

Peak Area		%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM													
				CarT		RajB		Ascor	MOWSE	Sequence							
		Protein Name	Gene	Phosphosites													
		A6RP TWF2	Y309										175.4	111.2	K.KIEIGDGAELTAFLYV	DEVHPK.Q	
		ABL interactor 1	AB1	Y213									22.0	50.0	K.TLEPVKPTVPNDYV	MTSPAR.L	
		ABL interactor 2	AB2	Y213									31.4	49.1	R.TLEPVRPPVVPNDYV	VPSPTR.N	
		Actin alpha, cardiac muscle	ACTB	Y93									42.4	27.6	K.IWHHTFYV	NELR.V	
		Actin alpha, cardiac muscle	ACTB	Y242									-0.2	66.0	R.SYVLELPGDQVITIGNR	.F	
		Actin binding LIM protein 1	ABLIM1	Y373									11.5	19.8	R.TSSIESIYRPGSSIPGSPGHTV	AK.V	
		Actin binding LIM protein 1	ABLIM1	Y406									12.3	15.9	K.AYDIERPDLITYV	EPFYTSGYDDK.Q	
		Actin gamma 1	ACTB	Y294									31.5	102.9	K.DLYVANTVLSGGTTMYPGIADR	.M	
		Actin gamma 1	ACTB	Y198									30.2	43.3	R.GYV	SFTTAER.E	
		Actin gamma 1	ACTB	Y218									48.5	47.0	K.LCYVVALDFEQEEMATAASSSLEK	.S	
		Actin related protein 10	ACTR10	Y4									105.1	119.3	M.PLYV	EGLSGGEEK.T	
		Actin related protein 3	ACTR3	Y109									56.5	27.6	R.AEPEDHYV	FLLTEPLTPENR.E	
		Acyl CoA synthetase long chain family member 4	ACSL4	Y582									26.0	63.4	K.LQAGEYV	VSGLK.V	
		ADAM9	ADAM9	Y769									100.0	26.5	R.EVPIV	ANR.F	
		Adenosine deaminase	ADA	Y29									13.0	46.5	K.VELVHLDGSIKPEITYV	YGR.R	
		Aldolase 3	ALDOC	Y358									35.4	56.8	K.YEGSGEDGGAQAQSLY	IANHY.-	
		ALS2CR7	CDK14	Y63									16.9	34.4	K.LGEGSYV	ATVYK.G	
		Angiotensin II receptor associated protein	AGTRAP	Y133									10.9	39.7	R.SAYV	QTIDSAEAPDPFAVPEGR.S	
		Ankyrin repeat domain 13	ANKRD13	Y485									136.4	77.7	R.NVHLQDEDYV	EIMQFAIQSSLSSR.S	
		Annexin II	ANXA2	Y24									12.2	80.8	K.LSLEGDHSTPPSAVY	GSVK.A	
		Annexin VI	ANXA6	Y30									38.4	64.7	R.GSHDFPGFDNQDAEALY	TAMK.G	
		Annexin VI	ANXA6	Y302									22.5	20.1	K.SLYV	SMIK.N	
		ARF2/3 protein complex subunit p21	ARPC3	Y47									13.9	62.3	K.DTDIVDEALY	YFK.A	
		Ataxin 2 domain protein	ATXN2L	Y349									100.0	24.1	K.VYV	IPLPOR.V	
		ATP binding cassette 50	ABCF1	Y378									100.0	31.1	K.VYV	EELR.A	
		ATP citrate lyase	ACLY	Y682									74.7	68.6	R.TTDGVYV	EGVAIGDGRYPGTFMDHVLRY	
		ATP citrate lyase	ACLY	Y131									100.0	55.0	R.EGDYV	FLFHGGVDVGDVDAK.A	
		ATP1A1	ATP1A1	Y260									16.9	30.9	R.GIVYV	TGDR.T	
		BCR	BCR	Y177									100.0	50.9	K.GHQGPQGADEKPYV	VNVEFHER.G	
		BCR downstream signaling 1	STAP1	Y168									15.9	46.1	K.KEPTEDYV	VDVLNPMFACFYTVSR.K	
		BH3 interacting domain death agonist	BID	Y54									40.7	44.3	R.ELDALGHELPLVAPQWEGYV	DELQTDGNR.S	
		BLK	BLK	Y501									100.0	23.6	R.QYV	ELQP.-	
		BLK	BLK	Y187									22.0	79.0	R.QLDEGGYV	YISPR.I	
		BLK	BLK	Y389									32.1	91.9	R.IIDSEYV	TAQEGAK.F	
		BLK	BLK	Y188									16.9	88.8	R.QLDEGGYV	YISPR.I	
		Bruton's tyrosine kinase	BTX	Y551									16.9	86.8	R.YVLDDYV	TSSVGSK.F	
		Bruton's tyrosine kinase	BTX	Y361									26.9	62.8	K.HLFTSTPELNV	YHOHNSAGLSRL.L	
		Bruton's tyrosine kinase	BTX	Y223									16.0	54.9	K.VVALYV	DYMPMINANDQLR.K	
		Bruton's tyrosine kinase	BTX	Y225									7.3	54.7	K.VVALYV	DYMPMINANDQLR.K	
		Bruton's tyrosine kinase	BTX	Y344									6.2	39.2	R.HYVVCSTPQSQYV	YLAEK.H	
		Bruton's tyrosine kinase	BTX	Y334									55.5	48.1	R.HYV	WCSTPQSQYVLAEK.H	
		C20ORF77 protein	RPRD1B	Y185									5.2	61.8	R.TFQIQIEEDDDYV	PGSYVSPDPSAGPLLTELK.A	
		C4orf14 protein	NOA1	Y77									95.3	31.0	R.FLPEYV	ILDEPQPTR.E	
		Calmodulin 1	CALM2	Y100									58.0	85.0	R.VFDKDGNGYV	ISAAELR.H	
		Calmodulin 1	CALM3	Y139									50.6	43.3	R.EADIDGQGVNV	YEEFQMMTAK.-	
		Calumenin	CALU	Y47									3.0	26.2	K.VHNDQAQSFYV	DHDAFLGAEAAKT	
		Cask-interacting protein 2	CASKIN2	Y253									27.4	123.7	R.NTVV	NOTALDIWQFTTSQASR.E	
		CBL	CBL	Y674									24.1	52.1	K.IKPSSSANAIV	YSLAARPLVPK.L	
		CBL	CBL	Y667Y674									14.0	34.7	K.IKPSSSANAIV	YSLAARPLVPK.L	
		CblB	CBLB	Y665Y672									32.0	37.8	K.VFSNGHLGSEEVY	VPVPRSLPPPVTLLPSIK.C	
		CblB	CBLB	Y885Y889									7.9	26.9	K.TNRTV	SQDYV	DQLPSCSDGSOAPARPPKPRPR.R
		CblB	CBLB	Y889									30.5	33.0	R.TSQDYV	DQLPSCSDGSOAPARPPKPRPR.R	
		CblB	CBLB	Y665									9.2	16.8	K.VFSNGHLGSEEVY	VPVPRSL	
		CD19	CD19	Y508									100.0	42.2	R.GILYV	AAPQLR.S	
		CD19	CD19	Y348									28.4	41.5	K.VTPPPGSGPONQYV	GNVLSLPTTSLGLRA	
		CD2 associated protein	CD2AP	Y361									17.8	24.4	K.YV	FSLKPEEK.D	
		CD28	Y191T195										21.1	27.7	R.LLHSDYV	MMNMTPR.R	
		CD28	Y191										19.3	40.1	R.LLHSDYV	MMNMTPR.R	
		CD28	Y209										37.1	21.1	R.KHYQYV	APPR.D	
		CD28	Y189Y191										67.1	31.8	R.LLHSDYV	MMNMTPR.R	
		CD28	Y218										100.0	35.7	R.DFAAYV	RS	
		CD28	Y206										27.3	19.8	R.KHYV	QPYAPPR.D	

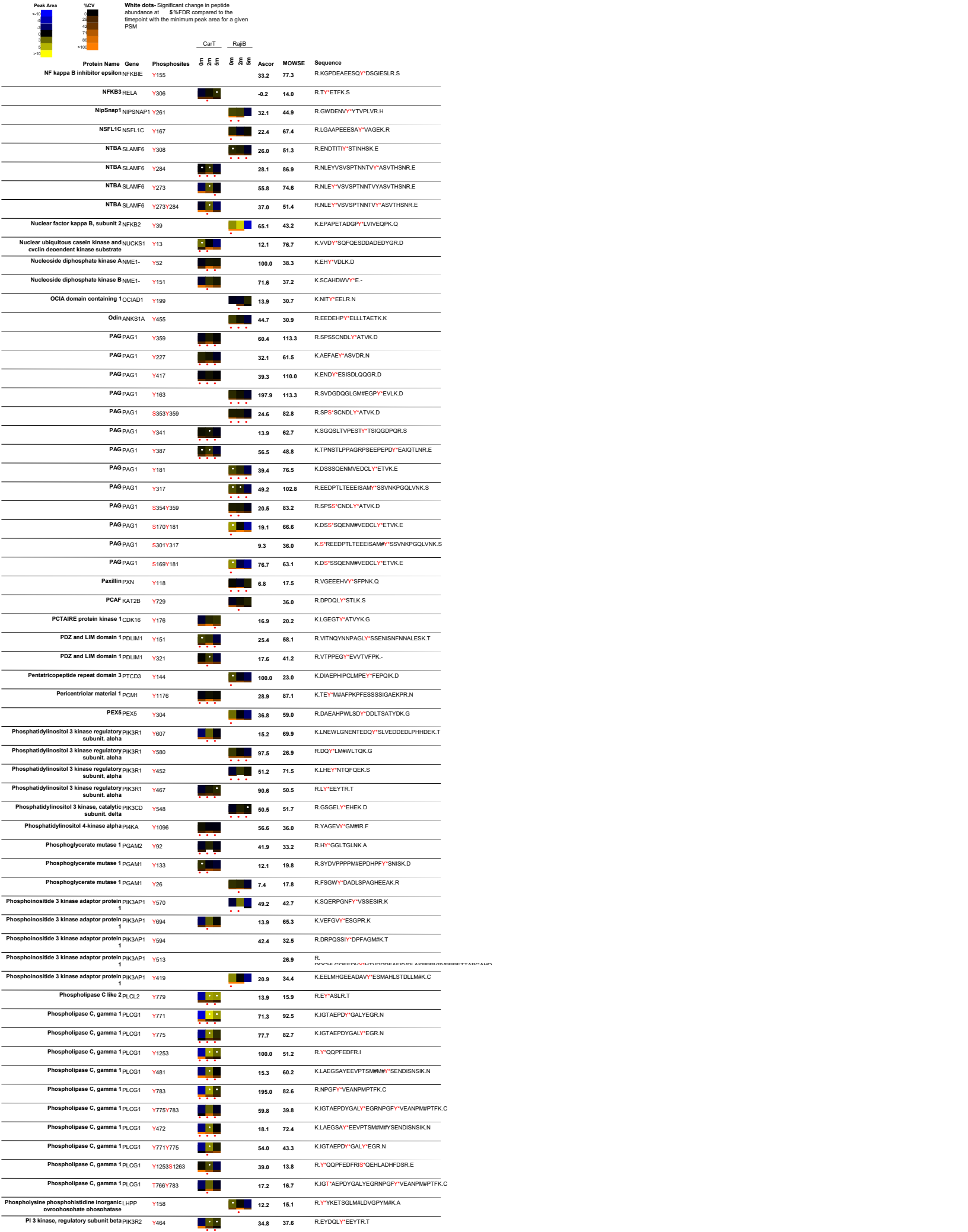
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		Protein Name	Gene	Phosphosites						
		CD3 gamma	CD3G	Y160				80.6	50.1	K.QTLLPNDQLY*QPLKDR.E
		CD3 gamma	CD3G	Y171				13.9	13.5	R.EDDQY*SHLQGNQLR.R
		CD31	PECAM1	Y713				27.6	61.0	K.DTETVY*SEVR.K
		CD37	CD37	Y274				100.0	36.4	R.NLDHVVY*NRL
		CD3E	CD3E	Y199				39.9	49.3	R.DLY*SGLNQR.R
		CD3E	CD3E	Y188				100.0	41.2	K.ERPPPVPNPDY*EPIRK.G
		CD5	CD5	S439Y453				24.1	24.2	R.S*HAENPTASHVDNEY*SQPPR.N
		CD5	CD5	Y453				25.2	18.3	R.SHAENPTASHVDNEY*SQPPR.N
		CD7	CD7	Y222				38.2	38.3	R.DKNSAACVVY*EDMSHSR.C
		CD84	CD84	Y262				39.8	57.7	K.TIV*TYIMASR.N
		CD84	CD84	Y299				32.3	94.6	K.EEPVNTVY*SEVQFADK.M
		CD84	CD84	Y324				12.1	63.9	K.ASTQDSKPPGTSSY*EIVI.-
		CD84	CD84	Y279				112.4	34.0	R.IY*DEILQSK.V
		CDC2	CDK1	Y15				16.9	76.3	K.IGEGTY*GVVYK.A
		CDC2	CDK1	T14Y15				69.8	74.1	K.IGEGTY*GVVYK.A
		CDC2	CDK1	Y19				33.2	47.9	K.IGEGTYGVVY*K.A
		CDC37	CDC37	Y298				58.0	38.4	R.LGPGGLDPVEVY*ESLPEELQK.C
		CDV3 homolog	CDV3	Y190				39.3	83.9	R.KTPQGPPEIY*SDTQFPSLQSTAK.H
		CDV3 homolog	CDV3	Y244				100.0	102.8	K.LQLDNGY*AVLENQK.S
		CDV3 homolog	CDV3	Y95				16.9	21.1	K.EVDY*SGLR.V
		Centaurin delta 2	ARAP1	Y497				16.4	56.5	K.HY*SVVLPTVSHSGFLYK.T
		Centaurin delta 2	ARAP1	Y231				11.5	20.9	R.LFPEFDSDY*DEVP EEGPGAPAR.V
		Chaperonin containing T complex polypeptide 1 subunit 4	CCT4	Y269				20.7	30.7	K.TDM#DNQIVSDY*AQMIDR.V
		Chaperonin containing T complex polypeptide 1, subunit 7	CCT7	Y263				40.0	88.2	R.VHTVEDY*QAIVDAEWNLIDYK.L
		Chemokine orphan receptor 1	ACKR3	Y354				32.1	97.9	R.VSETEY*SALEQSTK.-
		CHERP	CHERP	Y894				31.0		K.GVGVALDDPY*ENYRR.N
		Chromosome 11 open reading frame 59	LAMTOR1	Y40				26.0	38.0	K.ALNGAEPNY*HSLPSAR.T
		Chromosome 12 open reading frame 44	ATG101	Y164				100.0	26.1	R.HEY*LPK.M
		Chromosome 9 open reading frame 86	RABL6	Y683				100.0	33.4	R.HPGGGDY*EEL.-
		Chromosome condensation protein G	NCAPG	Y929				10.9	17.7	K.EVY*MTPLR.G
		Cingulin	CGN	Y105				101.1	24.5	K.GANDQGASGALSDELPENY*SQVK.G
		Clathrin, heavy polypeptide	CLTC	Y634				93.7	54.8	R.ALEHFTDLY*DIKRA
		Clathrin, heavy polypeptide	CLTC	Y430				52.2	24.9	K.Y*ESLELCRPVLQQR.K
		Clathrin, heavy polypeptide	CLTC	Y1477				37.7	85.3	K.SVNESLNNLFITEEDY*QALR.T
		Clathrin, heavy polypeptide	CLTC	Y1096				100.0	45.4	R.AY*EFAER.C
		Clathrin, heavy polypeptide	CLTC	Y1487				18.4	56.7	R.TSIDAY*DNFONISLAQR.L
		CLNS1A	CLNS1A	Y214				29.6	86.9	R.TEDSIROY*EDGM#EVDTTPTVAGGFEDADV#H.-
		Cofilin 1	CFL1	Y89				16.9	51.3	R.YALYDATY*ETK.E
		Cofilin 1	CFL1	Y68				22.0	71.0	K.EILVGDVGQTVDDPY*ATFVK.M
		Cofilin 1	CFL1	Y140				100.0	75.8	K.HELOANCY*EEVKDR.C
		Complement receptor 2	CR2	Y1029				29.3	15.4	R.EVYSVDPY*NPAS.-
		Coronin 1C	CORO1C	Y301				33.4	45.3	R.YFEITDESPLY*VHYLNTFSSK.E
		Cortactin	CTTN	Y421				55.8	61.0	R.LPSSPVY*EDAASFKA
		CRK	CRK	Y190				49.2		K.VDPAEAEVAVLINDM#EESGUBRIIDDEGSDVAVDQV#DRIIDM#Q
		CRKL	CRKL	Y132				15.1	43.1	R.TLY*DFPGNDAEDLPFKK.G
		Cyclin dependent kinase 5	CDK5	Y15				16.9	67.6	K.IGEGTY*GTVFKA
		Cyclin M3	CNNM3	Y301				19.2	15.0	R.GGGDPY*SDLSK.G
		Cysteine string protein	DNAJC5	Y149				26.0	52.8	K.APEGEETEFY*VSPEDLEAQLQSDER.E
		Cytoplasmic FMR1 interacting protein 1	CYFIP2	Y108				100.0	13.6	R.VEIY*EKT
		Cytoskeleton associated protein 1	TBCB	Y98				82.3	76.1	R.LGEY*EDVSR.V
		D4, zinc and double PHD fingers family 2	DPP2	Y172				55.5	54.6	R.ILEPDRLFDDDEDY*EEDTPK.R
		DAPP1	DAPP1	Y139				9.1	38.7	K.VEEPSIY*ESVR.V
		DDX20	DDX20	Y756				62.9	38.4	R.LQTEAQEDDWY*DCHR.E
		DDX3	DDX3X	Y69				16.9	65.4	K.DKDAY*SSFGR.S
		DDX3	DDX3X	Y104				45.2	58.8	R.SDY*DGIGSR.G
		DDX3	DDX3X	Y283				100.0	56.0	R.ELAVQY*EEAR.K
		DDX3	DDX3X	Y462				39.0	51.5	K.KGADSLEDFLY*HEGYACTSIHGDR.S
		DDX3	DDX3X	Y525				62.7	32.2	K.HVINFDLPSDIEEY*VHR.I
		DDX3	DDX3X	Y243				13.9	58.2	K.TA AFLPLISQY*SDGPGEALR.A
		DDX3Y	DDX3Y	Y103				45.2	57.4	R.SDY*DGIGNR.E
		Decapping enzyme hDcp1b	DCP1B	Y191				32.5	50.0	K.KITSSSAIY*DNPNLIKPIPVKPSNQQR.I
		Dedicator of cytokinesis 2	DOCK2	Y212				28.2	33.0	K.DOPDYAM#Y*SR.I

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		5	6				5	6	5	6			
<10	0			Diaphanous related formin 1	DIAPH1	Y374					10.9	93.1	R.VQLNVFDEQEEDSY*DLKGR.L
10-20	1			Diazepam binding inhibitor	OBI	Y46					31.5	67.8	K.TKPSDEEM#LFY*GHYK.Q
20-30	2			Diazepam binding inhibitor	OBI	Y49					9.1	34.6	K.TKPSDEEM#LFYGHY*K.Q
30-40	3			Dicer1, Dcr-1 homolog	DICER1	Y1438					49.9	29.3	K.EEADY*EDDFLEYDQEHIR.F
40-50	4			DNA methyltransferase 1	DNMT1	Y399					13.9	58.7	K.LSIFDANESGFESY*EALPQHK.L
50-60	5			DNA topoisomerase I	TOP1	Y723					100.0	14.6	K.LNY*LDPR.I
60-70	6			Docking protein 1	DOK1	Y315					22.5	67.8	R.IAPCPSQDSL*Y*SDPLDSTAQAAGEGVQR.K
70-80	7			Docking protein 1	DOK1	Y409					40.7	70.5	R.VKEEGYELPYNPATDD*AVPPPR.S
80-90	8			Docking protein 1	DOK1	Y382					109.7	40.6	K.EDPIY*DEPEGLAPVPPQGLYDLPR.E
90-100	9			Docking protein 1	DOK1	Y296					38.9	49.4	K.LPSPPGPOELDSPAL*Y*AEPLDSLRI
>100	10			Docking protein 1	DOK1	Y449					90.6	72.8	K.SHNSALY*SQVQK.S
				Docking protein 2, 56kDa	DOK2	Y299					100.0	98.1	R.GQEGEY*AVPFDAVAR.S
				Docking protein 3	DOK3	Y398					44.9	53.9	R.ASGPPGNEHLY*ENLCVLEASPTLHGGEPEPEHGPGR.S
				Docking protein 3	DOK3	S389Y398						15.1	K.RAS*GPPGNEHLY*ENLCVLEASPTLHGGEPEPEHGPGR.S
				Docking protein 3	DOK3	Y432					12.0	57.7	R.SPITSPRY*HNGQQLSWPGPANDSTLEAQYR.R
				Dual-specificitytyrosine phosphorylation-regulated kinase 2	DYRK4	Y382					22.5	55.7	R.VYTY*IQSR.F
				DynaminII	DCTN2	Y91					39.4	96.3	R.TGYESGEY*EMILGEGLVK.E
				DynaminII	DCTN2	Y318					14.7	16.5	K.VHQLY*ETIQR.W
				DYRK1B	DYRK1A	Y271					33.4	49.5	R.IY*QYIQSR.F
				DYRK1B	DYRK1A	Y273					39.3	44.8	R.IYQY*IQSR.F
				DYRK3	DYRK3	Y369					22.5	32.5	K.LYTY*IQSR.F
				EBNA2 coactivator p100	SND1	Y113					5.8	17.0	R.EYGMHLY*LGK.D
				EBNA2 coactivator p100	SND1	Y109					18.6	26.4	R.EY*GMHLYLGK.D
				EBNA2 coactivator p100	SND1	Y908					12.1	45.5	R.ADDADEFGY*SR.-
				EH domain containing 1	EHD1	Y453					12.1	27.0	K.DKPTYDEIFY*TLSPVNGKI
				Elongation factor 1 alpha 1	EEF1A1	Y86					10.6	50.5	K.YY*VTIIDAPGHR.D
				Elongation factor 1 alpha 1	EEF1A1	Y141					23.9	65.7	R.EHALLAY*TLGVK.Q
				Elongation factor 1 alpha 1	EEF1A1	Y85					8.2	44.9	K.YY*VTIIDAPGHR.D
				Elongation protein 3	ELP3	Y202					50.5	57.2	R.NLHDALSGHTSNNIY*EAVK.Y
				Emerin	EMD	Y161					55.6	55.4	R.DSAY*QSITHYRPVSASR.S
				Engulfment and cell motility 2	ELMO2	Y717					19.8	58.5	K.EPSSYDFVY*HYG.-
				Enhancer of filamentation 1	NEDD9	Y92					100.0	22.9	K.LY*QVPNPQAAPR.D
				Enhancer of filamentation 1	NEDD9	Y164					10.9	15.3	R.TGHGY*VVEYPSR.Y
				Enhancer of filamentation 1	NEDD9	Y345					100.0	30.7	R.DGVY*DVPLHNPPDAK.G
				Enhancer of filamentation 1	NEDD9	Y166					27.8	23.4	R.TGHGYVY*EYPSR.Y
				Enhancer of filamentation 1	NEDD9	Y317					6.3	50.1	R.RHQSLSFNHPPQLGQSVGSQNDA*Y*DVPR.G
				Enhancer of filamentation 1	NEDD9	Y261					40.4	15.1	R.QAGRPLRPEGVY*DIPTCTKPAGK.D
				Enolase 1	ENO1	Y44					40.0	46.9	R.AAVPSGASTGY*EALELRNDK.T
				Enolase 2	ENO3	Y44					93.0	104.8	R.AAVPSGASTGY*EALELR.D
				EPS15R	EPS15L1	Y564					63.3	60.0	R.SLEQY*QVLDGAHGASLTDLANLSEGVSLAER.G
				Erbin	ERBIN	Y884					40.7	63.2	K.IY*DILSONGPOQPSTTVK.I
				Erbin	ERBIN	Y1104					32.3	55.6	R.AQIEGDDY*LSYR.E
				ERK1	MAPK3	Y204					25.5	111.1	R.IADPEHDHTGFLTEY*VATR.W
				ERK1	MAPK3	T198Y204					16.5	52.8	R.IADPEHDHT*GFLTEY*VATR.W
				ERK1	MAPK3	T202Y204					40.7	95.4	R.IADPEHDHTGFLTEY*VATR.W
				ERK2	MAPK1	Y187					31.5	104.6	R.VADPDHDHTGFLTEY*VATR.W
				ERK2	MAPK1	T185Y187					16.5	75.7	R.VADPDHDHTGFLTEY*VATR.W
				ERK2	MAPK1	T181Y187					11.7	47.0	R.VADPDHDHT*GFLTEY*VATR.W
				Erythrocyte membrane protein band 4.1 like	EPB41L5	Y499					8.0	34.1	R.LPQLGEPEVEY*ETLKDTSEK.L
				Eukaryotic translation elongation factor 1 beta 2	EEF1B2	Y79						48.7	K.Y*GPADVEDTTGSGATDSKDDDDIDLFSGDDEESEAEKRL
				Eukaryotic translation elongation factor 2	EEF2	Y760					77.9	21.8	R.LMEPIYLVIEQCEQVGGY*GVLNR.K
				Eukaryotic translation initiation factor 2A	EIF2A	Y250					45.3	88.5	K.TGASY*YGEQTLHYIATNGESAVQLPK.N
				Expressed in T cells and eosinophils in FAF2 atopic dermatitis	FAF2	Y79					29.0	15.4	R.IY*SYVWSRPQPR.G
				Ezrin	EZR	Y354					100.0	33.9	R.LQDY*EEK.T
				Ezrin	EZR	Y116					16.5	41.1	K.EGILSDEIY*CPPETAVLLGSYAVQAK.F
				Fatty acid synthase	FASN	Y1047					28.4	15.3	K.HGLY*LPTR.V
				Fc receptor like protein 2	FCRL2	Y502					16.9	22.0	K.DSQVIY*SSVK.K
				Fc receptor like protein 3	FCRL3	Y722					100.0	89.9	R.AHEEDEENY*ENVPR.V
				Fc receptor like protein 3	FCRL3	Y692					15.2	35.0	K.ENSANCPMMHQEHEELTVLY*SELK.K
				FGFR1 oncogene partner	FGFR1OP	Y337					48.0	79.0	K.IGSLGLGTGEDDDY*VDDFNSTSHR.S
				Fgr	FGR	Y208					33.8	82.4	K.LDMGGY*YITTR.V
				Fgr	FGR	Y34					88.1	63.1	R.SYGAAHY*GPDPTKA

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<10	0	Fgr	FGR					22.9	22.1	K.TGCPISNYVAPVDSIAEEVY*FGK.I
10-20	1	Filamin B	FLNB					32.1	35.5	R.SSTETCVY*SAIPK.A
20-30	2	FK506 binding protein 4	FKBP4					46.5	35.0	K.GEHSIVY*LPKYAFGSVGK.E
30-40	3	Flightless 1	FLII					120.1	63.5	K.VGLGLGY*LELPQINYK.L
40-50	4	Flightless 1	FLII					60.4	17.7	R.YWVPVEY*EEEEK.K
50-60	5	Fodrin beta	SPTBN1					3.8	33.4	K.IVSSSDVGHDEY*STQSLVK.K
60-70	6	Fumarase	FH					14.3	64.3	K.ETAIELGY*LTAEQFDEWVKPK.D
70-80	7	FYB	FYB1					100.0	32.6	K.Y*GY*VLR.S
80-90	8	FYB	FYB1					32.3	79.2	K.TTAVEIDY*DSLK.L
90-100	9	FYB	FYB1					44.7	41.1	K.Y*GYVLR.S
>100	10	FYB	FYB1					10.9	23.3	R.GSY*GYIK.T
		FYB	FYB1					100.0	28.4	K.FKY*DGEIR.V
		FYB	FYB1					16.9	38.3	K.YGY*VLR.S
		Fyn	YES1					39.9	51.3	K.GAY*SLSIR.D
		Fyn	YES1					16.9	76.4	R.LIEDNEY*ITAR.Q
		FYVE, RhoGEF and PH domain containing 6	FGD6					31.1	45.1	R.HYEEIPEY*ENLPFIMAIR.K
		G protein signalling modulator 3	GPSM3					11.0	24.0	R.EQLY*STILSHQCQR.M
		GAB2	GAB2					9.4	20.2	R.AGDNSSQSVY*IPM#SPGAHHFDSLGYPTTLPVHR.G
		GART	GART					42.3	17.1	K.GYPGDY*TK.G
		GDP dissociation inhibitor 2	GDI2					20.5	41.9	R.TDDYLDQPCY*ETINR.I
		GGA2	GGA2					100.0	60.1	R.RPGQAPPDQDALQVVY*ER.C
		GIT1	GIT1					23.4	47.0	R.LQPFHSTLEDDAIY*SVHVPAGLYR.I
		Glucocorticoid receptor DNA binding factor	ARHGAP3					16.9	59.9	R.NEEENIY*SVPHDSTQGK.I
		Glucocorticoid receptor DNA binding factor	ARHGAP3					7.9	40.9	K.SVSSSPWLPQDGFDPDSDY*AEPM#DAVVKPR.N
		Glucose-6-phosphate dehydrogenase	G6PD					46.9	64.4	R.VGFQY*EGTYK.W
		Glucose-6-phosphate dehydrogenase	G6PD					43.7		R.VQPNEAIV*TK.M
		Glutamate dehydrogenase 1	GLUD1					30.5	63.8	R.DSNY*HLLMSVQESLR.K
		Glutamate oxaloacetate transaminase, GOT2 mitochondrial						100.0	44.2	K.NLDKEY*LPIGGLAEFCCK.A
		Glutathione S transferase 3	GSTP1					76.7	59.4	M.PPYTVVY*FPVR.G
		Glycogen debranching enzyme	AGL					28.1	56.5	R.EAM#SAY*NSHEEGR.L
		Glycogen phosphorylase, brain type	PYGB					106.0	22.4	K.ARPEY*MI LPVHFYGR.V
		Glycogen synthase kinase 3 beta	GSK3B					16.9	51.4	R.GEPNVSY*ICSR.Y
		Glycogen synthase kinase 3 beta	GSK3B					29.0	31.4	R.GEPNVSY*ICSR.Y
		Glycogen synthase kinase 3 beta	GSK3B					22.1	39.2	R.GEPNVSY*ICSR.Y
		Glyoxylate reductase	GRHPR					78.2	79.5	R.GDVVNQDDL Y*QALASGK.I
		Golgi autoantigen, golgin subfamily A, 4	GOLGA4					13.9	21.3	K.NVY*ATTVGTPYK.G
		Golgi phosphoprotein 4	GOLIM4					65.0	77.0	R.QQAHY*DAMDNIVQGAEDQGIQEGEEGAYER.D
		Golgi phosphoprotein 4	GOLIM4					100.0	30.7	R.EEHY*EEEEEEEDGAVAEK.S
		Golgin 160	GOLGA3					10.9	27.1	R.GTY*GILSK.T
		Golgin 160	GOLGA3					16.9	19.3	K.EY*SFLR.T
		GRB2 associated binding protein 3	GAB3					100.0	59.8	R.VDY*VQVDEQK.T
		Grb4	NCK2					100.0	65.1	R.IY*DLNIPAFVK.F
		Grb4	NCK2					25.5	35.7	R.DAS*PTPSTDAEYPANGSGADRIH*DLNIPAFVK.F
		Grb4	NCK2					14.7	35.7	R.TGY*VPSNYVER.K
		GRID	GRAP2					45.3	47.5	K.LSDHPPTLPQQHQHQPPQY*APAPQQLQPPQQR.Y
		GRID	GRAP2					42.3	72.6	K.AELSGOEGY*VPKN
		GRID	GRAP2					0.7	27.9	R.KLSDHPPTLPQQHQHQPPQY*APAPQQLQPPQQR.Y
		GRID	GRAP2					11.0	36.6	R.KLS*DHPPTLPQQHQHQPPQY*APAPQQLQPPQQR.Y
		GRID	GRAP2					100.0	28.1	R.Y* LQHHHFHQR.R
		Growth arrest specific 7	GAS7					0.5	17.4	R.Y*ASVEKARK.A
		GRP1 associated scaffold protein	GRASP					8.4	30.1	R.LVHGLVKDPSY*DTLESVR.S
		H2B Histone family, member E	HIST1H2B					9.1	24.3	R.KESYSY*VYK.V
		H4 Histone family, member A	HIST1H4A					32.3	50.5	R.ISGLIY*EETR.G
		HBS1L	HBS1L					25.4	47.4	R.DKPSVEPVEEYDY*EDLK.E
		HBS1L	HBS1L					21.2	23.6	R.DKPSVEPVEEYDYEDLKESNSVSNHQLSGFDQAR.L
		Hck	HCK					16.9	82.6	R.VIEDNEY*ITAR.E
		Heat shock 10 KD protein	HSPe1					18.4	53.4	K.VLLPEY*GGTK.V
		Heat shock 60 KD protein 1 (chaperonin)	HSPD1					39.3	45.8	R.GVISPY*FINTSK.G
		Heat shock 70 KD protein 1A	HSPA1L					16.9	90.3	R.TTTPSY*VAFDTTER.L
		Heat shock 70 kDa protein 8	HSPA8					27.7	116.7	K.GPAVGIDLGTTY*SCVGVFQHGK.V
		Heat shock 70kDa protein 4	HSPA4					143.9	66.0	K.EDIY*AVEVGATR.I
		Heat shock 70kDa protein 4	HSPA4					32.1	61.3	K.NAVEEYV*EM#R.D

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		CarT					RajiB					
		Protein Name	Gene	Phosphosites	0m	3m	6m	9m	12m	Ascor	MOWSE	Sequence
		Heat shock 70kDa protein 4	HSPA4	Y624						32.1	56.2	K.NAVEEY ^Y VEMR.D
		Heat shock 70kDa protein 4	HSPA4	Y660						46.6	18.9	K.LEDTENWL ^Y EDGEDQPK.Q
		Heat shock protein 105 kDa	HSPH1	Y641						32.1	56.5	K.NAVEEY ^Y VEFR.D
		Heat shock protein 105 kDa	HSPH1	Y677						62.1	54.6	R.LLTETEDWL ^Y EEGEDQAK.Q
		Helicase ATP binding 1	ASCC3	Y459						38.3	16.6	R.IPYSEPMPLSFEKPY ^Y IQDLDEIGQLAFK.G
		Hematopoietic cell specific LYN substrate 1	HCLS1	Y378						35.3	23.5	R.TLEGLQVEEYPYEAPEPEPEPEPENDY ^Y EDVEEMDR.H
		Hematopoietic cell specific LYN substrate 1	HCLS1	Y360						25.8	34.7	R.TLEGLQVEEYPY ^Y EAEPEPEPEPEPENDY ^Y EDVEEMDR.H
		Hematopoietic cell specific LYN substrate 1	HCLS1	Y103						67.1	58.2	K.SAVGHEY ^Y VAEVEK.H
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	Y137						30.2	19.0	R.MY ^Y SYPAR.V
		Heterogeneous nuclear ribonucleoprotein H1	HNRNP1	Y306						7.8	35.8	K.ATENDY ^Y NFFSPLPVR.V
		Heterogeneous nuclear ribonucleoprotein H3	HNRNP3	Y296						22.4	85.5	R.DGMDNQGGSY ^Y GSVGR.M
		Heterogeneous nuclear ribonucleoprotein M	HNRNPM	Y681						100.0	23.1	K.DKFNECGHLY ^Y ADIK.M
		Heterogeneous nuclear ribonucleoprotein U	HNRNPU	Y466						6.6	49.1	K.EKPY ^Y FPIPEEYTFIGNVPLEDR.V
		Heterogeneous nuclear ribonucleoprotein U	HNRNPU	Y473						13.1	34.0	K.EKPYFPIPEEY ^Y TFIGNVPLEDR.V
		Hexokinase domain containing 1	HKDC1	Y497						100.0	24.7	R.AELEY ^Y GLKKK.S
		HGAL GCSAM	Y107							40.2	49.7	R.VLCTRPSGSAEEY ^Y ENVPCK.A
		HGAL GCSAM	Y148							66.2	53.4	R.SPEDEY ^Y ELLMIPHR.I
		HGAL GCSAM	Y128							14.0	34.7	R.ESLGGTETY ^Y SLHMPSTDPR.H
		HGAL GCSAM	Y86							15.2	67.0	R.MSSTPIQDNVDQTYSEELCY ^Y TLNHR.V
		HGAL GCSAM	S99Y107							12.8	19.5	R.VLCTRPS ^Y GNSAEEY ^Y ENVPCK.A
		HGAL GCSAM	Y106							66.5	44.4	R.VLCTRPSGSAEEY ^Y ENVPCK.A
		HGAL GCSAM	S102Y107							12.7	35.5	R.VLCTRPSGNS ^Y AEEY ^Y ENVPCK.A
		HGAL GCSAM	S69Y86							13.7	31.2	R.M ^Y SS ^Y TPIQDNVDQTYSEELCY ^Y TLNHR.V
		HIP55 DBNL	Y162							32.2	52.6	R.FQDVGPQAPGSVY ^Y QK.T
		HIPK1 HIPK2	Y352							39.9	67.8	K.AVCSTY ^Y LQSR.Y
		HIV 1 REV binding protein	AGFG1	Y327						20.9	61.2	K.AGLQTADKY ^Y AALANLNFISAGQGGQDGSFGTTGKA
		HLA DR associated protein I	ANP32A	Y148						33.2	36.8	K.LLPQLTYLDGY ^Y DR.E
		HLA-DMB	Y248							8.0	37.6	R.AGHSSY ^Y TPLPGSNYSEGWHIS.-
		Homeodomain interacting protein kinase 3	HIPK3	Y359						16.9	68.0	K.TVCSTY ^Y LQSR.Y
		HP1-BP74	HP1BP3	Y379						19.3	41.4	K.YVLENHPGTNSNY ^Y QMHLLKK
		HSP90A	HSP90AA1	Y492						48.6	70.9	K.HIY ^Y ITGETK.D
		HSP90A	HSP90AB1	Y197						32.1	67.9	K.EDQTEY ^Y LEER.W
		HSP90A	HSP90AB1	Y284						100.0	17.5	K.Y ^Y IDQEELNK.T
		HSP90B	HSP90AB1	Y484						33.8	53.1	K.SIY ^Y ITGESK.E
		Hypothetical protein FLJ10769	NAXD	Y85						35.4	66.2	R.IGVVGCCQEY ^Y TGAPYFAAISALK.V
		Hypothetical protein FLJ38482	TMEM192	Y209						28.2	64.6	K.IY ^Y AYPSNITSETGFR.T
		ICT1	MRPL58	Y49						19.3	26.2	K.SIYSLDKLY ^Y PESQGSOTAWR.V
		Ig alpha	CD79A	Y210						15.2	71.3	R.GLQGTY ^Y QDVGSLNIGDVQLEKP.-
		Ig beta	CD79B	Y207						12.1	54.3	K.AGMWEEHDHYEGLDIDQATY ^Y EDIVTLR.T
		IGF-1 receptor	INSR	Y1165						26.0	34.4	R.DIYETDY ^Y YR.K
		IK factor Iκ	Y114							40.7	60.9	R.DGVNKDY ^Y EETELISTTANYR.A
		Interferon gamma receptor 1	IFNGR1	Y304						29.1	70.0	K.Y ^Y VSLTISYQPSLEK.E
		Intersectin 2	ITSN2	Y967						100.0	66.5	R.EEPEALY ^Y AAVNK.K
		Intersectin 2	ITSN2	Y552						100.0	49.4	K.LIY ^Y LVPEK.Q
		Intestinal cell (MAK-like) kinase	ICK	T157Y159						12.9	26.5	R.SKPPY ^Y TDY ^Y VSTR.W
		Intestinal cell (MAK-like) kinase	ICK	Y156T157						7.6	24.4	R.SKPPY ^Y TDY ^Y VSTR.W
		Intestinal cell (MAK-like) kinase	ICK	Y156Y159						-0.2	14.9	R.SKPPY ^Y TDY ^Y VSTR.W
		IQ motif and Sec7 domain 1	IQSEC1	Y343						100.0	27.9	R.AGGAAPDY ^Y WALAHKEDK.A
		ITK	ITK	Y512						40.2	56.3	R.FVLDDQY ^Y TSSTGTKFPVK.W
		Janus kinase 2	JAK2	Y570						22.3	16.1	R.EVGDY ^Y QQLHETVELLK.V
		Janus kinase 3	JAK3	Y785						5.7	54.9	R.DLNLSSSDY ^Y ELLSDPTGALAPR.D
		JAW1	LRMP	Y26						30.2	46.3	R.EY ^Y SSLPLPR.H
		Junction adhesion molecule 1	F11R	Y280						16.9	15.3	K.VIY ^Y SQPSAR.S
		Karyopherin beta 1	KPNB1	Y752						-0.9	18.8	K.SDY ^Y DMVDYLNELR.E
		Karyopherin beta 3	PO5	Y838						135.3	94.1	K.RODEDY ^Y DEQVEESLQDEDDNDVILTK.V
		KCC1	SLC12A4	Y17						85.5	40.1	R.RGDY ^Y DNLEGLSWVDYGER.A
		KIAA0317	AREL1	Y47						35.1	15.0	R.TIY ^Y DYVR.G
		KIAA1949	PPP1R18	Y230						6.8	26.6	R.LSPGESAY ^Y QK.L
		Lactate dehydrogenase A	LDHA	Y239						39.3	56.0	K.QVVEASAY ^Y EVIK.L
		Lactate dehydrogenase A	LDHA	Y10						100.0	37.0	K.DQLIY ^Y NLLK.E
		Lactate dehydrogenase B	Y240							26.0	48.8	K.MVVEASAY ^Y EVIK.L
		Laminin receptor 1	RPSA	Y139						19.1	87.3	R.ADHQPLTEASY ^Y VNLPTALCNTDSPLR.Y

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		0	1				0	1	0	1			
<10	0			LAT like membrane associated protein	LAX1	Y294					142.7	57.9	R.DY*ENVPAAADPSGSQQQAQK.D
10-20	1			LAT like membrane associated protein	LAX1	Y93					100.0	42.8	K.NIVYDILPWR.Q
20-30	2			LAT like membrane associated protein	LAX1	Y373					31.5	88.3	K.HREEM#SNEDSSDY*ENVLTAKL
30-40	3			LBA	LRBA	Y1110					164.7	74.8	K.SIVEEEEDDDYVELK.V
40-50	4			Lck	LCK	Y192					44.7	70.4	R.NLDNGGFYISPR.I
50-60	5			Lck	LCK	Y505					19.7	29.8	R.SVLEDDFTATEGQY*QPOP.-
60-70	6			Lck	LCK	Y414					26.0	58.7	K.WTAPEAINY*GFTFIK.S
70-80	7			Lck	LCK	Y470					100.0	19.4	R.MWVRPDCNPEELY*QLMR.L
80-90	8			Lck interacting transmembrane adaptor 1	LIME1	Y235					25.4	39.1	K.GQGAILALAGLAY*QTLPLR.A
>10	>10			Leucyl cystinyl aminopeptidase	LNPEP	Y70					28.2	49.6	R.GLGEHEM#EEDDEEY*ESSAK.L
				Leupaxin	LFXN	Y22					20.8	53.4	R.STLQDSDEY*SNAPPLDQHSR.K
				Lim and SH3 protein 1	LASP1	Y171					7.4	31.2	R.RPLEQQQPHIPTSAPVY*QQPQQPVAGSYGGYKE
				LIM domain only 7	LMO7	Y185					50.1	41.7	K.AQSNPY*YNGPHNLNKA
				LIM domain only 7	LMO7	Y186					9.5	33.4	K.AQSNPY*YNGPHNLNKA
				Linker for activation of T cells	LAT	Y220					120.8	94.5	R.EY*VNVSQELHPGAAK.T
				Linker for activation of T cells	LAT	Y220S224					100.0	51.7	R.EY*VNVS*QELHPGAAK.T
				Liver-specific bHLH-Zip transcription factor	LSR	Y551					37.5	14.0	R.SRDPIHY*DDFR.S
				Lupus brain antigen 1	TRANK1	Y779					42.4	15.7	R.LTEEVS*YKK
				Lupus brain antigen 1	TRANK1	Y2350					100.0	55.5	K.EGVQEDDY*ENEVEDFGLRPR.R
				Lymphocyte antigen 9	LY9	Y626					32.1	73.2	K.EESSATVY*CSIR.K
				Lymphocyte cytosolic protein 1	LCP1	Y299					77.7		K.AY*YHLLQVAPK.G
				Lymphocyte cytosolic protein 1	PLS3	Y124					100.0	51.1	K.YYAFVNWINK.A
				Lymphocyte cytosolic protein 1	LCP1	Y28					67.6	160.6	K.VDTDGNGYISFNLNDFLK.A
				Lymphocyte cytosolic protein 1	LCP1	Y598					100.0	47.3	R.VY*ALPDELVEVNPK.M
				Lymphocyte cytosolic protein 1	LCP1	Y300					-0.1	72.8	K.AY*YHLLQVAPK.G
				Lymphocyte cytosolic protein 1	LCP1	Y417					8.0	29.5	R.VNHLV*SDLSDALVFQLEYK.I
				Lymphocyte specific protein	LSP1	Y125					62.5	50.9	R.SPEGEQEDRPLGHAY*EK.E
				Lymphocyte specific protein	LSP1	S111Y125					100.0	37.5	R.S*PEGEQEDRPLGHAY*EK.E
				Lymphocyte specific protein	LSP1	Y234					33.8	122.1	K.IDQWLEQY*QTAIETAGRT
				Lyn	LYN	Y194					39.9	79.3	R.SLDNGGY*ISPR.I
				Lyn	LYN	Y473					100.0	55.0	R.VENCPDELY*DIM#K.M
				Lyn	LYN	Y316					37.7	59.0	R.EEPIY*ITEYMAK.G
				Lyn	LYN	Y508					67.3	39.5	K.EKAEERPTFDYLSVLDDFY*ATEGQYQQQP.-
				Lyn	LYN	Y501					30.1	35.9	K.EKAEERPTFDYLSVLDDFY*ATEGQYQQQP.-
				Lyn	LYN	Y306					87.6	41.8	R.LY*AVVTR.E
				LysM, peptidoglycan-binding, domain containing 2	LYSMD2	Y208					22.4	27.9	R.DEESPY*ATSLYHS.-
				MAGOH	MAGOH	Y40					7.3	41.5	R.YANNSNY*KNVDM#IR.K
				Malate dehydrogenase mitochondrial	MDH2	Y56					40.5	82.7	R.LTYL*DIATHPGVAADLSHIETK.A
				MAP4K4	MINK1	Y36					10.3	88.7	R.DPAGIFELVEVVGNGTY*GVVYK.G
				MAPK11	MAPK11	Y190					10.9	70.6	R.QADEMTGY*VATR.W
				MAPK12	MAPK12	Y185					32.1	104.6	R.QADSEMTGY*VATR.W
				MAPK14	MAPK14	Y182					41.9	66.2	R.HTDDEMTGY*VATR.W
				MAPK14	MAPK14	T180Y182					51.8	101.0	R.HTDDEMT*GY*VATR.W
				MAPK14	MAPK14	T175Y182					28.4	19.1	R.HT*DDEMTGY*VATR.W
				Matrin 3	MATR3	Y250					32.1	45.4	K.FDSEY*ER.M
				Matrin 3	MATR3	Y219					100.0	26.2	R.MDY*EDDLR.D
				MBC2	ESYT1	Y822					26.4	71.1	K.HLSPY*ATLTVGDSSH.T
				MCM2 minichromosome maintenance deficient 2, mitotin	MCM2	Y137					1.6	30.1	R.GLYV*DSDEEDEERPAR.K
				MCM3	MCM3	Y708					14.6	29.4	K.DGDSYDPY*DFSDTEEM#PQVHTPK.T
				MCM3	MCM3	Y708T722					20.8	26.2	K.DGDSYDPY*DFSDTEEM#PQVHT*PK.T
				Melanoregulin	MREG	Y37					25.4	40.0	R.ALPEKEPLVSDNNPY*SSFSGATLVR.D
				Microtubule associated protein 4	MAP4	Y47					10.4	55.1	K.TDY*IPLLDVEK.T
				Moesin	MSN	Y116					11.9	44.8	K.EGILNDDY*CPETAULLASYAVQSK.Y
				Myelin protein zero like 1	MPZL1	Y263					46.9	41.4	K.SESVY*ADIR.K
				Myosin heavy chain 9, nonmuscle	MYH9	Y1408					100.0	37.6	K.VAAV*DKLEK.T
				Myosin heavy chain 9, nonmuscle	MYH9	Y151					12.9	28.3	R.HEM#PPHY*AITDAYR.S
				Myosin heavy chain 9, nonmuscle	MYH9	Y11					20.1	54.8	K.YLY*VDKNFINPLAQADWAAK.K
				Myosin IG	MYO1G	Y72					46.5	36.7	R.ELY*ERPPHLYAVANAAYKA
				Myotubularin related protein 10	MTMR10	Y708					76.6	80.1	R.SGPLACY*GELGQSR.M
				NCK1	NCK1	Y105					211.4	68.7	R.LY*DLNMPAYVK.F
				NCK1	NCK1	S85Y105					12.9	36.3	K.RKPS*VPDASPADDPSFVDPGERLY*DLNMPAYVK.F
				Nectin 1	NECTIN1	Y468					5.6	62.3	K.YDEDAKRPY*FTVDEAEAR.Q



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<10	(0		PI 3 kinase, regulatory subunit beta	PIK3R2	Y605			6.1	37.3	K.NETEDQ ^Y ALM#EDEDLPH ^{HEER} .T
10-20	1-2		PI 3 kinase, regulatory subunit beta	PIK3R2	Y460			10.8	37.4	R.E ^Y DQLYEYTR.T
20-30	3-4		PLC, gamma 2	PLCG2	Y680			16.9	88.0	R.EGSDS ^Y AITFRA
30-40	5-6		PLC, gamma 2	PLCG2	Y753			41.9	63.1	R.DINSL ^Y DVSR.M
40-50	7-8		PLC, gamma 2	PLCG2	Y1245			106.8	73.8	K.EFSVNEQLQL ^Y QEK.C
50-60	9-10		PLC, gamma 2	PLCG2	Y1217			46.4	68.8	R.QEELNNQLFL ^Y DTHONLR.N
60-70	11-12		PLC, gamma 2	PLCG2	Y759			20.9	38.0	R.M ^Y ^Y VDPSEINSPMPOR.T
70-80	13-14		Pleckstrin homology domain-containing family G member 1	PLEKHG1	Y1280			75.6	57.5	K.ETDGEDD ^Y VEIK.S
80-90	15-16		Poly(I)C binding protein 2	PCBP2	Y201			61.3	50.1	K.GVTIPYRKPSSSPVIFAGGAYTIQ ^Q ^Y AIPQD ^{LT} K.L
90-100	17-18		Polyadenylate binding protein 1	PABPC1	Y364			70.0	67.5	R.IVATKPL ^Y VALAQR.K
100-110	19-20		Polypyrimidine tract binding protein 1	PTBP1	Y127			49.2	45.3	R.GQPI ^Y IQFSNHK.E
110-120	21-22		Prolyl endopeptidase	PREP	Y71			32.1	61.2	R.MITEL ^Y DYPK.Y
120-130	23-24		Proteasome 26S subunit, non-ATPase, 14S	PSMD14	Y32			28.2	72.9	R.LGGGM#PGLGQGPPDAPAVDTAEQ ^Y ISSALLK.M
130-140	25-26		Proteasome subunit alpha type 2	PSMA2	Y101			33.4	56.3	K.LAQQYYLV ^Y QEIPTAQLQVR.V
140-150	27-28		Proteasome subunit alpha type 2	PSMA2	Y57			44.6	23.8	K.SIL ^Y DER.S
150-160	29-30		Protein kinase C delta	PRKCD	Y313			120.0	53.6	R.RSDSASSEPVGI ^Y QGFEK.K
160-170	31-32		Protein kinase C delta	PRKCD	S304Y313			27.6	48.3	R.SD ^S ASSEPVGI ^Y QGFEK.K
170-180	33-34		Protein kinase C delta	PRKCD	Y374			100.0	14.1	R.GE ^Y FAIK.A
180-190	35-36		Protein kinase C delta	PRKCD	S306Y313			32.2	18.6	R.RSDSAS ^S SEPVGI ^Y QGFEK.K
190-200	37-38		Protein kinase C delta	PRKCD	Y64			40.7	26.8	K.STFDAHI ^Y EGR.V
200-210	39-40		Protein THEMIS2	THEMIS2	Y632			100.0	53.6	R.QDLDD ^Y EEILEQFQK.T
210-220	41-42		Protein tyrosine kinase TXK	TXK	Y420			32.1	68.2	R.YVLDEE ^Y VSSFGAK.F
220-230	43-44		Protein tyrosine phosphatase receptor type C	PTPRC	Y681			112.6	17.0	R. ^Y VDLPYDYNR.V
230-240	45-46		Protein tyrosine phosphatase, non-receptor	PTPN11	Y580			100.0	91.4	R. ^Y ^Y ENVGLMQQK.S
240-250	47-48		Protein tyrosine phosphatase, non-receptor	PTPN11	Y62			22.0	100.5	K.IQNTGD ^Y VDLYGGEK.F
250-260	49-50		Protein tyrosine phosphatase, non-receptor	PTPN11	Y542			16.9	46.7	R.KGHE ^Y TNIK.Y
260-270	51-52		Protein tyrosine phosphatase, non-receptor	PTPN6	Y536			13.9	56.3	K.GQESE ^Y GNITYPAMIK.N
270-280	53-54		Protein tyrosine phosphatase, non-receptor	PTPN6	Y564			111.4	53.4	K.HKEDV ^Y ENLHTK.N
280-290	55-56		Protein tyrosine phosphatase, non-receptor	PTPN6	Y301			26.0	66.9	R.DSNIGSD ^Y INANYIK.N
290-300	57-58		Protein tyrosine phosphatase, receptor	PTPRA	Y798			26.7	70.1	K.VVQEIYIDAFSD ^Y ANFK.-
300-310	59-60		PRP4 pre-mRNA processing factor 4 homolog B	PRPF4B	Y849			52.3	82.5	K.LCDFGSASHVADNDITP ^Y LVSR.F
310-320	61-62		PRP4 pre-mRNA processing factor 4 homolog B	PRPF4B	S839Y849			26.4	58.7	K.LCDFGSAS ^S HVADNDITP ^Y LVSR.F
320-330	63-64		PRP4 pre-mRNA processing factor 4 homolog B	PRPF4B	S837Y849			31.0	69.8	K.LCDFGS ^S ASHVADNDITP ^Y LVSR.F
330-340	65-66		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y580			16.9	58.6	R.YIEDED ^Y K.A
340-350	67-68		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y579Y580			40.0	64.4	R.YIEDED ^Y ^Y KASVTRL
350-360	69-70		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y849			77.7	57.3	K.EVG ^Y LEFTGPPQKPPRL
360-370	71-72		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y402			89.5	99.9	R.SHLSESCSIED ^Y AEIPDETLR.R
370-380	73-74		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y579			25.4	23.5	R.YIEDED ^Y ^Y KASVTRL
380-390	75-76		PTK2B protein tyrosine kinase 2 beta	PTK2B	Y819			100.0	45.8	K.QMIVED ^Y QWLR.Q
390-400	77-78		PTPRF interacting protein binding protein 1	PPIFBP1	Y336			32.8	22.5	K.GKDGE ^Y EELLNSSISSLLDAQGFSOLEK.S
400-410	79-80		Putative translation initiation factor	EIF1	Y30			36.4	35.5	K.GDOLLPA ^Y GHIR.I
410-420	81-82		Pyruvate dehydrogenase complex, E1-alpha polypeptide 1	PDHA1	Y366			24.1	23.1	K.EIEDAAQFATADPEPPEELG ^Y HIYSSDPF ^Y EVRL.G
420-430	83-84		Pyruvate dehydrogenase complex, E1-alpha polypeptide 1	PDHA1	Y369			6.9	19.3	R.KEIEDAAQFATADPEPPEELGY ^{HI} SSDPF ^Y EVRL.G
430-440	85-86		Pyruvate dehydrogenase E1 alpha subunit, testis specific form	PDHA1	S293Y299			3.1	34.0	R.YHGHSM ^S DPOGVS ^Y R.T
440-450	87-88		Pyruvate dehydrogenase E1 alpha subunit, testis specific form	PDHA1	S291Y299			6.4	21.3	R.YHGH ^S MSDPGVS ^Y R.T
450-460	89-90		Pyruvate dehydrogenase E1 alpha subunit, testis specific form	PDHA1	Y287S293			0.7	20.8	R. ^Y ^Y HGHSM ^S DPOGVS ^Y R.T
460-470	91-92		Pyruvate kinase 3	PKM	Y105			59.4	70.4	R.TATESFASDPI ^Y RPVAVALDTK.G
470-480	93-94		Pyruvate kinase 3	PKM	Y148			96.5	49.3	K.ITLDNAY ^Y MEK.C
480-490	95-96		Pyruvate kinase 3	PKM	Y390			100.0	49.1	R.EAEAAI ^Y HLQLFEELRR.L
490-500	97-98		Pyruvate kinase 3	PKM	Y175			193.2	81.7	K.I ^Y ^Y VDDGLISLQVK.Q
500-510	99-100		RAB GTPase activating protein 1 like	RABGAP1	Y455			80.2	70.7	K.GHTNAGDA ^Y EVSLQRE
510-520	101-102		RAB10	RAB10	Y6			12.1	32.5	K.KT ^Y DLLFK.L
520-530	103-104		RAB7	RAB7A	Y183			20.6	28.2	K.QETEEV ^Y NEFPEPIKLDK.N
530-540	105-106		RAC GTPase activating protein 1	RACGAP1	Y241			7.3	22.0	K.TTVTVPNDGGPIEAVSTIETVP ^Y WTR.S
540-550	107-108		Raf kinase inhibitor protein	PEBP1	Y181			96.6	45.3	K.L ^Y EQLSGK.-
550-560	109-110		Raft linking protein	RFTN1	Y20			30.2	42.2	K.RPGNI ^Y STLK.R
560-570	111-112		Raft linking protein	RFTN1	Y122			21.4	57.3	K.TDLHNEG ^Y IELDCCSSLDP ^Y TDQK.L
570-580	113-114		Rap guanine nucleotide exchange factor	RAPGEF6	Y29			19.3	23.1	R.TPEDLNTI ^Y SYLHGMEILSNLR.E
580-590	115-116		Ras related protein Rab35	RAB35	Y5			100.0	14.6	R.D ^Y DHLFKL
590-600	117-118		RasGAP	RASA1	Y460			44.7	29.6	K.EI ^Y NTIR.R
600-610	119-120		Replication factor C1	RFC1	Y282S283			6.0	21.9	R.S ^Y ^S PR.S
610-620	121-122		Retinoblastoma 1	RB1	Y790S794			23.2	34.1	R.SP ^Y ^Y KFPS ^S SPLR.I

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		0	>10	0	>10	0	>10			
<10	<10									
10	10									
20	20									
30	30									
40	40									
50	50									
60	60									
70	70									
80	80									
90	90									
>100	>100									
Protein Name	Gene	Phosphosites								
Rho GTPase-activating protein 27	ARHGAP2	Y28						100.0	49.5	R.ALPAQDVDDPPEPVY*ANIER.Q
Rho guanine nucleotide exchange factor 2	ARHGEF2	Y893						7.8	46.3	R.SLPAGDALY*LSFNPPQPSR.G
Ribosomal protein L10a	rPL10A	Y11						28.9	28.2	R.DTLY*EAVR.E
Ribosomal protein L3	rPL3	Y307						32.1	73.1	K.NNASTDY*DLSDK.S
Ribosomal protein S10	rPS10-	Y12						100.0	50.4	R.IAY*ELLFK.E
Ribosomal protein S2	rPS2	Y133						100.0	58.5	K.AFVAIGDY*NGHVGGLGVK.C
Ribosomal protein S3a	rPS3A	Y256						66.6	27.3	R.ADGY*EPPVQESV.-
Ribosomal protein S8	rPS8	Y117						15.7	20.4	R.QWYESHY*ALPLGR.K
Ribosomal protein, large, P0	rPLP0	Y24						100.0	49.1	K.IIQLLDDY*PK.C
RNA polymerase II subunit 2	POLR2B	Y845						100.0	67.6	R.HAIY*DKLDDDLIAPGVR.V
ROCK2	ROCK2	Y722						67.6	60.7	K.IY*ESIEEAK.S
SEC16 homolog A	SEC16A	Y991						32.1	88.1	K.ANHSSHQEDTY*GALDFTLSR.T
Secretory carrier membrane protein 3	SCAMP3	Y35						60.4	64.6	R.QY*ATLDVYNPFETR.E
septin 1	SEPT1	Y5						100.0	49.3	K.EY*VGFAALPNQLHR.K
Septin 9	SEPT9	Y278						56.9	48.7	K.APVDFGY*VGDISLEQMIR.R
Serine/threonine protein kinase 9	CDKL5	Y171						32.1	108.1	R.NLSEGNNANYEY*VATR.W
SERPINE1 mRNA binding protein 1	SERBP1	Y207						13.9	19.4	R.SFSHY*SGLK.H
Seryl tRNA synthetase 2	SARS2	Y52						10.0	46.7	R.EGY*SALPOLDIER.F
SET protein	SET	Y133						89.3	53.2	R.IDFYFDENPY*FENK.V
SH3 protein expressed in lymphocytes	SASH3	Y189						42.4	59.2	R.VHTDFTSPSY*DHDLSK.L
SHC (Src homology 2 domain containing) transformino orotein 1	SHC1	Y427						21.2	85.9	R.ELFDDPSY*VNVQNLDK.A
SHC (Src homology 2 domain containing) SHC1 transforming protein 1	SHC1	Y349						89.6	25.2	R.MIAGFDGSAWDEEEEPDHOY*YINDFPKG.E
SHIP1	INPP5D	Y864						100.0	36.1	K.LY*DFVK.T
SHIP1	INPP5D	Y914						68.0	60.9	R.APPCSGSSITEINPNY*MIKGVGFPGPMPLMHVK.Q
SHIP1	INPP5D	Y1021						24.2	42.7	K.NAGDTLPQEDLPLTKPEM#FENPLY*GSLSSFPPKAPR.K
SHIP1	INPP5D	Y795						39.1	62.4	K.LKPIISDPEY*LLDQHILSIK.S
SHIP1	INPP5D	Y372						56.6	21.6	K.EY*VFADSK.K
SHIP1	INPP5D	Y1021S 1023						10.3	20.0	K.NAGDTLPQEDLPLTKPEM#FENPLY*GS*LSSSFPPKAPR.K
SHIP2	INPPL1	Y1135						76.7	82.2	K.TLSEVDY*APAGPAR.S
SHIP2	INPPL1	Y886						146.2	80.4	R.LY*EWISIDKDEAGAK.S
SHIP2	INPPL1	Y986						62.7	55.5	K.NSFNNPAY*YLEGVPHQLLPPEPPSPARA
Signal recognition particle 14 kDa	SRP14	Y27						26.0	63.2	R.TSGSVY*ITLK.K
Signaling lymphocytic activation molecule	SLAMF1	Y281						55.2	46.6	K.SLTIY*AQVQKPGPLQK.K
Single stranded DNA binding protein 1	SSBP1	Y73						48.0	50.2	R.SGDSEY*QLGDVSQK.T
SIT	SIT1	Y148						161.6	79.5	K.Y*SEVVLDEPK.S
SIT	SIT1	Y90						33.5	60.2	R.SGESVEEVPLY*GNLHYLQTGR.L
SIT	SIT1	Y127						13.9	38.9	R.AAEVW#WCY*TSLQLRPPQGR.I
SIT	SIT1	Y95						24.3	67.7	R.SGESVEEVPLYGNLHY*LOTGR.L
SIT	SIT1	Y188						13.3	21.8	R.ASFDDQY*ANSQPAAS.-
SKAP55	SKAP1	Y232						22.8	62.4	K.EETY*DDIDGFDSPSCGSCRPTILPGSVGIK.E
SKAP55	SKAP1	Y271						13.8	42.0	K.EPTEEKEEDIY*EVLPOEHDLEDESGTR.R
Small nuclear ribonucleoprotein 70 kD	SNRNP70	Y126						100.0	33.9	R.EFEY*GPIKR.I
SMARCA6	HELLS	S60Y65						25.4	13.9	R.ES*TEIRY*R.R
Solute carrier family 38, member 2	SLC38A2	Y41						10.8	58.3	K.SHY*ADVPENQNFLESNLGK.K
Splicing factor 3A, subunit 3	SF3A3	Y479						25.3	63.1	R.WQPOTEEEY*EDSSGNVVKK.T
Splicing factor 3B subunit 4	SF3B4	Y16						32.1	32.7	R.NQDATY*VGGLDEK.V
Splicing factor, proline and glutamine rich	SFPQ	Y488						25.4	18.5	R.FAQHGTFEY*EYSQR.W
Sprouty homolog 1	SPRY1	Y53						16.9	73.9	R.GSNEY*TEGPSVKR.R
SRp30c	SRBF9	S211Y214						16.8	32.5	R.GS*PHY*FSPFRPY.-
SRp30c	SRBF9	Y214S216						5.2	25.7	R.GSPHY*FS*PFRPY.-
SRp30c	SRBF9	Y214						3.3	42.1	R.GSPHY*FSPFRPY.-
STE20 like kinase MST1	STK4	Y433						100.0	41.9	K.IPQDGDY*EFLK.S
Structure specific recognition protein 1	SSRP1	Y441						3.1	40.7	K.EGM#NPSYDEY*ADSDEDQHDAYLER.M
SUGT1	SUGT1	Y317						26.0	29.6	R.LFQQIY*SDGSDEVKRA
Switch associated protein 70	SWAP70	Y517						100.0	18.8	R.KQALEQY*EEVKK.K
SYK	SYK	Y352						42.4	58.6	R.EALPMDTEVYESPY*ADPEIRPK.E
SYK	SYK	Y323						40.6	63.6	R.QESTVSFNPY*EPELAPWAADK.G
SYK	SYK	Y348						33.2	62.6	R.EALPMDTEVY*ESPYADPEIRPK.E
SYK	SYK	Y74						16.9	76.7	R.ELNGTY*AIAGGR.T
SYK	SYK	Y28						34.8	41.4	R.EEAEDY*LVQGMDSGLYLLR.Q
Synapse associated protein 1	SYAP1	Y327						51.4	61.3	K.ELQQLQOEY*EVVTESEKR.D
T cell antigen receptor, zeta		Y142						68.3	88.3	R.RKGHDGLY*QGLSTATKD

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		<10	>10				5 6 7 8	5 6 7 8					
				T cell antigen receptor, zeta		Y83					100.0	44.3	R.REEYDVLDK.R
				T cell antigen receptor, zeta		Y153					33.7	38.6	K.DTYDALHMQALPPR.T
				T cell antigen receptor, zeta		Y72					54.3	25.1	R.SADAPAYQGQNQLYNELNLGR.R
				T cell antigen receptor, zeta		Y64Y72					61.4	56.7	R.SADAPAYQGQNQLYNELNLGR.R
				T cell antigen receptor, zeta		Y111					100.0	31.6	R.RKNPQEGLYNELQK.D
				T cell antigen receptor, zeta		Y123						14.2	K.DKMIAEAYSEIGMK.G
				T cell receptor T3 delta chain CD3D		Y149					100.0	37.4	R.NDQVYQPLR.D
				T cell receptor T3 delta chain CD3D		Y160					10.3	18.5	R.DDAQYSHLGGNWAR.N
				T Complex 1 TCP1		Y545					-0.1	14.2	K.DDKHGSYEDAVHSGALND.-
				T Complex 1 TCP1		Y181					16.9	23.5	K.YTDIR.G
				Tara like proteinTRIOBP		Y612					41.5	35.0	K.YQDVYVELSHIK.T
				TATSF1HTATSF1		Y650						27.6	K.VFDDSEDEKEDEEYADEK.G
TBC1 domain family member 15 (Fragment)				TBC1D15		Y116					74.9	55.6	K.SLSQSFENLLDEPAYGLIQK.I
				Tec tyrosine kinase TEC		Y519					16.9	65.7	R.YVLDDQYTSSSGAK.F
				Tensin 3 TNS3		S332Y354					57.7	66.6	R.WDSYENLSADGEVLHTQGPVDGSLYAK.V
				Tensin 3 TNS3		Y333Y354					10.2	29.1	R.WDSYENLSADGEVLHTQGPVDGSLYAK.V
				Thioredoxin reductase 1 TXNRD1		Y183					56.3	57.8	K.VVYENAYGQFIGPHR.I
				Tight junction protein 2 TJP2		Y1118					100.0	19.8	K.HPDIYAVPIK.T
				TRA2A TRA2A		Y87T88					-0.1	21.4	R.SYTPPEYR.R
				Transgelin 2 TAGLN3		Y192					13.9	45.9	R.GASQAGMTGYGMPR.Q
				Transgelin 2 TAGLN2		Y8					15.8	29.3	R.GPAYGLSR.E
				Transketolase TKT		Y275					12.3	66.4	K.NMAEQIIQEYSIQISK.K
				Tripartite motif containing protein 9 TRIM9		Y60					32.1	73.3	R.AAGSGVSDYDYLDLDM.K
				Tripeptidyl peptidase II TPP2		Y645					11.7	36.8	K.VNESSHYDLAFTDVHFQKQIR.R
				Tropomyosin 1 alpha chain TPM2		Y162					100.0	36.8	K.YEEVAR.K
				Tropomyosin 3 TPM3		Y162					100.0	17.2	K.HIAEEADRYEEVAR.K
				Tubulin, beta TUBB		Y50					13.9	23.3	R.ISVYNEATGGK.Y
				TUFM TUFM		Y249					16.9	70.9	K.LLDAVDTYIPVPAR.D
				TUFM TUFM		Y269					15.2	69.4	R.DLEKPFLLPVEAVYVPGR.G
Tumor necrosis factor receptor superfamily, member 9				TYK2 TYK2		Y222					100.0	26.5	K.LLYIFK.Q
				TYK2 TYK2		Y292					100.0	40.7	R.LLAQAGEGPCYIR.D
				TYK2 TYK2		Y433					10.9	43.4	R.LTADSSHLCHEVAPPR.L
				Tyrosine kinase, non-receptor, 2 TNK2		Y284					100.0	41.8	R.ALPNQNDHYVMQEHR.K
				Tyrosine kinase, non-receptor, 2 TNK2		Y827					29.1	56.1	K.YATPQVIQAPGPRA
				Tyrosine kinase, non-receptor, 2 TNK2		Y859					10.3	14.3	K.VSSTHYLLPERPSYLER.Y
				Tyrosine protein kinase ABL2 ABL1		Y439					10.9	41.9	R.LMFTGDTYTAHAGAK.F
				Tyrosine protein kinase ABL2 ABL2		Y231					53.8	58.6	K.VYVTAESR.F
				Tyrosine-protein kinase PRAG1 PRAG1		Y413					17.3	19.5	R.EATQPEPHYAESTKR.K
				Ubiquitin activating enzyme 1 UBA1		Y55					86.5	75.1	K.NGSEADIDEGLYSR.Q
				UNC112 related protein 2 FERMT3		Y11					46.9	72.9	K.TASGDYIDSSWELR.V
				UNC119 UNC119		Y194					6.3	32.7	K.NTCEHIYDFPPLSEELUSEMIR.H
				UNQ5783 SCIMP		Y131					22.1	31.2	K.TVISPISEYIPEDDYDDVEIPANTEK.A
				Uridine 5'-monophosphate synthase UMPS		Y37					46.9	56.6	K.SGLSSPHYDLR.G
				Vacuolar protein sorting 35 vPS35		Y791					48.5	27.6	R.ESPESEGPYEGIL.-
				Vasodilator stimulated phosphoprotein VASP		Y39					14.8	14.5	R.VQIYHNPTANSFR.V
				VAV1 VAV1		Y267					91.2	92.5	K.EALGTPGAANLYQVFIK.Y
				VAV1 VAV1		Y844					30.2	20.0	R.VGWFPANYVEEDYSEY.C.-
				VAV1 VAV1		Y791					100.0	25.4	K.ARYDFCAR.D
				VAV1 VAV1		Y826					100.0	20.5	R.GEYYGR.V
				VAV2 VAV2		Y142					37.1	64.0	K.GIRPFPSEETTENDDDVYR.S
				VAV3 VAV3		Y539					28.2	49.8	R.GTFYQGYLQFK.C
				VAV3 VAV3		Y265					93.0	100.9	K.NDQNLYYQVFINYK.E
				VAV3 VAV3		Y367					100.0	26.5	K.DLAQYVNEVK.R
				Vigilin HDLBP		Y437					100.0	16.8	R.MDYVEINIDHK.F
				Vimentin VIM		Y61					43.2	63.1	R.SLYASSPGGVYATR.S
				Vimentin VIM		Y53					13.4	26.9	R.SLYASSPGGVYATR.S
				WD repeat protein 1 WDR1		Y238					53.7	109.7	K.AHDGGIYAISWSPDSTHLLSASGDK.T
Williams Beuren syndrome chromosome EIF4H reation 1				Y12							33.8	33.7	R.AYSSFGGGR.G
				Wiskott-aldrich syndrome protein WAS		Y291					100.0	94.4	K.LIYDFIEDQGGLEAVR.Q
				Wiskott-Aldrich syndrome-like WASL		Y256					100.0	39.1	K.VIYDFIEK.T
				ZAP70 ZAP70		Y492					16.9	97.4	K.ALGADDYYTAR.S
				ZAP70 ZAP70		Y292					32.3	55.2	R.IDTLNSDGYTPEPAR.I

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				5	6	5	6			
<10	0									
10	1									
20	2									
40	4									
60	6									
70	7									
80	8									
90	9									
>100	>100									
Protein Name	Gene	Phosphosites								
ZAP70	ZAP70	Y397						100.0	54.3	R.EAQIMHQLDNP ^Y IVR.L
ZAP70	ZAP70	Y492Y493						28.4	81.2	K.ALGADDS ^Y ^Y TAR.S
ZAP70	ZAP70	Y493						16.9	79.0	K.ALGADDS ^Y ^Y TAR.S
ZAP70	ZAP70	S491Y493						12.1	27.4	K.ALGADDS ^Y ^Y ^Y TAR.S
ZAP70	ZAP70	T286Y292						9.7	45.8	R.RIDT ^T LNSDG ^Y TPEPAR.I
ZAP70	ZAP70	Y319						7.3	30.7	R.ITSPDKPRPMPMDTSVYES ^P ^Y SDPEELKDK.K
ZAP70	ZAP70	Y315						9.4	19.5	R.ITSPDKPRPMPMDTSV ^Y ESPYSDPEELKDK.K
Zinc finger protein 147	TRIM25	Y278						39.3	57.9	K.FDTI ^Y QILLK.K
Zinc finger protein 289, ID1 regulated	ARFGAP2	Y445						100.0	21.0	R.EVDAE ^Y EAR.S
Zinc finger protein 598	ZNF598	Y306						100.0	71.1	R.RNEG ^V VGGED ^Y EEVDR.Y
Zinc finger protein A20	TNFAIP3	Y443						20.8	43.0	R.GEAY ^E EPLAWNPEESTGGPHSAPPTAPSPFLSETTAMIK.C
Zinc finger protein, subfamily 1A, member 3	KZF3	Y96						46.9	20.1	R.EYNE ^Y ENIK.L
ZAP70	ZAP70	Y319						7.3	30.7	R.ITSPDKPRPMPMDTSVYES ^P ^Y SDPEELKDK.K