TSS*TDEVLSLEEK.D
	Transcription fact	tor E3 <sub>TFE3</sub>	S568			8.9	12.2	R.RSS*FSMEEES
Tra	anscription factor	E4F1 <sub>E4F1</sub>	S642S643			100.0	19.6	R.RS'S'RAPR.Q
	Transcription fact	or EB <sub>TFEB</sub>	S109S122		•	56.9	24.2	K.FAAHIS*PAQGSPKPPPAAS*PGVR.A
-	Transcription fact	or EB <sub>TFEB</sub>	S467			12.1	61.3	R.RSS*FSMEEGDVL
	Transcription fact	or EB <sub>TFEB</sub>	S332			31.8	97.9	R.VHGLPTTS*PSGMNMAELAQQVVK.Q
	Transcription fact	or EB <sub>TFEB</sub>	\$133\$134\$142			12.9	56.5	R.AGHVLSS*S*AGNSAPNS*PMAMLHIGS*NPER.E
<u> </u>	Transcription fact	or EB <sub>TFEB</sub>	S122			66.9	28.5	K.FAAHISPAQGSPKPPPAAS*PGVR.A
	Transcription fact		S138			4.3	75.2	R.AGHVLSSSAGNS*APNSPMAMLHIGSNPER.E
	Transcription fact		T331			5.8	24.8	R.VHGLPTT*SPSGMNMAELAQQVVK.Q
	Transcription fact		S138S142				52.2	R.AGHVLSSSAGNS*APNS*PMAMLHIGSNPER.E
						22.4		
	Transcription factor		S114S122			26.5	21.6	K.FAAHISPAQGS*PKPPPAAS*PGVR.A  R.AGHVLSS*S*AGNSAPNSPMAMLHIGSNPER.E
			S133S134			10.4	86.0	
	Transcription fact		S133S134S151			14.7	46.0	R.AGHVLSS*S*AGNSAPNSPMAMLHIGS*NPER.E
	Transcription fact		S134				83.7	R.AGHVLSSS*AGNSAPNSPMAMLHIGSNPER.E
	Transcription fact	or EB <sub>TFEB</sub>	S134S138S142			6.8	16.5	R.AGHVLSSS*AGNS*APNS*PMAM#LHIGS*NPER.E
		TFEB	S134S138S142		<u> </u>	16.3	61.4	R.AGHVLSSS*AGNS*APNS*PMAMLHIGSNPER.E
	Transcription fact	or EB <sub>TFEB</sub>	S133S134S138			9.9	49.7	R.AGHVLSS*S*AGNS*APNSPMAMLHIGS*NPER.E
	Transcription fact	or EB <sub>TFEB</sub>	S133			15.6	78.3	R.AGHVLSS*SAGNSAPNSPMAMLHIGSNPER.E
	Transcription fact	or EB <sub>TFEB</sub>	S142			3.9	16.8	R.AGHVLSSSAGNSAPNS'PMAMLHIGSNPER.E
-	Transcription fact	or EB <sub>TFEB</sub>	S133S151			21.2	77.8	R.AGHVLSS*SAGNSAPNSPMAMLHIGS*NPER.E
	Transcription fact	or EB <sub>TFEB</sub>	S109S114		• • •	85.4	22.9	K.FAAHIS*PAQGS*PKPPPAASPGVR.A

Peak Area	0 29	abundand	ots-Significant cha be at 5%FDR of with the minimum	compared to	the			
3	71 86 >100			CarT	RajiB			
>10	Protein Name Transcription factor EB 7		-	£ £ £	9 H H		MOWSE	Sequence RAGHVLSS*SAGNS*APNS*PMAMLHIGS*NPER.E
	Transcription factor EB		\$133\$138\$142 \$138\$151			6.4	38.8	RAGHVLSSSAGNS'APNSPMAMLHIGS'NPER.E
	Transcription factor EB		\$138\$151 \$334			2.3	40.1	R.VHGLPTTSPS*GM#NMAELAQQVVK.Q
	Transcription factor EB		\$466\$467		=	13.8	15.5	R.RS*S*FSMEEGDVL-
	Transcription factor EB		S134S138			11.8	74.9	R.AGHVLSSS'AGNS'APNSPMAMLHIGSNPER.E
	Transcription factor EB		\$133\$138\$142			14.9	58.6	RAGHVLSS*SAGNS*APNS*PMAMLHIGSNPER.E
	Transcription factor EB		\$133\$134\$142		•	9.1	29.2	RAGHVLSS'S'AGNSAPNS'PMAMLHIGSNPER.E
Tr	anscription factor ELF 1	LF1	S187			21.9	16.8	K.TKPPRPDS*PATTPNISVK.K
Ti	ranscription factor ELYS,	HCTF1	\$1577			75.8	68.3	R.NLS'FNELYPSGTLK.L
	ranscription factor ELYS,		S1980			32.1	45.6	R.EVS*PSDVR.E
	ranscription factor ELYS,		S1195		•	26.9	25.6	R.SLPSSSQLKGS*PQAISR.A
	Transcription factor IID	AF1	S328			7.6	12.3	K.SLWNYDYAPPPPPEQCLS*DDEITMMAPVESK.F
Transcription	factor IIF, alpha subunit	STF2F1	\$305\$307\$308			100.0	33.4	K.GVDEQS*DS*S*EES*EEEKPPEEDKEEEEEK.K
	factor IIF, alpha subunit		S385T389			31.9	76.1	R.GNS'RPGT'PSAEGGSTSSTLR.A
		TF2F1	S217S218S221			100.0	36.4	R.IHDLEDDLEM#S*S*DAS*GEEGGRVPK.A
Transcription	factor IIF, alpha subunit	STF2F1	S385S391	• • •		12.8	52.0	R.GNS*RPGTPS*AEGGSTSSTLR.A
	tor like nuclear regulator		S883				11.8	R.RAIS*PR.E
	Transcription factor Sp3		S73			176.2	105.7	K.IGPPS*PGDDEEEAAAAAGAPAAAGATGDLASAQLGGAPNR.W
	Transcription factor Sp4		\$73 \$770				105.7	R.IVTVAAISQDS*NPATPNVSTNMEEF.
	Transcription factor Sp4					21.4		R.IVTVAAISQDSNPAT'PNVSTNMEEF
	Transcription factor YY1		T774 S118			1.1	12.0 82.2	REEVVGDDS*DGLRA
	Transcription factor YY1		\$247			100.0	87.9	K.DIDHETVVEEQIIGENS*PPDYSEYMTGK.K
	termination factor, RNA				• • •	67.5		K.DFQHLIS*SPLKK.S
	polymerase 1		S64	-			18.4	K.GS*VPSPSPRPQALDATQVPS*PLPLAQPST*PPVR.R
			S296S314T323			14.6	10.8	
	ional coactivator MMS19		S1027			11.8	36.9	R.GEWFLLGS*PGS.
	ntermediary factor 1 beta		\$473			94.5	79.0	R.S'GEGEVSGLMR.K
			S598		===	7.2	95.4	R.LASPSGS*TSSGLEVVAPEGTSAPGGGPGTLDDSATICR.V
	ntermediary factor 1 beta		T599			5.3	105.6	RLASPSGST*SSGLEVVAPEGTSAPGGGPGTLDDSATICRV
	ntermediary factor 1 beta		\$823			16.6	35.5	K.FSAVLVEPPPMSLPGAGLS*SQELSGGPGDGP
	ntermediary factor 1 beta		S601			6.0	46.1	RLASPSGSTSS*GLEVVAPEGTSAPGGGPGTLDDSATICRV
	ntermediary factor 1 beta		\$33				31.8	R.S'TAPSAAASASAAASSPAGGGAEALELLEHCGVCR.E
	ntermediary factor 1 beta		S816			4.9	22.1	K.FSAVLVEPPPMS*LPGAGLSSQELSGGPGDGP
			T541			17.6	55.1	R. GAAAAATGQPGTAPAGT*PGAPPLAGMAIVK.E
	ntermediary factor 1 beta		S50			18.9	71.4	R.STAPSAAASASAAASS'PAGGGAEALELLEHCGVCR.E
	ntermediary factor 1 beta		S45			3.9	24.6	R.STAPSAAASASAS'AAASSPAGGGAEALELLEHCGVCR.E
	ntermediary factor 1 beta		<b>S</b> 49		•	4.6	26.3	R.STAPSAAASASAAAS SPAGGGAEALELLEHCGVCR.E
	ntermediary factor 1 beta		S824			4.8	17.3	K.FSAVLVEPPPMSLPGAGLSS'QELSGGPGDGP
	ntermediary factor 1 beta		S594		<u>-</u>		76.4	RLAS'PSGSTSSGLEVVAPEGTSAPGGGPGTLDDSATICR.V
	ntermediary factor 1 beta		T599S612			5.8	32.2	R.LASPSGST*SSGLEVVAPEGTS*APGGGPGTLDDSATICR.V
	nal intermediary factor 1 q qamma		T1102S1105			62.9	82.2	R.TFAPLPEFEQEEDDGEVT*EDS*DEDFIQPR.R
	nal intermediary factor 17 gamma		\$803\$808T815	•		24.1	12.6	R.S'ACMLS'SPESSLT'PPLSTNLHLESELDALASLENHVK.I
	nal intermediary factor 1 q gamma		S1119	-		100.0	12.1	R.LKS*DERPVHIK
	ermediary factor 1, alpha		S1019S1025			4.0	59.8	R.NES*EDNKFS*DDSDDDFVQPR.K
	ermediary factor 1, alpha		S663S667		•	6.0	11.6	R.TVQSPNS*SVPS*PGLAGPVTMTSVHPPIR.S
	ermediary factor 1, alpha		S768S771			3.8	31.1	R.SILTSLLLNSS'QSS'TSEETVLR.S
	ermediary factor 1, alpha		\$660\$667	-		12.8	70.6	R.TVQS'PNSSVPS'PGLAGPVTMTSVHPPIR.S
	ermediary factor 1, alpha		T657 <b>S</b> 667			4.2	14.1	R.T'VQSPNSSVPS'PGLAGPVTMTSVHPPIR.S
	ermediary factor 1, alpha		S767S771			11.3	44.6	R.SILTSLLLNS*SQSS*TSEETVLR.S
	ermediary factor 1, alpha		S1019S1028	-		11.7	73.3	R.NES"EDNKFSDDS"DDDFVQPR.K
	ermediary factor 1, alpha		S768S770	-		-0.4	24.4	R.SILTSLLLNS8'QS"STSEETVLR.S
	ermediary factor 1, alpha		S1025S1028			7.6	46.9	R.NESEDNKFS*DDS*DDDFVQPR.K
Transcriptional re	egulator protein HCNGP s	AP30BP	S69S72S77	-		9.6	16.1	R.LGGDEDGYEEEEDENS'RQS'EDDDS'ETEKPEADDPK.D
Transcriptional re	egulator protein HCNGP s				•	1.2	20.6	K.GGLVSDAY*GEDDFSR.L
		AP30BP				4.8	16.5	K.NVLSSLAVYAEDS*EPES*DGEAGIEAVGSAAEEK.G
Transcriptional re	egulator protein HCNGP					8.7	13.1	K.NVLS*S*LAVYAEDSEPESDGEAGIEAVGSAAEEK.G
	regulator protein HCNGP s	AP30BP	S9S10	•			14.9	K.NVLSSLAVY*AEDSEPES*DGEAGIEAVGSAAEEK.G
Transcriptional re						2.3	14.0	
Transcriptional re	egulator protein HCNGP s	AP30BP	Y14S22			2.3 45.1	38.1	R.RPPS'PDVIVLSDNEQPS'SPR.V
Transcriptional re	regulator protein HCNGP s	AP30BP	Y14S22 S100S113					R RPPS*PDVIVLSDNEQPS*SPR V KGTTATSAQANSTPTSVASVVTSAES*PASR Q
Transcriptional re Transcription Transcriptio	regulator protein HCNGP segulator protein HCNGP sonal repressor p66 alpha (	AP30BP GATAD2A GATAD2A	Y14S22 \$ \$100\$113			45.1	38.1	
Transcriptional re Transcriptional re Transcriptio Transcriptio	egulator protein HCNGP segulator protein HCNGP sonal repressor p66 alpha conal repressor p66 alp	AP30BP GATAD2A GATAD2A	Y14S22 \$100S113 \$340 \$100S107S114	• • • •		45.1 14.6	38.1 83.8	K.GTTATSAQANSTPTSVASVVTSAES'PASR.Q
Transcriptional re Transcription Transcriptio Transcriptio Transcriptio Transcriptio	regulator protein HCNGPs regulator protein HCNGPs conal repressor p66 alpha conal repressor p66 alpha conal repressor p66 alpha conal repressor p66 alpha	AP30BP SATAD2A SATAD2A SATAD2A	Y14S22 \$100S113 \$340 \$100S107S114 \$100S107S113	• • • •		45.1 14.6 33.4	38.1 83.8 40.0	K.GTTATSAQANSTPTSVASVVTSAES:PASR.Q RRPPS:PDVIVLS:DNEQPSS:PR.V

10 0 ab 	undance	at <b>5</b> %FDRc	nge in pepti ompared to	the			
	epoint v	vith the minimum					
3 86 5 >100			CarT	RajiB			
>10 Protein Name Ge	ne	Phosphosites	9 H H	5 m 9	Ascor	MOWSE	Sequence
Transducer of regulated cAMP response CR element binding protein 2	TC2	S170			5.7	33.2	R.TS*SDSALHTSVMNPSPQDTYPGPTPPSILPSR.R
Transducer of regulated cAMP response CR <sup>*</sup> element binding protein 2	TC2	S173			0.1	14.9	R.TSSDS*ALHTSVMNPSPQDTYPGPTPPSILPSR.R
Transducer of regulated cAMP response CR element binding protein 2	TC2	T187			8.7	31.0	R.TSSDSALHTSVMNPSPQDT*YPGPTPPSILPSR.R
Transducer of regulated cAMP response CR element binding protein 2	TC2	S178			6.5	35.6	R.TSSDSALHTS*VM#NPSPQDTYPGPTPPSILPSR.R
Transducer of regulated cAMP response CR*	TC2	S70S79S90			27.8	38.8	R.SSHYGGS*LPNVNQIGS*GLAEFQSPLHS*PLDSSR.S
Transducer of regulated cAMP response CR element binding protein 2	TC2	S456T458			5.2	38.5	K.QFS"PT"MSPTLSSITQGVPLDTSK.L
Transducer of regulated cAMP response CR*	TC2	S70S86S90		•	25.0	31.0	R.SSHYGGS*LPNVNQIGSGLAEFQS*PLHS*PLDSSR.S
Transducer of regulated cAMP response CR	TC2	S456S460			6.9	52.2	K.QFS*PTMS*PTLSSITQGVPLDTSK.L
Transducer of regulated cAMP response CR	TC2	S623			5.5	14.1	R.HGSGPNIILTGDS*SPGFSK.E
element binding protein 2  Transducer of regulated cAMP response CR	TC2	S613			26.7	23.8	R.HGS*GPNIILTGDSSPGFSK.E
element binding protein 2  Transducer of regulated cAMP response CR	TC2	S183	•		11.8	15.0	R.TSSDSALHTSVMNPS*PQDTYPGPTPPSILPSR.R
element binding protein 2  Transducer of regulated cAMP response CR		\$456			9.1	36.9	K.QFS*PTMSPTLSSITQGVPLDTSK.L
element binding protein 2  Transducer of regulated cAMP response CR		S456T462		-	5.7	25.6	K.QFS*PTMSPT*LSSITQGVPLDTSK.L
element binding protein 2  Transducer of regulated cAMP response CR							K.QFS*PTMSPTLS*SITQGVPLDTSK.L
element binding protein 2  Transducin like enhancer of split 3 <sub>TLE</sub>		S456S464	-		10.6	48.2	K.DAPT*SPASVASSSSTPSSK.T
Transducin like enhancer of split 3 <sub>TLE</sub>		T285			27.8	46.5	
		S203			26.0	106.2	R.ESSANNSVS*PSESLR.A
Transducin like enhancer of split 3 <sub>TLE</sub>		S240S245T259			21.6	32.8	R.YDS*DGDKS*DDLVVDVSNEDPAT*PR.V
Transducin like enhancer of split 3 <sub>TLE</sub>		Y238S240T259			11.1	22.2	R.Y*DS*DGDKSDDLVVDVSNEDPAT*PR.V
Transducin like enhancer of split 3 <sub>TLE</sub>	3	S263S267	Ţ.		100.0	15.6	R.VS*PAHS*PPENGLDK.A
Transducin like enhancer of split 3 <sub>TLE</sub>	3	S286	·		13.9	48.7	K.DAPTS*PASVASSSSTPSSK.T
Transducin like enhancer of split 3 <sub>TLE</sub>	3	Y238S245T259			9.3	13.1	R.Y*DSDGDKS*DDLVVDVSNEDPAT*PR.V
Transducin-like enhancer protein 3 <sub>TLE</sub> (Fragment)	3	S37S38			100.0	11.6	R.CENELGGPGAS*S*R.F
Transgelin 2 <sub>TAC</sub>	3LN2	S163			100.0	60.5	R.NFS*DNQLQEGK.N
Transketolase TKT	г	Y275			10.9	66.5	K.NMAEQIIQEIY*SQIQSK.K
Translation machinery-associated protein TM	A16	S192S193S195		<del></del>	3.3	20.3	K.TIITVDQDLGELELNDES*S*DS*DEEMTAVA
Translocated promoter region TPF	٦	S2155	•		85.5	46.5	R.TDGFAEAIHS*PQVAGVPR.F
Translocated promoter region TPF		T2116	•••		100.0	85.4	R.GLQLT*PGIGGMQQHFFDDEDR.T
Translocated promoter region TPF		S2136	•		15.7	53.0	R.TVPS*TPTLVVPHR.T
Translocated promoter region TPF		S522	-				R.DEEVS*SADISSSSEVISQHLVSYR.N
Translocated promoter region TPF				<del>-</del>	12.1	76.9	R TVPS*TPTI VVPHRTDGEAFAIHS*POVAGVPR F
Translocation associated membrane protein TRA		S2136S2155			17.5	11.0	
1		S365			28.7	60.2	K.KGTENGVNGTLTSNVADS*PR.N
Transmembrane and coiled coil domains 1 <sub>TM</sub>		<b>S</b> 90			13.9	58.9	K.ALGVISNFQSS*PK.Y
Transmembrane and coiled coil domains 1 <sub>TM</sub>		S89		-	19.3	11.4	K.ALGVISNFQS*SPK.Y
Transmembrane and coiled coil domains 1 <sub>TM</sub>	CC1	S58			100.0	29.4	R.NKFGS*ADNIPNLK.D
transmembrane and coiled coil domains 3 TM	CC3	S46			4.4	25.8	R.GGS*DTNLNFDVPDGILDFHK.V
Transmembrane protein 181 TMI	EM181						
Transmembrane protein 181 TM		S580Y586			23.5	88.6	K.DNPAFSMLNDS*DDDVIY*GSDYEEMPLQNGQAIR.A
Transmembrane protein for IMI	EM181				23.5	53.3	K.DNPAFSMLNDS*DDDVIY*GSDYEEMPLQNGQAIR.A  K.DNPAFSMLNDSDDDVIYGS*DYEEMPLQNGQAIR.A
Transmembrane protein 181 <sub>TMI</sub>		S588		<del></del>			
	EM181	\$588 \$580			-0.7	53.3	K.DNPAFSMLNDSDDDVIYGS*DYEEMPLQNGQAIR.A
Transmembrane protein 181 <sub>TMi</sub>	EM181	\$588 \$580 \$609\$611		 	-0.7 5.9	53.3 63.8	K.DNPAFSMLNDS:DDDVIYGS:DYEEMPLONGQAIR.A  K.DNPAFSMLNDS:DDDVIYGSDYEEMPLONGQAIR.A
Transmembrane protein 181 <sub>TM</sub> Transmembrane protein 181 <sub>TM</sub> Transmembrane protein 181 <sub>TM</sub>	EM181 EM181 EM181	\$588 \$580 \$609\$611 \$580Y590			-0.7 5.9 7.5	53.3 63.8 16.2	K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D
Transmembrane protein 181 <sub>TMI</sub> Transmembrane protein 181 <sub>TMI</sub> Transmembrane protein 181 <sub>TMI</sub>	EM181 EM181 EM181	\$588 \$580 \$609\$611 \$580Y590			-0.7 5.9 7.5 -1.0	53.3 63.8 16.2 41.8 74.8	K.DNPAFSMLNDS*DDDDVIYGS*DYEEMPLQNQQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNQQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEM#PLQNQQAIR A
Transmembrane protein 181 TMI	EM181 EM181 EM181 EM181	\$588 \$580 \$609\$611 \$580Y590 Y586 \$580\$588			-0.7 5.9 7.5 -1.0 -0.3	53.3 63.8 16.2 41.8 74.8	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES'DS'D K.DNPAFSMLNDS/DDDVIYGSDY'EEM#PLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDY'EEM#PLQNGQAIR A
Transmembrane protein 181 TMI	EM181 EM181 EM181 EM181 EM181	\$588 \$580 \$609\$611 \$580Y590 Y586 \$580\$588			-0.7 5.9 7.5 -1.0	53.3 63.8 16.2 41.8 74.8 49.9	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES/DS/D K.DNPAFSMLNDS/DDDVIYGSDY'EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A
Transmembrane protein 181 TMI	EM181 EM181 EM181 EM181 EM181 EM181	\$588 \$580 \$609\$611 \$580Y590 Y586 \$580\$588 \$575Y586 Y586\$588			-0.7 5.9 7.5 -1.0 -0.3	53.3 63.8 16.2 41.8 74.8 49.9 43.1	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS-DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A
Transmembrane protein 181 TMI	EM181 EM181 EM181 EM181 EM181 EM181 EM181	\$588 \$588 \$580 \$609\$611 \$5609\$60 \$7586 \$5759\$66 \$75966\$88 \$588588 \$588590			-0.7 5.9 7.5 -1.0 -0.3 7.7	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9	K.DNPAFSMLNDSDDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGSDY'EEMPLQNGQAIR A K.YKEES'DS'D K.DNPAFSMLNDS'DDDVIYGSDY'EEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIY'GS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIY'GS'DYEEMPLQNGQAIR A
Transmembrane protein 181 TMI	EM181 EM181 EM181 EM181 EM181 EM181 EM181 EM181	\$588 \$588 \$580 \$580 \$609\$611 \$5807590 \$7586 \$5805588 \$5757586 \$75865588 \$5887590 \$59			-0.7 5.9 7.5 -1.0 -0.3	53.3 63.8 16.2 41.8 74.8 49.9 43.1	K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGSDYEEMPLQNGQAIR A K.YKEES'DS'D K.DNPAFSMLNDS'DDDVIYGSDY'EEMBPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGSDYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DY'EEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DY'EEMPLQNGQAIR A
Transmembrane protein 181 TMI Transmembrane protein 388 TMI	EM181	\$588 \$580 \$580 \$580 \$609\$611 \$55807500 \$7586 \$55805588 \$5757586 \$75865588 \$5587500 \$9 \$6			-0.7 5.9 7.5 -1.0 -0.3 7.7	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9	K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEMBPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A
Transmembrane protein 181 TMI Transmembrane protein 388 TMI Transmembrane protein 388 TMI	EM181	\$588 \$580 \$580 \$580 \$609\$611 \$5809\$601 \$5809\$611 \$5809\$60 \$9586 \$580588 \$5757\$66 \$759566 \$580\$588 \$5887\$90 \$59 \$6			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9	K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGSDYEEMPLQNGQAIR A K.YKEES'DS'D K.DNPAFSMLNDS'DDDVIYGSDY'EEMBPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGSDYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DY'EEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS'DY'EEMPLQNGQAIR A
Transmembrane protein 181 TMI Transmembrane protein 388 TMI	EM181	\$588 \$580 \$580 \$580 \$609\$611 \$5809\$601 \$5809\$611 \$5809\$60 \$9586 \$580588 \$5757\$66 \$759566 \$580\$588 \$5887\$90 \$59 \$6			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9	K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEMBPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A
Transmembrane protein 181 TMI Transmembrane protein 388 TMI Transmembrane protein 388 TMI	EM181	\$588 \$580 \$580 \$580 \$609\$611 \$5807590 \$7586 \$580588 \$5757586 \$7586588 \$5887590 \$9 \$6 \$549 \$540			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9	K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDVIYGS*DYEEMPLQNGQAIR A
Transmembrane protein 181 TMI Transmembrane protein 388 TMI Transmembrane protein 37A TMI Transmembrane protein 87A TMI	EM181	\$588 \$580 \$580 \$5800 \$6009\$611 \$58007590 \$7586 \$580588 \$5757586 \$75865588 \$5887590 \$9 \$6 \$549 \$540 \$5540 \$5540 \$5534			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES/DS/D K.DNPAFSMLNDS/DDDVIYGSDY'EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A R.STS-YQELSEELVQVVENSELADEQDKETVR.V MALLLS*VLR.V K.WVEENVPSSVTDVALPALLDS*DEER.M KAQEDDLKWYEENVPSSVTDVALPALLDS*DEER.M
Transmembrane protein 181 TMI Transmembrane protein 381 TMI Transmembrane protein 374 TMI Transmembrane protein 674 TMI Transmembrane protein 678 TMI Transmembrane protein 678 TMI Transmembrane protein 678 TMI	EM181	\$588 \$580 \$580 \$5800 \$6009\$611 \$58007590 \$7586 \$580588 \$5757586 \$75865588 \$5887590 \$9 \$6 \$549 \$540 \$5540 \$5540 \$5534			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0 52.0	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS*DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A R.STS*YGELSEELVQVVENSELADEQDKETVR.V MALLLS*VLR.V K.WVEENVPSSVTDVALPALLDS*DEER.M K.AQEDDLKWVEENVPSSVTDVALPALLDS*DEER.M K.AQEDDLKWVEENVPSSVTDVALPALLDS*DEER.M
Transmembrane protein 181 TMI Transmembrane protein 358 TMI Transmembrane protein 878 TMI Transmembrane protein 878 TMI Transmembrane protein 878 TMI Transmembrane protein 878 TMI	EM181	\$588 \$580 \$580 \$5800\$\$\$\$609\$\$611 \$\$5807590 \$\$7586 \$\$580568 \$\$5757586 \$\$75865588 \$\$5757586 \$\$9 \$\$540 \$\$5540 \$\$5540 \$\$5534 \$\$5469 \$\$\$			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2	53.3 63.8 16.2 41.8 41.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0 70.1 50.0	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS/DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS*DY*EEMPLQNGQAIR A R.STS*YQELSEELVQVVENSELADEQDKETVR V MAILLLS*VLR.V K.WVEENVPSSVTDVALPALLDS*DEER M K.AQEDDLKWVEENVPSSVTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPVLVOS*DEEMTR S R.YAFMPLIDDS*DDEIEEFMVTSENLTEGIK L
Transmembrane protein 181 TMI Transmembrane protein 38 TMI Transmembrane protein 37 TMI Transmembrane protein 87 TATMI Transmembrane protein 87 TMI	EM181 EM206 EM35B EM87A EM87B EM87B EM87B	\$588 \$580 \$580 \$5800\$\$ \$5800\$\$611 \$5800590 \$7586 \$5800588 \$5757586 \$7586588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$7580588 \$758058 \$75			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2 23.2 95.9	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 88.0 70.1 50.0 50.0	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS-DDDVIYGSDY-EEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS-DDDVIYGSDY-EEMPLQNGQAIR A K.DNPAFSMLNDS-DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS-DY-EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS-DY-EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS-DY-EEMPLQNGQAIR A R.STS-YQELSEELVQVVENSELADEQDKETVR-V MALLLS*VLR-V K.WVEENVPSSVTDVALPALLDS*DEER M K.WVEENVPSSVTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEEMTR.S R.YAFMPLIDDS*DDEIEFMVTSENLTEGIK.L R.S*MAAAAAASLGQPRA
Transmembrane protein 181 TMI Transmembrane protein 38 TMI Transmembrane protein 37 TMI	EM181 EM206 EM35B EM87A EM87B EM87B EM87B EM87B	\$588 \$580 \$580 \$5800\$611 \$5800590 \$7586 \$5800588 \$5750588 \$5750588 \$5750588 \$580588 \$5880590 \$9 \$6 \$540 \$5540 \$5544 \$5469 \$5137 \$5243			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2 23.2 95.9 52.0	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0 52.0 70.1	K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDSDDDVIYGS*DYEEMPLQNGQAIR A K.WVEENVPSSVTDVALPALLDS*DEER M K.WVEENVPSSVTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPVLVOS*DEEMTR.S R.YAFMPLIDDS*DDEIEEFMVTSENLTEGIKL R.S*MAAAAAASLGGPRA
Transmembrane protein 181 TMI Transmembrane protein 358 TMI Transmembrane protein 358 TMI Transmembrane protein 378 TMI Transmembrane protein 378 TMI Transmembrane protein 378 TMI Transmembrane protein 97 TMI Transmembrane protein 97 TMI Transmembrane protein 97 TMI Transmembrane protein 97 TMI TRAP150 THI	EM181 EM206 EM358 EM87A EM87A EM87A	\$588 \$580 \$580 \$580 \$609\$611 \$5807590 \$7586 \$580588 \$5757586 \$7586588 \$58058 \$580580 \$58058 \$58058 \$58058 \$58058 \$58058 \$58058 \$58058 \$58058 \$580580			1.5 100.0 149.2 23.2 95.9 52.0 43.9 29.8	53.3 53.8 16.2 41.8 16.2 41.8 43.9 43.1 45.9 39.0 59.9 10.9 89.0 52.0 70.1 50.0 70.1 34.5	K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS*DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMIPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDVIYGS*DY*EEMPLQNGQAIR A K.WVEENIPS*STDVALPALLDS*DEER M K.WVEENIPS*SYTDVALPALLDS*DEER M K.WVEENIPS*SYTDVALPALLDS*DEER M K.WVEENIPS*SYTDVALPALLDS*DEER M K.WVEENIPS*SYTDVALPALLDS*DEER M K.WYEENIPS*SYTDVALPALLDS*DEER M K.WYEENIPS*SYTDVALPALDS*DEER M K.WYEENIPS*SYTDVAL
Transmembrane protein 181 TM Transmembrane protein 358 TM Transmembrane protein 37A TM Transmembrane protein 37A TM Transmembrane protein 87B TM Transmembrane protein 87B TM Transmembrane protein 87B TM Transmembrane protein 9TM TRAP150 THE TRAP150 THE TRAP150 THE	EM181	\$588 \$580 \$580 \$5800 \$600\$\$611 \$5800\$\$600\$\$611 \$5800\$\$600\$\$611 \$5800\$\$600 \$5800\$\$600 \$5800\$\$600 \$5800\$\$600 \$58757\$\$68 \$587575686 \$5887500 \$99 \$66 \$5840 \$5834 \$5400 \$5834 \$5400 \$5334 \$5400 \$5334 \$5400 \$5337 \$5243 \$5240 \$5939 \$5379 \$5379			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 23.2 95.9 52.0 43.9 29.8	53.3 53.8 16.2 41.8 74.8 43.9 43.1 48.9 39.0 59.9 10.9 89.0 50.0 70.1 34.5 113.1 79.2	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS-DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS*DY*E
Transmembrane protein 181 TM  Transmembrane protein 388 TM  Transmembrane protein 37A TM  Transmembrane protein 37A TM  Transmembrane protein 37B TM  Transmembrane protein 37B TM  Transmembrane protein 37B TM  Transmembrane protein 37B TM  Transmembrane protein 37 TM  Transmembrane protein 37 TM  Transmembrane protein 37 TM  TRAP150 THI  TRAP150 THI  TRAP150 THI  TRAP150 THI  TRAP150 THI	EM181	\$588 \$580 \$5800 \$5800 \$611 \$58007590 \$7586 \$5800588 \$5800588 \$5757586 \$757586 \$759586 \$5887590 \$80 \$540 \$540 \$540 \$540 \$540 \$540 \$540 \$54			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2 23.2 95.9 52.0 43.9 29.8 19.8	53.3 53.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 88.0 50.0 70.1 34.5 1113.1 79.2 64.1	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS-DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGSDY*EEMIPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS*DY*EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS*DY*E
Transmembrane protein 181 TM  Transmembrane protein 358 TM  Transmembrane protein 37A TM  Transmembrane protein 37A TM  Transmembrane protein 37B TM  TRAP150 TH  TRAP150 TH  TRAP150 TH  TRAP150 TH	EM181 EM206 EM87B	\$588 \$580 \$580 \$5800\$\$\$\$609\$\$611 \$\$5807590 \$\$7586 \$\$580568 \$\$5757586 \$\$5757586 \$\$5757586 \$\$587565588 \$\$5549 \$\$5540 \$\$5540 \$\$5540 \$\$534 \$\$5400 \$\$534 \$\$5400 \$\$534 \$\$5400 \$\$5370 \$\$5243 \$\$5240 \$\$5279 \$\$5279 \$\$59287941 \$\$5682			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 23.2 95.9 52.0 43.9 29.8	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0 52.0 70.1 34.5 113.1 79.2 64.1	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS*DDDVIYGSDY*EEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS*DDDVIYGSDY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GSDY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DY*EEMPLQNGQAIR A K.SNPAFMPLDDS*DDDVIY*GS*DY*EEMPLQNGQAIR A K.WVEENIPSSTTDVALPALLDS*DEER M K.WVEENIPSSTTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.SNSAAAAASLGGPRA R.ASAVS*ELS*PRE K.FSGEEGEIEDDES*GTENRE K.GSFS*DTGLGDGK.M K.FS*GEEGEIEDDES*GTENRE R.RIDIS*PSTFRK.H
Transmembrane protein 181 TM  Transmembrane protein 87 TM  Transmembrane protein 87A TM  Transmembrane protein 87A TM  Transmembrane protein 87B TM  TRAP150 TH  TRAP150 TH  TRAP150 TH  TRAP150 TH  TRAP150 TH	EM181 EM206 EM35B EM87A EM87B	\$588 \$580 \$5800 \$5800 \$611 \$58007590 \$7586 \$5800588 \$5800588 \$5757586 \$757586 \$759586 \$5887590 \$80 \$540 \$540 \$540 \$540 \$540 \$540 \$540 \$54			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 74.9 58.2 23.2 95.9 52.0 43.9 29.8 19.8	53.3 53.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 88.0 50.0 70.1 34.5 1113.1 79.2 64.1	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS-DDDVIYGSDY-EEMPLQNGQAIR A K.YKEES*DS*D K.DNPAFSMLNDS-DDDVIYGSDY-EEMPLQNGQAIR A K.DNPAFSMLNDS-DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.DNPAFSMLNDS/DDDVIYGS-DY-EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS-DY-EEMPLQNGQAIR A K.DNPAFSMLNDS/DDVIYGS-D
Transmembrane protein 181 TMI Transmembrane protein 385 TMI Transmembrane protein 374 TMI Transmembrane protein 378 TMI TRAP150 THI	EM181	\$588 \$580 \$580 \$5800\$\$\$\$609\$\$611 \$\$5807590 \$\$7586 \$\$580568 \$\$5757586 \$\$5757586 \$\$5757586 \$\$587565588 \$\$5549 \$\$5540 \$\$5540 \$\$5540 \$\$534 \$\$5400 \$\$534 \$\$5400 \$\$534 \$\$5400 \$\$5370 \$\$5243 \$\$5240 \$\$5279 \$\$5279 \$\$59287941 \$\$5682			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 100.0 149.2 74.9 58.2 23.2 95.9 52.0 43.9 29.8 19.8 40.6	53.3 63.8 16.2 41.8 74.8 49.9 43.1 48.9 39.0 59.9 10.9 89.0 52.0 70.1 34.5 113.1 79.2 64.1	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS*DDDVIYGSDY*EEMPLQNGQAIR A K.YKEES*DS*D- K.DNPAFSMLNDS*DDDVIYGSDY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GSDY*EEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DYEEMPLQNGQAIR A K.DNPAFSMLNDS*DDDVIY*GS*DY*EEMPLQNGQAIR A K.SNPAFMPLDDS*DDDVIY*GS*DY*EEMPLQNGQAIR A K.WVEENIPSSTTDVALPALLDS*DEER M K.WVEENIPSSTTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.WVEENIPSSFTDVALPALLDS*DEER M K.SNSAAAAASLGGPRA R.ASAVS*ELS*PRE K.FSGEEGEIEDDES*GTENRE K.GSFS*DTGLGDGK.M K.FS*GEEGEIEDDES*GTENRE R.RIDIS*PSTFRK.H
Transmembrane protein 181 TM  Transmembrane protein 38 TM  Transmembrane protein 38 TM  Transmembrane protein 37 TM  TRAP150 TH  TRAP150 TH  TRAP150 TH  TRAP150 TH  TRAP150 TH	EM181	\$588 \$580 \$580 \$5800 \$600\$\$611 \$5800\$\$600\$\$611 \$5800\$\$600 \$5800\$\$600 \$5800\$\$68 \$55757\$\$66 \$5800\$\$68 \$55757\$\$60 \$5900 \$59			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 100.0 149.2 74.9 95.9 52.0 43.9 29.8 19.8 40.6 36.8 57.8	53.3 63.8 16.2 41.8 74.8 43.9 43.1 48.9 39.0 59.9 10.9 88.0 50.0 70.1 50.0 70.1 70.1 70.2 64.1 24.4	K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGSDYEEMPLONGQAIR A K.YKEES'DS'D K.DNPAFSMLNDS'DDDVIYGSDY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DYEEMPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDVIYGS'DY'EEMIPLONGQAIR A K.DNPAFSMLNDS'DDVIYGS'DY'EEMIPLONGQAIR A K.MVEENIPSSYTDVALPALLDS'DEERM K.WVEENIPSSYTDVALPALLDS'DEERM K.WVEENIPSSYTDVALPALLDS'DEEMTR.S R.YAFMPLIDDS'DDEIEEFMVTSENLTEGIKL R.S'MAAAAASLGGPRA R.ASAVS'ELS'PRE R.ASAVS'ELS'PRE R.ASAVS'ELS'PRE R.ASAVS'ELS'PRE R.FSGEEGEIEDDES'GTENRE R.RIDIS'PSTFRKH K.WAHDKFS'GEEGEIEDDES'GTENRE R.ERS'PALKS'PLOSVVVRR
Transmembrane protein 181 TMI Transmembrane protein 385 TMI Transmembrane protein 374 TMI Transmembrane protein 378 TMI TRAP150 THI	EM181 EM206 EM35B EM87A	\$588 \$580 \$580 \$5800 \$600\$\$611 \$5800\$\$600 \$600\$\$611 \$5800\$\$60 \$7586 \$5800\$\$68 \$5757\$\$66 \$75865588 \$5757\$\$66 \$75865588 \$580590 \$9 \$6 \$540 \$5544 \$540 \$5544 \$540 \$5243 \$5240 \$5245\$\$650 \$600 \$600 \$600 \$600 \$600 \$600 \$60			-0.7 5.9 7.5 -1.0 -0.3 7.7 8.2 1.5 100.0 149.2 23.2 95.9 52.0 43.9 29.8 19.8 40.6 36.8 57.8 81.6	53.3 63.8 16.2 41.8 74.8 49.9 43.1 44.9 39.0 59.9 10.9 89.0 52.0 70.1 50.0 50.0 113.1 79.2 64.1 24.4 92.4	K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLONGQAIR A K.DNPAFSMLNDS/DDDVIYGSDYEEMPLONGGAIR A K.YKEES*DS*D K.DNPAFSMLNDS-DDDVIYGSDY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGSDY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS/DYEEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DYEEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDVIYGS*DY*EEMPLONGGAIR A K.DNPAFSMLNDS/DDVIYGS*DY*DV

Peak Area	abundand	ts-Significant cha se at 5%FDR of with the minimum	ompared to peak area f	the or a given			
5 >100 >100 Protein Name	Gene	Phosphosites	# # # # # # # # # # # # # # # # # # #	RajiB E E E	Ascor	MOWSE	Sequence
TRAP150		S534			-0.3	26.9	K.SS*SPPPR.K
TRAP150		\$535 \$24\$26\$28\$30			13.6	13.1	K.SSS'PPPR.K  R.S'RS'FS'KS'R.S
TRAP150		Y54S55			10.9	32.3	R.SY"S"PAHNR.E
	BCLAF1	S672			100.0	23.2	K.S'PEIHRR.I
TRAP150	THRAP3	S119			13.9	29.8	R.QAYS*PR.R
TRAP150		S320			36.3	87.3	K.S*PPSTGSTYGSSQK.E
	THRAP3	S399S406			20.1	13.6	K.TDS'EKPFRGS'QSPK.R  K.S'PVGKS'PPSTGSTYGSSQK.E
TRAP150		\$315\$320 \$51\$53\$55		•••	17.7	75.4 32.4	R.S'RS'YS'PAHNR.E
	THRAP3	S26S28S30			100.0	20.6	R.S'FS'KS'R.S
TRAP150	THRAP3	S406S408			23.6	19.2	K.TDSEKPFRGS'QS'PK.R
TRAP150		S134S136		<u> </u>	100.0	20.3	R.RS*PS*PR.R
TRAP150		S53Y54S55	<u></u>		-0.1	15.2	R.SRS"Y"S"PAHNR.E
TRAP150	THRAP3	S698	-		100.0	36.2	K.HGLAHDEMKS*PR.E  K.FS*GEEGEIEDDESGTENR.E
	THRAP3	\$928 \$253	=		5.8 42.4	15.2	K.S*PLQSVVVR.R
TRAP150		S51Y54S55			13.7	13.9	R.S'RSY'S'PAHNR.E
TRAP150	THRAP3	S51S53Y54		•	1.9	11.4	R.S'RS'Y'SPAHNR.E
TRAP150	THRAP3	<b>S</b> 377	<u> </u>		7.2	72.4	K.GS*FSDTGLGDGK.M
TRAP150		S24S26S28			100.0	11.5	R.S'RS'FS'K.S
TRAP150		S323	=		-20.9	87.8	K.SPPS*TGSTYGSSQK.E
TRAP220		\$1207T1215 \$1479\$1482	-		42.4	18.6	K.LAS'PMKPVPGT'PPSSK.A  K.SYQNS'PSS'DDGIRPLPEYSTEK.H
Treacle		S1479S1462 S1301			17.7	97.9	K.LGAGEGGEASVS*PEK.T
Treacle	TCOF1	\$270\$272\$273		•••	65.8	46.2	R.AKKPEEES'ES'S'EEGS'ES'EEEAPAGTR.S
Treacle	TCOF1	S1151			13.9	96.1	K.LDSS*PSVSSTLAAK.D
Treacle	TCOF1	S1073			6.5	13.5	K.KQEGPATQVDSAVGTLPATS*PQSTSVQAK.G
Treacle		T78587918794	Ħ		5.2	33.3	K.AVATAAQAQT*GPEEDS*GSS*EEES*DS*EEEAETLAQVKPSGK.T
Treacle	TCOF1	T785S791S793	_		9.3	29.9	K.AVATAAQAQT*GPEEDS*GS*SEEES*DS*EEEAETLAQVKPSGK.T  R.TETLVEETAAES*S*EDDVVAPSQSLLSGYMTPGLTPANSQASK.A
	TCOF1	S1113S1114 T1102T1104			25.4	77.0 53.5	R.T*ET*LVEETAAESSEDDVVAPSQSLLSGYMTPGLTPANSQASK.A
Treacle	TCOF1	S1273	•	• • •	100.0	74.3	R.KLS*GDQPAAR.T
Treacle	TCOF1	S304			24.2	55.5	K.TSQVGAASAPAKES*PR.K
Treacle	TCOF1	S829			100.0	44.8	R.AALAPAKES*PR.K
Treacle	TCOF1	S156			11.3	42.0	K.TVANLLSGKS*PR.K
-	TCOF1	S505			10.9	33.4	K.SLGNILQAKPTS*SPAKGPPQK.A
	TCOF1	\$426 \$506			72.1	71.0	K.S*PQVKPASTMGMGPLGK.G  K.SLGNILQAKPTSS*PAKGPPQK.A
Treacle		S1114S1122			3.5	51.0	R.TETLVEETAAESS'EDDVVAPS'QSLLSGYMTPGLTPANSQASK.A
Treacle	TCOF1	S1114S1124			0.9	42.1	R.TETLVEETAAESS'EDDVVAPSQS'LLSGYMTPGLTPANSQASK.A
Treacle	TCOF1	T504	• •		79.5	29.8	K.SLGNILQAKPT*SSPAKGPPQK.A
Treacle	TCOF1	T1072	Ţ.		10.3	36.0	K.KQEGPATQVDSAVGTLPAT*SPQSTSVQAK.G
Treacle		T1109S1122S11		·	1.0	15.6	R.TETLVEET AAESSEDDVVAPS QS LLSGYMTPGLTPANSQASK.A
Treacle Treacle		\$1122\$1124 T779T785\$791			0.9	44.2 54.3	R.TETLVEETAAESSEDDVVARS*QS*LLSGYMTPGLTPANSQASK.A  K.AVAT*AAQAQT*GPEEDS*GS*S*EEESDSEEAETLAQVKPSGK.T
Trinucleotide repeat containing 6		Y1574			0.0	43.9	R.LEESPFVPY*DFMNSSTSPASPPGSIGDGWPRA
Trinucleotide repeat containing 6	TNRC6A	S1585			26.0	47.7	R.LEESPFVPYDFMNSSTSPAS*PPGSIGDGWPRA
Trinucleotide repeat containing 6	TNRC6A	Y1574S1585			14.6	39.6	R.LEESPFVPY*DFMNSSTSPAS*PPGSIGDGWPR.A
Trinucleotide repeat containing 6	TNRC6A	Y1574T1581			2.1	25.3	R.LEESPFVPY*DFMNSST*SPASPPGSIGDGWPR.A
Trinucleotide repeat containing 6		S1579S1585			9.7	35.6	R.LEESPFVPYDFMNS*STSPAS*PPGSIGDGWPR.A
Trinucleotide repeat containing 6  Trinucleotide repeat containing 6		S1579S1580			5.5	11.9	R.LEESPFVPYDFMNS'S'TSPASPPGSIGDGWPR.A  R.LEESPFVPYDFMNSST'SPAS'PPGSIGDGWPR.A
Trinucleotide repeat containing 6		T1581S1585 S1012			9.6	44.8 25.9	R.MGS*PAPLLPGDLLGGGSDSI
Trinucleotide repeat containing 6E		Y630T640			4.5	11.5	R.GGSPY'NQFDIIPGDT'LGGHTGPAGDSWLPAKSPPTNK.I
Trinucleotide repeat containing 6E	TNRC6B	Y630S657			6.3	17.1	R.GGSPY*NQFDIIPGDTLGGHTGPAGDSWLPAKS*PPTNK.I
Trinucleotide repeat containing 6E	TNRC6B	Y630	-	<u>.                                    </u>	9.8	15.8	R.GGSPY*NQFDIIPGDTLGGHTGPAGDSWLPAK.S
Trinucleotide repeat containing 6E		T640	<b>—</b>		4.7	11.2	R.GGSPYNQFDIIPGDT*LGGHTGPAGDSWLPAK.S
Trinucleotide repeat containing protein 15		S376		•••	31.2	21.2	R.VGVEASEETPQTSSS*SARPGTPSDHQSQEASQFER.K
Trinucleotide repeat containing protein 15  Trinucleotide repeat containing protein 15		\$384 \$26\$30			0.3	30.6	R.VGVEASEETPQTSSSSARPGTPS*DHQSQEASQFER.K  R.ALSSGGSITS*PPLS*PALPK.Y
Trinucleotide repeat containing protein 15		\$26\$30 \$160			20.9	37.2	R.SQS*WEER.G

Peak Area %CV White do	ots-Significant cha ce at 5%FDR ( with the minimum	ange in peptio	the			
.s 42 PSM	with the minimum	треак агеа то	or a given			
3 86 5 5 >100 5 10		CarT	RajiB			
Protein Name Gene Trinucleotide repeat containing protein 15 GIGYF2	-	9 H H	£ £ £	Ascor	MOWSE	Sequence R.WRPHS*PDGPR.S
Trinucleotide repeat containing protein 15GIGYF2	S236			100.0	49.2	
	S26		•	23.9	87.6	RALSSGSITS*PPLSPALPK.Y
Trinucleotide repeat containing protein 15 GIGYF2	T25S30			22.8	35.1	R.ALSSGGSIT*SPPLS*PALPK.Y
Trinucleotide repeat containing protein 15 GIGYF2	T373			7.4	16.8	R.VGVEASEETPQT*SSSSARPGTPSDHQSQEASQFER.K
Trinucleotide repeat containing protein 15 <sub>GIGYF2</sub>	S374		<b>-</b>	0.3	16.8	R.VGVEASEETPQTS*SSSARPGTPSDHQSQEASQFER.K
Trinucleotide repeat containing protein 15 <sub>GIGYF2</sub>	T25		•	17.8	18.4	R.ALSSGGSIT*SPPLSPALPK.Y
Trinucleotide repeat-containing gene 6C TNRC6C protein	S1000			49.0	87.2	R.S*PLLGPVSSGWGEMPNVHSK.T
TRIO TRIO	S1724			-0.3	26.2	R.SS*MEMEGIFNHK.D
Triosephosphate isomerase 1 <sub>TPI1</sub>	S21			108.0	119.5	R.KQS*LGELIGTLNAAK.V
Tripartite motif containing 45 <sub>TRIM45</sub>	S451			100.0	12.1	K.KDS*PVR.T
tRNA modification GTPase GTPBP3, GTPBP3 mitochondrial	T22S23			100.0	17.9	R.RT'S'PRLR.R
tRNA-yW synthesizing protein 3 homolog TYW3	S236			14.1	15.0	K.ES*DEELENDDDDDLGINVTIFPEDY
Tropomodulin 3 <sub>TMOD3</sub>	S25			18.4	65.1	K.YKDLDEDELLGNLS*ETELK.Q
TRPC6 TRPC6	S14		•	8.9	20.0	R.RGSS'PR.G
Tryptophanyl tRNA synthetase WARS	S467			100.0	36.6	R.KLS'FDFQ
Tryptophanyl tRNA synthetase WARS	S8			4.3	35.9	M.PNSEPAS*LLELFNSIATQGELVR.S
TSC22 domain family 4 TSC22D4	S279	•••		100.0	49.6	K.S*PDPFGAVAAQK.F
TSC22 domain family 4 TSC22D4	S165			23.2	90.8	R.S'FTGGLGQLVVPSK.A
TSC22 domain family 4 TSC22D4	S260S263			11.4	12.0	R.MELGAPEEMGQVPPLDS*RPS*SPALYFTHDASLVHK.S
TSC22 domain family 4 TSC22D4	T167	-		-0.5	82.4	R.SFT*GGLGQLVVPSK.A
TSC22 domain family 4 TSC22D4	T229		Ė	16.0	29.9	RT'PPLSRR
TTK protein kinase <sub>TTK</sub>	<b>S</b> 455		•	16.9	54.2	K.TPS*SNTLDDYMSCFR.T
Tuberin <sub>TSC2</sub>	S1386			-0.1	87.8	K.SS*SSPELQTLQDILGDPGDK.A
Tuberin <sub>TSC2</sub>	S1387S1411			22.0	21.6	K.SSS*SPELQTLQDILGDPGDKADVGRLS*PEVK.A
Tuberin <sub>TSC2</sub>	S1388S1411			39.8	24.3	K.SSSS*PELQTLQDILGDPGDKADVGRLS*PEVK.A
TuberinTSC2	T1422	=		-0.5	86.4	R.SQSGT"LDGESAAWSASGEDSR.G
Tuberin TSC2	S1387			9.5	40.8	K.SSS*SPELOTLQDILGDPGDK.A
Tuberous sclerosis 1 <sub>TSC1</sub>	T339T345		•		38.5	R.LIT'EPPOAT'LWSPSMVCGMTTPPTSPGNVPPDLSHPYSK.V
Tubulin alpha 1 <sub>TUBA1B</sub>	S340			104.7	72.4	R.S*IQFVDWCPTGFK.V
Tubulin tyrosine ligase-like family, member TTLL4	S121S122		===	13.9	16.1	RRS'S'YR.Q
4 Tubulin tyrosine ligase-like family, member TTLL4	S122Y123				12.1	RRSS*Y*RQ
Tubulin tyrosine ligase-like family, memberTTLL4			_	5.0		RRS'SY'RQ
Tubulin, alpha 2 <sub>TUBA1</sub> C	\$121Y123 \$48		╸.	11.4	13.2	K.TIGGODDS'FNTFFSETGAGK.H
Tubulin, alpha, brain specific TUBA18				46.9	142.5	K.DYEVGVDS*VEGEGEEGEEY
Tubulin, beta TUBB		•		63.6		RISVYYNEAT'GGK.Y
Tuftelin interacting protein 11 <sub>TFIP11</sub>	T55		• •	12.7	30.3	K.GAAEEAELEDS'DDEEKPVKQDDFPK.D
Tuftelin interacting protein 11 <sub>TFIP11</sub>	S98			100.0	66.5	R.TTQSMQDFPVVDS*EEEAEEEFQK.E
	S210	•		86.3	85.7	R.DS'DDERPSEGK.R
TFIP11  Tuftelin interacting protein 11 <sub>TFIP11</sub>	S59	=		40.7	26.2	
	Y51			11.9	13.2	K.EEATY'GVWAERDSDDERPSFGGK.R
Tumor necrosis factor receptor superfamily, member 9	Y222			100.0	26.5	KLLY'IFKQ
Tumor protein D52 <sub>TPD52</sub>	T180			7.4	47.6	K.VGGTKPAGGDFGEVLNSAANASATTTEPLPEKI*QESL
Tumor protein D52 <sub>TPD52</sub>	S183			17.6	66.5	K.VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQES*L-
Tumor protein D52 like 2 <sub>TPD52L2</sub>			•	32.1	100.2	K.GLLSDS*MTDVPVDTGVAAR.T
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>				29.0	36.7	R.QSQQPMKPIS*PVKDPVS*PASQK.M
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>				7.6	13.5	R.GSGEKPVS*APGDDTESLHS*QGEEEFDMPQPPHGHVLHR.H
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>				8.6	32.9	R.GSGEKPVSAPGDDT*ESLHS*QGEEEFDMPQPPHGHVLHR.H
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>				19.2	37.7	R.GSGEKPVSAPGDDTES*LHS*QGEEEFDMPQPPHGHVLHR.H
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1202S1208				14.6	R.GS*GEKPVS*APGDDTESLHSQGEEEFDMPQPPHGHVLHR.H
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S380			20.1	50.4	R.STPFIVPSS'PTEQEGR.Q
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	<b>S</b> 552			27.3	35.8	R.IDEDGENTQIEDTEPMS*PVLNSK.F
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	<b>S</b> 500			104.3	117.8	K.NS*PEDLGLSLTGDSCK.L
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S294			112.6	108.0	K.S'PEPEVLSTQEDLFDQSNK.T
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S366	نب		88.2	76.0	R.SLVQDSLSTNSSDLVAPS*PDAFR.S
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1114			9.0	87.0	K.MVIQGPSS*PQGEAMVTDVLEDQK.E
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1462			-0.5	96.3	R.SDS*PEIPFQAAAGPSDGLDASSPGNSFVGLR.V
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1460			7.2	52.6	R.S*DSPEIPFQAAAGPSDGLDASSPGNSFVGLR.V
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1758S1759	·-		20.1	48.1	R.SKLPDGPTGS*S*EEEEFLEIPPFNK.Q
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	\$635\$639\$640	1		100.0	87.1	R.S'EALS'S'VLDQEEAMEIK.E
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1462S1481		•	5.8	56.6	R.SDS*PEIPFQAAAGPSDGLDASS*PGNSFVGLR.V
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1426S1430	••-		24.4	41.4	R.ETAVPGPLGIEDIS*PNLS*PDDKSFSR.V
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1462S1480			19.5	39.2	R.SDS*PEIPFQAAAGPSDGLDAS*SPGNSFVGLR.V
Tumor protein p53 binding protein 1 <sub>TP53BP1</sub>	S1460S1462			-0.5	16.3	R.S'DS'PEIPFQAAAGPSDGLDASSPGNSFVGLR.V
			•			

Peak Area	0 29 t	abundano	ts-Significant char ce at 5%FDR o with the minimum	ompared to	the or a given			
>10	Protein Name		Phosphosites		5 H B	Ascor	MOWSE	Sequence
	binding protein 1 <sub>T</sub>				•	7.8	23.3	KLMLSTSEYSQS'PK.M
1 umor protein p53	binding protein 1 <sub>T</sub>	P53BP1				2.3	38.4	R GSGEKPVSAPGDDT*ES*LHSQGEEEFDMPQPPHGHVLHR.H  KMVIQGPS*SPQGEAMMVTDVLEDQK.E
Tumor protein p53	binding protein 1 <sub>T</sub>				-	8.0	41.5	R.IDEDGENTQIEDT'EPMSPVLNSK.F
Tumor protein p53 in			S14		•	50.1	46.4	K.KHS*QTDLVSR.L
Tumor protein, translation	onally controlled 1 <sub>T</sub>	PT1	T39				56.0	R. TECHNINDS INCOMESCEDECITESTITO/UNIAMILLI DETSETY
Tumor r	ejection antigen 1 <sub>H</sub>	ISP90B1	S306	•	•	100.0	61.1	K.EES*DDEAAVEEEEEEKKPK.T
Tumor r	ejection antigen 1 <sub>H</sub>	ISP90B1	T468			100.0	33.9	R.KT*LDMIKK.I
	g subtransferable T candidate 4		S320	Ţ.		-0.6	11.9	K.SS'SPEDPGAEV
	g subtransferable T		S132	•••		100.0	15.1	R.S"PVEGLGRA
Tumor suppressin	g subtransferable T candidate 4 Twist neighbor T		S321			20.1	21.6	K.SSS*PEDPGAEV  R.KHS*EEAEFTPPLKCS*PK.R
Tyrosine pro	otein kinase ABL2A		S316S328 S631	•		47.2 35.4	33.7	R.DKS*PSSLLEDAK.E
	ein kinase PRAG1 P		S696		=	28.9	68.8	K.SAS*FAFEFPK.D
Tyrosine-prote	ein kinase PRAG1 p	RAG1	S826			46.3	15.3	R.AAS*SPDGFFWTQGSPKPGTASPK.L
Tyrosine-prote	ein kinase PRAG1 p	RAG1	S694			8.0	40.3	K.S'ASFAFEFPK.D
Tyrosyl DNA pho	osphodiesterase 1 <sub>T</sub>	DP1	T147S148		•	26.2	91.7	R.LKEEEDEYET*S*GEGQDIWDMLDK.G
Tyrosyl DNA pho	sphodiesterase 1 <sub>T</sub>	DP1	S13S14S15S18			10.6	25.2	R.WTIS'S'S'DES'EEEKPKPDKPSTSSLLCAR.Q
	osphodiesterase 1 <sub>T</sub>		T11S13S14S15			6.9	16.3	R.WT'IS'S'S'DESEEEKPKPDKPSTSSLLCAR.Q
	osphodiesterase 1 <sub>T</sub>		Y145T147	_		4.2	68.0	R.LKEEDEY'ET'SGEGQDIWDMLDK.G
	ted SR140 protein U		\$202 \$67			100.0	15.5	KKKS'NLELFKE  RESLCDS'PHONLSRPLLENKL
	ted SR140 protein U		S946S948			100.0	34.5	R.VKS'PS'PK.S
	ted SR140 protein ∪		S970S974		• • •	10.2	16.7	R.SS'HKDS'PR.D
U2-associat	ted SR140 protein ∪	2SURP	S930T931S934			16.3	21.3	R.RHS'T'SPS'PSR.S
U2-associat	ted SR140 protein U	2SURP	S930S932S934	••	Ļ	7.3	16.6	R.RHS*TS*PS*PSR.S
U2-associat	ted SR140 protein ∪	2SURP	<b>S</b> 49		•	25.1	11.3	R.TRPKS*PR.K
	ted SR140 protein ∪		T931S932S934			17.1	18.7	R.RHST*S'PS*PSR.S
	ted SR140 protein ∪		S930T931S932			12.4	22.6	R.RHS"T"S"PSPSR.S
U2-associat	ted SR140 protein U		\$930\$934\$936	=		10.0	14.6	R.RHS-TSPS-PS-R.S
	U2AF65 U		\$62 \$28\$30			42.4	16.0	R.S"KPLTR.G
	U2AF65 U		S79			100.0	16.9	K.EEHGGLIRS'PR.H
	U5 200kD S	NRNP20	S225			100.0	115.0	R.EEAS*DDDM#EGDEAVVR.C
Ubiquitin ac	tivating enzyme 1 U	BA1	S24			2.0	26.0	R.RVSGPDPKPGSNCS*PAQSVLSEVPSVPTNGMAK.N
Ubiquitin ac	tivating enzyme 1 U	BA1	S13S24			8.0	21.2	R.RVS*GPDPKPGSNCS*PAQSVLSEVPSVPTNGMAK.N
Ubiquitin ac	tivating enzyme 1 U	BA1	S13S28			22.3	29.3	R.RVS*GPDPKPGSNCSPAQS*VLSEVPSVPTNGMAK.N
	tivating enzyme 1 U		S21			49.5	23.9	R.RVSGPDPKPGS*NCSPAQSVLSEVPSVPTNGMAK.N
	tivating enzyme 1 U		S13	÷		4.8	13.9	R.RVS*GPDPKPGSNCSPAQSVLSEVPSVPTNGMAK.N
	tivating enzyme 1 U		S13S31			11.7	41.1	R.RVS*GPDPKPGSNCSPAQSVLS*EVPSVPTNGMAK.N  R.RVS*GPDPKPGS*NCSPAQSVLSEVPSVPTNGMAK.N
Ubiquitin associate			S13S21			20.0	41.1	R.S'LSSLQALQATVAR K
Ubiquitin carboxyl ten	ntaining protein A		S128	•		13.4	12.7	K.FLEESVS*MSPEER.A
Ubiquitin carboxyl ter	minal esterase L3 U	ICHL3	S130			11.3	26.9	K.FLEESVSMS'PEERA
Ubiquitin carboxyl ten	minal hydrolase 4 ∪	ISP4	S675S680	بب	•	16.2	28.3	K.EQLS'ETEGS'GEDEPGNDPSETTQKK.I
Ubiquitin carboxyl-term	ninal hydrolase 24 U	ISP24	T42				33.8	K.NDINEAVALLT*NERPGLDYGGYEPMDSGGGPSPGGGPR.G
Ubiquitin carboxyl-ten	minal hydrolase 8 U	ISP8	S718	-		14.3	34.1	R.SYS*SPDITQAIQEEEKR.K
Ubiquitin carboxyl-ten			Y717			-0.5	22.8	R.SY*SSPDITQAIQEEEKR.K
Ubiquitin conjugati			S268	•••		-1.5	48.8	R.RLSTS*PDVIQGHQPR.D
Ubiquitin conjugati  Ubiquitin conjugati			S251			26.0	40.1	K.NTSMS*PR.Q
Ubiquitin conjugati			T267			-0.4	40.8	R.RLST*SPDVIQGHQPR.D  R.RLS*T\$PDVIQGHQPR.D
	ating enzyme E2Q U		\$266 Y160T181			7.2	45.0 15.6	K.
	degradation 1 like U		S299		-	10.4	45.7	RFVAFSGEGGS*LRK
Ubiquitin p	orotein ligase E3C ∪	BE3C	T347S350				25.9	R.VLQT*FLS*QLPVSPASASCHDSASDSEESEEADKPSSPEDGR.L
Ubiquitin p	rotein ligase EDD ∪	BR5	S2486	Ţ.		79.1	49.8	R.S*VVDMDLDDTDDGDDNAPLFYQPGKR.G
Ubiquitin protein	ligase NEDD4 like N	EDD4L	S428	••		20.1	99.3	R.SLS"SPTVTLSAPLEGAK.D
	ligase NEDD4 like N		S429	Ţ.		-0.4	79.0	R.SLSS*PTVTLSAPLEGAK.D
	pecifc protease 16 ∪		S552	<b>.</b>		10.9	89.4	K.NINMDNDLEVLTSS'PTR.N
	ecifc protease 16 ∪		S415		Ļ	39.6	42.1	K.TVEDEDQDS*EEEKDNDSYIK.E
Ubiquitin specific pep			S2436			17.2	51.9	R.RPYTGNPQYTYNNWS*PPVQSNETSNGYFLER.S
Ubiquitin sp	ecific protease 10 U	SP10	S576			130.6	126.8	K.NHSVNEEEQEEQGEGS*EDEWEQVGPR.N

<-10 0 abundano		compared to	the			
.5 25 timepoint .3 42 PSM	with the minimum	peak area f	or a given			
3 85 >100 >100		CarT	RajiB			
Protein Name Gene Ubiquitin specific protease 10 USP10	Phosphosites \$211	£ £ £	5 2 B	Ascor 24.3	MOWSE 71.9	Sequence R.TCNS*PQNSTDSVSDIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	<b>S</b> 80	••		10.0	83.3	R.TPSYSIS*STLNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	T74			10.9	152.0	R.T*PSYSISSTLNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	T82			10.3	53.7	R.TPSYSISST*LNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	<b>S</b> 76			17.7	68.4	R.TPS*YSISSTLNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	S211S215S220			7.5	52.6	R.TCNS*PQNS*TDSVS*DIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	S81			12.2	29.7	R.TPSYSISS*TLNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	T216		•	0.2	20.3	R.TCNSPQNST*DSVSDIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	T208			2.5	26.1	R.T*CNSPQNSTDSVSDIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	S78	•••		3.5	92.5	R.TPSYS*ISSTLNPQAPEFILGCTASK.I
Ubiquitin specific protease 10 USP10	S211S215T216			1.7	44.8	R.TCNS*PQNS*T*DSVSDIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	S211S215S218			6.1	40.9	R.TCNS'PQNS'TDS'VSDIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 10 USP10	S211S218S220			3.2	55.3	R.TCNS*PQNSTDS*VS*DIVPDSPFPGALGSDTR.T
Ubiquitin specific protease 14 USP14	S143			16.3	85.8	R.AS*GEMASAQYITAALR.D
Ubiquitin specific protease 14 <sub>USP14</sub>	S148			18.5	67.9	R.ASGEMAS'AQYITAALR.D
Ubiquitin specific protesse 15 USP15	S965			0.7	31.4	K.GASAATGIPLESDEDS*NDNDNDIENENCMHTN
Ubiquitin specific protease 15 USP15  Ubiquitin specific protease 15 USP15	S961			25.5	42.3	K.GASAATGIPLES*DEDSNDNDNDIENENCMHTN  K.GASAATGIPLES*DEDS*NDNDNDIENENCMHTN
Ubiquitin specific protease 15 USP15  Ubiquitin specific protease 15 USP15	S961S965	•		25.3	32.9	K.S*PGASNFSTLPK.I
Ubiquitin specific protease 20 USP20	S229 S132S134			100.0	29.0	K.S PGASNFS I LPK.I  K.AVPIAVADEGES ES EDDDLKPR.G
Ubiquitin specific protease 24 USP24	\$1325134 \$1887	•	•	57.8	46.8	R.VSDQNS*PVLPK.K
Ubiquitin specific protease 24 <sub>USP24</sub>	S250			33.6	141.1	R.TIS*AQDTLAYATALLNEK.E
Ubiquitin specific protease 24 USP24	T254			14.2	86.5	R.TISAQDT*LAYATALLNEK.E
Ubiquitin specific protease 34 USP34	\$483\$486\$487		• • •	14.7	11.8	K.AQLS*KQS*S*FAS*LLNTNIPIGNKK.E
Ubiquitin specific protease 34 USP34	S2488			46.9	58.7	K.GPENPQVEVLS*EEEGEEEEEEDILSLAEEK.Y
Ubiquitin specific protease 39 USP39	S82			100.0	28.6	R.EVDEDS'EPER.E
Ubiquitin specific protease 47 USP47	T844		••	22.4	53.6	R.ELEQHIQT*SDPENFQSEER.S
Ubiquitin specific protease 47 USP47	S744			22.4	18.4	R.LFVLLPEQS*PVSYSK.R
Ubiquitin specific protease 6 USP6	S1214		• •	100.0	31.1	R.LRLPQIGS*K.N
Ubiquitin specific protease 7 USP7	S18	•		68.9	76.8	K.AGEQQLS*EPEDMEMEAGDTDDPPR.I
Ubiquitin-associated protein 2-like UBAP2L	<b>S</b> 478			18.0	49.6	K.STSAPQMS*PGSSDNQSSSPQPAQQK.L
Ubiquitin-associated protein 2-like UBAP2L	\$478\$488			20.8	42.4	K.STSAPQMS*PGSSDNQSSS*PQPAQQK.L
Ubiquitin-associated protein 2-like UBAP2L	S473S488			20.8	26.0	K.STS*APQMSPGSSDNQSSS*PQPAQQK.L
Ubiquitin-associated protein 2-like UBAP2L	<b>S</b> 473			8.7	26.7	K.STS*APQMSPGSSDNQSSSPQPAQQK.L
Ubiquitin-associated protein 2-like UBAP2L	S481		•	7.4	33.4	K.STSAPQMSPGS*SDNQSSSPQPAQQK.L
Ubiquitin-associated protein 2-like UBAP2L	S486S488			5.7	17.0	K.STSAPQMSPGSSDNQS*SS*PQPAQQK.L
Ubiquitin-conjugating enzyme E2Z UBE2Z	S231S232		<b>-</b>	4.6	35.5	R.LHNENAEMDSDS*S*SSGTETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S231S232			19.9	77.7	R.LHNENAEMDS*DS*S*S*SGTETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S231S232		<u>.</u>	15.1	38.6	R.LHNENAEMDS'DS'S'S'S'GTETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S232			6.9	65.6	R.LHNENAEMDS*DSS*SSGTETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S232S233			11.2	54.3	R.LHNENAEMDS*DSS*S*SGTETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z  Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S231S232			21.9	74.0	R.LHNENAEMDS*DS*S*SS*GTETDLHGSLR.V  R.LHNENAEMDS*DS*S*S*S*GT*ETDLHGSLR.V
Ubiquitin-conjugating enzyme E2Z UBE2Z  Ubiquitin-conjugating enzyme E2Z UBE2Z	S229S232S233		■.	13.5	20.9	R.LHNENAEMDSDS'S'S'S'GT'ETDLHGSLR.V
Ubiquitination factor E4B protein UBE4B	\$231\$232\$233 \$79			10.6	33.6	R.SQSS*EGVSSLSSSPSNSLETQSQSLSR.S
Ubiquitination factor E4B protein UBE4B	S87			6.1	15.6 48.7	R.SQSSEGVSSLSS*SPSNSLETQSQSLSR.S
Ubiquitously transcribed TPR protein on KDM6A	S769			58.3	75.1	K.S*PGLLSSDNPQLSALLMGK.A
the X chromosome  UBX domain containing 7 UBXN7	S288			34.4	134.4	R.SESLIDASEDS*QLEAAIR.A
UBX domain containing 7 UBXN7	S280S288			18.6	93.6	R.SES*LIDASEDS*QLEAAIR.A
UBX domain containing 7 UBXN7	S350			100.0	42.5	K.S*PHKDLGHR.K
UBX domain containing 7 UBXN7	S285			6.0	31.7	R.SESLIDAS*EDSQLEAAIR.A
UBX domain containing 7 UBXN7	S280			13.6	29.4	R.SES*LIDASEDSQLEAAIR.A
Unactive progesterone receptor 23KD PTGES3	S113			75.8	100.0	K.DWEDDS*DEDMSNFDR.F
Unactive progesterone receptor 23KD PTGES3	S151			10.0	58.6	R.FSEMMNNMGGDEDVDLPEVDGADDDSQDS*DDEKMPDLE
Unactive progesterone receptor 23KD PTGES3	S148			4.3	34.8	R.FSEMMNNMGGDEDVDLPEVDGADDDS*QDSDDEKMPDLE
Unactive progesterone receptor 23KD PTGES3	S124	•••			19.3	R.FS*EMMNNMGGDEDVDLPEVDGADDDSQDSDDEKMPDLE
Unactive progesterone receptor 23KD PTGES3	<b>S</b> 100			17.0	58.4	K.LNWLS*VDFNNWKDWEDDSDEDMSNFDR.F
Unactive progesterone receptor 23KD PTGES3	S113S118			100.0	55.0	K.DWEDDS*DEDMS*NFDR.F
Unc 51 like kinase 1 ULK1	S556		•	33.7	37.8	R.LHS*APNLSDLHVVRPK.L
Unc 51 like kinase 1 ULK1	S638			16.9	101.3	K.TPS*SQNLLALLAR.Q
Unc 51 like kinase 1 ULK1	T709S716				42.9	K.AAFGT*QAPDPGS*TESLQEKPMEIAPSAGFGGSLHPGAR.A
Unc 51 like kinase 1 ULK1	S716S719			30.6	43.3	K.AAFGTQAPDPGS*TES*LQEKPMEIAPSAGFGGSLHPGAR.A
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Peak Area	0 abundan		compared to	the			
-5 -3	timepoint 42 PSM	t with the minimum	ı peak area f	or a given			
5 >10	>100		CarT	RajiB E E E			•
	Protein Name Gene Unc 51 like kinase 1 <sub>ULK1</sub>	Phosphosites T660	5 m	9 4 6	Ascor 31.4	MOWSE 12.8	Sequence R.T*LPDLSEVGPFHGQPLGPGLRPGEDPK.G
	Unc 93 homolog B1 UNC93B1	S547S550			27.8	25.1	R.YLEEDNS*DES*DAEGEHGDGAEEEAPPAGPRPGPEPAGLGR.R
	Unc 93 homolog B1 <sub>UNC93B1</sub>					19.4	R.Y*LEEDNS*DESDAEGEHGDGAEEEAPPAGPRPGPEPAGLGR.R
	IC112 related protein 2 <sub>FERMT3</sub>		-		20.6	52.8	K.TAS*GDYIDSSWELR.V
	IC112 related protein 2 <sub>FERMT3</sub>	S484 T482	-		7.6	125.8	R.TGS*GGPGNHPHGPDASAEGLNPYGLVAPR.F  R.T*GSGGPGNHPHGPDASAEGLNPYGLVAPR.F
	UNC119 UNC119	T12T14S16	-		5.5	12.5	к.
	UNC119	T12T14S16S21				13.0	K.  VOCCACTATICE ADDRESSOR VADIDODDATE ESCRETEDACD
	UNC13D UNC13D	<b>S</b> 150			12.8	61.0	K.DVSGFSDPYCLLGIEQGVGVPGGS*PGSR.H
Uncharacteriz	zed membrane protein C19orf24 C19orf24	T113S117	<del></del>		4.4	11.7	R.YGLLANTEDPT'EM#AS'LDSDEETVFESR.N
Uncharacteriz	zed membrane protein C19orf24 C19orf24	S120	•		24.4	84.9	R.YGLLANTEDPTEMASLDS*DEETVFESR.N
	zed membrane protein C19orf24 C19orf24	S117S120	•••		31.2	119.9	R.YGLLANTEDPTEMAS*LDS*DEETVFESR.N
	zed membrane protein C19orf24 C19orf24	S117		. 🗜	12.0	97.0	R.YGLLANTEDPTEMAS*LDSDEETVFESR.N
	zed membrane protein C19orf24 C19orf24 zed membrane protein C19orf24	T109S120			3.9	13.7	R.YGLLANT*EDPTEM#ASLDS*DEETVFESR.N  R.YGLLANT*EDPT*EM#ASLDSDEETVFESR.N
	C19orf24 zed membrane protein C19orf24	T109T113			20.0	11.7 36.8	R.YGLLANTEDPT*EM#ASLDS*DEETVFESR.N
	C19orf24	\$101\$102			100.0	23.4	R.RS*S*LPRR.G
Uncharacteriz	red protein (Fragment)	<b>S</b> 96			6.5	24.2	R.RSS*GWPR.T
Uncharacte	rized protein C11orf96 C11orf96	<b>S</b> 86			12.1	45.5	K.SFLQS*LECLR.R
Uncharacte	rized protein C6orf132 C6orf132	S1151			26.1	13.1	R.S'PYTTTR.Y
	osin-XVIIIa (Fragment) MYO18A	S332	Ţ.		100.0	24.8	R.AAS*IRR.S
	0505 protein C16orf62 C16orf62	T434			100.0	17.6	R.ALLT*EM#MER.C
	latory element binding HUWE1 protein 1	S2362S2365			44.1	107.4	R.DGGS*GNS*TIIVSR.S  R.GSGTAS*DDEFENLR.I
	protein 1	\$1907 \$718			41.9	103.2	R.
	protein 1 latory element binding HUWE1	S726S727			-3.7	46.5	R. R. CHILLARE A STORE DEFECTION AND SENSO ON SETEMBLOOM (CTEE
Upstream regul	atory element binding HUWE1	S3919T3924			35.3	25.7	K.DEPPPLS*PAPLT*PATPSSLDPFFSR.E
Upstream regul	latory element binding HUWE1	S2619			40.5	102.1	R.S*DDELLDDFFHDQSTATSQAGTLSSIPTALTR.W
Upstream regul	latory element binding HUWE1 protein 1	S3373			22.2	83.6	KACS*PCSSQSSSSGICTDFWDLLVK.L
Upstream regul	latory element binding HUWE1 protein 1	S1395			100.0	51.2	R.AES*PEEVACR.K
	latory element binding HUWE1 protein 1	T3924			0.8	29.5	K.DEPPPLSPAPLT*PATPSSLDPFFSR.E
	latory element binding HUWE1 protein 1	T2635			10.9	51.1	R.SDDELLDDFFHDQSTAT*SQAGTLSSIPTALTR.W
	latory element binding HUWE1 protein 1 latory element binding HUWE1	\$3919T3924T39			33.6	34.1	K.DEPPPLS*PAPLT*PAT*PSSLDPFFSR.E  R.
	protein 1	\$740\$743 \$649			12.1	95.9	R.RSS*DPLGDTASNLGSAVDELMR.H
	protein 1 latory element binding HUWE1	S3379		-	5.8	25.0	K.ACSPCSSQS*SSSGICTDFWDLLVK.L
Upstream regul	atory element binding HUWE1	<b>S</b> 3919			1.6	45.0	K.DEPPPLS*PAPLTPATPSSLDPFFSR.E
Upstream regul	latory element binding HUWE1	<b>S</b> 3757			41.9	112.7	R.LGSSGLGS*ASSIQAAVR.Q
Upstream regul	latory element binding HUWE1 protein 1	S740T744			-2.8	37.5	R.
	latory element binding HUWE1 protein 1	S3919T3927			24.0	15.5	K.DEPPPLS*PAPLTPAT*PSSLDPFFSR.E
	latory element binding HUWE1 protein 1	S3816			8.0	66.5	R.REESPMDVDQPS*PSAQDTQSIASDGTPQGEK.E
	latory element binding HUWE1 protein 1	S718S726	÷			86.3	R. SGEDES'QEDVLMDEAPSNLSQASTLQANR.E
	protein 1  latory element binding HUWE1	S2377 S2632		-	2.4	66.3 22.8	R.SGEDES*QEDVLMDEAPSNLSQASTLQANR.E  R.SDDELLDDFFHDQS*TATSQAGTLSSIPTALTR.W
	protein 1	S726T749	-		0.1	26.4	R.
	protein 1 latory element binding HUWE1 protein 1	T2633		-	16.0	74.4	R.SDDELLDDFFHDQST*ATSQAGTLSSIPTALTR.W
Upstream regul	protein 1 latory element binding HUWE1 protein 1	S2636			-0.1	58.7	R.SDDELLDDFFHDQSTATS*QAGTLSSIPTALTR.W
U	racil DNA glycosylase UNG	<b>S</b> 23		•	34.3	45.7	R.HAPS*PEPAVQGTGVAGVPEESGDAAAIPAK.K
U	racil DNA glycosylase UNG	T60S63	•		19.6	56.7	K.KAPAGQEEPGT*PPS*SPLSAEQLDR.I
U	racil DNA glycosylase <sub>UNG</sub>	T60S64	• •		33.8	60.9	K.KAPAGQEEPGT*PPSS*PLSAEQLDR.I
Uridine m	nonophosphate kinase UCK2	S254			32.1	63.6	R.QAS*ESSSRPH
	USP6 N terminal like USP6NL	T276T279			100.0	11.8	R.T*PFT*LNLR.I
	UTP14A UTP14A	S29S31 S341S343			51.0	102.5 37.5	K.DYLLS'ES'EDEGDNDGER.K  K.LQVAS'ES'EEEEGGTEDVEELLVPDVVNEVQMNADGPNPWMLR.
UTP	14, U3 small nucleolar UTP14A	\$341\$343 \$405\$407		-	38.7	24.3	K.EAATQEDPEQLPELEAHGVS*ES*EGEERPVAEEEILLR.E
ribonuc	leoprotein. homolog A  Utrophin UTRN	\$405\$407 \$1866			-0.3	34.4	R.SS*LLPTDYLVEINK.I
	Utrophin (Fragment) UTRN	S211S213			10.1	19.5	R.LGYLPVQTVLEGDNLETPS*QS*PQLFHDDTHSR.I
	Utrophin (Fragment) UTRN	T200S213			9.9	17.6	R.LGYLPVQT*VLEGDNLETPSQS*PQLFHDDTHSR.I
	Utrophin (Fragment) UTRN	T209S211		<b></b>	8.3	24.2	R.LGYLPVQTVLEGDNLET*PS*QSPQLFHDDTHSR.I
	Utrophin (Fragment) UTRN	T209S213		<b>.</b>	10.6	31.0	R.LGYLPVQTVLEGDNLET*PSQS*PQLFHDDTHSR.I
	Vac14 homolog VAC14	S539S540			100.0	11.3	K.RFS*S*ER.K
Vacuo	lar protein sorting 13C VPS13C	S829Y835			-0.2	51.1	K.GLLGTSLLLDTVES*ESDDEY*FDAEDGEPQTCK.S

<-10 -5	abundand	ots-Significant cha ce at 5%FDR of with the minimum	compared to	the			
3 86 86 5100 >10				_RajiB_			
Protein Name Vacuolar protein sorting 13C		Phosphosites T826Y835	9 g g	9 % E	Ascor	MOWSE 41.2	Sequence K.GLLGTSLLLDT"VESESDDEY"FDAEDGEPQTCK
Vacuolar protein sorting 13C	VPS13C	T826S831		•	0.7	37.1	K.GLLGTSLLLDT*VESES*DDEYFDAEDGEPQTCK
Vacuolar protein sorting 13C	VPS13C	S831Y835	• •	-	-2.1	27.3	K.GLLGTSLLLDTVESES*DDEY*FDAEDGEPQTCK
Vacuolar protein sorting 13C	/PS13C	T826\$829		<b>—</b>	13.7	43.9	K.GLLGTSLLLDT"VES"ESDDEYFDAEDGEPQTCK
Vacuolar protein sorting 13C	VPS13C	S829S831			9.4	54.7	K.GLLGTSLLLDTVES*ES*DDEYFDAEDGEPQTCK
Vacuolar protein sorting 13C		S821T826			12.4	33.3	K.GLLGTS*LLLDT*VESESDDEYFDAEDGEPQTCK
Vacualar protein sorting 13D		S1724		<u></u>	28.1	43.8	R.S*LPSHMEEAPNVFQLYQRPTSASR.K
Vacuolar protein sorting 13D v		S1034		<u> </u>	2.3	18.1	K.NLSFDIPTGS*LRDSR.A
Vacuolar protein sorting 13D \ Vacuolar protein sorting 24(		T2862S2864			-0.4	33.3	R.ST*AS*LTNLEHQIYAR.A  K.VT*DALPEPEPPGAMAASEDEEEEEEALEAMQS
Vacuolar protein sorting 24(		T185			45.6	25.7 33.1	K.VTDALPEPEPPGAMAAS*EDEEEEEALEAMQS  K.VTDALPEPEPPGAMAAS*EDEEEEEALEAMQS
Valosin containing protein		\$200 \$770			100.0	33.1	R.GFGS*FR.F
Vanilloid receptor like 3		S374			22.4	24.7	K.RLRSLS*R.K
Vanilloid receptor like protein 1		S751			8.4	25.3	R.TLENPVLASPPKEDEDGAS*EENYVPVQLLQSN.
Vanilloid receptor like protein 1	TRPV2	S741			3.6	20.4	R.TLENPVLAS*PPKEDEDGASEENYVPVQLLQSN.
Vanilloid receptor like protein 1	TRPV2	Y755			6.7	15.6	R.TLENPVLASPPKEDEDGASEENY*VPVQLLQSN.
Vasodilator stimulated phosphoprotein	/ASP	S323			-0.2	54.7	K.SS*SSVTTSETQPCTPSSSDYSDLQR.V
Vasodilator stimulated phosphoprotein	VASP	T335			15.7	64.4	K.SSSSVTTSETQPCT*PSSSDYSDLQR.V
VAV1	VAV1	Y826		•	100.0	24.5	R.GEIY*GR.V
VAV2	VAV2	S768S769	- •		9.0	11.9	R.AS*S*RSPVFTPR.V
VAV2	VAV2	S768S771		-	10.0	21.1	R.AS*SRS*PVFTPR.V
VAV2 <sub>1</sub>		S768T775			6.9	14.6	R.AS*SRSPVFT*PR.V
VCIP135		S997S998			-0.3	18.3	R.SRES*S*PSHGLLK.L
VCIP135 \		S1198	Ļ		3.1	40.9	R.GNS*VEELEEMDSQDAEMTNTTEPMDHS
VCIP135 \		S994S997			8.0	13.5	R.S*RES*SPSHGLLK.L
VDAC1		S104			26.0	85.0	K.LTFDSSFS*PNTGKK.N
Ventricular zone expressed PH domain homolog 1		S783			100.0	15.2	R.DRS*LPR.A
Vesicle associated membrane protein 4		<b>S</b> 30	<b></b>		100.0	117.8	R.NLLEDDS*DEEEDFFLR.G
Vesicle docking protein p115		S942		•	62.5	69.0	K.DLGHPVEEEDELES*GDQEDEDDESEDPGKDLD
Vigilin : Vimentin \( \)		S944			100.0	22.1	K.DCDPGS*PR.R  R.SI YAS*SPGGVYATR S
Vimentin		S55			27.3	82.0	R.SLYAS*SPGGVYATR.S  R.SLYASS*PGGVYATR.S
Vimentin		\$56 Y61			29.1	83.8 62.1	R.SLYASSPGGW*ATR.S
Vimentin		Y61 S39			17.8	24.6	R.TYS*LGSALRPSTSR.S
Vimentin		S51			10.8	28.4	R.S'LYASSPGGVYATR.S
Vimentin v		S83			55.6	11.6	R.LLQDS*VDFSLADAINTEFK.N
Vinexin beta					8.2	42.5	R.LCDDGPQLPTS*PR.L
Vinexin beta s					14.7	52.8	R.GPSHPLDLGTSS*PNTSQIHWTPYRA
Vinexin beta	SORBS3	S605			9.2	25.8	R.GPSHPLDLGTS*SPNTSQIHWTPYRA
Vinexin beta	SORBS3	T529				26.5	R.LCDDGPQLPT*SPR.L
Voltage dependent anion selective channel protein 2	VDAC2	S130			28.4	44.1	K.LTFDTTFS*PNTGKK.S
Vpr binding protein [	DCAF1	S1000			4.0	53.9	R.HLPS*PPTLDSIITEYLR.E
WAS protein homology region 2 domain containing 1	WHAMM	S481S484	<b>—</b>	•	100.0	14.0	R.AS*LRS*R.K
WASP interacting protein	WIPF1	<b>S</b> 340	•		44.7	82.2	R.NLS*LSSSTPPLPSPGR.S
WAVE1\	WASF1	\$336\$339			12.0	18.0	R.TPVFVSPTPPPPPPPPPPPSALS*TSS*LR.A
WAVE1	WASF1	S336T337			3.5	11.2	R.TPVFVSPTPPPPPPPPPPPSALS*T*SSLR.A
WAVE1 \	WASF1	\$544\$546\$550		-	26.1	14.3	R.IAVEYS*DS*EDDS*EFDEVDWLE
WD repeat and HMG box DNA binding protein 1	WDHD1	S868	-		120.5	52.7	R.NQVEEDAEDS*GEADDEEKPEIHKPGQNSFSK.
	WDHD1	<b>S</b> 333			55.2	56.1	K.DYNDLFDGDDM#S*NAGDFLNDNAVEIPSFSK.G
WD repeat and HMG box DNA binding protein 1	WDHD1	<b>S</b> 407			64.8	13.3	K.EEEEDGQEGS*IHNLPLVTSQRPFYDGPMPTPR
WD repeat and HMG box DNA binding protein 1	WDHD1	S348			17.4	20.2	K.DYNDLFDGDDMSNAGDFLNDNAVEIPS*FSK.G
WD repeat domain 22 [	DCAF5	S531S533			5.4	49.0	R.LLALSNES*DS*EENVCEVELDTDLFPRPR.S
WD repeat domain 3 (		S241	-		10.6	87.8	K.GSS*PGIQDTLEAEDGAFETDEAPEDR.I
WD repeat domain 42A [		<b>S</b> 99	-		100.0	81.1	R.S*EEEEEEEEEEEEQPR.R
WD repeat domain 42A [		S129S130			69.4	34.3	R.DQDS*S*DDERALEDWVSSETSALPRPR.W
WD repeat domain 44 \		<b>S</b> 403			-0.3	44.2	K.EYVSNDAAQS*DDEEKLQSQPTDTDGGR.L
WD repeat domain 44 \		\$470\$471\$472	<b></b>		54.0	58.8	R.DEVFHTDQDDPS*S*S*DDEGMPYTRPVK.F
WD repeat domain 44		S161		<u> </u>	12.1	84.5	K.LTQTS*STEQLNVLETETEVLNK.E
WD repeat domain 44 \		S162		•	8.0	78.7	K.LTQTSS*TEQLNVLETETEVLNK.E
WD repeat domain 50 (		T180S186			14.5	62.9	R.KT*SSDDES*EEDEDDLLQR.T
WD repeat domain 50 (		S182S186			38.8	133.1	R.KTSS*DDES*EEDEDDLLQR.T
WD repeat domain 50 (	JTP18	T180S182S186			14.6	49.6	R.KT*SS*DDES*EEDEDDLLQR.T

Peak Area	%cv	White do	White dots-Significant change in peptide abundance at. 5%FDR compared to the threport with the minimum peak area for a given									
-6 -3	29 42 71											
3 5 >10	86 >100			CarT	RajiB							
	Protein Name WD repeat domain 5		Phosphosites S97S100	9m 2m 5m	5 ¥ £	Ascor	MOWSE	Sequence R.VQEHEDS*GDS*EVENEAK.G				
	WD repeat domain 5		\$181\$182\$186		• • •	23.8	53.8	R.KTS*S*DDES*EEDEDDLLQR.T				
	WD repeat domain 5	UTP18	T180S182			6.2	22.0	R.KT*SS*DDESEEDEDDLLQR.T				
	WD repeat domain 5	UTP18	S181S186			15.6	68.8	R.KTS*SDDES*EEDEDDLLQR.T				
	WD repeat domain 5	UTP18	T180S181S186			2.8	47.1	R.KT*S*SDDES*EEDEDDLLQR.T				
	WD repeat domain 5	UTP18	T180S181S182	•		7.8	18.2	R.KT*S*S*DDESEEDEDDLLQR.T				
	WD repeat domain 5	WDR55	S14			39.2	60.9	R.TCEERPAEDGS*DEEDPDSMEAPTR.I				
	WD repeat domain 70	WDR70	S638			103.6	63.8	K.TMFAQVES*DDEEAK.N				
	WD repeat domain 7	WDR75	S779S782			57.6	20.0	K.EIPEDVDMEEEKES*EDS*DEENDFTEK.V				
	WD repeat domain 7	WDR75	T798			0.3	107.9	K.VQDTSNT*GLGEDIIHQLSK.S				
	WD repeat domain 7	WDR75	<b>S</b> 796			17.7	113.8	K.VQDTS*NTGLGEDIIHQLSK.S				
	WD repeat domain 79		T489	<u> </u>		94.9	30.2	R.VFPEPT*ESGDEGEELGLPLLSTR.H				
	WD repeat domain 79		S491			2.3	38.9	R.VFPEPTES*GDEGEELGLPLLSTR.H				
	nain, phosphoinositid interacting	2	<b>S</b> 412		•	14.5	18.5	K.GTYVPS*SPTR.L				
WD repeat don	nain, phosphoinositid interacting	2	T408		-	8.4	16.4	K.GT*YVPSSPTR.L				
	WD repeat protein 1:		S116				36.0	R.GS*YQLQAQMNR.A				
	WD repeat protein 1:		S113Y117		===	3.2	18.1	R.SVS*RGSY*QLQAQMNR.A				
WD rappa	WD repeat protein 1: t-containing protein 4:		S113S116			6.2	26.3	R.SVS*RGS*YQLQAQMNR.A  K.DEENGEDRDT*AS*EK.E				
	WEE 1 tyrosine kinası		T656S658			100.0	58.1	R.S*PRPDHPGT*PPHK.T				
	WEE 1 tyrosine kinase		\$165T173 \$139	-		100.0	15.7 46.6	K.SPAAPYFLGSSFS*PVR.C				
	se interacting protein		S153			26.0	43.4	K.RPAAAAAAGSAS'PR.S				
	yndrome chromosome	PLAT2	S106			9.2	56.1	R.HGS*EEAYIDPIAMEYYNWGR.F				
	region : or 1 associated protein	5	\$305		• •	16.4	11.7	R.EGNTTEDDFPS*SPGNGNK.S				
Wilms tum	or 1 associated protein	1WTAP	\$306			13.9	33.6	R.EGNTTEDDFPSS*PGNGNK.S				
Wiskott-ald	drich syndrome protei	1WAS	S483S484			100.0	50.7	R.AIHS*S*DEGEDQAGDEDEDDEWDD				
Wiskott	-Aldrich syndrome-like	WASL	\$484\$485			100.0	30.3	K.AIHS*S*DEDEDEDDEEDFEDDDEWED				
	WNT-4 protein	nWNT4	S251S252			100.0	12.3	R.RVGS*S*R.A				
	WNT-4 protein	nWNT4	S252	•	<b>.</b>	8.9	16.4	R.RVGSS*R.A				
Wolf-Hirschhorn	syndrome candidate	2 NELFA	T277			100.0	66.3	K.T*LDAEVVEKPAK.E				
Wolf-Hirschhorn	syndrome candidate	<sup>2</sup> NELFA	Y377S379				21.8	R. ADMINISTED SPATDED AND TOD TOTTOD ANADITOTOD MARKANDO				
WW don	main binding protein 1	<b>1</b> WBP11	\$353\$361\$364			60.2	69.2	R.EVEEFS*EDDDEDDS*DDS*EAEKQSQK.Q				
	main binding protein 1		S237			16.9	36.9	R.DEDMLYS*PELAQR.G				
	ing adaptor with coiled coi	1	S523S535		-	6.8	44.1	R.S*PSPGPNHTSNSS*NASNATVVPQNSSAR.S				
	ing adaptor with coiled	ı	S64			51.2	22.5	R.RSDS*PENK.Y				
	ing adaptor with coile coi	ı	S525S534			5.6	31.3	R.SPS*PGPNHTSNS*SNASNATVVPQNSSAR.S				
	ing adaptor with coiled coi ing adaptor with coiled	ı	T457S470	•		13.7	16.2	R.IST*PQTNTVPIKPLIS*TPPVSSQPK.V  R.SPS*PGPNHTSNSSNAS*NATVVPQNSSAR.S				
	coi	ı	S525S538 T457T471			1.7	42.1	R.SPS*PGPNH1SNSSNAS*NA1VVPQNSSAR.S				
	coi	ı	\$534\$535	-		7.9	31.0	R.SPSPGPNHTSNS*S*NASNATVVPQNSSAR.S				
	coi ing adaptor with coile	I IWAC	S534S535 S525S535		. <u></u>	7.9	30.5	R.SPS'PGPNHTSNSS'NASNATVVPQNSSAR.S				
	coi ing adaptor with coile	I IWAC	S523S534			13.1	20.0	R.S'PSPGPNHTSNS'SNASNATVVPQNSSAR.S				
	coi ing adaptor with coile	I IWAC	S523S525	•		4.8	27.6	R.S'PS'PGPNHTSNSSNASNATVVPQNSSAR.S				
WW domain contain	coi	WAC	S523S538			-1.6	30.5	R.S*PSPGPNHTSNSSNAS*NATVVPQNSSAR.S				
WW domain containi	coi ing adaptor with coile coi	WAC	S523T531			2.4	23.0	R.S*PSPGPNHT*SNSSNASNATVVPQNSSAR.S				
,	WWC family member		<b>S</b> 927		•*	-0.5	10.9	R.SDS*DSSTLPR.K				
Xeroderma	pigmentosum group ( complementing proteil	XPC	S883S884			41.4	110.5	K.SEAAAPHTDAGGGLS*S*DEEEGTSSQAEAAR.I				
Xeroderma	pigmentosum group ( complementina protei	XPC	S122S129			27.6	102.1	R.GATMNEDS*NEEEEES*ENDWEEVEELSEPVLGDVR.E				
Xeroderma	pigmentosum group ( complementina proteil	XPC	T117S129			3.7	49.1	R.GAT*MNEDSNEEEEES*ENDWEEVEELSEPVLGDVR.E				
		XPC	T117S122			5.4	71.1	R.GAT*M#NEDS*NEEEEESENDWEEVEELSEPVLGDVR.E				
		XI-C					118.4					
	XPA binding protein		S338	-	_	53.8		R.GTLDEEDEEADS*DTDDIDHR.V				
	XPA binding protein XPA binding protein	1 <sub>GPN1</sub>	\$338 \$314			23.4	56.4	R.GTLDEEDEADS*DTDDIDHR.V  K.DSLS*PVLHPSDLILTR.G				
	XPA binding protein  XPA binding protein	1 <sub>GPN1</sub>					56.4 18.0	K.DSLS*PVLHPSDLILTR.G  K.DS*LSPVLHPSDLILTR.G				
	XPA binding protein  XPA binding protein  XRCC	1 <sub>GPN1</sub> 1 <sub>GPN1</sub> 1 <sub>GPN1</sub> 1 <sub>GPN1</sub>	S314		<b></b>	23.4		K.DSLS*PVLHPSDLILTR.G  K.DS*LSPVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASSA*PVSR.A				
	XPA binding protein  XPA binding protein  XRCC	1GPN1 1GPN1 1GPN1 1XRCC1	S314 S312			23.4	18.0	K.DSLS*PVLHPSDLILTR.G  K.DS*LS*PVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLOASSAASSÆ*PVSR.A  R. IODOCCEMOEDDVAGS**THEM**INSCELLGEDDVI DVIDEI ONCEYOLG				
	XPA binding protein  XPA binding protein  XRCC:  XRCC:  XRCC	1 Process of the second of the	\$314 \$312 T198\$226 \$518T519T523 \$241		····	23.4 11.6 11.5	18.0	K.DSLS*PVLHPSDLILTR.G  K.DS*LS*PVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASSA*PVSR.A  R. IDBOACELMSENDVAOS****INEST**INESECUAEDDNI BADEI DIEEFOOL  R.AIGSTSKPQES*PK.G				
	XPA binding protein  XPA binding protein  XRCC:  XRCC:  XRCC:  XRCC:	1GPN1 1GPN1 1XRCC1 1XRCC1 1XRCC1 1XRCC1	\$314 \$312 \$198\$226 \$518\$519\$523 \$241 \$199\$226			23.4 11.6 11.5 11.9	18.0 68.4 24.9	K.DSLS*PVLHPSDLILTR.G  K.DS*LSPVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASS&*PVSR.A  R. IGBOOGEEMIGENDVAGS**PINEM**PREELINEEDDNI BIJBEI BREEDON  R. AIGSTSKPQES*PK.G  R.INKTS**PVTASDPAGPSYAAATLQASSAASS&*PVSR.A				
	XPA binding protein  XPA binding protein  XRCC  XRCC  XRCC  XRCC  XRCC	1GPN1 1GPN1 1GPN1 1XRCC1 1XRCC1 1XRCC1 1XRCC1	\$314 \$312 T198\$226 \$518T519T523 \$241 \$199\$226 \$226		-	23.4 11.6 11.5 11.9	18.0 68.4 24.9 39.9 95.3	K.DSLS*PVLHPSDLILTR.G  K.DS*LS*PVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASSA*PVSR.A  R. INGONCESIACENDYADS**THEM**PRSCEUACEDDNI DAIGCI ONCEYADA  R.AIGSTSKPQES*PK.G  R.INKTS*PVTASDPAGPSYAAATLQASSAASSA*PVSR.A  K.TSPVTASDPAGPSYAAATLQASSAASSA*PVSR.A				
	XPA binding protein  XPA binding protein  XRCC  XRCC  XRCC  XRCC  XRCC	1GPN1 1GPN1 1TGPN1 1TGP	\$314 \$312 T198\$226 \$518T519T523 \$241 \$199\$226 \$226 Y515\$518T519		-	23.4 11.6 11.5 11.9 32.2 16.7 22.8	18.0 68.4 24.9 39.9 95.3 106.3	K.DSLS*PVLHPSDLLTR.G  K.DS*LS*PVLHPSDLLTR.G  R.INKT'SPVTASDPAGPSYAAATLQASSAASSA*PVSR.A  R. IODOCCEMPENDVAGS***PNEM***INSECUREDOM DIJDEI ONCECOME RAIGSTSKPQES*PK.G  R.INKTS*PVTASDPAGPSYAAATLQASSAASSA*PVSR.A  K.TSPVTASDPAGPSYAAATLQASSAASSA*PVSR.A  R. IODOCCEMPENDWAGS****INSECUREDOM DIJDEI ONCECOME R.				
	XPA binding protein  XPA binding protein  XRCC  XRCC  XRCC  XRCC  XRCC  XRCC	1GPN1 1GPN1 1GPN1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1	\$314 \$312 \$198\$226 \$518\$519\$523 \$241 \$199\$226 \$226 \$226 \$7515\$518\$519 \$34			23.4 11.6 11.5 11.9 32.2	18.0 68.4 24.9 39.9 95.3 106.3 19.1	K.DSLS*PVLHPSDLILTR.G  K.DS*LS*PVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASSA*PVSR.A  R. 10000000000000000000000000000000000				
	XPA binding protein  XPA binding protein  XRCC  XRCC  XRCC  XRCC  XRCC  XRCC	1GPN1 1GPN1 1GPN1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1 1XRCC1	\$314 \$312 T198\$226 \$518T519T523 \$241 \$199\$226 \$226 Y515\$518T519			23.4 11.6 11.5 11.9 32.2 16.7 22.8	18.0 68.4 24.9 39.9 95.3 106.3	K.DSLS*PVLHPSDLILTR.G  K.DSLS*PVLHPSDLILTR.G  R.INKT*SPVTASDPAGPSYAAATLQASSAASS&*PVSR.A  R. IDBOACELMICENDRVACS*PTINEM**IDECEMICEDDIN DIJDEI DICECOM  R.INKTS*PVTASDPAGPSYAAATLQASSAASS&*PVSR.A  K.TSPVTASDPAGPSYAAATLQASSAASS&*PVSR.A  R. IDBOACELMICENDRVAAGS**TINEM**IDECEMICEDDIN DIJDEI DICECOM  K.				

Peak Area %CV	White dot abundano	s-Significant cha	inge in pept	ide the			
-5 29 42 71		with the minimum					
3 85 5 >100 >10				RajiB			
Protein Name	Gene YBX1	Phosphosites \$176	F E E	£ £ £	Ascor 22.0	MOWSE 56.7	Sequence R.NYQQNYQNSESGEKNEGSES*APEGQAQQR.R
YB-1	YBX1	Y162S165			5.5	13.3	R.NYQQNY"QNS"ESGEKNEGSESAPEGQAQQR.R
YB-1	YBX1	S314			10.8	30.1	K.AADPPAENSS*APEAEQGGAE
YB-1	YBX1	S174			32.1	83.7	K.NEGS*ESAPEGQAQQR.R
YB-1	YBX1	<b>S</b> 313				12.5	K.AADPPAENS*SAPEAEQGGAE
YB-1	YBX1	Y162			17.3	31.6	R.NYQQNY"QNSESGEK.N
YB-1	YBX3	S102	ı,		30.6	42.9	R.S*VGDGETVEFDVVEGEK.G
	YBX1	S167	ı,		6.3	12.1	R.NYQQNYQNSES*GEK.N
YLP motif containing		\$398			22.4	64.4	R.GPASQFYITPSTSLS*PR.Q
YLP motif containing YLP motif containing		S1119			100.0	45.7	R.RAGS*QER.G
	YRDC	S394		•	7.8	12.9	R.GPASQFYITPS*TSLSPR.Q  R.LFRPPS*PAPAAPGAR.L
YTH domain containing 2		\$37 \$1090	• • •		100.0	34.5 40.8	R.VDGIPNDSS*DSEMEDK.T
YTH domain containing 2		\$1090 \$1089			22.0	49.7	R.VDGIPNDS*SDSEMEDK.T
YTH domain family 1	YTHDF1	S291		• •		35.3	K. ADVIDOGADE DA ADDDOGVA ADDDOGVOEDO DDOT
YY1 associated factor 2	YAF2	T8			1.6	30.1	K.SPT*RPK.R
YY1 associated factor 2	YAF2	S6			22.7	27.9	K.S'PTRPK.R
ZAK	MAP3K20	<b>S</b> 648			16.9	42.6	K.NFS*SLHLNSR.D
ZAP70	ZAP70	Y492Y493			12.9	43.1	K.ALGADDSY*Y*TAR.S
Zinc and ring finger 2	ZNRF2	S82			106.1	77.9	R.S*LGGAVGSVASGAR.A
Zinc and ring finger protein	ZNRF1	S123			100.0	67.4	R.AS*LADALPLHIAPR.W
Zinc and ring finger protein f		\$50\$53			8.1	62.8	R.S*VSS*VAGMGMDPSTAGGVPFGLYTPASR.G
Zinc and ring finger protein		S120S123			14.4	31.7	R.DGMLYLGS*RAS*LADALPLHIAPR.W
Zinc and ring finger protein		S50S62			6.7	35.1	R.S'VSSVAGMGMDPS'TAGGVPFGLYTPASR.G
Zinc and ring finger protein a		<b>S</b> 50			18.0	54.5	R.S'VSSVAGMGMDPSTAGGVPFGLYTPASR.G  R.SVS'SVAGMGMDPS'TAGGVPFGLYTPASR.G
Zinc and ring finger protein		\$52\$62 \$50\$52	=		5.1	34.5 57.6	R.S*VS*SVAGMGMDPSTAGGVPFGLYTPASR.G
Zinc finger and BTB domain containing 10		T646	•		48.0	59.0	R.NVNANLLAEAGT*SQDGGDAGTSHDFK.Y
Zinc finger antiviral protein				• • •	82.0	101.2	R.FLENGS*QEDLLHGNPGSTYLASNSTSAPNWK.S
Zinc finger antiviral protein	ZC3HAV1	S312			5.2	18.6	R.ARPPSGS*SK.A
Zinc finger antiviral protein	ZC3HAV1	S235			12.1	18.6	R.APS*SHRR.N
Zinc finger antiviral protein	ZC3HAV1	S271T273S275			46.8	15.2	R.S*CT*PS*PDQISHR.A
Zinc finger antiviral protein	ZC3HAV1	T347 <b>S</b> 355			9.3	42.8	R.FLENGSQEDLLHGNPGST*YLASNSTS*APNWK.S
Zinc finger antiviral protein	ZC3HAV1	S257			90.1	88.6	R.FFQGS*QEFLASASASAER.S
Zinc finger antiviral protein					4.0	56.1	R.FLENGSQEDLLHGNPGS*TYLASNSTSAPNWK.S
Zinc finger antiviral protein					16.3	44.3	R.FLENGS*QEDLLHGNPGSTYLASNSTS*APNWK.S
Zinc finger antiviral proteir  Zinc finger antiviral proteir					13.4	38.9	R.FLENGSQEDLLHGNPGS*TYLASNSTS*APNWK.S
Zinc finger antiviral protein			•		-0.4	31.3	R.SS*LGSLQTPEAVTTR.K  R.AS*LEDAPVDDLTR.K
Zinc finger antiviral protein					22.2	28.7	K.T*VFSPTLPAAR.S
Zinc finger antiviral protein					11.4	33.8	K.TVFS*PTLPAAR.S
Zinc finger antiviral protein					4.0	18.1	R.ARPPS*GSSK.A
Zinc finger CCCH-type antiviral protein					49.7	64.1	R.NLVPTTPGESTAPAQVSTLPQB*PAALSSSNR.A
Zinc finger CCCH-type containing 11	ZC3H11B	S761			9.2	33.0	R.RLSSAS*TGKPPLSVEDDFEK.L
Zinc finger CCCH-type containing 11A	ZC3H11A	S171			27.0	51.3	K.VESSENVPSPTHPPVVINAADDDEDDDDQFS*EEGDETK.T
Zinc finger CCCH-type containing 11.6					6.1	48.2	R.RLSSAS*T*GKPPLSVEDDFEK.L
Zinc finger CCCH-type containing 114			,		3.5	38.2	R.RLS*SASTGKPPLSVEDDFEK.L
Zinc finger CCCH-type containing 11A		S758S761	÷		13.6	56.3	R.RLS*SAS*TGKPPLSVEDDFEK.L
Zinc finger CCCH-type containing 13		S198			100.0	59.0	K.EVS*PEVVR.S
Zinc finger CCCH-type containing 13		\$207\$209	-		27.0	25.0	R.SKLS'PS'PSLR.K
Zinc finger CCCH-type containing 13  Zinc finger CCCH-type containing 13		S877			9.9	53.1	R.SLS*PSHLTEDR.Q  R.SAS*PY*PSHSLSS*PQR.K
Zinc finger CCCH-type containing 13		\$372Y374\$381 \$1456Y1462\$1			2.3	32.8	K.LDDAHSLGS*GAGEGY*EPIS*DDELDEILAGDAEK.R
Zinc finger CCCH-type containing 13		\$1456Y1462\$1 \$387			100.0	20.4	R.KQS*PPR.H
Zinc finger CCCH-type containing 13		\$387 \$77			18.4	28.7	R.S'PERPTGDLR.E
Zinc finger CCCH-type containing 13		S1014S1017			31.8	71.6	K.SKGDS*DIS*DEEAAQQSK.K
Zinc finger CCCH-type containing 13		T263S265			100.0	40.3	R.T*PS*PPPPIPEDIALGKK.Y
Zinc finger CCCH-type containing 13	ZC3H13	T317S318S325			10.2	16.3	R.ST*S*PAGQHHS*PISSR.H
Zinc finger CCCH-type containing 13	ZC3H13	\$370\$372\$380			22.3	16.8	R.S*AS*PYPSHSLS*SPQR.K
Zinc finger CCCH-type containing 13	ZC3H13	S372Y374S378			5.8	10.8	R.SAS"PY"PSHS"LSSPQR.K
Zinc finger CCCH-type containing 13	ZC3H13	\$372 <b>Y</b> 374 <b>\$</b> 380			1.3	23.3	R.SAS'PY'PSHSLS'SPQR.K
Zinc finger CCCH-type containing 13	ZC3H13	T134S137		•	50.1	23.5	K.ERT*PES*EEENVEWETNR.D

<-10 0 abundan	ots-Significant cha ce at 5%FDR of with the minimum	compared to the	given			
3 86 86 86 8100 PSW			RajiB			
>10 Protein Name Gene	Phosphosites		E E ,	Ascor	MOWSE	Sequence
Zinc finger CCCH-type containing 13 ZC3H13  Zinc finger CCCH-type containing 13 ZC3H13	S1453S1456S1			12.4	56.5	KLDDAHS'LGS'GAGEGYEPIS'DDELDEILAGDAEKR  R.DORPSS'PIR.H
Zinc finger CCCH-type containing 13 <sub>ZC3H13</sub>	\$643 \$1010\$1014\$1			56.9	59.0	K.S'KGDS'DIS'DEEAAQQSK.K
Zinc finger CCCH-type containing 13 ZC3H13	\$875	<del></del> -			47.1	R.S'LSPSHLTEDR.Q
Zinc finger CCCH-type containing 13 ZC3H13	S370S372S378			3.4	19.4	R.S'AS'PYPSHS'LSSPQR.K
Zinc finger CCCH-type containing 13 ZC3H13	S875S877		2	24.2	18.2	R.S'LS'PSHLTEDR.Q
Zinc finger CCCH-type containing 13 ZC3H13	<b>S</b> 110		7	7.8	18.6	R.NTEESSS*PVRK.E
Zinc finger DHHC domain containing \$ZDHHC5	S296S299		1	10.9	15.0	K.S'KGS'LEITESQSADAEPPPPPKPDLSR.Y
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub> Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>	<b>S</b> 423			21.2	41.6	K.SFHFDPLSS*GSR.S
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>				1.6	64.3	R.SSS'LKS'AQGTGFELGQLQSIR.S  R.SS'S'LKSAQGTGFELGQLQSIR.S
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>				15.4	100.5	K.S*AQGTGFELGQLQSIR.S
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>	<b>S</b> 422			37.2	36.0	K.SFHFDPLS*SGSR.S
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>	<b>S</b> 425		9	0.1	37.9	K.SFHFDPLSSGS*R.S
Zinc finger DHHC domain containing 5 <sub>ZDHHC5</sub>	S429T436	-	1	1.9	50.0	R.SSS'LKSAQGT'GFELGQLQSIR.S
Zinc finger FYVE domain containing 26 ZFYVE26	S1762			5.2	79.6	R.S'PSAEFSPAAPPGISSIHSPSLR.E
Zinc finger FYVE domain containing 26 ZFYVE26				7.6	55.0	R.SPS'AEFSPAAPPGISSIHSPSLR.E
Zinc finger protein 106 ZNF106  Zinc finger protein 106 ZNF106	\$1370 \$1025\$1026			78.7	53.1	R.AAHVPENS'DTEQDVLTVKPVRK.V  R.ATGDGS'S'PELPSLER.K
Zinc finger protein 183 RNF113A			• •	86.4	27.0	R.KRPACDPEPGES*GS*S*DEGCTVVRPEK.K
Zinc finger protein 183 RNF113A		<del></del>	_	88.2	55.8	KAAYGDLS'S'EEEEENEPESLGWYK.S
Zinc finger protein 183 RNF113A	S253		8	37.6	107.2	R.YGVYEDENYEVGS*DDEEIPFK.C
Zinc finger protein 183 RNF113A	Y80S84		2	25.5	13.7	K.AAY*GDLS*SEEEENEPESLGWYK.S
Zinc finger protein 206 ZSCAN10	S333	<b></b>	-	0.2	10.8	K.SFGRS*SILK.L
Zinc finger protein 22 ZNF22	<b>S</b> 49	•	4	13.5	22.1	R.S'LDDKPYK.C
Zinc finger protein 261 ZMYM3  Zinc finger protein 261 ZMYM3	S256T257				28.6	R.RAEPPKPEVVDS*T*ESIPVSDEDSDAMVDDPNDEDFVPFRPR.R
Zinc finger protein 261 ZMYM3  Zinc finger protein 261 ZMYM3	\$957\$960 \$263\$267			16.5	18.5	K.ASSDLCDLVS*NQS*AEGLLEDCDLFGPAR.D  R.RAEPPKPEVVDSTESIPVS*DEDS*DAMVDDPNDEDFVPFRPR.R
Zinc finger protein 262 ZMYM4	S122			15.8	46.2	R.VTQHES*DNENEIQIQNK.L
Zinc finger protein 262 ZMYM4	S1542S1547			22.3	46.2	K.SEDS'DVELS'D
Zinc finger protein 262 ZMYM4	\$1088T1089		8	3.9	32.2	K.DQGS*T*YSGDLESEAVSTPHSWEEELNHYALK.S
Zinc finger protein 262 ZMYM4	S1088S1091	Ė	1	16.8	11.1	K.DQGS*TYS*GDLESEAVSTPHSWEEELNHYALK.S
Zinc finger protein 265 ZRANB2	S153		1	112.6	109.7	K.EVEDKES*EGEEEDEDEDLSK.Y
Zinc finger protein 265 ZRANB2	\$305\$307		5	53.8	36.9	R.S'RS'PESQVIGENTK.Q
Zinc finger protein 265 ZRANB2	S188			16.5	77.4	R.ES*DGEYDEFGRKK
Zinc finger protein 265 ZRANB2	T303S305S307				29.7	R.T'RS'PESQVIGENTK.Q
Zinc finger protein 265 ZRANB2	\$266\$267				12.4	R.SHRGS'S'SPR.K
Zinc finger protein 265 ZRANB2	<b>S</b> 307		3	37.8	77.4	R.S'PESQVIGENTK.Q
Zinc finger protein 265 ZRANB2	T303S307S310		1	12.3	11.5	R.T'RSRS'PES'QVIGENTK.Q
Zinc finger protein 265 ZRANB2	\$305\$307\$310	<b>—</b>	1	10.5	11.9	R.TRS'RS'PES'QVIGENTK.Q
Zinc finger protein 272 ZNF460  Zinc finger protein 272 ZNF460	T492	=		9.8	19.6	R.RSPLT*RH
Zinc finger protein 272 ZNF460  Zinc finger protein 28 (KOX 24) ZNF28	\$489 \$427			15.8	14.2	RRS*PLTRH  RCKS*HLERH
Zinc finger protein 289, ID1 regulated ARFGAP:				3.5	17.2	R.SSVSHS*VLSEMQVIEQETPVSAK.S
Zinc finger protein 289, ID1 regulated ARFGAP					15.3	K.
Zinc finger protein 289, ID1 regulated ARFGAP	<sup>2</sup> S146		<b>1</b> 3	36.2	18.2	R.HGTDLWIDNMSSAVPNI-S*PEKK.D
Zinc finger protein 295 ZBTB21	<b>S</b> 345		1	13.6	84.5	R.SLS*MDSQVPVYSPSIDLK.S
Zinc finger protein 316 ZNF316	S112		<u> </u>	100.0	14.1	K.S'PVLQEK.G
Zinc finger protein 318 ZNF318  Zinc finger protein 318 ZNF318	S136				59.2	R.S*PGLCSDSLEK.S
Zinc tinger protein 318 ZNF318  Zinc finger protein 318 ZNF318	\$173 \$79\$81		<del></del>		28.2	RLGS'PVDNLEDMDRDDLTDDSVFTR.S  RRVS'PS'PPR.A
Zinc finger protein 318 ZNF318	S89S91		<u></u>		24.7	R.RGS*PS*PPR.G
Zinc finger protein 318 ZNF318	S214	=			45.5	R.YISQEEGPLS*PFLGQLDEDYR.T
Zinc finger protein 318 ZNF318	S69S71		1	100.0	18.1	R.RAS*PS*PPR.G
Zinc finger protein 318 ZNF318	T686S698	į	2	24.7	16.7	R.EAHHSNT*HSPEVSHPHPPS*PVDPYLLTK.N
Zinc finger protein 318 ZNF318	S684S698		. 2	26.3	16.9	R.EAHHS"NTHSPEVSHPHPPS"PVDPYLLTK.N
Zinc finger protein 318 ZNF318	Y205S214				32.0	R.Y'ISQEEGPLS'PFLGQLDEDYR.T
Zinc finger protein 330 ZNF330  Zinc finger protein 36 ZKSCAN	S291	===			143.7	R.KDS*DTESSDLFTNLNLGR.T  R.ALPAAHIPAPPHEGS*PR.D
Zinc finger protein 36 C3H type like 2 ZFP36L2					34.1	R.ALPAAHIPAPPHEGS*PR.D  R.RHS*ASNLHALAHPAPSPGSCSPK.F
Zinc finger protein 36 C3H type like 2 ZFP36L2		<del></del>		19.3	17.0	R.RHSAS*NLHALAHPAPSPGSCS*PK.F

Peak Area %CV	White do	ts-Significant cha	inge in pepti	ide the			
.5 25 42 71	timepoint PSM	with the minimum					
3 86 5 >100 >100			CarT	RajiB			
Protein Name Zinc finger protein 36 C3H type like 2		Phosphosites S59	5 % B	£ £ £	Ascor 4.6	MOWSE 15.7	Sequence R.RHSAS*NLHALAHPAPSPGSCSPK.F
Zinc finger protein 363		S257			100.0	25.5	R.RIS*LDQQ
Zinc finger protein 40	HIVEP1	S536			32.1	83.5	K.SSFTPS*SPENVIGDFLLQDR.S
Zinc finger protein 40	HIVEP1	S537			15.2	55.3	K.SSFTPSS*PENVIGDFLLQDR.S
Zinc finger protein 40	HIVEP1	T569S577		• • •	6.4	15.1	K.VVVHHVT*VSPLRTDS*PK.A
Zinc finger protein 444	ZNF444	S104			33.0	63.2	R.QPQSGEEAVALLEELWGPAAS*PDGSSATR.V
Zinc finger protein 483	ZNF483	T404S406			17.5	18.0	R.RST*LS*R.R
Zinc finger protein 483	ZNF483	\$403\$406			13.9	12.3	R.RS'TLS'R.R
Zinc finger protein 581		S30S36				49.5	R.S*PEPGPS*SSIGSPQASSPPRPNHYLLIDTQGVPYTVLVDEESQR.
Zinc finger protein 581		S45T58			12.1	53.2	R.SPEPGPSSSIGSPQAS*SPPRPNHYLLIDT*QGVPYTVLVDEESQR.
Zinc finger protein 581		S45S46			7.1	24.5	R.SPEPGPSSSIGSPQAS*S*PPRPNHYLLIDTQGVPYTVLVDEESQR.
Zinc finger protein 581  Zinc finger protein 581		Y53T58			-2.7	18.9	R.SPEPGPSSSIGSPQASSPPRPNHY*LLIDT*QGVPYTVLVDEESQR.
Zinc finger protein 592		\$46T58 \$142\$145\$146	=		-0.4	40.6	R.SPEPGPSSSIGSPQASS*PPRPNHYLLIDT*QGVPYTVLVDEESQR.  C  K.SEPLPTFNQFS*PIS*S*PEPEDPIKDNGFGIKPK.H
Zinc finger protein 592		\$142\$145\$146 \$689			9.9	42.0	K.GLTSGS*ASPPPPALPLYPDPVR.L
Zinc finger protein 592		T137S145S146	•		10.1	21.7	K.SEPLPT*FNQFSPIS*S*PEPEDPIKDNGFGIKPK.H
Zinc finger protein 592		S691			7.3	49.4	K.HGLTSGSAS*PPPPALPLYPDPVR.L
Zinc finger protein 592	ZNF592	S132T137S142	•			21.5	K.S*EPLPT*FNQFS*PISSPEPEDPIKDNGFGIKPK.H
Zinc finger protein 609	ZNF609	S842Y845S849			22.1	58.7	K.TNS*PAY*SDIS*DAGEDGEGKVDSVK.S
Zinc finger protein 609	ZNF609	S842S846S849			17.8	75.8	K.TNS*PAYS*DIS*DAGEDGEGKVDSVK.S
Zinc finger protein 609	ZNF609	Y845S846S849			8.4	12.7	K.TNSPAY"S"DIS"DAGEDGEGKVDSVK.S
Zinc finger protein 638	ZNF638	\$508\$510		•	32.7	12.8	R.S*RS*PMHYMYRPR.S
Zinc finger protein 638	ZNF638	<b>S</b> 552		• • • •	100.0	16.1	R.IRNPFRGS*PK.C
Zinc finger protein 646	ZNF646	S930			54.7	123.2	R.S*PPLQLSEAELLNQLQR.E
Zinc finger protein 646	ZNF646	S936			8.2	89.0	R.SPPLQLS*EAELLNQLQR.E
Zinc finger protein 687	ZNF687	S251			42.3	15.2	K.ATDIPAS*ASPPPVAGVPFFK.Q
Zinc finger protein 687	ZNF687	S253			13.4	36.3	K.ATDIPASAS*PPPVAGVPFFK.Q
Zinc finger protein 687		S1057	<u> </u>		100.0	25.2	R.HGLQLGAQS*PGR.G
Zinc finger protein 687		T191S197				11.9	R.EGALT*PPPFPS*SFELAQENGPGMQPPVSSPPLGALK.Q
Zinc finger protein 687		S198S215	<u> </u>		17.8	11.1	R.EGALTPPPFPSS*FELAQENGPGMQPPVSS*PPLGALK.Q
Zinc finger protein 740  Zinc finger protein 800		S44			100.0	50.4	R.AGS*PDVLR.C  R.DSITPDIATKPGQPLFLDS*ISPK.K
Zinc finger protein 99	ZNF8UU	\$334 \$2			82.1	38.8	M#S*FWSEK.C
Zinc finger protein A20	TNEAIP3	S381		Ξ	46.9	13.2 54.3	R.EGHAQNPMEPSVPQLS*LMDVK.C
Zinc finger protein A20		S376S381			100.0	45.0	R.EGHAQNPMEPS*VPQLS*LMDVK.C
Zinc finger protein A20	TNFAIP3	T454			7.2	30.2	R.GEAYEPLAWNPEEST*GGPHSAPPTAPSPFLFSETTAMK.C
Zinc finger protein A20	TNFAIP3	S645			32.1	13.9	K.VS*PTASR.F
Zinc finger protein A20	TNFAIP3	<b>S</b> 459			23.2	39.5	R.GEAYEPLAWNPEESTGGPHS*APPTAPSPFLFSETTAMK.C
Zinc finger protein A20	TNFAIP3	T463			7.1	45.2	R.GEAYEPLAWNPEESTGGPHSAPPT*APSPFLFSETTAMK.C
Zinc finger protein A20	TNFAIP3	<b>S</b> 453			4.2	45.9	R.GEAYEPLAWNPEES*TGGPHSAPPTAPSPFLFSETTAMK.C
Zinc finger protein A20	TNFAIP3	S573S575			37.5	37.8	R.S*PS*PHSCHR.A
Zinc finger protein A20	TNFAIP3	\$453\$471			10.1	17.0	R.GEAYEPLAWNPEES*TGGPHSAPPTAPSPFLFS*ETTAMK.C
Zinc finger protein A20	TNFAIP3	\$459\$466			12.8	14.6	R.GEAYEPLAWNPEESTGGPHS*APPTAPS*PFLFSETTAMK.C
Zinc finger protein A20		T454S459			1.5	35.3	R.GEAYEPLAWNPEEST*GGPHS*APPTAPSPFLFSETTAMK.C
Zinc finger protein A20		S453S459		•	6.4	30.0	R.GEAYEPLAWNPEES*TGGPHS*APPTAPSPFLFSETTAMK.C
Zinc finger protein A20		S466				19.2	R.GEAYEPLAWNPEESTGGPHSAPPTAPS*PFLFSETTAMK.C
Zinc finger protein A20		\$453T454			15.3	30.1	R.GEAYEPLAWNPEBS*T*GGPHSAPPTAPSPFLFSETTAMK.C
Zinc finger protein A20		S220			23.6	26.1	R.SLES*GSNFAPLK.V
Zinc finger protein A20		T454S466		-	13.5	21.9	R.GEAYEPLAWNPEEST*GGPHSAPPTAPS*PFLFSETTAMK.C
Zinc finger protein A20  Zinc finger protein AEBP2		S453T463		=	0.6	37.1	R.GEAYEPLAWNPEES*TGGPHSAPPT*APSPFLFSETTAMK.C
Zinc finger protein hRit1 alph		S206			49.2	24.9	R.RGS*LEMSSDGEPLSR.M  R.ELAGNSS*TPPPVS*PGR.G
Zinc finger protein hRit1 alph		S375S381			26.8	51.2	R.ELAGNSST*PPPVS*PGR.G
Zinc finger protein hRit1 alph		T376S381 S129	•		14.7	57.1	R.KVSEPVEIGIQVTPDEDDHLLS*PTK.G
Zinc finger protein hRit1 alph		\$129 \$496\$497			21.9	43.0	R.SDDGLSAAS*S*PEPGTSELAGEGLK.A
Zinc finger protein hRit1 alph		S398			100.0	43.7	R.LLNPFQPS*PK.S
Zinc finger protein hRit1 alph		T406T417			54.5	24.8	K.SPFLST*PPLPPMPPGGT*PPPQPPAK.S
Zinc finger protein hRit1 alph		S493S496			6.6	25.6	R.SDDGLS*AAS*SPEPGTSELAGEGLK.A
Zinc finger protein hRit1 alph	BCL11B	\$493\$496\$497			1.1	25.5	R.SDDGLS*AAS*S*PEPGTSELAGEGLK.A
Zinc finger protein hRit1 alph	BCL11B	\$401T417			56.4	19.0	K.S'PFLSTPPLPPMPPGGT'PPPQPPAK.S
Zinc finger protein hRit1 alph	BCL11B	S401	ij		30.6	19.4	K.S*PFLSTPPLPPMPPGGTPPPQPPAK.S
Zinc finger protein hRit1 alph	BCL11B	\$488\$493\$496			25.2	30.6	R.S*DDGLS*AAS*S*PEPGTSELAGEGLK.A

Peak Are	ea %CV	White dots-Significant change in peptide abundance at 5%FDR compared to the										
<-10 -5 -3	0 29 42 71		eat 5% FDR o with the minimum									
3 5 >10	86 >100			CarT	RajiB							
_	Protein Name		Phosphosites	5 4 5	9 K K	Ascor	МО					
Zino	finger protein hRit1 alph	BCL11B	\$401\$405T417	•••		42.2	14.6					
	, subfamily 1A, member 1		S409			42.6	45.					
Zinc finger protein	, subfamily 1A, member 1	IKZF1	S17T23	Ţ.		11.7	39.					
	, subfamily 1A, member 1		S361S364			32.1	69.0					
	, subfamily 1A, member 1		S445		<del></del>	34.4	57.0					
	, subfamily 1A, member 1		S364			8.7	49.9					
Zinc finger protein	, subfamily 1A, member 1	IKZF1	S21T23			1.0	48.9					
Zinc finger protein	, subfamily 1A, member 1	IKZF1	S361			9.2	71.3					
	, subfamily 1A, member 1		S63			39.7	47.					
Zinc finger protein	, subfamily 1A, member 1	IKZF1	S17S21T23			42.7	45.4					
		IKZF2	<b>S</b> 56	•		65.7	63.4					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	\$369T372\$375			59.6	72.2					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S433			20.3	27.					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S369	•		100.0	17.6					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	<b>S</b> 40			17.0	20.					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S31S40			20.6	35.2					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	T30S40			7.4	19.6					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S78S79			50.0	62.0					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	\$32\$40	·		7.3	39.0					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S23S40	<b>F</b>		23.7	32.6					
Zinc finger protein	, subfamily 1A, member 2	IKZF2	S23T30				28.4					
	, subfamily 1A, member 2		S23				27.9					
Zinc finger protein	, subfamily 1A, member 3	IKZF3	S378S382S386		-		12.2					
Zinc fin	nger, AN1-type domain 2B	ZFAND2B	S183			18.6	110					
Zinc fin	nger, AN1-type domain 2B	ZFAND2B	T185			6.0	78.8					
Zinc finger, Co	CHC domain containing 6	ZCCHC6	T13			100.0	12.8					
Zinc finger, CW typ	e with coiled-coil domain	MORC2	S681			50.7	32.0					
Zinc finger, CW typ	e with coiled-coil domain	MORC2	S553			100.0	17.0					

Zinc finger, CW type with coiled-coil domain MORC2 \$715S717

Zinc finger, FYVE domain containing 19 ZFYVE19 \$344

Zinc finger, FYVE domain containing 19 ZFYVE19 S134

Znf HX ATRX Y1009S1012S1

Znf HX ATRX T1989S1995

Znf HX ATRX S1990S1991

Znf HX ATRX T1346S1352

Znf HX ATRX \$1348\$1352

Znf HX ATRX S729S731

Znf HX ATRX T724S731

Znf HX ATRX Y1009S1011S10

Znf HX ATRX T1989Y2002

Znf HX ATRX S1991S1995

Znf HX ATRX S1996Y2002

ZNF635 POGZ S746

Zyxin ZYX \$308

Zyxin ZYX \$344

Zuotin related factor 1 DNAJC2 S49

Zuotin related factor 1 DNAJC2 S47

Zuotin related factor 1 DNAJC2 847S49

Znf HX ATRX \$101181012810

Znf HX ATRX Y1009S1011S10

K.S\*PFLS\*TPPLPPMPPGGT\*PPPQPPAK.S R.S\*GLIYLTNHIAPHAR.N

R.S\*NHS\*AQDSAVENLLLLSK.A R.AASENS\*QDALR.V R.SNHS\*AQDSAVENLLLLSK.A

R.S\*NHSAQDSAVENLLLLSK.A K VETOS\*DEENGR A

K.LEMQS\*DEECDRKPLSR.E R.IERPIS\*RET\*ADS\*HENNMDGPISLIRPK.S

R.KQS\*PAYMK.E

K.RT\*KDR.G R.SVAVS\*DEEEVEEEAER.R

R.S\*PPLPAVIR.N

K.WS\*PPQNYK.K

K.KDSNELS\*DS\*AGEEDSADLKR.A

K.MEQQY\*ESS\*S\*DGTEKLPER.E

R.HKLT\*VSDGES\*GEEKK.T

R.HKLTVS\*DGES\*GEEKK.T

K.MEQQYES\*S\*S\*DGTEKLPER.E

K.QSETVDQNS\*DS\*DEMLAILK.E

K.QSET\*VDQNSDS\*DEMLAILK.E

K.MEQQY\*ES\*SS\*DGTEKLPER.E

K.MEQQY\*ES\*S\*SDGTEKLPER.E

R.KMS\*VMGR.Q

R.NASAS\*FQELEDKK.E

R.NAS\*ASFQELEDK.K

R.NAS\*AS\*FQELEDKK.E

R.S\*PGAPGPLTLK.E

K.LGHPEALSAGTGS\*PQPPSFTYAQQR.E

K.AT\*SSSNPSSPAPDWY\*KDFVTDADAEVLEHSGK.M

K.ATSS\*SNPS\*SPAPDWYKDFVTDADAEVLEHSGK.M

K.ATSSSNPSS\*PAPDWY\*KDFVTDADAEVLEHSGK.M

K.AT\*SSSNPS\*SPAPDWYKDFVTDADAEVLEHSGK.M

K.ATS\*S\*SNPSSPAPDWYKDFVTDADAEVLEHSGK.M

R.LPDS\*DDDEDEETAIQR.V

100.0 17.6

133.0 99.6

67.4 30.2

2.3 36.6

5.9 39.7

20.3 58.4

10.2 41.7

61.1 71.1

9.3 18.1

10.1 17.6

30.6 33.5

4.3 14.2

10.3 74.7

100.0 15.8

12.1 55.7

100.0 39.3

54.8 40.8

39.3 73.0

15.7 44.6

-2.0 25.6

13.8 61.9

19.3

29.4 62.4 K.ES\*PPVSDT\*PDEGDEPMPIPEDLSTTSGGQQSSK.S

K.ESPPVS\*DT\*PDEGDEPMPIPEDLSTTSGGQQSSK.S

K.ES\*PPVS\*DT\*PDEGDEPMPIPEDLSTTSGGQQSSK.S

R.EHSNMAIDLTSSTPNGQHAS\*PSHMTSTNSVK.L R.EHSNMAIDLTS\*STPNGQHAS\*PSHMTSTNSVK.L R.EHSNMAIDLT\*SSTPNGQHAS\*PSHMTSTNSVK.L R.GHDEGS\*S\*LEEPLIESSEVADNR.K R.EHSNMAIDLTSS\*TPNGQHAS\*PSHMTSTNSVK.L R.EHS\*NMAIDLTSSTPNGQHAS\*PSHMTSTNSVK.L R.EHS\*NMAIDLT\*SSTPNGQHASPSHMTSTNSVK.L R.EHS\*NMAIDLTSSTPNGQHASPSHMTSTNSVK.L R.GLS\*PNNS\*GHDS\*T\*DT\*DS\*NHEER.Q R.SPS\*WTAPPVIALQNGLSEDEALQR.A R.SPSWT\*APPVIALQNGLSEDEALQR.A