

## Supplemental Tables:

- Supplemental Table S1. Phosphosites which exhibit increased phosphorylation after GH treatment.
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- Supplemental Table S3. Phosphoproteomics data from the first 5 min GH treatment experiment.
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- Supplemental Table S5. Phosphoproteomics data from the 15 min GH treatment experiment.

The data sets generated by this project may be accessed from the Tranche data repository ([www.proteomecommons.org](http://www.proteomecommons.org): under 'browse data', search for 'Carter-Su C').

The Hash codes for the data sets are:

1) MSMS peak lists:

VkNbKTbCv4khOExPkFJqN+Tb3O3Xm0eAmylXmQTRwKN5zJRUX34Ozs  
w5fjPn0+T2TATDyp/rYMvALluT+LEbhE/TVtQAAAAAAAAALTw==

2) RAW data files:

d3O/sgIU9t9fDTFC2GDO9YJ05Gh5bBo1SYxT7BtQJ1xd79X07CphAHIEIK  
xgx6s03WWzHfEcc7WcNtdFmZswh7EwqHkAAAAAAB/dQ==

Supplemental Table S1. Phosphosites which exhibit increased phosphorylation after GH treatment.									
Gene Name	Protein Name	Phosphosite <sup>1</sup>	# of phosphosites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite	Function of protein <sup>4</sup>
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Max. ratio <sup>3</sup>		
9-Sep	Septin 9	[Ser41 =Thr42]	1	[1.4]	-	-	1.4	Unknown	Cytoskeleton, binds cytoskeleton, cytokinesis, exocytosis, GTP binding protein
6330577E15 Ri	Uncharacterized protein C10 of 78 homolog	[Thr70 =Ser71]	1	-	-	[1.5]	1.5	Unknown	Unknown
Acin1	Apoptotic chromatin condensation inducer in the nucleus	Ser710	1	-	1.8	-	1.8	Unknown	Apoptosis, chromatin condensation
Acly	ATP-citrate lyase	Ser455	1	1.5	-	-	1.5	Increases catalytic activity (1)	Metabolic process, acetyl-CoA synthesis, lipid synthesis
Ahnak	AHNAK nucleoprotein 1	[Ser5557 >Ser5566 =Thr5567]	1	[2.1]	-	-	2.1	Unknown	Cytoskeleton
Ahnak	AHNAK nucleoprotein 1	[Thr5569 >Thr5567 >Thr5571 >Ser5555 >Ser5566]	2	[2.5]	-	-	2.5	Unknown	Cytoskeleton
Ahnak	Ahnak	Ser136	1	3.4	4.5	5.2	5.2	Unknown	Cytoskeleton
Ahnak	Ahnak	Ser217	1	-	-	2.4	2.4	Unknown	Cytoskeleton
Ahnak	Ahnak	Ser4890	1	2.2	2.5	3.7	3.7	Unknown	Cytoskeleton
Ahnak2	AHNAK nucleoprotein 2	Ser652	1	-	2.4	-	2.4	Unknown	Cytoskeleton
Akap1	A-kinase anchor protein 1, mitochondrial	Ser109 - isoforms 1,3,5,6 (Ser142 - isoforms 2,4)	1	1.5	-	-	1.5	Unknown	Adaptor
Akap2	A-kinase anchor protein 2	[Thr738 >Ser740] [(Thr982 >Ser984)]	1	-	[2.2]	-	2.2	Unknown	Adaptor
Akap2	A kinase anchor protein 2	Ser740 (Ser984)	1	-	1.9	1.6	1.9	Unknown	Adaptor
Akt1s1	Proline-rich AKT1 substrate 1 (PRAS40)	Ser184 (Ser255)	1	-	2.2	3.9	3.9	Regulates PRAS40 interaction with raptor (2)	Apoptosis, mTORC1 complex
Akt1s1	Proline-rich AKT1 substrate 1 (PRAS40)	Thr247 (Thr318)	1	3.8	-	-	3.8	Prevents PRAS40 inhibition of mTORC1 (3)	Apoptosis, mTORC1 complex
Arfgap2	ADP-ribosylation factor GTPase-activating protein 2	Ser145	1	-	1.7	-	1.7	Unknown	GAP
Atp6v0a2	V-type proton ATPase 116 kDa subunit a isoform 2	Ser695	1	1.4	-	-	1.4	Unknown	Endosomal pH sensing

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Bat2	Large proline-rich protein BAT2	Ser761	1	-	1.5	-	1.5	Unknown	mRNA processing, RNA splicing
Bckdha	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	Ser334 (Ser338)	1	1.6	1.0 <sup>s</sup>	-	1.6	Unknown	Metabolic process, leucine oxidation, (maple syrup urine disease <sup>5</sup> )
Bcl9l	B-cell CLL/lymphoma 9-like protein	[Ser116 >Ser118]	1	-	[2.8]	-	2.8	Unknown	Transcription, interacts with $\beta$ -catenin, nuclear import
Bcl9l	B-cell CLL/lymphoma 9-like protein	Ser118	1	-	2.4	-	2.4	Unknown	Transcription, interacts with $\beta$ -catenin, nuclear import
Bclaf1	Bcl-2-associated transcription factor 1	Ser383	1	1.6	1.3 <sup>s</sup>	1.0 <sup>s</sup>	1.6	Unknown	Transcription, transcription factor, apoptosis,
Cad	Carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Ser1859	1	-	1.9	-	1.9	Unknown	Metabolic process, pyrimidine synthesis
Cast	Calpastatin	Ser219	1	-	1.5	-	1.5	Unknown	Protease inhibitor, inhibits calpain
Cbx5	Chromobox protein homolog 5	Ser95 (Ser93)	1	-	2.0	-	2.0	Unknown	Transcription, interacts with methylated histone H3, epigenic repression
Cd2ap	CD2-associated protein	Ser458	1	-	1.5	-	1.5	Unknown	Adaptor, cytoskeleton, cell migration, filtration in kidney, (focal segmental glomerulosclerosis <sup>5</sup> )
Cic	Protein capicua homolog	[Ser2280 >Thr2283 =Ser2284 >Ser2275 =Thr2277]	2	[1.4]	-	-	1.4	Unknown	Transcription
D930048N14 Rik	Novel protein	Thr15	1	-	4.1	-	4.1	Unknown	Unknown
Dact3	Dapper homolog 3	Ser409	1	2.2	-	-	2.2	Unknown	Antagonist of $\beta$ -catenin
Dap	Death-associated protein 1	Thr56	1	-	22	-	22	Unknown	Autophagy, negatively regulates autophagy, apoptosis, inhibition of NF- $\kappa$ B transcription factor
Dcaf8	DDB1- and CUL4-associated factor 8; Wdr42a	Ser123, Ser124	2	1.5	-	-	1.5	Unknown	Ubiquitin, ubiquitination
Dpysl3	Collapsin response mediator protein 4A isoform 3	Ser101	1	-	1.7	-	1.7	Unknown	Cytoskeleton, cytoskeletal remodeling, axon guidance
Eif4b	Eukaryotic translation initiation factor 4B	[Thr420 >Ser422]	1	-	[3.1]	-	3.1	Increases interaction Eif4b with Eif3 (4) and Eif4b activity (5)	Translation, binding mRNA to ribosomes

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				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Max. ratio <sup>3</sup>		
Finc	Filamin-C	Ser2234	1	3.3	2.3	1.7	3.3	Unknown	Cytoskeleton
Fnbp11	Formin-binding protein 1-like	Ser295	1	-	2.5	-	2.5	Unknown	Adaptor, promotes CDC42-induced actin polymeration, membrane invagination and tubulation
Frs2	Fibroblast growth factor receptor substrate 2	Thr326	1	1.8	-	-	1.8	Unknown	Adaptor, ras/MAPK pathway, cell proliferation, organ development
Gm15128	Novel protein similar to ovary testis transcribed (Ott)	Ser384, Ser388	2	-	1.5	-	1.5	Unknown	Unknown
Gsta3	Glutathione S-transferase A3	Thr68, Tyr74	2	-	-	1.7	1.7	Unknown	Metabolic process
Hmgn1	Non-histone chromosomal protein HMG-14	[Thr70 =Thr71 >Ser84 =Ser87]	2	-	[1.6]	-	1.6	Unknown	DNA binding, chromatin architecture
Irf2bp2	interferon regulatory factor 2 binding protein 2	Ser421	1	2.2	-	-	2.2	Unknown	Transcription, repressor
Irs2	Insulin receptor substrate 2	Ser556	1	-	1.5	-	1.5	Unknown	Adaptor, signal transduction
Itr3	Inositol 1,4,5-trisphosphate receptor type 3	Ser934	1	-	1.7	-	1.7	Unknown	Receptor, release of intercellular Ca
Kif21a	Kinesin-like protein KIF21A	Ser855	1	-	2.1	-	2.1	Unknown	Cytoskeleton, motor protein, neuronal axon transport
Larp7	La-related protein 7	[Thr251 >Ser253]	1	-	[1.6]	-	1.6	Unknown	Transcription, suppresses RNA polymerase II mediated transcription
Lima1	LIM domain and actin-binding protein 1	Ser230	1	-	1.5	-	1.5	Unknown	Cytoskeleton, actin binding, inhibits depolymerization of actin filaments
Map1b	Microtubule-associated protein 1B	Ser1793	1	-	-	1.6	1.6	Unknown	Cytoskeleton
Map1b	Microtubule-associated protein 1B	Ser614	1	-	-	1.6	1.6	Unknown	Cytoskeleton
Mapk1	Mitogen-activated protein kinase 1 (Erk2)	[Thr179 >Thr183 =Tyr185 =Thr188]	1	-	[8.7]	-	8.7	Function pThr179 and pThr188 unknown. pThr183 and pTyr185 required for activation (6)	Kinase
Mapk1	Mitogen-activated protein kinase 1 (Erk2)	Thr183 [Tyr185 =Thr188 >Thr179]	2	9.5	-	-	9.5	pThr183 and pTyr185 required for activation (6). Functionp Thr188 and pThr179 unknown.	Kinase
Mapk1	Mitogen-activated protein kinase 1 (Erk2)	Thr183, Tyr185	2	11	-	-	11	pThr183 and pTyr185 required for activation (6)	Kinase
Mapk1	Mitogen-activated protein kinase 1 (Erk2)	Tyr185	1	2.4	2.4	-	2.4	Required for kinase activation (6)	Kinase

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Mapk1	Mitogen-activated protein kinase 1 (Erk2)	Tyr185 [Thr179 =Thr183]	2	5.4	-	-	5.4	Function pThr179 unknown pThr183 and pTyr185 required for kinase activation (6)	Kinase
Mapk3	Mitogen-activated protein kinase 3 (Erk1)	[Thr208 >Tyr205]	1	-	[3.0]	-	3.0	Function pThr208 unknown. pTyr205 required for activation (6)	Kinase
Mapk3	Mitogen-activated protein kinase 3 (Erk1)	Thr199 [Thr203 =Tyr205]	2	6.7	-	-	6.7	Function of pThr199 unknown. pThr203 and pTyr185 required for activation (6)	Kinase
Mapk3	Mitogen-activated protein kinase 3 (Erk1)	Thr208 [Thr203 >Tyr205 >Thr199]	2	4.8	-	-	4.8	Function pThr208 and pThr199 unknown, pThr203 and pTyr205 required for activation (6)	Kinase
Mapk3	Mitogen-activated protein kinase 3 (Erk1)	Tyr205	1	3.5	2.9	-	3.5	Required for activation (6)	Kinase
Matr3	Matrin-3	Ser188	1	1.7	1.8	-	1.8	Unknown	mRNA processing, component of nuclear matrix
Matr3	Matrin-3	Ser195	1	-	2.0	-	2.0	Unknown	mRNA processing, component of nuclear matrix
Med19	Mediator of RNA polymerase II transcription subunit 19	Ser226 >Ser234 =Ser235 =Ser238 =Ser239 =Ser240 =Ser241 =S242	7	-	9.6	-	9.6	Unknown	Transcription, mediates RNA polymerase II transcription
Mia3	Melanoma inhibitory activity protein 3	Ser1915	1	-	-	1.7	1.7	Unknown	Vesicle-mediated transport
Myh9	Myosin-9	[Thr1938 =Ser1942] ([Thr1939 =Ser1943])	1	[1.4]	[1.1 <sup>§</sup> ]	[1.0 <sup>§</sup> ]	1.4	Unknown	Cytoskeleton, motor protein
Ncbp1	Nuclear cap-binding protein subunit 1	Ser22	1	-	2.2	-	2.2	Unknown	Translation, RNA splicing
Ncoa5	Nuclear receptor coactivator 5	Ser29, Ser34	2	-	1.6	-	1.6	Unknown	Transcription, interacts with steroid nuclear receptors
NdrG1	Protein NDRG1	Ser330	1	-	1.5	-	1.5	Primes NDRG1 for phosphorylation by GSK3 (7) and required for suppressive effect on NFκβ signaling (8)	Induced by hypoxia and stress, rab4a effector, interacts with p53 signaling, regulates growth and differentiation during development, (Charcot-Marie-Tooth disease type 4D <sup>5</sup> )
NdrG1	Protein NDRG1	Thr328	1	-	1.8	-	1.8	Primes NDRG1 for phosphorylation by GSK3 (7) and required for suppressive effect on NFκβ signaling (8)	Induced by hypoxia and stress, rab4a effector, interacts with p53 signaling, regulates growth and differentiation during development, (Charcot-Marie-Tooth disease type 4D <sup>5</sup> )
Nr3c1	Glucocorticoid receptor;	Thr159 (Thr168)	1	-	1.8	-	1.8	Unknown	Receptor, receptor for glucocorticoids, transcription factor

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Oxr1	Oxidation resistance protein 1	Ser113 (Ser201 or 194)	1	2.5	2.4	-	2.5	Unknown	Mitochondrial protein, induced by heat and oxidative stress
Oxr1	Oxidation resistance protein 1	Ser114 (Ser195)	1	-	2.1	-	2.1	Unknown	Mitochondrial protein, induced by heat and oxidative stress
Parva	Alpha-parvin	Thr16, Ser19	2	-	1.5	-	1.5	Unknown	Adaptor, actin cytoskeleton, cell adhesion
Pdcd4	Programmed cell death protein 4	Ser457	1	-	3.8	-	3.8	Results in nuclear translocation of Pdcd4 (9)	Apoptosis
Pdcd4	Programmed cell death protein 4	Ser76	1	-	3.5	-	3.5	Mediates Pdcd4 interaction with betaTRCP (10)	Apoptosis
Pgrmc1	Membrane-associated progesterone receptor component 1	Tyr180	1	1.4	1.3 <sup>s</sup>	-	1.4	Unknown	Receptor, receptor for progesterone
Phf3	PHD finger protein 3	[Ser658 >Ser660]	1	-	[3.5]	-	3.5	Unknown	Transcription,
Phldb2	Pleckstrin homology-like domain family B member 2	Thr468	1	-	1.8	-	1.8	Unknown	Vesicle protein, interacts with filamin-C
Pi4k2a	Phosphatidylinositol 4-kinase type 2-alpha	[Ser460 >Ser462]	1	-	-	[2.3]	2.3	Unknown	Kinase, lipid, inositol P3 pathway
Pkn2	Serine/threonine-protein kinase N2	[Ser581 =Ser582]	1	-	[6.7]		6.7	Unknown	Kinase, AGC kinase
Pkn2	Serine/threonine-protein kinase N2	Thr957	1	-		1.6	1.6	Unknown	Kinase, AGC kinase
Plec1	Plectin-1	[Ser4391 >Ser4392 >Ser4393] [(Ser4243 >Ser4244 >Ser4245)]	1	-	[2.1]	-	2.1	Unknown	Cytoskeleton, crosslinks actin, intermediate filaments, microtubules; scaffold - binds MAPK, RACK1, (epidermolysis bullosa simplex 1 <sup>5</sup> )
Plec1	Plectin-1	[Thr19 >Ser21]	1	-	-	[1.6]	1.6	Unknown	Cytoskeleton, crosslinks actin, intermediate filaments, microtubules; scaffold - binds MAPK, RACK1, (epidermolysis bullosa simplex 1 <sup>5</sup> )
Plec1	Plectin-1	Ser4393 (Ser4245)	1	1.6	2.1	1.3 <sup>s</sup>	2.1	Unknown	Cytoskeleton, crosslinks actin, intermediate filaments, microtubules; scaffold - binds MAPK, RACK1, (epidermolysis bullosa simplex 1 <sup>5</sup> )
Ppfbp1	Liprin-beta-1	Ser957, Ser961 (Ser992, Ser996)	2	-	1.5	-	1.5	Unknown	Adaptor, interacts with LAR protein tyrosine phosphatases, axon guidance and mammary development
Ppp1r12a	Protein phosphatase 1 regulatory subunit 12A	[Ser870 >Ser877]	1	-	[1.7]	-	1.7	Unknown	Phosphatase, regulates interaction of actin and myosin

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				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Max. ratio <sup>3</sup>		
Ppp1r12a	Protein phosphatase 1 regulatory subunit 12A	Ser507	1	6.9	8.6	-	8.6	Unknown	Phosphatase, regulates interaction of actin and myosin
Ppp1r12a	Protein phosphatase 1 regulatory subunit 12A	Ser509	1	4.0	-	-	4.0	Unknown	Phosphatase, regulates interaction of actin and myosin
Ppp1r12a	Protein phosphatase 1 regulatory subunit 12A	Ser861	1	1.5	-	-	1.5	Unknown	Phosphatase, regulates interaction of actin and myosin
Ptpn2	Protein tyrosine phosphatase, receptor type, N polypeptide 2, isoform	Ser89	1	-	104.9	-	104.9	Unknown	Phosphatase, protein tyrosine phosphatase
Rai14	Ankycorbin	Ser914	1	1.5	-	-	1.5	Unknown	Adaptor
Ranbp3	Ran-binding protein 3	Ser58	1	-	2.5	-	2.5	Important for nuclear export function (11)	Adaptor, nuclear export
Raver1	Ribonucleoprotein PTB-binding 1	Ser576	1	-	1.9	-	1.9	Unknown	mRNA processing, regulates switching between alternative RNA splicing events
Rbm17	Splicing factor 45	Ser155	1	1.7	1.4 <sup>§</sup>	1.0 <sup>§</sup>	1.7	Unknown	mRNA processing, RNA splicing
Rbmx	Heterogeneous nuclear ribonucleoprotein G	Ser165	1	-	1.5	-	1.5	Unknown	mRNA processing, RNA splicing
Rgs2	Regulator of G-protein signaling 2	Ser19	1	-	12.2	-	12.2	Unknown	GAP, brown fat cell differentiation
Rnf220	E3 ubiquitin-protein ligase Rnf220	Thr474	1	-	-	5.6	5.6	Unknown	Ubiquitin
Rptor	Regulatory-associated protein of mTOR (raptor)	Ser863	1	1.5	2.0	1.9	2.0	Required for hierarchical raptor phosphorylation and plays a critical role in mTOR activity (12, 13)	Adaptor, mTORC1
Sdpr	Serum deprivation-response protein	Ser359	1	1.6	-	-	1.6	Unknown	Lipid binding protein, binds phosphatidylserine
Senp7	Sentrin-specific protease 7	Ser12	1	-	2.7	-	2.7	Unknown	Protease, deconjugation of SUMO2 and SUMO3 chains
Sgta	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	[Ser303 >Thr305]	1	-	[2.0]	-	2.0	Unknown	Chaperone
Shc1	SHC-transforming protein 1	Tyr423	1	-	3.7	-	3.7	Binds Grb2 (14)	Adaptor, ras/MAPK pathway
Sipa1l2	Signal-induced proliferation-associated 1-like protein 2	Ser1461	1	-	-	1.6	1.6	Unknown	Regulation GTPase

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Slc9a1	Sodium/hydrogen exchanger 1 (Nhe1)	Ser707	1	-	7.3	3.3	7.3	Binds 14-3-3 and is required for serum-induced activation of Nhe1 (15)	Ion channel, regulates pH, regulation of cell growth, differentiation
Srrm1	Serine/arginine repetitive matrix protein 1	[Ser461 >Ser463]	1	-	[2.8]	-	2.8	Unknown	mRNA processing, RNA splicing, RNA export
Srrm2	Serine/arginine repetitive matrix protein 2	Ser2224	1	-	2.9	-	2.9	Unknown	mRNA processing, RNA splicing
Stat5a	Signal transducer and activator of transcription 5a	Tyr694	1	-	+GH only	+GH only	199	Required for Stat5a activation (16)	Transcription
Stat5b	Signal transducer and activator of transcription 5b	Tyr699	1	-	+GH only	+GH only	199	Required for Stat5b activation (16)	Transcription
Stk10	Serine/threonine kinase 10	Thr950	1	-	2	2.3	2.3	Unknown	Kinase, lymphocyte-oriented kinase
Stmn1	Stathmin	Ser25	1	-	7.6	-	7.6	Unknown	Cytoskeleton, promotes disassembly of microtubules
Tbc1d15	TBC1 domain family member 15	Ser201	1	-	-	1.6	1.6	Unknown	GAP, GAP for rab family proteins
Tnks1bp1	182 kDa tankyrase-1-binding protein	Ser1022	1	-	2.5	-	2.5	Unknown	Cytoskeleton, actin binding
Tnks1bp1	182 kDa tankyrase-1-binding protein	Ser1375	1	-	1.5	1.8	1.8	Unknown	Cytoskeleton, actin binding
Tns3	Tensin-3	Ser769	1	2.0	-	-	2.0	Unknown	Adaptor
Top2b	DNA topoisomerase 2-beta	Ser1387 (Ser1537)	1	1.5	1.9	1.0 <sup>§</sup>	1.9	Unknown	DNA binding, makes transient double strand breaks in DNA
Tpr	Nuclear pore complex-associated intranuclear protein TPR	Ser2149	1	-	6.3	-	6.3	Unknown	Nuclear matrix protein, mitotic cell cycle spindle assembly checkpoint
Trim28	Transcription intermediary factor 1-beta	Ser471	1	-	-	2.3	2.3	Unknown	Kinase, regulates transcription
Trim28	Transcription intermediary factor 1-beta	Ser473	1	-	1.5	2.4	2.4	Regulates Trim28 interaction with HP1beta (17)	Kinase, regulates transcription
Trim47	Tripartite motif-containing protein 47	Ser591 (Ser592)	1	-	-	2.0	2.0	Unknown	Ubiquitin
Trio	Triple functional domain protein	Ser2399, Ser2403 (Ser2575, 2579)	2	-	5.0	-	5.0	Unknown	GEF, protein kinase, apoptosis



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Tsc2	Tuberin	[Ser939 >Thr940 >Ser941] [(Ser937 >Thr938 >Ser939)]	1	-	[1.9]	-	1.9	Phosphorylation Ser939 promotes interaction with 14-3-3 and relieves inhibition of mTOR signaling (18)	GAP, negative regulator of mTOR signaling, tumor suppressor
Twist1	Twist-related protein 1	Ser68	1	1.6	-	-	1.6	Unknown	Transcription, binds E Box sequences, represses TNF $\alpha$ and IL1 $\beta$ , regulates FGFR2, forelimb morphogenesis, muscle development, neuronal migration
Twist2	Twist-related protein 2	Ser55	1	1.6	-	-	1.6	Unknown	Transcription, binds E Box consensus sequence, represses expression of TNF $\alpha$ and IL1 $\beta$
Usp10	Ubiquitin carboxyl-terminal hydrolase 10	Ser223	1	-	3.8	-	3.8	Unknown	Ubiquitin, disassembles ubiquitin chains
Wdr48	WD repeat-containing protein 48	Ser586	1	-	-	5.0	5.0	Unknown	Vesicle protein, lysosomal protein
Zc3hc1	Nuclear-interacting partner of ALK (Nipa)	Ser394	1	-	-	1.8	1.8	Unknown	Ubiquitin, nuclear protein, inactivation increases cyclin B1 levels and mitotic entry
Zc3hc1	Nuclear-interacting partner of ALK (Nipa)	Ser406	1	-	2.6	-	2.6	Unknown	Ubiquitin, nuclear protein, inactivation increases cyclin B1 levels and mitotic entry
Zyx	Zyxin	Ser336	1	-	1.8	-	1.8	Unknown	Cytoskeleton, focal adhesions, cell-cell adherens junctions
<sup>1</sup> Residue numbering is according to PhosphositePlus ( <a href="http://www.phosphosite.org">http://www.phosphosite.org</a> ).									
( ) When residue numbering varies between Phosphosite and MaxQuant, MaxQuant numbering is listed in parentheses.									
[ ] Residues in brackets refer to unlocalized sites (localization probability <0.75 and > 0.15, see Supplemental Tables 3 - 5).									
<sup>2</sup> Phosphosites with a significant (B<0.05) increase correspond to sites with an increase greater than ~40% (5 min <sup>a</sup> trial) and ~50% (5 min <sup>b</sup> and 15 min trials). For statistically significant phosphosites, if the same phosphosite was detected in another of the other trials, the ratio in the other trial is also listed in the table even if not significant. Ratios that are not significant are indicated with §. The ratios are normalized to correct for unequal amounts of "light" and "heavy" protein in the assay.									
<sup>3</sup> The maximum normalized ratio (+GH/-GH) in the three trials. To facilitate sorting, the ratio was defined as 199 for phosphosites detected in only the +GH condition.									
<sup>4</sup> Function of proteins that contain the phosphopeptides identified during the SILAC-based phosphoproteomic screens were classified according to the functions tabulated in Phosphosite Plus ( <a href="http://www.phosphosite.org">http://www.phosphosite.org</a> (January 28, 2011)). Information in Phosphosite includes information from UniProtKB. The first function listed is the category used to construct the pie charts in Fig 4A,B.									
<sup>5</sup> The disease in parentheses is caused by a mutation in the protein containing the identified phosphosite.									
<b>References (Supplemental Table 1)</b>									
1. Potapova IA, El-Maghrabi MR, Doronin SV, Benjamin WB 2000 Phosphorylation of recombinant human ATP:citrate lyase by cAMP-dependent protein kinase abolishes homotropic allosteric regulation of the enzyme by citrate and increases the enzyme activity. Allosteric activation of ATP:citrate lyase by phosphorylated sugars. <i>Biochemistry</i> 39:1169-1179									



Supplemental Table S2. Phosphosites which exhibit decreased phosphorylation after GH treatment.								
Gene Name	Protein Name	Phosphosite <sup>1</sup>	# of phosphosites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
9-Sep	Septin-9	Ser30	1	-	0.7	-	0.7	Unknown
9-Sep	Septin-9	Thr143	1	-	0.5	-	0.5	Unknown
Acaca	Acetyl-CoA carboxylase 1	Ser29 (S67)	1	-	0.2	-	0.2	Unknown
Ahnak	Ahnak protein	Ser5101	1	0.7	0.8	-	0.7	Unknown
Ahnak	Ahnak protein	Ser5510	1	-	0.7	-	0.7	Unknown
Ahnak	Ahnak protein	Ser5512	1	1.0 <sup>§</sup>	0.6	-	0.6	Unknown
Ahnak	Ahnak protein	Ser5553	1	-	0.7	-	0.7	Unknown
Ahnak	Ahnak protein	Ser5555	1	0.8	0.6	-	0.6	Unknown
Ahnak	Ahnak protein	Ser5563	1	-	0.6	-	0.6	Unknown
Ahnak	Ahnak protein	Thr5571 [Thr5567 ~Thr5569]	2	-	0.7	-	0.7	Unknown
Arhgef7	Rho guanine nucleotide exchange factor 7	Ser580	1	-	-	0.7	0.7	Unknown
BC089491	cDNA sequence BC089491	Ser225 [Ser228 =Thr229]	2	-	0.03	-	0.03	Unknown
Bcor	BCL-6 corepressor	Tyr977	1	0.4	-	-	0.4	Unknown
Bmp10	Bone morphogenetic protein 10	Thr94, Ser101	2	-	-	0.1	0.1	Unknown
Cav1	Caveolin-1	Tyr14	1	-	0.7	-	0.7	Phosphorylated Y14 interacts with Grb7 (1), required for localization to focal adhesions (2)
Clasp1	CLIP-associating protein 1	Ser794 (Ser795)	1	-	0.7	-	0.7	Unknown
Ctnnd1	Catenin delta-1	[Ser320 =Tyr321]	1	-	[0.7]	-	0.7	Unknown
Cx3cl1	Fractalkine	[Ser259 >Ser262]	1	-	[0.7]	-	0.7	Unknown
Cx3cl1	Fractalkine	Ser262	1	-	0.7	-	0.7	Unknown
Dclk1	Serine/threonine-protein kinase DCLK1	[Thr336 =Ser337]	1	-	[0.7]	-	0.7	Unknown
Dclk1	Serine/threonine-protein kinase DCLK1	Ser305	1	-	0.7	-	0.7	Unknown
Dhx9	ATP-dependent RNA helicase A	Ser136 (Ser137)	1	0.6	1.2 <sup>§</sup>	-	0.6	Unknown
Dock9	Dedicator of cytokinesis protein 9	Ser1384, Ser1378	2	-	0.1	-	0.1	Unknown
Dpf2	D4, zinc and double PHD fingers family 2	[Ser142]	1	-	-	[0.6]	0.6	Unknown

Gene Name	Protein Name	Phospho-site <sup>1</sup>	# of phospho-sites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
Dpf2	D4, zinc and double PHD fingers family 2	Ser142	1	1.2 <sup>§</sup>	-	-	1.2	Unknown
Dyrk1a	Dual specificity tyrosine-phosphorylation-regulated kinase 1A	[Tyr321]	1	-	-	[0.7]	0.7	Y321 is an autophosphorylation site that is required for full activity (3)
Dyrk1a	Dual specificity tyrosine-phosphorylation-regulated kinase 1A	Tyr321	1	1.0 <sup>§</sup>	1.1 <sup>§</sup>	-	1	Y321 is an autophosphorylation site that is required for full activity (3)
E130012A19 Rik	Uncharacterized protein C17orf96 homolog	Ser19, Thr24	2	0.04	-	-	0.04	Unknown
Eap1	Enhanced at puberty protein 1	Ser638 (Ser696)	1	1.3 <sup>§</sup>	-	0.5	0.5	Unknown
Eef2	Elongation factor 2	Thr57	1	-	0.6	-	0.6	Phosphorylation T57 inhibits activity (4)
Eif4g1	Eukaryotic translation initiation factor 4 gamma 1	Ser1189	1	-	0.7	-	0.7	Unknown
Epb4.1l2	Erythrocyte protein band 4.1-like 2	[Ser86 >Tyr87]	1	-	[0.7]	-	0.7	Unknown
Fat1	Cadherin FAT1 isoform +12	Ser4475 (Ser4483)	1	-	0.6	-	0.6	Unknown
Gas7	Growth arrest specific 7 similar to DNA cytosine-5 methyltransferase 3B2	Ser62	1	-	0.7	-	0.7	Unknown
Gm14490	DNA cytosine-5 methyltransferase 3B2	Ser290	1	0.04	-	-	0.04	Unknown
Hdgfrp2	Hepatoma-derived growth factor-related protein 2	Ser644	1	0.7	-	-	0.7	Unknown
Hmgn1	Non-histone chromosomal protein HMG-14	[Thr80 >Ser84 >Ser87]	1	-	-	[0.6]	0.6	Unknown
Hnmpul2	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Thr163	1	-	0.7	-	0.7	Unknown
KIAA1143 homolog	Uncharacterized protein KIAA1143 homolog	Ser50	1	0.7	-	-	0.7	Unknown
Kiaa1712	Uncharacterized protein KIAA1712	Thr287, Ser292	2	0.7	-	-	0.7	Unknown
Klc2	Klc2 protein	Ser579	1	0.7	-	-	0.7	Unknown

Gene Name	Protein Name	Phosphosite <sup>1</sup>	# of phosphosites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
Lmna	Lamin-A/C	Ser395 [Ser390 =Ser392 >Thr394]	2	-	0.3	-	0.3	Unknown
Lmna	Lamin-A/C	Thr394, Ser395	2	1.2 <sup>§</sup>	-	-	1.2	Unknown
Map3k2	Mitogen-activated protein kinase kinase kinase 2	Ser164 (Ser180)	1	-	0.6	-	0.6	Unknown
Mast4	Microtubule-associated serine/threonine-protein kinase 4	Ser204	1	0.7	-	-	0.7	Unknown
Mcm2	DNA replication licensing factor MCM2	Ser21	1	0.7	-	-	0.7	Unknown
Mical2	JRAB	Ser766	1		0.5		0.5	Unknown
Mrip	Myosin phosphatase Rho-interacting protein	Ser292	1	0.8	0.7	-	0.7	Unknown
Mre11a	Double-strand break repair protein MRE11A	Ser686	1	-	0.2	-	0.2	Unknown
Myadm	Myeloid-associated differentiation marker	[Ser17 >Ser15 =Ser16 =Thr18 >Thr14 =Thr19 >Thr12 =Thr13]	1	[0.7]	-	-	0.7	Unknown
Myo1c	Myosin-1c	Ser6	1		0.5		0.5	Unknown
Myr12	Myosin regulatory light polypeptide 9	[Thr19 =Ser20]	1	-	[0.6]	-	0.6	Unknown
Myr12	Myosin regulatory light polypeptide 9	Ser20	1	-	0.6	-	0.6	Unknown
Nadk	NAD kinase	Ser46	1	-	0.6	-	0.6	Unknown
Nap114	Nap114 protein	[Thr117 >Ser121 >Ser125 >Thr111]	1	[0.6]	-	-	0.6	Unknown
Ndrp1	N-myc downstream-regulated gene 1 protein	[Ser333 >Thr335 =Ser336 >Ser330 =S332 >Thr328 >Thr340]	1	-	[0.5]	-	0.5	Unknown

Gene Name	Protein Name	Phosphosite <sup>1</sup>	# of phosphosites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
Ndrp1	N-myc downstream-regulated gene 1 protein	[Ser333 >Thr335 =Ser336 >Ser332 >Ser330 >Thr328]	1	[1.3 <sup>§</sup> ]	-	-	1.3	Unknown
Nfia	Nuclear factor 1 A-type	S310	1	-	0.8	0.7	0.7	Unknown
Nherf1	Na(+)/H(+) exchange regulatory cofactor NHERF1	Ser285	1	0.7	-	-	0.7	Unknown
Npm1	Nucleophosmin	[Thr75 =Thr78 >Ser48 >Y67 =Ser70 =Thr42]	1	-	[0.1]	-	0.1	Unknown
Nptx1	Neuronal pentraxin-1	[Ser203, Ser207]	2	-	-	[0.04]	0.04	Unknown
Nudt1	7,8-dihydro-8-oxoguanine triphosphatase	[Tyr7 >Thr8 >Ser2 =Thr3 >Ser4]	2	-	[0.02]	-	0.02	Unknown
Palm	Paralemmin	Thr141, Thr145	2	-	0.6	-	0.6	Unknown
Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	[Thr231 =Ser232]	1	-	[0.7]	-	0.7	Unknown
Pdha1	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Ser232	1	-	0.7	0.9*	0.7	Unknown
Pdim2	PDZ and LIM domain protein 2	Ser199, Ser205	2	0.7	-	-	0.7	Unknown
Pdim2	PDZ and LIM domain protein 2	Ser199, Ser205	2	0.8	-	-	0.8	Unknown
Pgm1	Phosphoglucosyltransferase-1	[Thr115 =Ser117]	1	-	[0.6]	-	0.6	Unknown
Pgm1	Phosphoglucosyltransferase-1	Ser117	1	-	0.7	-	0.7	Unknown
Plec1	Plectin-1	Ser4620 (Ser4472)	1	-	0.7	0.4	0.4	Unknown
Ppap2a	Lipid phosphate phosphohydrolase 1	[Ser274 >Thr272 =Thr275 >Thr268 >Thr267]	1	-	[0.7]	-	0.7	Unknown
Ppap2a	Lipid phosphate phosphohydrolase 1	Ser274	1	0.8 <sup>§</sup>	-	-	0.8	Unknown
Ppap2a	Lipid phosphate phosphohydrolase 1	Thr271 (Thr272)	1	-	0.7	-	0.7	Unknown

Gene Name	Protein Name	Phospho-site <sup>1</sup>	# of phospho-sites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
Ppp1r12a	Ppp1r12a protein	[Ser693 >Thr694]	1	[0.9 <sup>§</sup> ]	-	-	0.9	Phosphorylation of S693 reduces phosphorylation of T694 (5)
Ppp1r12a	Ppp1r12a protein	Ser693	1	-	0.6	-	0.6	Phosphorylation of S693 reduces phosphorylation of T694 (5)
Ppp1r12a	Ppp1r12a protein	Thr694	1	1.1 <sup>§</sup>	0.6	-	0.6	Phosphorylation of T694 inhibits phosphatase activity (6)
Ppp1r2	Putative uncharacterized protein Ppp1r2	Thr117, Ser123 >Ser122 >Ser131	2	0.5	-	-	0.5	Unknown
Prkd3	Protein kinase D3	Ser44	1	0.4	-	-	0.4	Unknown
Pxn	Paxillin	Ser119	1	-	0.6	-	0.6	Unknown
Rad50	DNA repair protein RAD50	Thr564, Ser565 [Ser557 =Ser560]	3	-	[0.5]	-	0.5	Unknown
Rc3h2	Ring finger and CCCH-type zinc finger domain-containing protein 2	Ser895, Ser907	2	-	0.001	-	0.001	Unknown
Scrib	Protein scribble homolog	Ser1543, Ser1548 (Ser1550, Ser1555)	2	-	0.7	-	0.7	Unknown
Sfrs11	Splicing factor, arginine/serine-rich 11, isoform CRA_b	Ser389 (Ser477)	1	-	1.2 <sup>§</sup>	0.7	0.7	Unknown
Skiv2l	MCG15924, isoform CRA_a	[Ser242 >Ser240 =Ser244 =Thr246]	1	[0.6]	-	-	0.6	Unknown
Sntb2	Sntb2 protein	[Ser88 =Ser90]	1	-	-	[0.2]	0.2	Unknown
Sntb2	Beta-2-syntrophin	Ser88	1	-	1.1 <sup>§</sup>	-	1.1	Unknown
Sntb2	Beta-2-syntrophin	Ser90	1	0.9 <sup>§</sup>	0.9 <sup>§</sup>	-	0.9	Unknown
Srrm2	Serine/arginine repetitive matrix protein 2	[Ser1305]	1	-	-	[0.7]	0.7	Unknown
Srrm2	Serine/arginine repetitive matrix protein 2	Ser1305	1	1.1 <sup>§</sup>	1.1 <sup>§</sup>	-	1.1	Unknown
Svil	Supervillin	[Tyr809 >Tyr811] [(Tyr405 >Tyr407)]	1	-	[0.7]	-	0.7	Unknown
Synpo	Synaptopodin	Ser583	1	-	0.1	-	0.1	Unknown

Gene Name	Protein Name	Phosphosite <sup>1</sup>	# of phosphosites	Normalized ratio (+GH/-GH) <sup>2</sup>				Function of phosphosite
				5 min <sup>a</sup>	5 min <sup>b</sup>	15 min	Min. ratio <sup>3</sup>	
Tmpo	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/ilon/gamma	[Ser277 =Thr278]	1	[0.6]	-	-	0.6	Unknown
Tub	Tubby protein	Ser333	1	0.2			0.2	Unknown
Ubash3b	Ubiquitin-associated and SH3 domain-containing protein B	Ser542	1	-	0.2	-	0.2	Unknown
Vasp	Vasodilator-stimulated phosphoprotein	Ser317	1	-	0.5	-	0.5	Unknown
Vim	Vimentin	[Thr417 >Ser419 =Ser420 >Ser412]	1	-	[0.7]	-	0.7	Unknown
<sup>1</sup> Residue numbering is according to PhosphositePlus ( <a href="http://www.phosphosite.org">http://www.phosphosite.org</a> ).								
( ) When residue numbering varies between Phosphosite and MaxQuant, MaxQuant numbering is listed in parentheses.								
[ ] Residues in brackets refer to unlocalized sites (localization probability <0.75 and > 0.15, see Supplemental Tables 3 - 5).								
<sup>2</sup> Phosphosites with a significant (B<0.05) decrease correspond to sites with a decrease less than ~20%. Because the decrease required for significance is small, if borderline phosphosites were detected in a second trial, often the change falls below statistical relevance. To minimize the uncertainty associated with these peptides, for our analysis, we selected phosphosites that decreased by ≥ 30%. For statistically significant phosphosites, if the same phosphosite was detected in another trial, the ratio in the other trial is also listed in the table. Ratios that are not significant are indicated with a §. The ratios are normalized to correct for unequal amounts of "light" and "heavy" protein in the assay.								
<sup>3</sup> The minimum normalized ratio (+GH/-GH) in the three trials.								
<b>References (Supplemental Table 2)</b>								
<ol style="list-style-type: none"> <li>Lee H, Volonte D, Galbiati F, Iyengar P, Lublin DM, Bregman DB, Wilson MT, Campos-Gonzalez R, Bouzahzah B, Pestell RG, Scherer PE, Lisanti MP 2000 Constitutive and growth factor-regulated phosphorylation of caveolin-1 occurs at the same site (Tyr-14) in vivo: identification of a c-Src/Cav-1/Grb7 signaling cassette. <i>Mol Endocrinol</i> 14:1750-1775</li> <li>Nethe M, Anthony EC, Fernandez-Borja M, Dee R, Geerts D, Hensbergen PJ, Deelder AM, Schmidt G, Hordijk PL 2010 Focal-adhesion targeting links caveolin-1 to a Rac1-degradation pathway. <i>J Cell Sci</i> 123:1948-1958</li> <li>Himpel S, Panzer P, Eirnbter K, Czajkowska H, Sayed M, Packman LC, Blundell T, Kentrup H, Grotzinger J, Joost HG, Becker W 2001 Identification of the autophosphorylation sites and characterization of their effects in the protein kinase DYRK1A. <i>Biochem J</i> 359:497-505</li> <li>Redpath NT, Price NT, Severinov KV, Proud CG 1993 Regulation of elongation factor-2 by multisite phosphorylation. <i>Eur J Biochem/ FEBS</i> 213:689-699</li> <li>Wooldridge AA, MacDonald JA, Erdodi F, Ma C, Borman MA, Hartshorne DJ, Haystead TA 2004 Smooth muscle phosphatase is regulated in vivo by exclusion of phosphorylation of threonine 696 of MYPT1 by phosphorylation of Serine 695 in response to cyclic nucleotides. <i>J Biol Chem</i> 279:34496-34504</li> <li>Ichikawa K, Ito M, Hartshorne DJ 1996 Phosphorylation of the large subunit of myosin phosphatase and inhibition of phosphatase activity. <i>J Biol Chem</i> 271:4733-4740</li> </ol>								



Supplemental Table S3. Phosphoproteomics data from the first 5 min GH treatment experiment.														
No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Ph	Ratio Signific	Up-/Down-re	Phosphosites localized?
393	IPI00229328	1110037F02Rik protein	1110037F02Rik;Kiaa142	S1628	1	8	SFLSEPS5SPGR	SFLSEPS(0.05)/S(0.949)P	SFLSEPS(ph)PGR	WW GroupIV	1.1	0.36872		Yes
227	IPI00458153	Uncharacterized protein	6330577E15Rik;633057	S67	1	5	ENPPSPPTSPAAPQPR	ENPPS(0.999)PPT(0.00)	ENPPS(ph)PPTSPAAPQPR	WW GroupIV	0.9	0.2209		Yes
169	IPI00458153	Uncharacterized protein	6330577E15Rik;633057	T70	1	8	ENPPSPPTSPAAPQPR	ENPPS(0.122)PPT(0.85)	ENPPSPPT(ph)SPAAPQPR	CK1	0.9	0.15415		Yes
559	IPI00753321	Antigen containing epit	A230054D04Rik;AF013	S2909	1	3	SVSETSEDKKDEESDEEE	S(0.092)VS(0.276)ET(0.	SVS(ph)ETSEDKKDEESDEEE	PLGATTR				No
561	IPI00753321	Antigen containing epit	A230054D04Rik;AF013	S2912	1	6	SVSETSEDKKDEESDEEE	S(0.092)VS(0.276)ET(0.	SVS(ph)ETSEDKKDEESD	CK1				No
462	IPI00753321	Antigen containing epit	A230054D04Rik;AF013	S2920	1	14	SVSETSEDKKDEESDEEE	SVSETS(0.001)EDKKDEE	SVSETSEDKKDEES(ph)D	CK2	1.0	0.424		Yes
560	IPI00753321	Antigen containing epit	A230054D04Rik;AF013	T2911	1	5	SVSETSEDKKDEESDEEE	S(0.092)VS(0.276)ET(0.	SVS(ph)ETSEDKKDEESD	FHA1 Ra53p				No
150	IPI00458612	AP2-associated protein	Aak1;Kiaa1048;Aak1;Kia	T604	1	4	VQTTPTPTIQQGQK	VQT(0.005)T(0.995)PPP	VQTT(ph)PPTIQQGQK		0.9	0.1304		Yes
440	IPI00396671	ATP-binding cassette su	Abcf1;Abcf1	S103	1	5	LKQLSVPASDEEDEVPA	LKQLS(0.994)VPAS(0.00	LKQLS(ph)VPASDEEDEV	GSK3	1.1	0.4071		Yes
370	IPI00396671	ATP-binding cassette su	Abcf1;Abcf1	S107	1	9	LKQLSVPASDEEDEVPA	LKQLS(0.004)VPAS(0.99	LKQLSVPAS(ph)DEEDEV	CK2	1.0	0.35344		Yes
398	IPI00396671	ATP-binding cassette su	Abcf1;Abcf1	S138	1	13	GGNVFEALIQDDSEEEEE	GGNVFEALIQDDSD(1)EEE	GGNVFEALIQDDSD(ph)E	CK2	1.1	0.37209		Yes
407	IPI00922962	Apoptotic chromatin co	Acin1;RP23-94B13.1-00	S477	1	1	SLSPSLGTTDTK	S(0.643)LS(0.357)PLSGT	S(ph)LSPLSGTTDTK	NEK6	1.0	0.38041		No
238	IPI00922962	Apoptotic chromatin co	Acin1;RP23-94B13.1-00	S479	1	3	SLSPSLGTTDTK	S(0.178)LS(0.821)PLS(0.	SLS(ph)LSGTTDTK	CHK1/2	1.2	0.22542		Yes
562	IPI00922962	Apoptotic chromatin co	Acin1;RP23-94B13.1-00	S387	1	1	SQSPSPPLPEDLEK	S(0.418)QS(0.291)PS(0.	S(ph)SQSPSPPLPEDLEK	GSK3				No
186	IPI00922962	Apoptotic chromatin co	Acin1;RP23-94B13.1-00	S389	1	3	SQSPSPPLPEDLEK	S(0.12)QS(0.827)PS(0.0	SQSPSPPLPEDLEK		1.3	0.1683		Yes
49	IPI00126248	Putative uncharacterize	Acly;Acly;Acly;RP23-39	S455	1	3	TASFESRADEVAPAKK	T(0.185)AS(0.772)FS(0.	TAS(ph)FESRADEVAPAK	PKA/AKT	1.5	0.017006	Up	Yes
563	IPI00126248	Putative uncharacterize	Acly;Acly;Acly;RP23-39	S457	1	5	TASFESRADEVAPAKK	T(0.072)AS(0.051)FS(0.	TASF(ph)FESRADEVAPAK	CK1				No
564	IPI00126248	Putative uncharacterize	Acly;Acly;Acly;RP23-39	S459	1	7	TASFESRADEVAPAKK	T(0.072)AS(0.051)FS(0.	TASF(ph)FESRADEVAPAK	CK1				No
180	IPI00126248	Putative uncharacterize	Acly;Acly;Acly;RP23-39	S481	1	12	AKPAMPQDSVPSPPR	AKPAMPQDS(0.001)VP	AKPAMPQDSVPS(ph)PR	ERK/MAPK	0.9	0.1618		Yes
565	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S464	1	18	WLHSGRGDDASEEGQN	WLHSGRGDDAS(0.004)	WLHSGRGDDASEEGQN	GSK3				Yes
420	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S465	1	19	WLHSGRGDDASEEGQN	WLHSGRGDDASEEGQN	WLHSGRGDDASEEGQN	Polo box	1.0	0.39207		Yes
566	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1;	S679	1	12	TEEVLPDGSPPSKSPK	TEEVLPDGS(0.004)PS(0.	TEEVLPDGSPPSKSPK	GSK3				No
477	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1;	S681	1	14	TEEVLPDGSPPSKSPK	TEEVLPDGSPPSKS(0.94)	TEEVLPDGSPPSKS(ph)P	CDK2	1.1	0.44426		Yes
567	IPI00890205	AF4/FMR2 family, mem	Aff2;RP23-324H24.1-00	S580	1	2	LSTSDVTVSQR	LS(0.949)T(0.05)SVDTV	LS(ph)SVDTVTVSQR					Yes
367	IPI00553798	Ahnak protein	Ahnak	S116	1	7	SSEVVLGDDDEDYQR	SSEVVL(1)GDDEDYQR	SSEVVL(ph)GDDEDYQR		1.0	0.35164		Yes
13	IPI00553798	Ahnak protein	Ahnak	S136	1	3	LRSEEDGVEGDLGETQSR	LRS(1)EDGVEGDLGETQSR	LRS(ph)EDGVEGDLGETQ	CAMK2	3.4	9.769E-13	Up	Yes
408	IPI00553798	Ahnak protein	Ahnak	S211	1	7	TVIRLPSGSGPASPTTGS	T(0.003)VIRLPS(0.82)GS	TVIRLPS(ph)GSGPASPTT	PKD	1.0	0.38101		Yes
114	IPI00553798	Ahnak protein	Ahnak	S217	1	13	TVIRLPSGSGPASPTTGS	TVIRLPSGSGPAS(0.969)	TVIRLPSGSGPAS(ph)PTT	WW GroupIV	1.3	0.092133		Yes
22	IPI00553798	Ahnak protein	Ahnak	S4890	1	9	FKAEPALPSPK	FKAEPALPS(1)PK	FKAEPALPS(ph)PK	CDK1	2.2	3.346E-06	Up	Yes
515	IPI00553798	Ahnak protein	Ahnak	S5099	1	12	GPSLKGDLGASSPSMK	GPSLKGDLGAS(0.017)S	GPSLKGDLGASS(ph)PSM	Polo box	1.1	0.47333		Yes
50	IPI00553798	Ahnak protein	Ahnak	S5101	1	9	GDLGASSPSMK	GDLGASS(0.003)PS(0.99	GDLGASS(ph)MK	CK1	1.0	0.017137	Down	Yes
307	IPI00553798	Ahnak protein	Ahnak	S5504	1	8	GKGGVTGSPEASISGSK	GKGGVTGS(1)PEASISGS	GKGGVTGS(ph)PEASISG	GSK3	0.7	0.30559		Yes
168	IPI00553798	Ahnak protein	Ahnak	S5508	1	10	GGVTGSPEASISGSKGDL	GGVTGSPEAS(0.921)S	GGVTGSPEAS(ph)ISGSK	PLK1	0.9	0.15209		Yes
263	IPI00553798	Ahnak protein	Ahnak	S5512	1	14	GGVTGSPEASISGSKGDL	GGVTGSPEAS(0.099)S	GGVTGSPEASISGSK(ph)K	CK1	1.0	0.25891		Yes
144	IPI00553798	Ahnak protein	Ahnak	S5518	2	1	SSKASLGSLEGEVEAEASS	S(0.604)S(0.547)KAS(0.	S(ph)S(ph)KASLGSLEGE	GSK3	0.9	0.12359		No
145	IPI00553798	Ahnak protein	Ahnak	S5519	2	2	SSKASLGSLEGEVEAEASS	S(0.604)S(0.547)KAS(0.	S(ph)S(ph)KASLGSLEGE	NEK6	0.9	0.12359		No
268	IPI00553798	Ahnak protein	Ahnak	S5553	1	3	HRSNSFSDEREFSAPTPT	HRS(0.68)NS(0.159)FS	HRS(ph)NSFSDEREFSAPT	PIM1/2	1.0	0.26321		No
62	IPI00553798	Ahnak protein	Ahnak	S5555	1	5	HRSNSFSDER	HRS(0.08)NS(0.839)FS	HRSNS(ph)FSDER	PKA/AKT	0.8	0.027929	Down	Yes
25	IPI00553798	Ahnak protein	Ahnak	S5557	1	7	HRSNSFSDEREFSAPTPT	HRS(0.06)NS(0.06)FS(0.	HRSNS(ph)DEREFSAPT	CK1	2.1	2.512E-08	Up	No
569	IPI00553798	Ahnak protein	Ahnak	S5563	2	11	SNSFSDEREFSAPTPTG	S(0.312)NS(0.678)FS(0.	SNS(ph)FS(ph)DEREFSA	CAMK2				No
277	IPI00553798	Ahnak protein	Ahnak	S5566	2	14	SNSFSDEREFSAPTPTG	S(0.499)NS(0.436)FS(0.	S(ph)NSFSDEREFSAPT	CK1	1.0	0.27772		No
466	IPI00553798	Ahnak protein	Ahnak	T219	1	11	LPSGSGPASPTTGS	LPSGSGPAS(0.333)PT(0.	LPSGSGPAS(ph)PTTGS	FHA KAPP	1.1	0.42668		No
568	IPI00553798	Ahnak protein	Ahnak	T220	1	12	LPSGSGPASPTTGS	LPSGSGPAS(0.333)PT(0.	LPSGSGPAS(ph)PTTGS	CK1				No
18	IPI00553798	Ahnak protein	Ahnak	T5567	2	17	HRSNSFSDEREFSAPTPT	HRS(0.067)NS(0.19)FS	HRSNSFSDEREFSAPT	WW GroupIV	2.5	9.892E-08	Up	No
19	IPI00553798	Ahnak protein	Ahnak	T5569	2	19	HRSNSFSDEREFSAPTPT	HRS(0.067)NS(0.19)FS	HRSNSFSDEREFSAPT	CK1	2.5	9.892E-08	Up	No
414	IPI00553798	Ahnak protein;Ahnak p	Ahnak;Ahnak;MCG 178	S94	1	5	KGDRSPEPGQWTWTEVF	KGDRS(1)PEPGQWTWTEVF	KGDRS(ph)PEPGQWTWTEVF	FSSR	1.1	0.38612		Yes
507	IPI00850843	Putative uncharacterize	Ahnak2;AI450948	S286	1	3	DMSPTSTDETVHR	DMS(0.999)PTSTDETVHR	DMS(ph)PTSTDETVHR	CAMK2	1.1	0.4668		Yes
570	IPI00850843	Putative uncharacterize	Ahnak2;AI450948	S289	1	6	DMSPTSTDETVHR	DMS(0.419)PT(0.11)S(0.	DM(ox)S(ph)PTSTDETV	CK1				No
113	IPI00677756	AHNAK nucleoprotein 2	Ahnak2;AI450948	S35	1	3	KLSFSMPR	KLS(1)FSMPR	KLS(ph)FSMPR	PKA/AKT	1.3	0.090351		Yes
131	IPI00677756	AHNAK nucleoprotein 2	Ahnak2;AI450948	S37	1	5	KLSFSMPR	KLS(0.5)FS(0.5)MPR	KLS(ph)FSM(ox)PR	NEK6	1.3	0.10946		No
267	IPI00230591	A kinase anchor protein	Akap1;Akap;Akap1;RP2	S136	1	3	SESSGNLPSVADTR	S(0.179)ES(0.82)S(0.00	SES(ph)SGNLPSVADTR	PKA/AKT	1.2	0.26099		Yes
63	IPI00230591	A kinase anchor protein	Akap1;Akap;Akap1;RP2	S142	1	11	RRESSGNLPSVADTR	RRESSGNLPS(0.984)VA	RRESSGNLPS(ph)VADTR		1.5	0.028525	Up	Yes
11	IPI00857073	Proline-rich AKT1 subst	Akt1s1;Pras	T318	1	3	LNTSDFQK	LNT(0.999)S(0.001)DFQ	LNT(ph)SDFQK	PKA/AKT	3.8	2.178E-15	Up	Yes
161	IPI00223838	Ankyrin repeat domain	Ankrd57	S82	1	6	FCTGDSPPLEAK	FCTGDS(1)PPLEAK	FCTGDS(ph)PPLEAK		0.9	0.14002		Yes
191	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	S760	1	8	HSSLPTESDEDIAPAQR	HSSLPT(0.002)ES(0.998)	HSSLPTES(ph)DEDIAPAQR		0.9	0.17344		Yes
571	IPI00119913	Adenomatous polyposi	Apc;Apc;MCG_121500;	S2330	2	4	NSISPRNGISPPNK	NS(0.185)S(0.815)PGR	NSIS(ph)PGRNGIS(ph)P	CDK2				Yes
572	IPI00119913	Adenomatous polyposi	Apc;Apc;MCG_121500;	S2337	2	11	NSISPRNGISPPNK	NS(0.185)S(0.815)PGR	NSIS(ph)PGRNGIS(ph)P	PNK				Yes
251	IPI00170307	Apollipoprotein A-I bind	Apoa1bp;Aibp	S43	1	3	RGSETMAGAAVK	RG(0.997)ET(0.003)M	RG(ph)ETMAGAAVK	PKA/AKT	1.0	0.23934		Yes
112	IPI00170084	DCC-interacting protein	App1;Dip13a;Kiaa1428	S401	1	12	VNQSALEAVTPSPFQQ	VNQSALEAVT(0.012)PS	VNQSALEAVTPSPFQQ		0.9	0.089849		Yes
61	IPI00123183	Aquaporin-1;Aquaporin	Aqp1	S262	1	19	VWVTSGQVEEYDLDDADD	VWVTSGQVEEYDLDDADD	VWVTSGQVEEYDLDDADD	CK2	0.8	0.025407	Down	Yes
244	IPI00652831	Arginine and glutamate	Arglu1;Arglu1	S74	1	2	ASSPPDRIDIFGR	AS(0.865)S(0.135)PPDR	AS(ph)SSPPDRIDIFGR	PKA	1.2	0.23205		Yes
435	IPI00652831	Arginine and glutamate	Arglu1;Arglu1	S75	1	3	ASSPPDRIDIFGR	AS(0.071)S(0.929)PPDR	ASS(ph)PPDRIDIFGR	PKA/AKT	1.1	0.40244		Yes
101	IPI00465761	Rho guanine nucleotide	Arhgef17;Kiaa0337	S689	1	4	ALVSPETPTPGALR	ALVS(0.999)PET(0.001)	ALVS(ph)PETPTPGALR		0.8	0.076054		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?	
156	IPI00127472	Armadillo repeat prote	Arvcf;Arvcf;Arvcf;Arvcf;	S865	1	11	GTPSSGGFDDSTLPLVDK	GTPSSGGFDD(S)(0.5)T(0.0)	GTPSSGGFDD(ph)TLPLVDK		1.3	0.13333	No		
152	IPI00127472	Armadillo repeat prote	Arvcf;Arvcf;Arvcf;Arvcf;	T637	1	4	NFDTLDLPK	NFDT(1)LDLPK	NFDT(ph)LDLPK	FHA2 Rad53p	0.9	0.13159	Yes		
302	IPI00349032	Arf-GAP with SH3 doma	Asap1;Ddef1;Kiaa1249;	S1045	1	7	SHTGDLSPNVQSR	SHTGDL(S)(0.999)PNVQS	SHTGDL(ph)PNVQSR	CK1	1.2	0.30243	Yes		
536	IPI00380770	Activating transcription	Atf7ip;Mcaf1	S112	1	12	NKQEDLNSEALSPSITCD	NKQEDLN(S)(0.108)EALS	NKQEDLNSEAL(ph)PSIT	CK1	1.1	0.4902	Yes		
573	IPI00556827	Putative uncharacterize	Atp2b1	S1219	1	17	SATSSSPGSPHLHLETSL	SATSSSPGSPHLH(S)(0.001)	SATSSSPGSPHLHETS(ph)PLK1				Yes		
69	IPI00135975	V-type proton ATPase 1	Atp6v0a2;Atp6n1b;Tj6;	S695	1	3	KDEEEVSLGNQDIEEG	KDS(0.997)EEV(S)(0.003)	KDS(ph)EEVSLGNQDI	CHK1/2	1.4	0.039482	Up	Yes	
516	IPI00458001	Ataxin-2-like protein;At	Atxn2l;A2lp;Atxn2l;A2lj	S556	1	6	LQPSSSPETGLDPPFR	LQPSS(0.001)(S)(0.999)P	LQPSS(ph)PETGLDPPFR	Polo box	1.1	0.47361	Yes		
444	IPI00458001	Ataxin-2-like protein;At	Atxn2l;A2lp;Atxn2l;A2lj	S591	1	13	EVDGLTSDPMGSPVSSK	EVDGLTSDPMG(S)(1)PV	EVDGLTSDPMG(ph)P	GSK3	1.0	0.41141	Yes		
162	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S177	1	1	SQSPAASDCSSSSASLPS	S(0.814)QS(0.168)PAAS	S(ph)QSPAASDCSSSSASLPS	SSGR	0.9	0.14037	Yes		
574	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S179	6	3	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	CAMK2			No		
575	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S183	6	7	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	GSK3			No		
576	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S186	6	10	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	CK1			No		
577	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S187	6	11	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	GSK3			No		
578	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S188	6	12	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)DCS	SSAS(ph)LPS	SSGR			No	
579	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S193	6	17	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	CK1			No		
580	IPI00387388	BCL2-associated athanc	Bag3;Bag3;Bis;MNCb-2	S197	6	21	SQSPAASDCSSSSASLPS	S(0.538)QS(0.55)PAAS	S(ph)QS(ph)PAAS(ph)D	NEK6			No		
213	IPI00380722	Large proline-rich prote	Bat2	T609	1	14	EGPEPPEEVPPTTPAPP	EGPEPPEEVPPTT(0.007)	EGPEPPEEVPPTT(ph)P	WW GroupIV	0.9	0.20405	Yes		
313	IPI00330171	BAT2 domain-containin	Bat2d1;Bat2d;Kiaa1096	T2625	1	12	AFGSGIDIKPGTPIPIIG	AFGSGIDIKPGT(1)PIPIG	AFGSGIDIKPGT(ph)PIPIG	ERK/MAPK	1.0	0.308	Yes		
37	IPI00331555	2-oxoisovalerate dehyd	Bckdha	S338	1	5	IGHHSTSDSSAYR	IGHHS(0.834)T(0.082)S	IGHHS(ph)TSDSSAYR		1.6	0.0086446	Up	Yes	
581	IPI00331555	2-oxoisovalerate dehyd	Bckdha	S348	2	15	IGHHSTSDSSAYRVSDE	IGHHS(0.189)T(0.189)S	IGHHSTSDSS(ph)SAYR	CK2			No		
122	IPI00331555	2-oxoisovalerate dehyd	Bckdha	S363	2	30	IGHHSTSDSSAYRVSDE	IGHHS(0.153)T(0.153)S	IGHHSTSDSSAYRS(ph)S	VEVNYWQDQHPIS	1.3	0.098488	No		
196	IPI00115094	[3-methyl-2-oxobutano	Bckdk	S31	1	1	STSATDTHHVELAR	S(0.545)T(0.397)(S)(0.058)	S(ph)TSATDTHHVELAR	CAMK2	1.3	0.18052	No		
258	IPI00115094	[3-methyl-2-oxobutano	Bckdk	T32	1	2	STSATDTHHVELAR	S(0.161)T(0.742)(S)(0.085)	T(ph)TSATDTHHVELAR	PKA	1.2	0.25122	No		
451	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S177	1	10	KAEGEPQEEPSLPSK	KAEGEPQEE(S)(1)PLKSK	KAEGEPQEE(ph)PLKSK	CDK2	1.1	0.41887	Yes		
43	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S383	1	17	GRADGDWDDQEVLDYF	GRADGDWDDQEVLDY	GRADGDWDDQEVLDY	CK2	1.5	0.013077	Up	Yes	
140	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S387	1	21	GRADGDWDDQEVLDYF	GRADGDWDDQEVLDY	GRADGDWDDQEVLDY	CK1	1.3	0.11723	Yes		
394	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S395	1	4	FHDSEGDTEETEDYR	FHDS(1)EGDDTEETEDY	FHDS(ph)EGDDTEETEDYR		1.0	0.3697	Yes		
513	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S656	1	4	IDISPALSALR	IDIS(1)PSALSALR	IDIS(ph)PSALSALR		1.1	0.472	Yes		
533	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	S658	1	7	RIDISPALSALR	RIDIS(0.5)PS(0.5)ALR	RIDIS(ph)PSALSALR		1.1	0.48683	No		
524	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;Bcl	T400	1	11	QKFHDESGDDTEETEDY	QKFHDS(0.033)EGDDT	QKFHDESGDDT(ph)EETEDYR		1.1	0.48036	Yes		
15	IPI00229530	BCL-6 corepressor;BCL-	Bcor;Kiaa1575;Bcor;Kia	Y977	1	7	IANSAGYVGRDFK	IANS(0.001)AGY(0.999)	IANSAGY(ph)VGRDFK	EGFR	0.4	9.716E-10	Down	Yes	
55	IPI00114352	Myc box-dependent-int	Bin1;Amphl;Sh3p9;Bin1	S296	1	1	SPSPPPDGSPPAATPEIR	S(0.973)NPE(0.027)PPDP	S(ph)SPSPPPDGSPPAATPEIR		0.8	0.022192	Down	Yes	
327	IPI00114352	Myc box-dependent-int	Bin1;Amphl;Sh3p9;Bin1	S298	1	16	AQPSDNAPEKGNKSPSP	AQPSDNAPEKGNK(S)(0.0)	AQPSDNAPEKGNKSPS(ph)PPDPDGSPPAATPEIR		1.2	0.31709	Yes		
303	IPI00114352	Myc box-dependent-int	Bin1;Amphl;Sh3p9;Bin1	S304	1	9	SPSPPPDGSPPAATPEIR	SPSPPPDGS(0.994)PAA	SPSPPPDGS(ph)PAAATPEIR		1.2	0.30269	Yes		
192	IPI00268218	Zinc finger protein basc	Bnc2;Bnc2;Bnc2	S431	1	7	TEPACVPIQNSAPVDSL	T(0.002)EPACV(S)(0.998)	TEPACV(ph)PIQNSAPVDSL		1.3	0.17359	Yes		
486	IPI00410792	Bromodomain-containi	Brd3;Frg2;Brd3;Frg2;B	S262	1	3	SESPPLSEPK	S(0.095)ES(0.905)PPLS	SES(ph)PPLSEPK	14-3-3 binding	1.1	0.45071	Yes		
293	IPI00118762	Bystin	Bysl	S97	1	10	LGPGLPQDGSDEEEDVE	LGPGLPQDGS(1)DEEED	LGPGLPQDGS(ph)DEED	CK2	1.2	0.28944	Yes		
143	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;Rf	S270	1	10	LPAPQEDTASEAGTPQG	LPAPQEDT(0.066)AS(0.4)	LPAPQEDTAS(ph)EAGTPQGEVQTR		0.9	0.12314	Yes		
582	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;Rf	T268	1	8	LPAPQEDTASEAGTPQG	LPAPQEDT(0.475)AS(0.4)	LPAPQEDT(ph)ASEAGT	CK2			No		
142	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;Rf	T274	1	14	LPAPQEDTASEAGTPQG	LPAPQEDT(0.06)AS(0.06)	LPAPQEDTASEAGT(ph)PQGEVQTR		0.9	0.12216	Yes		
472	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;Rf	S135	1	4	GRLSVPVPR	GRLS(1)PVPVPR	GRLS(ph)PVPVPR	PKA	1.1	0.43325	Yes		
348	IPI00380280	Carbamoyl-phosphate	Cad;mCG_23490;Cad	S1859	1	5	IHRASDPLPAEPEK	IHRAS(1)DPGLPAEPEK	IHRAS(ph)DPGLPAEPEK	PKA	1.2	0.33964	Yes		
288	IPI00775950	Putative uncharacterize	Cald1;Cald1	S254	1	9	LKQTENAFSPSR	LKQT(0.001)ENAF(S)(0.999)	LKQTENAFS(ph)PSR	CDK2	1.0	0.28635	Yes		
437	IPI00119618	Calnexin	Canx	S582	1	10	AEEDEILNRSR	AEEDEILNRS(1)PR	AEEDEILNRS(ph)PR	CDK1	1.1	0.40453	Yes		
278	IPI00776341	Peripheral plasma mem	Cask	S571	1	5	TQSSCEDLPSTTQPK	TQS(0.001)S(0.113)S(0.0)	TQSSS(ph)CEDLPSTTQPK	CK1	1.0	0.27901	Yes		
314	IPI00653604	Coiled-coil domain-con	Ccdc102a	S12	1	4	LAESPQLSK	LAES(1)PQLSK	LAES(ph)PQLSK	NEK6	1.2	0.30823	Yes		
378	IPI00170037	Malcavernin;Cerebral c	Ccm2;Osm;Ccm2;Osm	S393	1	6	GIITDSFGR	GIITDS(1)FGR	GIITDS(ph)FGR		1.0	0.35947	Yes		
385	IPI00752728	Cyclin-H	Ccnh	Y178	1	1	YPMLENPEILRK	Y(1)PMLENPEILRK	Y(ph)PMLENPEILRK	ALK	1.0	0.36155	Yes		
255	IPI00336973	Cyclin-L1;Cyclin Ania-6	Ccnl1;Ania6a;Ccn1	S358	1	5	AEEKSPVSNV	AEEKS(0.995)PVS(0.005)	AEEKS(ph)PVSINVK		1.2	0.24467	Yes		
501	IPI00308149	Cyclin-Y;Cyclin fold pr	Ccny;Cfp1;Ccny;Cfp1	S326	1	4	RSASADNLLPR	RSAS(1)ADNLLPR	RSAS(ph)ADNLLPR	PKA/AKT	1.1	0.46264	Yes		
376	IPI00753875	Putative uncharacterize	Ccny1	S352	1	4	RSLSADNFIQIR	RSLS(1)ADNFIQIR	RSLS(ph)ADNFIQIR	CHK1	1.0	0.35777	Yes		
506	IPI00464128	Cell division cycle 2-like	Cdc215;Kiaa1791;Cdc21	T1245	1	5	IILETPEDRPR	IILET(1)PEDRPR	IILET(ph)PEDRPR	NEK6	1.1	0.46395	Yes		
583	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	S1679	1	2	HSTPSNNSNPSPGPPSPNS	HS(0.28)T(0.28)PS(0.10)	HS(ph)TSPNSNPSPGPPSPNS	CK1			No		
67	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	S1692	1	15	HSTPSNNSNPSPGPPSPNS	HSTPSNNSNPSPGPPS(0.9)	HSTPSNNSNPSPGPPS(ph)WW GroupIV		0.8	0.034312	Down	Yes	
585	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	S1695	1	18	HSTPSNNSNPSPGPPSPNS	HSTPSNNSNPSPGPPS(0.5)	HSTPSNNSNPSPGPPS(ph)WW GroupIV				No		
584	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	T1680	1	3	HSTPSNNSNPSPGPPSPNS	HS(0.28)T(0.28)PS(0.10)	HS(ph)TSPNSNPSPGPPSPNS	Polo box			No		
389	IPI00471127	Cdc42 effector protein	Cdc42ep1;Borg5;Cep1	S207	1	4	RSDSLLSFR	RSDS(1)LLSFR	RSDS(ph)LLSFR	CHK1/2	1.0	0.36634	Yes		
354	IPI00138190	Cadherin-11;Osteoblast	Cdh11;Cad-11	S714	1	9	PGLRPAPNSVDVDFINT	PGLRPAPNS(1)VDVDF	PGLRPAPNS(ph)VDVDFINTR		1.2	0.34494	Yes		
97	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	S621	2	1	SQLDDHPESDEENFVDV	S(0.589)QLDDHPES(0.2)	S(ph)QLDDHPESDEENFVDV	GGDS(ph)DDEKFTDA	1.4	0.069273	No		
100	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	S629	2	9	SQLDDHPESDEENFVDV	S(0.002)QLDDHPES(0.9)	SQLDDHPES(ph)DEENF	CK2	1.4	0.073937	Yes		
285	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	S641	2	21	SQLDDHPESDEENFVDV	S(0.095)QLDDHPES(0.9)	SQLDDHPES(ph)DEENF	CK2	1.2	0.28263	Yes		
586	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	T647	2	27	SQLDDHPESDEENFVDV	S(0.003)QLDDHPES(0.9)	SQLDDHPES(ph)DEENF	FHA1 Rad53p			No		
75	IPI00653910	Protein capicua homolo	Cic;Kiaa0306;Cic;Kiaa03	S2280	2	20	FAELPFRPEEVLPSPTLQ	FAELPFRPEEVLPS(0.24)	FAELPFRPEEVLPSPTLQ	GSK3	1.4	0.047282	Up	No	
102	IPI00653910	Protein capicua homolo	Cic;Kiaa0306;Cic;Kiaa03	S2284	2	24	FAELPFRPEEVLPSPTLQ	FAELPFRPEEVLPS(0.03)	FAELPFRPEEVLPSPTLQ	CDK1	1.4	0.084232	Yes		
298	IPI00672213	CLIP-associating protei	Clasp1;Kiaa0622;Clasp1	S598	1	1	SRSIDIVNAAASAK	S(0.76)RS(0.24)DIVNAA	S(ph)SRSIDIVNAAASAK	NEK6	1.0	0.29916	Yes		
421	IPI00672213	CLIP-associating protei	Clasp1;Kiaa0622;Clasp1	S600	1	3	SRSIDIVNAAASAK	S(0.092)RS(0.908)DIVN	SRS(ph)SRSIDIVNAAASAK	CHK1/2	1.0	0.39313	Yes		

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
211	IPI00857273	CAP-Gly domain-contain	Clip1;Kiaa4046;Rsn;Clip	S203	1	14	TASESINLSLEAGSVK	TASESINLSLEAGS(1)VK	TASESINLSLEAGS(ph)VK	CK1	0.9	0.1993		Yes
274	IPI00467854	CAP-Gly domain-contain	Clip2;Cynl2;Kiaa0291;C	S295	1	7	IGFPSTSPAK	IGFPST(0.003)S(0.996)P	IGFPSTS(ph)PAK	CDK2	1.0	0.27355		Yes
322	IPI00124248	Chloride channel regula	Clns1a;Cln	S100	1	10	LGEEKSKEPLSDEDEEDN	LGEEKSKEPLS(1)DEDEED	LGEEKSKEPLS(ph)DEDEEDNDDVEIPESEFR		1.0	0.31394		Yes
587	IPI00230426	Chymase;Alpha-chymas	Cma1;Mcp5	S193	2	14	MRLQEQPOACKHFTSFR	MRLQEQPOACKHFT(1)S	M(ox)RQEQPOACKHFT(ph)S(ph)FR		1.0	0.34722		Yes
363	IPI00135512	Protein canopy homolo	Cnpy2;Msap;Tmem4;Zs	S115	1	4	NGESSELDLQGR	NGES(0.95)S(0.045)EL	NGES(ph)SELDLQGR		1.0	0.34722		Yes
383	IPI00112963	Catenin alpha-1;102 kD	Ctnn1;Catna1	S641	1	8	TPEELDDSDFTEDFDVDR	T(0.139)PEELDDSD(0.859)	TPEELDDSD(ph)DFETDF	CK2	1.1	0.3608		Yes
229	IPI00112963	Catenin alpha-1;102 kD	Ctnn1;Catna1	T645	1	12	TPEELDDSDFTEDFDVDR	TPEELDDSD(0.67)DFET	TPEELDDSDFT(ph)EDFDVDR		0.9	0.22167		Yes
588	IPI00112963	Catenin alpha-1;102 kD	Ctnn1;Catna1;Ctnna2;	S652	1	1	SRTSVQTEDDQLIAGQSA	S(0.42)RT(0.29)S(0.29)	S(ph)RTSVQTEDDQLIAGQSA					No
91	IPI00125899	Catenin beta-1;Beta-ca	Ctnnb1;Catnb;Ctnnb1	S552	1	3	RTSMGGTQQQFVEGVDR	RT(0.012)S(0.988)MGG	RTS(ph)M(ox)GGTQQQ	AURORA-A	0.8	0.062974		Yes
589	IPI00125899	Catenin beta-1;Beta-ca	Ctnnb1;Catnb;Ctnnb1	T556	1	7	RTSMGGTQQQFVEGVDR	RT(0.161)S(0.42)MGGT	RTS(ph)M(ox)GGTQQQFVEGVDR					No
494	IPI00120919	RNA polymerase-associ	Ctr9;Kiaa0155;Sh2bp1;	T925	1	13	KGGFEDEFVNDTDDDD	KGGFEDEFVNDT(1)DD	KGGFEDEFVNDT(ph)D	FHA1 Rad53p	1.1	0.45883		Yes
104	IPI00118143	Src substrate cortactin	Cctn;Ems1;Cctn;mCG	S405	3	7	KQTPPASPSQPPIEDRPP	KQT(0.984)PPAS(0.691)	KQT(ph)PPAS(ph)PSPQ	WW GroupIV	1.4	0.081257		No
178	IPI00118143	Src substrate cortactin	Cctn;Ems1;Cctn;mCG	S407	3	9	KQTPPASPSQPPIEDRPP	KQT(0.985)PPAS(0.209)	KQT(ph)PPASPS(ph)PQPIEDRPPSPPIY	(ph)EDAAP	1.3	0.16083		Yes
590	IPI00118143	Src substrate cortactin	Cctn;Ems1;Cctn;mCG	S417	3	19	KQTPPASPSQPPIEDRPP	KQT(0.984)PPAS(0.691)	KQT(ph)PPAS(ph)PSPQ	CAMK2				No
591	IPI00118143	Src substrate cortactin	Cctn;Ems1;Cctn;mCG	S418	3	20	KQTPPASPSQPPIEDRPP	KQT(0.984)PPAS(0.691)	KQT(ph)PPAS(ph)PSPQ	WW GroupIV				No
24	IPI00754924	Dapper homolog 3	Dact3	S409	1	3	SOSETLLGR	S(0.094)QS(0.903)ET	SOS(ph)ETSLGR	PKA/AKT	2.2	4.57E-06	Up	Yes
84	IPI00128975	Death-associated prote	Dap	S49	1	9	DKDDQEWESTSPPKPTV	DKDDQEWES(0.736)T	DKDDQEWES(ph)TSPPKTVFISGVIAR		0.8	0.056888		No
349	IPI00128975	Death-associated prote	Dap	S51	1	11	DKDDQEWESTSPPKPTV	DKDDQEWES(0.013)T	DKDDQEWESTS(ph)PK	CDK2	1.2	0.34		Yes
402	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1l;Dcl;Dcl	S32	2	6	VNGLSPSTHSAHCSFYR	VNGLPS(0.86)PT(0.04)	VNGLPS(ph)PTHSAHCS	GSK3	1.1	0.37752		Yes
403	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1l;Dcl;Dcl	S40	2	14	VNGLSPSTHSAHCSFYR	VNGLPS(0.86)PT(0.04)	VNGLPS(ph)PTHSAHCS	CK1	1.1	0.37752		Yes
592	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1l;Dcl;Dcl	S337	1	8	SPSPSPTSPGSLR	SPSPS(0.001)PT(0.499)	SPSPSPT(ph)SPGSLR	WW GroupIV				No
593	IPI00130114	mRNA-decapping enzyr	Dcp1a;Mtc1;Smif	S542	1	2	ASSPSPLTVGTAESQR	AS(0.497)S(0.497)PS	AS(ph)SPSPLTVGTAESQ	CHK1/2				No
594	IPI00130114	mRNA-decapping enzyr	Dcp1a;Mtc1;Smif	S543	1	3	ASSPSPLTVGTAESQR	AS(0.497)S(0.497)PS	AS(ph)SPSPLTVGTAESQ	Polo box				No
275	IPI00120691	Nucleolar RNA helicase	Ddx21;Ddx21;mCG_113	S118	1	8	EIITEEPEEEEEADMPKPK	EIITEEPS(1)EEEDAMPK	EIITEEPEEEEEADMPK	CK2	1.0	0.27364		Yes
214	IPI00329839	ATP-dependent RNA he	Ddx42;Ddx42	S185	1	23	YMAENPTAGVVQEEEE	YMAENPTAGVVQEEEE	YMAENPTAGVVQEEEEEDNLEYDS	(ph)JDNPIAPSK	1.2	0.2045		Yes
281	IPI00329839	ATP-dependent RNA he	Ddx42;Ddx42	Y183	1	21	YMAENPTAGVVQEEEE	YMAENPTAGVVQEEEE	YMAENPTAGVVQEEEEEDNLEYD	(ph)DSDGNPIAPSK	1.2	0.2803		Yes
299	IPI00339468	ATP-dependent RNA he	Dhx9;Ddx9	S137	1	16	AEAEENNSGVESGYS	AEAEENNSGVESGYS(0.00)	AEAEENNSGVESGYS(ph)	CK1	0.6	0.0006943	Down	Yes
537	IPI00761536	Dedicator of cytokines	Dock5;Lr2;Rlc	S1765	1	1	SLQLVDSR	S(1)QLVDSR	S(ph)QLVDSR	CAMK2	1.1	0.49021		Yes
151	IPI00816914	Dedicator of cytokines	Dock7;Gm430;Kiaa177	S1422	1	3	SPSGAFSGQENLR	S(0.017)PS(0.982)GS	SPS(ph)SGAFSGQENLR	PKA/AKT	1.3	0.13156		Yes
595	IPI00816914	Dedicator of cytokines	Dock7;Gm430;Kiaa177	S896	1	1	SLNSNPDISGTPSPDD	S(0.456)LS(0.272)NS	S(ph)LSNSNPDISGTPSPD	PKA/AKT				No
347	IPI00882020	Putative uncharacterize	Dpf2;Dpf2;Req;Ubid4	S142	1	5	VDDDSLGEFPVNSNR	VDDDS(1)LGEFPVNSNR	VDDDS(ph)LGEFPVNSNR	PLK	1.2	0.33951		Yes
247	IPI00857720	Protein dpy-19 homolo	Dpy19l1	S22	1	11	SGPPPLSGASEVDAGELG	S(0.626)S(0.374)PPPLS	S(ph)SPPLSGASEVDAG	CK1	1.0	0.25115		No
596	IPI00406447	Collapsin response me	Dpysl3;Dpysl3;Drp3;Uli	S635	1	11	GGTPAGSTRGSPTRPNP	GGT(0.001)PAGS(0.082)	GGTPAGST(ph)RGSPTPR	CDK2	0.9			No
146	IPI00230692	Bullous pemphigoid ant	Dst;Bpag1;Dst;Bpag1;D	S3240	1	5	PHVCSDLR	PHVCS(1)DLR	PHVCS(ph)DLR		1.0	0.1245		Yes
371	IPI00118849	Dual specificity tyrosine	Dyrk1a;Dyrk;Dyrk1a;RP	Y321	1	4	IYQYIQSR	IYQY(1)QSR	IYQY(ph)QSR		1.0	0.35384		Yes
1	IPI00223156	Uncharacterized protei	E130012A19Rik	S19	2	10	LAVPASPRGSPCPTPLK	LAVPAS(0.086)PRG(S	LAVPASPRGS(ph)PCSPTR	PKA	0.04	1.54E-81	Down	Yes
183	IPI00848728	Enhanced at puberty pr	Eap1;Kiaa1865	S584	1	3	KASPEPPDASAESALK	KAS(1)PEPPDASAESALK	KAS(ph)PEPPDASAESALK	PKA/AKT	0.9	0.16633		Yes
130	IPI00848728	Enhanced at puberty pr	Eap1;Kiaa1865	S696	1	4	NSSSPVSPASVPGQR	NS(0.001)S(0.003)S	NSSS(ph)PVSPASVPGQR	Polo box	1.3	0.10888		Yes
220	IPI00467435	ER degradation-enhanc	Edem1;Edem	S214	1	2	DSTVQVFATIR	DS(0.5)T(0.5)VQVFATI	DS(ph)TVQVFATIR		0.9	0.21204		No
202	IPI00320208	Elongation factor 1-bet	Eef1b;Eef1b2	S106	1	28	YGPSSVEDTTGSGAADA	YGPSSVEDTTGSGAADA	YGPSSVEDTTGSGAADA	CK2	1.2	0.18995		Yes
599	IPI00320208	Elongation factor 1-bet	Eef1b;Eef1b2	S90	1	12	YGPSSVEDTTGSGAADA	Y(0.103)GPS(0.1)S	YGPSSVEDT(ph)TSGGAADAKDDDDIDLFGSDDEESEEAKK					No
597	IPI00320208	Elongation factor 1-bet	Eef1b;Eef1b2	T87	1	9	YGPSSVEDTTGSGAADA	Y(0.103)GPS(0.1)S	YGPSSVEDT(ph)TSGGA	FHA KAPP				No
598	IPI00320208	Elongation factor 1-bet	Eef1b;Eef1b2	T88	1	10	YGPSSVEDTTGSGAADA	Y(0.103)GPS(0.1)S	YGPSSVEDT(ph)TSGGAADAKDDDDIDLFGSDDEESEEAKK					No
601	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S492	1	2	LSSLEKSSPTPR	LS(0.325)S(0.325)LEKS	LS(ph)SLEKSSPTPR	PKA				No
602	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S493	1	3	LSSLEKSSPTPR	LS(0.325)S(0.325)LEKS	LS(ph)SLEKSSPTPR	CAMK2				No
603	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S497	1	7	LSSLEKSSPTPR	LS(0.325)S(0.325)LEKS	LS(ph)SLEKSSPTPR	NEK6				No
262	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S498	1	8	LSSLEKSSPTPR	LS(0.001)SLEKS(0.07)	SLSLEKSS(ph)PTPR	Polo box	1.0	0.25683		Yes
523	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S512	1	10	ATAPQTQHVSPMR	ATAPQTQHV(1)PMR	ATAPQTQHV(1)PMR	CDK2	1.1	0.47902		Yes
115	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	S541	1	18	GATPAEDDEDKIDILFGS	GATPAEDDEDKIDILFGS	GATPAEDDEDKIDILFGS	CK2	1.3	0.092139		Yes
400	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef1	T508	1	6	ATAPQTQHVSPMR	AT(0.001)APQT(0.499)	ATAPQT(ph)QHVSPM(ox)R					No
422	IPI00402968	EH domain-containing	Ehd2	S438	1	20	MGPFVERGDEAIEDGE	MGPFVERGDEAIEDGE	MGPFVERGDEAIEDGEGS	(ph)EDDAEWWVTK	1.1	0.39472		Yes
92	IPI00402968	EH domain-containing	Ehd2	T447	1	29	MGPFVERGDEAIEDGE	MGPFVERGDEAIEDGE	M(ox)GPFVERGDEAIEDGEGSEDDAEWVVT	(ph)	1.4	0.064192		Yes
364	IPI00261239	Translation initiation fa	Eif2b5	S540	1	3	AGSPQLDDIR	AGS(1)PQLDDIR	AGS(ph)PQLDDIR	CAMK2	1.2	0.34829		Yes
223	IPI00229859	Eukaryotic translation	Eif3b;Eif3s9	S75	1	14	AKPAAQSEETATSPAAS	AKPAAQSEETAT(0.003)	AKPAAQSEETATS(ph)P	GSK3	0.9	0.21569		Yes
604	IPI00229859	Eukaryotic translation	Eif3b;Eif3s9	S79	2	18	AKPAAQSEETATSPAAS	AKPAAQS(0.001)EET	(0)AKPAAQSEETATS(ph)P	CK1				No
605	IPI00229859	Eukaryotic translation	Eif3b;Eif3s9	T81	2	20	AKPAAQSEETATSPAAS	AKPAAQS(0.001)EET	(0)AKPAAQSEETATS(ph)P	FHA KAPP				No
345	IPI00421179	Eukaryotic translation	Eif4g1;Eif4g1;Eif4g1;Eif	S1187	1	1	SFSKEVEER	S(1)FSKEVEER	S(ph)FSKEVEER		1.2	0.33736		Yes
120	IPI00776162	Eukaryotic translation	Eif4g2;Nat1;Eif4g2;Nat	T507	1	3	TQTPPLGQTPQLGLK	T(0.036)QT(0.958)PPLG	TQTP(ph)PPLGQTPQLGLK	CAMK2	0.9	0.097918		Yes
468	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S137	1	11	TARPNSAEPLSGSEDA	T(0.001)ARPNS(0.026)	TARPNSAEPLS(ph)GSE	CK2	1.1	0.43005		Yes
399	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S215	1	7	SVPTVDSGNEDDSSFK	SVPTVDS(1)GNEDDSS	SVPTVDS(ph)GNEDDSS	CK2	1.0	0.37228		Yes
607	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S223	3	15	SVPTVDSGNEDDSSFK	S(0.289)VPT(0.84)VDS	(SVPT(ph)VDS(ph)GNE	PLK1				No
606	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	T212	3	4	SVPTVDSGNEDDSSFK	S(0.289)VPT(0.84)VDS	(SVPT(ph)VDS(ph)GNE	CK1				Yes
141	IPI00309309	RNA polymerase II elon	Ell;Ell;mCG_23118	S299	1	12	KLCQPQNATDSSPPREH	KLCQPQNATD(0.886)	KLCQPQNATD(ph)SPPREHGR		1.3	0.11973		Yes
219	IPI00403406	Epb4.112 protein;Erythr	Epb4.112;Epb4.112	S596	1	11	ATPLPAEGKSSHETLNVV	ATPLPAEGKS(0.071)S	(0)ATPLPAEGKS(ph)HETLNVVEEK		0.9	0.20905		Yes
608	IPI00229300	Band 4.1-like protein 3;	Epb4113;Dal1;Epb4.113;	S749	1	8	VESTSVGSISPGGAK	VESTSVGS(0.5)S(0.5)P	VESTSVGS(ph)ISPGGAK	CK1				No
474	IPI00229300	Band 4.1-like protein 3;	Epb4113;Dal1;Epb4.113;	S751	1	10	VESTSVGSISPGGAK	VESTSVGS(0.077)S	(0.9)VESTSVGS(ph)ISPGGAK			0.44317		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
324	IPI00420185	Epidermal growth factor	Egfr;Egfr;Egfr;Egfr;Egfr	S255	1	18	STPSHGVSLSNSTGSLSP	STPSHGVSLSNSTGSLSP	STPSHGVSLSNSTGSLSP	CDK1	1.2	0.31583		Yes
392	IPI00154109	Protein FAM122A	Fam122a	S73	1	8	HGLLLPASVPR	HGLLLPAS(1)PVR	HGLLLPAS(ph)PVR	WW GroupIV	1.1	0.36679		Yes
208	IPI00223670	Protein FAM40A;Protein	Fam40a;Kiaa1761;Fam40	S335	1	3	AASPPASASDLIEQQQK	AAS(1)PPASASDLIEQQQK	AAS(ph)PPASASDLIEQQQK	CAMK2	0.9	0.19813		Yes
276	IPI00874398	Protein FAM65A	Fam65a;Kiaa1930	S90	1	1	SQSFAGVLGSHER	S(0.644)QS(0.356)FAGV	S(ph)QSFAFVGLGSHER		1.0	0.27455		No
129	IPI00874398	Protein FAM65A	Fam65a;Kiaa1930	S92	1	3	SQSFAGVLGSHER	S(0.176)QS(0.824)FAGV	SQS(ph)FAGVGLGSHER	PKD	0.9	0.10656		Yes
292	IPI00344835	Protein FAM65C	Fam65c	S24	1	3	SASFAGFSAQSR	S(0.081)AS(0.919)FAGF	SAS(ph)FAGFSAQSR	PKD	1.2	0.28731		Yes
428	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1	S427	1	11	ACTLELGHQPSALPK	ACT(0.001)LELGHQPS(0)	ACTLELGHQPS(ph)PALPK		1.1	0.39715		Yes
386	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1;Farp1	T24	1	11	LGAPENSGISTLER	LGAPENSGIS(0.06)T(0.9)	LGAPENSGIST(ph)LER		1.1	0.36214		Yes
609	IPI00929902	Fas;Tumor necrosis fact	Fas;Fas;Apt1;Tnfrsf6	S217	1	8	ETIPMNASNLNLSK	ET(0.15)IPMNAS(0.297)	ETIPM(ox)NAS(ph)NLSK					No
448	IPI00929902	Fas;Tumor necrosis fact	Fas;Fas;Apt1;Tnfrsf6	S220	1	11	ETIPMNASNLNLSK	ETIPMNAS(0.005)NLS(0)	ETIPMNASNLNLSK	CK1	1.1	0.41371		Yes
610	IPI00849967	Putative uncharacterize	Fez1	S150	4	9	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GSK3				No
611	IPI00849967	Putative uncharacterize	Fez1	S154	4	13	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	CK1				No
613	IPI00849967	Putative uncharacterize	Fez1	S178	4	37	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GINEEPLLTADQVIEIEEEM(ox)MQNSPDPPEEEEEVLEEDGGEISSQ				No
614	IPI00849967	Putative uncharacterize	Fez1	S197	4	56	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GINEEPLLTADQVIEIEEEM(ox)MQNSPDPPEEEEEVLEEDGGEISSQ				No
615	IPI00849967	Putative uncharacterize	Fez1	S198	4	57	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GSK3				No
616	IPI00849967	Putative uncharacterize	Fez1	S202	4	61	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	CK1				No
247	IPI00849967	Putative uncharacterize	Fez1	S220	4	79	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GINEEPLLTADQVIEIEEEM	1.2	0.23641		No
612	IPI00849967	Putative uncharacterize	Fez1	T163	4	22	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GINEEPLLTADQVIEIEEEM(ox)MQNSPDPPEEEEEVLEEDGGEISSQ				No
617	IPI00849967	Putative uncharacterize	Fez1	T212	4	71	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	GINEEPLLTADQVIEIEEEM(ox)MQNSPDPPEEEEEVLEEDGGEISSQ				No
618	IPI00849967	Putative uncharacterize	Fez1	T214	4	73	EEEEFNKSEKENDSGINEE	EEEEFNKES(0.271)ENDS	EEEEFNKES(ph)ENDS(ph)	NEK6				No
82	IPI00223046	FH1/FH2 domain-conta	Fhod1;Fhos1	S370	1	1	SLEGGGCPVR	S(1)LEGGGCPVR	S(ph)LEGGGCPVR	AURORA	0.8	0.055184		Yes
14	IPI00664670	Filamin-C;Gamma-filam	FlnC;Abp1;Fln2;FlnC;Abp	S2234	1	3	LGSFGSITR	LGS(1)FGSITR	LGS(ph)FGSITR	PKA/AKT	3.3	2.696E-12	Up	Yes
222	IPI00664670	Filamin-C;Gamma-filam	FlnC;Abp1;Fln2;FlnC;Abp	S2237	1	6	LGSFGSITR	LGSFGS(0.881)IT(0.119)	LGSFGS(ph)ITR	CK1	0.9	0.21372		Yes
98	IPI00652813	Fn1 protein;Fibronectin	Fn1;Fn1;Fn1	S2359	1	24	TNTNVNCPICFCMPLDV	TNTNVNCPICFCMPLDV	TNTNVNCPICFCMPLDV	CAMK2	0.8	0.072399		Yes
350	IPI00119242	Formin-binding protein	Fnbp4;Fbp30;Kiaa1014	S65	1	7	RPILQLSPPGPR	RPILQLS(1)PPGPR	RPILQLS(ph)PPGPR	NEK6	1.0	0.34031		Yes
619	IPI00170120	Forkhead box protein N	Foxn4	S217	2	3	TGSLPVSEIYFNM	T(0.999)GS(0.992)LPVS	T(ph)GS(ph)LPVSEIYFNM	GSK3				Yes
410	IPI00338635	FERM domain-containi	FrmD6;FrmD6	S544	1	4	HLSLDDDIR	HLS(1)LDDDIR	HLSL(ph)LDDDIR		1.0	0.38347		Yes
620	IPI00224112	Fibroblast growth facto	Frs2;Frs2a	S327	1	3	LTSTSTSDTQININNSAQR	LT(0.391)S(0.391)T(0.06)	LT(ph)S(ph)TSDTQININNSAQR	PKA/AKT				No
163	IPI00224112	Fibroblast growth facto	Frs2;Frs2a	S331	1	9	GRLTSTSTSDTQININNSA	GRLT(0.003)S(0.003)T(0)	GRLTSTSTSDTQININNSA	CK1	1.3	0.14169		Yes
30	IPI00224112	Fibroblast growth facto	Frs2;Frs2a	T326	1	4	GRLTSTSTSDTQININNSA	GRLT(0.805)S(0.154)T(0)	GRLTSTSTSDTQININNSA	PKA	1.8	0.0012258	Up	Yes
621	IPI00224112	Fibroblast growth facto	Frs2;Frs2a	T328	1	4	LTSTSTSDTQININNSAQR	LT(0.32)S(0.32)T(0.32)	LT(ph)S(ph)TSDTQININNSAQR	NEK6				No
248	IPI00122521	Fragile X mental retard	Fxr1;Fxr1h;Fxr1;Fxr1h	S643	1	9	AINGPPTSASGDEIPKLR	AINGP(0.002)S(0.113)	AINGP(ox)S(ph)GDEIPKLR	CK2	1.2	0.23921		Yes
135	IPI00126389	Fragile X mental retard	Fxr2;Fxr2h;RP23-422L1	S603	2	4	TDGSIQDRQPVTVADYI	T(0.288)DGS(0.856)IS(0)	TDGSIQDRQPVTVADYI	PLK1	1.3	0.11611		Yes
136	IPI00126389	Fragile X mental retard	Fxr2;Fxr2h;RP23-422L1	S605	2	6	TDGSIQDRQPVTVADYI	T(0.234)DGS(0.808)IS(0)	TDGSIQDRQPVTVADYI		1.3	0.11611		Yes
622	IPI00130455	Phospholemmann;FXD	Fxyd1;Plm	S82	1	13	TGEPDEEETFRSSIR	TGEPDEEETFRS(0.5)S(0)	TGEPDEEETFRS(ph)SIR					No
259	IPI00130455	Phospholemmann;FXD	Fxyd1;Plm	S83	1	14	TGEPDEEETFRSSIR	TGEPDEEETFRS(0.374)	TGEPDEEETFRS(ph)SIR	AURORA	1.0	0.25183		No
546	IPI00130095	Ras GTPase-activating p	G3bp1;G3bp;G3bp1;G3	S229	1	1	STSPAPADVAPAEQDLR	S(0.564)T(0.218)S(0.21)	S(ph)TSPAPADVAPAEQDLR		1.1	0.49147		No
66	IPI00124245	Ras GTPase-activating p	G3bp2;G3bp2	S225	1	1	SATPPPAEASLPQEPKP	S(0.956)AT(0.044)PPPA	S(ph)ATPPPAEASLPQEPKP		0.8	0.032515	Down	No
207	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	S259	1	3	VDSITCLFPVEEK	VDS(0.993)T(0.006)T(0)	VDS(ph)TCLFPVEEK	CHK1/2	0.9	0.19754		Yes
312	IPI00473912	PERQ amino acid-rich w	Gigyf2;Kiaa0642;Perq2	S26	1	10	ALSSGGISITPPLSPALPK	ALSSGGISIT(0.132)S(0.8)	ALSSGGISIT(ph)PPLSPA	CK1	1.0	0.30792		Yes
441	IPI00473912	PERQ amino acid-rich w	Gigyf2;Kiaa0642;Perq2	T383	1	21	AGAEASEEVPQTSLSAR	AGAEASEEVPQTSLS(0.0)	AGAEASEEVPQTSLSAR	ERK/MAPK	1.0	0.4078		Yes
2	IPI00749815	similar to DNA cytosine	Gm14490	S290	1	12	RTTNDPAASESPPPKR	RTTNDPAASES(0.013)S(0)	RTTNDPAASES(ph)PPKR	Polo box	0.04	2.182E-80	Down	Yes
270	IPI00222461	Guanine nucleotide-bin	Gnl3;Ns;Gnl3;Ns	S505	1	3	ELSPQSTAGKPSDSSA	ELS(0.914)PQ(0.058)	ELS(ph)PQSTAGKPSDSSA	CAMK2	1.0	0.2668		Yes
623	IPI00222461	Guanine nucleotide-bin	Gnl3;Ns;Gnl3;Ns	S509	1	21	NAEISDVAVPEETRELSPE	NAEISDVAVPEET(0.153)	NAEISDVAVPEETRELSPE	CK1				No
624	IPI00138860	Golgin subfamily A men	Golga4;Golga4;Golga4	T39	1	1	TSSFTDQLDDVTPNR	T(0.394)S(0.202)S(0.20)	T(ph)SSFTDQLDDVTPNR	PKA/AKT				No
157	IPI00131457	Probable G-protein cou	Gpr124;Tem5	S1104	1	10	ALPTATEDGSPVLGEGPA	ALPTATEDGS(1)PVLGEG	ALPTATEDGS(ph)PVLGEG	CK1	0.9	0.13382		Yes
72	IPI00648141	Glycogen synthase kina	Gsk3a;Gsk3b	Y279	1	7	GEPNVSYICSR	GEPNVSY(0.02)Y(0.998)	GEPNVSY(ph)ICSR		0.8	0.041235	Down	No
625	IPI00113686	General transcription fa	Gtf2i;Bap135;Diws1;G	S674	1	1	SPGNSKVPVEIETVGGP	S(0.498)P(0.41)NS(0)	S(ph)PNSKVPVEIETVGGP	WW GroupIV				No
309	IPI00340529	General transcription fa	Gtf3c3;AL022818	S42	1	3	GKSSPKENPDDSEVPSSS	GKS(0.864)S(0.136)PKE	GKS(ph)SPKENPDDSEVPSSS	GIDSAK	1.0	0.30677		Yes
626	IPI00340529	General transcription fa	Gtf3c3;AL022818	S43	1	4	GKSSPKENPDDSEVPSSS	GKS(0.286)S(0.286)PKE	GKS(ph)SPKENPDDSEVPSSS	Polo box				No
627	IPI00340529	General transcription fa	Gtf3c3;AL022818	S51	1	12	GKSSPKENPDDSEVPSSS	GKS(0.286)S(0.286)PKE	GKS(ph)SPKENPDDSEVPSSS	GSK3				No
628	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	S170	4	3	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	PKD				No
629	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	S173	4	6	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	CK2				No
634	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	S187	4	20	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	EGTPTDGFVLSTK				No
630	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T174	4	7	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	EGTPTDGFVLSTK				No
631	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T175	4	8	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	EGTPTDGFVLSTK				No
543	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T178	1	11	AASADSTTEGTPDGFV	AA(0.001)T(0.001)	AASADSTTEGTPDGFV	FHA1 Rad53p	1.1	0.49074		Yes
632	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T180	4	13	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	EGTPTDGFVLSTK				No
633	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T184	4	17	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	FHA KAPP				No
635	IPI00378480	Core histone macro-H2	H2afy;H2afy;H2afy	T188	4	21	AASADSTTEGTPDGFV	AA(0.441)ADS(0.441)T	AA(ox)ADS(ph)T(ph)T	FHA2 Rad53p				No
377	IPI00117011	Hematopoietic lineage	Hcls1;Hs1;Hcls1	S112	2	16	SAVGHEYVADVEKHSSQ	S(0.958)AVGHEY(0.042)	S(ph)AVGHEYVADVEKHSSQ	PKD	1.1	0.35916		Yes
331	IPI00117011	Hematopoietic lineage	Hcls1;Hs1;Hcls1	S97	2	1	SAVGHEYVADVEKHSSQ	S(0.958)AVGHEY(0.042)	S(ph)AVGHEYVADVEKHSSQ	QTDAAR	1.2	0.31943		Yes
492	IPI00114232	Histone deacetylase 1	Hdac1	S393	1	22	MLPHAPGVQMQAIPED	MLPHAPGVQMQAIPED	M(ox)LPHPAGVQMQAIPED	CK2	1.1	0.45695		Yes
511	IPI00114232	Histone deacetylase 1	Hdac1	S421	2	8	IACEEFSDSDEEGGRR	IACEEFS(1)DS(1)DEEG	IACEEFS(ph)DS(ph)DEEG	GRRK	1.1	0.47198		Yes
512	IPI00114232	Histone deacetylase 1	Hdac1	S423	2	10	IACEEFSDSDEEGGRR	IACEEFS(1)DS(1)DEEG	IACEEFS(ph)DS(ph)DEEG	CK2	1.1	0.47198		Yes
549	IPI00137668	Histone deacetylase 2;	Hdac2;Yy1bp	S394	1	22	MLPHAPGVQMQAIPED	MLPHAPGVQMQAIPED	MLPHAPGVQMQAIPED	CK2	1.1	0.49234		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
175	IPI00137668	Histone deacetylase 2; Hdac2;Yy1bp	Hdac2;Yy1bp	S422	2	8	IACDEEFSDEDEGEGR	IACDEEFS(1)DS(1)EDEG	IACDEEFS(ph)DS(ph)ED	CK2	1.3	0.15866		Yes
176	IPI00137668	Histone deacetylase 2; Hdac2;Yy1bp	Hdac2;Yy1bp	S424	2	10	IACDEEFSDEDEGEGR	IACDEEFS(1)DS(1)EDEG	IACDEEFS(ph)DS(ph)ED	CK2	1.3	0.15866		Yes
551	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S165	1	9	RAGDVLEDS(1)PK	RAGDVLEDS(1)PK	RAGDVLEDS(ph)PK	CK2	1.1	0.49303		Yes
413	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S202	1	5	NSTPSEPDGQGGPAEE	NS(0.023)T(0.136)PS(0.	NSTPS(ph)EPDGGQGGP	CK1	1.0	0.38531		Yes
636	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S206	1	9	NSTPSEPDGQGGPAEE	NS(0.132)T(0.132)PS(0.	NSTPS(ph)EPDGGQGGP	CK1				No
38	IPI00116442	Hepatoma-derived gro	Hdgfrp2;Hdgfrp2	S644	1	10	GGSEELHDS(1)PRNS	GGSEELHDS(1)PRNS	GGSEELHDS(ph)PRNS	CDK1	0.7	0.0091446	Down	Yes
174	IPI00420246	HEAT repeat-containing	Heatr6	S646	1	15	TFPAGSLEEAASLSPK	TFPAGSLEEAASL(0.009	TFPAGSLEEAASL(ph)P	Polo box	0.9	0.15844		Yes
210	IPI00331597	Histone H1.3;H1 VAR.4	Hist1h1d;H1f3	S62	2	1	SETAPAAPAAPAPVEK	S(1)ET(1)APAAPAAPAP	S(ph)ET(ph)APAAPAAPV	PKA	1.2	0.19929		Yes
419	IPI00623776	Histone H4	Hist1h4a;Hist1h4b;H4	S103	1	3	RISGLIYEETR	RIS(1)GLIYEETR	RIS(ph)GLIYEETR	PKA	1.1	0.39185		Yes
271	IPI00314240	High mobility group prc	Hmg1a;Hmgi;Hmgiy;Hn	S102	2	14	KLEKEEEEGISQESSEEE	KLEKEEEEGISQES(1)S(1)	KLEKEEEEGISQES(ph)S	CK2	1.2	0.26859		Yes
272	IPI00314240	High mobility group prc	Hmg1a;Hmgi;Hmgiy;Hn	S103	2	15	KLEKEEEEGISQESSEEE	KLEKEEEEGISQES(1)S(1)	KLEKEEEEGISQES(ph)S	CK2	1.2	0.26859		Yes
556	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S84	2	23	QADVADQQTTELPAEN	QADVADQQT(0.001)T(0.	QADVADQQTTELPAEN	CK1	1.1	0.4994		No
206	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S87	2	26	QADVADQQTTELPAEN	QADVADQQT(0.001)T(0.	QADVADQQTTELPAEN	CK2	1.2	0.19612		No
111	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S95	1	34	QADVADQQTTELPAEN	QADVADQQTTELPAEN	QADVADQQTTELPAEN	GETENQSPASEEKEAKS	1.3	0.088666		Yes
637	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	T80	2	19	QADVADQQTTELPAEN	QADVADQQTTELPAEN	QADVADQQTTELPAEN	GET(ph)ENQSPASEEKEAKS				No
54	IPI00314755	Hematological and neu	Hn1	S87	1	3	SNSSEASSGDFLDLK	S(0.011)NS(0.983)S(0.	SNS(ph)SEASSGDFLDLK	CAMK2	0.8	0.02151	Down	Yes
397	IPI00553777	Heterogeneous nuclear	Hnrnpa1;Fli-2;Hnrpa1;	S4	1	1	SESPKEPEQLR	S(0.959)ES(0.041)PKEP	S(ph)JESPKPEQLR		1.0	0.37078		Yes
269	IPI00553777	Heterogeneous nuclear	Hnrnpa1;Fli-2;Hnrpa1;	S6	1	3	SESPKEPEQLR	S(0.007)ES(0.993)PKEP	SES(ph)PKEPEQLR	CDK1	1.2	0.26534		Yes
256	IPI00224729	Heterogeneous nuclear	Hnrnp1;Hnrph1;RP23;	S104	1	6	HTGPNSPDTANDGFVR	HTGPNNS(0.992)PDT(0.	HTGPNNS(ph)PDTANDGF	WW GroupIV	1.2	0.24584		Yes
216	IPI00224729	Heterogeneous nuclear	Hnrnp1;Hnrph1;RP23;	T107	1	9	HTGPNSPDTANDGFVR	HTGPNNS(0.008)PDT(0.	HTGPNNS(ph)PDTANDGF	FHA1 Rad53p	1.2	0.20495		Yes
199	IPI00229080	Heat shock protein 84b	Hsp90ab1;Hsp84b;Hsp	S255	1	6	IEDVGSDEEDDSGDKK	IEDVGS(1)DEEDDSGDKD	IEDVGS(ph)DEEDDSGDK	CK2	1.3	0.18597		Yes
365	IPI00229080	Heat shock protein 84b	Hsp90ab1;Hsp84b;Hsp	S261	1	12	IEDVGSDEEDDSGDKK	IEDVGS(0.5)DEEDDS(0.	IEDVGS(ph)DEEDDSGDK	CK2	1.0	0.35149		No
490	IPI00123802	Heat shock protein 105	Hsp11;Hsp105;Hsp110;	S810	1	3	IESPKLER	IES(1)PKLER	IES(ph)PKLER	CDK1	1.1	0.45577		Yes
232	IPI00221566	HIV Tat-specific factor	Htatsf1	S645	1	6	VFDSDSDIEEEEADEE	VFDSDSD(1)DDIEEEEADE	VFDSDSD(ph)DDIEEEEADE	CECEDADKCEDNDID	1.2	0.2223		Yes
319	IPI00463909	E3 ubiquitin-protein lig	Huwe1;Klaa0312;Ureb1	S1907	1	6	GSSTASDDEFENLR	GS(0.004)GT(0.004)AS	GSSTAS(ph)DDEFENLR	CK2	1.0	0.31334		Yes
357	IPI00120225	Insulin-like growth fact	Igf1r	S1260	1	4	MRPSFLEIIGSIK	MRPS(1)FLEIIGSIK	M(ox)RPS(ph)FLEIIGSIK	PKA	1.2	0.34515		Yes
461	IPI00120225	Insulin-like growth fact	Igf1r	S1267	1	11	MRPSFLEIIGSIK	MRPS(0.126)FLEIIGS(0.	M(ox)RPSFLEIIGS(ph)IK		1.1	0.4239		Yes
638	IPI00308971	Cation-independent ma	Igf2r	S2476	1	8	LVSFHDDSDDELLHI	LVSFHDDSD(1)DEDLHI	LVSFHDDSD(ph)DEDLHI					Yes
639	IPI00124436	Interleukin-22 receptor	Il22ra1	S420	2	8	DSTPGILSTPKYLTKT	DSTPGILS(0.876)T(0.12)	DSTPGILS(ph)TPKY(ph)L	LTKT				Yes
640	IPI00124436	Interleukin-22 receptor	Il22ra1	Y424	2	12	DSTPGILSTPKYLTKT	DSTPGILS(0.876)T(0.12)	DSTPGILS(ph)TPKY(ph)E	EGFR				Yes
439	IPI00308094	Integrator complex sub	Ints3;Ints3	S500	1	11	EKFPEFCSSPPVVEK	EKFPEFC(0.011)S(0.04)	EKFPEFCSSPS(ph)PPVE	CK1	1.1	0.40553		Yes
491	IPI00468004	IQ domain-containing p	Iqce;Iqce	S661	1	12	ETVSLTPSGASPPSLR	ETVSLTPS(0.001)GS(0.	ETVSLTPSGAS(ph)PPSL	CK1	1.1	0.4559		No
641	IPI00854942	Putative uncharacterize	Irf2bp2	S419	1	4	RPASVSSAAAEHEAR	RPAS(0.462)VS(0.462)S	RPAS(ph)VSSAAAEHEAR	CAMK2	2.2	3.864E-06	Up	Yes
23	IPI00854942	Putative uncharacterize	Irf2bp2	S421	1	6	RPASVSSAAAEHEAR	RPAS(0.141)VS(0.841)S	RPASV(ph)VSSAAAEHEAR		0.8	0.040344	Down	Yes
71	IPI00854942	Putative uncharacterize	Irf2bp2	S536	1	4	RKPSPEPEGEVGPVK	RKPS(1)PEPEGEVGPVK	RKPS(ph)PEPEGEVGPVK	PKA/AKT	2.2	0.040344	Down	Yes
642	IPI00119627	Insulin receptor substra	Irs1;Irs-1;Irs1;mCG_203	S1096	1	2	HSSETFSAPTR	HS(0.49)S(0.49)ET(0.01)	HS(ph)SETFSAPTR	PKA				No
417	IPI00119627	Insulin receptor substra	Irs1;Irs-1;Irs1;mCG_203	S1097	1	3	HSSETFSAPTR	HS(0.065)S(0.934)ET(0.	HSS(ph)JTFFSAPTR	PIM1/2	1.1	0.38948		Yes
166	IPI00923679	Insulin receptor substra	Irs2;Irs2	S1165	1	5	HNSASVENVSLR	HNS(0.007)AS(0.993)VE	HNSAS(ph)VENVSLR		0.9	0.14548		Yes
643	IPI00923679	Insulin receptor substra	Irs2;Irs2	S515	1	1	SNTPESIAETPPAR	S(0.941)NT(0.059)PESIA	S(ph)NTPESIAETPPAR	CK1				Yes
124	IPI00923679	Insulin receptor substra	Irs2;Irs2	T517	1	3	SNTPESIAETPPAR	S(0.104)NT(0.896)PESIA	SNT(ph)PESIAETPPAR	CAMK2	1.3	0.10202		Yes
554	IPI00410790	Iroquois-class homeod	Irx1;Irx1a;Irx1	S267	1	4	DQSSPLSAAETLK	DQS(0.006)S(0.993)PLS	DQSS(ph)PLSAAETLK	Polo box	1.1	0.49435		Yes
195	IPI00856218	Iron-sulfur cluster asse	Iscu;Nifun	S15	1	4	RAASALLLR	RAAS(1)ALLLR	RAAS(ph)ALLLR	CHK1/2	0.9	0.17898		Yes
644	IPI00649251	Integrin beta-4;Integrin	Irgb4;Irgb4;Irgb4;RP23-	S1086	1	6	FQVQLSNPK	FQVQLS(1)NPK	FQVQLS(ph)NPK					Yes
645	IPI00831223	Intersectin-1;EH and SH	Itns1;Ese1;Itns1;Itns1;E	S900	1	12	SAFTPATATGSSPVLG	SAFTPATATGS(0.044)S	SAFTPATATGSS(ph)PSP	Polo box				No
95	IPI00831223	Intersectin-1;EH and SH	Itns1;Ese1;Itns1;Itns1;E	S902	1	14	SAFTPATATGSSPVLG	SAFTPATATGS(0.015)S	SAFTPATATGSS(ph)PSP	CK1	0.8	0.064821		Yes
544	IPI00122143	Tyrosine-protein kinase	Jak2	S523	1	10	TNGISDVQISPTLQR	TNGISDVQIS(0.5)PT(0.5)	TNGISDVQIS(ph)PTLQR		1.1	0.49101		No
545	IPI00122143	Tyrosine-protein kinase	Jak2	T525	1	12	TNGISDVQISPTLQR	TNGISDVQIS(0.5)PT(0.5)	TNGISDVQIS(ph)PTLQR		1.1	0.49101		No
172	IPI00469103	Lysyl-tRNA synthetase;	Kars;Kars	S422	1	3	RISMVEELEK	RIS(1)MVEELEK	RIS(ph)MVEELEK	AURORA-A	0.9	0.15608		Yes
45	IPI00381078	Uncharacterized protei	Klaa1712	S292	2	11	VTLLETMLLSK	VTLLET(1)EMLLS(1)K	VTLLET(ph)EMLLS(ph)K		0.7	0.013382	Down	Yes
44	IPI00381078	Uncharacterized protei	Klaa1712	T287	2	6	VTLLETMLLSK	VTLLET(1)EMLLS(1)K	VTLLET(ph)EMLLS(ph)K	NEK6	0.7	0.013382	Down	Yes
464	IPI00411082	Kinesin-like protein KIF	Kif1b;Kif1b	S1057	1	4	SGLSLEELR	SGLS(1)LEELR	SGLS(ph)LEELR	CK2	1.0	0.42554		Yes
53	IPI00753928	Klc2 protein;Kinesin lig	Klc2;mCG_8395;Klc2	S579	1	3	ASSLNFNLK	AS(0.049)S(0.951)NFLN	ASS(ph)NFLNLK	PKA	0.7	0.017685	Down	Yes
483	IPI00230429	Importin subunit alpha	Kpna3;Qip2;Kpna3	S60	1	11	NVPQEESLESDVDADF	NVPQEESLEDS(1)DVDA	NVPQEESLEDS(ph)DVD	NEK6	1.1	0.4497		Yes
337	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S81	1	15	ESPRPAAAEAPAGSDG	ESPRPAAAEAPAGS(1)T	ESPRPAAAEAPAGS(ph)	CK2	1.0	0.32485		Yes
646	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	T503	1	3	AVTPVPKTEEVSNLK	AVT(0.499)PVPT(0.499)	AVT(ph)PVPTKTEEVSNL	CAMK2				No
647	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	T507	1	7	AVTPVPKTEEVSNLK	AVT(0.499)PVPT(0.499)	AVT(ph)PVPTKTEEVSNL	CK2				No
453	IPI00112339	LIM domain and actin-b	Lima1;D15Ert366E;Epl	S360	1	13	SEAQQPMHPKPLSPDAR	SEAQQPMHPKPLS(1)PD	SEAQQPM(ox)HPKPLS	WW GroupIV	1.0	0.42056		Yes
415	IPI00112339	LIM domain and actin-b	Lima1;D15Ert366E;Epl	S488	1	22	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNAG	WW GroupIV	1.0	0.38831		Yes
226	IPI00620256	Lamin-A/C	Lmna;Lmn1	S573	1	5	GSHCSGSDPAEYNLR	GS(0.003)HCS(0.997)G	GSHCS(ph)GSDPAEYN	CK1	0.9	0.22		Yes
484	IPI00620256	Lamin-A/C	Lmna;Lmn1	S633	1	5	SVGGSGGSGFDNLVTR	S(0.004)VGGSG(0.996)G	SVGGSGGSG(ph)GSGFDNL	GSK3	1.1	0.44989		Yes
246	IPI00620256	Lamin-A/C	Lmna;Lmn1	S637	1	9	SVGGSGGSGFDNLVTR	SVGGSGGSGS(1)FGDNLV	SVGGSGGSGS(ph)FGDNL	CK1	1.0	0.23435		Yes
534	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn1	S390	1	4	LRLSPSPTSQR	LRLS(0.885)PS(0.099)PT	LRLS(ph)PSPTSQR	PKA	1.1	0.48753		Yes
336	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn1	S392	1	4	LRLSPSPTSQR	LS(0.001)PS(0.99)PT(0.	LRLSPS(ph)PTSQR	NEK6	1.0	0.32349		Yes
326	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn1	S395	2	9	LRLSPSPTSQR	LRLS(0.055)PS(0.055)PT	LRLSPS(ph)S(ph)QR	CK1	1.2	0.31608		Yes
299	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn1	S458	1	3	NKSNEQDSMGNWQIR	NKS(1)NEDQSMGNWQ	NKS(ph)NEDQSM(ox)G	PKA/AKT	1.0	0.2998		Yes
243	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn1	S546	1	1	SLTMVEDNEDDEDGEE	S(0.57)LT(0.43)MVEDN	S(ph)LTMVEDNEDDED	NEK6	1.0	0.2296		No

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
325	IPI00620256	Lamin-A/C;Lamin-A/C/L	Lmna;Lmn1;Lmna;Lmn1	T394	2	8	LRLSPSPTSQR	LRLS(0.055)PS(0.055)PT	LRLSPSPT(ph)S(ph)QR		1.2	0.31608		Yes
128	IPI00659447	LIM domain only 7	Lmo7	S194	1	4	REDSFESLDSLGSR	REDS(0.939)FES(0.02)LS	REDS(ph)FESLDSLGSR	PLK1	0.9	0.10641		Yes
209	IPI00474873	Leucine-rich repeat-cor	Lrrc16a;Carmil;Lrrc16;L	S971	1	1	SSGLISELPSSEGR	S(0.554)S(0.393)GLIS(O	S(ph)SSGLISELPSSEGR		0.9	0.19852		No
171	IPI00474873	Leucine-rich repeat-cor	Lrrc16a;Carmil;Lrrc16;L	S972	1	3	RSSGLISELPSSEGR	RS(0.107)S(0.893)GLISE	RSS(ph)GLISELPSSEGR	PKA	1.3	0.15603		Yes
137	IPI00762483	Putative uncharacterize	Lrrfp1;Lrrfp1;Lrrfp1;F	S98	1	3	RGSGDTSISMDEEASR	RGS(0.989)GDT(0.009)S	RGS(ph)GSDTSISM(ox)D	PKA	0.9	0.11626		Yes
193	IPI00607974	Protein MAK16 homolo	Mak16;Rbm13	S197	2	9	ALEKQEAESDEDEE	ALEKQEAES(1)DS(1)EDE	ALEKQEAES(ph)DS(ph)E	CK2	1.3	0.17634		Yes
194	IPI00607974	Protein MAK16 homolo	Mak16;Rbm13	S199	2	11	ALEKQEAESDEDEE	ALEKQEAES(1)DS(1)EDE	ALEKQEAES(ph)DS(ph)E	CK2	1.3	0.17634		Yes
425	IPI00676243	Microtubule-associated	Map1a;Mtap1;Mtap1a;	S764	2	5	ELALSSPEDLTQDFEELKR	ELALS(1)S(1)PEDLTQDF	ELALS(ph)S(ph)PEDLTQ	CK2	1.0	0.39651		Yes
426	IPI00676243	Microtubule-associated	Map1a;Mtap1;Mtap1a;	S765	2	6	ELALSSPEDLTQDFEELKR	ELALS(1)S(1)PEDLTQDF	ELALS(ph)S(ph)PEDLTQ	Polo box	1.0	0.39651		Yes
406	IPI00223621	Microtubule-associated	Map1s;Bpy2ip1;Map8;f	S658	1	1	STSPHDVLDLVSPEFSH	S(0.778)T(0.111)S(0.11	S(ph)STSPHDVLDLVSPE	PKA	1.1	0.38036		Yes
531	IPI00123967	Putative uncharacterize	Map3k7;Map3k7;Tak1;	S439	1	3	RRSIQDLTVGTGTEPGQVS	RRS(1)QDLTVGTGTEPGG	RRS(ph)QDLTVGTGTEPG	AURORA-A	1.1	0.48457		Yes
296	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;Mt	S598	1	11	GQSTVPPCTASPEPVK	GQSTVPPCT(0.001)AS(D	GQSTVPPCTAS(ph)PEPVK		1.0	0.29258		Yes
411	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;Mt	S667	1	21	AAVGVGTGNDIITPPNKE	AAVGVGTGNDIITPPNKE	AAVGVGTGNDIITPPNKE	WW GroupIV	1.0	0.38366		Yes
457	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;Mt	T788	1	6	ATSPSTLVSTGSSSR	AT(0.06)S(0.06)PS(0.06	ATSPST(ph)LVSTGSSSR	CK1	1.1	0.42246		Yes
8	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkn	T179	2	9	VADPDHDHTGFLTEYVA	VADPDHDHT(0.6)GFLT	VADPDHDHT(ph)GFLTE	FHA2 Rad53p	5.3	1.50E-23	Up	No
3	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkn	T183	2	13	VADPDHDHTGFLTEYVA	VADPDHDHTGFLT(1)EY	VADPDHDHTGFLT(ph)EY	(ph)VATR	10.9	3.47E-47	Up	Yes
4	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkn	T188	2	18	VADPDHDHTGFLTEYVA	VADPDHDHT(0.177)GFL	VADPDHDHTGFLT(ph)EY	(ph)VATR	9.5	1.003E-41	Up	No
20	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkn	Y185	1	15	VADPDHDHTGFLTEYVA	VADPDHDHTGFLT(0.00	VADPDHDHTGFLTEY(ph)	VATR	2.4	2.44E-07	Up	Yes
6	IPI00230277	Mitogen-activated prot	Mapk3;Erk1;Prkm3;Ma	T199	2	9	IADPEHDHTGFLTEYVAT	IADPEHDHT(0.992)GFL	IADPEHDHT(ph)GFLT	(ph)FHA2 Rad53p	6.7	3.98E-30	Up	Yes
9	IPI00230277	Mitogen-activated prot	Mapk3;Erk1;Prkm3;Ma	T208	2	18	IADPEHDHTGFLTEYVAT	IADPEHDHT(0.156)GFL	IADPEHDHTGFLT(ph)EY	VAT(ph)R	4.8	7.763E-21	Up	Yes
12	IPI00230277	Mitogen-activated prot	Mapk3;Erk1;Prkm3;Ma	Y205	1	15	IADPEHDHTGFLTEYVAT	IADPEHDHTGFLT(0.012	IADPEHDHTGFLTEY(ph)	VATR	3.5	1.164E-13	Up	Yes
648	IPI00229534	Myristoylated alanine-r	Marcks;Macs	S138	1	8	AEDGAAPSPSSETPKKK	AEDGAAPS(0.25)PS(0.2	AEDGAAPS(ph)PSSETPKK					No
649	IPI00229534	Myristoylated alanine-r	Marcks;Macs	S141	1	11	AEDGAAPSPSSETPKKK	AEDGAAPS(0.004)PS(O	AEDGAAPSPS(ph)ETPK	CK1				No
493	IPI00622008	Microtubule-associated	Mast2;Mast205;Mast2	S149	1	7	NQSLGQSPSLTAGLK	NQSLGQS(0.99)APS(0.0	NQSLGQS(ph)APSLTAGI	NEK6	1.1	0.45868		Yes
48	IPI00677823	Microtubule-associated	Mast4;Mast4	S204	1	7	SQALGQSPSLTAGLK	SQALGQS(0.823)APS(O	SQALGQS(ph)APSLTAGI	NEK6	0.7	0.015541	Down	Yes
33	IPI00453826	Matrin-3	Matr3	S188	1	3	RDSFDDRGPSPSLNPLV	RDS(0.826)FDDRGRS(0.	RDS(ph)FDDRGPSPSLNP	PKA	1.7	0.003376	Up	Yes
650	IPI00453826	Matrin-3	Matr3	S195	1	10	RDSFDDRGPSPSLNPLV	RDS(0.5)FDDRGRS(0.5)	RDS(ph)FDDRGPSPSLNP	CAMK2				No
68	IPI00117098	MAP3K12-binding inhib	Mbip	S22	1	7	SLEQCSSPLLTR	SLEQCS(0.002)S(0.998)	SLEQCSS(ph)PLLTR	Polo box	0.8	0.036854	Down	Yes
41	IPI00323820	DNA replication licensi	Mcm2;Bm28;Cdc1;Kiaa	S21	1	3	RISDPLTSSPGR	RIS(0.997)DPLT(0.002)S	RIS(ph)DPLTSSPGR	PKA	0.7	0.012453	Down	Yes
412	IPI00323820	DNA replication licensi	Mcm2;Bm28;Cdc1;Kiaa	S27	1	8	ISDPLTSSPGR	ISDPLTS(0.002)S(0.998)	ISDPLTS(ph)PGR	Polo box	1.0	0.384		Yes
138	IPI00753701	Mediator of DNA dama	Mdc1;Kiaa0170	S168	1	17	VLLAADSEEEGDFPSPG	VLLAADS(1)EEEGDFPSP	VLLAADS(ph)EEEGDFPS	CK2	0.9	0.11676		Yes
123	IPI00857417	Mediator of RNA polym	Med24;D11Erdt307e;T	S890	1	14	LLSSDDDDANILSSPTDR	LLSSDDDDANILS(0.039)	LLSSDDDDANILSS(ph)P	T	0.9	0.098768		Yes
204	IPI00850543	Mitochondrial fission fa	Mff;Mff	S146	1	3	NDSIPVLR	NDS(1)IPVLR	NDS(ph)IPVLR	CHK1/2	0.9	0.19261		Yes
416	IPI00116372	Myeloid leukemia facto	Mlf2	S237	1	9	LAIQGPEDSPSR	LAIQGPEDS(0.94)PS(O	LAIQGPEDS(ph)PSR	CDK2	1.0	0.38884		Yes
149	IPI00856176	Putative uncharacterize	Mobk1a;Mobk1a;Mob	T35	1	5	HAEAT1JLGSNLR	HAEAT(1)JLGSNLR	HAEAT(ph)JLGSNLR	PLK1	0.9	0.12741		Yes
173	IPI00720036	Myosin phosphatase Rf	Mrip;Kiaa0864;Mrip;R	S1018	1	1	SKSVIEQVSWDN	S(0.999)KS(0.001)VIEQ	S(ph)KSVIEQVSWDN		1.3	0.15621		Yes
480	IPI00720036	Myosin phosphatase Rf	Mrip;Kiaa0864;Mrip;R	S1020	1	3	SKSVIEQVSWDN	S(0.096)KS(0.904)VIEQ	SKS(ph)VIEQVSWDN	CAMK2	1.1	0.4469		Yes
56	IPI00720036	Myosin phosphatase Rf	Mrip;Kiaa0864;Mrip;R	S292	1	13	AEEQLPPLSPSPSPH	AEEQLPPLS(0.019)PPS	AEEQLPPLSPSPS(ph)P	WW GroupIV	0.8	0.023892	Down	Yes
651	IPI00720036	Myosin phosphatase Rf	Mrip;Kiaa0864;Mrip;R	S294	1	15	AEEQLPPLSPSPSPH	AEEQLPPLS(0.001)PPS	AEEQLPPLSPSPS(ph)T	GSK3				No
652	IPI00720036	Myosin phosphatase Rf	Mrip;Kiaa0864;Mrip;R	T295	1	16	AEEQLPPLSPSPSPH	AEEQLPPLS(0.001)PPS	AEEQLPPLSPSPS(ph)T	WW GroupIV				No
81	IPI00128196	Myotubularin-related p	Mtmr2;Mtmr2;RP23-13	S74	1	3	SSCESLGAQLPAAR	S(0.171)S(0.075)S(0.75	SSS(ph)CESLGAQLPAAR	CHK1	0.8	0.052329		Yes
653	IPI00132938	Myeloid-associated diff	Myadm;Mug	S16	4	9	TTTTTTSSSTTVGSSAR	T(0.509)T(0.449)T(0.53	T(ph)TTTTSSSTTVGSSA	CK1				Yes
39	IPI00132938	Myeloid-associated diff	Myadm;Mug	S17	1	10	TTTTTTSSSTTVGSSAR	T(0.001)T(0.001)T(0.00	TTTTTTSSS(ph)TVGSA	CK1	0.7	0.010051	Down	No
528	IPI00331361	Myb-binding protein 1A	Mybbp1a;P160;Mybbp	S1253	1	10	SPAPSNPTLSPSTPAK	SPAPSNPT(0.041)LS(O	SPAPSNPTLSPSTPAK		1.1	0.48276		Yes
535	IPI00757312	Myosin, heavy polypep	Myh10;RP23-396M19.2	S1993	1	13	RQLHIEGASLELSDDDTE	RQLHIEGASLELS(0.993)	RQLHIEGASLELS(ph)DD	NEK6	1.1	0.48999		Yes
442	IPI00757312	Myosin, heavy polypep	Myh10;RP23-396M19.2	T1997	1	17	RQLHIEGASLELSDDDTE	RQLHIEGASLELS(0.036)	RQLHIEGASLELSDDDT	(ph)ESK	1.0	0.41008		Yes
212	IPI00752027	Acyl-CoA synthetase sh	Myh7b;Acss2;RP23-26D	S30	1	3	GWSPPEVVR	GWS(1)PPEVVR	GWS(ph)PPEVVR	PKA/AKT	0.9	0.20299		Yes
351	IPI00123181	Myosin-9;Myosin heav	Myh9	S1943	1	7	KGTGDCSDEEVDGKADG	KGT(0.003)GDCS(0.997	KGTGDCS(ph)DEEVDGK	CK2	1.2	0.34123		Yes
70	IPI00123181	Myosin-9;Myosin heav	Myh9	T1939	1	3	KGTGDCSDEEVDGKADG	KGT(0.5)GDCS(0.5)DEE	KGT(ph)GDCSDEEVDGK	PKA	1.4	0.040104	Up	No
295	IPI00849670	Myof protein;Myoferlin	Myof;Myof;Fer13;Kiaa	S175	1	17	GPSGTVSEALQR	GPSGT(0.003)VS(0.997)	GPSGTVSEALQR	CK1	1.0	0.29216		Yes
447	IPI00133977	Nap14 protein;Nucleos	Nap14;mCG_129001;N	S125	1	8	EFITGDVEPTDAESAWHS	EFITGDVEPTDAESAWHS	EFITGDVEPTDAESAWHS	CK2	1.0	0.41272		Yes
28	IPI00133977	Nap14 protein;Nucleos	Nap14;mCG_129001;N	T117	1	10	EFITGDVEPTDAESAWHS	EFIT(0.05)GDVEPT(0.51	EFITGDVEPT(ph)DAESA	CK2	0.6	0.000647	Down	No
290	IPI00317794	Nucleolin;Protein C23	Ncl;Nuc	S145	2	7	NAKKEDSDEDEDEEDED	NAKKEDS(1)DEDEDEED	NAKKEDS(ph)DEDEDEE	EDDS(ph)DEDEDEEDED	1.2	0.28729		Yes
291	IPI00317794	Nucleolin;Protein C23	Ncl;Nuc	S157	2	19	NAKKEDSDEDEDEEDED	NAKKEDS(1)DEDEDEED	NAKKEDS(ph)DEDEDEE	EDDS(ph)DEDEDEEDED	1.2	0.28729		Yes
436	IPI00116968	Nuclear receptor coact	Ncoa2;Grip1;Tif2;Ncoa	S699	1	7	LLQDSSPVDLAK	LLQDSS(0.052)S(0.948)	LLQDSS(ph)PVDLAK	Polo box	1.1	0.40325		Yes
187	IPI00113730	Nuclear receptor coact	Ncoa2;RP23-120P1.1-0	S846	1	3	AVSLDSPVSVSGSPVVK	AVS(0.999)LDS(0.001)P	AVS(ph)LDSPVSVSGSPV	CAMK2	0.9	0.16935		Yes
87	IPI00123871	Nuclear receptor corep	Ncor2;Smrt;Ncor2;Smrt	S1255	1	6	IVGEDSPSRLDR	IVGEDS(0.5)PS(0.5)R	IVGEDS(ph)PSRLDR	CDK2	1.4	0.058043		No
188	IPI00123871	Nuclear receptor corep	Ncor2;Smrt;Ncor2;Smrt	S1257	1	8	IVGEDSPSRLDR	IVGEDS(0.5)PS(0.5)R	IVGEDS(ph)PSRLDR		1.4	0.058043		No
89	IPI00125960	Protein NDRG1;N-myc c	Ndr1;Ndr1;Ndr1;Tdd5	S333	1	6	TASGSSVTSLEGR	T(0.001)AS(0.003)GS(O	TASGSS(ph)VTSLEGR	CK1	1.3	0.17265		No
443	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	S281	1	3	RPSDDDLTDEDNDMD	RPS(0.5)PDDDLT(0.5)D	RPS(ph)PDDDLTDEDND	PKA	1.1	0.4111		No
76	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	S309	1	4	RQISEEDVDGPDNR	RQIS(1)EDVDGPDNR	RQIS(ph)EDVDGPDNR	CAMK2	1.0	0.04888	Down	Yes
308	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	T287	1	13	TQWKRSPDDDLTDEDN	T(0.001)QWKRSPDDDLT	T(ph)QWKRSPDDDLT	(ph)FHA1 Rad53p	0.8	0.30577		Yes
654	IPI00554928	Neurofilament light pol	Nefl;Nf68;Nfl	S11	4	11	MSSFYDYPFSTYKRR	MSSFYDYPFYS(1)T(1)S	MSSFYDYPFYS(ph)T(ph)S	(ph)Y(ph)KRR				Yes
656	IPI00554928	Neurofilament light pol	Nefl;Nf68;Nfl	S13	4	13	MSSFYDYPFSTYKRR	MSSFYDYPFYS(1)T(1)S	MSSFYDYPFYS(ph)T(ph)S	(ph)Y(ph)KRR				Yes
655	IPI00554928	Neurofilament light pol	Nefl;Nf68;Nfl	T12	4	12	MSSFYDYPFSTYKRR	MSSFYDYPFYS(1)T(1)S	MSSFYDYPFYS(ph)T(ph)S	(ph)Y(ph)KRR				Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
657	IPI0054928	Neurofilament light pol	Nefl;Nf68;Nfl	Y14	4	14	MSSFGYDPYFSTYKRR	MSSFGYDPYF(1)T(1)S(	MSSFGYDPYF(ph)T(ph)S	S(ph)Y(ph)KRR				Yes
658	IPI00409935	Nuclear factor of activa	Nfat4;Nfat3;Nfatc4;NF	S334	1	3	RTSSEQAVALPR	RT(0.057)S(0.887)S(0.0	RTS(ph)SEQAVALPR	PKA				Yes
449	IPI00421052	Nipped-B-like protein;D	Nipbl;Nipbl	S2652	1	10	AITSLGGGSPK	AITSLGGG(S1)PK	AITSLGGG(ph)PK	CDK1	1.1	0.41415		Yes
659	IPI00421052	Nipped-B-like protein;D	Nipbl;Nipbl;Nipbl	S305	1	16	GSRPPLILQSQSLPCSSPR	GS(0.004)RPPILQSQ(0.0	GSRPPLILQSQSLPCSS(ph)	NEK6				No
475	IPI00421052	Nipped-B-like protein;D	Nipbl;Nipbl;Nipbl	S306	1	17	GSRPPLILQSQSLPCSSPR	GS(0.001)RPPILQSQ(0.0	GSRPPLILQSQSLPCSS(ph)	Polo box	1.1	0.44318		Yes
404	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S536	1	9	SSPKVEEVAEPEEAASPTT	SSPKVEEVA(S1)PEEAAS	SSPKVEEVA(ph)PEEAAS	CK2	1.1	0.37815		Yes
74	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S543	1	16	SSPKVEEVAEPEEAASPTT	SSPKVEEVAEPEEAAS(0.5	SSPKVEEVAEPEEAAS(ph)PTTPK		0.8	0.044601	Down	Yes
231	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	S509	1	8	HIKEEPLSEEEPCSTAVPR	HIKEEPLS(0.977)EEEPC	HIKEEPLS(ph)EEEPCST	CK2	0.9	0.22227		Yes
660	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	T515	1	14	HIKEEPLSEEEPCSTAVPR	HIKEEPLS(0.175)EEEPC	HIKEEPLSEEEPC(ph)ST	FHA KAPP				No
661	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;Np	S106	1	3	CGSGPVHISGQHLVAVEH	CGS(0.322)GPVHIS(0.32	CGS(ph)GPVHISGQHLVAVE	DAEAEDEDEEDVKLLGM(ox)SGK				No
85	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;Np	S112	1	9	CGSGPVHISGQHLVAVEH	CGS(0.094)GPVHIS(0.81	CGSGPVHIS(ph)GQHLVAVE	DAEAEDEDEEDVKLL	1.4	0.057059		Yes
155	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;Np	S125	1	22	CGSGPVHISGQHLVAVEH	CGSGPVHISGQHLVAVEH	CGSGPVHISGQHLVAVEH	CK2	1.3	0.13318		Yes
305	IPI00894870	tRNA (cytosine-5'-)met	Nsun2;D13Wsu123e;M	S723	1	12	EGVILTNENAASPEQPGI	EGVILTNENAAS(1)PEQPG	EGVILTNENAAS(ph)PEQPG	DEDAK	1.0	0.30543		Yes
359	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S368	1	5	AQRLSQETALGR	AQRLS(1)QETALGR	AQRLS(ph)QETALGR	PKA	1.2	0.346202		Yes
154	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S456	1	14	KVPEQPPELPQLDSQHL	KVPEQPPELPQLDS(1)QH	KVPEQPPELPQLDS(ph)QHL		0.9	0.13293		Yes
94	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	T371	1	8	AQRLSQETALGR	AQRLS(0.198)QET(0.80	AQRLSQET(ph)EALGR	CK1	0.8	0.064681		Yes
663	IPI00341869	Nuclear ubiquitous case	Nucks1;Nucks	S14	1	5	VVDYSQFQESDDADEDY	VVDY(0.134)S(0.421)QF	VVDYS(ph)QFQESDDADEDY	GRDSSGPPAK				No
548	IPI00341869	Nuclear ubiquitous case	Nucks1;Nucks	S19	1	11	KVVDYSQFQESDDADEDY	KVVDYSQFQES(1)DDAD	KVVDYSQFQES(ph)DDADEDY	GR	1.1	0.49233		Yes
527	IPI00341869	Nuclear ubiquitous case	Nucks1;Nucks	S30	1	21	VVDYSQFQESDDADEDY	VVDY(0.007)S(0.014)QF	VVDYSQFQESDDADEDY	PKA	1.1	0.48153		No
662	IPI00341869	Nuclear ubiquitous case	Nucks1;Nucks	Y13	1	5	KVVDYSQFQESDDADEDY	KVVDY(0.426)S(0.13)QF	KVVDY(ph)SQFQESDDADEDY	GRDSSGPPAK				No
664	IPI00341869	Nuclear ubiquitous case	Nucks1;Nucks	Y26	1	17	VVDYSQFQESDDADEDY	VVDY(0.025)S(0.04)QF	VVDYSQFQES(ph)DDAD	SRC				No
342	IPI00263048	Putative uncharacterize	Numa1	S1739	1	14	TQPDGTSVPGEPASPIQ	TQPDGTSVPGEPAS(0.99	TQPDGTSVPGEPAS(ph)P	WW GroupIV	1.2	0.33401		Yes
240	IPI00420602	Nucleoporin NUP188 h	Nup188;Kiaa0169	S1719	1	5	GAPSSPAAGVLPSPQK	GAPS(0.012)S(0.988)PA	GAPSS(ph)PAAGVLPSPC	WW GroupIV	0.9	0.2259		Yes
445	IPI00918049	Oxysterol-binding prote	Osbp11	S192	1	10	SFSLASSGNSPISQR	SFSLASS(0.001)GNS(0.9	SFSLASSGNS(ph)PISQR	CK1	1.0	0.4115		Yes
170	IPI00462728	MKIAA0704 protein;Ox	Osbp3;mkIAA0704;Ost	S302	1	3	LHSSNPMLSTLDFGEEK	LHS(0.818)S(0.145)NPN	LHS(ph)SNPMLSTLDFGE	CAMK2	0.9	0.15547		Yes
297	IPI00462728	MKIAA0704 protein;Ox	Osbp3;mkIAA0704;Ost	S303	1	4	LHSSNPMLSTLDFGEEK	LHS(0.083)S(0.909)NPN	LHSSNPMLSTLDFGE	NEK6	1.0	0.2928		Yes
17	IPI00911135	Putative uncharacterize	Oxr1;Oxr1;C7;Gm1238;	S201	1	3	VVSSSTEEEAFATEK	VVS(0.927)S(0.001)T(0	VVS(ph)STEEEAFATEK	CAMK2	2.5	5.976E-08	Up	Yes
518	IPI00223738	Serine/threonine-prote	Oxsr1;Oxr1;Oxr1;mkIA	S339	1	12	LHKTEDEGGWEVSDDEF	LHKTEDEGGWEV(S1)DD	LHKTEDEGGWEV(ph)D	CK2	1.1	0.47645		Yes
286	IPI00129298	Paralemmin;Paralemm	Palm;Palm	T145	1	14	SETLVNAQQTPLGTPK	SETLVNAQQTPLGT(1)PK	SETLVNAQQTPLGT(ph)P	CDK1	1.0	0.28403		Yes
253	IPI00719927	Protocadherin 1 isoform	Pcdh1;Pcdh1;Pcdh1	S823	1	14	SNPLPISQLQPSPASISQ	SNPLPISQLQP(S0.998)	SNPLPISQLQP(S)P	WW GroupIV	1.0	0.24212		Yes
665	IPI00464318	PCF11;Pcf11 protein	Pcf11;Pcf11	S279	1	1	SRAGPSLQMQDLK	S(0.995)RAGPS(0.005)L	S(ph)RAGPSLQMQDLK	ox)QDLK				Yes
504	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S1805	2	4	NVRSDVSDQEEDEESER	NVRS(1)DV(S1)DQEEDE	NVRS(ph)DV(S)DQEEDE	ESERCPVSINLSK	1.1	0.46326		Yes
505	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S1808	2	7	NVRSDVSDQEEDEESER	NVRS(1)DV(S1)DQEEDE	NVRS(ph)DV(S)DQEE	CK2	1.1	0.46326		Yes
260	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S65	1	6	VITNAISPESPGVGR	VITNAIS(1)PESPGVGR	VITNAIS(ph)PESPGVGR	GSK3	1.0	0.25481		Yes
499	IPI00352475	28 kDa heat- and acid-s	Pdap1	S57	2	1	SLDSEDESEDEDDYQQK	S(0.983)LDS(0.017)DES	S(ph)LDSDES(ph)EDED	AURORA	1.1	0.46188		Yes
310	IPI00352475	28 kDa heat- and acid-s	Pdap1	S60	2	5	KSLDSESEDEDDYQQK	KS(0.036)LDS(0.982)DE	KSLD(S)DES(ph)EDED	CK1	1.2	0.30724		Yes
482	IPI00352475	28 kDa heat- and acid-s	Pdap1	S63	2	7	SLDSESEDEDDYQQK	S(0.983)LDS(0.017)DES	S(ph)LDSDES(ph)EDED	CK2	1.1	0.44855		Yes
463	IPI00352475	28 kDa heat- and acid-s	Pdap1	Y70	2	14	SLDSESEDEDDYQQK	S(0.034)LDS(0.966)DES	SLD(S)DES(ph)EDED	DDYQQK	1.1	0.42547		No
64	IPI00130881	cAMP-specific 3',5'-cyc	Pde4a;Pde4a;Pde4a;Pd	T331	1	4	LVHTGSLNINVPR	LVHT(0.911)GS(0.089)L	LVHT(ph)GSLNINVPR	NEK6	0.8	0.0312	Down	Yes
73	IPI00153375	PDZ and LIM domain pr	Pdlim2;Pdlim2	S199	2	5	VLLHSPGRPSSPR	VLLHS(1)PGRPS(0.074)	VLLHS(ph)PGRPSS(ph)P	CDK2	0.8	0.041921	Down	Yes
330	IPI00153375	PDZ and LIM domain pr	Pdlim2;Pdlim2	S204	1	10	VLLHSPGRPSSPR	VLLHS(0.161)PGRPS(0.6	VLLHSPGRPS(ph)SPR	PKA	1.0	0.31847		No
52	IPI00153375	PDZ and LIM domain pr	Pdlim2;Pdlim2	S205	2	11	VLLHSPGRPSSPR	VLLHS(1)PGRPS(0.074)	VLLHS(ph)PGRPSS(ph)P	PKC	0.7	0.017657	Down	Yes
529	IPI00317401	Sister chromatid cohesi	Pds5b;Aprin;As3;Kiaa0	S1356	1	3	AESPETSAVESTQSTPQK	AES(1)PETSAVESTQSTP	AES(ph)PETSAVESTQST	CAMK2	1.1	0.48399		Yes
667	IPI00317401	Sister chromatid cohesi	Pds5b;Aprin;As3;Kiaa0	S1360	1	7	AESPETSAVESTQSTPQK	AES(0.333)PET(0.333)S	AES(ph)PETSAVESTQST	CK2				No
666	IPI00317401	Sister chromatid cohesi	Pds5b;Aprin;As3;Kiaa0	T1359	1	7	AESPETSAVESTQSTPQK	AES(0.492)PET(0.492)S	AES(ph)PETSAVESTQST	CK1				No
400	IPI00856504	Pyridoxal-dependent de	Pdxdc1;Pdxdc1;Pdxdc1	T687	1	6	VQGTGVTTPPTPLGTR	VQGTGVT(1)PPTPLGTR	VQGTGVT(ph)PPTPLGTR		1.0	0.3743		Yes
358	IPI00554862	6-phosphofructokinase	Pfk1;Pfk-1;Pfk1;Pfk1	S775	1	3	TLSIDKGF	TLS(1)DKGF	TLS(ph)DKGF	CAMK2	1.2	0.34558		Yes
479	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	S181	1	9	EGEETPVYSDDEEPEKDE	EGEETP(0.001)JVY(0.07	EGEETPVY(S)DDEEPEK	CK2	1.1	0.44677		Yes
668	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	T178	1	6	EGEETPVYSDDEEPEKDE	EGEETP(0.325)JVY(0.32	EGEETP(ph)YVSDDEEPEK	PLK1				No
669	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	T190	1	18	EGEETPVYSDDEEPEKDE	EGEETP(0.105)JVY(0.20	EGEETPVYSDDEEPEKDE	(ph)AR				No
77	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	Y180	1	8	EGEETPVYSDDEEPEKDE	EGEETP(0.116)JVY(0.76	EGEETPVY(ph)SDDEEPEKDE	TAR	1.4	0.049488	Up	Yes
328	IPI00377615	Phf3 protein	Phf3	S377	1	12	NTVDIVDKPENSQRNEL	NT(0.001)JVYDVKPENS	NTVDIVDKPENS(ph)PQ	CDK2	1.2	0.31766		Yes
670	IPI00400215	Plectin-1;Plectin-6;Plect	Plec1;Plec1;Plec1;Plec1	S4243	1	1	SSSVGSSSSYPISAGPR	S(0.359)S(0.294)S(0.29	S(ph)SSVSSSSYPISAG	PKA/AKT				No
40	IPI00400215	Plectin-1;Plectin-6;Plect	Plec1;Plec1;Plec1;Plec1	S4245	1	3	SSSVGSSSSYPISAGPR	S(0.164)S(0.09)S(0.747	SSS(ph)JVGSSSSYPISAG	PKA/AKT	1.6	0.010563	Up	No
177	IPI00400215	Plectin-1;Plectin-6;Plect	Plec1;Plec1;Plec1;Plec1	S580	1	9	ARNDESQSLSPATR	ARNDES(0.08)QLS(0.91	ARNDESQSLS(ph)PATR	CK1	0.9	0.15866		Yes
473	IPI00400215	Plectin-1;Plectin-6;Plect	Plec1;Plec1;Plec1;Plec1	T3889	1	4	KQITVEELVR	KQIT(1)VEELVR	KQIT(ph)VEELVR	PKD	1.1	0.44235		Yes
423	IPI00229810	MKIAA1686 protein;Ple	Plekha5;mkIAA1686;Ple	S1241	1	1	SLSPSPDSSTAADPPTP	S(0.571)LS(0.385)PS(0.0	S(ph)LSPSPDSSTAADPP	GSK3	1.0	0.39542		No
671	IPI00403031	Pleckstrin homology do	Plekho2;Plekho2	S393	1	1	SSSLGDLRL	S(0.421)S(0.29)S(0.29)L	S(ph)SSSLGDLRL					No
323	IPI00403031	Pleckstrin homology do	Plekho2;Plekho2	S395	1	3	SSSLGDLRL	S(0.01)S(0.005)S(0.985	SSS(ph)JGDLRL	CAMK2	1.0	0.31445		No
86	IPI00223459	Lipid phosphate phosph	Ppap2a;Hpic53;Lp1;Pp	S274	1	14	KEEDPHHTLHETASSR	KEEDPHHT(0.01)T(0.08)L	KEEDPHHTLHETAS(ph)SR		0.8	0.057114		Yes
93	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S445	1	4	KTGSYGALAEISASK	KT(0.044)GS(0.911)Y(0.	KTGS(ph)YGALAEISASK	PKD	1.4	0.064677		Yes
5	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S507	1	3	LASTSDIEEKENR	LAS(0.912)T(0.079)S(0.	LAS(ph)TSDIEEKENR	CAMK2	6.9	5.622E-31	Up	Yes
10	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S509	1	6	RLASTSDIEEK	RLAS(0.057)T(0.057)S(0	RLASTS(ph)DIEEK	CK2	4.0	2.25E-16	Up	Yes
57	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S861	1	11	STGVSFWTQDSDENEQE	S(0.001)T(0.001)GVS(0.	STGVSFWTQDSDENEQ	(ph)DENEQ	1.5	0.023908	Up	Yes
165	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S870	1	20	STGVSFWTQDSDENEQE	S(0.001)T(0.001)GVS(0.	STGVSFWTQDSDENEQ	PKA	1.3	0.1454		No
674	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_122391	S876	1	26	STGVSFWTQDSDENEQE	S(0.002)T(0.002)GVS(0.	STGVSFWTQDSDENEQ	(ph)DEN	1.0			No

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
675	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	S877	1	27	STGVSWFTQSDSENEEQ	S(0.002)T(0.002)GVS(0.0)	STGVSWFTQDS(ph)DEN	CK2				No
673	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	T508	1	5	RLASTSDIEEK	RLAS(0.482)T(0.482)S(0)	RLAS(ph)TSDIEEK	NEK6				No
672	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	Y446	1	5	KTGSYGALAEISASK	KT(0.096)GS(0.39)T(0.3)	KTGS(ph)YALAEISASK	ALK				No
228	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	S693	1	1	STQGVTLTDLQEAEK	S(0.645)T(0.355)QGVTL	S(ph)TQGVTLTDLQEAEK	PKA	0.9	0.22132		No
489	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	T694	1	3	RSTQGVTLTDLQEAEK	RS(0.032)T(0.968)QGVTL	RST(ph)QGVTLTDLQEAEK	PKA	1.1	0.45385		Yes
503	IPI00671847	PPP1r12a protein;MCG	PPP1r12a;mCG_122391	T698	1	7	RSTQGVTLTDLQEAEK	RS(0.204)T(0.204)QGVTL	RSTQGVTL(ph)TDLQEAEK	FHA1 Rad53p	1.1	0.46312		No
495	IPI00856140	Putative uncharacterize	PPP1r2	S122	2	6	TREQESSGEEDNLSPEE	TREQES(1)S(1)GEEEDND	TREQES(ph)S(ph)GEEEDN	CK2	1.1	0.46065		Yes
496	IPI00856140	Putative uncharacterize	PPP1r2	S123	2	7	TREQESSGEEDNLSPEE	TREQES(1)S(1)GEEEDND	TREQES(ph)S(ph)GEEEDN	CK2	1.1	0.46065		Yes
21	IPI00856140	Putative uncharacterize	PPP1r2	T117	2	1	TREQESSGEEDNLSPEE	T(0.933)REQES(0.494)S	T(ph)REQES(ph)S(ph)GEEEDNLSPEE		0.5	2.386E-06	Down	Yes
287	IPI00380331	Protein phosphatase 2A	PPP2r5d;mCG_2696	S81	1	3	RQSSFPFNLNK	RQS(0.5)S(0.5)FPFNLNK	RQS(ph)SFPFNLNK	PKA	1.0	0.28627		No
280	IPI00380331	Protein phosphatase 2A	PPP2r5d;mCG_2696	S82	1	4	RQSSFPFNLNK	RQS(0.279)S(0.721)FPF	RQSS(ph)SFPFNLNK	CAMK2	1.0	0.28019		No
83	IPI00119575	Putative uncharacterize	Prkar1a;Prkar1a;Prkar1	S212	1	9	TDSREDEISPPPPNPVVK	TDSREDEIS(1)PPPPNPV	TDSREDEIS(ph)PPPPNPVVK		0.8	0.055375		Yes
676	IPI00119575	Putative uncharacterize	Prkar1a;Prkar1a;Prkar1	T204	1	1	TDSREDEISPPPPNPVVK	T(0.49)DS(0.1)REDEIS(0	T(ph)DSREDEISPPPPNPVVK					No
597	IPI00169788	Protein kinase, cAMP de	Prkar2a;mCG_16488;Pr	S97	1	3	RVSVCATFNPDDEEEDN	RVS(1)VCATFNPDDEEEDN	RVS(ph)VCATFNPDDEEEDN	AURORA-A	1.2	0.2406		Yes
117	IPI00169788	Protein kinase, cAMP de	Prkar2a;mCG_16488;Pr	T102	1	8	RVSVCATFNPDDEEEDN	RVS(0.5)VCAT(0.5)FNPD	RVS(ph)VCATFNPDDEEEDN	PKA	1.3	0.093751		No
217	IPI00224570	cAMP-dependent prote	Prkar2b	S112	1	3	RASVCAEAYNPDEEEDN	RAS(1)VCAEAYNPDEEEDN	RAS(ph)VCAEAYNPDEEEDN	AURORA-A	1.2	0.20697		Yes
233	IPI00126939	Protein kinase C delta-1	Prkcdpb;Srbc	S165	2	29	AFQKVPPELLGPEDLQVLG	AFQKVPPELLGPEDLQVLG	AFQKVPPELLGPEDLQVLG	CK2	1.2	0.2239		Yes
234	IPI00126939	Protein kinase C delta-1	Prkcdpb;Srbc	S166	2	30	AFQKVPPELLGPEDLQVLG	AFQKVPPELLGPEDLQVLG	AFQKVPPELLGPEDLQVLG	CK2	1.2	0.2239		Yes
146	IPI00895452	Protein kinase D3;Serin	Prkd3;Prkcn;Prkd3;Prk	S44	1	5	LSNGFSAPSLTNSR	LS(0.007)NGS(0.982)FS	LSNGS(ph)FAPSLTNSR	CK1	0.4	2.67E-08	Down	Yes
339	IPI00417140	Protein arginine N-met	Prmt3;Hrmt113;Prmt3;H	S22	2	12	GAELGPEPLELSDSGDDA	GAELGPEPLELS(1)DS(1)	GAELGPEPLELS(ph)DS(1)	NEK6	1.0	0.33149		Yes
340	IPI00417140	Protein arginine N-met	Prmt3;Hrmt113;Prmt3;H	S24	2	14	GAELGPEPLELSDSGDDA	GAELGPEPLELS(1)DS(1)	GAELGPEPLELS(ph)DS(1)	NEK6	1.0	0.33149		Yes
360	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Prf	S852	1	21	LCDFGSAHVADNDITPY	LCDFGSAHVADNDITPY	LCDFGSAHVADNDITPY	PKA	1.2	0.34647		Yes
99	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Prf	S94	1	12	EVIEASDKGELSPAKR	EVIEASDKGELS(1)PAKR	EVIEASDKGELS(ph)PAKR	CDK2	1.4	0.073754		Yes
116	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Prf	Y849	1	18	LCDFGSAHVADNDITPY	LCDFGSAHVADNDITPY	LCDFGSAHVADNDITPY	PKA	1.3	0.092502		Yes
355	IPI00337948	Tyrosine-protein phosph	Ptpn12;Ptpn12;mCG_61	S434	1	3	NLSFEIK	NLS(1)FEIK	NLS(ph)FEIK	CHK1/2	1.0	0.34495		Yes
452	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	S42	1	10	ATEEPSGTGSDELK	ATEEPS(0.007)GT(0.076)	ATEEPSGTGS(ph)DELK	CK1	1.0	0.42006		Yes
343	IPI00112203	Pumilio homolog 2;Put	Pum2;Kiaa0235;Pum2;	S136	1	4	GKASPFEEQNR	GKAS(1)PFEEQNR	GKAS(ph)PFEEQNR	CK2	1.0	0.33505		Yes
677	IPI00320422	Periodic tryptophan pr	Pwp1	S486	1	5	GLSVSGPCGSRSPQQTPN	GLS(0.072)VS(0.428)GP	GLSVS(ph)GPCGSRSPQQTPN	NEK6				No
678	IPI00320422	Periodic tryptophan pr	Pwp1	S491	1	10	GLSVSGPCGSRSPQQTPN	GLS(0.072)VS(0.428)GP	GLSVS(ph)GPCGSRSPQQTPN	PKA				No
485	IPI00320422	Periodic tryptophan pr	Pwp1	S493	1	12	GLSVSGPCGSRSPQQTPN	GLS(0.001)VS(0.001)GP	GLSVSGPCGSRSPQQTPN	PKA	1.1	0.45002		Yes
265	IPI00461460	R3hdm1 protein	R3hdm1	S381	1	3	ASSFSGISVLR	AS(0.06)S(0.936)FS(0.0)	ASSF(ph)SFGISVLR	PKD	1.0	0.25977		Yes
679	IPI00461479	RAB3A-interacting prot	Rab3ip	S215	1	7	TLVLSSTPSTQPELAAA	T(0.001)LVLS(0.044)S(0)	TLVLS(ph)SPTQPELAAA	Polo box				No
680	IPI00461479	RAB3A-interacting prot	Rab3ip	T217	1	9	TLVLSSTPSTQPELAAA	TLVLS(0.001)S(0.006)S	TLVLS(ph)SPTQPELAAA	CK1				Yes
118	IPI00845537	Rab GTPase-binding eff	Rabep1;Rab5ep;Rab5ep	S407	1	4	RAQSTDSLGTSSSLQSK	RAQS(0.892)T(0.104)DS	RAQS(ph)TDSLGTSSSLQSK	CHK1/2	0.9	0.094146		Yes
58	IPI00453820	Ankyrin;Ankyrin reg	Rai14;Kiaa1334;Norpeg	S914	1	3	RQSQQLDLQQLQVVK	RQS(1)QQLDLQQLQVVK	RQS(ph)QQLDLQQLQVVK	PKA	1.5	0.024355	Up	Yes
530	IPI00135190	Ran-binding protein 3	Ranbp3	S28	3	1	SAGSSSPEAGEDSDHEDC	S(0.832)AGS(0.19)S(0.1)	S(ph)AGSSS(ph)PEAGEDC	GSK3	1.1	0.48406		Yes
181	IPI00135190	Ran-binding protein 3	Ranbp3	S31	3	4	SAGSSSPEAGEDSDHEDC	S(0.187)AGS(0.604)S(0.	SAGS(ph)S(ph)PEAGEDC	CK1	0.9	0.16504		No
182	IPI00135190	Ran-binding protein 3	Ranbp3	S32	3	5	SAGSSSPEAGEDSDHEDC	S(0.187)AGS(0.604)S(0.	SAGS(ph)S(ph)PEAGEDC	CK2	0.9	0.16504		No
224	IPI00135190	Ran-binding protein 3	Ranbp3	S33	2	6	SAGSSSPEAGEDSDHEDC	S(0.004)AGS(0.02)S(0.1)	SAGSSS(ph)PEAGEDC	Polo box	0.9	0.21611		Yes
225	IPI00135190	Ran-binding protein 3	Ranbp3	S40	2	13	SAGSSSPEAGEDSDHEDC	S(0.004)AGS(0.02)S(0.1)	SAGSSS(ph)PEAGEDC	CK2	0.9	0.21611		Yes
519	IPI00116031	RNA-binding protein 10	Rbm10;Kiaa0122;Rbm1	S723	1	8	LASDDRSPPR	LASDRPS(1)PPR	LASDRPS(ph)PPR	CDK2	1.1	0.47774		Yes
34	IPI00170394	Splicing factor 45;45 kD	Rbm17;Spf45	S155	1	6	RPPDPSDEDEYERER	RPPDPS(1)DEDEYERER	RPPDPS(ph)DEDEYERER		1.7	0.0034046	Up	Yes
221	IPI00229472	RNA-binding protein 28	Rbm28	S231	2	8	VEEQVEDSDDEEDDSSH	VEEQVEDS(0.999)DDEE	VEEQVEDS(ph)DDEEDD	CK2	1.0	0.31382		Yes
230	IPI00229472	RNA-binding protein 28	Rbm28	S239	2	16	VEEQVEDSDDEEDDSSH	VEEQVEDS(0.999)DDEE	VEEQVEDS(ph)DDEEDDSSH	PKA	0.9	0.22176		Yes
105	IPI00229472	RNA-binding protein 28	Rbm28	S248	2	25	VEEQVEDSDDEEDDSSH	VEEQVEDS(0.12)DDEE	VEEQVEDS(ph)DDEEDDSSH	PKA	1.4	0.081931		Yes
106	IPI00229472	RNA-binding protein 28	Rbm28	T249	2	26	VEEQVEDSDDEEDDSSH	VEEQVEDS(0.12)DDEE	VEEQVEDS(ph)DDEEDDSSH	PK1	1.4	0.081931		Yes
241	IPI00223371	RNA-binding protein 39	Rbm39;Caper;Rncp2;R	S136	1	3	DKSPVREPIDNLTPEER	DKS(1)PVREPIDNLTPEER	DKS(ph)PVREPIDNLTPEER	CDK2	0.9	0.22854		Yes
478	IPI00380766	E3 ubiquitin-protein lig	Rnf20;Bre1a;Kiaa4116;	S138	1	13	ALVVPPEPDSDSNQER	ALVVPPEPDS(0.01)DS	ALVVPPEPDS(ph)JNC	CK2	1.1	0.44644		Yes
264	IPI00453849	mRNA cap guanine-N7	Rnmt;Kiaa0398;Rnmt;K	S15	1	9	ASVASDPESPPGGNEPA	ASVASDPES(1)PPGGNE	ASVASDPES(ph)PPGGNE	ERK/MAPK	1.0	0.25962		Yes
301	IPI00111412	60S ribosomal protein	Rpl4	S295	1	4	ILKSPFQIR	ILKS(1)PFQIR	ILKS(ph)PFQIR		1.0	0.30236		Yes
391	IPI00314950	60S acidic ribosomal pr	Rplp0;Arbp	S304	2	7	AEAKEESEDEDMGFLFD	AEAKES(1)EES(1)DEDM	AEAKES(ph)EES(ph)DEDM	GFLFD	1.1	0.36662		Yes
396	IPI00314950	60S acidic ribosomal pr	Rplp0;Arbp	S307	2	10	AEAKEESEDEDMGFLFD	AEAKES(1)EES(1)DEDM	AEAKES(ph)EES(ph)DE	CK1	1.1	0.37076		Yes
125	IPI00113377	60S acidic ribosomal pr	Rplp1	S101	2	4	KEESESEDEDMGFLFD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDMGF	GFLFD	1.3	0.10222		Yes
126	IPI00113377	60S acidic ribosomal pr	Rplp1	S104	2	7	KEESESEDEDMGFLFD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDM	CK1	1.3	0.10222		Yes
283	IPI00139795	60S acidic ribosomal pr	Rplp2	S102	2	4	KEESESEDEDMGFLFD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDM	GFLFD	1.2	0.28092		Yes
284	IPI00139795	60S acidic ribosomal pr	Rplp2	S105	2	7	KEESESEDEDMGFLFD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDM	CK1	1.2	0.28092		Yes
469	IPI00134599	40S ribosomal protein	Rps3	T221	1	7	DEILPTTPISEQK	DEILPT(0.06)T(0.94)PIS	DEILPTT(ph)PISEQK	WW GroupIV	1.1	0.43151		Yes
103	IPI00114333	Ribosomal protein S6 k	Rps6ka3;Rps6ka-rs1;R	S715	1	3	NQSPVLEPVGR	NQS(1)PVLEPVGR	NQS(ph)PVLEPVGR	CHK1/2	0.8	0.078735		Yes
354	IPI00849948	40S ribosomal protein	Rps8;Rps8;OTTMUSG0	T143	1	5	GAKLTPEEEILNK	GAKLT(1)PEEEILNK	GAKLT(ph)PEEEILNK	CK2	1.0	0.34271		Yes
65	IPI00411051	Regulatory-associated	Rptor;Raptor;Raptor;Rap	S863	1	14	ILDTSSTLQSQAPASPTNK	ILDTSSTLQS(0.009)APAS	ILDTSSTLQSQAPAS(ph)PTNK	WW GroupIV	1.5	0.031364	Up	Yes
465	IPI00468702	Ras-related GTP-bindin	Rragc;Rragc	S94	1	11	MSPNETLFLFSTNK	MSPNETLFLS(0.997)T(1	M(sp)SPNETLFLS(ph)TNK		1.1	0.42644		Yes
446	IPI00323822	Ras-related protein R-R	Rras2	S186	1	10	KFQEQCECPSPPEPTRK	KFQEQCECPSP(1)PEPTRK	KFQEQCECPSP(ph)PEPTRK	WW GroupIV	1.1	0.41215		Yes
215	IPI00420344	RRP12-like protein	Rrp12;Kiaa0690	S1073	1	3	GDSIEEILADSEDEDEEE	GDS(0.5)IEEILADS(0.5)E	GDS(ph)IEEILADSEDEDEE	CK2	1.2	0.20491		No
375	IPI00420344	RRP12-like protein	Rrp12;Kiaa0690	S1081	1	11	GDSIEEILADSEDEDEEE	GDSIEEILADS(1)EDEDEE	GDSIEEILADS(ph)EDEDEE	CK2	1.1	0.35737		Yes
205	IPI00471271	Rsrc2 protein	Rsrc2	S30	1	8	KKEQSDISISPR	KKEQS(0.003)DIS(0.884)	KKEQSDIS(ph)ISPR	PLK1	0.9	0.1946		Yes
362	IPI00471271	Rsrc2 protein	Rsrc2	S32	1	10	KKEQSDISISPR	KKEQS(0.307)S(0.695)	KKEQSDIS(ph)ISPR	CDK1	1.2	0.3469		No



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?	
681	IPI00649426	Runt-related transcript	Runx1t1;RP23-134H12	S590	1	1	STTPGTPSTIETTPR	S(0.445)T(0.277)T(0.27)	S(ph)TTPGTPSTIETTPR					No	
682	IPI00649426	Runt-related transcript	Runx1t1;RP23-134H12	T601	3	12	STTPGTPSTIETTPR	S(0.443)T(0.403)T(0.17)	S(ph)TTPGTPSTIETTPR					No	
683	IPI00649426	Runt-related transcript	Runx1t1;RP23-134H12	T602	3	13	STTPGTPSTIETTPR	S(0.443)T(0.403)T(0.17)	S(ph)TTPGTPSTIETTPR	CDK1				No	
395	IPI00122174	MKIAA0138 protein;Sc	Safb2;mkIAA0138;Safb	S404	1	7	APTAALSPQDQSKEDVKA	APTAALS(1)PEPQDQSKED	APTAALS(ph)PEPQDQSKED	CK1	1.1	0.36992		Yes	
431	IPI00719971	Serine/threonine-prote	Saps3;D19ErtD703e;Kia	S617	1	9	IQQFDDGGSSDEEDIWEE	IQQFDDGGSS(1)DEEDIWEE	IQQFDDGGSS(ph)DEEDIWEE	CK2	1.1	0.39925		Yes	
353	IPI00338954	SAM and SH3 domain-c	Sash1	S400	1	3	TCSFGGFDLTNR	T(0.008)CS(0.392)FGGF	TCS(ph)GGFDLTNR	CAMK2	1.0	0.34363		Yes	
684	IPI00338954	SAM and SH3 domain-c	Sash1	S805	1	1	SLPVSICR	S(1)LPVSICR	S(ph)LPVSICR	AURORA-A				Yes	
159	IPI00177200	Scavenger receptor clas	Scarf2;Srec2	S672	1	9	HSAAAAAPSPPPAGR	HSAAAAAPSP(1)PPAGR	HSAAAAAPSP(ph)PPAGR		0.9	0.13631		Yes	
335	IPI00474285	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S1361	1	3	RVSLVGADDLR	RVS(1)LVGADDLR	RVS(ph)LVGADDLR	AURORA-A	1.2	0.32214		Yes	
108	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S192	3	1	SLEETHHNVDLSSDDELP	S(0.545)LEET(0.543)LHN	S(ph)LEET(ph)LHNVDLS	CK2	1.4	0.084632		No	
557	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S203	3	12	SLEETHHNVDLSSDDELP	S(0.025)LEET(0.024)LHN	SLEETHHNVDLS(ph)S(ph)DDELPRDEEALEDSP	(ph)	1.1	0.5		Yes	
334	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S204	3	13	SLEETHHNVDLSSDDELP	S(0.025)LEET(0.024)LHN	SLEETHHNVDLS(ph)S(ph)CK2		1.2	0.31998		Yes	
558	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S218	3	27	SLEETHHNVDLSSDDELP	S(0.255)LEET(0.225)LHN	SLEETHHNVDLS(ph)S(ph)CK2		1.1	0.5		Yes	
685	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S283	2	2	ASSGKSSPFKVSPLSFR	AS(0.25)S(0.25)GKS(0.2)	AS(ph)GKSSPFKVS(ph)GSK3					No	
686	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S284	2	3	ASSGKSSPFKVSPLSFR	AS(0.046)S(0.318)GKS(0.	ASS(ph)GKSSPFKVS(ph)GSK3					No	
687	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S287	2	6	ASSGKSSPFKVSPLSFR	AS(0.009)S(0.061)GKS(0.	ASSGKSS(ph)SPFKVS(ph)CK1					No	
688	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S288	2	7	ASSGKSSPFKVSPLSFR	AS(0.009)S(0.061)GKS(0.	ASSGKSS(ph)SPFKVS(ph)Polo box					No	
201	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S293	2	12	ASSGKSSPFKVSPLSFR	AS(0.046)S(0.318)GKS(0.	ASS(ph)GKSSPFKVS(ph)PLSFR			1.2	0.1881		Yes
36	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S359	1	5	RGNNSAVGNSADLTIEE	RGNNNS(0.761)AVGNS(0.2	RGNNNS(ph)AVGNSADLT	GSK3	1.6	0.005584	Up	Yes	
160	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	S363	1	9	RGNNSAVGNSADLTIEE	RGNNNS(0.021)AVGNS(0.9	RGNNNSAVGNS(ph)NADLT	CK1	1.3	0.13831		Yes	
109	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	T366	3	5	SLEETHHNVDLSSDDELP	S(0.545)LEET(0.543)LHN	S(ph)LEET(ph)LHNVDLS	PLK1	1.4	0.084632		No	
79	IPI00135660	Serum deprivation-resp	Sdpr;Sdr	T368	1	14	RGNNSAVGNSADLTIEE	RGNNNSAVGNS(0.055)NAD	RGNNNSAVGNSADLT(ph)PLK		1.4	0.051611		Yes	
458	IPI00648142	Sec23ip protein;SEC23-	Sec23ip;Sec23ip	S748	1	3	KLSVGYAVYSVR	KLS(1)VGYAVYSVR	KLS(ph)VGYAVYSVR	CAMK2	1.1	0.42292		Yes	
438	IPI00133030	Protein transport prote	Sec61b	S14	1	13	PGPTPSGTNVGSSGRSP	PGPTPSGTNVGSS(0.084)	PGPTPSGTNVGSS(ph)GRSPSK		1.0	0.40494		Yes	
689	IPI00133030	Protein transport prote	Sec61b	S17	1	16	PGPTPSGTNVGSSGRSP	PGPTPSGTNVGSS(0.057)	PGPTPSGTNVGSS(ph)G	CDK2				No	
481	IPI00114945	Septin-2;Neural precurs	Sept2;Nedd5;Nedd5	S218	1	9	IYHLPADEADEDEDFKQ	IYHLPADES(1)DEDEDFKQ	IYHLPADES(ph)DEDEDFKQ		1.1	0.44779		Yes	
381	IPI00923056	Sept5 protein;Septin-5;	Sept5;Sept5;Pnut1;Sep	S225	1	13	FGIHVYQFPECDSDDEED	FGIHVYQFPECDSD(1)DEED	FGIHVYQFPECDSD(ph)DEED	QQR	1.1	0.36055		Yes	
78	IPI00457611	Septin-9;SL3-3 integrat	Sept9;Kiaa0991;Sint1;S	S41	1	12	SFEVEEIEPPNSTPPR	SFEVEEIEPPNS(0.5)T(0.	SFEVEEIEPPNS(ph)TTPR		1.4	0.050031		No	
424	IPI00457611	Septin-9;SL3-3 integrat	Sept9;Kiaa0991;Sint1;S	T42	1	13	SFEVEEIEPPNSTPPR	SFEVEEIEPPNS(0.003)T	SFEVEEIEPPNST(ph)PPR	Polo box	1.0	0.39618		Yes	
197	IPI00116284	Splicing factor 1;Zinc fir	Sf1;Zfm1;Zfp162;Sf1;Zf	S80	2	14	TGDLGIPNPEDRSPSP	TGDLGIPNPEDRS(1)PS	TGDLGIPNPEDRS(ph)PS	PEPINSEGR	1.3	0.18521		Yes	
198	IPI00116284	Splicing factor 1;Zinc fir	Sf1;Zfm1;Zfp162;Sf1;Zf	S82	2	16	TGDLGIPNPEDRSPSP	TGDLGIPNPEDRS(1)PS	TGDLGIPNPEDRS(ph)P	CAMK2	1.3	0.18521		Yes	
134	IPI00420807	Splicing factor, arginine	Sfrs1	S199	1	8	VKVDGPRSPSYGR	VKVDGPRS(0.984)PS(0.	VKVDGPRS(ph)PSYGR	WW GroupIV	1.3	0.11386		Yes	
690	IPI00420807	Splicing factor, arginine	Sfrs1	S201	1	10	VKVDGPRSPSYGR	VKVDGPRS(0.496)PS(0.	VKVDGPRS(ph)PSYGR	CAMK2				No	
110	IPI00848672	Putative uncharacterize	Sfrs11;mcG_11658;Sfrs	S235	1	10	LNHVAAGLVSPSLK	LNHVAAGLV(0.992)PS	LNHVAAGLV(ph)PSLK		1.4	0.085157		Yes	
235	IPI00310880	Splicing factor arginine	Sfrs4;RP23-13A13.2-00	S118	1	7	LIVENLSSR	LIVENLS(0.5)S(0.5)R	LIVENLS(ph)SR	GSK3	1.2	0.2253		No	
553	IPI00310880	Splicing factor arginine	Sfrs4;RP23-13A13.2-00	S119	1	8	LIVENLSSR	LIVENLS(0.107)S(0.893)	LIVENLS(ph)R		1.1	0.49397		Yes	
356	IPI00310880	Putative uncharacterize	Sfrs6;mcG_1675	S303	1	3	SHSPLPAPPSK	S(0.008)HS(0.992)PLPA	SHS(ph)PLPAPPSK	CAMK2	1.0	0.34506		Yes	
514	IPI00120052	Sphingosine-1-phospha	Sgpp1;Spp1;Spph1	S101	1	3	RNSLTGEEGELVK	RNS(0.999)LT(0.001)GE	RNS(ph)LTGEEGELVK	PKA/AKT	1.1	0.47231		Yes	
294	IPI00120052	Sphingosine-1-phospha	Sgpp1;Spp1;Spph1	T103	1	5	RNSLTGEEGELVK	RNS(0.5)LT(0.5)GEEGEL	RNS(ph)LTGEEGELVK	CK2	1.0	0.29132		No	
127	IPI00828245	SH3-domain binding pr	Sh3bp1;AL592169.1-00	S535	1	12	ERTEADLPKPTPK	ERTEADLPKPT(0.09)S(0.	ERTEADLPKPT(ph)PK	WW GroupIV	0.9	0.10384		Yes	
133	IPI00280250	SH3 and PX domain-cor	Sh3pxd2a;Fish;Sh3md1	S1032	1	6	AASQGSSEPLLTQQR	AAS(0.008)QGS(0.984)E	AASQGS(ph)ESPLLTQQR	CK1	0.9	0.11065		Yes	
185	IPI00453688	Signal-induced prolifere	Sipa11;Kiaa0440;Sipa1	S1528	1	6	LIDLESPTPESQK	LIDLES(0.931)PT(0.069)	LIDLES(ph)PTPESQK		1.3	0.16802		Yes	
203	IPI00454140	MCG15924, isoform CR	Skiv2;SKI;Stk19;mcG_1	S240	1	5	GDNASPSPSGTPLVLR	GDNAS(0.991)PS(0.008)	GDNAS(ph)PSPSGTPLVLR	GSK3	0.9	0.19082		Yes	
27	IPI00454140	MCG15924, isoform CR	Skiv2;SKI;Stk19;mcG_1	S242	1	7	GDNASPSPSGTPLVLR	GDNAS(0.115)PS(0.655)	GDNAS(ph)PSGTPLVLR		0.6	0.0001013	Down	No	
450	IPI00454140	MCG15924, isoform CR	Skiv2;SKI;Stk19;mcG_1	S253	1	3	ASSLEDLVK	AS(0.003)S(0.997)LEDL	ASS(ph)LEDLVK	CHK1/2	1.0	0.41585		Yes	
502	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S697	1	3	LDSPTLSR	LDS(1)PTLSR	LDS(ph)PTLSR	GSK3	1.1	0.46287		Yes	
550	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S790	1	20	SKEPSSPGTDDVFTPGSS	SKEPSSPGTDDVFTPGS(0.	SKEPSSPGTDDVFTPGSS	CK1	1.1	0.49299		Yes	
46	IPI00109311	Na(+)/H(+) exchange re	Slc9a3r1;Nherf;Nherf1	S285	1	3	SASSDTSSEELNSQDSPKR	S(0.148)AS(0.837)S(0.0	SAS(ph)SDTSEELNSQDS	CHK1/2	0.7	0.015072	Down	Yes	
221	IPI00229571	SAFB-like transcription	Sltm;Met;Sltm;Met;Sltm	S289	1	9	DVQDAIAQSPKEAK	DVQDAIAQS(1)PEKEAK	DVQDAIAQS(ph)PEKEAK	CDK2	1.2	0.21304		Yes	
460	IPI00127941	Small acidic protein;Sid	Smap;Sid2057	S15	1	2	RSASPDDDLGSNNWEAA	RS(0.863)AS(0.136)PDD	RS(ph)ASPDDDLGSNNWEA	ADLNGNEER	1.0	0.4232		Yes	
432	IPI00127941	Small acidic protein;Sid	Smap;Sid2057	S17	1	3	SASPDDDLGSNNWEAA	S(0.13)AS(0.87)PDDDLG	SAS(ph)PDDDLGSNNWEA	PKA	1.0	0.39927		Yes	
691	IPI00127941	Small acidic protein;Sid	Smap;Sid2057	S24	1	11	RSASPDDDLGSNNWEAA	RS(0.194)AS(0.194)PDD	RSASPDDDLGSNNWEA	ADLNGNEER				No	
692	IPI00127941	Small acidic protein;Sid	Smap;Sid2057	S25	1	12	RSASPDDDLGSNNWEAA	RS(0.25)AS(0.25)PDDDL	RS(ph)ASPDDDLGSNNWEA	CK2				No	
333	IPI00396739	SWI/SNF-related matrix	Smarca5;Snf2h	S65	1	32	GGPEGGAAPAAPCAAGS	GGPEGGAAPAAPCAAGS	GGPEGGAAPAAPCAAGS	CDK2	1.2	0.31989		Yes	
200	IPI00459742	SWI/SNF complex subu	Smarca2;Baf170;Smarca	S283	1	8	TLTDEVNSPDSRRR	TLTDEVNS(1)PDSRRR	TLTDEVNS(ph)PDSRRR	ERK/MAPK	0.9	0.18612		Yes	
164	IPI00129918	Survival motor neuron	Smn1;Smn	S25	2	6	RGTGQSDSDIWDDTAL	RGT(0.158)GQS(0.844)I	RGTGQS(ph)DDSDIWDDTAL		1.3	0.14443		Yes	
184	IPI00129918	Survival motor neuron	Smn1;Smn	S28	2	9	RGTGQSDSDIWDDTAL	RGT(0.158)GQS(0.844)I	RGTGQS(ph)DDSDIWDDTAL	CK1	0.9	0.16694		Yes	
242	IPI00929261	Sntb2 protein;Beta-2-5y	Sntb2;Sntb2;Snt2b2	S90	1	9	GPAGEASASPPYR	GPAGEAS(0.024)AS(0.9)	GPAGEASAS(ph)PPYR		0.9	0.22867		Yes	
487	IPI00342755	Sorting nexin-33;SH3 ar	Snx33;Sh3px3	S169	1	8	APLERQDSLASAK	APLERQDS(1)LASAK	APLERQDS(ph)LASAK	CHK1/2	1.1	0.45112		Yes	
245	IPI00654133	Protein SOLO;Protein S	Solo;Solo;Solo;Solo;Sol	S959	1	10	IQQLGEEASPR	IQQLGEEAS(1)PR	IQQLGEEAS(ph)PR	CDK1	1.0	0.2339		Yes	
693	IPI00648688	C-jun-amino-terminal k	Spag9;Jip4;Jsap2;Kiaa0	S732	1	5	SASQSSLDKLDQELK	S(0.065)AS(0.043)QS(0.	SASQS(ph)SLDKLDQELK	CK1				No	
694	IPI00648688	C-jun-amino-terminal k	Spag9;Jip4;Jsap2;Kiaa0	S733	1	6	SASQSSLDKLDQELK	S(0.065)AS(0.043)QS(0.	SASQS(ph)SLDKLDQELK	CK1				No	
695	IPI00404721	Serine protease inhibit	Spink6;Spink6	S93	1	1	SSGKINKLHR	S(0.691)S(0.309)GKINKL	S(ph)SGKINKLHR	NEK6				No	
218	IPI00319830	Spectrin beta chain, bra	Sptbn1;Elf;Sptn-2;Sptn	S2340	1	16	AQTLPTSVMVTIETSSSPGK	AQTLPTSVMVT(0.009)TIT	AQTLPTSVMVTIETSSSPGK	Polo box	1.2	0.20816		Yes	
552	IPI00319830	Spectrin beta chain, bra	Sptbn1;Elf;Sptn-2;Sptn	S2102	1	4	RPPSPDPNTK	RPPS(0.973)PDPNT(0.0)	RPPS(ph)PDPNTK	WW GroupIV	1.1	0.49338		Yes	
509	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S915	2	5	KETESEAEDNLDLDER	KET(1)ES(1)EAEDNLDL	KET(ph)ES(ph)EAEDNLDL	CK2	1.1	0.469		Yes	

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
508	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	T913	2	3	KETESAEDDNLDDLDER	KET(1)ES(1)EAEDDNLDE	KET(ph)ES(ph)EAEDDNL	PKA	1.1	0.469		Yes
318	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S220	1	3	EKSELPPEPSVR	EKS(1)PELPEPSVR	EKS(ph)PELPEPSVR	PKA	1.2	0.31314		Yes
119	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S448	1	3	RESPSAPKPKR	RES(0.88)PS(0.12)PAPK	RES(ph)PSAPKPKR	PKA	0.9	0.096192		Yes
320	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S450	1	5	RESPSAPKPKR	RES(0.051)PS(0.949)PAPK	RES(ph)PSAPKPKR	PKA	1.0	0.31342		Yes
538	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S572	2	3	RRSPSPAPKPKR	RRS(1)PS(1)PAPKPKR	RRS(ph)PSAPKPKR	PKA/AKT	1.1	0.49021		Yes
539	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S574	2	5	RRSPSPAPKPKR	RRS(1)PS(1)PAPKPKR	RRS(ph)PSAPKPKR	PKA/AKT	1.1	0.49021		Yes
696	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S713	1	5	APQTSPPVPR	APQT(0.004)S(0.498)SAPQTS	APQT(ph)SPPVPR					No
366	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S714	1	6	APQTSPPVPR	APQT(0.001)S(0.01)SAPQTS	APQT(ph)SPPVPR	Polo box	1.0	0.35151		Yes
158	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2535	1	4	RVPSPTPVPK	RVPS(0.906)PT(0.094)P	RVPS(ph)PTPVPK	PKA	0.9	0.1344		Yes
433	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T2537	1	6	RVPSPTPVPK	RVPS(0.002)PT(0.998)P	RVPSPT(ph)PVPK		1.1	0.39957		Yes
374	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1068	1	3	SSSPVTELTAR	S(0.097)S(0.054)S(0.84)SSS	(ph)PVTELTAR	CHK1/2	1.1	0.35687		Yes
388	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1151	1	4	DKFSPTQDRPESSTVVK	DKFS(0.978)PT(0.022)Q	DKFS(ph)PTQDRPESSTVVK		1.1	0.36558		Yes
317	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1160	1	13	DKFSPTQDRPESSTVVK	DKFS(0.001)PT(0.013)Q	DKFSPTQDRPESSTVVK		1.2	0.31307		Yes
306	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1214	1	11	SEQPLSQVLPSPK	SEQPLSQVLP(0.5)LS(0.0)	SEQPLSQVLP(0.5)LS(ph)SPK		1.0	0.30556		No
430	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1216	1	13	SEQPLSQVLPSPK	SEQPLSQVLP(0.002)QVLP(0.0)	SEQPLSQVLP(0.002)QVLP(ph)SPK		1.1	0.39885		Yes
498	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1305	1	13	NSGPVSEVNTGFSPEVK	NSGPVSEVNTGFS(1)PEV	NSGPVSEVNTGFS(ph)PEVK		1.1	0.4618		Yes
701	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1338	1	2	RSSSELSPEVVEK	RS(0.468)S(0.468)S(0.0)	RS(ph)SSELSPEVVEK	PKA				No
188	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S1339	1	3	RSSSELSPEVVEK	RS(0.02)S(0.957)S(0.02)	RSS(ph)SSELSPEVVEK	PKA	1.3	0.17088		Yes
266	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2070	1	5	MSCFSRSPMSPTPLDR	MSCFS(0.744)RPS(0.25)M	(ox)SCFS(ph)RPSMSP	CK1	1.0	0.25982		No
521	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2073	1	8	MSCFSRSPMSPTPLDR	MSCFS(0.001)RPS(0.99)	M(ox)SCFSRSPMS(ph)M	ox)PKA	1.1	0.47864		Yes
698	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2075	1	10	MSCFSRSPMSPTPLDR	MS(0.075)CFS(0.081)R	M(ox)SCFSRSPMS(ph)P	PLDR				No
702	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2347	1	2	VSGRTSPLMLDR	VS(0.456)GRT(0.087)S(0.0)	(ph)GRTSPLM(ox)LD	PKA				No
346	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2351	1	6	VSGRTSPLMLDR	VSGRT(0.006)S(0.994)P	VSGRTS(ph)PLM(ox)LD	PKA	1.0	0.33946		Yes
459	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2404	1	19	MVQASSQSLPPAQDRP	MVQASSQSLPPAQDRP	M(ox)VQASSQSLPPAQ	WW GroupIV	1.1	0.42319		Yes
700	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S2411	1	26	MVQASSQSLPPAQDRP	MVQAS(0.135)S(0.079)	M(ox)VQASSQSLPPAQ	CK1				No
520	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S821	1	1	SGTPPRPGSVTNMQADE	S(0.55)GT(0.441)PPRP	S(ph)GTTPPRPGSVTNM	(ox)QADECTATPQR	1.1	0.47858		No
89	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	S829	2	9	SGTPPRPGSVTNMQADE	S(0.493)GT(0.439)PPRP	S(ph)GTTPPRPGSVTNM	VTN	0.8	0.060924		No
697	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T1153	1	6	DKFSPTQDRPESSTVVK	DKFS(0.277)PT(0.442)Q	DKFSPT(ph)QDRPESSTVVK					No
699	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T2077	1	12	MSCFSRSPMSPTPLDR	MS(0.075)CFS(0.081)R	M(ox)SCFSRSPMS(ph)P	FHA1 Rad53p				No
379	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T2350	1	1	TSPLMLDR	T(0.987)S(0.013)PLMLD	T(ph)SPLMLDR	CK1	1.0	0.35965		No
401	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T823	1	3	SGTPPRPGSVTNMQADE	S(0.194)GT(0.796)PPRP	SGT(ph)PPRPGSVTNM	CDK2	1.0	0.37655		Yes
90	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T831	2	11	SGTPPRPGSVTNMQADE	S(0.493)GT(0.439)PPRP	S(ph)GTTPPRPGSVTNM	(ox)QADECTATPQR	0.8	0.060924		No
102	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2;	T973	1	5	SMLQTTPDQNLGSGK	SMLQT(1)PPDQNLGSGK	SM(ox)LQT(ph)PPDQNL	FHA1 Rad53p	0.8	0.076776		Yes
273	IPI00830670	Sperm-specific antigen	Ssfa2;Kiaa1927;Krap;Ss	S738	1	3	SQSLPTLLSPVPR	S(0.097)QS(0.901)LP	SQSL(ph)PTLLSPVPR	14-3-3 binding	1.0	0.27111		Yes
542	IPI00830670	Sperm-specific antigen	Ssfa2;Kiaa1927;Krap;Ss	S90	1	6	TPLGASLDEQSSGTPK	TPLGAS(1)LDEQSSGTPK	TPLGAS(ph)LDEQSSGTP	CK2	1.1	0.49073		Yes
405	IPI00311020	Sarcospan;K-ras oncoge	Ssnp;Krag;Ssnp	S205	1	1	SLMASDGLQPKA	S(0.994)LMAS(0.006)D	S(ph)LM(ox)ASDGLQPK	GSK3	1.1	0.37995		Yes
540	IPI00755329	Translocan-associated	Ssr1	S268	1	28	VEMGTSSQNDVDMSW	VEMGTSSQNDVDM(0.0)	VEMGTSSQNDVDM(0.0)	CDK2	1.1	0.49051		Yes
289	IPI00755329	Translocan-associated	Ssr1	T260	1	20	VEMGTSSQNDVDMSW	VEMGT(0.001)S(0.002)	VEMGTSSQNDVDM(0.001)	POET(ph)LNQINKASPR	1.2	0.28652		No
329	IPI00131311	Striamin protein	Strm;Strn2	S67	1	10	IQALTAQLPSPLGR	IQALTAQLPS(1)PLGR	IQALTAQLPS(ph)PLGR		1.2	0.31818		Yes
455	IPI00471361	STIP1 homology and U	Stub1;Chip	S20	1	8	LGTGGGGSPDKPSAQE	LGT(0.007)GGGG(0.99)	LGTGGGGSPDKPS(ph)P	CDK2	1.0	0.42157		Yes
315	IPI00471361	STIP1 homology and U	Stub1;Chip	T15	1	3	LGTGGGGSPDKPSAQE	LGT(0.919)GGGG(0.08)	LGT(ph)GGGGSPDKPS	CAMK2	1.0	0.31043		Yes
344	IPI00170232	Supervillin;Archivillin;p	Svil;Svil;Svil;Svil	S227	1	10	SISFPEVPRSPK	SISFPEVPRS(1)PK	SISFPEVPRS(ph)PK	WW GroupIV	1.2	0.33695		Yes
467	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S116	1	8	KVMTASGSSPVPR	KVMTAS(0.012)GS(0.80)	KVM(ox)TASGS(ph)SSP	CK1	1.1	0.42682		Yes
132	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S118	1	10	KVMTASGSSPVPR	KVMT(0.001)AS(0.017)	KVM(ox)TASGSS(ph)P	Polo box	0.9	0.1102		Yes
418	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S134	1	3	STSFTEIDLK	S(0.006)T(0.049)S(0.94)	STS(ph)FTEIDLK	PKA/AKT	1.0	0.38955		Yes
454	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo;	S535	1	6	LLGQRSPLVLR	LLGQRS(1)PVLR	LLGQRS(ph)PVLR		1.0	0.42156		Yes
341	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo;	S672	1	4	DRASPAEAEEAVPEWAS	DRAS(1)PAAEAEEAVPEW	DRAS(ph)PAAEAEEAVPE	PKA	1.0	0.33338		Yes
703	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S107	1	7	KKEPAISSQNSPEAR	KKEPAIS(0.333)S(0.333)	KKEPAIS(ph)SQNSPEAR	GSK3				No
704	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S108	1	8	KKEPAISSQNSPEAR	KKEPAIS(0.333)S(0.333)	KKEPAIS(ph)SQNSPEAR					No
471	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S111	1	11	KKEPAISSQNSPEAR	KKEPAISSQNS(1)PEAR	KKEPAISSQNS(ph)PEAR	CK1	1.1	0.43291		Yes
96	IPI00828809	Transcription factor E3;	Tcf3;RP23-109E24.7-0	S553	1	11	AASDPLLSVSPAVSK	AASDPLLSVS(0.999)PAV	AASDPLLSVS(ph)PAVSK	CK1	0.8	0.06702		Yes
517	IPI00115660	Treacle protein;Treache	Tcof1;Tcof1	S169	1	13	KSAEPLANTVLASETEEEK	KS(0.002)AEPLANTVL(0.0)	KSAEPLANTVLAS(ph)ET	CK2	1.1	0.47583		Yes
547	IPI00115660	Treacle protein;Treache	Tcof1;Tcof1;Tcof1	S1191	1	3	KLSGDLGAGAPK	KLS(1)GDLEAGAPK	KLS(ph)GDLEAGAPK	PKA	1.1	0.49212		Yes
179	IPI00848939	Tensin-like C1 domain-c	Tenc1;Tns2;Tenc1;Tns2	S1089	1	5	HLPGSGQQPSPPAR	HLPGS(0.862)GQQPS(0.0)	HLPGS(ph)GQQPSPPAR	NEK6	0.9	0.16105		Yes
373	IPI00848939	Tensin-like C1 domain-c	Tenc1;Tns2;Tenc1;Tns2	S1094	1	10	HLPGSGQQPSPPAR	HLPGS(0.002)GQQPS(0.0)	HLPGSGQQPS(ph)PPAR		1.2	0.35512		Yes
476	IPI00848939	Tensin-like C1 domain-c	Tenc1;Tns2;Tenc1;Tns2	Y483	1	8	GPLDGSYPYIAQVQR	GPLDGSYPY(1)AQVQR	GPLDGSYPY(ph)AQVQR	ALK	1.1	0.44323		Yes
250	IPI00807764	29 kDa protein	Tfpt	S180	1	9	TTATLDPTSPAPGEGP	TTATLDPT(0.5)S(0.5)PA	TTATLDPT(ph)SPAPGEG	WW GroupIV	1.2	0.23922		No
249	IPI00807764	29 kDa protein	Tfpt	T179	1	8	TTATLDPTSPAPGEGP	TTATLDPT(0.5)S(0.5)PA	TTATLDPT(ph)SPAPGEG	NEK6	1.2	0.23922		No
261	IPI00556768	Thyroid hormone recep	Thrap3;Trap150;Thrap3	S243	1	7	ASVSDLSR	ASVSDLS(1)PR	ASVSDLS(ph)PR	CDK1	1.2	0.25485		Yes
332	IPI00556768	Thyroid hormone recep	Thrap3;Trap150;Thrap3	S679	1	4	IDISPSTFR	IDIS(1)PSTFR	IDIS(ph)PSTFR		1.2	0.31973		Yes
235	IPI00556768	Thyroid hormone recep	Thrap3;Trap150;Thrap3	S681	1	7	RIDISPSTFR	RIDIS(0.499)PS(0.499)T	RIDIS(ph)PSTFR					No
706	IPI00114862	THUMP domain-containi	Thumpd1	S86	2	9	FIDKDDQPSGSEGEDDD	FIDKDDQPS(1)GS(1)EG	FIDKDDQPS(ph)GS(ph)E	CK2	0.9	0.22536		Yes
237	IPI00114862	THUMP domain-containi	Thumpd1	S88	2	11	FIDKDDQPSGSEGEDDD	FIDKDDQPS(1)GS(1)EG	FIDKDDQPS(ph)GS(ph)E	CK2	0.9	0.22536		Yes
488	IPI00461642	Tight junction-associate	Tjp1;Pilt;Tjp4	S527	1	3	KDSLTAQEQGTVLS	KDS(0.959)LT(0.041)QA	KDS(ph)LTQAQEQGTVL	CHK1/2	1.1	0.45183		Yes
31	IPI00828976	Putative uncharacterize	Tmpo;Tmpe;Tmpe;Lap2	S277	1	9	IDGAVISESTPIAETIK	IDGAVISES(0.5)T(0.5)PI	IDGAVISES(ph)TPIAETIK		0.6	0.0017421	Down	No
32	IPI00828976	Putative uncharacterize	Tmpo;Tmpe;Tmpe;Lap2	T278	1	10	IDGAVISESTPIAETIK	IDGAVISES(0.5)T(0.5)PI	IDGAVISES(ph)TPIAETIK	Polo box	0.6	0.0017421	Down	No

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-reg	Phosphosites localized?
282	IPI00896574	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S157	1	1	SSTPLPTVSSSAENR	S(0.528)S(0.236)T(0.236)	S(ph)STPLPTVSSSAENR	CK1	1.2	0.28071	No	
706	IPI00896574	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S165	1	9	SSTPLPTVSSSAENR	S(0.066)S(0.047)T(0.047)	SSTPLPTVSSSAENR				No	
707	IPI00896574	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S167	1	11	SSTPLPTVSSSAENR	S(0.066)S(0.047)T(0.047)	SSTPLPTVSSSAENR	CK1			No	
525	IPI00896574	Putative uncharacterize	Tmpo;Tmpo;Tmpo;mc	S66	2	6	GPPDFSSDEEREPTVLG	GPPDF(S)(0.777)S(0.777)	GPPDF(S)(ph)S(ph)DEERE	CK2	1.1	0.48121	Yes	
526	IPI00896574	Putative uncharacterize	Tmpo;Tmpo;Tmpo;mc	S67	2	7	GPPDFSSDEEREPTVLG	GPPDF(S)(0.777)S(0.777)	GPPDF(S)(ph)S(ph)DEERE	CK2	1.1	0.48121	Yes	
279	IPI00121341	Thioredoxin-related tra	Tmx1;Txndc;Txndc1	S245	1	14	KVEEQEQAEEEDVSEEEA	KVEEQEQAEEEDV(S)1EE	KVEEQEQAEEEDV(S)(ph)CK2		1.2	0.27982	Yes	
153	IPI00121341	Thioredoxin-related tra	Tmx1;Txndc;Txndc1	S256	1	25	KVEEQEQAEEEDVSEEEA	KVEEQEQAEEEDV(S)0.5	KVEEQEQAEEEDV(S)(ph)GSK3		1.3	0.13214	No	
300	IPI00459443	182 kDa tankyrase-1-bi	Tnks1bp1;Kiaa1741;Ta	S1063	1	7	MQAESQSPTNVDLDEK	MQAESQ(0.082)QS(0.917)	M(ox)QAESQ(S)(ph)PTNVDLDEK		1.0	0.30129	Yes	
708	IPI00459443	182 kDa tankyrase-1-bi	Tnks1bp1;Kiaa1741;Ta	S1373	1	4	SSGSLSPGLETEDEPLER	S(0.056)S(0.033)GS(0.4)	SSGS(ph)LSPGLETEDEPLER	CK1			No	
709	IPI00459443	182 kDa tankyrase-1-bi	Tnks1bp1;Kiaa1741;Ta	S1375	1	6	SSGSLSPGLETEDEPLER	S(0.056)S(0.033)GS(0.4)	SSGS(ph)LSPGLETEDEPLER	CK1			No	
147	IPI00459443	182 kDa tankyrase-1-bi	Tnks1bp1;Kiaa1741;Ta	T533	1	11	GEGVSVQVPGTTPAPES	GEGVSVQVPGT(1)PPAP	GEGVSVQVPGT(ph)PPA	ERK/MAPK	0.9	0.12659	Yes	
434	IPI00378438	Putative uncharacterize	Tns1	S1346	1	9	TVGNTTTPSPGFR	TVGT(0.001)NT(0.021)F	TVGNTTTPS(ph)PGFR	WW GroupIV	1.0	0.40177	Yes	
26	IPI00353237	Tensin-3;Tensin-like SH	Tns3;Tens1	S769	1	3	KLISGQYDNDAAASQVTF	KL(0.998)IGQY(0.002)I	KL(ph)IGQYDNDAAASQV	PKA/AKT	2.0	6.292E-05	Up	Yes
594	IPI00751137	Putative uncharacterize	Tomm70a	S92	1	8	KTPTEGRASPALGSGHHD	KT(0.051)PEGRAS(0.753)	KTPTEGRAS(ph)PALGSGH	PKA	1.1	0.47873	Yes	
47	IPI00135443	DNA topoisomerase 2-t	Top2b	S1387	1	4	VKASPIITNDGDEFVPSD	VKAS(0.824)PIT(0.176)	VKAS(ph)PITNDGDEFVPSD	GDKLDEYAFSSG	1.5	0.015322	Up	Yes
372	IPI00135443	DNA topoisomerase 2-t	Top2b	S1400	2	17	VKASPIITNDGDEFVPSD	VKAS(0.984)PIT(0.017)	VKAS(ph)PITNDGDEFVPSD	DGLDKDEYAFSSG	1.2	0.35489	Yes	
710	IPI00135443	DNA topoisomerase 2-t	Top2b	S1563	1	3	KTSFDQDSDVDFIPSDFT	KT(0.464)S(0.464)FDQD	KT(ph)SFDQDSDVDFIPSDFT	SEPPALPR			No	
541	IPI00135443	DNA topoisomerase 2-t	Top2b	S1568	1	8	KTSFDQDSDVDFIPSDFT	KT(0.005)S(0.005)FDQD	KTSFDQD(S)(ph)DVIDFIPSDFT	SEPPALPR	1.1	0.49068	Yes	
311	IPI00135443	DNA topoisomerase 2-t	Top2b	T1390	1	7	VKASPIITNDGDEFVPSD	VKAS(0.196)PIT(0.803)	VKASPIIT(ph)ITNDGDEFV	CK1	1.2	0.30745	Yes	
382	IPI00135443	DNA topoisomerase 2-t	Top2b	Y1408	2	25	VKASPIITNDGDEFVPSD	VKAS(0.499)PIT(0.499)	VKAS(ph)PITNDGDEFVPSD	GDKLDEYAFSSG	1.0	0.3607	No	
254	IPI00755183	Tumor protein D52-like	Tpd52l;RP23-33L3.2-0	S189	1	7	NSATFKSFEDR	NSATFKS(1)FEDR	NSATFKS(ph)FEDR		1.2	0.24246	Yes	
167	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trin	S471	1	1	SRSGEGEVSGLLR	S(0.701)RS(0.299)GEGE	S(ph)RSGEGEVSGLLR	NIMA	1.3	0.14593	No	
555	IPI00480497	Tripartite motif-contain	Trim47;Trim47;Trim47	S591	1	6	SGALASPTDPFQSR	SGALAS(0.994)PT(0.006)	SGALAS(ph)PTDPFQSR		1.1	0.49457	No	
711	IPI00480497	Tripartite motif-contain	Trim47;Trim47;Trim47	T593	1	9	RSGALASPTDPFQSR	RSGALAS(0.497)PT(0.497)	RSGALAS(ph)PTDPFQSR				No	
409	IPI00623570	Cbp37	Trip12;Gtl6;cbp37	S310	1	1	SESPPAELPSLR	S(0.663)ES(0.337)PPAE	S(ph)ESPPAELPSLR	CK1	1.0	0.38212	No	
190	IPI00623570	Cbp37	Trip12;Gtl6;cbp37	S312	1	4	RSEPPAELPSLR	RS(0.108)ES(0.892)PPAE	RSE(ph)PPAELPSLR	14-3-3 binding	0.9	0.17328	Yes	
304	IPI00229801	Transformation related	Trp53bp1;RP23-437L13	S267	1	6	SEDRPSPQVSVAAVETK	S(0.002)EDRPS(0.902)S	SEDRPS(ph)SPQVSVAAV	PKA	1.0	0.30373	Yes	
532	IPI00229801	Transformation related	Trp53bp1;RP23-437L13	S268	1	7	SEDRPSPQVSVAAVETK	SEDRPSS(1)PQVSVAAV	SEDRPSS(ph)PQVSVAAV	WW GroupIV	1.1	0.48655	Yes	
384	IPI00229801	Transformation related	Trp53bp1;RP23-437L13	S382	1	9	STPFIVPSSPTEQGGGR	STPFIVP(S)(0.057)S(0.887)	STPFIVPSS(ph)PTEQGGG	WW GroupIV	1.1	0.36103	Yes	
7	IPI00119314	Tubby protein;Tubby pr	Tub;Rd5;Tub;Rd5	S333	1	1	SNLMGTFKFTVYDNGVNP	S(1)NLMGTFKFTVYDNGV	S(ph)NLMGTFKFTVYDNGV	PKD	0.2	8.043E-26	Down	Yes
35	IPI00115425	Twist-related protein 1	Twist1;Twist	S68	1	24	SAGGSAGPGGATGGGIG	SAGGSAGPGGAT(0.201)	SAGGSAGPGGATGGGIG	ERK/MAPK	1.6	0.0049247	Up	Yes
42	IPI00848643	Twist homolog 2 (Dros	Twist2;Twist2;Dermo1	S55	1	3	KGSPSAQSFEELQSQSR	KGS(0.956)PS(0.022)AC	KGS(ph)PSAQSFEELQSQSR		1.5	0.012927	Up	Yes
712	IPI00848643	Twist homolog 2 (Dros	Twist2;Twist2;Dermo1	S57	1	5	KGSPSAQSFEELQSQSR	KGS(0.5)PS(0.5)AQSFEE	KGS(ph)PSAQSFEELQSQSR				No	
338	IPI00113746	Splicing factor U2AF 65	U2af2;U2af65	S79	1	12	GAKEEHGGLIRSP	GAKEEHGGLIR(S)1PR	GAKEEHGGLIR(S)(ph)PR	CDK1	1.2	0.33033	Yes	
497	IPI00112597	Ubiquitin conjugation f	Ube4b;Ufd2;Ube4b;RP2	S103	1	1	SQSMIDIGVSCER	S(0.746)QS(0.254)MDIC	S(ph)QSMDIDIGVSCER	NEK6	1.1	0.46143	No	
713	IPI00420949	Regulator of nonsense	Upf1;Rent1;Upf1;Rent1	S915	2	2	ESLMQFSKPRK	ES(1)LMQFS(1)KPRK	ES(ph)LMQFS(ph)KPRK	AURORA			Yes	
714	IPI00420949	Regulator of nonsense	Upf1;Rent1;Upf1;Rent1	S920	2	7	ESLMQFSKPRK	ES(1)LMQFS(1)KPRK	ES(ph)LMQFS(ph)KPRK				Yes	
470	IPI00128071	General vesicular trans	Uso1;Vdp;Uso1;Vdp;U	S940	1	14	LKDLGHPVEEEDSGDQL	LKDLGHPVEEED(S)1G	LKDLGHPVEEED(S)(ph)GDQ	EDDDDEIDDGDKDQ	1.1	0.43172	Yes	
148	IPI00405227	Vinculin;Metavinculin	Vcl	S290	1	9	GWLRDPNASPDGAGEQ	GWLRDPNAS(1)PGDAG	GWLRDPNAS(ph)PGDAGEQ	AIR	0.9	0.12659	Yes	
715	IPI00122549	Voltage-dependent anik	Vdac1;Vdac5;Vdac1;Vd	S114	1	5	LTFDSSFSPNTGKK	LT(0.001)FDS(0.332)S(0	LTFD(S)(ph)SFPNTGKK				No	
716	IPI00122549	Voltage-dependent anik	Vdac1;Vdac5;Vdac1;Vd	S115	1	6	LTFDSSFSPNTGKK	LT(0.001)FDS(0.332)S(0	LTFD(S)(ph)SFPNTGKK	PLK1			No	
717	IPI00122549	Voltage-dependent anik	Vdac1;Vdac5;Vdac1;Vd	S117	1	8	LTFDSSFSPNTGKK	LT(0.001)FDS(0.332)S(0	LTFD(S)(ph)SFPNTGKK	CK1			No	
429	IPI00226275	WD repeat-containing g	Wdr26	S101	1	3	RLSQSDDEDVIR	RLS(0.977)QS(0.023)DE	RLS(ph)QSDEDVIR	PKA	1.1	0.39859	No	
59	IPI00229856	WD repeat-containing g	Wdr42a;D1Ucla4;H326	S123	2	4	DQDSSDDERALEDWVSS	DQDS(1)S(1)DDEERALED	DQDS(S)(ph)SDDERALED	WVSSSETALPRPR	1.5	0.024848	Up	Yes
60	IPI00229856	WD repeat-containing g	Wdr42a;D1Ucla4;H326	S124	2	5	DQDSSDDERALEDWVSS	DQDS(1)S(1)DDEERALED	DQDS(S)(ph)SDDERALED	CK2	1.5	0.024848	Up	Yes
719	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nsep	S166	1	9	NYQQNYQNSSEGEKNEC	NYQQNY(0.015)QNS(0.	NYQQNYQNS(ph)ESGEKNEGS	ESAPEGQAQR			No	
387	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nsep	S168	1	11	NYQQNYQNSSEGEKNEC	NYQQNY(0.005)QNS(0.	NYQQNYQNS(ph)ESGEKNEGS	ESAPEGQAQR	1.1	0.3638	Yes	
500	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nsep	S175	1	18	NYQQNYQNSSEGEKNEC	NYQQNYQNS(0.007)ES	NYQQNYQNSSEGEKNEGS	(ph)ESAPEGQAQR	1.1	0.4626	Yes	
121	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nsep	S177	1	20	NYQQNYQNSSEGEKNEC	NY(0.008)QNNY(0.02)Q	NYQQNYQNSSEGEKNEC	CK2	0.9	0.098281	No	
718	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nsep	Y163	1	6	NYQQNYQNSSEGEKNEC	NY(0.114)QNNY(0.373)	NYQQNY(ph)QNSSEGEKNEGS	ESAPEGQAQR			No	
80	IPI00676162	YEATS domain-containi	Yeats2;Kiaa1197;Yeats2	S462	1	3	IVSGSPITSPSPPLPR	IVS(0.924)GS(0.075)PIS	IVS(ph)GSPITSPSPPLPR		0.8	0.052188	No	
456	IPI00515528	Zinc finger CCCH type c	Zc3h13	S242	1	7	KAADVASPLLDQQR	KAADVAS(1)PLLDQQR	KAADVAS(ph)PLLDQQR	ERK/MAPK	1.1	0.42223	Yes	
510	IPI00461416	Zinc finger CCCH domai	Zc3h14	S515	1	10	DLVQPKDPKASPK	DLVQPKDPAS(1)PK	DLVQPKDPAS(ph)PK	WW GroupIV	1.1	0.47088	Yes	
390	IPI00673693	Zinc finger CCCH domai	Zc3h18;Nhn1	S554	1	6	LGVSIVSPSR	LGVSIVS(1)PSR	LGVSIVS(ph)PSR	CDK2	1.1	0.36656	Yes	
720	IPI00673693	Zinc finger CCCH domai	Zc3h18;Nhn1	S556	1	8	LGVSIVSPSR	LGVS(0.004)VS(0.498)P	LGVSIVS(ph)PSR	CK1			No	
369	IPI00673693	Zinc finger CCCH domai	Zc3h18;Nhn1;Zc3h18;N	S114	2	27	GPAGSPCEEEDVVEEDG	GPAGS(1)PCEEEDVVEE	GPAGS(ph)PCEEEDVVEE	DGTSDLRDEASS(ph)VT	1.2	0.35318	No	
368	IPI00673693	Zinc finger CCCH domai	Zc3h18;Nhn1;Zc3h18;N	S92	2	5	GPAGSPCEEEDVVEEDG	GPAGS(1)PCEEEDVVEE	GPAGS(ph)PCEEEDVVEE	CK2	1.2	0.35318	Yes	
239	IPI00453824	MKIAA1227 protein;Put	Zfp295;MKIAA1227;Zfp	S462	1	6	IKTEPSPSLDPSDIIR	IKTEPS(0.906)S(0.093)P	IKTEPS(ph)SPLDPSDIIR	GSK3	1.2	0.22577	Yes	
721	IPI00453824	MKIAA1227 protein;Put	Zfp295;MKIAA1227;Zfp	S463	1	7	IKTEPSPSLDPSDIIR	IKT(0.006)EPS(0.497)S	(IKTEPS(ph)SPLDPSDIIR	WW GroupIV			No	
427	IPI00467729	Zinc finger protein 462	Zfp462	S1994	1	12	KHVQYGSVPAVSAVKG	KHVQYGSVPAVS(1)AAV	KHVQYGSVPAVS(ph)AAV	KGLR	1.1	0.39665	Yes	
361	IPI00123531	Zinc finger protein 148	Znf148;Zfp89;Zfp148;Z	S306	1	15	GGLLTSEEDSGFSTSPK	GGLLTSEEDSGFSTS(1)P	GGLLTSEEDSGFSTS(ph)P	CDK1	1.0	0.34675	Yes	
139	IPI00421031	Zinc finger protein 521	Znf521;Evi3;Zfp521;Znf	S273	1	10	HIAECPHPCSPNEDR	HIAECPHPC(S)1PNEDR	HIAECPHPC(S)(ph)PNEDR	CK2	0.9	0.11693	Yes	
316	IPI00227314	Zinc finger protein 609	Znf609;Kiaa0295;Zfp60	S1057	1	3	APSLTDLVK	APS(0.999)LT(0.001)DL	APS(ph)TDLVK	PKD	1.2	0.31059	Yes	
380	IPI00463399	Zinc finger protein 740	Znf740;Zfp740;Znf740	S19	1	3	AGSPDVLIR	AGS(1)PDVLIR	AGS(ph)PDVLIR	CAMK2	1.1	0.36021	Yes	
51	IPI00320990	Uncharacterized protein	KIAA1143 homolog	S50	1	13	IQPQLPDEDGNHSDKED	IQPQLPDEDGNH(S)1DK	IQPQLPDEDGNH(S)(ph)D	CK2	0.7	0.01748	Down	Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabil	Modified Sequence	Best Motifs	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-re	Phosphosites localized?
The End														
	<sup>1</sup> The ratios are normalized to correct for unequal amounts of "light" and "heavy" protein in the assay. For the peptides where a value for "Ratio of Phosphorylations (+GH/-GH), Normalized" is not listed, one or both peptide signals in the corresponding peptide pair (light and heavy) were below the threshold for quantification.													

Supplemental Table S4. Phosphoproteomics data from the second 5 min GH treatment experiment.														
No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phc	Ratio Signific	Up-/Down-r	Localized phosphosite?
676	IPI00229328	1110037F02Rik protein	1110037F02Rik;Kiaa14	S1627	1	7	SFLSEPPSPGR	SFLSEPS(0.5)S(0.5)PGR	SFLSEPS(ph)SPGR	CK1	1.0	0.34135	No	
677	IPI00229328	1110037F02Rik protein	1110037F02Rik;Kiaa14	S1628	1	8	SFLSEPPSPGR	SFLSEPS(0.5)S(0.5)PGR	SFLSEPS(ph)SPGR	WW GroupIV	1.0	0.34135	No	
421	IPI00336929	Phostensin;Protein phc	2310014H01Rik;RP24	S5510	1	7	SCLVKGSPER	SCLVKG(1)PER	SCLVKG(ph)PER	CDK2	1.0	0.2203	Yes	
79	IPI00109044	Putative uncharacterize	2900073G15Rik;mcG	S20	1	3	ATSNVFMFQDSQIQEAF	AT(0.082)S(0.918)NVFAMF	AT(0.082)S(0.918)NVFAMF	CDK2	0.6	0.002444	Down	Yes
100	IPI00109044	Putative uncharacterize	2900073G15Rik;mcG	T19	1	2	ATSNVFMFQDSQIQEAF	AT(0.5)S(0.5)NVFAMF	AT(0.5)S(0.5)NVFAMF	PKA	0.6	0.0012963	Down	Yes
445	IPI00874907	Putative uncharacterize	4933425L03Rik	S472	1	11	AGEEDEGEVDSDDPETS	AGEEDEGEVDS(0.902)T	AGEEDEGEVDS(ph)DSDPETS	SAK	1.2	0.2326	Yes	
299	IPI00223634	Ankyrin repeat-contain	6330439K17Rik;RP23	S541	2	3	LISATVHEDGVEYSIR	LIS(0.982)AT(1)VHEDG	LIS(ph)AT(ph)VHEDG	CHK1	0.9	0.12587	Yes	
300	IPI00223634	Ankyrin repeat-contain	6330439K17Rik;RP23	T543	2	5	LISATVHEDGVEYSIR	LIS(0.982)AT(1)VHEDG	LIS(ph)AT(ph)VHEDG	CK2	0.9	0.12587	Yes	
313	IPI00458153	Uncharacterized protei	6330577E15Rik;63305	S67	1	5	ENPPSPPTSPAAPQPR	ENPPS(0.967)PPT(0.01	ENPPS(ph)PPTSPAAP	WW GroupIV	0.9	0.14004	Yes	
575	IPI00458153	Uncharacterized protei	6330577E15Rik;63305	S71	2	9	ENPPSPPTSPAAPQPR	ENPPS(0.082)PPT(0.95	ENPPSPPT(ph)S(ph)PA	WW GroupIV	1.2	0.28816	Yes	
576	IPI00458153	Uncharacterized protei	6330577E15Rik;63305	T70	2	8	ENPPSPPTSPAAPQPR	ENPPS(0.082)PPT(0.95	ENPPSPPT(ph)S(ph)PA	CK1	1.2	0.28816	Yes	
256	IPI00753321	Antigen containing epit	A230054D04Rik;AF013	S2920	1	14	SVSETSEDKKDEESDEEE	SVSETSEDKKDEES(1)DE	SVSETSEDKKDEES(ph)	CK2	0.9	0.099002	Yes	
680	IPI00458612	AP2-associated protein	Aak1;Kiaa1048;Aak1,Ki	S621	2	8	VGSLTPPSPK	VGSLT(0.105)PPS(0.914	VGSLTPPS(ph)S(ph)PK	PKA	1.0	0.34209	Yes	
562	IPI00458612	AP2-associated protein	Aak1;Kiaa1048;Aak1,Ki	S622	2	9	VGSLTPPSPK	VGSLT(0.105)PPS(0.914	VGSLTPPS(ph)S(ph)PK	WW GroupIV	1.0	0.28288	Yes	
1403	IPI00762360	ATP-binding cassette, s	Abcf1	S187	1	1	SKPAAADSEGEEDTAK	S(0.343)KPAAAD(0.32	S(ph)KPAAADSEGEEDTAK				No	
1005	IPI00762360	ATP-binding cassette, s	Abcf1	S194	1	8	SKPAAADSEGEEDTAK	SKPAAAD(1)EGEEEDT	SKPAAAD(ph)EGEEEDT	CK2	1.1	0.47857	Yes	
974	IPI00762360	ATP-binding cassette, s	Abcf1;Abcf1	S103	1	3	QLSVPASDEEDEVPAIP	QLS(0.851)VPAS(0.149	QLS(ph)VPASDEEDEV	GSK3	1.1	0.46542	Yes	
900	IPI00762360	ATP-binding cassette, s	Abcf1;Abcf1	S107	1	7	QLSVPASDEEDEVPAIP	QLSVPAS(1)DEEDEVPAI	QLSVPAS(ph)DEEDEV	CK2	1.1	0.43963	Yes	
612	IPI00762360	ATP-binding cassette, s	Abcf1;Abcf1	S138	1	13	GGNVFALIQQDSEEEEE	GGNVFALIQQD(1)EE	GGNVFALIQQD(ph)	CK2	1.0	0.30591	Yes	
451	IPI00798483	Abl interactor 1;Abelso	Abi1;Sh3bp1;Abi1;RP2	S296	1	3	HNSSTTSSTGGYR	HNS(0.804)T(0.079)T	HNS(ph)TTSSTGGYR	PKD	1.0	0.23412	Yes	
827	IPI00467530	Actin-binding LIM prot	Ablim1;Ablim;Kiaa0055	S475	1	3	TLSPTPSAEGYQDVR	T(0.089)LS(0.869)PT(0	TLSPTPSAEGYQDVR	PKA/AKT	1.0	0.40352	Yes	
208	IPI00467530	Actin-binding LIM prot	Ablim1;Ablim;Kiaa0055	S479	2	7	TLSPTPSAEGYQDVR	T(0.473)LS(0.43)PT(0.2	T(ph)LSPTPS(ph)AEGY	CK1	0.8	0.061165	No	
1096	IPI00467530	Actin-binding LIM prot	Ablim1;Ablim;Kiaa0055	S494	1	1	STSQGSINSVPYSR	S(0.475)T(0.262)S(0.26	S(ph)TSQGSINSVPYSR				No	
1100	IPI00467530	Actin-binding LIM prot	Ablim1;Ablim;Kiaa0055	T473	2	1	TLSPTPSAEGYQDVR	T(0.473)LS(0.43)PT(0.2	T(ph)LSPTPS(ph)AEGY	CK1			No	
28	IPI00848443	Acetyl-CoA carboxylase	Acaca;Acac;Gm738;Ac	S67	1	11	FIIGSVSEDNSEDEISNLV	FIIGSVSEDN(1)EISNLV	FIIGSVSEDN(ph)EISNLV	CK2	0.2	2.298E-25	Down	Yes
1401	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S895	1	23	SLIPDIKPLAGQEAIVDLH	SLIPDIKPLAGQEAIVDLH	SLIPDIKPLAGQEAIVDLH	HADD(1)RISEDETER			No	
452	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S898	1	26	SLIPDIKPLAGQEAIVDLH	S(0.005)LIPDIKPLAGQE	SLIPDIKPLAGQEAIVDLH	PKA	1.2	0.2342	No	
1402	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	T902	1	30	SLIPDIKPLAGQEAIVDLH	S(0.009)LIPDIKPLAGQE	SLIPDIKPLAGQEAIVDLH	HADD(1)RISEDETER			No	
408	IPI00911143	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S886	1	14	EAVVDLHADD(1)RISEDE	EAVVDLHADD(0.175)F	EAVVDLHADD(1)RISEDE	PKA	1.0	0.21153	Yes	
666	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S1003	1	6	TAQVPSPPR	TAQVPS(1)PPR	TAQVPS(ph)PPR	ERK/MAPK	1.2	0.33752	Yes	
945	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S477	1	3	SLSPLSGTTDTK	S(0.606)LS(0.393)PLS(0	S(ph)SPLSGTTDTK	NEK6	1.1	0.45474	No	
511	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S479	1	1	SLSPLSGTTDTK	S(0.013)LS(0.985)PLSG	SLS(ph)SPLSGTTDTK	CHK1/2	1.0	0.26193	No	
924	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S482	1	6	SLSPLSGTTDTK	S(0.167)LS(0.147)PLS(0	SLS(ph)SPLSGTTDTK	CK1	1.1	0.44719	No	
118	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S710	1	3	HLSHPEPEQQHVIR	HLS(1)HPEPEQQHVIR	HLS(ph)HPEPEQQHVIR	PIM1/2	1.7	0.0034146	Up	Yes
647	IPI00922962	Apoptotic chromatin cc	Acin1;RP23-94B13.1-0	S216	1	11	SSSFSSEKESDDEKPR	SSSFS(0.001)EEKGES(0.	SSSFSSEKES(ph)DDE	CK2	1.2	0.32598	Yes	
617	IPI00126248	Putative uncharacterize	Acly;Acly;RP23-39213.9	S481	1	12	AKPAMPQDSVPSPR	AKPAMPQDS(0.004)VP	AKPAMPQDSVPS(ph)P	ERK/MAPK	1.2	0.30928	Yes	
200	IPI00314443	Putative uncharacterize	Adam17;Adam17;Tace	S813	1	1	SFEDLTHPVR	S(1)FEDLTHPVR	S(ph)FEDLTHPVR	CK1	0.8	0.055126	Yes	
170	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S427	1	22	KYSDVEVPASVTGHFSFAS	KYS(0.001)DVEVPASVT	KYSDVEVPASVTGHFSF	F box bTrCP	0.8	0.035387	Down	No
1394	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S431	1	25	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSF	F box bTrCP			No	
1395	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S436	1	30	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSF	PKA			No	
714	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	S465	1	13	GDDASEEGQNGSSPK	GDDASEEGQNGS(0.087	GDDASEEGQNGSS(ph)	Polo box	1.0	0.35742	Yes	
1396	IPI00136000	Alpha-adducin;Erythro	Add1;Add1	T429	1	23	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSFAS	YSDVEVPASVTGHFSF	CSPLRHSFK			No	
447	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1	S677	1	10	TEEVLSPDGSPKSPK	TEEVLSPDGS(0.801)PSI	TEEVLSPDGS(ph)PSK	CDK2	1.0	0.2332	Yes	
809	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1	S679	1	12	TEEVLSPDGSPKSPK	TEEVLSPDGS(0.076)PSI	TEEVLSPDGS(ph)PSK	GSK3	1.0	0.39558	Yes	
532	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1	S681	1	14	TEEVLSPDGSPKSPK	TEEVLSPDGS(0.005)PSI	TEEVLSPDGS(ph)PSK	CDK2	1.0	0.26792	Yes	
163	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1	S683	1	16	TEEVLSPDGSPKSPK	TEEVLSPDGS(0.113)PSI	TEEVLSPDGS(ph)PSK	CK1	0.8	0.03083	Down	No
1241	IPI00387580	Gamma-adducin;Adduc	Add3;Add1;Add3;Add1	T668	1	1	TEEVLSPDGSPKSPK	T(0.223)EVL(1.01)PD	T(ph)EVLSPDGSPKSPK				No	
805	IPI00467327	Actin filament-associat	Afap1;Kiaa3018	S669	1	8	SGTSSPQSPVFR	SGTSSPQS(1)PVFR	SGTSSPQS(ph)PVFR	WW GroupIV	1.0	0.39438	Yes	
742	IPI00420172	Arf-GAP domain and FC	Afg1;Hrb;Rip;Afg1;H	S181	1	6	GTPSQSPVGR	GTPSQS(1)PVGR	GTPSQS(ph)PVGR	CK1	1.0	0.369	Yes	
1379	IPI00553798	Ahnak protein	Ahnak	S111	1	2	SSEVLSGDDEYQYR	S(0.293)S(0.331)EVL	SS(ph)EVLSDGDEYQYR	PKA			No	
505	IPI00553798	Ahnak protein	Ahnak	S116	1	7	SSEVLSGDDEYQYR	SSEVLS(1)GDDEYQYR	SSEVLS(ph)GDDEYQYR		1.0	0.25954	Yes	
34	IPI00553798	Ahnak protein	Ahnak	S136	1	3	LRSDEGVGDLGETQSR	LRS(1)EDGVEGLGETQ	LRS(ph)EDGVEGLGETQ	CAMK2	4.5	3.024E-16	Up	Yes
1378	IPI00553798	Ahnak protein	Ahnak	S149	1	16	LRSDEGVGDLGETQSR	LRS(0.12)EDGVEGLGET	LRSDEGVGDLGET(ph)QSR				No	
637	IPI00553798	Ahnak protein	Ahnak	S211	1	3	LPSGSGPASPTTGSVAVD	LPS(0.999)GS(0.001)GP	LPS(ph)GSGPASPTTGS	PKD	1.0	0.32037	Yes	
437	IPI00553798	Ahnak protein	Ahnak	S213	2	5	LPSGSGPASPTTGSVAVD	LPS(0.077)GS(0.923)GP	LPSGSGPASPTTGS(ph)P	GSK3	1.0	0.22784	Yes	
222	IPI00553798	Ahnak protein	Ahnak	S217	1	9	LPSGSGPASPTTGSVAVD	LPS(0.005)GS(0.001)GP	LPSGSGPASPTTGS(ph)P	WW GroupIV	1.4	0.06832	Yes	
1377	IPI00553798	Ahnak protein	Ahnak	S222	2	14	LPSGSGPASPTTGSVAVD	LPS(0.294)GS(0.39)GP	LPSGSGPASPTTGS(ph)P	AVDIR			No	
51	IPI00553798	Ahnak protein	Ahnak	S4890	1	9	FKAEPALPSK	FKAEPALPS(1)PK	FKAEPALPS(ph)PK	CDK1	2.5	6.232E-07	Up	Yes
157	IPI00553798	Ahnak protein	Ahnak	S5099	1	7	GDLGASSPSMK	GDLGAS(0.007)S(0.986	(ca)GDLGASS(ph)PSM	Polo box	0.8	0.027932	Down	Yes
165	IPI00553798	Ahnak protein	Ahnak	S5101	1	9	GDLGASSPSMK	GDLGAS(0.001)S(0.01)H	(ca)GDLGASS(ph)JM	CK1	0.8	0.031585	Down	Yes
279	IPI00553798	Ahnak protein	Ahnak	S5333	1	16	GPSFNVASPESDFGVSLK	GPSFNVASPESDFGV(1)	GPSFNVASPESDFGV(ph)	LKGP	0.9	0.10943	Yes	
743	IPI00553798	Ahnak protein	Ahnak	S5504	1	6	GGVTGSPASISGSK	GGVTGS(1)PEASISGSK	GGVTGS(ph)PEASISG	GSK3	1.0	0.37001	Yes	
117	IPI00553798	Ahnak protein	Ahnak	S5510	1	14	GKGGVTGSPASISGSK	GKGGVT(0.001)GS(0.0	GKGGVTGSPASIS(ph)G	GSKDLK	0.7	0.0027616	Down	Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Ph	Ratio Signif	Up-/Down-r	Localized phosphosite?
72	IPI00553798	Ahnak protein	Ahnak	S5512	1	14	GGVTGSPEASISGSKGDL	GGVTGSPEAS(0.006)IS	_GGVTGSPEASISGS(ph)	CK1	0.6	7.486E-05	Down	Yes
359	IPI00553798	Ahnak protein	Ahnak	S5518	2	1	SSKASLGSLEGEVEAEAS	S(0.528)S(0.489)KAS(0	_S(ph)S(ph)KASLGSLEGE	GSK3	0.9	0.17445		No
1382	IPI00553798	Ahnak protein	Ahnak	S5519	2	2	SSKASLGSLEGEVEAEAS	S(0.528)S(0.489)KAS(0	_S(ph)S(ph)KASLGSLEGE	NEK6				No
465	IPI00553798	Ahnak protein	Ahnak	S5522	1	2	ASLGSLEGEVEAEASSPK	AS(0.813)LGS(0.182)LE	AS(ph)LGSLEGEVEAEAE	AURORA	1.2	0.24139		Yes
864	IPI00553798	Ahnak protein	Ahnak	S5525	1	5	ASLGSLEGEVEAEASSPK	ASLGS(1)LEGEVEAEASS	ASLGS(ph)LEGEVEAEAE	CK1	1.1	0.42219		Yes
214	IPI00553798	Ahnak protein	Ahnak	S5535	1	15	ASLGSLEGEVEAEASSPK	AS(0.052)LGS(0.052)LE	ASLGSLEGEVEAEAS(ph)SPK		0.8	0.064438		No
225	IPI00553798	Ahnak protein	Ahnak	S5536	1	16	ASLGSLEGEVEAEASSPK	ASLGSLEGEVEAEASS(1)	ASLGSLEGEVEAEASS(ph)Polo box		1.4	0.071596		Yes
101	IPI00553798	Ahnak protein	Ahnak	S5553	1	1	SNSFSDER	S(0.955)NS(0.044)FS(0	_S(ph)SNSFSDER	PIM1/2	0.7	0.0013621	Down	Yes
97	IPI00553798	Ahnak protein	Ahnak	S5555	1	3	SNSFSDER	S(0.001)NS(0.999)FS(0	_SNS(ph)FSDER	PKA/AKT	0.6	0.0011776	Down	Yes
210	IPI00553798	Ahnak protein	Ahnak	S5557	1	7	HRSNSFSDER	HRS(0.081)NS(0.047)FS	(ca)HRSNSFSDER	CK1	1.4	0.061857		Yes
93	IPI00553798	Ahnak protein	Ahnak	S5563	1	3	EFSAPTPTGTLEFAGGD	EF(0.988)APS(0.012)TT	EF(ph)APSTPTGTLEF	CAMK2	0.6	0.000947	Down	Yes
1371	IPI00553798	Ahnak protein	Ahnak	S5566	2	6	EFSAPTPTGTLEFAGGD	EF(0.988)APS(0.042)IT	EF(ph)APS(ph)TPTGT	CK1				No
755	IPI00553798	Ahnak protein	Ahnak	S5607	1	10	SKGHYEVTGSDDEAGKL	SKGHYEVTGS(1)DDEAG	_SKGHYEVTGS(ph)DDE	CK2	1.0	0.37371		Yes
1372	IPI00553798	Ahnak protein	Ahnak	S5617	1	20	SKGHYEVTGSDDEAGKL	S(0.004)KGHY(0.004)EV	SKGHYEVTGSDDEAGK	NEK6				No
1373	IPI00553798	Ahnak protein	Ahnak	S5620	1	23	SKGHYEVTGSDDEAGKL	S(0.004)KGHY(0.004)EV	SKGHYEVTGSDDEAGK	CK1				No
1375	IPI00553798	Ahnak protein	Ahnak	S5623	1	26	SKGHYEVTGSDDEAGKL	S(0.004)KGHY(0.004)EV	SKGHYEVTGSDDEAGK	CK1				No
1385	IPI00553798	Ahnak protein	Ahnak	T147	1	14	LRSEdGVEGDLGELTQSR	LRS(0.12)EDGVEGDLGE	_LRSEdGVEGDLGELT(ph)	NEK6				No
1386	IPI00553798	Ahnak protein	Ahnak	T205	2	1	TVIRLPSGSGPASPTTGA	T(0.342)VIRLPS(0.265)G	_T(ph)VIRLPSGSGPASPTT	(ph)GSAVDIR				No
1384	IPI00553798	Ahnak protein	Ahnak	T219	1	11	LPSGSGPASPTTGSADV	LPSGSGPAS(0.481)PT(0	_LPSGSGPAS(ph)PTTGS	FHA KAPP				No
201	IPI00553798	Ahnak protein	Ahnak	T220	1	12	LPSGSGPASPTTGSADV	LPSGS(0.01)GPAS(0.08	_LPSGSGPASPTT(ph)GS	CK1	1.4	0.055541		No
230	IPI00553798	Ahnak protein	Ahnak	T5567	1	7	EFSAPTPTGTLEFAGGD	EF(0.013)APS(0.102)TT	EFSAPT(ph)PTGTLEF	WW GroupIV	1.4	0.074758		Yes
95	IPI00553798	Ahnak protein	Ahnak	T5569	2	9	EFSAPTPTGTLEFAGGD	EFSA(0.071)T(0.496)	EFSAPT(ph)PTGT(ph)	CK1	0.6	0.0011054	Down	No
105	IPI00553798	Ahnak protein	Ahnak	T5571	2	11	EFSAPTPTGTLEFAGGD	EFSA(0.071)T(0.496)	EFSAPT(ph)PTGT(ph)	LEFAGGD	0.7	0.0016383	Down	Yes
96	IPI00553798	Ahnak protein	Ahnak	T5571	2	11	EFSAPTPTGTLEFAGGD	EFSA(0.071)T(0.496)	EFSAPT(ph)PTGT(ph)	CK1	0.6	0.0011054	Down	No
673	IPI00553798	Ahnak protein	Ahnak	T5605	1	6	GHYEVTGSDDEAGLQ	GHY(0.002)EVT(0.802)G	(ca)GHYEVT(ph)GSD	FHA1 Rad53p	1.2	0.34115		Yes
1387	IPI00553798	Ahnak protein	Ahnak	Y5602	1	3	GHYEVTGSDDEAGLQ	GHY(0.317)EVT(0.124)G	GHY(ph)EVTGSDDEAGL	QSGVSLASK				No
312	IPI00553798	Ahnak protein;Desmoy	Ahnak;Ahnak	S893	1	3	AESEPMENVLPK	AE(1)PEMENVLPK	AE(1)PEMENVLPK		0.9	0.13854		Yes
834	IPI00553798	Ahnak protein;Ahnak p	Ahnak;Ahnak;mcG	T107	1	18	KGDRSPEPGQTWTHEV	KGDRSPEPGQT(0.009)Y	KGDRSPEPGQTWTHEV	GSK3	1.0	0.40759		Yes
941	IPI00553798	Ahnak protein;Ahnak p	Ahnak;Ahnak;mcG	T107	1	5	KGDRSPEPGQTWTHEV	KGDRS(1)PEPGQTWTH	KGDRS(ph)PEPGQTWTHE	VFSSR	1.1	0.4542		Yes
1047	IPI00553798	Ahnak protein;Ahnak p	Ahnak;Ahnak;mcG	T102	1	13	KGDRSPEPGQTWTHEV	KGDRS(0.002)PEPGQT	KGDRSPEPGQTWTH	(ph)HEVFSSR	1.1	0.49552		No
1017	IPI00850843	Putative uncharacterize	Ahnak2;AI450948	S286	1	3	DMSPTDTEVHR	DMS(0.982)PT(0.017)S	_DMS(ph)PTDTEVHR	CAMK2	1.1	0.48437		Yes
652	IPI00677756	AHNAK nucleoprotein	Ahnak2;AI450948	S35	1	3	KLSFSMPR	KL(0.998)FS(0.002)MP	KL(ph)FSMPR	PKA/AKT	1.0	0.33001		Yes
61	IPI00677756	AHNAK nucleoprotein	Ahnak2;AI450948	S652	1	6	DTTQRSVPVHQPTAR	DT(0.025)T(0.136)QRS	DTTQRS(ph)PVVHQPT	CK1	2.4	4.127E-06	Up	Yes
533	IPI00230591	A kinase anchor protei	Akap1;Akap;Akap1,RP2	S88	1	3	RLSEACPGVLSVAPT	RLS(1)EEACPGVLSVAPT	RLS(ph)EEACPGVLSVA	PKA	1.2	0.26807		Yes
276	IPI00123709	A-kinase anchor protei	Akap1;Gag12;Ssecks;A	S584	1	17	GPSEAPQEAEEAGATS	GPSEAPQEAEEAGAT(0	_GPSEAPQEAEEAGAT	CK2	0.9	0.1082		Yes
1391	IPI00123709	A-kinase anchor protei	Akap12;Gag12;Ssecks;A	T583	1	16	GPSEAPQEAEEAGATS	GP(0.002)EAPQEAEE	GPSEAPQEAEEAGAT	(ph)SDGEKKR				No
88	IPI00649060	A kinase (PRKA) anchor	Akap2;Palm2;RP23-33	S984	1	3	TLSMIEEIR	T(0.087)LS(0.913)MIEE	TL(ph)MIEEIR	CAMK2	1.9	0.0005411	Up	Yes
68	IPI00649060	A kinase (PRKA) anchor	Akap2;Palm2;RP23-33	T982	1	1	TLSMIEEIR	T(0.561)LS(0.439)MIEE	T(ph)LSMIEEIR		2.2	3.454E-05	Up	No
633	IPI00321739	A-kinase anchor protei	Akap8;Akap95	S320	2	3	ADSDGDLSENDGAGDI	ADS(1)DGDL(1)ENDDC	ADS(ph)DGDL(ph)EN	CHK1/2	1.2	0.31756		Yes
634	IPI00321739	A-kinase anchor protei	Akap8;Akap95	S325	2	8	ADSDGDLSENDGAGDI	ADS(1)DGDL(1)ENDDC	ADS(ph)DGDL(ph)EN	DDGAGDLR	1.2	0.31756		Yes
65	IPI00857073	Proline-rich AKT1 subst	Akt1s1;Pras	S255	1	14	SLPVSVPVWAFK	S(1)LPVSVPVWAFK	S(ph)LPVSVPVWAFK	GSK3	2.2	1.792E-05	Up	Yes
1392	IPI00453512	Alkylated DNA repair p	Alkbh5;Abh5;Ofoxd	S384	1	1	KSYESSEDCEPAASSPTR	KSYESSEDCEPAAS(0.47	_KSYESSEDCEPAAS(ph)S	PTR				No
1393	IPI00453512	Alkylated DNA repair p	Alkbh5;Abh5;Ofoxd	S385	1	15	KSYESSEDCEPAASSPTR	KSYESSEDCEPAAS(0.47	_KSYESSEDCEPAAS(ph)	Polo box				No
448	IPI00309844	Alsin;Amyotrophic late	Als2	S1456	1	1	SESPPEGYVVTSSGLL	S(0.58)ES(0.412)PEPGY	S(ph)ESPEPGYVVTSSG	CK1	1.2	0.23334		No
694	IPI00223838	Ankyrin repeat domain	Ankrd57	S82	1	6	FCTGDSPPLEAK	FCTGDS(1)PPLEAK	FCTGDS(ph)PPLEAK		1.2	0.3481		Yes
828	IPI00831258	Acidic leucine-rich nucl	Anp32b;Pal31	T265	1	4	KRETDDDEGEDD	KRET(1)DDEGEDD	KRET(ph)DDEGEDD	PKA	1.1	0.40441		Yes
161	IPI00648295	Amine oxidase (Flavin d	Aof2;RP23-426N4.2-00	S132	2	10	EMDESLANLSEDEYSEE	EMDESLANLS(0.993)ED	EM(ox)DESLANLS(ph)	CK2	0.8	0.029713	Down	Yes
162	IPI00648295	Amine oxidase (Flavin d	Aof2;RP23-426N4.2-00	S138	2	16	EMDESLANLSEDEYSEE	EMDESLANLS(0.993)ED	EM(ox)DESLANLS(ph)	CK2	0.8	0.029713	Down	Yes
879	IPI00130444	AP-3 complex subunit c	Ap3b1	S276	1	5	NFYEEEEEEKEK	NFY(0.001)ES(0.999)E	NFY(1)EEEEEEKEK	CK2	1.1	0.42911		Yes
736	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	S754	1	3	RHSSLPTESDEDIAPAQR	RHS(0.613)S(0.229)LPT	RHS(ph)SLPTESDEDIA	PKA	1.2	0.36612		No
1397	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	S755	1	4	RHSSLPTESDEDIAPAQR	RHS(0.081)S(0.306)LPT	RHS(ph)SLPTESDEDIA	PIM1/2				No
540	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	S760	1	8	RHSSLPTESDEDIAPAQR	HSSLPTES(1)DEDIAPAQR	HSSLPTES(ph)DEDIAPAQR		1.0	0.27118		Yes
1031	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	S784	1	15	VDIITEEMPENALPSDED	VDIITEEMPENALPS(0.9	_VDIITEEMPENALPS(ph)	DEDDKDPNDP	1.1	0.48893		Yes
1399	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	T758	1	6	HSSLPTESDEDIAPAQR	HS(0.003)S(0.003)LPT	(ca)HSSLPT(ph)SEDED	FHA1 Rad53p				No
983	IPI00117811	AP-3 complex subunit c	Ap3d1;Ap3d	Y795	1	26	VDIITEEMPENALPSDED	VDIITEEMPENALPS(0.5	_VDIITEEMPENALPS(ph)	ALK	1.1	0.46816		No
472	IPI00170307	Apolipoprotein A-I-bind	Apoa1bp;Aibp	S43	1	3	RGSEPMAGAAVK	RGS(1)ETMAGAAVK	RGS(ph)ETMAGAAVK	PKA/AKT	1.2	0.24424		Yes
147	IPI00625950	Adenine phosphoribos	Aprt;aprt	S15	1	1	SFPDFPIPVGLFR	S(1)FPDFPIPVGLFR	S(ph)FPDFPIPVGLFR	CAMK2	0.8	0.017005	Down	Yes
166	IPI00123183	Aquaporin-1;Aquaporin	Aqp1	S262	1	19	VWTSQGVVEYDLADDI	VWTSQGVVEYDLADDI	VWTSQGVVEYDLADDI	CK2	0.8	0.032489	Down	Yes
146	IPI00123183	Aquaporin-1;Aquaporin	Aqp1	T246	1	3	VWTSQGVVEYDLADDI	VWT(0.544)S(0.177)G	VWT(ph)SQGVVEYDLADD	INSRVM(ox)JKPK	0.8	0.016653	Down	No
122	IPI00109656	ADP-ribosylation factor	Arfgap2;Zfp289;Znf289	S145	1	17	HGTDLWIDSMNSAPSH	HGTDLWIDSMNSAPS(0	_HGTDLWIDSMNSAPSH	CDK2	1.7	0.0068805	Up	Yes
464	IPI00111931	ADP-ribosylation factor	Arfgap3	S332	1	18	SGISHSVTSDMQTIEQES	SGISHSVTSDMQT(0.00	_SGISHSVTSDMQTIEQES	(ph)PTLAKPR	1.2	0.24109		Yes
1112	IPI00137087	ADP-ribosylation factor	Arfgaf2;RP23-216D20	S218	1	12	ELEKPMQSKPQSPVIAQT	ELEKPMQ(0.05)KQPS(	ELEKPMQSKPQSPVIA	WW GroupIV				No
1115	IPI00137087	ADP-ribosylation factor	Arfgaf2;RP23-216D20	S227	1	12	ELEKPMQSKPQSPVIAQT	ELEKPMQSKPQ(0.002	ELEKPMQSKPQSPVIA	CDK1				No
1120	IPI00137087	ADP-ribosylation factor	Arfgaf2;RP23-216D20	T224	1	21	ELEKPMQSKPQSPVIAQT	ELEKPMQSKPQ(0.002	ELEKPMQSKPQSPVIA	FHA KAPP				No
644	IPI00652831	Arginine and glutamate	Arglu1;Arglu1	S74	1	2	ASSPPDRIDIFGR	AS(0.5)S(0.5)PPDRIDIF	AS(ph)SPPDRIDIFGR	PKA	1.2	0.32551		No
597	IPI00652831	Arginine and glutamate	Arglu1;Arglu1	S75	1	3	ASSPPDRIDIFGR	AS(0.113)S(0.887)PDR	ASS(ph)PPDRIDIFGR	PKA/AKT	1.2	0.30003		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
376	IPI00322312	Rho GDP-dissociation	Arhgdia;C87222;Gdi1	T7	1	6	AEQEPTAEQLAQIAAEN	AEQEPT(1)AEQLAQIAA	AEQEPT(ph)AEQLAQIAA	AEENEDEHSVNYKPPAQ	0.9	0.18516		Yes
1044	IPI00310764	Rho guanine nucleotide	Arhgef2;Kiaa0651;Lbc1	S585	1	1	SLPAGDALYLSFNPPQPS	S(0.997)LPAGDALY(0.00	S(ph)LPAGDALYLSFNPP	AURORA-A	1.1	0.49328		Yes
1307	IPI00230704	Rho guanine nucleotide	Arhgef7;Kiaa0142;Pak3	S578	1	21	VTSVSNPTIKPHSVPSHTI	VTSVSNPTIKPHS(0.001)	VTSVSNPTIKPHSVPSHTDLS	(ph)KSPK	1.1		No	
1309	IPI00230704	Rho guanine nucleotide	Arhgef7;Kiaa0142;Pak3	S580	1	23	VTSVSNPTIKPHSVPSHTI	VTSVSNPTIKPHS(0.001)	VTSVSNPTIKPHSVPSHTDLS	CDK1	1.1		No	
913	IPI00230704	Rho guanine nucleotide	Arhgef7;Kiaa0142;Pak3	S497	1	2	MSGFYQGGK	MS(1)GFYQGGK	M(ox)S(ph)GFYQGGK	_PKA	1.1	0.44449		Yes
773	IPI00757909	Armadillo repeat-conta	Armc10	S43	1	1	SAEDLTGSGYDDILNAEQ	S(1)AEDLTGSGYDDILNAEQ	S(ph)AEDLTGSGYDDILNAEQ	LK	1.2	0.37962		Yes
234	IPI00918646	cAMP-regulated phosph	Arpp19;Arpp19;Ensa;E	S95	1	4	YFDSGDYNNMAK	YFDS(1)GDYNNMAK	YFDS(ph)GDYNNMAK	(ox)AK	0.9	0.080352		Yes
184	IPI00127472	Armadillo repeat prote	Arvcf;Arvcf;Arvcf;Arvcf	T637	1	4	NFDT1LIDLPK	NFDT(1)LIDLPK	NFDT(ph)LIDLPK	FHA2 Rad53p	0.8	0.044151	Down	Yes
766	IPI00556827	Putative uncharacterize	Atp2b1	S1155	1	4	IEDSEPHIPLIDDDTAEDD	IEDS(0.97)EPIHLIDDDT	IEDS(ph)EPIHLIDDDTDAEDD	DAPTKR	1.2	0.3771		Yes
235	IPI00857253	Alpha thalassemia/mer	Atrx;RP23-170G19.5-0	S92	1	4	YVESDDEKPTDENVNEK	Y(0.165)VES(0.834)DDE	(ca)YVES(ph)DDEKPTDCK2		1.4	0.080726		Yes
621	IPI00857253	Alpha thalassemia/mer	Atrx;RP23-170G19.5-0	Y89	1	1	YVESDDEKPTDENVNEK	Y(0.962)VES(0.038)DDE	Y(ph)VESDDEKPTDENVNEK		1.2	0.31092		Yes
705	IPI00605902	Ataxin-1-like;Brother o	Atxn1;Boat	T328	1	11	VEVAAPAHRGTPDPTDLE	VEVAAPAHRG(0.999)H	VEVAAPAHRG(ph)PD	PKA	1.2	0.35365		Yes
789	IPI00458001	Ataxin-2-like protein;A	Atxn2;A2lp;Atxn2;A2l	S109	1	5	GPPQSPVFEVGVYNNRS	GPPQS(0.999)PVFEVGV	GPPQS(ph)PVFEVGVYNN	WW GroupIV	1.0	0.38607		Yes
238	IPI00387388	BCL2-associated athan	Bag3;Bag3;Bis;MNCb-2	S177	1	1	SQSPAASDCSSSSSSASL	S(0.61)QS(0.39)PAAASD	S(ph)QSPAASDCSSSSSSASL	PSGR	0.9	0.082893		No
1278	IPI00222731	Brain-specific angiogen	Baiap2;Baiap2;Baiap2;	S365	1	1	SSSMAAGLER	S(0.448)S(0.276)S(0.27	S(ph)SSSMAAGLER	NEK6			No	
1284	IPI00222731	Brain-specific angiogen	Baiap2;Baiap2;Baiap2;	S366	1	2	SSSMAAGLER	S(0.193)S(0.404)S(0.40	SS(ph)SM(ox)AAGLER	PKA			No	
159	IPI00222731	Brain-specific angiogen	Baiap2;Baiap2;Baiap2;	S367	1	3	SSSMAAGLER	S(0.097)S(0.054)S(0.84	SSS(ph)MAAGLER	_CHK1/2	0.8	0.028214	Down	Yes
882	IPI00129519	Brain acid soluble prote	Basp1;Nap22	T36	1	12	KAEGAGTEEEGTKEPESE	KAEGAGT(0.004)EEEGT	KAEGAGTEEEGT(ph)P	CDK1	1.1	0.42972		Yes
176	IPI00380722	Large proline-rich prote	Bat2	S761	1	5	ERSDSSGSSSEPFER	ERS(0.017)DS(0.818)GC	ERSDS(ph)GSSSEPFER	F box bTrCP	1.5	0.040394	Up	Yes
889	IPI00380722	Large proline-rich prote	Bat2	T608	1	13	EGPEPPEEVPPPTTPPAP	EGPEPPEEVPPPT(0.5)T	EGPEPPEEVPPPT(ph)T	PPAP	1.1	0.43249		No
660	IPI00380722	Large proline-rich prote	Bat2	T609	1	14	EGPEPPEEVPPPTTPPAP	EGPEPPEEVPPPT(0.017	EGPEPPEEVPPPT(ph)T	WW GroupIV	1.0	0.33403		Yes
868	IPI00130381	Large proline-rich prote	Bat3;Bat3	S995	1	4	ENASAPAGTTAEAEAMSR	ENAS(0.999)PAGTTAE	ENAS(ph)PAGTTAEAEAM	(ox)SR	1.1	0.42282		Yes
885	IPI00923656	Tyrosine-protein kinase	Baz1b;Wbscr9;Wstf;Ba	S1464	1	8	LADDEGDSDESVEGQSR	LADDEGDS(1)DESVEGQ	LADDEGDS(ph)DESVEGQ	CK2	1.1	0.43123		Yes
492	IPI00923656	Tyrosine-protein kinase	Baz1b;Wbscr9;Wstf;Ba	S1468	2	12	LADDEGDSDESVEGQSR	LADDEGDS(0.691)DS(0.	LADDEGDS(ph)DESVEGQ	GSK3	1.2	0.2534		No
601	IPI00625898	HMG box transcription	Bbx;Hbp2;Bbx;Hbp2;B	S811	1	7	TADGRVSPAGGLDLDK	T(0.004)ADGRVS(0.82)	TADGRVS(ph)PAGGLT	PKA	1.2	0.30226		Yes
512	IPI00742368	Novel protein (BC0056	BC005624;RP23-2210	S261	1	12	VGDTEKPEPERSPPNR	VGDTEKPEPERS(1)PPNR	VGDTEKPEPERS(ph)PPNR		1.2	0.26197		Yes
5	IPI00330070	cDNA sequence BC0894	BC089491	S225	2	9	LSTISPAPFSFGSTK	LSTIS(0.002)PAPFS(0.99	LSTISPAPFS(ph)FGS	(ph)CK1	0.03	7.97E-105	Down	Yes
6	IPI00330070	cDNA sequence BC0894	BC089491	S228	2	12	LSTISPAPFSFGSTK	LSTIS(0.002)PAPFS(0.99	LSTISPAPFS(ph)FGS	(ph)CK2	0.03	7.97E-105	Down	No
7	IPI00330070	cDNA sequence BC0894	BC089491	T229	2	13	LSTISPAPFSFGSTK	LSTIS(0.002)PAPFS(0.99	LSTISPAPFS(ph)FGS	(ph)FHA2 Rad53p	0.03	7.97E-105	Down	No
589	IPI00331555	2-oxoisovalerate dehyd	Bckdha	S338	1	5	IGHHSTSDSSAYR	IGHHS(0.991)T(0.008)S	IGHHS(ph)TSDSSAYR		1.0	0.29372		Yes
545	IPI00331555	2-oxoisovalerate dehyd	Bckdha	S348	1	1	SVDEVNYYWQDKQDHP	S(1)VDEVNYYWQDKQDHP	S(ph)VDEVNYYWQDKQD	CK2	1.0	0.27408		Yes
1406	IPI00115094	[3-methyl-2-oxobutano	Bckdk	S31	1	1	STATDTHHVELAR	S(0.429)T(0.271)S(0.27	S(ph)STATDTHHVELAR	CAMK2			No	
415	IPI00321499	Bcl-2-like protein 13;P	Bcl2l13;Mii1;Bcl2l13	S343	1	5	AEKTSPTPSVFLVEEEL	AEKT(0.027)S(0.707)PT	AEKTS(ph)PTPSVFLVEL	GSK3	1.3	0.21601		No
1250	IPI00321499	Bcl-2-like protein 13;P	Bcl2l13;Mii1;Bcl2l13	T342	1	4	AEKTSPTPSVFLVEEEL	AEKT(0.305)S(0.305)PT	AEKTS(ph)PTPSVFLVEEEL	AVTARPEAVER			No	
1254	IPI00321499	Bcl-2-like protein 13;P	Bcl2l13;Mii1;Bcl2l13	T345	1	7	AEKTSPTPSVFLVEEEL	AEKT(0.305)S(0.305)PT	AEKTS(ph)PTPSVFLVEEEL	AVTARPEAVER			No	
896	IPI00321499	Bcl-2-like protein 13;P	Bcl2l13;Mii1;Bcl2l13	T361	1	23	AEKTSPTPSVFLVEEEL	AEKT(0.024)S(0.024)PT	AEKTSPTPSVFLVEEEL	AVTARPEAVER	1.1	0.4371		Yes
416	IPI00453751	B-cell CLL/lymphoma 9	Bcl9l;B9l;Bcl9l;B9l	S116	1	1	SVSVDSEGEQR	S(0.665)VS(0.335)VDSE	S(ph)SVSVDSEGEQR	CAMK2	2.8	3.05E-08	Up	No
59	IPI00453751	B-cell CLL/lymphoma 9	Bcl9l;B9l;Bcl9l;B9l	S118	1	3	SVSVDSEGEQR	S(0.156)VS(0.821)VDSE	SVS(ph)VDSEGEQR	PKA/AKT	2.4	3.154E-06	Up	Yes
790	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S177	1	10	KAEGEPQEEESPLK	KAEGEPQEEES(1)PLK	KAEGEPQEEES(ph)PLK	CDK2	1.1	0.38646		Yes
1239	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S261	1	7	NTPSQHSHSIQHSPE	NT(0.172)PS(0.156)QHS	NTPSQHSHSIQHSI	CK1			No	
639	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S263	1	9	NTPSQHSHSIQHSPE	NT(0.005)PS(0.01)QHS	NTPSQHSHSIQHSI	GSK3	1.2	0.32327		No
663	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S267	1	13	NTPSQHSHSIQHSPE	NTPSQHS(0.001)HS(0.0	NTPSQHSHSIQHSI	(ph)CDK2	1.0	0.33583		Yes
281	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S383	1	17	GRADGDWDDQEVLDYF	GRADGDWDDQEVLDY(0.6	GRADGDWDDQEVLDY	CK2	1.3	0.11201		Yes
1236	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S387	1	19	ADGDWDDQEVLDYFSD	ADGDWDDQEVLDY(0.0	ADGDWDDQEVLDYFSD	CK1			No	
880	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S395	1	4	FHDSEGDTEETEDYR	FHDS(1)EGDTEETEDYR	FHDS(ph)EGDTEETEDYR		1.1	0.42925		Yes
628	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S494	1	5	KEVQSPQEVK	KEVQS(1)PEQVK	KEVQS(ph)PEQVK	ERK/MAPK	1.2	0.31548		Yes
433	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S510	1	8	LKELFDYSPPLHK	LKELFDYS(1)PPLHK	LKELFDYS(ph)PPLHK		1.2	0.22732		Yes
706	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S656	1	5	RIDISPSALR	RIDIS(1)PSALR	RIDIS(ph)PSALR		1.2	0.35374		Yes
1027	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	S658	1	6	IDISPSALR	IDIS(0.242)PS(0.758)AL	(ca)IDISPS(ph)ALR		1.1	0.48724		No
996	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	Y381	1	13	ADGDWDDQEVLDYFSD	ADGDWDDQEVLDY(0.6	ADGDWDDQEVLDY(ph)FSDKESAK		1.1	0.47532		No
701	IPI00415385	Bcl-2-associated transc	Bclaf1;Btf;Kiaa0164;B	Y509	1	5	ELFDYSPPLHK	ELFDY(0.5)S(0.5)PPLHK	(ca)ELFDY(ph)PPLHK		1.0	0.35028		No
389	IPI00114352	Myc box-dependent-in	Bin1;Amphl;Sh3p9;Bin	S296	1	1	SPSPPPDGSAAATPEIR	S(0.938)PS(0.062)PPDP	S(ph)SPSPPPDGSAAATPEIR		0.9	0.19761		Yes
811	IPI00114352	Myc box-dependent-in	Bin1;Amphl;Sh3p9;Bin	S298	1	16	AQPSDNAMEKGNKSPS	AQPS(0.006)DNAMEKGN	AQPSDNAMEKGNKSPS	(ph)PPPDGSPAATPEIR	1.1	0.39683		Yes
195	IPI00114352	Myc box-dependent-in	Bin1;Amphl;Sh3p9;Bin	S304	1	9	SPSPPPDGSAAATPEIR	S(0.001)PS(0.002)PPDP	SPSPPPDGS(ph)PAAATPEIR		0.8	0.05335		Yes
1226	IPI00114352	Myc box-dependent-in	Bin1;Amphl;Sh3p9;Bin	T308	1	13	SPSPPPDGSAAATPEIR	S(0.228)PS(0.257)PPDP	(ca)SPS(ph)PPPDGSPA	FHA2 Rad53p			No	
1184	IPI00850963	BCL2/adenovirus E1B 1	Bnip3l;Nix;Bnip3l;mcG	S118	1	4	DHSSQSEEEVVEGK	DHS(0.029)S(0.486)QS	DHSS(ph)QSEEEVVEGK	CK2			No	
1187	IPI00850963	BCL2/adenovirus E1B 1	Bnip3l;Nix;Bnip3l;mcG	S120	1	6	DHSSQSEEEVVEGK	DHS(0.029)S(0.486)QS	DHSS(ph)QSEEEVVEGK	CK2			No	
268	IPI00410792	Bromodomain-containi	Brd3;Fsr2;Brd3;Fsr2;	S262	1	3	SESPPLSEPK	S(0.029)ES(0.971)PPLS	SES(ph)PPLSEPK	14-3-3 binding	0.9	0.10612		Yes
251	IPI00153284	BUD13 homolog;BUD1	Bud13;Bud13	S297	1	5	AHHESPDLELHK	AHHES(1)PDLELHK	AHHES(ph)PDLELHK		1.4	0.094306		Yes
987	IPI00118762	Bystin	Bysl	S97	1	10	LGGLPQDGSDEEDEF	LGGLPQDGS(1)DEEDEF	LGGLPQDGS(ph)DEEDEF	CK2	1.1	0.46989		Yes
683	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;R	S270	1	10	LPAPQEDTASEAGTPQG	LPAPQEDT(0.007)AS(0.	LPAPQEDTAS(ph)EAGTPQ	GEVQTR	1.2	0.34386		Yes
929	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;R	T268	1	8	LPAPQEDTASEAGTPQG	LPAPQEDT(0.946)AS(0.	LPAPQEDT(ph)ASEAGT	CK2	1.1	0.44882		Yes
480	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;R	T274	2	14	LPAPQEDTASEAGTPQG	LPAPQEDT(0.212)AS(0.	LPAPQEDTAS(ph)EAGT	(ph)PQGEVQTR	1.2	0.24771		Yes
535	IPI00828741	HnRNP-associated with	C130057N11Rik;Raly;R	S1335	1	4	GRLSVPVPR	GRLS(1)PVPVPR	GRLS(ph)PVPVPR	PKA	1.2	0.26993		Yes
90	IPI00380280	Carbamoyl-phosphate	Cad;mcG 23490;Cad	S1859	1	5	IHRASDPGLPAEPEK	IHRAS(1)DPGLPAEPEK	IHRAS(ph)DPGLPAEPEK	PKA	1.9	0.0006648	Up	Yes
640	IPI00775950	Putative uncharacterize	Cald1	S254	1	9	LKQTFNAFSPSR	LKQT(0.001)ENAFS(0.9	LKQTFNAFSPS(ph)PSR	CDK2	1.2	0.32369		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
140	IPI00406790	Calcium/calmodulin-de	Camk2d;Kiaa4163;Cam	T371	1	9	ESTESSNTTIEDVDK	ES(0.013)T(0.013)ES(0.013)	ESTESSNTT(ph)IIEDEDV	FHA1 Rad53p	0.8	0.014907	Down	Yes
609	IPI00119618	Calnexin	Canx	S553	1	3	QKSDAEEDGVTGSQDEE	QKS(0.999)DAEEDGVT	QKS(ph)DAEEDGVTGS	CK2	1.2	0.30554		Yes
698	IPI00119618	Calnexin	Canx	S563	1	11	SDAEEDGVTGSQDEE	SDAEEDGVT(0.096)GS	SDAEEDGVTGS(ph)QD	CK2	1.2	0.34914		Yes
826	IPI00119618	Calnexin	Canx	S582	1	10	AEDEILNRSR	AEDEILNRS(1)PR	AEDEILNRS(ph)PR	CDK1	1.1	0.40275		Yes
515	IPI00133349	Calcium-regulated heat	Carhsp1	S42	1	6	GNVVPSPLPTRR	GNVVPS(1)PLPTRR	GNVVPS(ph)PLPTRR	ERK/MAPK	1.0	0.26322		Yes
354	IPI00133349	Calcium-regulated heat	Carhsp1	S53	1	3	TFSATVR	TFS(1)ATVR	TFS(ph)ATVR	PKA/AKT	1.3	0.17121		Yes
414	IPI00133349	Calcium-regulated heat	Carhsp1	T46	1	10	GNVVPSPLPTR	GNVVPS(0.5)PLPT(0.5)P	(ca)GNVVPS(ph)PLPTR		1.0	0.21559		No
308	IPI00776341	Peripheral plasma mem	Cask	S569	1	3	TQSSCEDLPSTTQPK	T(0.152)QS(0.628)S(0.1)	TQS(ph)SSCEDLPSTTQ	PKA/AKT	0.9	0.13415		No
1359	IPI00776341	Peripheral plasma mem	Cask	S570	1	4	TQSSCEDLPSTTQPK	T(0.004)QS(0.031)S(0.4)	TQSS(ph)SSCEDLPSTTQ	CK2	1.0	0.25016		No
486	IPI00776341	Peripheral plasma mem	Cask	S571	1	5	TQSSCEDLPSTTQPK	T(0.001)QS(0.007)S(0.0)	TQSS(ph)CEDLPSTTQ	CK1	1.0	0.25016		Yes
1360	IPI00776341	Peripheral plasma mem	Cask	T567	1	1	TQSSCEDLPSTTQPK	T(0.22)QS(0.204)S(0.20)	T(ph)QSSCEDLPSTTQ	CK1				No
187	IPI00409176	Calpastatin;Calpain inh	Cast;Cast;Cast;Cast;Cas	S219	1	9	EQKPFPTASPVQSTPSKP	EQKPFPT(0.009)PAS(0.9)	EQKPFPTAS(ph)PVQST	WW GroupIV	1.5	0.045872	Up	Yes
197	IPI00409176	Calpastatin;Calpain inh	Cast;Cast;Cast;Cast;Cas	S226	1	16	EQKPFPTASPVQSTPSKP	EQKPFPT(0.037)PAS(0.2)	EQKPFPTASPVQSTPS	CK1	1.4	0.05451		No
350	IPI00409176	Calpastatin;Calpain inh	Cast;Cast;Cast;Cast;Cas	S442	1	1	SLSESELIGLSADDFDR	S(0.66)LS(0.34)SESELIGE	S(ph)LSESELIGLSADDF	CK2	0.9	0.16792		No
148	IPI00409176	Calpastatin;Calpain inh	Cast;Cast;Cast;Cast;Cas	T479	1	7	SNDSQTTPGETVPR	S(0.002)NDT(0.001)S(0.0)	SNDSQT(ph)PGETVPR		0.8	0.017165	Down	Yes
131	IPI00117829	Caveolin-1	Cav1;Cav	Y14	1	9	YVYSEGHLYTVPIR	YVYSEGHLY(0.931)T(0.1)	YVYSEGHLY(ph)TVPIR	ABL	0.7	0.010847	Down	Yes
1070	IPI00677454	Chromobox homolog 3	Cbx3;Cbx3	S176	1	5	LTWHSCEPEDEAQ	LTWHS(1)CPEDEAQ	LTWHS(ph)CPEDEAQ	CK2				Yes
1033	IPI00677454	Chromobox homolog 3	Cbx3;Cbx3	S93	1	1	SLSDESDDSK	S(0.994)LS(0.006)DSE	S(ph)SLSDESDDSK	AURORA-A	1.1	0.48941		Yes
950	IPI00677454	Chromobox homolog 3	Cbx3;Cbx3	S95	1	3	SLSDESDDSK	S(0.088)LS(0.912)DSE	SLS(ph)SLSDESDDSK	CK2	1.1	0.45682		Yes
1067	IPI00677454	Chromobox homolog 3	Cbx3;Cbx3	S97	1	5	SLSDESDDSKSK	S(0.089)LS(0.415)DS(0.0)	SLS(ph)SLSDESDDSKSK	NEK6				No
1263	IPI00123755	Chromobox protein ho	Cbx5;Hp1a	S92	1	2	KSSFNSADDIK	KS(0.5)S(0.5)FS(0.001)N	KS(ph)SSFNSADDIK	PKA				No
80	IPI00123755	Chromobox protein ho	Cbx5;Hp1a	S93	1	3	KSSFNSADDIK	KS(0.06)S(0.935)FS(0.0)	KSS(ph)SSFNSADDIK	PKA	2.0	0.0002769	Up	Yes
949	IPI00321848	Coiled-coil and C2 dom	Cc2d1a	S435	1	8	LANHDEGSDDEEETPK	LANHDEGS(1)DDEEET	LANHDEGS(ph)DDEE	CK2	1.1	0.45577		Yes
322	IPI00653604	Coiled-coil domain-con	Ccdc102a	S12	1	4	LAESPQLSK	LAES(1)PQLSK	LAES(ph)PQLSK	NEK6	0.9	0.14416		Yes
1297	IPI00319221	Coiled-coil domain-con	Ccdc12	S165	1	21	GQEDSLASAVDATTGQE	GQEDSLASAVDATT(0.00)	GQEDSLASAVDATTGQEA	CD5(ph)D				Yes
824	IPI00133032	Coiled-coil domain-con	Ccdc43;D11ErtD707e;C	T137	1	11	AALLAQYADVTDEEAEI	AALLAQY(0.001)ADVT(0.0)	AALLAQYADVT(ph)DE	CK2	1.0	0.40166		Yes
215	IPI00402914	Coiled-coil domain-con	Ccdc86;Cyclon;D19ErtD	S18	1	11	RLEGLKPLSPENLPPV	RLEGLKPLS(1)PENLPPV	RLEGLKPLS(ph)PENLP	WW GroupIV	1.4	0.064616		Yes
491	IPI00170037	Malcavernin;Cerebral c	Ccm2;Osm;Ccm2;Osm	S393	1	6	GIITDSFGR	GIITDS(1)FGR	GIITDS(ph)FGR		1.0	0.25269		Yes
273	IPI00654283	Putative uncharacterize	Ccnk;Ccnk	S341	1	5	AVVVS1PKKENK	AVVVS(1)PKKENK	AVVVS(ph)PKKENK	ERK/MAPK	1.4	0.10743		Yes
457	IPI00336973	Cyclin-L1;Cyclin Ania-6	Ccnl1;Ania6a;Ccn1	S358	1	5	AEEKSPVSNVVK	AEEKS(0.993)PVS(0.007)	AEEKS(ph)PVSINVK		1.2	0.23732		Yes
450	IPI00308149	Cyclin-Y;Cyclin fold pro	Ccny;Cfp1;Ccny;Cfp1	S324	1	1	SASADNLILPR	S(0.642)AS(0.358)ADNL	S(ph)ASADNLILPR	PKA	1.0	0.23399		No
517	IPI00308149	Cyclin-Y;Cyclin fold pro	Ccny;Cfp1;Ccny;Cfp1	S326	1	3	SASADNLILPR	S(0.112)AS(0.888)ADNL	SAS(ph)ADNLILPR	PKA/AKT	1.0	0.26341		Yes
570	IPI00753875	Putative uncharacterize	Ccny1	S350	1	1	SLSADNFIGIQR	S(0.663)LS(0.337)ADNF	S(ph)SLSADNFIGIQR	NIMA	1.0	0.28563		No
599	IPI00753875	Putative uncharacterize	Ccny1	S352	1	1	SLSADNFIGIQR	S(0.096)LS(0.904)ADNF	SLS(ph)ADNFIGIQR	CHK1	1.0	0.3008		Yes
167	IPI00268688	CD2-associated protein	Cd2ap;Mets1	S458	1	3	SVLDLDAFVAR	S(1)VDLDAFVAR	S(ph)VDLDAFVAR	CAMK2	1.5	0.033948	Up	Yes
700	IPI00110050	PITSLRE serine/threoni	Cdc21i;Cdc21	S47	1	3	RDSLEEGELR	RDS(1)LEEGELR	RDS(ph)LEEGELR	AURORA-A	1.0	0.34994		Yes
1024	IPI00464128	Cell division cycle 2-like	Cdc215;Kiaa1791;Cdc21	T871	1	11	LYSSESRPYTNK	LYSSESRPY(0.001)T(0.1)	LYSSESRPY(ph)TNK	CAMK2	1.1	0.48698		Yes
764	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	S1692	1	15	HSTPSNNSNPGPPSPNS	HSTPSNNSNPGPPS(0.5)	HSTPSNNSNPGPPS(ph)	WW GroupIV	1.0	0.37698		No
765	IPI00114613	Serine/threonine-prote	Cdc42bpb;Kiaa1124	S1695	1	18	HSTPSNNSNPGPPSPNS	HSTPSNNSNPGPPS(0.5)	HSTPSNNSNPGPPS(ph)	WW GroupIV	1.0	0.37698		No
325	IPI00471127	Cdc42 effector protein	Cdc42ep1;Borg5;Cep1	S207	1	4	RSDSLLSFR	RSDS(1)LLSFR	RSDS(ph)LLSFR	CHK1/2	0.9	0.14464		Yes
778	IPI00124906	Cdc42 effector protein	Cdc42ep4;Borg4;Cep4;	S64	1	8	AREADDESLEQASASK	AREADDES(1)LEQASA	AREADDES(ph)LEQA	PLK	1.2	0.38299		Yes
1366	IPI00125505	Cdc42 GTPase-activatin	Cdgap;Kiaa1204	S1092	1	4	HRPSSLNLDSATPIADLFR	HRPS(0.49)S(0.49)LNLD	HRPS(ph)SLNLDSATPI	PKA				No
1370	IPI00125505	Cdc42 GTPase-activatin	Cdgap;Kiaa1204	S1093	1	5	HRPSSLNLDSATPIADLFR	HRPS(0.49)S(0.49)LNLD	HRPS(ph)SLNLDSATPI	CAMK2				No
806	IPI00138190	Cadherin-11;Osteoblas	Cdh11;Cad-11	S714	1	9	PGLRPAAPNSVDVDFDIF	PGLRPAAPNS(1)VDVDFD	PGLRPAAPNS(ph)VDVDFD	INTR	1.0	0.39453		Yes
460	IPI00138190	Cadherin-11;Osteoblas	Cdh11;Cad-11	S788	1	7	LADLYGSKDTFDDDS	LADLY(0.001)GS(0.991)	LADLYGS(ph)KDTFDD	NEK6	1.0	0.2391		Yes
1311	IPI00138190	Cadherin-11;Osteoblas	Cdh11;Cad-11	Y786	1	5	LADLYGSKDTFDDDS	LADLY(0.417)GS(0.417)	LADLY(ph)GSKDTFDD					No
602	IPI00133537	Cyclin-dependent kinas	Cdkn1b;Cdkn1b	S10	1	5	VSNGLPSLER	VSNGLS(0.94)PS(0.06)LE	VSNGLS(ph)PSLER	CK1	1.0	0.30306		Yes
255	IPI00353932	Cerebellar degeneratio	Cdr2l;Gm21	S180	1	4	LHSSLELGRPRLEQENEF	LHS(0.136)S(0.728)S(0.0)	LHSS(ph)SLELGRPRLEC	CK2	0.9	0.098741		No
702	IPI00468999	Phosphatidate cytidilyl	Cds2;Cds2;RP23-33N1S	S32	1	22	EDAPPEDKESSEAKLDG	EDAPPEDKESSEAKLDG	EDAPPEDKESSEAKLD	CK2	1.2	0.35061		Yes
730	IPI00468999	Phosphatidate cytidilyl	Cds2;Cds2;RP23-33N1S	S34	1	9	LDGETASDESER	LDGET(0.004)AS(0.151)	LDGETASDS(ph)ESR	CK1	1.0	0.36183		Yes
722	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	S629	2	9	SQLDDHPESDEENFVDV	S(0.003)QLDDHPES(0.9)	SQLDDHPES(ph)DEEN	CK2	1.2	0.35872		Yes
723	IPI00752710	CCAAT/enhancer-bindin	Cebpz;Cb2;Cebpa-rs1	S641	2	21	SQLDDHPESDEENFVDV	S(0.003)QLDDHPES(0.9)	SQLDDHPES(ph)DEEN	CK2	1.2	0.35872		Yes
252	IPI00667973	Centrosomal protein of	Cep170;Kiaa0470	S1102	1	1	LGEASDSELADADK	LGEAS(0.922)DS(0.078)	LGEAS(ph)DSELADAD	CK2	1.4	0.095599		Yes
397	IPI00667973	Centrosomal protein of	Cep170;Kiaa0470	S1155	1	1	SDSEATISR	S(0.969)DS(0.031)EATIS	S(ph)DSEATISR	CK2	0.9	0.20389		Yes
897	IPI00667973	Centrosomal protein of	Cep170;Kiaa0470	S1157	1	3	SDSEATISR	S(0.102)DS(0.898)EATIS	SDS(ph)EATISR	CAMK2	1.1	0.43846		Yes
220	IPI00222386	Charged multivesicular	Chmp2b	S199	1	4	ATISDEEIER	AT(0.001)S(0.999)DEE	ATIS(ph)DEEIER	CK2	0.8	0.067351		Yes
1026	IPI00785520	CBF1-interacting corep	Cir;Cir;Cir	S202	1	14	NLTANDPQSDYVASDCE	NLTANDPQSDYVASDCE	NLTANDPQSDYVAS(ph)	CK2	1.1	0.48702		Yes
110	IPI00672213	CLIP-associating protei	Clasp1;Kiaa0622;Clasp	S795	1	5	VLSTDTLEAAVADALK	VLST(0.05)T(0.05)S(0.87)	VLSTS(ph)TDLEAAVAD	NEK6	0.7	0.0002348	Down	Yes
413	IPI00672213	CLIP-associating protei	Clasp1;Kiaa0622;Clasp	S600	1	3	SRSIDIVNAAASAK	S(0.097)RS(0.903)DIDV	SRS(ph)DIDVNAASAK	CHK1/2	1.0	0.21373		Yes
775	IPI00467854	CAP-Gly domain-conta	Clip2;Clyn2;Kiaa0291;C	S924	1	10	VLLLEANRHSPPGER	VLLLEANRHS(1)PGPER	VLLLEANRHS(ph)PGPE	PKA	1.2	0.38159		Yes
440	IPI00124248	Chloride channel regul	Clns1a;Icln	S100	1	10	LGEESKEPLSDEEEDND	LGEES(0.003)KEPLS(0.9)	LGEESKEPLS(ph)DEEEDND	VPEIFEFR	1.0	0.22986		Yes
444	IPI00915083	Putative uncharacterize	Cnot2;Cnot2;Cnot2;Cn	S175	1	11	TNSMSSGLGSPNRR	TNSMSSGLGS(1)PNRR	TNSMSSGLGS(ph)PN	CDK2	1.2	0.2312		Yes
951	IPI00277028	Negative elongation fac	Cobra1;Nelfb;MNCB-5	S557	1	3	KPSPTQAAETPALDPLP	KPS(0.5)PT(0.5)QAAETF	KPS(ph)PTQAAETPAL	PKA	1.1	0.45716		No
952	IPI00277028	Negative elongation fac	Cobra1;Nelfb;MNCB-5	T559	1	5	KPSPTQAAETPALDPLP	KPS(0.5)PT(0.5)QAAETF	KPS(ph)PTQAAETPAL	FHA KAPP	1.0	0.45716		No
1312	IPI00132076	Catechol O-methyltran	Comt;Comt1;Comt;Cor	S260	1	8	AVYQGGPSSPVKS	AVY(0.306)QGGPS(0.30)	(ca)AVY(ph)QGGPSSPVKS					No
496	IPI00132076	Catechol O-methyltran	Comt;Comt1;Comt;Cor	S261	1	9	AVYQGGPSSPVKS	AVYQGGPS(0.005)S(0.9)	AVYQGGPS(ph)PVKS	Polo box	1.0	0.25477		Yes



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
1316	IPI00132076	Catechol O-methyltran	Comt;Comt1;Comt;Cor	S265	1	13	AVYQGGSSPVKS	AVY(0.001)QGGPS(0.08	(ca)AVYQGGSS(ph)PK1	CK1			No	No
1319	IPI00132076	Catechol O-methyltran	Comt;Comt1;Comt;Cor	Y255	1	3	AVYQGGSSPVKS	AVY(0.306)QGGPS(0.30	(ca)AVY(ph)QGGSSP	ABL			No	No
942	IPI00649269	Cell division cycle 2-rel	Crkrs;Crk7;Kiaa0904;Cr	S1079	1	16	KETTSGTAEPRKNNKSPA	KETTSGT(0.001)AEPVK	KETTSGTAEPRKNNKSPA	PAP/PAPVK	1.1	0.45422	Yes	Yes
804	IPI00330591	DNA-binding protein A	Csda;Msy4;Ybx3;Csda;	S328	1	1	SRPLNAVSDQDGK	S(1)RPLNAVSDQDGK	S(ph)RPLNAVSDQDGK	PKA	1.1	0.39396	Yes	Yes
795	IPI00116929	Cleavage stimulation fa	Cstf3	S691	1	6	RPNEDSDEEEKGAVVP	RPNEDS(1)DEEEKGAV	RPNEDS(ph)DEEEKGAV	PPVHDIYR	1.0	0.38919	Yes	Yes
995	IPI00116929	Cleavage stimulation fa	Cstf3	Y708	1	23	RPNEDSDEEEKGAVVP	RPNEDS(0.418)DEEEK	RPNEDSDEEEKGAVVP	PPVHDIYR	1.1	0.47517	Yes	Yes
664	IPI00112963	Catenin alpha-1;102 kD	Ctnna1;Catna1	S641	1	8	TPPEELDDSFETEDFV	TPPEELDDSFETEDF	TPPEELDDSFETEDF	CK2	1.0	0.33602	Yes	Yes
618	IPI00112963	Catenin alpha-1;102 kD	Ctnna1;Catna1	T634	1	1	TPPEELDDSFETEDFV	T(0.98)PEELDDSF(0.02)D	T(ph)PEELDDSFETEDF	CK2	1.0	0.30956	Yes	Yes
1328	IPI00112963	Catenin alpha-1;102 kD	Ctnna1;Catna1	T645	1	12	TPPEELDDSFETEDFV	T(0.316)PEELDDSF(0.34	TPPEELDDSFETEDFV				No	No
392	IPI00125899	Catenin beta-1;Beta-ca	Ctnnb1;Catnb;Ctnnb1	S552	1	3	RTSMGGTQQQVFEGVR	RT(0.096)S(0.904)MGG	RTS(ph)MGGTQQQVF	AURORA-A	1.3	0.19966	Yes	Yes
1334	IPI00125899	Catenin beta-1;Beta-ca	Ctnnb1;Catnb;Ctnnb1	T551	1	2	RTSMGGTQQQVFEGVR	RT(0.431)S(0.138)MGG	RT(ph)SMGGTQQQVF	PKA			No	No
1337	IPI00125899	Catenin beta-1;Beta-ca	Ctnnb1;Catnb;Ctnnb1	T556	1	7	RTSMGGTQQQVFEGVR	RT(0.431)S(0.138)MGG	RT(ph)SMGGTQQQVFEGVR				No	No
189	IPI00752108	Catenin delta-1;p120 c	Ctnnd1;Catsn;Kiaa0384	S230	1	15	HYEDGYPGGSDNYGSL	HYEDGYPGGSDNYGSL(0.01	(ca)HYEDGYPGGSDNYGSL	(ph)LSR	0.8	0.047488	Down	Yes
1351	IPI00752108	Catenin delta-1;p120 c	Ctnnd1;Catsn;Kiaa0384	S232	1	17	HYEDGYPGGSDNYGSL	HYEDGYPGGSDNYGSL(0.001)D	HYEDGYPGGSDNYGSL	(ph)LSR			No	No
107	IPI00752108	Catenin delta-1;p120 c	Ctnnd1;Catsn;Kiaa0384	S320	1	3	LRSYEDMIGEEVPPDQY	LRSY(0.5)Y(0.5)EDMIGEE	LRYS(ph)YEDMIGEEVPP	PKA/AKT	0.7	0.0019583	Down	No
1353	IPI00752108	Catenin delta-1;p120 c	Ctnnd1;Catsn;Kiaa0384	Y228	1	13	HYEDGYPGGSDNYGSL	HYEDGYPGGSDNYGSL(0.49	HYEDGYPGGSDNYGSL	(ph)ALK			No	No
108	IPI00752108	Catenin delta-1;p120 c	Ctnnd1;Catsn;Kiaa0384	Y321	1	4	LRSYEDMIGEEVPPDQY	LRSY(0.5)Y(0.5)EDMIGEE	LRYS(ph)YEDMIGEEVPP	ALK	0.7	0.0019583	Down	No
1020	IPI00120919	RNA polymerase-associ	Ctr9;Kiaa0155;Sh2bp1;	T925	1	13	KGGEFDEFVNDTDDDD	KGGEFDEFVNDT(1)DD	KGGEFDEFVNDT(ph)	FHA1 Rad53p	1.1	0.48584	Yes	Yes
186	IPI00118143	Src substrate cortactin	Ctnn;Ems1;Ctnn;mCG	S407	1	9	KQTPPASPSQPPIEDRPP	KQT(0.166)PPAS(0.166	KQTPPASPS(ph)PQPIEDR	PPSSPIEDAAPFK	0.8	0.04546	Down	No
1139	IPI00118143	Src substrate cortactin	Ctnn;Ems1;Ctnn;mCG	S417	1	19	KQTPPASPSQPPIEDRPP	KQT(0.001)PPAS(0.005	KQTPPASPSQPPIEDRPP	CAMK2			No	No
1141	IPI00118143	Src substrate cortactin	Ctnn;Ems1;Ctnn;mCG	S418	1	20	KQTPPASPSQPPIEDRPP	KQT(0.001)PPAS(0.005	KQTPPASPSQPPIEDRPP	WW GroupIV			No	No
169	IPI00118143	Src substrate cortactin	Ctnn;Ems1;Ctnn;mCG	T401	1	3	KQTPPASPSQPPIEDRPP	KQT(0.955)PPAS(0.043	KQT(ph)PPASPSQPPIE	FHA KAPP	0.8	0.035312	Down	Yes
774	IPI00854018	CUG-BP- and ETR-3-li	Cugbp2;Celf2;Napor;Cu	S27	1	9	ETATELGSPPSNGTANK	ETATELGS(0.026)G(S0.77	ETATELGS(ph)PPSNG	NEK6	1.2	0.38131	Yes	Yes
1317	IPI00854018	CUG-BP- and ETR-3-li	Cugbp2;Celf2;Napor;Cu	S30	1	12	ETATELGSPPSNGTANK	ET(0.018)AT(0.018)ELS	ETATELGS(ph)PPSNG	CK1			No	No
133	IPI00127811	Fractalkine;C-X3-C mot	Cx3cl1;Cx3c;Fkn;Scyd1;	S259	1	1	SLGSEIINPVHTDNQFERS	(0.599)LGS(0.401)EINP	S(ph)LGSSEIINPVHTDN	PLK1	0.7	0.011573	Down	No
124	IPI00127811	Fractalkine;C-X3-C mot	Cx3cl1;Cx3c;Fkn;Scyd1;	S262	1	4	SLGSEIINPVHTDNQFERS	(0.15)LGS(0.85)EINP	SLGS(ph)EINPVHTDN	CK1	0.7	0.0082169	Down	Yes
35	IPI00224867	Novel protein;Novel p	D930048N14Rik;RP23	T15	1	3	SLTSSADSPDEALER	S(0.188)LT(0.792)CS(0	(ca)SLT(ph)CSSADSP	PKA/AKT	4.1	1.364-14	Up	Yes
402	IPI00128975	Death-associated prote	Dap	S49	1	9	DKDDQEWESTSPPKPTV	DKDDQEWES(0.797)T(C	DKDDQEWES(ph)TSPPK	TVFISGVIAR	0.9	0.20696	Yes	Yes
964	IPI00128975	Death-associated prote	Dap	S51	1	11	DKDDQEWESTSPPKPTV	DKDDQEWES(0.083)T(C	DKDDQEWESTS(ph)P	CDK2	1.1	0.46046	Yes	Yes
309	IPI00128975	Death-associated prote	Dap	T50	1	10	DKDDQEWESTSPPKPTV	DKDDQEWES(0.054)T(C	DKDDQEWEST(ph)SPPK	TVFISGVIAR	0.9	0.13472	No	No
8	IPI00128975	Death-associated prote	Dap	T56	1	2	PTVFISGVIARGDK	PT(0.983)VFIS(0.017)G	(ca)PT(ph)VFISGVIAR	AURORA	21.0	4.26E-65	Up	Yes
596	IPI00135475	Drebrin;Developmenta	Dbn1;Drba;Dbn1;Drba;	S142	1	2	LSSPVLHR	LS(0.003)S(0.997)PVLH	LSS(ph)PVLHR	CHK1/2	1.0	0.29703	Yes	Yes
126	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S305	1	4	SKSPASTSSVNGTPGSQ	S(0.839)KS(0.052)PAS(0	(ca)S(ph)KSPASTSSVN	PKA	0.7	0.0086256	Down	Yes
1310	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S307	1	4	RSKSPASTSSVNGTPGS	RS(0.038)KS(0.459)PAS	RSKS(ph)PASTSSVNGT	CAMK2			No	No
245	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S32	1	6	VNGLPSPTSAHCSFYR	VNGLPS(0.957)PT(0.02	VNGLPS(ph)PTSAHCS	GSK3	0.9	0.088939	Yes	Yes
160	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S36	2	10	VNGLPSPTSAHCSFYR	VNGLPS(0.267)PT(0.62	VNGLPSPT(ph)HS(ph)	GSK3	0.8	0.029142	Down	No
1314	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S40	2	14	VNGLPSPTSAHCSFYR	VNGLPS(0.226)PT(0.22	VNGLPSPTS(ph)AHC	CK1	1.0	0.22	No	No
317	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	T34	2	8	VNGLPSPTSAHCSFYR	VNGLPS(0.267)PT(0.62	VNGLPSPT(ph)HS(ph)	FHA KAPP	0.9	0.14251	No	No
202	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	Y42	2	16	VNGLPSPTSAHCSFYR	VNGLPS(0.942)PT(0.18	VNGLPS(ph)PTSAHCSFY	(ph)R	0.8	0.055917	No	No
259	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S330	2	1	SPSPSPTSPGSLR	S(0.588)PS(0.411)PS(0	S(ph)SPSPSPT(ph)SPGS	CK1	1.0	0.099837	Yes	Yes
1330	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S334	1	5	SPSPSPTSPGSLR	S(0.002)PS(0.008)PS(0	SPSPS(ph)PTSPGSLR	CK1			No	No
289	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S337	1	5	SPSPSPTSPGSLR	SPSPS(0.001)PT(0.009)	SPSPSPTS(ph)PGSLR	WW GroupIV	0.9	0.11851	Yes	Yes
443	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	S340	1	11	SPSPSPTSPGSLR	S(0.001)PS(0.001)PS(0	(ca)SPSPSPTSPGS(ph)	CK1	1.0	0.23093	Yes	Yes
112	IPI00468380	Serine/threonine-prote	Dck1;Dcamk1;Dckl;Dc	T336	1	7	SPSPSPTSPGSLR	SPSPSPT(0.5)S(0.5)PS	SPSPSPT(ph)SPGSLR		1.7	0.0023412	Down	No
574	IPI00896604	Probable ATP-depende	Ddx10	T587	1	14	LASGDGDEEQDEETE	LASGDGDEEQDEETE(1)E	LASGDGDEEQDEETE(ph	CK2	0.2	0.28731	Yes	Yes
707	IPI00120691	Nucleolar RNA helicase	Ddx21;Ddx21;mCG	S118	1	8	EITEEPEEEADMPKPK	EITEEPEE(1)EEADMPK	EITEEPEE(ph)EEEADM	CK2	1.2	0.35397	Yes	Yes
770	IPI00113576	ATP-dependent RNA he	Ddx24;Ddx24	S126	1	5	AQAVSEEEEEEGSSSP	AQAVS(1)EEEEEEEGSS	AQAVS(ph)EEEEEEEG	CK2	1.2	0.37858	Yes	Yes
745	IPI00329839	ATP-dependent RNA he	Ddx42;Ddx42	S185	1	23	YMAENPTAGVVQEEED	YMAENPTAGVVQEEED	YMAENPTAGVVQEEED	NLEYS(ph)DGNPIAPS	1.2	0.37075	Yes	Yes
1404	IPI00329839	ATP-dependent RNA he	Ddx42;Ddx42	S193	1	31	YMAENPTAGVVQEEED	Y(0.078)MAENPT(0.027	YMAENPTAGVVQEEED	NLEYS(ph)DGNPIAPS	1.2	0.37075	Yes	Yes
587	IPI00474721	Putative uncharacteriz	Ddx54;Ddx54	S774	1	6	IDDRDS1JEEEGPSNQR	IDDRDS(1)JEEEGPSNQR	IDDRDS(ph)JEEEGPSN	PKA	1.2	0.29263	Yes	Yes
759	IPI00339468	ATP-dependent RNA he	Dhx9;Ddx9	S137	1	16	AEAENNSGVESGYGSP	AEAENNSGVESGYGSL(1	AEAENNSGVESGYGSL	CK1	1.2	0.37521	Yes	Yes
175	IPI00331314	Disco-interacting prote	Dip2b;Kiaa1463	Y97	1	1	YRSDIHTAEVQAALAK	Y(0.877)RS(0.123)DIHT	Y(ph)RSDIHTAEVQAAL	SRC	0.8	0.04027	Down	Yes
915	IPI00113635	H/ACA ribonucleoprote	Dck1;Dck1;BC068171	S481	1	5	TVLESGGTGDGDNDDTT	T(0.009)VL(0.99)GGE	TVLES(ph)GGTGDGDD	CK2	1.1	0.44543	Yes	Yes
799	IPI00113635	H/ACA ribonucleoprote	Dck1;Dck1;BC068171	S508	1	8	VKVVEEMSE	VKVVEEMS(1)E	VKVVEEMS(ph)E		1.0	0.39186	Yes	Yes
632	IPI00113635	H/ACA ribonucleoprote	Dck1;Dck1;BC068171	T485	1	9	TVLESGGTGDGDNDDTT	T(0.032)VL(0.089)GG	TVLESGGT(ph)GGDNDD	TK	1.0	0.31639	No	No
1063	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	S694	1	5	NKDQSEQETSADQHQV	NKDQS(0.333)EQET(0.3	NKDQS(ph)EQETSADQ	CK2			No	No
1064	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	S699	1	10	NKDQSEQETSADQHQV	NKDQS(0.052)EQET(0.4	NKDQSEQET(ph)SDAQ	HVTSNASDESSEYR			No	No
1068	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	S707	1	18	NKDQSEQETSADQHQV	NKDQS(0.004)EQET(0.0	NKDQSEQETSADQHQV	(ph)NASDESSEYR			No	No
771	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	S710	1	21	NKDQSEQETSADQHQV	NKDQSEQETSADQHQV	NKDQSEQETSADQHQV	CK2	1.0	0.37939	No	No
1071	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	T698	1	9	NKDQSEQETSADQHQV	NKDQS(0.052)EQET(0.4	NKDQSEQET(ph)SDAQ	FHA KAPP			No	No
1073	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlgl1;Dlgh1	T706	1	17	NKDQSEQETSADQHQV	NKDQSEQETSADQHQV	NKDQSEQETSADQHQV	FHA KAPP			No	No
1354	IPI00875866	Dnal (Hsp40) homolog	Dnajc5;RP23-33L3.3-00	S12	1	5	SLSTSGESLYHVLGLDKN	S(0.164)LS(0.148)T(0.1	SLSTS(ph)GESLYHVLG	NEK6			No	No
936	IPI00875866	Dnal (Hsp40) homolog	Dnajc5;RP23-33L3.3-00	S8	1	5	SLSTSGESLYHVLGLDKN	S(0.613)LS(0.356)T(0.0	(ca)S(ph)LSTSGESLYH	CAMK2	1.1	0.45117	Yes	Yes
400	IPI00469323	DNA (cytosine-5)-meth	Dnmt1;Dnmt;Met1;Uir	S724	1	17	EADDDDEADDVSEMP	EADDDDEADDVSEMP	EADDDDEADDVSEMP	CDK2	0.9	0.20554	No	No
370	IPI00816914	Dedicator of cytokines	Dock7;Gm430;Kiaa177	S1422	1	3	SPSGSAFGSQENLR	S(0.111)PS(0.82)GS(0.0	SPS(ph)SGSAFGSQENL	PKA/AKT	0.9	0.18208	Yes	Yes
1061	IPI00816914	Dedicator of cytokines	Dock7;Gm430;Kiaa177	S896	1	1	SLSNSNPDISGTPSPDDI	S(0.467)LS(0.267)NS(0	S(ph)SLSNSNPDISGTP	PKA/AKT			No	No



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
685	IPI00330289	Erythrocyte protein ba	Epb4.112;Epb4112;Epb4	S38	1	12	AKEVENEQTPVSEPEEEK	AKEVENEQ(T.0.04)PVSI	AKEVENEQTPVSI(ph)E	CK2	1.0	0.34423	Yes	Yes
127	IPI00330289	Erythrocyte protein ba	Epb4.112;Epb4112;Epb4	S86	1	1	SYNLVVAK	S(0.738)Y(0.262)NLVVA	S(ph)YNLVAK	PKD	0.7	0.0099869	Down	No
1405	IPI00229295	Band 4.1-like protein 3	Epb413;Dal1;Epb4.113	S790	1	8	VESTSVGSIISPGGAK	VESTSVGS(0.5)S(0.5)P	VESTSVGSIISPGGAK	CK1	1.1	0.073783	Yes	Yes
228	IPI00229295	Band 4.1-like protein 3	Epb413;Dal1;Epb4.113	S792	1	10	VESTSVGSIISPGGAK	VESTSVGS(0.019)S(0.9)	VESTSVGSIISPGGAK	CK1	1.4	0.073783	Yes	Yes
384	IPI00875692	Excision repair cross-co	Erc5;Erc5;Erc5;Xpg	S384	1	12	NSGATADAGSISPR	NSGATADAGSIS(1)PR	NSGATADAGSIS(ph)P	CDK1	1.3	0.19444	Yes	Yes
851	IPI00154109	Protein FAM122A	Fam122a	S32	1	1	SNSAPLIHGLSDSPVQ	S(0.531)NS(0.449)APLI	S(ph)NSAPLIHGLSDSP	NIMA	1.1	0.41723	Yes	No
955	IPI00154109	Protein FAM122A	Fam122a	S34	1	3	SNSAPLIHGLSDSPVQ	S(0.25)NS(0.673)APLI	SNS(ph)APLIHGLSDSP	14-3-3 binding	1.1	0.45792	No	No
968	IPI00468516	Protein FAM21;Protein	Fam21;D6Wsu116e;Kia	S388	1	15	ARPAQAPVSEELPPSPK	ARPAQAPVSEELPPS(1)P	ARPAQAPVSEELPPSP	WW GroupIV	1.1	0.46233	Yes	Yes
297	IPI00223670	Protein FAM40A;Prote	Fam40a;Kiaa1761;Fam	S335	1	3	AASPPASASDLIEQ	AAS(0.976)PPAS(0.02)A	AAS(ph)PPASASDLIEQ	CAMK2	0.9	0.12522	Yes	Yes
461	IPI00266942	Extended synaptotagm	Fam62b;D12Erd551e;	S662	1	3	SSSLLASPSHIAAK	S(0.023)S(0.018)S(0.94	SSS(ph)SLLASPSHIAAK	CHK1/2	1.2	0.23969	Yes	Yes
1179	IPI00266942	Extended synaptotagm	Fam62b;D12Erd551e;	S679	2	5	EPTPSIASDISLIATQELR	EPT(0.312)PS(0.447)IAS	EPTPS(ph)IASDISLIATQELR		1.1	0.35766	No	No
716	IPI00266942	Extended synaptotagm	Fam62b;D12Erd551e;	S682	2	8	EPTPSIASDISLIATQELR	EPT(0.036)PS(0.036)IAS	EPTPSIAS(ph)DISLIATQELR	CK1	1.2	0.35766	Yes	Yes
717	IPI00266942	Extended synaptotagm	Fam62b;D12Erd551e;	S685	2	11	EPTPSIASDISLIATQELR	EPT(0.036)PS(0.036)IAS	EPTPSIAS(ph)DISLIATQELR	PLK1	1.2	0.35766	Yes	Yes
754	IPI00874398	Protein FAM65A	Fam65a;Kiaa1930	S417	1	7	FSTYSQSPPTPSLR	FS(0.005)T(0.005)Y(0.0	FSTYSQSPPTPSLR	CK1	1.0	0.37362	Yes	Yes
1245	IPI00344835	Protein FAM65C	Fam65c	S635	1	7	LASPNLSR	LASPNLS(1)R	LASPNLS(ph)R	CK1	1.1	0.39815	Yes	Yes
294	IPI00678532	Regulator of microtubu	Fam82a2;Fam82c;1200	S46	1	3	SHSLPNSLDYQAQASER	S(0.117)HS(0.882)LPNS	SHS(ph)PNSLDYQAQASER	14-3-3 binding	1.3	0.12303	Yes	Yes
239	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1	S373	1	1	SLVSQPTAPNSEVPK	S(0.981)LV(0.019)QPT	S(ph)LVSQPTAPNSEV	CK1	0.9	0.083133	Yes	Yes
282	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1	S427	1	11	ACTLELGHQSPALPK	ACTLELGHQSP(1)PALPK	ACTLELGHQSP(ph)PALPK		0.9	0.11227	Yes	Yes
816	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1	S892	1	12	SPDEATAADQESDDL	SPDEATAADQES(1)EDD	SPDEATAADQES(ph)EDD	JLSDSASR	1.0	0.39815	Yes	Yes
990	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1;Farp1	S23	1	10	LGAPENSGISTLER	LGAPENS(0.006)GIS(0.8	LGAPENSGIS(ph)TLER	CK2	1.1	0.47137	Yes	Yes
822	IPI00757373	Farp1 protein;Farp1 pr	Farp1;Farp1;Farp1	T24	1	11	LGAPENSGISTLER	LGAPENSGIS(0.046)T(0	LGAPENSGIST(ph)LER		1.0	0.4006	Yes	Yes
86	IPI00623114	Cadherin FAT1 isoform	Fat1;Fat1;Fath	S4483	1	7	DMPAAGSLGSSSR	DMPAAGS(0.997)LGS(0)	DMPAAGS(ph)LGS	GSK3	0.6	0.0004696	Down	Yes
1291	IPI00623114	Cadherin FAT1 isoform	Fat1;Fat1;Fath	S4486	3	10	DMPAAGSLGSSSR	DMPAAGS(0.75)LGS(0)	DMPAAGS(ph)LGS	CK1	1.1	0.4006	No	No
1296	IPI00623114	Cadherin FAT1 isoform	Fat1;Fat1;Fath	S4487	3	11	DMPAAGSLGSSSR	DMPAAGS(0.75)LGS(0)	DMPAAGS(ph)LGS	NEK6	1.1	0.4006	No	No
1301	IPI00623114	Cadherin FAT1 isoform	Fat1;Fat1;Fath	S4488	3	12	DMPAAGSLGSSSR	DMPAAGS(0.75)LGS(0)	DMPAAGS(ph)LGS	S(ph)SR	1.1	0.4006	No	No
767	IPI00228716	Protocadherin Fat 4;FA	Fat4;Fatj	S4878	1	7	LSQVNESDADDEDNYGA	LSQVNES(1)DADDEDNY	LSQVNES(ph)DADDEDNY	GAR	1.0	0.37784	Yes	Yes
419	IPI00378206	F-box/WD repeat-conta	Fbxw8;Fbxw8	S84	1	1	SRSPPDRDATEPEPLVDC	S(0.536)RS(0.459)PPDR	S(ph)RSPPDRDATEPEPLVDC	CK1	1.3	0.21729	Yes	Yes
927	IPI00378206	F-box/WD repeat-conta	Fbxw8;Fbxw8	S86	1	3	SRSPPDRDATEPEPLVDC	S(0.183)RS(0.817)PPDR	SRS(ph)RSPPDRDATEPEPLVDC	14-3-3 binding	1.1	0.44798	Yes	Yes
502	IPI00223046	FH1/FH2 domain-conta	Fhod1;Fhos1	S370	1	1	SLEGGGCPVR	S(1)LEGGGCPVR	S(ph)LEGGGCPVR	AURORA	1.0	0.25805	Yes	Yes
813	IPI00881462	Pre-mRNA 3'-end-proce	Fip11;Fip11;Fip11	S493	1	3	DHSPTPSVFNSEDER	DHS(0.984)PT(0.008)PS	DHS(ph)PTPSVFNSEDER	PKA/AKT	1.1	0.39743	Yes	Yes
832	IPI00881462	Pre-mRNA 3'-end-proce	Fip11;Fip11;Fip11	T495	1	7	ERDHSPTPSVFNSEDER	ERDHS(0.163)PT(0.827	ERDHSPT(ph)PSVFNSEDER		1.1	0.40595	Yes	Yes
1023	IPI00458068	FK506-binding protein	Fkbp15;Fkbp133;Kiaa0	S1091	1	3	RLSLTPDEPEKPPALPD	RLS(0.982)LT(0.018)PD	RLS(ph)LTPEPEKPPALPD	PKA/AKT	1.1	0.48689	Yes	Yes
842	IPI00921658	Filamin, alpha;Filamin	Flna;RP23-436K3.1-003	S2152	1	4	RAPSVANIGSHCDLSLK	RAPS(1)VANIGSHCDLSLK	RAPS(ph)VANIGSHCDLSLK	PKA/AKT	1.1	0.41011	Yes	Yes
63	IPI00664670	Filamin-C;Gamma-filam	Flncc;Abpl;Fln2;Flncc;Abp	S2234	1	3	LGSFGSITR	LGS(1)FGSITR	LGS(ph)FGSITR	PKA/AKT	2.3	6.094E-06	Up	Yes
869	IPI00345373	Formin-like protein 2;P	Fmnl2;Kiaa1902;Man;F	S687	2	6	ITQKASSKVTLLEANR	IT(0.983)QKAS(0.508)S	(ca)IT(ph)QKAS(ph)SK	CK1	1.1	0.4233	No	No
999	IPI00345373	Formin-like protein 2;P	Fmnl2;Kiaa1902;Man;F	S688	2	7	ITQKASSKVTLLEANR	IT(0.984)QKAS(0.128)S	(ca)IT(ph)QKAS(ph)KVTLEANR		1.1	0.4772	Yes	Yes
933	IPI00345373	Formin-like protein 2;P	Fmnl2;Kiaa1902;Man;F	T683	2	2	ITQKASSKVTLLEANR	IT(0.984)QKAS(0.128)S	(ca)IT(ph)QKAS(ph)K	FHA KAPP	1.1	0.45013	Yes	Yes
456	IPI00876259	Formin binding protein	Fnbp1;RP23-24313.2-00	S295	1	3	TVSDNLSLSSK	T(0.008)VS(0.992)DNSL	TVS(ph)DNSLSSK	PKA	1.0	0.23668	Yes	Yes
1207	IPI00876259	Formin binding protein	Fnbp1;RP23-24313.2-00	S298	1	6	TVSDNLSLSSK	T(0.09)VS(0.431)DNSL	TVS(ph)DNSLSSK	PLK1	1.0	0.23668	No	No
503	IPI00761177	Formin-binding protein	Fnbp1;Toca1;Fnbp1;T	S295	1	3	TISDGTISAAK	T(0.027)IS(0.949)DGT	TIS(ph)DGTISAAK	PKD	2.5	8.11E-07	Up	Yes
194	IPI00761177	Formin-binding protein	Fnbp1;Toca1;Fnbp1;T	S501	1	15	HSSDINHVLTVQGRESPE	HS(0.001)DINHVLTV(0.0	HSSDINHVLTVQGRESPE	PKA	0.8	0.052042	Yes	Yes
150	IPI00761177	Formin-binding protein	Fnbp1;Toca1;Fnbp1;T	T496	1	10	HSSDINHVLTVQGRESPE	HS(0.002)S(0.008)DINH	HSSDINHVLTV(ph)QGRESPE	YDDANQEV	0.8	0.018956	Down	No
522	IPI00229601	Fibronectin type III don	Fndc3b;Fad104;Kiaa41	S208	1	3	LNSPPTIYK	LNS(0.993)PPS(0.003)T	LNS(ph)PPPTIYK	CAMK2	1.0	0.26587	Yes	Yes
518	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	S292	1	25	LEQLGKDPVSGSGAGNT	LEQLGKDPVSGSGAGNT	LEQLGKDPVSGSGAGNT	F box bTrCP	1.0	0.26353	Yes	No
1229	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	S327	1	3	LTSTSTSDTQNNINSAQR	LT(0.484)S(0.484)T(0.0	LT(ph)STSTSDTQNNINSAQR	PKA/AKT	1.0	0.26353	Yes	No
1231	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	S329	1	5	LTSTSTSDTQNNINSAQR	LT(0.23)S(0.23)T(0.23)	LT(ph)STSTSDTQNNINSAQR		1.0	0.26353	No	No
1233	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	S331	1	7	LTSTSTSDTQNNINSAQR	LT(0.18)S(0.18)T(0.18)	LT(ph)STSTSDTQNNINSAQR	CK1	1.0	0.26353	No	No
1237	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	T326	1	2	LTSTSTSDTQNNINSAQR	LT(0.484)S(0.484)T(0.0	LT(ph)STSTSDTQNNINSAQR	PKA	1.0	0.26353	No	No
1240	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	T328	1	4	LTSTSTSDTQNNINSAQR	LT(0.027)S(0.473)T(0.4	LTS(ph)STSTSDTQNNINSAQR	NEK6	1.0	0.26353	No	No
1244	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	T330	1	6	LTSTSTSDTQNNINSAQR	LT(0.18)S(0.18)T(0.18)	LT(ph)STSTSDTQNNINSAQR	CK1	1.0	0.26353	No	No
1247	IPI00224112	Fibroblast growth fact	Frs2;Frs2a	T333	1	9	LTSTSTSDTQNNINSAQR	LT(0.117)S(0.117)T(0.1	LTSTSTSDT(ph)QNNINSAQR	FHA2 Rad53p	1.0	0.26353	No	No
763	IPI00119124	FUN14 domain-contain	Fundc1	S13	1	9	NPPPPQDYSDDESVEYL	NPPPPQDY(0.096)ES(0.9	NPPPPQDYES(ph)DDES	CK2	1.2	0.37664	Yes	Yes
1200	IPI00119124	FUN14 domain-contain	Fundc1	S17	1	13	NPPPPQDYSDDESVEYL	NPPPPQDY(0.073)ES(0.0	NPPPPQDYSDDES(ph)PLK1		1.0	0.37664	Yes	Yes
1208	IPI00119124	FUN14 domain-contain	Fundc1	T24	1	20	NPPPPQDYSDDESVEYL	NPPPPQDY(0.073)ES(0.0	NPPPPQDYSDDES(ph)NEK6		1.0	0.37664	No	No
615	IPI00119124	FUN14 domain-contain	Fundc1	Y11	1	7	NPPPPQDYSDDESVEYL	NPPPPQDY(0.5)ES(0.5)D	NPPPPQDY(ph)ESDDESVEYL	DLTEYAR	1.2	0.30751	No	No
1213	IPI00119124	FUN14 domain-contain	Fundc1	Y18	1	14	NPPPPQDYSDDESVEYL	NPPPPQDY(0.14)ES(0.22	NPPPPQDYES(ph)DDES	EGFR	1.0	0.30751	No	No
1217	IPI00119124	FUN14 domain-contain	Fundc1	Y26	1	22	NPPPPQDYSDDESVEYL	NPPPPQDY(0.073)ES(0.0	NPPPPQDYSDDES(ph)YEVLDL	TEYAR	1.0	0.30751	No	No
1190	IPI00126389	Fragile X mental retard	Fxr2;Fxr2h;RP23-4221	T600	1	1	TDGSIQDRQPVTVADYI	T(0.498)DGS(0.413)S(0.0	T(ph)DGSIQDRQPVTVADYI	FHA KAPP	1.0	0.30751	No	No
1193	IPI00126389	Fragile X mental retard	Fxr2;Fxr2h;RP23-4221	S455	1	16	TGGPAYGSSDPSTASE	TGGPAYGSP(0.002)S(0.	TGGPAYGSSDPST(ph)CK2		1.0	0.30336	No	No
604	IPI00130095	Ras GTPase-activating	G3bp1;G3bp;G3bp1;G	S149	1	17	YQDEVFGGVTPEQEEIS	YQDEVFGGVTPEQEEIS	YQDEVFGGVTPEQEEIS	CK2	1.0	0.30336	Yes	Yes
874	IPI00130095	Ras GTPase-activating	G3bp1;G3bp;G3bp1;G	S229	1	1	STSPAPADVAPAQEDLR	S(0.526)T(0.237)S(0.23	S(ph)TSPAPADVAPAQEDLR		1.1	0.42707	No	No
1183	IPI00130095	Ras GTPase-activating	G3bp1;G3bp;G3bp1;G	S231	1	3	STSPAPADVAPAQEDLR	S(0.147)T(0.113)S(0.74	STS(ph)PAPADVAPAQEDLR	PKD	1.0	0.42707	No	No
853	IPI00124245	Ras GTPase-activating	G3bp2;G3bp2	S225	1	1	SATPPPAEPASLPQEPK	S(0.646)AT(0.354)PPPA	S(ph)ATPPPAEPASLPQEPK		1.1	0.41804	No	No
527	IPI00874964	Glyceraldehyde-3-phos	Gapdh;Gapd;Gapdh;AK	T186	1	22	VHIDNFVIGVEGLMTTVAH	VHIDNFVIGVEGLMTTVAH	VHIDNFVIGVEGLMTTVAH	ITAT(ph)QK	1.0	0.26732	Yes	Yes
151	IPI00460042	GTPase-activating Rap	Garn1;Kiaa0884;Tulip1	S796	1	3	SSSSTDILEPFTVER	S(0.106)S(0.074)S(0.67	SSS(ph)STDILEPFTVER	PKA/AKT	0.8	0.019035	Down	No
1326	IPI00869450	Growth arrest specific	Gas7;mcG 133182;Ga	S60	1	22	YYVNTTNETTWERPSS	YYVNTTNETTWERPSS	YYVNTTNETTWERPSS	CK1	1.0	0.019035	No	No

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
113	IPI00869450	Growth arrest specific	Gas7;mcCG_133182;Gas	S62	1	24	YYVNTTNETTWERPSS	YYVNTTNETTWERP(S)	YYVNTTNETTWERPSSPGISAS(ph)PGPHR	0.7	0.0023958	Down	Yes	
1259	IPI00463493	Gbf1 protein	Gbf1	S1298	1	10	ADAPDAGAQSDELSPSY	ADAPDAGAQS(0.497)D	ADAPDAGAQS(ph)DSECK2				No	
835	IPI00463493	Gbf1 protein	Gbf1	S1300	1	12	ADAPDAGAQSDELSPSY	ADAPDAGAQS(0.194)D	ADAPDAGAQS(ph)DSECK2	1.0	0.40817		Yes	
887	IPI00463493	Gbf1 protein	Gbf1	S1318	1	4	GYTSDSEVYTDHGRPGK	GY(0.022)T(0.062)S(0.8)	GYTS(ph)DSEVYTDHGRPGK	1.1	0.43158		Yes	
961	IPI00463493	Gbf1 protein	Gbf1	S1320	1	6	GYTSDSEVYTDHGRPGK	GY(0.028)T(0.028)S(0.1)	(ca)GYTSDS(ph)EYVTDHGRPGK	1.1	0.45966		Yes	
972	IPI00463493	Gbf1 protein	Gbf1	T1317	1	3	GYTSDSEVYTDHGRPGK	GY(0.105)T(0.789)S(0.1)	GYT(ph)DSEVYTDHGRPGK	1.1	0.46435		Yes	
1264	IPI00463493	Gbf1 protein	Gbf1	T1324	1	10	GYTSDSEVYTDHGRPGK	GY(0.085)T(0.085)S(0.0)	(ca)GYTSDSEVYTDHGRPGK				No	
1279	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	S259	1	3	VDSSTCLFPVEEK	VDS(0.487)T(0.487)T(0.0)	VDS(ph)TCLFPVEEK	CHK1/2			No	
1285	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	T260	1	4	VDSSTCLFPVEEK	VDS(0.487)T(0.487)T(0.0)	VDS(ph)TCLFPVEEK	FHA2 Rad53p			No	
1292	IPI00127267	Glycine dehydrogenase	Gldc	S103	2	5	TVPASIRLK	T(1)VPAS(1)IRLK	(ca)T(ph)VPAS(ph)IRLK	CK1			Yes	
381	IPI00123429	Zinc finger protein GLI3	Gli3;Gli3;Gli3	S445	1	9	IKPDEDLPSPGSR	IKPDEDLPS(0.991)PGS(T)	IKPDEDLPS(ph)PGSR		0.9	0.19151		Yes
1308	IPI00351252	GMP synthase [glutam]	Gmps	S332	1	7	TLNMTTSPPEEK	TLNMT(0.037)T(0.482)T	TLNMTT(ph)SPEEK	CK2			No	
1313	IPI00351252	GMP synthase [glutam]	Gmps	T331	1	6	TLNMTTSPPEEK	TLNMT(0.037)T(0.482)T	TLNMTT(ph)SPEEK	CK2			No	
687	IPI00762316	Guanine nucleotide-bir	Gnl1;Gna-rs1;Mmr1	S51	1	8	REEQTDSDSGSVTHHIR	REEQT(0.004)DT(0.134)	REEQTDTS(ph)DGSV	CK2	1.2	0.34563		Yes
781	IPI00222461	Guanine nucleotide-bir	Gnl3;Ns;Gnl3;Ns	S505	1	3	ELSPQSTAGKPSDGS	ELS(0.962)PEQS(0.018)	ELS(ph)EQSTAGKPSD	CAMK2	1.0	0.38461		No
1338	IPI00222461	Guanine nucleotide-bir	Gnl3;Ns;Gnl3;Ns	S509	1	7	ELSPQSTAGKPSDGS	ELS(0.332)PEQS(0.332)	ELS(ph)EQSTAGKPSD	CK1			No	
1342	IPI00222461	Guanine nucleotide-bir	Gnl3;Ns;Gnl3;Ns	T510	1	8	ELSPQSTAGKPSDGS	ELS(0.332)PEQS(0.332)	ELS(ph)EQSTAGKPSD	GSSALDR			No	
453	IPI00341196	G patch domain-contai	Gpatch8;Gpatch8;Kiaa0	S1037	1	1	SQSPHYFQSGR	S(0.959)QS(0.041)PHYF	S(ph)QSPHYFQSGR		1.0	0.23432		Yes
1049	IPI00122054	GPN-loop GTPase 1;XP	Gpn1;Mbdin;Xab1	S338	1	12	GTLDDEEEDSDDTDI	GTLDDEEEDS(0.989)	GTLDDEEEDS(ph)D	DDDDIHR	1.1	0.49838		Yes
271	IPI00131457	Probable G-protein cou	Gpr124;Tem5	S1104	1	10	ALPTATEDGSPVLGEG	ALPT(0.011)AT(0.014)E	ALPTATEDGSPVLGEG	CK1	0.9	0.1066		Yes
902	IPI00757356	G-protein coupled rece	Gpr98;Kiaa0686;Mass1	T1994	1	14	TRPLSVEEATQNVTL	TRPLSVEEATQNV(T)0.95	TRPLSVEEATQNV(T)ph	FHA2 Rad53p	1.1	0.44142		Yes
753	IPI00750061	Glycogen synthase kina	Gsk3b;Gsk3a	S215	1	6	GEPNVSYICSR	GEPNV(S)0.5Y(0.5)ICSR	GEPNV(ph)YICSR	GSK3	1.2	0.37348		No
1306	IPI00750061	Glycogen synthase kina	Gsk3b;Gsk3a	S219	1	10	GEPNVSYICSR	GEPNV(S)0.012Y(0.494)	(ca)GEPNVSY(ph)ICSR	CK1			No	
836	IPI00750061	Glycogen synthase kina	Gsk3b;Gsk3a	Y216	1	7	GEPNVSYICSR	GEPNV(S)0.002Y(0.998)	GEPNVSY(ph)ICSR		1.0	0.40828		Yes
873	IPI00114232	Histone deacetylase 1	Hdac1	S393	1	22	MLPHAPGVQMQAIPED	MLPHAPGVQMQAIPED	(ca)MLPHAPGVQMQA	CK2	1.1	0.42684		Yes
1019	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S165	1	9	RAGDVLEDSPK	RAGDVLEDS(1)PK	RAGDVLEDS(ph)PK	CDK2	1.1	0.48541		Yes
1040	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S202	1	5	NSTPSEPDGQPPAE	NS(0.124)T(0.124)PS(0)	NSTP(ph)EPDQGGP	CK1	1.1	0.49115		No
557	IPI00116442	Hepatoma-derived gro	Hdgfrp2;Hdgfrp2;Hdgfr	S629	1	8	AQEDGQDSEDGPR	AQEDGQD(S)1JEDGPR	AQEDGQD(ph)JEDGPR		1.2	0.27888		Yes
458	IPI00123379	Vigilin;High density lip	Hdlbp;Hdlbp	S31	1	6	VATLNSIEEENDPPTYK	VATLNS(1)JEEENDPPTYK	VATLNS(ph)JEEENDPPT	CK2	1.0	0.23743		Yes
690	IPI00222813	HIRA-interacting protei	Hirip3	S575	1	4	TLDSEEEQPR	T(0.006)LDS(0.994)EEE	TLDS(ph)EEEQPR	CK2	1.0	0.3463		Yes
331	IPI00228616	Histone H1.1;H1 VAR.3	Hist1h1a;H1f1	T15	1	14	SETAPVAQAASTATEK	S(0.009)ET(0.007)APVA	SETAPVAQAASTAT(ph)CK1		0.9	0.15312		No
581	IPI00230133	Histone H1.5;H1 VAR.5	Hist1h1b;H1f5	S2	1	11	SETAPAEAAPAPVEK	S(0.57)ET(0.43)APAETA	S(ph)ETAPAEAAPAPVEK		1.0	0.29111		No
561	IPI00223713	Histone H1.2;H1 VAR.4	Hist1h1c;H1f2	S2	1	1	SEAAPAAPAAPAPAEK	S(ph)EAAAPAAPAAPAEK	SEAAPAAPAAPAPAEK	CK2	1.0	0.28197		Yes
829	IPI00331597	Histone H1.3;H1 VAR.4	Hist1h1d;H1f3	S2	1	1	SETAPAAPAAPAPVEK	S(0.946)ET(0.054)APAA	S(ph)ETAPAAPAAPAPVEK		1.0	0.40456		Yes
494	IPI00223714	Histone H1.4;H1 VAR.2	Hist1h1e;H1f4	S2	1	1	SETAPAAPAAPAPVEK	S(0.908)ET(0.092)APAA	S(ph)ETAPAAPAAPAPAEK		1.0	0.25447		Yes
787	IPI00623776	Histone H4	Hist1h4a;Hist1h4b;H4-	S103	1	3	RISGLIYEETR	RIS(1)GLIYEETR	RIS(ph)GLIYEETR	PKA	1.1	0.38569		Yes
548	IPI00624711	High mobility group pr	Hmga1;Hmgi;Hmgi;Hr	S88	2	11	KLEKEEEEIGISQESSE	KLEKEEEEIGIS(0.761)QE	KLEKEEEEIGIS(ph)QES	GSK3	1.2	0.27484		No
403	IPI00624711	High mobility group pr	Hmga1;Hmgi;Hmgi;Hr	S91	1	14	KLEKEEEEIGISQESSE	KLEKEEEEIGISQES(0.94)	KLEKEEEEIGIS(ph)S	CK2	1.3	0.20876		Yes
233	IPI00624711	High mobility group pr	Hmga1;Hmgi;Hmgi;Hr	S92	2	15	KLEKEEEEIGISQESSE	KLEKEEEEIGISQES(1)S(1)	KLEKEEEEIGISQES(ph)S	CK2	1.4	0.079098		Yes
459	IPI00331612	High mobility group pr	Hmga2;Hmgic	S104	1	14	KPAQETTESQESAED	KPAQETTESQES(0.001)Q	KPAQETTESQES(ph)CK2		1.2	0.23813		Yes
1013	IPI00331612	High mobility group pr	Hmga2;Hmgic;Hmga2	S44	1	11	KQQQEPTCEPSPK	KQQQEPTCEP(S)1PK	KQQQEPTCEP(ph)PK	CDK2	1.1	0.48214		Yes
1398	IPI00331707	Hydroxymethylglutaryl	Hmgcs1	S486	1	18	RPFTNDHSLDEGMGLV	RPFT(0.053)NDHS(0.09)	RPFTNDHSLDEGMGLV	NEK6			No	
635	IPI00331707	Hydroxymethylglutaryl	Hmgcs1	S495	1	27	RPFTNDHSLDEGMGLV	RPFTNDHSLDEGMGLV	RPFTNDHSLDEGMGLV	CDK2	1.0	0.31866		Yes
940	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S84	1	23	QADVADQQTTELPAEN	QADVADQQTTELPAEN	(ca)QADVADQQTTEL	CK1	1.1	0.45309		No
667	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S87	1	26	QADVADQQTTELPAEN	QADVADQQTTELPAEN	QADVADQQTTELPAEN	CK2	1.2	0.33864		Yes
128	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	T70	2	9	QADVADQQTTELPAEN	QADVADQQT(0.512)T(0)	QADVADQQT(ph)TEL	FHA2 Rad53p	1.6	0.010135	Up	No
129	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	T71	2	10	QADVADQQTTELPAEN	QADVADQQT(0.512)T(0)	QADVADQQT(ph)TELPAEN	ENQ(S)ph)PASE1	1.6	0.010135	Up	No
1270	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	T80	2	19	QADVADQQTTELPAEN	QADVADQQT(0.408)T(0)	(ca)QADVADQQT(ph)TELPAEN	ENQ(S)ph)PASE1	1.6	0.010135	Up	No
782	IPI00553777	Heterogeneous nuclear	Hnrnpa1;Fli-2;Hnrpa1;	S4	1	1	SESPKPEQLR	S(0.976)ES(0.024)PKPE	S(ph)ESPKPEQLR		1.1	0.38498		Yes
793	IPI00553777	Heterogeneous nuclear	Hnrnpa1;Fli-2;Hnrpa1;	S6	1	3	SESPKPEQLR	S(0.002)ES(0.998)PKPE	SES(ph)PKPEQLR	CDK1	1.0	0.38734		Yes
1015	IPI00269661	Heterogeneous nuclear	Hnrnpa3;Hnrpa3;Hnrnp	Y361	1	6	SSGSPYGGYSGGGGSG	S(0.011)S(0.007)GS(0.0)	SSGSPY(ph)GGYSGGGGSG	YGSR	1.1	0.48312		Yes
649	IPI00874321	Heterogeneous nuclear	Hnrnpc;Hnrpc;Hnrnpc;	S306	1	15	DDEKEPEEGEDDRDSAN	DDEKEPEEGEDDRDS(0)	DDEKEPEEGEDDRDS(ph)PKA		1.2	0.32698		Yes
303	IPI00874321	Heterogeneous nuclear	Hnrnpc;Hnrpc;Hnrnpc;	S313	1	22	DDEKEPEEGEDDRDSAN	DDEKEPEEGEDDRDS(0)	DDEKEPEEGEDDRDS(ph)ANGEDDS		0.9	0.13065		No
693	IPI00874321	Heterogeneous nuclear	Hnrnpc;Hnrpc;Hnrnpc;	S241	1	4	NEKSEEEQSSASVK	NEKS(1)JEEEQSSASVK	NEKS(ph)JEEEQSSASVK	CK2	1.0	0.34762		Yes
572	IPI00874321	Heterogeneous nuclear	Hnrnpc;Hnrpc;Hnrnpc;	S268	1	10	MESEAGADDSAEEDLL	MESEAGADDS(1)AEEGI	M(ox)ESEAGADDS(ph)CK2		1.0	0.28671		Yes
1368	IPI00330958	Heterogeneous nuclear	Hnrnpd;Auf1;Hnrpd;Hr	S80	1	13	IDASKNEEDEGHNSSPR	IDAS(0.002)KNEEDEGH	IDASKNEEDEGHNSSPR				No	
724	IPI00330958	Heterogeneous nuclear	Hnrnpd;Auf1;Hnrpd;Hr	S82	1	15	IDASKNEEDEGHNSSPR	IDAS(0.001)KNEEDEGH	(ca)IDASKNEEDEGHNS	(ph)SPR	1.2	0.35951		Yes
607	IPI00330958	Heterogeneous nuclear	Hnrnpd;Auf1;Hnrpd;Hr	S83	1	16	IDASKNEEDEGHNSSPR	IDASKNEEDEGHNS(0.006)	IDASKNEEDEGHNS(S)Polo box		1.2	0.30502		Yes
338	IPI00224729	Heterogeneous nuclear	Hnrnp2;Hnrp2;Hnrnp	S104	1	6	HTGPNSPDTANDGFR	HTGPN(S)0.995PDT(0.0)	HTGPN(ph)PDTANDG	WW GroupIV	1.3	0.16125		Yes
261	IPI00224729	Heterogeneous nuclear	Hnrnp2;Hnrp2;Hnrnp	T107	1	9	HTGPNSPDTANDGFR	HTGPN(S)0.006PDT(0.9)	HTGPNPDT(ph)ANDG	FHA1 Rad53p	1.4	0.10104		Yes
382	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	S116	1	14	KIIPTEELGLQLPSPATS	KIIPTEELGLQLP(S)0.95P	KIIPTEELGLQLP(ph)PATS	QLPLESDA	1.3	0.19329		Yes
1374	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	T118	1	16	KIIPTEELGLQLPSPATS	KIIP(T)0.093LEELGLQLP	KIIPTEELGLQLP(ph)P	FHA KAPP			No	
1376	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	T120	1	18	KIIPTEELGLQLPSPATS	KIIP(T)0.001LEELGLQLP	KIIPTEELGLQLPSPAT	FHA2 Rad53p			No	
890	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	S284	1	6	DYDDMSIPR	DYDDMS(1)PR	DYDDMS(ph)PR	CDK2	1.1	0.43322		Yes
1381	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	T13	1	13	METEPEETFPNTEG	MET(0.229)EQPEET(0.2)	M(ox)ETEPEETFPNT	(ph)ETNGEFGK			No	
1383	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrpk;	T15	1	15	METEPEETFPNTEG	MET(0.229)EQPEET(0.2)	M(ox)ETEPEETFPNT	CK2			No	

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
871	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrnpk;	T3	1	3	METEQQEETFPNTETNG	MET(0.997)EQPEET(0.0)	MET(ph)EQPEETFPNTETNGEFGK		1.1	0.42591		Yes
735	IPI00458583	Heterogeneous nuclear	Hnrnpu;Hnrpu;hnrnp	S247	1	3	AKSPQPVVEEEDHFD	AKS(1)PQPPVEEEDHFD	AKS(ph)PQPPVEEEDHFD	CAMK2	1.2	0.36592		Yes
481	IPI00458583	Heterogeneous nuclear	Hnrnpu;Hnrpu;hnrnp	T262	1	18	AKSPQPVVEEEDHFD	AKS(0.268)PQPPVEEED	AKSPQPVVEEEDHFD	PLK1	1.2	0.24776		No
758	IPI00458583	Heterogeneous nuclear	Hnrnpu;Hnrpu;hnrnp	T268	1	24	AKSPQPVVEEEDHFD	AKS(0.039)PQPPVEEED	AKSPQPVVEEEDHFD	YVCLDT(ph)YVCLDHF	1.2	0.37512		Yes
697	IPI00123501	Heterogeneous nuclear	Hnrnpul1;Hnrnpul1;Hnr	S195	1	3	GRSPQPAEEDDDDF	GRS(1)PQPAEEDDDDF	GRS(ph)PQPAEEDDD	CAMK2	1.2	0.34868		Yes
966	IPI00123501	Heterogeneous nuclear	Hnrnpul1;Hnrnpul1;Hnr	T210	1	19	GRSPQPAEEDDDDF	GRS(0.287)PQPAEED	GRSPQPAEEDDDDF	PLK1	1.1	0.46176		No
399	IPI00123501	Heterogeneous nuclear	Hnrnpul1;Hnrnpul1;Hnr	T216	1	25	GRSPQPAEEDDDDF	GRS(0.075)PQPAEED	GRSPQPAEEDDDDF	YVCLDT(ph)YVCLDHF	0.9	0.20481		No
614	IPI00123501	Heterogeneous nuclear	Hnrnpul1;Hnrnpul1;Hnr	Y217	1	26	GRSPQPAEEDDDDF	GRS(0.176)PQPAEED	GRSPQPAEEDDDDF	EGFR	1.2	0.30668		No
531	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	S224	1	1	SKSPPPPEEAKDEEEDQ	S(0.552)KS(0.448)PPPP	S(ph)SKSPPPPEEAKDEEEDQ	TLVNLDTYSDLHF	1.2	0.26768		No
1388	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	S251	1	28	SKSPPPPEEAKDEEEDQ	S(0.103)KS(0.105)PPPP	SKSPPPPEEAKDEEEDQ	TLVNLDTYSDLHF	1.2	0.26768		No
1389	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	S258	1	35	SKSPPPPEEAKDEEEDQ	S(0.156)KS(0.151)PPPP	SKSPPPPEEAKDEEEDQ	TLVNLDTYSDLHF	1.2	0.26768		No
1390	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	T250	1	27	SKSPPPPEEAKDEEEDQ	S(0.071)KS(0.071)PPPP	SKSPPPPEEAKDEEEDQ	FHA2 Rad53p	1.2	0.26768		No
1006	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	S159	1	1	SGDETPGSEAPGDK	S(1)GDETPGSEAPGDK	S(ph)GDETPGSEAPGDK	CK2	1.1	0.47987		Yes
130	IPI00849047	Heterogeneous nuclear	Hnrnpul2;Hnrnpul2;Mar	T163	1	5	SGDETPGSEAPGDK	S(0.023)GDETP(0.861)PG	SGDETP(ph)GSEAPGDK	FHA KAPP	0.7	0.010421	Down	Yes
956	IPI00121760	Heterogeneous nuclear	Hnrpl1;Hnrpl1	S37	1	11	LKTEEGEIVYSAEESNR	LKTEEGEIVY(0.01)S(0.9)	LKTEEGEIVY(ph)AEESCK2	CK2	1.1	0.45814		Yes
720	IPI00330804	Heat shock protein Hsp	Hsp90aa1;Hsp86;Hsp8	S263	1	13	ESDDKPEIEDVGSDEE	ESDDKPEIEDVGS(1)DEE	ESDDKPEIEDVGS(ph)DCK2	CK2	1.2	0.35851		Yes
841	IPI00229080	Heat shock protein 84b	Hsp90ab1;Hsp84b;Hsp	S255	1	6	IEDVGSDEEDDSGDKK	IEDVGS(1)DEEDDSGDK	IEDVGS(ph)DEEDDSGDK	CK2	1.0	0.40961		Yes
928	IPI00229080	Heat shock protein 84b	Hsp90ab1;Hsp84b;Hsp	S261	1	12	IEDVGSDEEDDSGDKK	IEDVGS(0.175)DEEDDS	IEDVGSDEEDDS(ph)GDKDK	CK2	1.1	0.4481		Yes
814	IPI00123802	Heat shock protein 105	Hsp11;Hsp105;Hsp110	S810	1	3	IESPFLER	IES(1)PKLER	IES(ph)PKLER	CDK1	1.0	0.39802		Yes
670	IPI00221566	HIV Tat-specific factor	Htatsf1	S724	1	5	LFDDSDER	LFDDSDER	LFDDSDER	CDK1	1.0	0.34036		Yes
678	IPI00463909	E3 ubiquitin-protein lig	Huwe1;Kiaa0312;Urb	S1395	1	3	AESPEEVACR	AES(1)PEEVACR	AES(ph)PEEVACR	CAMK2	1.2	0.34139		Yes
903	IPI00463909	E3 ubiquitin-protein lig	Huwe1;Kiaa0312;Urb	S1907	1	6	GSSTASDDEFENLR	GS(0.011)GT(0.011)AS	GSSTAS(ph)DDEFENLR	CK2	1.1	0.44152		Yes
1400	IPI00761863	Insulin-like growth fact	Igf2bp2;Imp2;Vickz2;I	S161	1	10	ISYIPDEEVSSPSPHHR	IS(0.003)Y(0.008)PDEE	ISYIPDEEVSSPSPHHR	ERK/MAPK	1.1	0.47798		No
1001	IPI00761863	Insulin-like growth fact	Igf2bp2;Imp2;Vickz2;I	S162	1	11	ISYIPDEEVSSPSPHHR	ISYIPDEEVSSPSPHHR	ISYIPDEEVSSPSPHHR	ERK/MAPK	1.1	0.47798		No
850	IPI00761863	Insulin-like growth fact	Igf2bp2;Imp2;Vickz2;I	S164	1	13	ISYIPDEEVSSPSPHHR	ISYIPDEEVSSPSPHHR	ISYIPDEEVSSPSPHHR	ERK/MAPK	1.1	0.41352		Yes
737	IPI00331315	Insulin-like growth fact	Igf2bp3;Vickz3	S165	1	15	VAYIPDETAQQNPSPQ	VAYIPDETAQQNPSP(1)	VAYIPDETAQQNPSP(ph)PQLR	CK2	1.0	0.36621		Yes
582	IPI00308971	Cation-independent m	Igf2r	S2401	1	14	AEALSSLHGDDQDSEDE	AEALSSLHGDDQDSEDE	AEALSSLHGDDQDSEDE	CK2	1.0	0.2913		Yes
1356	IPI00308971	Cation-independent m	Igf2r	S2476	1	8	LVSFHDSDDEDLHI	LVSFHDSDDEDLHI	(ca)LVSFHDSDDEDLHI	CK2	1.0	0.2913		Yes
1358	IPI00308971	Cation-independent m	Igf2r	T2407	1	20	AEALSSLHGDDQDSEDE	AEALS(0.002)S(0.014)LE	AEALSSLHGDDQDSEDE	CK2	1.0	0.2913		No
224	IPI00120155	Interleukin-6 receptor	Il6st	S665	1	7	SHIAQWSPHTPPR	SHIAQWS(0.991)PHT(0.0)	SHIAQWS(ph)PHTPPR	CK2	0.8	0.070977		Yes
1010	IPI00319956	Protein IMPACT;Impr	Impact	S137	1	2	TEEVEVEEEDDPILEHPP	TEEVEVES(1)EEDDPILEH	TEEVEVES(ph)EEDDPILEHPP	PKA	1.1	0.48116		Yes
866	IPI00319956	Protein IMPACT;Impr	Impact	T130	1	8	KTEEVEVEEEDDPILEHPP	KT(0.5)EEVEVES(0.5)E	KT(ph)EEVEVEEEDDPILEHPP	PKA	1.1	0.42239		No
750	IPI00896646	Tyrosine-protein kinase	Insr;mcg_3075;Insr;	S989	1	6	ELGQGSFGMVYEGLAR	ELGQGS(0.5)FGMVY(0.0)	(ca)ELGQGS(ph)FGMVYEGLAR	CK2	1.0	0.37209		No
751	IPI00896646	Tyrosine-protein kinase	Insr;mcg_3075;Insr;	Y994	1	11	ELGQGSFGMVYEGLAR	ELGQGS(0.5)FGMVY(0.0)	(ca)ELGQGS(ph)FGMVYEGLAR	CK2	1.0	0.37209		No
411	IPI00453578	Interferon regulatory f	Irf2bp1;Irf2bp1	S384	1	3	KASPEPEGETAGK	KAS(0.997)PEPEGET(0.0)	KAS(ph)PEPEGETAGK	PKA/AKT	1.3	0.21337		Yes
1029	IPI00453578	Interferon regulatory f	Irf2bp1;Irf2bp1	S436	1	9	NVAEALGHSPKDPGGG	NVAEALGH(1)PKDPGG	NVAEALGH(ph)PKDPGG	CDK1	1.1	0.48864		Yes
982	IPI00854942	Putative uncharacterize	Irf2bp2	S362	1	11	LEEPELNRQSPNPR	LEEPELNRQSPNPR	LEEPELNRQSPNPR	PKA	1.1	0.4681		Yes
1327	IPI00854942	Putative uncharacterize	Irf2bp2	S419	1	4	RPASVSSAAAEHEAR	RPAS(0.462)VS(0.462)S	RPAS(ph)VSSAAAEHEAR	CAMK2	1.0	0.4681		No
1329	IPI00854942	Putative uncharacterize	Irf2bp2	S421	1	6	RPASVSSAAAEHEAR	RPAS(0.462)VS(0.462)S	RPAS(ph)VSSAAAEHEAR	CK2	1.0	0.4681		No
892	IPI00854942	Putative uncharacterize	Irf2bp2	S536	1	4	RKPSPEPEGEVGGPK	RKPS(1)PEPEGEVGGPK	RKPS(ph)PEPEGEVGGPK	PKA/AKT	1.1	0.43479		Yes
311	IPI00119627	Insulin receptor substr	Irs1;Irs-1;Irs1;mcg_20	S1097	1	3	HSETFSAPTR	HS(0.004)S(0.996)ETFS	HSS(ph)ETFSAPTR	PIM1/2	0.9	0.13779		Yes
190	IPI00923679	Insulin receptor substr	Irs2;Irs2	S556	1	3	RVSGDGAQDLDR	RVS(1)GDGAQDLDR	RVS(ph)GDGAQDLDR	PKA	1.5	0.048389	Up	Yes
125	IPI00137400	Inositol 1,4,5-trisphosp	Itp3	S934	1	3	KQSVFGASSLPAGVGVY	KQS(0.714)VFGAS(0.14)	KQS(ph)VFGASSLPAGVGVY	CAMK2	1.7	0.0084638	Up	No
963	IPI00831223	Intersectin-1;EH and S	Itns1;Ese1;Itns1;Itns1;E	S334	1	6	LPEEPSSEDEQQPEK	LPEEPS(0.886)S(0.114)	LPEEPS(ph)SEDEQQPEK	CK2	1.1	0.46033		Yes
348	IPI00831223	Intersectin-1;EH and S	Itns1;Ese1;Itns1;Itns1;E	S335	1	7	LPEEPSSEDEQQPEK	LPEEPS(0.113)S(0.887)	LPEEPS(ph)SEDEQQPEK	CK2	0.9	0.16673		Yes
818	IPI00876351	potassium channel tetr	Kctd18	S349	1	17	AAQCSVATGASGHAPAS	AAQCSVATGAS(0.002)K	AAQCSVATGASGHAPAS	WW GroupIV	1.1	0.39934		Yes
367	IPI00464324	Uncharacterized protei	Kiaa0754	S275	1	5	EKTESELKFEEDER	EKT(0.119)ES(0.881)EL	EKTES(ph)ELKFEEDER	CK2	1.3	0.18108		Yes
73	IPI00454081	Kinesin-like protein KIF	Kif21a;Kiaa1708;Kif21a	S855	1	3	KLSSESAPADTGGSSAAS	KLS(0.97)S(0.026)S(0.0)	KLS(ph)SSESAPADTGGSSAAS	PKA	2.1	8.458E-05	Up	Yes
434	IPI00120089	Kinesin light chain 4;Kir	Klc4;Kns18	S590	1	3	AASLNLYNQPNAAAPLQV	AA(0.999)LN(0.001)LP	AAS(ph)LNLYNQPNAAAPLQV	PKA	1.0	0.2274		Yes
918	IPI00230429	Importin subunit alpha	Kpna3;Oip2;Kpna3	S60	1	11	NVPOQESLEDSVDADDF	NVPOQESLEDS(1)DVDA	NVPOQESLEDS(ph)DVDA	NEK6	1.1	0.44648		Yes
594	IPI00129792	Importin subunit alpha	Kpna4;Oip1	S60	1	11	NVPOQEDICEDSDIDGDYR	NVPOQEDICEDS(1)DIDG	NVPOQEDICEDS(ph)DIDGDYR	CK2	1.0	0.29583		Yes
739	IPI00311761	Protein KRI1 homolog	Kri1	S148	1	7	YVDEDNSDGETVDHR	YVDEDNS(0.953)DGET	YVDEDNS(ph)DGETVDHR	CK2	1.2	0.36726		Yes
364	IPI00623208	Kinase suppressor of R	Ksr1;Ksr;Ksr1;Ksr;Ksr1;	S518	1	19	TDVLGVHEAEAEPEAG	TDVLGVHEAEAEPEAG	TDVLGVHEAEAEPEAG	CK2	0.9	0.17871		Yes
855	IPI00122559	Kinectin;Kinectin;Kine	Ktn1;Ktn1;Ktn1;Ktn1;K	S75	1	10	EIQNGTLRESDESHPVPR	EIQNGT(0.002)LR(0.9)S	EIQNGTLRES(ph)DSEH	PKA	1.1	0.41931		Yes
1165	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S298	1	12	VEPAWHDDQDTSVSKSD	VEPAWHDDQDET(0.059)	VEPAWHDDQDTS(ph)GSK3	CK2	1.0	0.37197		No
1169	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S299	1	13	VEPAWHDDQDTSVSKSD	VEPAWHDDQDET(0.168)	VEPAWHDDQDTS(ph)VKSDGAGGAR	CK2	1.0	0.37197		Yes
1174	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S302	1	16	VEPAWHDDQDTSVSKSD	VEPAWHDDQDET(0.059)	VEPAWHDDQDTS(ph)GSK3	CK2	1.0	0.37197		No
679	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S525	1	5	GLSASLPDLDESSEWIEVK	GLS(0.113)AS(0.886)LP	GLSAS(ph)LPDLDESSEWIEVK	NEK6	1.0	0.34169		Yes
733	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S751	1	9	SLPTTVPEPSPNYR	SLPTTVPEPSPNYR	SLPTTVPEPSPNYR	ERK/MAPK	1.0	0.36309		Yes
749	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	S81	1	15	ESPRPPAAAEEAPAGSDG	ESPRPPAAAEEAPAGS(1)	ESPRPPAAAEEAPAGS(ph)CK2	CK2	1.0	0.37197		Yes
859	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	T626	1	7	ILIVTQTPPYMR	ILIVTQ(0.997)PPY(0.0)	ILIVTQ(ph)PPY(ox)R	CK2	1.1	0.42052		Yes
1177	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	Y754	1	12	SLPTTVPEPSPNYR	SLPTT(0.003)VPES(0.49)	SLPTTVPEPSPNYR	CK2	1.0	0.37197		No
144	IPI00340860	La-related protein 7;La	Larp7;D3Wsu161e	T251	1	1	TASEGSEAEETPEAPK	T(0.613)AS(0.383)EGS	T(ph)ASEGSEAEETPEAPK	PKA	1.6	0.016033	Up	No
616	IPI00474486	RNA polymerase-assoc	Leo1;Gm185	S631	1	4	KLNSDEEGESSGK	KLNS(1)DEEGESSGK	KLNS(ph)DEEGESSGK	CK2	1.2	0.30911		Yes
588	IPI00474486	RNA polymerase-assoc	Leo1;Gm185	S659	1	5	KYVISDEEEEDD	KY(0.003)VIS(0.997)DE	KYVIS(ph)DEEEEDD	CK2	1.2	0.29372		Yes
516	IPI00229517	Galectin-1;Lectin galact	Lgals1;Gbp	S8	1	7	ACGLVASNLNLKPGCE	ACGLVAS(1)NLNLKPGCE	ACGLVAS(ph)NLNLKPGCE	NEK6	1.0	0.2633		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
223	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	S225	1	3	RLSENNCLDDWEIGAG	RLS(0.985)ENNCS(0.01)	RLS(ph)ENNCSLDDWEI	PKA	1.4	0.070318		Yes
185	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	S230	1	8	RLSENNCLDDWEIGAG	RLS(0.046)ENNCS(0.95)	RLSENNCS(ph)LDDWEI	GAGHLSAAFNSEK	1.5	0.044672	Up	Yes
1045	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	S360	1	13	SEAAQPMHPKPLSPDAR	SEAQPMHPKPLS(1)PG	SEAQPMHPKPLS(ph)	WW GroupIV	1.1	0.49473		Yes
943	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	S485	1	19	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNAG	(ph)PHSPGVEDAPIA	1.1	0.45436		No
981	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	S488	1	22	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNA	WW GroupIV	1.1	0.4678		Yes
1225	IPI00112339	LIM domain and actin-	Lima1;D15ErtD366e;Ep	T472	1	6	SDNEETLGRPAQPPNAG	S(0.208)DNEET(0.412)	SDNEETLGRPAQPP	PLK1				No
1251	IPI00620256	Lamin-A/C	Lmna;Lmn1	S570	1	2	GSHCSGSGDPAEYNLR	GS(0.454)HCS(0.454)GS	(ca)GS(ph)HCSGSGDP	PKA				No
504	IPI00620256	Lamin-A/C	Lmna;Lmn1	S573	1	5	GSHCSGSGDPAEYNLR	GS(0.005)HCS(0.995)GS	GSHCS(ph)GSGDPAEY	CK1	1.0	0.25889		Yes
1255	IPI00620256	Lamin-A/C	Lmna;Lmn1	S575	1	7	GSHCSGSGDPAEYNLR	GS(0.333)HCS(0.333)GS	GS(ph)HCSGSGDPAEY	NLR				No
552	IPI00620256	Lamin-A/C	Lmna;Lmn1	S629	1	1	SVGGSGGSGFDNLVTR	S(0.925)VGG(0.073)GS	S(ph)VGGSGGSGFDN	CK1	1.0	0.27809		Yes
344	IPI00620256	Lamin-A/C	Lmna;Lmn1	S633	1	5	SVGGSGGSGFDNLVTR	S(0.021)VGG(0.979)GS	SVGGSG(ph)GGSGFDN	GSK3	0.9	0.16454		Yes
688	IPI00620256	Lamin-A/C	Lmna;Lmn1	T548	1	3	SLTMVEDNEDDDEGEE	S(0.15)LT(0.85)IMVEDN	SLT(ph)IMVEDNEDDDE	CHK1/2	1.2	0.34584		Yes
1293	IPI00620256	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	S17	1	6	SGAQASSTPLSPTR	S(0.001)GAQAS(0.333)P	SGAQAS(ph)STPLSPTR					No
335	IPI00620256	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	S18	1	7	SGAQASSTPLSPTR	SGAQAS(0.004)S(0.936)	SGAQAS(ph)TPLSPTR	GSK3	0.9	0.15599		Yes
519	IPI00620256	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	S22	1	11	SGAQASSTPLSPTR	SGAQASSTPLS(0.994)P	SGAQASSTPLS(ph)PTR	WW GroupIV	1.2	0.26362		Yes
792	IPI00400300	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	S570	1	25	SLTMVEDNEDDDEGEE	SLTMVEDNEDDDEGEE	SLTMVEDNEDDDEGEE	PKA	1.0	0.38726		Yes
692	IPI00400300	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	S572	1	27	SLTMVEDNEDDDEGEE	SLTMVEDNEDDDEGEE	SLTM(ox)VEDNEDDDEGEE	LLHHRV5(ph)GSF	1.0	0.34709		No
218	IPI00620256	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	T19	1	8	SGAQASSTPLSPTR	S(0.001)GAQAS(0.019)P	SGAQASST(ph)PLSPTR	Polo box	0.8	0.065483		Yes
854	IPI00620256	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	T24	1	13	SGAQASSTPLSPTR	SGAQASSTPLS(0.5)PT(0	SGAQASSTPLS(ph)PTR	NEK6	1.1	0.41827		No
689	IPI00400300	Lamin-A/C;Lamin-A/C	Lmna;Lmn1;Lmna;Lmn	T548	1	3	SLTMVEDNEDDDEGEE	S(0.15)LT(0.85)IMVEDN	SLT(ph)IMVEDNEDDDE	CHK1/2	1.2	0.34584		Yes
352	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S390	1	4	LRLSPSPTSQR	LRLS(0.928)PS(0.071)P	(ca)LRLS(ph)PSPTSQR	PKA	0.9	0.17006		Yes
192	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S392	1	6	LRLSPSPTSQR	LRLS(0.029)PS(0.971)P	LRLSPS(ph)PTSQR	NEK6	0.8	0.05045		Yes
41	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S395	2	9	LRLSPSPTSQR	LRLS(0.386)PS(0.386)P	LRLS(ph)PSPTS(ph)QR	CK1	0.3	2.007E-11	Down	No
1132	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S403	1	2	ASSHSSQSQGGGSVTK	AS(0.455)S(0.455)HS(0	AS(ph)SHSSQSQGGGS	PKA				No
1136	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S404	1	3	ASSHSSQSQGGGSVTK	AS(0.455)S(0.455)HS(0	AS(ph)SHSSQSQGGGS	PKA/AKT				No
1137	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S406	1	5	ASSHSSQSQGGGSVTK	AS(0.114)S(0.114)HS(0	ASSHS(ph)SQSQGGGS	CK1				No
1140	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S407	1	6	ASSHSSQSQGGGSVTK	AS(0.114)S(0.114)HS(0	ASSHS(ph)SQSQGGGS	CK1				No
1142	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	T394	2	8	LRLSPSPTSQR	LRLS(0.386)PS(0.386)P	LRLS(ph)PSPTS(ph)QR					No
1138	IPI00849159	similar to DNA cytosine	LOC100048887	S217	1	9	TTGVGGTGSATSCR	TTGVGGT(0.05)GS(0.3)	(ca)TTGVGGTGS(ph)ATSCR					No
498	IPI00849159	similar to DNA cytosine	LOC100048887	S220	1	12	TTGVGGTGSATSCR	TTGVGGT(0.017)GS(0.1	(ca)TTGVGGTGSATS(p	CK1	1.0	0.25752		Yes
740	IPI00172202	Protein LSM14 homolo	Lsm14a;Fam61a	S216	1	2	RSVPARPLPPTSQK	RS(1)PVPARPLPPTSQK	RS(ph)PVPARPLPPTSQ	PKA	1.2	0.36826		Yes
979	IPI00874393	Latent-transforming gr	Ltbp2;Ltbp2	S491	1	13	VRGELDPVLEDNSVTR	VRGELDPVLEDNS(0.974	VRGELDPVLEDNS(ph)	PLK1	1.1	0.4673		Yes
484	IPI00607974	Protein MAK16 homolo	Mak16;Rbm13	S197	2	9	ALEKQEAESDESEDEEE	ALEKQEAES(1)DS(1)ED	ALEKQEAES(ph)DS	CK2	1.2	0.24977		Yes
485	IPI00607974	Protein MAK16 homolo	Mak16;Rbm13	S199	2	11	ALEKQEAESDESEDEEE	ALEKQEAES(1)DS(1)ED	ALEKQEAES(ph)DS	CK2	1.2	0.24977		Yes
1021	IPI00676243	Microtubule-associated	Map1a;Mtap1;Mtap1a	S2027	1	9	VPSAPGQESVPVPTK	VPS(0.001)APGQES(0.9	VPSAPGQES(ph)VPVPTK		1.1	0.48585		Yes
206	IPI00676243	Microtubule-associated	Map1a;Mtap1;Mtap1a	S905	1	12	AEELEEMEVHPSDEEE	AEELEEMEVHPS(1)DEE	AEELEEMEVHPS(ph)D	CK2	0.8	0.060625		Yes
1106	IPI00223621	Microtubule-associated	Map1s;Bpy2lp1;Map8	S658	1	1	STSPHDVLDLCLVSPCF	S(0.396)T(0.302)S(0.30	S(ph)TSPHDVLDLCLVSP	PKA				No
623	IPI00223621	Microtubule-associated	Map1s;Bpy2lp1;Map8	S660	1	4	RSTSPHDVLDLCLVSPCF	RS(0.206)T(0.206)S(0.5	RSTS(ph)PHDVLCLVCS	CAMK2	1.2	0.3114		No
1109	IPI00223621	Microtubule-associated	Map1s;Bpy2lp1;Map8	T659	1	3	RSTSPHDVLDLCLVSPCF	RS(0.333)T(0.333)S(0.3	RS(ph)TSPHDVLDLCLV	CHK1/2				No
87	IPI00874452	72 kDa protein	Map3k2	S180	1	4	DRSSPPPGYIPDELQIAH	DRS(0.011)S(0.989)PPP	DRSS(ph)PPGYIPDEL	Polo box	0.6	0.0005296		Yes
407	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S345	1	18	DVAPPMEEEIVPGNDT	DVAPPMEEEIVPGNDT(I	DVAPPMEEEIVPGNDT	CDK1	1.3	0.2109		Yes
691	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S475	1	3	DMSPLPESEVTLGK	DMS(1)PLPESEVTLGK	DMS(ph)PLPESEVTLGK	CHK1	1.0	0.3465		Yes
791	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S506	1	11	VAEFNNVTLSEEEVTSV	VAEFNNVT(0.007)PLS(0	VAEFNNVTPS(ph)EE	CK2	1.1	0.38705		Yes
671	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S517	1	3	DMPSAETAAPLAK	DMS(1)PSAETAAPLAK	DMS(ph)PSAETAAPLAK		1.0	0.3405		Yes
1129	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T343	1	16	DVAPPMEEEIVPGNDT	DVAPPMEEEIVPGNDT(I	DVAPPMEEEIVPGNDT	(ph)TSPK				No
1133	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T344	1	17	DVAPPMEEEIVPGNDT	DVAPPMEEEIVPGNDT(I	DVAPPMEEEIVPGNDT	(ph)TSPK				No
1126	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T522	1	8	DMPSAETAAPLAK	DMS(0.312)PS(0.204)A	(ca)DM(ox)PSAET(ph	CK1				No
565	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S1046	1	3	VGSLDNVGHLPAGGAVK	VGS(1)LDNVGHLPAGGAV	VGS(ph)LDNVGHLPAGG	AVK	1.0	0.28441		Yes
699	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S667	1	21	AAVGTGNDITTPPNK	AAVGT(0.001)GNDIT(I	AAVGTGNDITTPPNK	WW GroupIV	1.2	0.34942		Yes
232	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S785	1	3	ATSPSTLVSTGSSR	AT(0.077)S(0.923)PS(0	ATS(ph)PSTLVSTGSS	PKD	0.9	0.075848		Yes
503	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S914	1	3	VGSTENIK	VGS(0.991)T(0.009)ENI	VGS(ph)TENIK	CK1	1.0	0.2585		Yes
1148	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T784	1	2	ATSPSTLVSTGSSR	AT(0.497)S(0.497)PS(0	AT(ph)PSTLVSTGSS	CK1				No
856	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T915	1	6	SKVGSTENIK	SKVGS(0.072)T(0.928)E	SKVGST(ph)ENIK	FHA2 Rad53p	1.1	0.41966		Yes
229	IPI00923108	Map4k4 protein;MKIA	Map4k4;Map4k4;MKIA	S684	1	3	RDSPQLQGGQQNQSQAG	RDS(1)PLQGGQQNQSQ	RDS(ph)PLQGGQQNQ	CHK1/2	0.9	0.074322		Yes
22	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkr	T179	1	9	VADPDHDHTGFLTEYVA	VADPDHDHT(0.442)GFL	VADPDHDHT(ph)GFL	FHA2 Rad53p	8.7	5.009E-33	Up	No
58	IPI00119663	Mitogen-activated prot	Mapk1;Erk2;Mapk;Prkr	Y185	1	15	VADPDHDHTGFLTEYVA	VADPDHDHTGFL(0.09	VADPDHDHTGFLTEY	(ph)VATR	2.4	2.421E-06	Up	Yes
43	IPI00230277	Mitogen-activated prot	Mapk3;Erk1;Prkm3;Ma	T208	1	18	IADPEHDHTGFLTEYVAT	IADPEHDHT(0.068)GFL	IADPEHDHTGFLTEYV	(ph)R	3.0	1.82E-09	Up	No
44	IPI00230277	Mitogen-activated prot	Mapk3;Erk1;Prkm3;Ma	Y205	1	15	IADPEHDHTGFLTEYVAT	IADPEHDHTGFL(0.105	IADPEHDHTGFLTEY	(ph)VATR	2.9	1.695E-08	Up	Yes
1009	IPI00229534	Myristoylated alanine-	Marcks;Macs	S138	1	8	AEDGAAPSPSSETPK	AEDGAAPS(0.878)PS(0	AEDGAAPS(ph)PSSETPK		1.1	0.48113		Yes
221	IPI00229534	Myristoylated alanine-	Marcks;Macs	S140	1	10	AEDGAAPSPSSETPK	AEDGAAPS(0.145)PS(0	AEDGAAPS(ph)SETPKK		1.4	0.067963		No
994	IPI00229534	Myristoylated alanine-	Marcks;Macs	S141	1	11	AEDGAAPSPSSETPK	AEDGAAPS(0.05)S(0	AEDGAAPS(ph)ET	CK1	1.1	0.47516		Yes
746	IPI00229534	Myristoylated alanine-	Marcks;Macs	S46	1	6	VNGDASPAAPGPAK	VNGDAS(1)PAAAPGPAK	VNGDAS(ph)PAAAPGPA		1.2	0.3709		Yes
947	IPI00229534	Myristoylated alanine-	Marcks;Macs	T143	1	13	AEDGAAPSPSSETPK	AEDGAAPS(1)PK	AEDGAAPS(1)PK	CDK2	1.1	0.45551		Yes
1051	IPI00281011	MARCKS-related protei	Marcks1;Mlp;Mrp	T85	1	8	GEVAPKETP	GEVAPKET(1)PK	GEVAPKET(ph)PK	CDK2	1.1	0.49883		Yes
154	IPI00554855	Serine/threonine-prote	Mark2;Emk;Mark2;Emk	T208	1	3	LDTFCGSPYAAPELFGK	LDT(1)FCGSPYAAPEL	LDT(ph)FCGSPYAAPEL	FGK	0.8	0.024203	Down	Yes
116	IPI00453826	Matrin-3	Matr3	S188	1	3	RDSFDDRGSLNPLVDYI	RDS(0.999)FDDRGPS(0	RDS(ph)FDDRGSLNPL	PKA	1.8	0.0026584		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
84	IPI00453826	Matrin-3	Matr3	S195	1	10	RDSFDDRRGSLNPVLDY	RDS(0.056)FDDRRG(S)0.28	RDSFDDRRGSLNPVLDYDHGSR	CAMK2	2.0	0.0003883	Up	Yes
1294	IPI00453826	Matrin-3	Matr3	S206	1	21	RDSFDDRRGSLNPVLDY	RDS(0.28)FDDRRG(S)0.28	RDSFDDRRGSLNPVLDYDHGSR					No
302	IPI00453826	Matrin-3	Matr3	S604	2	9	SYSPDGGKESPSDKK	S(0.435)Y(0.282)S(0.28)	S(ph)YSPDGGKES(ph)PSDKK		1.3	0.12941		Yes
334	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S139	1	6	GLLYDSSEDEERPAR	GLLY(0.002)DS(0.86)S(0.86)	GLLYDS(ph)SEDEERPAR	CK2	1.3	0.15596		Yes
216	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S140	1	8	RGLLYDSSEDEERPAR	RGLLY(0.201)DS(0.201)	RGLLYDS(ph)SEDEERPAR		1.4	0.065241		No
1185	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S26	1	8	RISDPLTSSPGR	RIS(0.059)DPLT(0.466)S	RISDPLT(ph)SSPGR					No
432	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S27	1	8	ISDPLTSSPGR	ISDPLTSS(1)PGR	ISDPLTSS(ph)PGR	Polo box	1.2	0.22522		Yes
1188	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	T25	1	7	RISDPLTSSPGR	RIS(0.059)DPLT(0.466)S	RISDPLT(ph)SSPGR					No
227	IPI00108338	DNA replication licensi	Mcm3;Mcmd;Mcmd3	S668	1	3	KASEDESDLEDEEEKSQE	KAS(0.785)EDES(0.213)	KAS(ph)EDESDEDEEE	CK2	1.4	0.073538		Yes
374	IPI00108338	DNA replication licensi	Mcm3;Mcmd;Mcmd3	S672	1	7	KASEDESDLEDEEEKSQE	KAS(0.031)EDES(0.969)	KASEDESDLEDEEE	CK2	1.3	0.18467		Yes
390	IPI00753701	Mediator of DNA dama	Mdc1;Kiaa0170	S168	1	7	VLLAADSEEEGDFPSSGR	VLLAADS(1)EEEGDFPSSGR	VLLAADS(ph)EEEGDFPSSGR		1.3	0.19899		Yes
310	IPI00129226	E3 ubiquitin-protein lig	Mdm2;Mdm2;Mdm2	S183	1	1	SLSFDPSSLGLCEL	S(0.644)LS(0.356)FDPSS	S(ph)LSFDPSSLGLCEL	PKA/AKT	1.3	0.13546		No
538	IPI00224399	Mediator of RNA polym	Med19	S226	1	4	NRHSPDHPGMSGSSQAS	NRHS(0.996)PDHPGMSG	NRHS(ph)PDHPGMSG	PKA	1.2	0.27081		Yes
15	IPI00224399	Mediator of RNA polym	Med19	S234	7	12	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	GSK3	9.6	2.659E-36	Up	No
16	IPI00224399	Mediator of RNA polym	Med19	S235	7	13	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	GSK3	9.6	2.659E-36	Up	No
17	IPI00224399	Mediator of RNA polym	Med19	S238	7	16	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	CK1	9.6	2.659E-36	Up	No
18	IPI00224399	Mediator of RNA polym	Med19	S239	7	17	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	CK1	9.6	2.659E-36	Up	No
19	IPI00224399	Mediator of RNA polym	Med19	S240	7	18	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	(ox)GS(ph)QAS(ph)	9.6	2.659E-36	Up	No
20	IPI00224399	Mediator of RNA polym	Med19	S241	7	19	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	CK1	9.6	2.659E-36	Up	No
21	IPI00224399	Mediator of RNA polym	Med19	S242	7	20	NRHSPDHPGMSGSSQAS	NRHS(0.992)PDHPGMSG	(ca)NRHS(ph)PDHPGMSG	CK1	9.6	2.659E-36	Up	No
980	IPI00228590	Microfibrillar-associate	Mfap1	T267	1	10	SLAALDALNTDDEENDEEE	S(0.153)LAALDALNT(0.4)	SLAALDALNT(ph)DDEE	CK2	1.1	0.46746		Yes
1080	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1765	1	14	HSASDPGAPVNVSSSR	HS(0.004)AS(0.017)DPG	HSASDPGAPVNVSSSR	(ph)GSK3				No
1082	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1766	1	15	HSASDPGAPVNVSSSR	HSASDPGAPVNVNS(0.0)	HSASDPGAPVNVSSSR	(ph)GSK3				No
1087	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1767	1	16	HSASDPGAPVNVSSSR	HSASDPGAPVNVNS(0.0)	HSASDPGAPVNVSSSR	(ph)GSK3				No
304	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1916	1	15	DSLPSGPREEAKPASPS	DSLPSGPREEAKPAS(0.9)	DSLPSGPREEAKPAS(ph)	WW GroupIV	1.3	0.1318		Yes
1076	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1918	1	9	EEAKPASPSVQDR	EEAKPAS(0.468)PS(0.46)	EEAKPAS(ph)PSSVQDR					No
1077	IPI00222037	Melanoma inhibitory a	Mia3;Kiaa0268;Mia3;K	S1919	1	18	DSLPSGPREEAKPASPS	DS(0.02)LP(0.01)GPRE	DSLPSGPREEAKPASPS	CK1				No
66	IPI00280103	JRAB;Putative uncharac	Micall2;JRAB;mcG_12	S766	1	16	RKPCPAGSGPSPALSP	RKPCPAGSGPSPALSP(0.0)	RKPCPAGSGPSPALSP	GSK3	0.5	1.862E-05	Down	Yes
833	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	S1018	1	3	SKSVIEQVSWDN	S(0.999)KS(0.001)VIEQ	S(ph)KSVIEQVSWDN		1.0	0.40644		Yes
695	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	S1020	1	3	SKSVIEQVSWDN	S(0.027)KS(0.973)VIEQ	SKS(ph)VIEQVSWDN	CAMK2	1.0	0.34813		Yes
134	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	S292	1	13	AEEQLPPLSPSPSPSP	AEEQLPPLSP(0.001)PSP	AEEQLPPLSPSPSPSP	(ph)WW GroupIV	0.7	0.011856		Yes
1248	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	S294	1	15	AEEQLPPLSPSPSPSP	AEEQLPPLSP(0.06)PSP	AEEQLPPLSPSPSPSP	(ph)PSP	0.2			No
1252	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	T295	1	16	AEEQLPPLSPSPSPSP	AEEQLPPLSP(0.06)PSP	AEEQLPPLSPSPSPSP	(ph)PSP	0.2			No
938	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	S543	1	3	SKTFDWAEFRPIQQAAL	S(0.926)KT(0.074)FDW	S(ph)KTFDWAEFRPIQQAAL	QER	1.1	0.45216		Yes
978	IPI00720036	Myosin phosphatase R	Mrip;Kiaa0864;Mrip;F	T545	1	1	SKTFDWAEFRPIQQAAL	S(0.137)KT(0.863)FDW	SKT(ph)FDWAEFRPIQQAAL	CAMK2	1.1	0.46704		Yes
29	IPI00118853	Double-strand break re	Mre11a;Mre11;Mre11	S686	1	2	GVDFESDEDDDDPFM	GVDFES(1)DEDDDDPFM	GVDFES(ph)DEDDDDPFM	(ox)SSCCPR	0.2	8.198E-25	Down	Yes
959	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S1371	2	6	ASLSPMDEPVPDSESPV	AS(0.657)LS(0.657)PM	AS(ph)LS(ph)PM	(ox)DEPVPDSESPVEK	1.1	0.45871		No
1201	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S1382	1	13	ASLSPMDEPVPDSESPV	ASLSPMDEPVPDPS(0.5)	ASLSPMDEPVPDPS(ph)	ESPVEK				No
1025	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S1384	1	15	ASLSPMDEPVPDSESPV	AS(0.139)LS(0.139)PM	ASLSPMDEPVPDSESPV	CK2	1.1	0.487		No
648	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S1422	1	4	RSESPFEKG	RS(0.001)ES(0.999)PFE	RSES(ph)PFEKG	CAMK2	1.0	0.32663		Yes
135	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S614	1	9	EVSSKEEQSPVKAIEVAEK	EVS(0.033)S(0.155)KEE	EVSSKEEQS(ph)PVKAE	CDK2	1.6	0.012416	Up	Yes
305	IPI00330599	Protein LYRIC;Lysine-ri	Mtdh;Lyric	S423	1	12	SQEPISNDQKVSDDDKKE	SQEPIS(0.014)NDQKVS	SQEPISNDQKVS(ph)DDDKKE		1.3	0.13182		Yes
470	IPI00226263	Matrix-remodeling-ass	Mxra7;Tmap1;Mxra7;R	S79	1	7	VAEPEESEAEPEAEGR	VAEPEES(1)EAEPEAEGR	VAEPEES(ph)EAEPEAE	CK2	1.0	0.24365		Yes
590	IPI00331361	Myb-binding protein 1	Mybbp1a;P160;Mybbp	S1325	1	3	SPSLQSGVK	S(0.094)PS(0.906)LLQS	SPS(ph)LLQSGVK	PKD	1.0	0.29491		Yes
1265	IPI00757312	Myosin, heavy polypep	Myh10;RP23-396M19	S1989	1	8	QLHIEGASLELSDDDTE	QLHIEGAS(0.498)LELS(0.498)	(ca)QLHIEGAS(ph)LELS	GSK3				No
857	IPI00757312	Myosin, heavy polypep	Myh10;RP23-396M19	S1993	1	13	QLHIEGASLELSDDDTE	QLHIEGASLELS(1)DD	QLHIEGASLELS(ph)DD	NEK6	1.1	0.4197		Yes
1269	IPI00757312	Myosin, heavy polypep	Myh10;RP23-396M19	T1997	1	17	QLHIEGASLELSDDDTE	QLHIEGAS(0.256)LELS	QLHIEGAS(ph)LELSDDDTESK					No
1043	IPI00123181	Myosin-9;Myosin heav	Myh9	S1943	1	7	KGTGDCSDEEVDGK	KGTGDCS(1)GDEVDGK	KGTGDCS(ph)DEEVDGK	CK2	1.1	0.49274		Yes
960	IPI00123181	Myosin-9;Myosin heav	Myh9	T1939	1	3	KGTGDCSDEEVDGK	KGT(0.881)GDCS(0.119)	(ca)KGT(ph)GDCSDEE	PKA	1.1	0.45885		Yes
682	IPI00649326	Myosin-XVIIIa;Myosin	Myo18a;Myspdz;Myo1	S2028	1	16	SSSPTSHWKLAPDPSDI	SSSPTSHWKLAPDPS(1)	SSSPTSHWKLAPDPS	CK2	1.0	0.34251		Yes
60	IPI00754649	Myosin-Ic;Myosin I be	Myo1c	S6	1	4	YRASALGSDGVR	Y(0.014)RAS(0.986)ALG	YRAS(ph)ALGSDGVR	PKA	0.5	3.449E-06	Down	Yes
1256	IPI00890268	Myosin Va;Myosin-Va	Myo5a;RP24-18912.1	T1650	1	1	TSSIADEGTYLDSILR	T(0.492)S(0.254)S(0.25)	T(ph)SSIADEGTYLDSILR	PKA	0.2			No
820	IPI00464223	Myoferlin;Fer-1-like pr	Myof;Fer13;Kiaa1207	S174	1	7	GPSGTVSEAQALR	GPSGTVS(1)EAQALR	GPSGTVS(ph)EAQALR	CK1	1.0	0.39948		Yes
976	IPI00111831	Nascent polypeptide-as	Naca;Gm1878;Naca	S2138	1	22	VQGEAVSNIQENTQTPT	VQGEAVSNIQENTQTPT	VQGEAVSNIQENTQTPT	CK2	1.1	0.46642		Yes
911	IPI00111831	Nascent polypeptide-as	Naca;Gm1878;Naca	T2133	1	17	VQGEAVSNIQENTQTPT	VQGEAVSNIQENTQTPT	VQGEAVSNIQENTQTPT	CK2	1.1	0.44377		Yes
69	IPI00115895	NAD kinase;Poly(P)/AT	Nadk;Nadk;RP23-183D	S46	1	1	SLSASPALGSTK	S(0.986)LS(0.014)ASPA	S(ph)SLSASPALGSTK	GSK3	0.6	3.6E-05	Down	Yes
67	IPI00458056	Nuclear cap-binding pr	Ncbp1	S22	1	3	KTSDANETEDHLESICK	KT(0.082)S(0.917)DANE	KTS(ph)DANETEDHLESICK	PKA	2.2	2.912E-05	Up	Yes
1117	IPI00309413	SH2/SH3 adaptor prote	Nck2;mNck-beta;mcG	S90	1	3	DASPTPSTDAEYPANGS	DAS(0.321)PT(0.321)PS	DAS(ph)PTPSTDAEYPA	CAMK2				No
1121	IPI00309413	SH2/SH3 adaptor prote	Nck2;mNck-beta;mcG	S94	1	7	DASPTPSTDAEYPANGS	DAS(0.321)PT(0.321)PS	DAS(ph)PTPSTDAEYPA	CK1				No
1124	IPI00309413	SH2/SH3 adaptor prote	Nck2;mNck-beta;mcG	T92	1	5	DASPTPSTDAEYPANGS	DAS(0.321)PT(0.321)PS	DAS(ph)PTPSTDAEYPANGSGADR					No
555	IPI00317794	Nucleolin;Protein C23	Ncl;Nuc	S145	2	4	KEDSDEDEDEEDEDSD	KEDS(1)DEDEDEEDED	KEDS(ph)DEDEDEEDED	(ph)DEDEDEEDEF	1.2	0.27879		Yes
556	IPI00317794	Nucleolin;Protein C23	Ncl;Nuc	S157	2	16	KEDSDEDEDEEDEDSD	KEDS(1)DEDEDEEDED	KEDS(ph)DEDEDEEDED	(ph)DEDEDEEDEF	1.2	0.27879		Yes
142	IPI00313525	Nuclear receptor coact	Ncoa5;Ncoa5;RP23-61	S29	2	3	DRSPIRGS	DRS(1)PIRGS(1)PR	DRS(ph)PIRGS(ph)PR	CDK2	1.6	0.015565	Up	Yes
143	IPI00313525	Nuclear receptor coact	Ncoa5;Ncoa5;RP23-61	S34	2	8	DRSPIRGS	DRS(1)PIRGS(1)PR	DRS(ph)PIRGS(ph)PR	CDK2	1.6	0.015565	Up	Yes
1016	IPI00274795	Nuclear receptor corep	Ncor1;Rxp13;Ncor1;N	S225	1	19	QQQLEEEAAKPPPEKPK	QQQLEEEAAKPPPEKPK	QQQLEEEAAKPPPEKPK	WW GroupIV	1.1	0.48331		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?	
203	IPI00123871	Nuclear receptor corep	Ncor2;Smrt;Ncor2;Smr	S1023	1	3	SRSVPVPAEK	S(0.112)RS(0.888)PVPP	_SRS(ph)PVPPAEK_		1.4	0.057045		Yes	
1302	IPI00123871	Nuclear receptor corep	Ncor2;Smrt;Ncor2;Smr	S359	1	6	VGQRGSLMSAAR	VGQRGS(1)GLMSAAR	(ca)VGQRGS(ph)GLSM	PKA				Yes	
172	IPI00125960	Protein NDRG1;N-myc	Ndr1;Ndr1;Ndr1;Tdd5	S330	1	3	TASGSSVTSLEGTR	T(0.001)AS(0.999)GSSV	TAS(ph)GSSVTSLEGTR	PKA/AKT	1.5	0.038342	Up	Yes	
54	IPI00125960	Protein NDRG1;N-myc	Ndr1;Ndr1;Ndr1;Tdd5	S333	1	6	TASGSSVTSLEGTR	T(0.007)AS(0.027)GS(O	TASGSS(ph)VTSLEGTR	CK1	0.5	9.506E-07	Down	No	
115	IPI00125960	Protein NDRG1;N-myc	Ndr1;Ndr1;Ndr1;Tdd5	T328	1	1	TASGSSVTSLEGTR	T(0.975)AS(0.025)GSSV	T(ph)ASGSSVTSLEGTR	PKA/AKT	1.8	0.0025862	Up	Yes	
709	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	S281	1	3	RSPDDDLTDEDNDMM	RPS(0.932)PDDDLT(O.0	RPS(ph)PDDDLTDEDN	PKA	1.0	0.35467		Yes	
992	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	S309	1	4	RQISEDVDPDNR	RQIS(1)EDVDPDNR	RQIS(ph)EDVDPDNR	CAMK2	1.1	0.47297		Yes	
810	IPI00462445	E3 ubiquitin-protein lig	Nedd4;Kiaa0093;Nedd	T287	1	9	RPSDDDLTDEDNDMM	RSPDDDLT(1)DEDND	RSPDDDLT(ph)DEDN	FHA1 Rad53p	1.0	0.39561		Yes	
568	IPI00649115	E3 ubiquitin-protein lig	Nedd4;Kiaa0439;Nedd	S475	1	1	SLSSPTVLSAPLEGAK	S(0.533)LS(0.395)S(O.0	S(ph)LSPTVLSAPLEG	PKD	1.2	0.28524		No	
917	IPI00127241	Serine/threonine-prote	Nek3	T477	1	6	LDEEDTDFEEDNENPDW	LDEEDT(1)DFEEDNENP	LDEEDT(ph)DFEEDNE	CK2	1.1	0.446		Yes	
173	IPI00131415	Nuclear factor 1 A-type	Nfia;Nfia;Nfia;Nfia	S310	1	8	SVEDEMDSPGEEPFYTG	SVEDEMDS(1)PGEPEFY	SVEDEMDS(ph)PGEEP	CK2	0.8	0.0388	Down	Yes	
378	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S312	1	6	DDMSSPTTMM	DDMSS(0.003)S(0.966)	DDMSS(ph)PTTMM_	Polo box	1.3	0.18755		Yes	
1235	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S325	1	8	KPEKPLFSSTSPQDSSPR	KPEKPLFS(0.24)S(0.24)	KPEKPLFS(ph)STSPQDSSPR					No	
1238	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S326	1	9	KPEKPLFSSTSPQDSSPR	KPEKPLFS(0.24)S(0.24)	KPEKPLFS(ph)STSPQD	NEK6				No	
336	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S328	1	11	KPEKPLFSSTSPQDSSPR	KPEKPLFS(0.009)T(O.0	KPEKPLFSST(ph)PQD	CK1	0.9	0.15764		Yes	
703	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S332	1	15	KPEKPLFSSTSPQDSSPR	KPEKPLFS(0.073)S(0.05	KPEKPLFSSTSPQDSS	ph CK1	1.2	0.35155		No	
1242	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	S333	1	16	KPEKPLFSSTSPQDSSPR	KPEKPLFSST(0.001)PQ	KPEKPLFSSTSPQDSS	(ph)Polo box				No	
243	IPI00130129	Nuclear factor 1 B-type	Nfib;Nfib;Nfib;Nfib	T327	1	10	KPEKPLFSSTSPQDSSPR	KPEKPLFS(0.058)S(0.05	KPEKPLFSST(ph)SPQDSSPR		0.9	0.086901		No	
326	IPI00137501	Nuclear factor 1 C-type	Nfic;Nfic;Nfic;Nfic	S322	1	11	NWTEDEIEGGISPVKK	NWTEDEIEGGIS(0.5)S(O	NWTEDEIEGGIS(ph)SPVK		1.3	0.14743		No	
327	IPI00137501	Nuclear factor 1 C-type	Nfic;Nfic;Nfic;Nfic	S323	1	12	NWTEDEIEGGISPVKK	NWTEDEIEGGIS(0.5)S(O	NWTEDEIEGGIS(ph)SPV	Polo box	1.3	0.14743		No	
997	IPI00331515	Nuclear factor 1;Nuclea	Nfix;Nfix;Nfix	S366	1	18	MAFTHHPLPVLAVRPG	MAFTHHPLPVLAVRPG	M(ox)AFTHHPLPVLAV	PKC	1.1	0.47634		Yes	
544	IPI00331515	Nuclear factor 1;Nuclea	Nfix;Nfix;Nfix;Nfix	S285	1	1	SIDSEMEESPVDVFPYG	S(0.607)IDD5(0.393)EM	S(ph)IDSEMEESPVDV	PKA	1.2	0.27349		No	
412	IPI00123474	Nuclear factor NF-kapp	Nfkb2	T425	1	13	DTDAGEGAEPRTPPEEA	DTDAGEGAEPRT(1)PP	DTDAGEGAEPRT(ph)	WW GroupIV	1.0	0.2134		Yes	
1014	IPI00421052	Nipped-B-like protein;C	Nipbl;Nipbl	S2652	1	10	AITSLGGGSPK	AITSLGGGS(1)PK	_AITSLGGG(ph)PK_	CDK1	1.1	0.48274		Yes	
1222	IPI00461536	Nucleolar protein 8	Nol8	S315	2	1	SSMSDDVDSEDELK	S(0.402)S(0.299)MS(O.2	S(ph)SM(ox)SDDVDSD	(ph)EDELK_				No	
626	IPI00461536	Nucleolar protein 8	Nol8	S324	2	10	SSMSDDVDSEDELK	S(0.402)S(0.299)MS(O.2	S(ph)SM(ox)SDDVDSD	CK2	1.2	0.31441		Yes	
944	IPI00720058	MKIAA0035 protein;Pu	Nolc1;MKIAA0035;Nolc	S563	1	5	AAKESEEEEEETEKK	AAKES(1)EEEEEEEEETE	AAKES(ph)EEEEEEEE	CK2	1.1	0.45445		Yes	
509	IPI00311453	Putative ribosomal RN	Nop2;Nol1	T169	1	15	AQDATAGVLWNEEDTD	AQDATAGVLWNEEDT(C	AQDATAGVLWNEEDT	FHA1 Rad53p	1.0	0.26113		Yes	
939	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S513	1	5	EELASDLEEMATSSAK	EELAS(1)DLEEMATSSAK	EELAS(ph)DLEEMATSS	CK2	1.1	0.45239		Yes	
1191	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S521	1	16	APKEELASDLEEMATSSA	APKEELAS(0.058)DLEEN	APKEELASDLEEMAT	(ph)SSAK				No	
1194	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S522	1	17	APKEELASDLEEMATSSA	APKEELAS(0.058)DLEEN	APKEELASDLEEMAT	(ph)SSAK				No	
357	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S529	2	3	KSSPKEEVAEPEEAAASPT	KS(0.142)S(0.858)PKEE	KSS(ph)PKEEVAAS(ph)	E Polo box	1.3	0.17259		Yes	
863	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S536	1	5	EEVASEPEEAAASPTPK	EEVAS(1)EEPEEAAASPTP	EEVAS(ph)EEPEEAAASPT	CK2	1.1	0.4217		Yes	
916	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S543	2	12	EEVASEPEEAAASPTPK	EEVAS(1)EEPEEAAAS(0.75	EEVAS(ph)EEPEEAAAS	(ph)PTTPK	1.1	0.44591		Yes	
776	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	T520	1	16	KAPKEELASDLEEMATSS	KAPKEELAS(0.002)DLEE	KAPKEELASDLEEMAT	(ph)FHA KAPP	1.2	0.38202		Yes	
454	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	S509	1	8	HIKEEPLSEEEPTSTAVP	HIKEEPLS(1)EEEPCTSTA	HIKEEPLS(ph)EEEPCT	CK2	1.2	0.23491		No	
1202	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	S516	1	15	HIKEEPLSEEEPTSTAVP	HIKEEPLS(0.002)EEEPCT	HIKEEPLSEEEPTCT	(ph)STAVPSPEKK_				Yes	
772	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	S521	1	20	HIKEEPLSEEEPTSTAVP	HIKEEPLS(0.089)EEEPCT	HIKEEPLSEEEPTCT	(ph)SERK/MAPK	1.2	0.37952		No	
1209	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	T515	1	14	HIKEEPLSEEEPTSTAVP	HIKEEPLS(0.002)EEEPCT	HIKEEPLSEEEPTCT	(ph)FHA KAPP				No	
1214	IPI00463468	Nucleolar protein 58;N	Nop58;Nol5	T517	1	16	HIKEEPLSEEEPTSTAVP	HIKEEPLS(0.002)EEEPCT	HIKEEPLSEEEPTCT	(ph)STAVPSPEKK				No	
404	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;RP	S70	1	25	TVSLGAGAKDELHIVEAE	T(0.001)VS(0.001)LGAG	TVSLGAGAKDELHIVEA	CDK2	1.3	0.20948		Yes	
13	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;RP	T75	1	30	TVSLGAGAKDELHIVEAE	T(0.056)VS(0.06)LGAG	TVSLGAGAKDELHIVEA	AURORA	0.1	8.074E-39	Down	No	
14	IPI00127415	Nucleophosmin;Nucleo	Npm1;Npm1;Npm1;RP	T78	1	33	TVSLGAGAKDELHIVEAE	T(0.056)VS(0.06)LGAG	TVSLGAGAKDELHIVEA	EAMNYEGSPIKVT	(ph)LA	0.1	8.074E-39	Down	No
296	IPI00856881	Glucocorticoid recepto	Nr3c1;Nr3c1;Gr1;Gr1	N168	1	10	SSTPAAGCATPTEKEFPQ	SSTPAAGCAT(0.838)PT	SSTPAAGCAT(ph)PTEK	CK2	1.8	0.0012795	Up	Yes	
286	IPI00664246	Putative uncharacterize	Nrbp1;Nrbp;Nrbp1;Ma	T439	1	1	TPTPEPAEVETR	T(0.643)PT(0.357)PEPA	T(ph)TPTPEPAEVETR	ERK/MAPK	1.3	0.11473		Yes	
373	IPI00664246	Putative uncharacterize	Nrbp1;Nrbp;Nrbp1;Ma	T441	1	3	TPTPEPAEVETR	T(0.006)PT(0.994)PEPA	TPT(ph)PEPAEVETR		1.3	0.18431		Yes	
254	IPI00648408	Nardilysin, N-arginine d	Nrd1;RP23-188A12.1-0	S85	1	6	LGAESEEEGR	LGADES(1)EEEGR	LGADES(ph)EEEGR	CK2	0.9	0.098462		Yes	
661	IPI00387232	NSFL1 cofactor p47;p9	Nsfl1c;Nsf1c;Nsf1c;Ns	S116	1	3	KKSPNELVDDLK	KKS(1)PNELVDDLK	_KKS(ph)PNELVDDLK_	PKA	1.2	0.33424		Yes	
240	IPI00894870	tRNA (cytosine-5)-met	Nsun2;D13Wsu123e;M	S23	1	15	RFQPPQPEGEEDASDG	RFQPPQPEGEEDAS(1)	RFQPPQPEGEEDAS	(ph)DGGR	0.9	0.084595		Yes	
934	IPI00894870	tRNA (cytosine-5)-met	Nsun2;D13Wsu123e;M	S723	1	12	EGVILTNNENASPEQPGD	EGVILT(N)ENASAS(1)PEQ	EGVILTNNENASAS	(ph)PEQPGDEDAK	1.1	0.45035		Yes	
1039	IPI00894870	tRNA (cytosine-5)-met	Nsun2;D13Wsu123e;M	T717	1	6	EGVILTNNENASPEQPGD	EGVILT(1)ENASAS(0.0	(ca)EGVILT(ph)NNENAS	PEQPGDEDAK_	1.1	0.49101		No	
307	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S81	1	1	SGKLSQELDFVSHNVR	S(0.893)GKLS(0.107)QE	S(ph)GKLSQELDFVSHN	GSK3	1.3	0.13325		Yes	
292	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S85	1	5	SGKLSQELDFVSHNVR	SGKLS(1)QELDFVSHNVR	SGKLS(ph)QELDFVSHN	CK1	1.3	0.1221		Yes	
1171	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S92	1	12	SGKLSQELDFVSHNVR	S(0.272)GKLS(0.261)QE	SGKLSQELDFVSHNVR					No	
1320	IPI00341869	Nuclear ubiquitinous cas	Nucks1;Nucks	S14	1	6	KVVDYSQFQESDDADEDY	KVVDY(0.078)S(0.461)Q	(ca)KVVDYS(ph)QFQESDD	DADEDYGR_				No	
668	IPI00341869	Nuclear ubiquitinous cas	Nucks1;Nucks	S19	1	10	VVDYSQFQESDDADEDY	VVDYSQFQES(1)DDADE	VVDYSQFQES(ph)DDADE	DADEDYGR	1.2	0.33938		Yes	
388	IPI00341869	Nuclear ubiquitinous cas	Nucks1;Nucks	S214	1	8	EEDEEAESPEPKK	EEDEEAES(1)PEPKK	EEDEEAES(ph)PEPKK	CK2	1.3	0.19373		Yes	
361	IPI00341869	Nuclear ubiquitinous cas	Nucks1;Nucks	S58	1	6	NSQEDSEDESEKDKV	NSQEDS(0.986)EDS(O.0	NSQEDS(ph)EDSEKDK	CK1	1.3	0.17803		Yes	
650	IPI00341869	Nuclear ubiquitinous cas	Nucks1;Nucks	S61	2	9	NSQEDSEDESEKDKV	NS(0.002)QEDS(0.998)	NSQEDS(ph)EDS(ph)E	CK1	1.2	0.32842		Yes	
1053	IPI00130438	7,8-dihydro-8-oxoguan	Nudt1;Mth1	S2	2	2	MSTSRlyTLVVLVLPQQR	MS(0.385)T(0.385)S(O.2	MS(ph)TSLRly(ph)TLVVL	LPQQR				No	
1054	IPI00130438	7,8-dihydro-8-oxoguan	Nudt1;Mth1	S4	2	2	MSTSRlyTLVVLVLPQQR	MS(0.339)T(0.339)S(O.2	MS(ph)TSLRly(ph)TLVVL	LPQQR				No	
1055	IPI00130438	7,8-dihydro-8-oxoguan	Nudt1;Mth1	T3	2	3	MSTSRlyTLVVLVLPQQR	MS(0.385)T(0.385)S(O.2	MS(ph)TSLRly(ph)TLVVL	FHA2 Rad53p				No	
1056	IPI00130438	7,8-dihydro-8-oxoguan	Nudt1;Mth1	T8	2	8	MSTSRlyTLVVLVLPQQR	MS(0.334)T(0.334)S(O.2	MS(ph)TSLRly(ph)TLVVL	CAMK2				No	
4	IPI00130438	7,8-dihydro-8-oxoguan	Nudt1;Mth1	Y7	2	7	MSTSRlyTLVVLVLPQQR	MS(0.385)T(0.385)S(O.2	MS(ph)TSLRly(ph)TLVVL	ALK	0.02	1E-109	Down	No	
360	IPI00263048	Putative uncharacterize	Numa1	S1739	1	14	TQPDGTSVPGEPASPI	TQPDGTSVPGEPAS(O.9	TQPDGTSVPGEPAS	(ph)WW GroupIV	1.3	0.17483		Yes	
1318	IPI00263048	Putative uncharacterize	Numa1	S1742	1	17	TQPDGTSVPGEPASPI	T(0.029)QPDGT(0.031)	TQPDGTSVPGEPAS	(ph)CK1				No	



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
1271	IPI00129535	Nuclear pore complex	Nup160;Gtl1-13;Kiaa0	S1113	1	14	LIRPEYAWIVQPASGAVS	LIRPEY(0.225)AWIVQPA	LIRPEYAWIVQPAS(ph)	GSK3				No
1274	IPI00129535	Nuclear pore complex	Nup160;Gtl1-13;Kiaa0	S1117	1	18	LIRPEYAWIVQPASGAVS	LIRPEY(0.225)AWIVQPA	LIRPEYAWIVQPAS(ph)	CK1				No
483	IPI00129535	Nuclear pore complex	Nup160;Gtl1-13;Kiaa0	S1123	1	24	LIRPEYAWIVQPASGAVS	LIRPEYAWIVQPAS(0.00)	LIRPEYAWIVQPASGAV	CDK2	1.2	0.24944		Yes
1280	IPI00129535	Nuclear pore complex	Nup160;Gtl1-13;Kiaa0	Y1105	1	6	LIRPEYAWIVQPASGAVS	LIRPEY(0.331)AWIVQPA	LIRPEY(ph)AWIVQPAS	ALK				No
213	IPI00474558	Nup98 protein;Nup98	Nup98;Nup98	S297	1	6	YGLQDSDEEEEEHPKK	Y(0.007)GLQDS(0.993)I	YGLQDS(ph)DEEEEEH	CK2	1.4	0.063441		Yes
365	IPI00474558	Nup98 protein;Nup98	Nup98;Nup98	S436	1	16	FGHIPKGETVQVEICSPR	FGHIPKGETE(0.002)VQ	FGHIPKGETVQVEICSP	CDK1	1.3	0.18047		Yes
1218	IPI00869414	NACHT and WD repeat	Nwd1	S1484	3	5	IIPTSNMGFMAPTSHGYLIR	IIPT(0.585)S(0.585)NGF	(ca)IIPT(ph)S(ph)NGFM	(ox)APTS(HG)Y(ph)LIR				No
1221	IPI00869414	NACHT and WD repeat	Nwd1	S1492	3	13	IIPTSNMGFMAPTSHGYLIR	IIPT(0.585)S(0.585)NGF	(ca)IIPT(ph)S(ph)NGFM	(ox)APTS(HG)Y(ph)LIR				No
1227	IPI00869414	NACHT and WD repeat	Nwd1	Y1495	3	16	IIPTSNMGFMAPTSHGYLIR	IIPT(0.585)S(0.585)NGF	(ca)IIPT(ph)S(ph)NGFM	(ox)APTS(HG)Y(ph)LIR				Yes
1072	IPI00750945	Outer dense fiber prote	Odf2;Odf84;Odf2;Odf8	S49	1	1	SSTPLPHVHVVDENTPVHH	S(0.374)S(0.313)T(0.31)	S(ph)STPLPHVHVVDENTPVHH					No
1065	IPI00162970	Olfactory receptor 62	OlfR2;RP23-154A15.3	S140	1	6	YKIVMSPLLR	YKIVMS(1)PLLR	YKIVM(ox)S(ph)PLLR					Yes
710	IPI00918049	Oxysterol-binding prote	Osbp11	S188	1	6	SFSLASSGNPISQQR	S(0.004)FS(0.004)LAS(0	SFSLAS(ph)SGNSPISQQR	CK1	1.0	0.35529		Yes
800	IPI00918049	Oxysterol-binding prote	Osbp11	S192	1	10	SFSLASSGNPISQQR	S(0.001)FS(0.001)LAS(0	SFSLASSGN(ph)PISQQR	CK1	1.0	0.39245		Yes
1143	IPI00462728	MKIAA0704 protein;Ox	Osbp13;mkIAA0704;Osi	S302	1	3	LHSSNPNLSTLDFGEEK	LHS(0.498)S(0.498)NPN	LHS(ph)SNPNLSTLDFG	CAMK2				No
1145	IPI00462728	MKIAA0704 protein;Ox	Osbp13;mkIAA0704;Osi	S303	1	4	LHSSNPNLSTLDFGEEK	LHS(0.498)S(0.498)NPN	LHS(ph)SNPNLSTLDFG	NEK6				No
1069	IPI00221706	Osteopetrosis-associat	Ostm1;Gl	S329	1	4	SSTSFAHQENAT	S(0.016)S(0.012)T(0.01	SSTS(ph)FAHQENAT	CK1				No
265	IPI00463065	Novel protein similar to	OTTMUSG0000001914	S384	1	3	DASPPGSEPEIDR	DAS(1)PPGSEPEIDR	DAS(ph)PPGSEPEIDR	CAMK2	1.4	0.10341		Yes
191	IPI00463065	Novel protein similar to	OTTMUSG0000001914	S388	2	7	DASPPGSEPEIDR	DAS(1)PPGSEPEIDR	DAS(ph)PPGSEPEIDR	CK2	1.5	0.048633	Up	Yes
62	IPI00654216	Putative uncharacterize	Oxr1;Oxr1;C7;Gm1238	S194	1	3	VVSTSEEEEEAFTEK	VVVS(0.994)S(0.001)T(0	VVVS(ph)TSEEEEEAFTEK	CAMK2	2.3	5.448E-06	Up	Yes
70	IPI00654216	Putative uncharacterize	Oxr1;Oxr1;C7;Gm1238	S195	1	4	VVSTSEEEEEAFTEK	VVVS(0.071)S(0.851)T(0	VVVS(ph)TSEEEEEAFTEK	CK2	2.1	5.388E-05	Up	Yes
819	IPI00119305	Proliferation-associate	Pa2g4;Ebp1;Pifap	S2	1	1	SGEDEQQEQTIAEDLVV	S(1)GEDEQQEQTIAEDLVV	S(ph)GEDEQQEQTIAEDLVV	VTK	1.1	0.39936		Yes
912	IPI00229884	Serine/threonine-prote	Pak2	S141	1	3	YLSFTTPEEK	YLS(0.997)FT(0.003)PP	YLS(ph)FTTPEEK		1.1	0.44405		Yes
284	IPI00830990	p21 (CDKN1A)-activate	Pak3;RP23-4506.1-009	S207	1	12	TASEPPLAPPVSEEEEEE	TASEPPLAPPV(1)EEED	TASEPPLAPPV(ph)EE	CK2	0.9	0.11283		Yes
77	IPI00129298	Paralemmin;Paralemm	Palm;Palm	T141	2	10	SETLVNAQQTPLGTGPK	SETLVNAQQT(1)PLGT(1)	SETLVNAQQT(ph)PLGT(ph)PK		0.6	0.0002022	Down	Yes
78	IPI00129298	Paralemmin;Paralemm	Palm;Palm	T145	2	14	SETLVNAQQTPLGTGPK	SETLVNAQQT(1)PLGT(1)	SETLVNAQQT(ph)PLGT(ph)PK		0.6	0.0002022	Down	Yes
158	IPI00470003	Alpha-parvin;Actopaxin	Parva;Actp;MNCb-030	S14	1	1	SPTPKPSSR	S(0.507)PT(0.076)PKS(0	(ca)S(ph)PTPKPSSR	WW GroupIV	0.8	0.028085	Down	No
174	IPI00470003	Alpha-parvin;Actopaxin	Parva;Actp;MNCb-030	T116	2	9	SPLVPKSPTPKSPSSR	SPLVPKS(0.215)PT(0.79	SPLVPKSPTPKSPSSR	PKS(ph)CDK1	1.5	0.038965	Up	Yes
1298	IPI00127707	Poly(rC)-binding protei	Pcbp2;Cbp;Hnrnp;Hnr	S183	1	11	GVTIYRPRKPSVIFAG	GVTI(0.001)PY(0.022)R	GVTIYRPRKPS(ph)S	SPVIFAGGQDR				No
922	IPI00127707	Poly(rC)-binding protei	Pcbp2;Cbp;Hnrnp;Hnr	S184	1	12	GVTIYRPRKPSVIFAG	GVTIYRPRKPS(0.133)S(0	GVTIYRPRKPS(ph)S	SPVIFAGGQDR	1.1	0.44715		No
1303	IPI00127707	Poly(rC)-binding protei	Pcbp2;Cbp;Hnrnp;Hnr	S185	1	13	GVTIYRPRKPSVIFAG	GVTIY(0.001)RPKPS(0	GVTIYRPRKPS(ph)S	Polo box				No
393	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S65	1	6	VTNAISPESPGVGR	VTNAIS(1)PESPGVGR	VTNAIS(ph)PESPGVGR	GSK3	1.3	0.2016		Yes
366	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S69	2	10	VTNAISPESPGVGR	VT(0.218)NAIS(0.744)P	VTNAIS(ph)PES(ph)P	Polo box	0.9	0.18082		Yes
306	IPI00115490	Choline-phosphate cyti	Pcyt1a;Ctptc;Pcyt1	S315	1	6	MLQAISPK	MLQAIS(1)PK	M(ox)LQAIS(ph)PK	CDK1	0.9	0.13221		Yes
1003	IPI00352475	28 kDa heat- and acid-s	Pdap1	S57	2	1	SLDSDSEDEDDDDYQQK	S(0.711)LDS(0.289)DES	S(ph)LDSDES(ph)EDE	AURORA	1.1	0.47813		No
1004	IPI00352475	28 kDa heat- and acid-s	Pdap1	S63	2	7	SLDSDSEDEDDDDYQQK	S(0.711)LDS(0.289)DES	S(ph)LDSDES(ph)EDE	CK2	1.1	0.47813		Yes
921	IPI00551454	Protein RRP5 homolog;	Pdcd11;Alg4;Kiaa0185	S1490	1	10	KSGAAEEDDSGVVYR	KS(0.005)GAAEEDDS(0	KSGAAEEDDS(ph)GVE	CK2	1.1	0.44706		Yes
36	IPI00323064	Programmed cell death	Pdcd4;Ma3;Tis	S457	1	4	RFVSEGGDGR	RFVS(1)EGDGGRR	RFVS(ph)EGDGGRR	PKA/AKT	3.8	2.594E-13	Up	Yes
39	IPI00323064	Programmed cell death	Pdcd4;Ma3;Tis	S76	1	7	DSGRGDSVSDNGSEAVR	DSGRGDS(0.988)VS(0.0	DSGRGDS(ph)VSDNGS	CAMK2	3.5	1.363E-11	Up	Yes
779	IPI00323064	Programmed cell death	Pdcd4;Ma3;Tis	S94	1	8	SGVAVPTSPK	SGVAVPT(0.072)S(0.92	SGVAVPT(ph)PK	WW GroupIV	1.1	0.38387		Yes
547	IPI00323064	Programmed cell death	Pdcd4;Ma3;Tis	T93	1	7	SGVAVPTSPK	SGVAVPT(0.913)S(0.08	SGVAVPT(ph)SPK		1.2	0.27483		Yes
852	IPI00885252	Programmed cell death	Pdcd5;Tfar19	S198	1	5	KVMDSDEDDADY	KVMDS(1)DEDDADY	KVM(ox)DS(ph)DEDDADY		1.1	0.41782		Yes
654	IPI00885252	Programmed cell death	Pdcd5;Tfar19	Y205	1	13	RKVMDSDEDDADY	RKVMDS(0.5)DEDDADY	RKVMDS(ph)DEDDADY		1.2	0.3309		No
137	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	S232	1	6	YGMGTSVER	YGMGT(0.039)S(0.961)	YGMGT(S)ph)VER		0.7	0.012838	Down	Yes
262	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	S293	1	5	YHGHSMDPVGYSYR	YHGHS(0.995)MS(0.005	YHGHS(ph)MDPVGYSYR		1.4	0.10133		Yes
1036	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	S295	1	7	YHGHSMDPVGYSYR	Y(0.007)HGHS(0.178)M	YHGHSM(ox)S(ph)DPVGYSYR		1.1	0.48975		Yes
226	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	S300	2	12	YHGHSMDPVGYSYR	Y(0.592)HGHS(0.404)M	Y(ph)HGHSMDPVGVS(ph)YR		0.8	0.072601		Yes
104	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	T231	1	5	YGMGTSVER	YGMGT(0.5)S(0.5)VER	YGMGT(ph)SVER	CK2	0.7	0.0016225	Down	No
196	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	Y289	2	1	YHGHSMDPVGYSYR	Y(0.592)HGHS(0.404)M	Y(ph)HGHSMDPVGVS(ph)YR		1.4	0.054334		Yes
1116	IPI00337893	Pyruvate dehydrogenase	Pdha1;Pdha-1	Y301	2	13	YHGHSMDPVGYSYR	Y(0.141)HGHS(0.753)M	YHGHS(ph)MDPVGVS(ph)YR					No
171	IPI00222496	Protein disulfide-isome	Pdia6;Txndc7	S433	1	13	DGELPVEDDIDLSVDL	DGELPVEDDIDLS(1)DVE	DGELPVEDDIDLS(ph)D	CK2	0.8	0.036903	Down	Yes
368	IPI00153375	PDZ and LIM domain pr	Pdlim2;Pdlim2	S204	1	10	VLLHSPGRPSSR	VLLHS(0.032)PGRPS(0.5	(ca)VLLHSPGRPS(ph)S	PKA	0.9	0.18123		Yes
558	IPI00153375	PDZ and LIM domain pr	Pdlim2;Pdlim2	S205	1	11	VLLHSPGRPSSR	VLLHS(0.001)PGRPS(0	VLLHSPGRPS(ph)PR	PKC	1.0	0.28019		Yes
478	IPI00323609	3-phosphoinositide-deg	Pdpk1;Pdk1;Pdpk1;Pdg	S244	1	3	ANSFVGTAAQVSPPELLTE	ANS(1)FVGTAAQVSPPELL	ANS(ph)FVGTAAQVSP	CAMK2	1.0	0.24617		Yes
815	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1358	1	3	AESPETSAVESTQSTPQK	AES(1)PETSAVESTQSTP	AES(ph)PETSAVESTQS	CAMK2	1.1	0.39803		Yes
1146	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1362	1	7	AESPETSAVESTQSTPQK	AES(0.324)PET(0.324)S	AES(ph)PETSAVESTQS	CK2				No
1176	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	T1361	1	6	AESPETSAVESTQSTPQK	AES(0.324)PET(0.324)S	AES(ph)PETSAVESTQS	CK1				No
1178	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	T1370	1	15	AESPETSAVESTQSTPQK	AES(0.088)PET(0.088)S	AESPETSAVESTQST(ph)	Polo box				No
1149	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1156	3	5	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	GSK3				No
1154	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1159	3	8	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	CK1				No
1159	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1160	3	9	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	CK1				No
1164	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1161	3	10	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	GSK3				No
1166	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1162	3	11	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	CK1				No
1172	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1165	3	14	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	CK1				No
1002	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1166	1	15	METVSNASSSSNPSSPG	METVSNASSSSNPSS(0.0	M(ox)ETVSNASSSSNP	WW GroupIV	1.1	0.47806		No
1181	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	T1154	3	3	METVSNASSSSNPSSPG	MET(0.439)VS(0.439)N	MET(ph)VSNAAS(ph)S	CAMK2				No
274	IPI00121013	Astrocytic phosphopro	Pea15;Pea15a;Pea15;P	S116	1	7	DIIRQPSSEEEIHK	DIIRQPS(1)EEIHK	DIIRQPS(ph)EEIHK	PKD	0.9	0.10757		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
109	IPI0055140	Phosphoglucosyltransferase-1	Pgm1;Pgm2;Pgm2;RP2	S117	1	10	AIGGILTASHNPPGGNG	AIGGILT(0.004)AS(0.9)	(ca)AIGGILTAS(ph)HN	NEK6	0.7	0.0021296	Down	Yes
98	IPI0055140	Phosphoglucosyltransferase-1	Pgm1;Pgm2;Pgm2;RP2	T115	1	8	AIGGILTASHNPPGGNG	AIGGILT(0.5)AS(0.5)HN	AIGGILT(ph)ASHNPPGGNGDFGIK		0.6	0.0012542	Down	No
762	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	S181	1	9	EGEPTVYSDDDEPKDET	EGEPT(0.001)YV(0.02)	EGEPTVYS(ph)DDEEPCCK2		1.2	0.37663	Down	Yes
1092	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	T178	1	6	EGEPTVYSDDDEPKDET	EGEPT(0.304)YV(0.30)	EGEPT(ph)YVSDDEEPLK1					No
288	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	Y180	1	8	EGEPTVYSDDDEPKDET	EGEPT(0.049)YV(0.76)	EGEPTVY(ph)SDDEEPKDETARK		1.3	0.11601	Down	Yes
1127	IPI00648030	Phosphatase and actin	Phactr4;Kiaa4120;Phac	S126	1	1	SSSPVLVEEPEER	S(0.475)S(0.263)S(0.26)	S(ph)SSSPVLVEEPEER	CK1				No
785	IPI00123868	PHD finger protein 2;G	Phf2	S873	1	8	DSDYVYPSLESDENPVF	DSDYVY(0.003)PS(0.87)	DSDYVYPS(ph)LESDENPVFK		1.0	0.38534	Down	Yes
861	IPI00123868	PHD finger protein 2;G	Phf2	S876	1	11	DSDYVYPSLESDENPVF	DSDYVYPS(0.009)LES(0)	DSDYVYPSLESDENPVFK		1.1	0.42124	Down	Yes
1369	IPI00377615	Phf3 protein	Phf3	S1147	1	23	KHSDNEAESLADALSSTT	KHS(0.043)DNEAES(0.0)	KHSDNEAESLADALSSTNLT(ph)SDFEEEKQESPK					No
895	IPI00377615	Phf3 protein	Phf3	S1157	1	33	KHSDNEAESLADALSSTT	KHS(0.001)DNEAES(0.0)	KHSDNEAESLADALSSTCDK1		1.1	0.4356	Down	No
396	IPI00377615	Phf3 protein	Phf3	S377	1	12	NTDIVDKPENSQRNE	NT(0.001)VDIVDKPENS(0)	NTDIVDKPENS(ph)PCDK2		1.3	0.20365	Down	Yes
40	IPI00377615	Phf3 protein;Phf3 prote	Phf3;Phf3	S658	1	1	SFSLDEPPLFIPDNIAVK	S(0.613)FS(0.387)JDEP	S(ph)FSLDEPPLFIPDNIAVK	CK1	3.5	1.428E-11	Up	No
1364	IPI00137302	PHD finger protein 6;Ph	Phf6;Kiaa1823;Phf6;Kia	S154	1	21	TAHNSADLEESFNEHEL	TAHNSADLEES(0.001)	TAHNSADLEESFNEHEL	NEK6				No
1365	IPI00137302	PHD finger protein 6;Ph	Phf6;Kiaa1823;Phf6;Kia	S155	1	22	TAHNSADLEESFNEHEL	TAHNSADLEES(0.001)	TAHNSADLEESFNEHEL	WW GroupIV				No
595	IPI00311490	PH-interacting protein;	Phip;Ndrp;Wdr11	S1783	1	9	TAFYNEDDSEEEQR	TAFYNEDDS(1)EEEQR	TAFYNEDDS(ph)EEEQR	CK2	1.0	0.29651	Down	No
1180	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S465	1	3	RLSAGTTVADVQK	RLS(0.333)AGT(0.333)T	RLS(ph)AGTTVADVQK	PKA				Yes
821	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S486	1	4	LQLSDEESVFEDALVCPD	LQLS(1)DEESVFEDALVC	LQLS(ph)DEESVFEDALV	CK2	1.0	0.39999	Down	Yes
893	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S490	1	8	LQLSDEESVFEDALVCPD	LQLS(0.105)DEES(0.89)	LQLSDEES(ph)VFEDALV	PLK	1.1	0.4349	Down	Yes
476	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S510	1	3	KGSLQDQVDVAGFNLGH	KGS(1)LQDQVDVAGFNLGH	KGS(ph)LQDQVDVAGFNLGH	PKA	1.2	0.24538	Down	Yes
111	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	T468	1	6	RLSAGTTVADVQK	RLS(0.112)AGT(0.777)T	RLSAGT(ph)TVADVQK	CK1	1.8	0.0023391	Up	Yes
1182	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	T469	1	7	RLSAGTTVADVQK	RLS(0.333)AGT(0.333)T	RLS(ph)AGTTVADVQK	FHA1 Rad53p				No
369	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S981	1	8	AHLPLGQSNCSGSLPH3	AHLPLGQS(0.561)NS(0)	AHLPLGQS(ph)NSCSGSLPH3	NEK6	1.3	0.18146	Down	No
1195	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S983	1	10	AHLPLGQSNCSGSLPH3	AHLPLGQS(0.498)NS(0)	AHLPLGQS(ph)NSCSGSLPH3LATMTK					No
643	IPI00403827	Pleckstrin homology-lik	Phldb2;L5b;Phldb2;L5	S986	1	13	AHLPLGQSNCSGSLPH3	AHLPLGQS(0.035)NS(0)	AHLPLGQSNCSGSLPH3	CK1	1.0	0.32465	Down	Yes
954	IPI00881116	PHD and RING finger do	Phrf1;Kiaa1542;Phrf1;K	S1201	1	3	EVSPAPATQGESR	EVS(1)PAPATQGESR	EVS(ph)PAPATQGESR	CAMK2	1.1	0.4576	Down	Yes
295	IPI00918347	Phosphatidylinositol-4-	Pip5k1c;Kiaa0589;Pip5	S554	1	3	TQSSGQDGRPQEEPAHA	T(0.167)QDS(0.696)S(0.1)	TQS(ph)SGQDGRPQEEPAHA	PKA/AKT	1.3	0.12314	Down	No
231	IPI00884540	Polycystin-2 delta 7 var	Pkd2;Pkd2	S806	1	1	SLDSEEDDEDSGHSR	S(0.558)LDDS(0.441)EE	S(ph)LDDSSEEDDEDSGHSR	GSK3	0.9	0.075253	Down	No
435	IPI00884540	Polycystin-2 delta 7 var	Pkd2;Pkd2	S810	1	5	SLDSEEDDEDSGHSR	LDDS(1)EEEDDEDSGH	LDDS(ph)EEEDDEDSGHSR	CK2	1.0	0.22764	Down	Yes
497	IPI00474711	Putative uncharacterize	Pkn1;Pkn1;Pkn1;Prk1;Pr	S925	1	18	TDVSNDFEFTGEAPTLS	TDVSNDFEFTGEAPT(0)	TDVSNDFEFTGEAPTLCCK2		1.0	0.25732	Down	Yes
1066	IPI00474711	Putative uncharacterize	Pkn1;Pkn1;Pkn1;Prk1;Pr	T781	1	1	TSTFCGTFEFLAPEVLTDT	T(0.327)S(0.224)T(0.22)	T(ph)STFCGTFEFLAPEVLTDTSYTR					No
26	IPI00312414	Serine/threonine-prote	Pkn2;Prkl2;Pkn2;Prkl	S581	1	2	ASSLGETDESSLER	AS(0.5)S(0.5)JLGETDESS	AS(ph)SLGETDESSLER	PKA	6.7	1.05E-25	Up	No
27	IPI00312414	Serine/threonine-prote	Pkn2;Prkl2;Pkn2;Prkl	S582	1	3	ASSLGETDESSLER	AS(0.5)S(0.5)JLGETDESS	AS(ph)SLGETDESSLER	CAMK2	6.7	1.05E-25	Up	No
1089	IPI00312414	Serine/threonine-prote	Pkn2;Prkl2;Pkn2;Prkl	T813	1	1	TSTFCGTFEFLAPEVLTET	T(0.306)S(0.231)T(0.23)	T(ph)STFCGTFEFLAPEVLTETSYTR					No
507	IPI00312414	Serine/threonine-prote	Pkn2;Prkl2;Pkn2;Prkl	T957	1	20	GREDVSNDFEFTSEAPI	GREDVSNDFEFTS(0.0)	GREDVSNDFEFTSEAPI	CK2	1.2	0.26053	Down	Yes
646	IPI00111169	Cytosolic phospholipase	Pla2g4a;Cpla2;Pla2g4;P	S437	1	10	HIVSNDSDDSDDEAQQ	HIVSNDSDDSD(1)DDEAQQ	HIVSNDSDDSD(ph)DDEAQQ	CK2	1.0	0.3258	Down	Yes
655	IPI00130046	Plcd1 protein;1-phosph	Plcd1;Plcd1;Plcd	S460	1	20	KLGLLPAGGENGPEAT	KLGLLPAGGENGPEAT	KLGLLPAGGENGPEATDVS(ph)DEDEAAEMED		1.0	0.33217	Down	Yes
1203	IPI00400215	Plectin-1;Plectin-6	Plec1	S20	1	3	RTSSEDNLYLAVLR	RT(0.333)S(0.333)S(0.3)	RT(ph)SSEDNLYLAVLR	PKA				No
204	IPI00400215	Plectin-1;Plectin-6	Plec1	S21	1	3	TSSSEDNLYLAVLR	T(0.083)S(0.035)S(0.88)	TSS(ph)EDNLYLAVLR	PKA	0.8	0.058354	Down	Yes
156	IPI00400215	Plectin-1;Plectin-6	Plec1	T19	1	2	RTSSEDNLYLAVLR	RT(0.748)S(0.126)S(0.1)	RT(ph)SSEDNLYLAVLR	CK2	0.8	0.027906	Down	No
71	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4243	1	1	SSSVGSSSSYPISAGPR	S(0.558)S(0.288)S(0.15)	S(ph)SSSVGSSSSYPISAGPR	PKA/AKT	2.1	6.85E-05	Up	No
74	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4245	1	3	SSSVGSSSSYPISAGPR	S(0.103)S(0.06)S(0.837)	SSS(ph)VGSSSSYPISAGPR	PKA/AKT	2.1	8.494E-05	Up	Yes
1272	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4255	1	13	SSSVGSSSSYPISAGPR	S(0.066)S(0.067)S(0.06)	SSSVGSSSSYPIS(ph)SA	CK1				No
1275	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4256	1	14	SSSVGSSSSYPISAGPR	S(0.066)S(0.067)S(0.06)	SSSVGSSSSYPIS(ph)SAGPR					No
138	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4472	1	4	GYYSPYVSGSGTAGSR	GY(0.004)Y(0.06)S(0.93)	GYYSPYVSGSGTAGSR		0.7	0.013447	Down	Yes
1253	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4477	1	9	GYYSPYVSGSGTAGSR	GY(0.055)Y(0.055)S(0.0)	GYYSPYVSGSGTAGSR	GSK3				No
1257	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4479	1	11	GYYSPYVSGSGTAGSR	GY(0.055)Y(0.055)S(0.0)	GYYSPYVSGSGTAGSR	CK1				No
1261	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4481	1	13	GYYSPYVSGSGTAGSR	GY(0.055)Y(0.055)S(0.0)	GYYSPYVSGSGTAGSR	GSK3				No
1266	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4485	1	17	GYYSPYVSGSGTAGSR	GY(0.055)Y(0.055)S(0.0)	GYYSPYVSGSGTAGSR	GSK3				No
534	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S580	1	7	NDESQLSPATR	NDESQLS(0.995)PAT(0)	NDESQLS(ph)PATR	CK1	1.0	0.26961	Down	Yes
466	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	T3889	1	4	KQITVEELVLR	KQIT(1)VEELVLR	KQIT(ph)VEELVLR	PKD	1.0	0.24158	Down	Yes
1281	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	T4482	1	14	GYYSPYVSGSGTAGSR	GY(0.055)Y(0.055)S(0.0)	GYYSPYVSGSGTAGSR	CK1				No
1286	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	Y4470	1	2	GYYSPYVSGSGTAGSR	GY(0.312)Y(0.312)S(0.3)	GY(ph)YVSGSGSGTAGSR					No
1289	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	Y4471	1	3	GYYSPYVSGSGTAGSR	GY(0.312)Y(0.312)S(0.3)	GY(ph)YVSGSGSGTAGSR					No
1162	IPI00403031	Pleckstrin homology do	Plekho2;Plekho1	S394	1	2	SSSLGDLRL	S(0.06)S(0.47)S(0.47)LC	SS(ph)SLGDLRL	PKA				No
605	IPI00403031	Pleckstrin homology do	Plekho2;Plekho1	S395	1	3	SSSLGDLRL	S(0.01)S(0.005)S(0.985)	SSS(ph)SLGDLRL	CAMK2	1.2	0.3042	Down	Yes
591	IPI00229072	Probable transcription	Pml;Pml	S17	1	7	VPAPPGSPCR	VPAPPGS(1)PCR	VPAPPGS(ph)PCR	ERK/MAPK	1.2	0.29534	Down	Yes
1287	IPI00229072	Probable transcription	Pml;Pml	S528	1	3	ATSPPHLDGTSNPSTVPE	AT(0.483)S(0.483)PPHL	AT(ph)SPPHLDGTSNPSTVPEKK					No
684	IPI00110298	DNA polymerase delta	Pold3;Pold3	S306	1	5	RVDLSDEEAETHEHLK	RVDLS(1)DEEAETHEHLK	RVDLS(ph)DEEAETHEHLK	CK2	1.2	0.34422	Down	Yes
580	IPI00944006	Putative uncharacterize	Ppan;mCG 67924;Ppan	S362	1	7	ARADGSDAEDPGAPP	ARADGDS(1)DAEDPGAPP	ARADGDS(ph)DAEDPGAPP	CK2	1.2	0.29033	Down	Yes
103	IPI00223459	Lipid phosphate phosph	Ppap2a;Hpic53;Lpp1;P	S274	1	14	KEEDPHTTLHETASSR	KEEDPHT(0.005)T(0.01)	KEEDPHTTLHETAS(ph)SR		0.7	0.0016143	Down	No
1234	IPI00223459	Lipid phosphate phosph	Ppap2a;Hpic53;Lpp1;P	S275	1	15	KEEDPHTTLHETASSR	KEEDPHT(0.018)T(0.03)	KEEDPHTTLHETAS(ph)GSK3					No
136	IPI00223459	Lipid phosphate phosph	Ppap2a;Hpic53;Lpp1;P	T272	1	12	KEEDPHTTLHETASSR	KEEDPHT(0.002)T(0.01)	KEEDPHTTLHETAS(ph)AS	NEK6	0.7	0.012605	Down	Yes
278	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfb	S788	1	4	RRPSDENSTPSEVQQW	RRPS(0.875)DENS(0.05)	RRPS(ph)DENSTPSEV	CHK1/2	1.4	0.10922	Down	Yes
363	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfb	S792	1	8	RRPSDENSTPSEVQQW	RRPS(0.169)DENS(0.56)	RRPSDENSTPSEV	PLK1	0.9	0.17826	Down	No
177	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfb	S992	2	6	DFAARSPASITDEDSNV	DFAARS(0.889)PS(0.17)	DFAARS(ph)PSAS(ph)I	GSK3	1.5	0.04098	Up	Yes
178	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfb	S996	2	10	DFAARSPASITDEDSNV	DFAARS(0.889)PS(0.17)	DFAARS(ph)PSAS(ph)I	CK1	1.5	0.04098	Up	Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
1260	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfit	S593	1	1	SQSTTFNPDMDSEPEFK	S(0.388)QS(0.3)T(0.3)T	_S(ph)QSTTFNPDMDSE	NIMA			No	
321	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfit	S595	1	3	SQSTTFNPDMDSEPEFK	S(0.114)QS(0.805)T(0.0	SOS(ph)ITTFNPDMDSE	PKA/AKT	0.9	0.14359	Yes	
543	IPI00664998	Liprin-beta-1;Protein ty	Ppfbp1;Kiaa1230;Ppfit	S573	1	16	SKGSQGSPPFPMSPSP	S(0.001)KGS(0.001)QGT	SKGSQGSPPFPMSPSP	WW GroupIV	1.0	0.27255	No	
998	IPI00554989	Peptidyl-prolyl cis-trans	Ppia	T5	1	12	MVNPVTFFDITADDEPL	MVNPT(1)VFDDITADDE	MVNPT(ph)VFFDITADDEPLGR		1.1	0.47679	Yes	
219	IPI00349306	Peptidyl-prolyl cis-trans	Ppig;Ppig;RP23-174C9	S395	1	5	SELNEIKENQRSPVLR	SELNEIKENQR(1)PVR	_SELNEIKENQR(ph)PV	CDK2	1.4	0.066505	Yes	
957	IPI00110280	Peptidyl-prolyl cis-trans	Ppil4	S178	1	23	INHVTLLDDPDDPDDLLI	INHVTLLDDPDDPDDLLI	INHVTLLDDPDDPDDLLIPDRS	(ph)PEPTKEQLDS	1.1	0.45832	Yes	
1346	IPI00110280	Peptidyl-prolyl cis-trans	Ppil4	S188	1	33	INHVTLLDDPDDPDDLLI	INHVT(0.075)VLLDDPDD	INHVTLLDDPDDPDDLLIPDRS	(ph)PEPTKEQLDSGR			No	
566	IPI00110280	Peptidyl-prolyl cis-trans	Ppil4	T159	1	4	INHVTLLDDPDDPDDLLI	INHVT(0.709)VLLDDPDD	INHVT(ph)VLLDDPDDPDD	FHA2 Rad53p	1.2	0.28453	No	
1349	IPI00110280	Peptidyl-prolyl cis-trans	Ppil4	T182	1	27	INHVTLLDDPDDPDDLLI	INHVT(0.02)VLLDDPDD	INHVTLLDDPDDPDDLLIPDRS	(ph)PEPTK			No	
757	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	S445	1	4	KTGSYGALAEISASK	KT(0.004)GS(0.993)Y(0	KTGS(ph)YGALAEISASK	PKD	1.2	0.37466	Yes	
23	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	S507	1	3	LASTSDIEEK	LAS(0.998)T(0.002)SDI	LAS(ph)TSDIEEK	CAMK2	8.6	9.464E-33	Up	
1083	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	S509	1	5	LASTSDIEEK	LAS(0.333)T(0.333)S(0	LAS(ph)TSDIEEK	CK2			No	
121	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	S870	1	20	STGVSFWTQDSDENEC	STGVSFWTQDSDENEC	STGVSFWTQDSDENEC	PKA	1.7	0.0050341	Up	
606	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	T443	1	1	TGSYGALAEISASK	T(0.628)GS(0.346)Y(0.0	T(ph)TGSYGALAEISASK	NIMA	1.2	0.305	No	
1088	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	T508	1	4	LASTSDIEEK	LAS(0.333)T(0.333)S(0	LAS(ph)TSDIEEK	NEK6			No	
75	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	S693	1	2	RSTQGVTLTDLQEA	RS(0.838)T(0.161)QGV	RST(ph)QGVTLTDLQEA	PKA	0.6	0.000121	Down	
76	IPI00671847	Ppp1r12a protein;MCG	Ppp1r12a;mCG_12239	T694	1	3	RSTQGVTLTDLQEA	RS(0.003)T(0.997)QGV	RST(ph)QGVTLTDLQEA	PKA	0.6	0.0001523	Down	
145	IPI00380331	Protein phosphatase 2	Pp2r5d;mCG_2696	S566	1	3	RKSELQPDVYTIK	RKS(1)ELQPDVYTIK	RKS(ph)ELQPDVYTIK	_CHK1/2	0.8	0.016576	Down	
1352	IPI00230005	cAMP-dependent prote	Prkaca;Pkaca;Prkaca;P	S213	1	18	TWTLGCTPEYLAPEILSK	T(0.269)WT(0.252)LCG	TWTLGCTPEYLAPEILSK	(ph)K			No	
438	IPI00230005	cAMP-dependent prote	Prkaca;Pkaca;Prkaca;P	T196	1	1	TWTLGCTPEYLAPEILSK	T(0.811)WT(0.162)LCG	T(ph)WTLGCTPEYLAPEI	FHA2 Rad53p	1.0	0.22839	Yes	
530	IPI00119575	Putative uncharacteriz	Prkar1a;Prkar1a;Prkar1	S212	1	9	TDSREDEISPPPPNPVK	TDSREDEIS(1)PPPPNPV	TDSREDEIS(ph)PPPPNPVK		1.0	0.2675	Yes	
1046	IPI00169788	Protein kinase, cAMP d	Prkar2a;mCG_16488;P	S97	1	3	RVSVCAETFPNDEEEDN	RVS(0.996)VCAET(0.00	RVS(ph)VCAETFPNDEE	AURORA-A	1.1	0.49507	Yes	
780	IPI00169788	Protein kinase, cAMP d	Prkar2a;mCG_16488;P	T102	1	8	RVSVCAETFPNDEEEDN	RVS(0.5)VCAET(0.5)FN	RVS(ph)VCAETFPNDEE	NDPR	1.1	0.38444	No	
847	IPI00224570	cAMP-dependent prote	Prkar2b	S112	1	3	RASVCAEAYNPDEEEDD	RAS(1)VCAEAYNPDEE	RAS(ph)VCAEAYNPDE	AURORA-A	1.0	0.41271	Yes	
180	IPI00321446	Protein kinase C alpha	Prkca;Pkca;Prkca;RP23	T497	1	1	TFCGTDPYIAPEIAYQPY	T(0.957)FCGT(0.042)P	T(ph)FCGTDPYIAPEIAYQ	PGK	0.8	0.041901	Down	
1262	IPI00227880	Protein kinase C delta	Prkcd;Pkcd;Prkcd;Pkcd	S530	1	2	ASTFCGTPDYIAPEILQGL	AS(0.5)T(0.5)FCGTPDYI	AS(ph)TFCGTPDYIAPEI	PKA			No	
1267	IPI00227880	Protein kinase C delta	Prkcd;Pkcd;Prkcd;Pkcd	T531	1	3	ASTFCGTPDYIAPEILQGL	AS(0.5)T(0.5)FCGTPDYI	AS(ph)TFCGTPDYIAPEI	CAMK2			No	
1273	IPI00227880	Protein kinase C delta	Prkcd;Pkcd;Prkcd;Pkcd	T535	1	7	ASTFCGTPDYIAPEILQGL	AS(0.328)T(0.328)FCGT	AS(ph)TFCGTPDYIAPEI	LQGLK			No	
807	IPI00122084	Serine/threonine-prote	Prkd1;Pkcmm;Pkd;Prkcm	S748	1	1	SVVGTTPAYLAPEVLR	S(1)VVGTTPAYLAPEVLR	S(ph)VVGTTPAYLAPEVLR	NIMA	1.1	0.39484	Yes	
1258	IPI00480507	Pre-mRNA-processing f	Prpf19;Prpf19;Snev;Prp	S2	1	1	SLICSISNEVPEHPCVSPV	S(0.373)LICS(0.313)S(0	S(ph)LICSISNEVPEHPC	GSK3			No	
1249	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Pr	S852	1	21	LCDFGSASHVADNDITP	LCDFGSASHVADNDIT(0	LCDFGSASHVADNDITP	(ph)LVSR			No	
410	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Pr	S94	1	12	EVIEASDKLEGLSPAK	EVIEAS(0.004)DKLEGLS	EVIEASDKLEGLS(ph)PA	CDK2	1.3	0.2119	Yes	
726	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Pr	Y849	1	18	LCDFGSASHVADNDITP	LCDFGSAS(0.001)HVAD	LCDFGSASHVADNDITP	(ph)LVSR	1.2	0.35996	Yes	
398	IPI00153950	Phosphoribosyl pyroph	Prpsap2	S227	1	23	LGVAVIHGEAQDAESDL	LGVAVIHGEAQDAESDL	LGVAVIHGEAQDAESDL	PKA	0.9	0.20478	Yes	
909	IPI00118248	Paired mesoderm hom	Prrx1;Pmx;Pmx1;Prrx1	S21	1	3	LDSPGNLDTLOAK	LDS(1)PGNLDTLOAK	LDS(ph)PGNLDTLOAK	CAMK2	1.1	0.44362	Yes	
919	IPI00115257	PC4 and SFRS1-interact	Psp1;Ledgf;Psp1;Ledg	S106	1	6	QSNASSDVEVEEK	QSNAS(0.08)S(0.92)VD	QSNASS(ph)DVEVEEK	CK2	1.1	0.4467	Yes	
270	IPI00115257	PC4 and SFRS1-interact	Psp1;Ledgf;Psp1;Ledg	S129	1	16	ETNVSKEDTDQEEKASNI	ETNVSKEDTDQEEKAS(0	ETNVSKEDTDQEEKAS	(ph)NEDVTK	1.4	0.10628	Yes	
272	IPI00115257	PC4 and SFRS1-interact	Psp1;Ledgf;Psp1;Ledg	T122	1	9	ETNVSKEDTDQEEKASNI	ET(0.003)NV(0.046)KE	ETNVSKEDT(ph)DQEE	PKD	1.4	0.10718	Yes	
825	IPI00331644	Proteasome subunit al	Psm3	S250	1	9	ESLKEEDESDDDDNM	ESLKEEDES(1)DDDDNM	ESLKEEDES(ph)DDDDNM		1.1	0.40247	Yes	
849	IPI00127989	Prostaglandin E synth	Ptges3;Sid3177;Tebp	S113	1	6	DWEDDSDSDMSNFDR	DWEDDS(1)DDMSNFDR	DWEDDSDSDMSNFDR	(ox)SNFDR	1.1	0.41335	Yes	
1219	IPI00387213	Protein tyrosine phosph	Ptpn12;mCG_6416	S326	1	18	IADGNEITGTMVSSIDS	IADGNEITGTMV(0.00	IADGNEITGTMVSSID	CK1			No	
1223	IPI00387213	Protein tyrosine phosph	Ptpn12;mCG_6416	S331	1	23	IADGNEITGTMVSSIDS	IADGNEITGTMV(0.00	IADGNEITGTMVSSIDS	(ph)EKQDSSPPKPPR			No	
727	IPI00387213	Protein tyrosine phosph	Ptpn12;mCG_6416;Ptp	S588	1	24	TVSSTPNSTAEAAHDLT	TVSSTPNSTAEAAHDLT	TVSSTPNSTAEAAHDLT	Polo box	1.0	0.36007	Yes	
3	IPI00459843	Putative uncharacteriz	Ptpn2	S89	1	2	LSRTDNMNFNNNNK	LS(0.975)RT(0.025)DNN	LS(ph)RTDNMNFNNNNK		104.9	2.42E-152	Up	
659	IPI00117689	Polymerase I and trans	Ptrf	S169	1	15	VMIYQDEVKLPKAKLSVSK	VMIYQDEVKLPKAKLS(0.9	VMIYQDEVKLPKAKLS	(ph)AURORA	1.2	0.33369	Yes	
1321	IPI00117689	Polymerase I and trans	Ptrf	S171	1	17	VMIYQDEVKLPKAKLSVSK	VMIY(0.014)QDEVKLP	VMIYQDEVKLPKAKLS	(ph)NEK6			No	
182	IPI00117689	Polymerase I and trans	Ptrf	S302	1	1	SFTPDHVVYAR	S(0.999)FT(0.001)PDHV	S(ph)FTPDHVVYAR	NIMA	0.8	0.042843	Down	
188	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	S38	1	6	AATEEPSGTGSDLEIKSQ	AT(0.035)EEPS(0.833)G	AATEEPS(ph)GTGSDLEI	GSK3	0.8	0.046839	Down	
610	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	S42	1	10	AATEEPSGTGSDLEIK	AATEEPS(0.001)GT(0.068	AATEEPSGTG(ph)DELH	CK1	1.0	0.30562	Yes	
1332	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	T34	1	2	AATEEPSGTGSDLEIK	AT(0.376)EEPS(0.196)G	AT(ph)EEPSGTGSDLEI	PKA			No	
537	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	T40	2	8	AATEEPSGTGSDLEIK	AATEEPS(0.989)GT(0.909	AATEEPS(ph)GT(ph)GSD	FHA1 Rad53p	1.0	0.27067	Yes	
550	IPI00330262	Pumilio homolog 1;Pun	Pum1;Kiaa0099;Pum1	T712	1	5	RDSLTTGSSDLYKR	RDS(0.075)LT(0.867)GS	RDSLTT(ph)GSSDLYKR	FHA KAPP	1.2	0.27782	Yes	
886	IPI00112203	Pumilio homolog 2;Put	Pum2;Kiaa0235;Pum2	S136	1	4	GKASPFEEQDNR	GKAS(1)PFEEQDNR	GKAS(ph)PFEEQDNR	CK2	1.1	0.43146	Yes	
989	IPI00128867	Transcriptional activat	Purb	S316	1	11	RGGSGGGGDESEGEV	RGGSGGGGDES(1)EGEE	RGGSGGGGDES(ph)EG	CK2	1.1	0.47112	Yes	
91	IPI00165881	Paxillin;Paxillin	Pxn;Pxn	S119	1	9	AGEEEHVYSPFNK	AGEEEHVY(0.148)S(0.8	AGEEEHVYS(ph)PFNK		1.0	0.0006659	Down	
567	IPI00165881	Paxillin;Paxillin	Pxn;Pxn	Y118	1	8	AGEEEHVYSPFNK	AGEEEHVY(0.991)S(0.0	AGEEEHVY(ph)SPFNK	ABL	0.6	0.28496	Yes	
257	IPI00480432	MKIAA0857 protein;Ra	Rab11fp5;mKIAA0857	S307	1	3	TYSDEASQLR	T(0.003)Y(0.001)S(0.99	TYS(ph)DEASQLR	PKA	1.4	0.099161	Yes	
55	IPI00108335	DNA repair protein RAC	Rad50;Rad50;Rad50	S557	3	1	SRHSDELTSLLGYFPNKK	S(0.612)RHS(0.39)DELT	(ca)S(ph)RHSDELTT	PKD	0.5	1.21E-06	Down	
56	IPI00108335	DNA repair protein RAC	Rad50;Rad50;Rad50	S565	3	9	SRHSDELTSLLGYFPNKK	S(0.612)RHS(0.39)DELT	(ca)S(ph)RHSDELTT	S(ph)LLGYFPNKK	0.5	1.21E-06	Down	
1163	IPI00135190	Ran-binding protein 3	Ranbp3	S28	2	1	SAGSSSPEAGEDSDHED	S(0.269)AGS(0.249)S(0	S(ph)AGSSSPEAGEDS	GSK3			No	
489	IPI00135190	Ran-binding protein 3	Ranbp3	S33	2	6	SAGSSSPEAGEDSDHED	S(0.006)AGS(0.026)S(0	SAGSSS(ph)PEAGEDS	Polo box	1.2	0.25132	Yes	
1028	IPI00135190	Ran-binding protein 3	Ranbp3	S40	1	13	SAGSSSPEAGEDSDHED	SAGSSSPEAGEDS(1)DH	SAGSSSPEAGEDS(ph)C	CK2	1.1	0.48795	Yes	
80	IPI00135190	Ran-binding protein 3	Ranbp3	S58	1	3	TSSLTHSSEK	T(0.001)S(0.055)S(0.94	TSS(ph)LTHSSEK	PKA/AKT	2.5	6.14E-07	Up	
55	IPI00719915	Ribonucleoprotein PTB	Raver1;Kiaa1978	S576	1	3	LLSPIASNR	LLS(1)PIASNR	LLS(ph)PIASNR	CAMK2	1.9	0.0004552	Up	
493	IPI00719915	Ribonucleoprotein PTB	Raver1;Kiaa1978	S626	1	4	HKMSPPPSFNEPR	HKMS(0.974)PPPS(0.02	HKMS(ph)PPPSFNEPR	GSK3	1.0	0.25422	Yes	
551	IPI00113372	RB1-inducible coiled-c	Rb1cc1;Cc1;Kiaa0203;R	S237	1	1	STELVLSPPDMPR	S(0.663)T(0.337)ELVLS	S(ph)TELVLSPPDMPR	NIMA	1.2	0.27802	No	

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
638	IPI00468834	RNA-binding protein 10	Rbm10;Kiaa0122;Rbm10	S646	1	8	LASDDRRSPRR	LASDDRRS(1)PPR	_LASDDRRS(ph)PPR	CDK2	1.2	0.32212		Yes
718	IPI00340815	Rbm15 protein	Rbm15	S293	1	3	SLSPGGAALGVR	S(0.096)LS(0.904)PGGA	SLS(ph)PGGAALGVR	CAMK2	1.2	0.35824		Yes
386	IPI00170394	Splicing factor 45;45 kD	Rbm17;Spf45	S155	1	6	RPDPDSDEDEDYER	RPDPDS(1)DEDEDYER	RPDPDS(ph)DEDEDYER		1.3	0.19537		Yes
905	IPI00421119	RNA-binding protein 25	Rbm25;Rbm25	S675	1	5	LGASNSPGQPNSVK	LGASNS(1)PGQPNSVK	LGASNS(ph)PGQPNSVK		1.1	0.44242		Yes
1038	IPI00828361	RNA-binding protein 26	Rbm26;Rbm26;Rbm26	S127	1	6	RLNHSPQQSSSR	RLNHS(0.972)PPQS(0.0	RLNHS(ph)PPQSSSR	NEK6	1.1	0.491		Yes
665	IPI00759858	RNA-binding protein 33	Rbm33;Prr8;Rbm33;Prr8	S243	1	6	DIKEESEDEDDDEESGR	DIKEES(1)DEDDDEES	DIKEES(ph)DEDDDEES	CK2	1.2	0.33633		Yes
712	IPI00759858	RNA-binding protein 33	Rbm33;Prr8;Rbm33;Prr8	S41	1	8	AAEEDWDSLEDDLLGE	AAEEDWDS(1)ELEDLL	AAEEDWDS(ph)ELEDLL	CK2	1.0	0.35682		Yes
920	IPI00223371	RNA-binding protein 39	Rbm39;Caper;Rnpc2;Rnpc2	S97	1	3	YRSPYSGPK	Y(0.004)RS(0.957)PY(0	YRS(ph)PYSGPK	PKA/AKT	1.1	0.44705		Yes
598	IPI00223371	RNA-binding protein 39	Rbm39;Caper;Rnpc2;Rnpc2	S136	1	3	DKSPVREPIDLNLTPEER	DKS(1)PVREPIDLNLTPEE	DKS(ph)PVREPIDLNLTPE	CDK2	1.2	0.30016		Yes
608	IPI00130160	RNA-binding protein 5	Rbm5;Luca15;Rbm5;Luca15	S59	1	4	DYDSEPERER	DYDS(1)PERER	DYDS(ph)PERER	CDK2	1.2	0.30512		Yes
715	IPI00130160	RNA-binding protein 5	Rbm5;Luca15;Rbm5;Luca15	S78	1	11	NSDRSEDGYHSDGDEYGR	NS(0.001)DRS(0.004)EG	NSDRSEDGYHSDGDEYGR		1.0	0.35761		Yes
672	IPI00410937	RNA-binding protein 8	Rbm8a;Rbm8;Rbm8a;Rbm8a	S56	1	7	MREDYDSEVQGDGDEPG	MREDYDS(1)VEQGDGE	M(ox)REDYDS(ph)VEQGDGDEPGPQR		1.2	0.34098		Yes
179	IPI00663587	Putative uncharacterized protein	Rbmxrt;Rbmx;Hnrnpq;Rbmxrt	S165	1	5	RSTPSGPVR	RSTPS(1)GPVR	_RSTPS(ph)GPVR	CK1	1.5	0.041863	Up	Yes
280	IPI00663587	Putative uncharacterized protein	Rbmxrt;Rbmx;Hnrnpq;Rbmxrt	T163	1	3	RSTPSGPVR	RS(0.008)T(0.984)PS(0	RST(ph)PSGPVR	Polo box	1.3	0.11197		Yes
1052	IPI00663587	Putative uncharacterized protein	Rbmxrt;Rbmx;RP23-37	S205	1	5	DVYLSR	DVYLS(1)PR	DVYLS(ph)PR	CDK1	1.1	0.49953		Yes
1	IPI00349293	Ring finger and CCHC-t	Rc3h2;Mnab;Rc3h2;Rc3h2	S895	2	9	EEDPIIPFSDGPIISKWGA	EEDPIIPFS(0.999)DGPII	(ca)EEDPIIPFS(ph)DGPIISKWGAIS(ph)R		0.001	0	Down	Yes
2	IPI00349293	Ring finger and CCHC-t	Rc3h2;Mnab;Rc3h2;Rc3h2	S907	2	21	EEDPIIPFSDGPIISKWGA	EEDPIIPFS(0.999)DGPII	(ca)EEDPIIPFS(ph)DGPIISKWGAIS(ph)R		0.003	2.75E-271	Down	Yes
345	IPI00123762	Putative uncharacterized protein	Rcc1;Rcc1;Chc1;Rcc1;W	S11	1	3	RRSPEDAIPK	RRS(1)PPEDAIPK	RRS(ph)PPEDAIPK	PKD	1.3	0.16541		Yes
593	IPI00395067	Negative elongation fact	Rdbp;D17h6s45;Nelfe	S115	1	3	SMSAEDLQEPSR	S(0.004)MS(0.996)ADE	SM(ox)S(ph)ADEDLQEPSR	CAMK2	1.2	0.29562		Yes
250	IPI00119795	RalBP1-associated eps	Reps1;Reps1	S708	1	3	LKSEDELRPDVEHTQK	LKS(0.998)EDELRPDVEH	LKS(ph)EDELRPDVEHTQK	PKA/AKT	1.4	0.094161		Yes
499	IPI00120529	Putative uncharacterized protein	Rfc1;Recc1	S68	2	5	IINDSDSESEETVQVK	IINDS(0.958)DS(0.958)E	IINDS(ph)DS(ph)ESEETVQVK	CK2	1.2	0.25794		Yes
500	IPI00120529	Putative uncharacterized protein	Rfc1;Recc1	S70	2	7	IINDSDSESEETVQVK	IINDS(0.958)DS(0.958)E	IINDS(ph)DS(ph)ESEETVQVK	CK2	1.2	0.25794		Yes
12	IPI00309304	Regulator of G-protein	Rgs2	S19	1	1	SAGNGPKVEEK	S(1)AGNGPKVEEK	(ca)S(ph)AGNGPKVEEK		12.1	5.602E-44	Up	Yes
1175	IPI00122131	Ras and Rab interactor	Rin1	S338	1	1	SMSSAFCSLLAPER	S(0.374)MS(0.309)S(0.3	S(ph)MSSAFCSLLAPER	NEK6				No
181	IPI00122131	Ras and Rab interactor	Rin1	S341	1	4	SMSSAFCSLLAPER	S(0.118)MS(0.079)S(0.8	SMSS(ph)AFCSLLAPER	CK1	0.8	0.042036	Down	Yes
217	IPI00122131	Ras and Rab interactor	Rin1	S345	1	8	SMSSAFCSLLAPER	S(0.098)MS(0.092)S(0.0	SMSSAFCS(ph)LLAPER	CK1	0.8	0.06532		No
675	IPI00453849	mRNA cap guanine-N7	Rnmt;Kiaa0398;Rnmt;Kiaa0398	S15	1	9	ASVASDPEPPGNEPA	ASVASDPE(1)PPGNE	ASVASDPE(ph)PPGNE	ERK/MAPK	1.0	0.34126		Yes
1198	IPI00403755	Likely ortholog of H. sa	RP23-102G9.3;RP23-102G9.3	Y313	1	11	MDLLTIVTQTHYK	MDLLT(0.001)T(0.001)N	MDLLTIVTQ(ph)HYK	ALK				No
529	IPI00869441	Uncharacterized protein	RP23-263M10.5;12000	S25	1	13	AEAPAGPALGLPSPVEVES	AEAPAGPALGLPS(1)PEV	AEAPAGPALGLPS(ph)PEVESGLER		1.2	0.26748		Yes
741	IPI00869441	Uncharacterized protein	RP23-263M10.5;12000	S30	1	18	AEAPAGPALGLPSPVEVES	AEAPAGPALGLPS(0.5)P	AEAPAGPALGLPS(ph)PEV	CK2	1.0	0.36863		No
830	IPI00111412	60S ribosomal protein	Rpl4	S295	1	4	ILKSPPIQR	ILKS(1)PIEIQ	(ca)ILKS(ph)PIEIQ		1.1	0.40568		Yes
802	IPI00314950	60S acidic ribosomal pr	Rplp0;Arbp	S304	2	7	AEAKEESEDEDMGFG	AEAKEES(1)EES(1)DEDN	AEAKEES(ph)EES(ph)DEDM(ox)GFGFLD		1.0	0.39277		Yes
803	IPI00314950	60S acidic ribosomal pr	Rplp0;Arbp	S307	2	10	AEAKEESEDEDMGFG	AEAKEES(1)EES(1)DEDN	AEAKEES(ph)EES(ph)DEDM(ox)GFGFLD		1.0	0.39277		Yes
875	IPI00113377	60S acidic ribosomal pr	Rplp1	S101	2	4	KEESESEDDMGFGFLD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDMGFGFLD		1.1	0.4273		Yes
876	IPI00113377	60S acidic ribosomal pr	Rplp1	S104	2	7	KEESESEDDMGFGFLD	KEES(1)EES(1)EDDMGF	KEES(ph)EES(ph)EDDM(ox)GFGFLD		1.1	0.4273		Yes
1034	IPI00139795	60S acidic ribosomal pr	Rplp2	S102	2	4	KEESESEDDMGFGFLD	KEES(1)EES(1)DDDMGF	KEES(ph)EES(ph)DDDM(ox)GFGFLD		1.1	0.48957		Yes
1035	IPI00139795	60S acidic ribosomal pr	Rplp2	S105	2	7	KEESESEDDMGFGFLD	KEES(1)EES(1)DDDMGF	KEES(ph)EES(ph)DDDM(ox)GFGFLD		1.1	0.48957		Yes
711	IPI00750262	Regulation of nuclear p	Rprd1b;Crept;Rprd1b;Crept	S165	1	18	TFQIQEEEDDDYPGSYS	TFQIQEEEDDDY(0.001)P	TFQIQEEEDDDYPGSYS(ph)PQDPSAGPLLTEL		1.2	0.35661		Yes
559	IPI00454123	Regulation of nuclear p	Rprd2;Kiaa0460;Rprd2;Kiaa0460	S392	1	8	DVEDMELSDVEDDGSK	DVEDMELS(1)DVEDDG	DVEDMELS(ph)DVEDDG	CK2	1.2	0.28031		Yes
969	IPI00173160	40S ribosomal protein	Rps27	S11	1	6	DLLHPSPEEKKR	DLLHS(1)PEEKKR	DLLHS(ph)PEEKKR	CK2	1.1	0.46315		Yes
798	IPI00134599	40S ribosomal protein	Rps3	S224	1	10	DEILPTPISEQK	DEILPT(0.069)T(0.197)E	DEILPTPISEQK	CK1	1.1	0.39151		No
881	IPI00134599	40S ribosomal protein	Rps3	T220	1	6	DEILPTPISEQK	DEILPT(0.5)T(0.5)PISEQ	DEILPT(ph)PISEQK	FHA2 Rad53p	1.1	0.42939		No
975	IPI00134599	40S ribosomal protein	Rps3	T221	1	7	DEILPTPISEQK	DEILPT(0.074)T(0.852)E	DEILPT(ph)PISEQK	WW GroupIV	1.1	0.46552		Yes
932	IPI00944141	Putative uncharacterized protein	Rps5;mCG_22552;Rps5	T2	1	1	TEWEAATPAVAETPDIK	T(0.997)EWEAAT(0.003	T(ph)EWEAATPAVAET	CK2	1.1	0.44979		Yes
1295	IPI00114333	Ribosomal protein S6 k	Rps6ka3;Rps6ka-rs1;Rps6ka3	S227	1	3	AYSCFGTVEYMAPEVNR	AY(0.489)S(0.489)FCGT	AY(ph)SCFGTVEYMAPEVNR					No
1300	IPI00114333	Ribosomal protein S6 k	Rps6ka3;Rps6ka-rs1;Rps6ka3	Y226	1	2	AYSCFGTVEYMAPEVNR	AY(0.489)S(0.489)FCGT	AY(ph)SCFGTVEYMAPEVNR					No
82	IPI00411051	Regulatory-associated	Rptor;Raptor;Rptor;Raptor	S863	1	14	ILDTSSLTQSAPASPTNK	ILDTSSLT(0.072)QS(0.0	ILDTSSLTQSAPAS(ph)PTNK	WW GroupIV	2.0	0.0003539	Up	Yes
613	IPI00323822	Ras-related protein R-R	Rras2	S186	1	10	KFQEQECPSPPEPTRK	KFQEQECPSP(0.999)PE	KFQEQECPSP(ph)PEPTRK	WW GroupIV	1.0	0.30625		Yes
277	IPI00110856	Ribosomal RNA process	Rrp1;Nnp1;Rrp1;Nnp1	S434	1	4	EAGSEAESSADPPGGR	EAGS(0.997)EAES(0.00	EAGS(ph)EAESSADPPGGR	CK2	0.9	0.10861		Yes
962	IPI00420344	RRP12-like protein	Rrp12;Kiaa0690	S1081	1	11	GDSIEEILADEDEEE	GDSIEEILADS(1)EDEEE	GDSIEEILADS(ph)EDEEE	CK2	1.1	0.46		Yes
269	IPI00458958	RRP15-like protein;Rib	Rrp15	S265	1	6	DWDKESGEEPPAGGR	DWDKES(1)EGEEPAGGR	DWDKES(ph)EGEEPAGGR	CK2	1.4	0.10616		Yes
948	IPI00471271	Rsrc2 protein	Rsrc2	S17	1	9	DGLALEKTPSPDREK	DGLALEKT(0.113)S(0.88	DGLALEKTS(ph)PDREK	CDK2	1.1	0.45571		Yes
656	IPI00471271	Rsrc2 protein	Rsrc2	S30	1	8	KKEQSDISISPR	KKEQSDIS(0.874)S(0.1	KKEQSDIS(ph)ISPR	PLK1	1.2	0.33288		Yes
473	IPI00471271	Rsrc2 protein	Rsrc2	S32	1	8	EQSDISISPR	EQSDIS(0.011)S(0.989)	EQSDISIS(ph)ISPR	CDK1	1.0	0.24433		Yes
898	IPI00471271	Rsrc2 protein	Rsrc2	T16	1	8	DGLALEKTPSPDREK	DGLALEKT(0.5)S(0.5)P	DGLALEKTS(ph)PDREK	FHA1 Rad53p	1.1	0.43901		No
1282	IPI00469392	Reticulon-4;Neurite ou	Rtn4;Kiaa0886;Nogo;Rtn4	S832	1	2	ESETSDSSPIIEIDFPFTF	ES(0.324)ET(0.324)FS(0	ES(ph)ETSDSSPIIEIDFPFTF	GSK3				No
1288	IPI00469392	Reticulon-4;Neurite ou	Rtn4;Kiaa0886;Nogo;Rtn4	S836	1	6	ESETSDSSPIIEIDFPFTF	ES(0.324)ET(0.324)FS(0	ES(ph)ETSDSSPIIEIDFPFTF	CK1				No
734	IPI00469392	Reticulon-4;Neurite ou	Rtn4;Kiaa0886;Nogo;Rtn4	S953	1	8	EAEKLPSTDEKEDR	EAEKLP(0.573)DT(0.4	EAEKLP(ph)STDEKEDR	CK2	1.2	0.36494		No
1290	IPI00469392	Reticulon-4;Neurite ou	Rtn4;Kiaa0886;Nogo;Rtn4	T834	1	4	ESETSDSSPIIEIDFPFTF	ES(0.324)ET(0.324)FS(0	ES(ph)ETSDSSPIIEIDFPFTF	FHA1 Rad53p				No
296	IPI00469392	Reticulon-4;Neurite ou	Rtn4;Kiaa0886;Nogo;Rtn4	S105	1	16	GPLPAAPPTAPERQPS	GPLPAAPPT(0.001)APE	GPLPAAPPTAPERQPS	CAMK2	0.9	0.12508		Yes
728	IPI00470167	RTN4;Reticulon 4	Rtn4;RP23-17605.4-00	S165	1	3	RGSVSVVVDLlyYR	RGS(0.897)GS(0.103)V	RGS(ph)GSVSVVVDLlyYR	PKA/AKT	1.0	0.36102		Yes
468	IPI00122174	MKIAA0138 protein;Sc	Safb2;mKIAA0138;Safb2	S404	1	7	APTAALSPEPQDSK	APTAALS(1)PEPQDSK	APTAALS(ph)PEPQDSK	CK1	1.2	0.24319		Yes
287	IPI00122174	MKIAA0138 protein;Sc	Safb2;mKIAA0138;Safb2	S410	1	13	APTAALSPEPQDSKEDV	APTAALS(0.011)PEPQD	APTAALSPEPQDS(ph)KEDV		1.3	0.11525		Yes
523	IPI00719971	Serine/threonine-prote	Saps3;D19Erd703e;Kia	S617	1	9	IQQFDGGSDDEIWE	IQQFDGG(1)DEEDIW	IQQFDGGS(ph)DEEDIW	CK2	1.0	0.26609		Yes
346	IPI00338954	SAM and SH3 domain-c	Sash1	S829	1	1	SHSLDQLGGDADVGK	S(0.645)HS(0.355)LDL	S(ph)SHSLDQLGGDADVGK	CK1	0.9	0.16552		No
877	IPI00344430	Splicing factor, arginine	Scaf1;Sfrs19	S676	2	3	APSPAPAVSPK	APS(1)PAPAVS(1)PK	APS(ph)PAPAVS(ph)PK	CAMK2	1.1	0.42825		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
878	IPI00344430	Splicing factor, arginine	Scaf1;Sfrs19	S682	2	9	APSPAPAVSPK	APS(1)PAPAVS(1)PK	_APS(ph)PAPAVS(ph)PK	CDK2	1.1	0.42825		Yes
320	IPI00177200	Scavenger receptor class	Scarf2;Srec2	S672	1	9	HSAAAAAPSPPPAGR	HSAAAAAPSP(1)PPPPAGR	HSAAAAAPSP(ph)PPPPAGR		0.9	0.14346		Yes
1299	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S1536	2	12	LAEAPSPAPTSPPTPLEDI	LAEAPSPAPT(0.002)PAPT(0.0	LAEAPSPAPT(ph)PTPLEDFGLQTSASPRGLS(ph)PDFVEELR				No	
132	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S1550	2	26	LAEAPSPAPTSPPTPLEDI	LAEAPSPAPT(0.001)P	LAEAPSPAPTSPPTPLED	CDK2	0.7	0.011522	Down	Yes
629	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S1555	2	31	LAEAPSPAPTSPPTPLEDI	LAEAPSPAPT(0.001)P	LAEAPSPAPTSPPTPLED	PKA	1.2	0.31593		Yes
1304	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	T1538	2	14	LAEAPSPAPTSPPTPLEDI	LAEAPSPAPT(0.002)PAPT(0.0	LAEAPSPAPT(ph)PT	CK2				No
152	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S1497	1	3	MKSLQEQDALR	MKS(1)LEQDALAR	M(ox)KS(ph)LEQDALAR	CAMK2	0.8	0.021854	Down	Yes
577	IPI00454106	Protein LAP4;Protein sc	Scrib;Kiaa0147;Lap4;Sc	S5508	1	17	RNEAFVCKPDPSPSPSE	RNEAFVCKPDPSP(0.003)	RNEAFVCKPDPSPSPS	CK2	1.2	0.28858		Yes
525	IPI00135660	Serum deprivation-res	Sdpr;Sdr	S287	2	1	SSPFKVSPLSFR	S(0.659)S(0.341)PFKVS	S(ph)SPFKVS(ph)PLSF	CK1	1.0	0.267		No
301	IPI00135660	Serum deprivation-res	Sdpr;Sdr	S288	2	7	ASSGKSSPFKVSPLSFR	AS(0.031)S(0.139)GKS	ASSGKSS(ph)PFKVS	Polo box	1.3	0.12823		No
1030	IPI00135660	Serum deprivation-res	Sdpr;Sdr	S293	1	7	SSPFKVSPLSFR	SSPFKVS(1)PLSFR	SSPFKVS(ph)PLSFR		1.1	0.48883		Yes
662	IPI00135660	Serum deprivation-res	Sdpr;Sdr	S359	2	5	RGNNSAVGSNADLTIEE	RGNNNS(0.969)AVGS(0.7	RGNNNS(ph)AVGS(ph)N	GSK3	1.0	0.33549		Yes
353	IPI00135660	Serum deprivation-res	Sdpr;Sdr	S363	1	9	RGNNSAVGSNADLTIEE	RGNNNS(0.003)AVGS(0.4	RGNNNSAVGS(ph)NAD	CK1	1.3	0.17081		Yes
248	IPI00135660	Serum deprivation-res	Sdpr;Sdr	T368	1	14	RGNNSAVGSNADLTIEE	RGNNNS(0.021)AVGS(0.2	RGNNNSAVGSNADLT	PLK	1.4	0.093523		No
784	IPI00648142	Sec23ip protein;SEC23	Sec23ip;Sec23ip	S748	1	3	KLSVGVAYVSSVR	KL(1)VGVAYVSSVR	KLS(ph)VGVAYVSSVR	CAMK2	1.0	0.38511		Yes
1084	IPI00648142	Sec23ip protein;SEC23	Sec23ip;Sec23ip	S755	1	10	KLSVGVAYVSSVR	KL(0.026)VGVAY(0.026)	KLSVGVAYSS(ph)VR					Yes
323	IPI00377592	Protein transport prote	Sec31a;Sec311	S614	2	2	DSQDVAQSDGEEESPAAB	DS(0.784)DQVAQS(0.75	DS(ph)DQVAQS(ph)D	NEK6	0.9	0.14455		No
669	IPI00377592	Protein transport prote	Sec31a;Sec311	S620	1	8	DSQDVAQSDGEEESPAAB	DSQDVAQS(1)DGEEESPA	DSQDVAQS(ph)DGEEES	CK2	1.0	0.33958		Yes
1204	IPI00133030	Protein transport prote	Sec61b	S13	1	12	PGPTPSGTNVGSSGRSP	PGPT(0.074)PS(0.126)G	PGPTPSGTNVGSS(ph)S	GSK3				No
937	IPI00133030	Protein transport prote	Sec61b	S14	1	13	PGPTPSGTNVGSSGRSP	PGPTPSGT(0.001)NVGS	PGPTPSGTNVGSS(ph)GR	SPSK	1.1	0.45198		Yes
155	IPI00133030	Protein transport prote	Sec61b	S17	1	16	PGPTPSGTNVGSSGRSP	PGPTPSGTNVGSS(0.002	(ca)PGPTPSGTNVGSS	CDK2	0.8	0.02503	Down	Yes
1210	IPI00133030	Protein transport prote	Sec61b	S19	1	18	PGPTPSGTNVGSSGRSP	PGPT(0.19)PS(0.19)GT	PGPTPSGTNVGSSGRS	CAMK2				No
930	IPI00133030	Protein transport prote	Sec61b	S7	1	6	PGPTPSGTNVGSSGRSP	PGPT(0.001)PS(0.531)G	PGPTPS(ph)GTNVGSSGR	SPSK	1.1	0.44919		No
1215	IPI00133030	Protein transport prote	Sec61b	T9	1	8	PGPTPSGTNVGSSGRSP	PGPT(0.175)PS(0.175)G	(ca)PGPT(ph)PSGTNVG	SSGRSPSK				No
946	IPI00134398	Translocation protein S	Sec62;Tloc1	T375	1	7	ELEEQTQDGDGDEEDDD	ELEEQT(1)DGDGDEED	ELEEQT(ph)DGDGDEE	FHA1 Rad53p	1.1	0.45482		Yes
48	IPI00403228	Sentrin-specific proteas	Senp7;Kiaa1707;Susp2	S12	1	3	RASSEIVTEGK	RAS(1)SEIVTEGK	_RAS(ph)SEIVTEGK	PKA	2.7	1.541E-07	Up	Yes
817	IPI00114945	Septin-2;Neural precur	Sept2;Nedd-5;Nedd5	S218	1	9	IYHLPAESEDDEDFEKQ	IYHLPAEAS(1)DEDEDFEK	IYHLPAEAS(ph)DEDEDFE	KQTR	1.0	0.39827		Yes
209	IPI00923056	Sept5 protein;Septin-5	Sept5;Sept5;Pnut1;Sep	S339	1	3	MESPILPLPTPAETEK	MES(1)PILPLPTPAET	M(ox)ES(ph)PILPLPT	CAMK2	0.8	0.061755		Yes
985	IPI00923056	Sept5 protein;Septin-5	Sept5;Sept5;Pnut1;Sep	S225	1	13	FGIHYVQFPECDSDDED	FGIHYVQFPECDSD(1)DEE	FGIHYVQFPECDSD(ph)DE	EDDFKQQR	1.1	0.46906		Yes
106	IPI00457611	Septin-9;SL3-3 integr	Sept9;Kiaa0991;Sint1;S	S530	1	1	SFEVEEIEPPNTPPR	S(1)FEVEEIEPPNTPPR	_S(ph)FEVEEIEPPNTPP	NIMA	0.7	0.0019236	Down	Yes
183	IPI00457611	Septin-9;SL3-3 integr	Sept9;Kiaa0991;Sint1;S	S585	1	9	LVDSLSQRSQPKPSLR	LVDS(0.006)LS(0.028)G	LVDSLSQRS(ph)PKPSL	CDK1	0.8	0.043848	Down	Yes
57	IPI00457611	Septin-9;SL3-3 integr	Sept9;Kiaa0991;Sint1;S	T143	1	9	RAEVLGHKTPPEVPR	RAEVLGHK(1)PEVPR	RAEVLGHK(ph)PEVPR		0.5	2.081E-06	Down	Yes
524	IPI00462466	MKIAA1732 protein	Setd2;BC031601;MKIA	S633	1	5	KLDESPLVKPEFIGHDGR	KLDES(1)PVLPKPEFIGHD	KLDES(ph)PVLPKPEFIGH	NEK6	1.0	0.26637		Yes
578	IPI00454015	Splicing factor 4	Sf4	S483	1	11	ALQQHQHQYDSDDEEVD	ALQQHQHQY(0.203)DS	ALQQHQHQYDSD(ph)D	CK2	1.2	0.28917		Yes
283	IPI00420807	Splicing factor, arginine	Sfrs1	S199	1	6	VDGPRSPSYGR	VDGPRS(0.984)PS(0.01	VDGPRS(ph)PSYGR	WW GroupIV	1.3	0.11234		Yes
1123	IPI00420807	Splicing factor, arginine	Sfrs1	S201	1	10	VKVDGPRSPSYGR	VKVDGPRS(0.237)PS(0.	VKVDGPRSPS(ph)YGR	CAMK2				No
383	IPI00848672	Putative uncharacterize	Sfrs11;mCG_11658;Sfr	S462	1	11	DYDEEEQGYDSEKEKK	DYDEEEQGY(0.003)DS	(ph)DYDEEEQGYDSEK	CK2	1.3	0.19444		Yes
696	IPI00848672	Putative uncharacterize	Sfrs11;mCG_11658;Sfr	S477	1	7	RPTAEVSPK	RPTAEV(1)PK	_RPTAEV(ph)PK	CDK1	1.2	0.34837		Yes
1075	IPI00848672	Putative uncharacterize	Sfrs11;mCG_11658;Sfr	S510	1	14	VNGDDHHEEDMDMSD	VNGDDHHEEDMDMS(1)	VNGDDHHEEDM(ox)D	M(ox)S(ph)D				Yes
721	IPI00474430	Putative uncharacterize	Sfrs2;Sfrs2;Pr264;Sfrs1	S26	1	9	VDNLTVRTSPDTLRR	VDNLT(0.004)Y(0.02)RT	VDNLTVRTS(ph)PDTLR	PKA	1.2	0.35856		Yes
249	IPI00474430	Putative uncharacterize	Sfrs2;Sfrs2;Pr264;Sfrs1	T25	1	12	VDNLTVRTSPDTLRR	VDNLT(0.004)Y(0.035)R	VDNLTVRT(ph)SPDTLR	FHA1 Rad53p	1.4	0.093959		No
1078	IPI00474430	Putative uncharacterize	Sfrs2;Sfrs2;Pr264;Sfrs1	T29	1	8	VDNLTVRTSPDTLRR	VDNLTVRT(0.001)S(0.4	VDNLTVRTS(ph)PDTLR	CK1				No
1170	IPI00874991	MKIAA3013 protein;Sfr	Sfrs2ip;mKIAA3013;Sfr	S884	1	11	ETVVESQSSQSPSPK	ET(0.001)VVES(0.029)G	ETVVESQSSQS(ph)PSP	CK1				Yes
431	IPI00874991	MKIAA3013 protein;Sfr	Sfrs2ip;mKIAA3013;Sfr	S886	1	13	ETVVESQSSQSPSPK	ETVVESQSSQS(0.001)P	ETVVESQSSQS(ph)P	CDK2	1.0	0.22498		Yes
704	IPI00310880	Putative uncharacterize	Sfrs6;mCG_1675	S301	1	1	SHSPLPAPPSK	S(0.642)HS(0.358)PLPA	S(ph)HSPLPAPPSK	CK1	1.2	0.35166		No
831	IPI00310880	Putative uncharacterize	Sfrs6;mCG_1675	S303	1	3	SHSPLPAPPSK	S(0.011)HS(0.989)PLPA	SHS(ph)PLPAPPSK	CAMK2	1.0	0.40577		Yes
560	IPI00310880	Putative uncharacterize	Sfrs6;mCG_1675	S45	1	11	NGYGFVEFEDSRDADDA	NGYGFVEFEDS(1)RDAD	NGYGFVEFEDS(ph)RDAD	DAVVELNSK	1.0	0.28138		Yes
83	IPI00116331	Small glutamine-rich te	Sgta;Sgt;Sgta;Sgt	S303	1	1	SRTPSASHEEQQE	S(0.585)RT(0.373)PS(0.	S(ph)RTPSASHEEQQE	GSK3	2.0	0.0003747	Up	No
291	IPI00116331	Small glutamine-rich te	Sgta;Sgt;Sgta;Sgt	T305	1	3	SRTPSASHEEQQE	S(0.138)RT(0.737)PS(0.	(ca)SRT(ph)PSASHEE	PKA/AKT	0.9	0.12122		No
991	IPI00116331	Small glutamine-rich te	Sgta;Sgt;Sgta;Sgt	T82	1	5	APDRTPPSEEDSAEAE	APDRTP(0.997)PPS(0.00	APDRTP(ph)PSEEDSAE	FHA KAPP	1.1	0.47187		Yes
394	IPI00116907	SH3 domain-binding pr	Sh3bp5;Kiaa1720;Sh3b	S377	1	3	RGSDIGVR	RGS(1)DIGVR	_RGS(ph)DIGVR	PKA/AKT	0.9	0.20231		Yes
1335	IPI00312752	Endophilin-A2;Endophi	Sh3gl1;Sh3d2b	S286	1	4	ITASSFR	ITAS(0.333)S(0.333)S	ITAS(ph)SFR					No
401	IPI00312752	Endophilin-A2;Endophi	Sh3gl1;Sh3d2b	S287	1	5	ITASSFR	ITAS(0.008)S(0.917)S	ITAS(ph)SFR	GSK3	0.9	0.2065		Yes
395	IPI00312752	Endophilin-A2;Endophi	Sh3gl1;Sh3d2b	S288	1	6	ITASSFR	ITAS(0.037)S(0.963)FR	ITASSS(ph)FR	GSK3	0.9	0.20297		Yes
199	IPI00466258	SH3 domain-containing	Sh3kbp1;Ruk;Seta;Sh3	S274	1	1	SIEVENDFLPVEK	S(1)IEVENDFLPVEK	_S(ph)IEVENDFLPVEK	CAMK2	1.4	0.054872		Yes
388	IPI00125298	SHC-transforming prot	Shc1;Shc;ShcA;Shc1;Sh	Y423	1	8	ELFDDPSYVNIQNLDK	ELFDDPS(0.067)Y(0.93	ELFDDPSYVNIQNL	EGFR	3.7	9.86E-13	Up	Yes
844	IPI00117932	Paired amphipathic hel	Sin3a;Sin3a;Sin3a;Sin3	S833	1	4	GDLSDVEEEEEEMDVED	GDLS(1)DVVEEEEEEMD	GDLS(ph)DVVEEEEEEM	CK2	1.1	0.4112		Yes
681	IPI00117932	Paired amphipathic hel	Sin3a;Sin3a;Sin3a;Sin3	T849	1	20	GDLSDVEEEEEEMDVED	GDLS(0.366)DVVEEEEE	GDLSDVEEEEEEMDVEAT	(ph)GAPK	1.0	0.34219		No
843	IPI00453688	Signal-induced prolifer	Sipa11;Kiaa0440;Sipa1	S1564	1	3	TLSDESIYSSQR	TLS(1)DESIYSSQR	_TLS(ph)DESIYSSQR	CHK1/2	1.1	0.41107		Yes
858	IPI00454140	MCG15924, isoform CR	Sktiv2;Ski;Ski19;mCG	S252	1	2	ASLLEDLVLK	AS(0.5)S(0.5)LEDLVLK	AS(ph)SLEDLVLK	PKA	1.1	0.42037		No
1018	IPI00454140	MCG15924, isoform CR	Sktiv2;Ski;Ski19;mCG	S253	1	3	ASLLEDLVLK	AS(0.003)S(0.997)LEDL	AS(ph)LEDLVLK	CHK1/2	1.1	0.48476		Yes
471	IPI00137194	Monocarboxylate trans	Slc16a1;Mct1	S213	1	4	SKESLQEAGK	SKES(1)LQEAGK	SKES(ph)LQEAGK	AURORA	1.0	0.24403		Yes
838	IPI00137194	Monocarboxylate trans	Slc16a1;Mct1	S461	1	8	EGKDEASTDVDEKPK	EGKDEAS(0.5)T(0.5)DV	EGKDEAS(ph)TDVDEKPK		1.1	0.40892		No
986	IPI00137194	Monocarboxylate trans	Slc16a1;Mct1	T462	1	9	EGKDEASTDVDEKPK	EGKDEAS(0.217)T(0.7	EGKDEAS(ph)DVDE	FHA1 Rad53p	1.1	0.46956		Yes
521	IPI00880321	Putative uncharacterize	Slc4a1ap;Slc4a1ap;Slc4	S258	1	6	MLGEDSDEEEEEANTTEG	MLGEDS(1)DEEEEAANT	M(ox)LGEDS(ph)DEEE	CK2	1.2	0.26499		Yes
592	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S697	1	3	LDSPTLSR	LDS(1)PTLSR	_LDS(ph)PTLSR	GSK3	1.0	0.29559		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phs	Ratio Signif	Up-/Down-r	Localized phosphosite?
1085	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S701	1	18	ITNYLTVPAHKLDSPTLSR	IT(0.023)NY(0.052)LT(0	ITNYLTVPAHKLDS(ph)	CK1				No
25	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S707	1	3	IGSDPLAYEYK	IGS(1)DPLAYEYK	IGS(ph)DPLAYEYK	PKA/AKT	7.3	4.139E-28	Up	Yes
205	IPI00109311	Na(+)/H(+) exchange re	Slc9a3r1;Nherf;Nherf1	S283	1	1	SASDSTSEELNSQDSQK	S(0.713)AS(0.276)JS(0.0	S(ph)ASDSTSEELNSQD	NEK6	0.8	0.060013		No
904	IPI00318935	SRA stem-loop-interact	Slirp	T104	1	7	ALHGAQTSDEER	ALHGAQT(0.963)S(0.03	ALHGAQT(ph)SDEER	CK2	1.1	0.44194		Yes
467	IPI00229571	SAFB-like transcription	Sltm;Met;Sltm;Met;Slt	S289	1	9	DVQDAIAQSQPEKAK	DVQDAIAQSQ(1)PEKAK	DVQDAIAQSQ(ph)PEKAK	CDK2	1.2	0.24218		Yes
977	IPI00127941	Small acidic protein;Sid	Smcp;Sid2057	S15	1	1	SASPDDDLGSSNWEEAAS	S(0.69)AS(0.31)PDDDLG	S(ph)ASPDGSSNWEEAADL	LGNEER	1.1	0.46645		No
953	IPI00127941	Small acidic protein;Sid	Smcp;Sid2057	S17	1	4	RSAPDDDLGSSNWEEAAS	RS(0.172)AS(0.6)PDDDLG	RSAS(ph)PDDDLGSSNW	PKA	1.1	0.45749		No
1192	IPI00127941	Small acidic protein;Sid	Smcp;Sid2057	S24	1	10	SASPDDDLGSSNWEEAAS	S(0.16)AS(0.151)PDDDLG	SASPDDDLGSSNWEEAADL	LGNEER				No
1196	IPI00127941	Small acidic protein;Sid	Smcp;Sid2057	S25	1	11	SASPDDDLGSSNWEEAAS	S(0.16)AS(0.151)PDDDLG	SASPDDDLGSSNWEEAADL	CK2				No
899	IPI00460668	Putative uncharacterize	Smarc4;Smarc4;Brg1	T1393	1	8	DSEAGSPTTSTR	DSEAGS(0.001)S(0.064)	DSEAGSST(ph)PTTSTR	Polo box	1.1	0.43935		Yes
891	IPI00459742	SWI/SNF complex subu	Smarc2;Baf170;Smarc	S347	1	6	DMDEPSPVNPVEEVLTP	DMDEPS(1)PVPNVEEVT	DMDEPS(ph)PVPNVEEVLTP		1.1	0.4337		Yes
747	IPI00132122	Structural maintenance	Smc3;Bam;Bmh;Cspg6	S1065	1	7	KGDVEGSSQSQDEGE	KGDVEGS(0.5)QS(0.5)Q	KGDVEGS(ph)QSQSQDEGE	GESER	1.2	0.37091		No
748	IPI00132122	Structural maintenance	Smc3;Bam;Bmh;Cspg6	S1067	1	9	KGDVEGSSQSQDEGE	KGDVEGS(0.5)QS(0.5)Q	KGDVEGS(ph)QSQSQDEGE	CK2	1.2	0.37091		No
571	IPI00420329	MKIAA0788 protein;Pu	Snrp200;Asc31;mkI	S225	1	4	EEASDDMMEGDEAVVR	EEAS(1)DDMMEGDEAVR	EEAS(ph)DDMMEGDEAVR		1.0	0.28577		Yes
796	IPI00625105	U1 small nuclear ribon	Snrnp70;Snrp70	S226	1	8	YDERPGSPPLPHR	YDERPGS(1)PLPHR	YDERPGS(ph)PLPHR		1.1	0.38931		Yes
1032	IPI00849318	Beta-2-syntrophin;59 k	Sntb2;Snt2b2;Sntb2	S88	1	7	GPAGEASASPPVRR	GPAGEAS(0.817)AS(0.1	GPAGEAS(ph)ASPPVRR		1.1	0.48918		Yes
342	IPI00849318	Beta-2-syntrophin;59 k	Sntb2;Snt2b2;Sntb2	S90	1	9	GPAGEASASPPVRR	GPAGEAS(0.003)AS(0.9	GPAGEASAS(ph)PPVRR		0.9	0.16237		Yes
1050	IPI00317298	SNW domain-containin	Snw1;Skipp	S224	2	4	GPPSPAPVMHSPSRK	GPPS(1)PPAPVMHS(0.6	GPPS(ph)PPAPVMHS(	WW GroupIV	1.1	0.49871		Yes
973	IPI00317298	SNW domain-containin	Snw1;Skipp	S232	2	12	GPPSPAPVMHSPSRK	GPPS(1)PPAPVMHS(0.6	GPPS(ph)PPAPVMHS(	CDK2	1.1	0.46529		No
935	IPI00317298	SNW domain-containin	Snw1;Skipp	S234	2	14	GPPSPAPVMHSPSRK	GPPS(0.996)PPAPVMHS	GPPS(ph)PPAPVMHSPS	(ph)RK	1.1	0.45079		No
168	IPI00654133	Protein SOLO;Protein S	Solo;Solo;Solo;Solo	S959	1	11	RIQQQLGEEASPR	RIQQQLGEEAS(1)PR	RIQQQLGEEAS(ph)PR	CDK1	0.8	0.035197	Down	Yes
549	IPI00828218	SON protein;MKIAA101	Son;Son;mkIAA101;S	S1723	1	11	ESQAQAVAVALSFK	ESQAQAVAVALS(1)PK	ESQAQAVAVALS(ph)PK	CDK1	1.2	0.27556		Yes
1090	IPI00129831	Soritin-related recepto	Sor1;Sor1	S1583	1	4	KMPASCVVNVYR	KMPAS(1)ACVNVVYR	(ca)KMPAS(ph)ACVNVVYR					Yes
355	IPI00753815	Spectrin alpha chain, b	Sptan1;Spna2;Spta2;Sp	S1029	1	7	KLDPAQASRENLEEQK	KLDPAQS(0.977)AS(0.0	KLDPAQS(ph)ASRENLEEQ	SIALR	0.9	0.17232		Yes
236	IPI00753815	Spectrin alpha chain, b	Sptan1;Spna2;Spta2;Sp	S1031	1	9	KLDPAQASRENLEEQK	KLDPAQS(0.044)AS(0.9	KLDPAQASAS(ph)RENLEEQ	SIALR	0.9	0.082263		Yes
358	IPI00753815	Spectrin alpha chain, b	Sptan1;Spna2;Spta2;Sp	S1217	1	1	SLQLLAEER	S(1)LQLLAEER	S(ph)LQLLAEER	CAMK2	0.9	0.17344		Yes
490	IPI00319830	Spectrin beta chain, br	Sptbn1;Elf;Sptn-2;Sptn	S2102	1	4	RPPSPDPNTK	RPPS(1)PDPNTK	RPPS(ph)PDPNTK	WW GroupIV	1.0	0.25207		Yes
427	IPI00319830	Spectrin beta chain, br	Sptbn1;Elf;Sptn-2;Sptn	T2107	1	9	RPPSPDPNTK	RPPSPDPNT(1)K	RPPSPDPNT(ph)K	FHA KAPP	1.0	0.22384		Yes
708	IPI00222801	Neuronal proto-oncoge	Src;Src;RP23-169M4.1	S17	1	1	SLEPSENVHGAGGAFPA	S(0.851)LEPS(0.149)EN	S(ph)LEPSENVHGAGG	AURORA-A	1.0	0.35449		Yes
651	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S915	1	5	KETESAEDDNLDDL	KETES(1)EAEDDNLDDL	KETES(ph)EAEDDNLDDL	CK2	1.2	0.32995		Yes
474	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	T913	2	3	KETESAEDDNLDDL	KET(1)ES(1)EAEDDNLDDL	KET(ph)ES(ph)EAEDDNL	PKA	1.2	0.24489		Yes
725	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S220	1	3	EKSELPPEPSVR	EKS(1)PELPPEPSVR	EKS(ph)PELPPEPSVR		1.2	0.35984		Yes
372	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S260	1	14	APKPEPVPPEKPSPEK	APKPEPVPPEKPS(1)PE	APKPEPVPPEKPS(ph)	CDK2	1.3	0.18367		Yes
462	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S387	2	3	RLSPASAPPR	RLS(0.992)PS(0.086)AS	(ca)RLS(ph)PSAS(ph)P	PKA/AKT	1.2	0.24051		Yes
463	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S391	2	7	RLSPASAPPR	RLS(0.935)PS(0.071)AS	RLS(ph)PSAS(ph)PPR	CDK2	1.2	0.24051		Yes
585	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S400	2	4	HRPSPATPPP	HRPS(0.986)S(0.899)PA	HRPS(ph)S(ph)PATPPP	PKA	1.2	0.29215		Yes
586	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S401	2	5	HRPSPATPPP	HRPS(0.986)S(0.899)PA	HRPS(ph)S(ph)PATPPP	PKA/AKT	1.2	0.29215		Yes
713	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S448	1	3	RESPSPAPKPR	RES(0.916)PS(0.084)PA	RES(ph)PSAPKPR	PKA	1.2	0.35731		Yes
330	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S450	1	5	RESPSPAPKPR	RES(0.071)PS(0.929)PA	(ca)RESPS(ph)PAPKPR		1.3	0.14992		Yes
47	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S461	1	5	KVELSEEDKGSK	KVELS(0.739)ES(0.217)	(ca)KVELS(ph)EEDK	CK2	2.8	4.712E-08	Up	No
356	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S463	1	7	KVELSEEDKGSK	KVELS(0.103)ES(0.895)	KVELSES(ph)EEDKGSK	NEK6	1.3	0.17238		Yes
487	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S572	2	3	RRSPSPAPPPPPPPPP	RRS(1)PS(1)PAPPPPPPP	RRS(ph)PS(ph)PAPPPPP	PKA/AKT	1.2	0.25054		Yes
488	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S574	2	5	RRSPSPAPPPPPPPPP	RRS(1)PS(1)PAPPPPPPP	RRS(ph)PS(ph)PAPPPPP	PKA/AKT	1.2	0.25054		Yes
641	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S616	1	3	RYSPPPIQR	RY(S)PPIQR	RY(S(ph)PPIQR	PKA	1.2	0.32378		Yes
418	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S635	1	3	TASPPPPPKR	T(0.014)AS(0.986)PPPP	TAS(ph)PPPPPKR	CAMK2	1.3	0.21719		Yes
1008	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S713	1	5	APQTSPPPPVR	APQT(0.002)S(0.956)S	APQTS(ph)SPPPPVR		1.1	0.48071		Yes
686	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S714	1	6	APQTSPPPPVR	APQT(0.012)S(0.159)S	APQTS(ph)SPPPPVR	Polo box	1.2	0.34472		Yes
1197	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	T712	1	4	APQTSPPPPVR	APQT(0.451)S(0.451)S	APQT(ph)SPPPPVR					No
379	IPI00874854	Srrm2 protein	Srrm2	S1269	1	17	AAETPAVASCWSGPQV	AAETPAVASCWSGPQV	AAETPAVASCWSGPQV	(ph)PEHK	0.9	0.18792		Yes
290	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2535	1	4	RVPSPTVPVK	RVPS(0.997)PT(0.003)P	RVPS(ph)PTVPVK	PKA	1.3	0.11908		Yes
340	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	T2537	1	6	RVPSPTVPVK	RVPS(0.001)PT(0.999)P	RVPSPT(ph)VPVK		1.3	0.16183		Yes
1230	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1066	1	1	SSSPVTELTAR	S(0.44)S(0.268)S(0.268	(ca)SSSPVTELTAR	NEK6				No
1048	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1068	1	3	SSSPVTELTAR	SSS(1)PVTELTAR	SSS(ph)PVTELTAR	CHK1/2	1.1	0.49704		Yes
783	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1077	2	12	SSSPVTELTARSPVQDK	S(0.174)S(0.148)S(0.64	SSS(ph)PVTELTAR	(ph)CDK2	1.1	0.385		No
884	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1097	1	4	SGMSPPEQSK	SGMS(1)PEQSK	SGMS(ph)PEQSK	CK1	1.1	0.43122		Yes
1224	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1101	1	8	SGMSPPEQSK	S(0.037)GMS(0.482)PE	SGMS(ph)PEQSK	CK1				No
719	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1151	1	4	DKFSPTQDRPESSTVLK	DKFS(0.887)PT(0.091)C	DKFS(ph)PTQDRPESSTVLK		1.2	0.35849		Yes
744	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1160	1	13	DKFSPTQDRPESSTVLK	DKFS(0.086)PT(0.086)C	DKFS(ph)PTQDRPESSTVLK		1.2	0.37029		No
808	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1278	1	5	ELSHSPPRENSFESLEFK	EL(S)HS(0.968)PPR	ELSHS(ph)PPRENSFES	CDK2	1.1	0.39492		Yes
910	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1305	1	13	NSGPVSEVNTGFSPEVK	NSGPVSEVNTGFS(1)PEV	NSGPVSEVNTGFS(ph)PEV		1.1	0.44365		Yes
1216	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1338	1	2	RSSSELSPEVVEK	RS(0.328)S(0.328)S(0.3	RS(ph)SSELSPEVVEK	PKA				No
253	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1339	1	3	RSSSELSPEVVEK	RS(0.06)S(0.935)S(0.00	RS(ph)SSELSPEVVEK	PKA	1.4	0.096684		Yes
1220	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1340	1	4	RSSSELSPEVVEK	RS(0.328)S(0.328)S(0.3	RS(ph)SSELSPEVVEK	CAMK2				No
925	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1359	1	2	VSSPVLETVQQR	VS(0.5)S(0.5)PVLETVQQR	VS(ph)SPVLETVQQR	CK1	1.1	0.44754		No
907	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S1360	1	3	VSSPVLETVQQR	VS(0.003)S(0.997)PVLE	VSSS(ph)PVLETVQQR	ERK/MAPK	1.1	0.44284		Yes
45	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2224	1	1	TPAAAAAMNLASPR	TPAAAAAMNLAS(1)PR	TPAAAAAMNLAS(ph)	CDK1	2.8	1.712E-08	Up	Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
1232	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2347	1	2	VSGRTSPLMLDR	V(0.47)GRT(0.47)S(0.0)	VS(ph)GRTSPLM(ox)LL	PKA			No	
542	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2351	1	6	VSGRTSPLMLDR	VSGRT(0.007)S(0.993)P	VSGRTS(ph)PLMLDR	PKA	1.2	0.27231	Yes	
738	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2360	1	1	SRTPPSAPSQSR	S(0.504)RT(0.407)PPS(0.0)	S(ph)RTPPSAPSQSR	CHK1/2	1.2	0.36684	Yes	
1228	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2368	1	9	SRTPPSAPSQSR	S(0.099)RT(0.43)PPS(0.0)	SRT(ph)PPSAPSQSR	CK1			No	
298	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2404	1	19	MVQASSQLLPPAQDRP	MVQASSQLLPPAQDRP	M(ox)VQASSQLLPPA	IWW GroupIV	1.3	0.12562	Yes	
1199	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2408	1	23	MVQASSQLLPPAQDRP	MVQASSQLLPPAQDRP	M(ox)VQASSQLLPPA	CK1			No	
1205	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2411	1	26	MVQASSQLLPPAQDRP	MVQAS(0.1)S(0.129)QS	MVQASSQLLPPAQDR	CK1			No	
1211	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2414	1	29	MVQASSQLLPPAQDRP	MVQAS(0.1)S(0.129)QS	MVQASSQLLPPAQDR	CK1			No	
422	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2656	1	4	RQPSQPSPR	RQPS(0.999)PQPS(0.00)	(ca)RQPS(ph)PQPSR	CAMK2	1.2	0.22181	Yes	
391	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S2660	1	8	RQPSQPSPR	RQPS(0.5)PQPS(0.5)PR	RQPS(ph)PQPSR	CDK1	1.3	0.19948	No	
658	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	T1153	1	6	DKFSPTQDRPESSTVLK	DKFS(0.009)PT(0.991)C	DKFSPT(ph)QDRPESSTVLK		1.2	0.33004	Yes	
198	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	T2077	1	7	PSMSPTPLDR	PSMS(0.003)PT(0.997)H	PSMSPT(ph)PLDR	FHA1 Rad53p	1.4	0.054801	Yes	
584	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	T2362	1	3	SRTPPSAPSQSR	S(0.12)RT(0.87)PPS(0.0)	SRT(ph)PPSAPSQSR	14-3-3 binding	1.2	0.29158	Yes	
339	IPI00785240	Serine/arginine repetit	Srrm2;Kiaa0324;Srrm2	S778	1	6	SLSGSSPCPK	SLSGS(0.107)S(0.893)P	SLSGSS(ph)PCPK	Polo box	1.3	0.1616	Yes	
569	IPI00830670	Sperm-specific antigen	Sfsa2;Kiaa1927;Krap;S	S90	1	6	TPLGASLDEQSSGTPK	T(0.008)PLGAS(0.977)L	TPLGAS(ph)LDEQSSG	CK2	1.0	0.28537	Yes	
554	IPI00407571	FACT complex subunit	Ssrp1;Ssrp1;Ssrp1;RP2	S444	1	13	EGINPGYDDYADSDDEQ	EGINPGYDDY(0.032)AD	EGINPGYDDYADSD	DEQHDAYLER	1.2	0.27863	Yes	
1186	IPI00407571	FACT complex subunit	Ssrp1;Ssrp1;Ssrp1;RP2	Y438	1	7	EGINPGYDDYADSDDEQ	EGINPGY(0.323)DDY(0.0)	EGINPGY(ph)DDYADSD	EGFR			No	
1189	IPI00407571	FACT complex subunit	Ssrp1;Ssrp1;Ssrp1;RP2	Y441	1	10	EGINPGYDDYADSDDEQ	EGINPGY(0.179)DDY(0.0)	(ca)EGINPGYDDY(ph)ADSDDEQHDAYLER				No	
343	IPI00312188	AMSH-like protease;AN	Stambpl1;Amshp;Stam	S242	1	10	SDGSNFANYSPVNR	SDGSNFANY(0.001)S(0.0)	SDGSNFANYS(ph)PPVNR		0.9	0.16407	Yes	
1130	IPI00153216	Signal-transducing ada	Stap2;Stap2	S19	1	7	LKGAPSHYYESFLEKK	LKGAPPS(0.329)HY(0.3)	(ca)LKGAPPS(ph)HYYESFLEKK				No	
1134	IPI00153216	Signal-transducing ada	Stap2;Stap2	Y21	1	9	LKGAPSHYYESFLEKK	LKGAPPS(0.329)HY(0.3)	(ca)LKGAPPS(ph)HYYESFLEKK				No	
553	IPI00153216	Signal-transducing ada	Stap2;Stap2	Y22	1	10	LKGAPSHYYESFLEKK	LKGAPPS(0.117)HY(0.1)	(ca)LKGAPSHYHY(ph)ESFLEKK		1.0	0.27857	Yes	
1118	IPI00114979	Signal transducer and a	Stat5a;Mgf;Mpf	Y694	1	5	AVDGYVKPQIK	AVDGY(1)VKPQIK	AVDGY(ph)VKPQIK	EGFR			Yes	
1122	IPI00114982	Signal transducer and a	Stat5b	Y699	1	5	AADGYVKPQIK	AADGY(1)VKPQIK	AADGY(ph)VKPQIK	EGFR			Yes	
81	IPI00831595	Serine/threonine kinas	Stk10;Stk10;Lok	T950	1	11	LSEEAERPTTPSK	LSEEAERPTT(0.008)T(0.0)	LSEEAERPTT(ph)PSK	IWW GroupIV	2.0	0.000348	Up	Yes
848	IPI00474228	Serine/threonine-prote	Stk3;Mess1;Mst2;Stk3	S316	1	15	HEEQRELEEEEEENSD	HEEQRELEEEEEENS(0.9)	HEEQRELEEEEEENS(ph)DEDELDSHTMVK		1.1	0.41318	Yes	
1277	IPI00474228	Serine/threonine-prote	Stk3;Mess1;Mst2;Stk3	S323	1	22	HEEQRELEEEEEENSD	HEEQRELEEEEEENS(0.4)	HEEQRELEEEEEENS(ph)DEDELDSHTMVK				No	
1283	IPI00474228	Serine/threonine-prote	Stk3;Mess1;Mst2;Stk3	T325	1	18	ELEEEEEENSDDELDSHT	ELEEEEEENS(0.249)DEDE	ELEEEEEENSDDELDS(ph)HTM(ox)VK				No	
24	IPI00551236	Stathmin;Phosphoprot	Stmn1;Lag;Lap18;Pr22	S25	1	11	ASGOAFELILSPR	ASGOAFELILS(1)PR	ASGOAFELILS(ph)PR	CDK1	7.6	4.22E-29	Up	Yes
840	IPI00352986	Striatin	Strn	S245	1	10	FLESAAADFSDEDEDED	FLESAAADFS(1)DEDEDE	FLESAAADFS(ph)DEDEDEDTDR		1.0	0.40947	Yes	
428	IPI00316469	Dolichyl-diphosphoolig	Stt3b;Simp	S495	1	8	ENPPVEDSDEDDKRNPI	ENPPVEDS(0.842)S(0.1)	ENPPVEDS(ph)SDEDD	CK2	1.2	0.22434	Yes	
1357	IPI00316469	Dolichyl-diphosphoolig	Stt3b;Simp	Y508	1	21	ENPPVEDSDEDDKRNPI	ENPPVEDS(0.339)S(0.3)	ENPPVEDS(ph)SDEDD	EGFR			Yes	
1079	IPI00471361	STIP1 homology and U	Stub1;Chip	S20	1	8	LGTGGGSPDKSQAQ	LGT(0.498)GGGGS(0.49)	LGT(ph)GGGSPDKSP	CDK2			No	
1081	IPI00471361	STIP1 homology and U	Stub1;Chip	S24	1	12	LGTGGGSPDKSQAQ	LGT(0.138)GGGGS(0.40)	LGTGGGGS(ph)PKSP	CK1			No	
1086	IPI00471361	STIP1 homology and U	Stub1;Chip	T15	1	3	LGTGGGSPDKSQAQ	LGT(0.498)GGGGS(0.49)	LGT(ph)GGGSPDKSP	CAMK2			No	
417	IPI00454050	Transcription elongatio	Supt6h;Kiaa0162	S125	1	3	KMSDDDEDEEYEGKEE	KMS(1)DDEDEEYEGY	KMS(ph)DDEDEEYEGKEHEK		1.3	0.21652	Yes	
212	IPI00918245	Putative uncharacterize	Svil	S260	1	5	ARYPSGEIPVVEDEEKVI	ARYP(0.013)PS(0.939)GS	ARYPS(ph)GSEIPVVED	PKA/AKT	1.4	0.062399	Yes	
984	IPI00918245	Putative uncharacterize	Svil;Svil;Svil	S556	1	3	RGSLGPNNSAAHLGDS	RGSL(1)LELGNPSAAHLG	RGSL(ph)LELGNPSAAH	AURORA-A	1.0	0.4687	Yes	
141	IPI00918245	Putative uncharacterize	Svil;Svil;Svil	T407	1	3	YQTQPVTLGEVEQVQSG	Y(0.11)QT(0.89)QPVTLC	YQT(ph)QPVTLGEVEQ	CAMK2	0.8	0.015004	Down	Yes
123	IPI00918245	Putative uncharacterize	Svil;Svil;Svil	Y405	1	1	YQTQPVTLGEVEQVQSG	Y(0.61)QT(0.39)QPVTLC	Y(ph)QPVTLGEVEQVQSGK		0.7	0.0070677	Down	No
349	IPI00317599	Synapse-associated pro	Syap1	T255	1	7	DDNLPLTEAVRPKTPPV	DDNLPLT(0.643)EAVRP	DDNLPLT(ph)EAVRPK	NEK6	0.9	0.16703	No	
837	IPI00317599	Synapse-associated pro	Syap1	T262	1	14	DDNLPLTEAVRPKTPPV	DDNLPLT(0.003)EAVRP	DDNLPLTEAVRPKTPPV	IWW GroupIV	1.0	0.40872	Yes	
526	IPI00856427	Symplekin	Sympk	S1260	1	4	DESPQNLSHAAVEEALK	DESP(0.097)QNLS(0.0)	DESP(ph)QNLSHAAVEEALK		1.0	0.26711	Yes	
603	IPI00469184	Synemin;Desmuslin;Syn	Synn;Dmn;Kiaa0353;S	S780	1	18	IDFSTPFQVEEVDVSP	IDFSTPFQVEEVDV(0.0)	IDFSTPFQVEEVDVSP	CDK1	1.0	0.30319	Yes	
1110	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S116	1	8	KVMTASGSSSPVPR	KVMTAS(0.003)GS(0.3)	KVMTASGS(ph)SSPVP	CK1			No	
1113	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S117	1	9	KVMTASGSSSPVPR	KVMTAS(0.003)GS(0.3)	KVMTASGS(ph)SSPVP	CK1			No	
1119	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S118	1	10	KVMTASGSSSPVPR	KVMTAS(0.003)GS(0.3)	KVMTASGS(ph)SSPVP	Polo box			No	
729	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S132	1	1	STSFTEIDLK	S(0.939)T(0.03)S(0.03)P	S(ph)TSFTEIDLK	NEK6	1.0	0.36113	Yes	
630	IPI00662157	Synaptopodin	Synpo;Kiaa1029	S134	1	3	STSFTEIDLK	S(0.009)T(0.004)S(0.98)	STS(ph)TFTEIDLK	PKA/AKT	1.0	0.31631	Yes	
931	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S1002	1	3	MRSQPASPAR	MRS(1)QPASPAR	MRS(ph)QPASPAR	CAMK2	1.1	0.49934	Yes	
263	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S1091	1	3	RGSLPTEASCTT	RGSL(1)LPTEASCTT	RGSL(ph)LPTEASCTT	AURORA-A	1.4	0.10136	Yes	
756	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S567	1	3	VRSPSYSTLYPSSDPKPS	VRSPSYSTLYPSSDPKPS(0.867)PPS(0.051)Y	VRSPSYSTLYPSSDPKPS	ERK/MAPK	1.2	0.37419	Yes	
9	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S583	1	19	VRSPSYSTLYPSSDPKPS	VRSPSYSTLYPSSDPKPS(0.021)Y	VRSPSYSTLYPSSDPKPS(ph)HLK		0.1	2.894E-59	Down	Yes
573	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S672	1	4	DRASPAEAEEAVPEWAS	DRAS(1)PAEAEEAVPEW	DRAS(ph)PAEAEEAVPEW	PKA	1.0	0.2872	Yes	
786	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S833	1	3	AASPAKPSLIDLVPNLR	AAS(0.999)PAKPSLIDLVP	AAS(ph)PAKPSLIDLVP	CDK2	1.0	0.38557	Yes	
1060	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S838	1	8	AASPAKPSLIDLVPNLR	AAS(0.179)PAKPS(0.41)	(ca)AASPAKPS(ph)SLDLVPLNLR				No	
1062	IPI00662157	Synaptopodin;Synapto	Synpo;Kiaa1029;Synpo	S839	1	9	AASPAKPSLIDLVPNLR	AAS(0.179)PAKPS(0.41)	(ca)AASPAKPS(ph)SLDLVPLNLR				No	
416	IPI00139383	TBC1 domain family me	Tbc1d10a;Epi64;Tbc1d	S441	1	16	AILDAEPGRPALQPS	AILDAEPGRPALQPS(0.0)	AILDAEPGRPALQPS(ph)NEK6		1.0	0.21614	Yes	
631	IPI00139383	TBC1 domain family me	Tbc1d10a;Epi64;Tbc1d	S443	1	18	AILDAEPGRPALQPS	AILDAEPGRPALQPS(0.0)	AILDAEPGRPALQPS(ph)IR		1.0	0.31634	Yes	
211	IPI00469012	TBC1 domain family me	Tbc1d10b	S22	1	8	HGAPAAPSPPPR	HGAPAAPSP(1)PPPR	HGAPAAPSP(ph)PPPR		1.0	0.062341	Yes	
469	IPI00110247	TBC1 domain family me	Tbc1d15	S201	1	1	SLSQSFENLDEPAGYLIC	S(0.964)LS(0.018)QS(0.0)	S(ph)LSQSFENLDEPAG	GSK3	0.8	0.24324	Yes	
788	IPI00453842	TBC1 domain family me	Tbc1d2b;Kiaa1055	S959	1	11	DTPSPDKGELVSDDEEDT	DTPSPDKGELVS(1)DEEEDT	DTPSPDKGELVS(ph)DEE	CK2	1.0	0.3859	Yes	
1074	IPI00453842	TBC1 domain family me	Tbc1d2b;Kiaa1055	T965	1	19	ERDTPSPDKGELVSDDEEDT	ERDTPSPDKGELVS(0.5)D	ERDTPSPDKGELVS(ph)DEEEDT				No	
1098	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S107	1	7	KKEPAISSQNSPEAR	KKEPAIS(0.333)S(0.333)	KKEPAIS(ph)SQNSPEAR				No	
1101	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S108	1	8	KKEPAISSQNSPEAR	KKEPAIS(0.333)S(0.333)	KKEPAIS(ph)SQNSPEAR				No	
901	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S111	1	11	KKEPAISSQNSPEAR	KKEPAISS(0.001)QNS(0.0)	KKEPAISSQNS(ph)PEA	CK1	1.1	0.44047	Yes	

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Localized phosphosite?
625	IPI00848939	Tensin-like C1 domain	Tenc1;Tns2;Tenc1;Tns2	S1094	1	10	HLPGSGQQPSPPAR	HLPGS(0.002)GQQPS(0.002)	HLPGSGQQPS(ph)PPAR		1.0	0.31395		Yes
862	IPI00112101	Tuftelin-interacting protein	Ttip11;Stip;Tip39	S211	1	13	TTQSLQDFPVADSEEEAE	TTQSLQDFPVADSI(1)EEAE	TTQSLQDFPVADSI(ph)CK2		1.1	0.42146		Yes
674	IPI00124572	Trans-Golgi network in	Tgoln2;Tgn2	S277	1	6	VSGPSSSENQEGTLTDSN	VSGPS(0.003)S(0.899)S	VSGPSS(ph)SENQEGTLCK1		1.0	0.34121		Yes
1167	IPI00124572	Trans-Golgi network in	Tgoln2;Tgn2	S278	1	7	VSGPSSSENQEGTLTDSN	VS(0.1)GPS(0.1)S(0.35)	VSGPSS(ph)ENQEGTLTDSMK					No
1173	IPI00124572	Trans-Golgi network in	Tgoln2;Tgn2	S288	1	17	VSGPSSSENQEGTLTDSN	VS(0.11)GPS(0.11)S(0.1)	VSGPSSSENQEGTLTDSNEK6					No
332	IPI00664886	THO complex 2;Putativ	Thoc2;RP23-300D2.1-0	S1419	1	9	KIDSHPSHSSTVK	KIDS(0.005)HPS(0.024)	KIDSHPS(ph)HSSTVK		1.3	0.15408		Yes
1042	IPI00664886	THO complex 2;Putativ	Thoc2;RP23-300D2.1-0	T1423	1	13	KIDSHPSHSSTVK	KIDSHPS(0.028)PIS(0.02)	KIDSHPSHSST(ph)VF	FHA1 Rad53p	1.1	0.49272		Yes
926	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S243	1	7	ASVSDLSR	ASVSDLS(1)PR	ASVSDLS(ph)PR	CDK1	1.1	0.44755		Yes
732	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S679	1	5	RIDISPSTFR	RIDIS(1)PSTFR	(ca)RIDIS(ph)PSTFR		1.2	0.36256		Yes
1093	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S681	1	7	RIDISPSTFR	RIDIS(0.496)PS(0.496)T	RIDIS(ph)PSTFR					No
275	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	T682	1	8	RIDISPSTFRK	RIDIS(0.208)PS(0.021)T	RIDISPST(ph)FRK	CK1	1.4	0.10778		Yes
794	IPI00323349	Tight junction protein 2	Tjp2;Zo2	S107	1	10	KVQVAPLQGSPPPLSHDD	KVQVAPLQGS(0.999)PS	KVQVAPLQGS(ph)PPL	NEK6	1.0	0.38894		Yes
620	IPI00323349	Tight junction protein 2	Tjp2;Zo2	S1136	1	5	GSYSDPEEEYR	GS(0.009)Y(0.009)GS(0.009)	GSYSDPEEEYR	CK2	1.0	0.3107		Yes
315	IPI00323349	Tight junction protein 2	Tjp2;Zo2	Y238	1	14	SYHEAYEPDYGGYSPY	SYHEAYEPDY(0.015)GG	SYHEAYEPDYGGY(ph)SPSYDRR		1.3	0.14053		Yes
439	IPI00845563	MKIAA1547 protein;Pu	Tle3;mkIAA1547;Tle3	S286	1	5	DAPTSVASVSSSPSSK	DAPT(0.014)S(0.986)PA	DAPTS(ph)PASVASSSS	WW GroupIV	1.2	0.22976		Yes
752	IPI00229647	Tln2 protein;Tln2 prote	Tln2;Tln2;Tln2;mkIAA0	T1844	1	5	LDEGTTPPEK	LDEGT(1)PPEK	LDEGT(ph)PPEK	CK2	1.2	0.37252		Yes
579	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S157	1	1	SSTPLTVSSSAENR	S(0.528)S(0.236)T(0.23)	S(ph)STPLTVSSSAEN	CK1	1.2	0.28977		No
1057	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S158	2	11	LREQGTERSSRSTPLPTV	LREQGT(0.238)ES(0.23)	LREQGTERSSR(ph)S(ph)	PKA				No
193	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	S165	2	9	SSTPLTVSSSAENR	S(0.379)S(0.308)T(0.30)	S(ph)STPLTVSSSAENR		1.5	0.051085		Yes
624	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;Lap	T159	1	3	SSTPLTVSSSAENR	S(0.079)S(0.03)T(0.891)	SST(ph)PLTVSSSAEN	Polo box	1.2	0.31291		Yes
1058	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;mc	S66	1	6	GPPDFSSDEEREPTVPLG	GPPDFS(0.493)S(0.493)	GPPDFS(ph)SDEEREPT	CK2				No
1059	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;mc	S67	1	7	GPPDFSSDEEREPTVPLG	GPPDFS(0.493)S(0.493)	GPPDFS(ph)SDEEREPT	CK2				No
314	IPI00828976	Putative uncharacterize	Tmpo;Tmpo;Tmpo;mc	T74	1	14	GPPDFSSDEEREPTVPLG	GPPDFSDEEREPT(1)PV	GPPDFSSDEEREPT(ph)	CAMK2	1.3	0.14031		Yes
1022	IPI00121341	Thioredoxin-related tra	Tmx1;Txndc;Txndc1	S245	1	14	KVEEEQEAEDEEDVSEEA	KVEEEQEAEDEEDVSI(1)EE	KVEEEQEAEDEEDVSI(ph)	CK2	1.1	0.48673		Yes
52	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1022	1	15	DVGHLEEGASGGLLSPST	DVGHLEEGASGGLLS(0.8)	DVGHLEEGASGGLLS(ph)	PSTPHSR	2.5	6.597E-07	Up	Yes
583	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1290	1	9	NMAPGAGCSPPGEP	NMAPGAGCS(1)PGEPR	NMAPGAGCS(ph)PGE	CK2	1.0	0.29152		Yes
164	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1375	1	6	SSGSLSPGLETEDPLEAR	S(0.014)S(0.01)GS(0.08)	SSGSLSPGLETEDPLEAR	CK1	1.5	0.030931	Up	Yes
513	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1611	2	4	VPSDEEVVEEPOQR	VPS(1)S(1)DEEVVEEQS	VPS(ph)S(ph)DEEVVEE	CAMK2	1.0	0.26304		Yes
514	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1612	2	3	VPSDEEVVEEPOQR	VPS(1)S(1)DEEVVEEQS	VPS(ph)S(ph)DEEVVEE	CK2	1.0	0.26304		Yes
241	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1657	1	3	NRSAAEEGEVTESK	NRS(1)AEEGEVTESK	NRS(ph)AEEGEVTESK	PKA/AKT	1.4	0.085639		Yes
318	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S236	1	17	SOEGTAEIPAECQEEHSI	SOEGTAEIPAECQEEHSI(1)	SOEGTAEIPAECQEEHSI(ph)	KTPEER	1.0	0.14323		No
657	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S300	1	11	LANISVPASESPR	LANISVPAS(0.909)ES(0.0)	LANISVPASESPR	CDK1	1.0	0.33302		Yes
441	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S527	1	5	GEGVSQVGPPTPAPES	GEGVS(0.518)QVGPPT	GEGVS(ph)QVGPPTPAPES	PR	1.0	0.23019		No
914	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S568	1	1	SPALLPSTVEGPPGAPLL	S(1)PALLPSTVEGPPGAP	S(ph)PALLPSTVEGPPG	WW GroupIV	1.1	0.44512		Yes
319	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	T238	1	19	SOEGTAEIPAECQEEHSI	SOEGTAEIPAECQEEHSI(1)	SOEGTAEIPAECQEEHSI	CK2	1.3	0.14323		Yes
371	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	T533	1	11	GEGVSQVGPPTPAPES	GEGVSQVGPPT(1)PPAP	GEGVSQVGPPT(ph)PP	ERK/MAPK	0.9	0.1821		Yes
449	IPI00378438	Putative uncharacterize	Tns1	S1468	1	12	HLGGSVVPSPSLDR	HLGGSVVPSPSLDR(0.002)VV	HLGGSVVPSPSPSLDR(ph)	ERK/MAPK	1.0	0.23373		Yes
1324	IPI00751137	Putative uncharacterize	Tomm70a	S105	1	13	ASPALGSGHHHDGSGDSL	AS(0.325)PALGS(0.325)	AS(ph)PALGSGHHHDGSGDSL	SLEMSLDR				No
622	IPI00751137	Putative uncharacterize	Tomm70a	S94	1	2	ASPALGSGHHHDGSGDSL	AS(1)PALGSGHHHDGSG	AS(ph)PALGSGHHHDGSG	PKA	1.2	0.31124		Yes
1322	IPI00751137	Putative uncharacterize	Tomm70a	S99	1	7	ASPALGSGHHHDGSGDSL	AS(0.497)PALGS(0.497)	AS(ph)PALGSGHHHDGSGDSL	EM(ox)SSLDR				No
424	IPI00109764	DNA topoisomerase 1	Top1;Top-1;Top1	S114	1	8	EKENGFSPPR	EKENGFS(0.071)S(0.92)	(ca)EKENGFS(ph)PPR	Polo box	1.0	0.2232		Yes
988	IPI00135443	DNA topoisomerase 2	Top2b	S1363	1	6	YTFDFSEEDDDAAAADI	Y(0.008)T(0.007)FDFS	YTFDFSEEDDDAAAADI	CK2	1.1	0.47035		Yes
1344	IPI00135443	DNA topoisomerase 2	Top2b	S1376	1	19	YTFDFSEEDDDAAAADI	Y(0.214)T(0.216)FDFS	YTFDFSEEDDDAAAADD	(ph)NDLEELK				No
242	IPI00135443	DNA topoisomerase 2	Top2b	S1387	1	4	VKASPIITNDGDEFPVSD	VKAS(0.977)PIT(0.023)I	VKAS(ph)PITNDGDEFPVSD	GLDKDEYAFSSGK	1.4	0.086086		Yes
425	IPI00135443	DNA topoisomerase 2	Top2b	S1509	2	7	IVETINSDSDFEFGIPK	IVETINS(1)DS(0.996)DS	IVETINS(ph)DS(ph)DS	GSK3	1.2	0.22335		Yes
426	IPI00135443	DNA topoisomerase 2	Top2b	S1511	2	9	IVETINSDSDFEFGIPK	IVETINS(1)DS(0.996)DS	IVETINS(ph)DS(ph)DS	CK2	1.2	0.22335		Yes
92	IPI00135443	DNA topoisomerase 2	Top2b	S1537	1	3	KASGSENEGDNYPGR	KAS(0.923)GS(0.077)EN	KAS(ph)GSENEGDNYP	PKA	1.9	0.0007518	Up	Yes
1340	IPI00135443	DNA topoisomerase 2	Top2b	S1563	1	3	KTSFDQDSDVDFPDSFT	KT(0.481)S(0.481)FDQ	KT(ph)SFDQDSDVDFPDSFT	SEPPALPR				No
536	IPI00135443	DNA topoisomerase 2	Top2b	S1568	1	8	KTSFDQDSDVDFPDSFT	KT(0.013)S(0.013)FDQ	KTSFDQDSDVDFPDSFT	SEPPALPR	1.0	0.27037		Yes
420	IPI00135443	DNA topoisomerase 2	Top2b	T1390	1	7	VKASPIITNDGDEFPVSD	VKAS(0.5)PIT(0.5)INDGE	VKAS(ph)PITNDGDEFE	CK1	1.2	0.21899		No
642	IPI00135443	DNA topoisomerase 2	Top2b	T1562	1	1	TSFDQDSDVDFPDSFTS	T(0.52)S(0.406)FDQDS	T(ph)SFDQDSDVDFPDS	FHA1 Rad53p	1.2	0.32426		No
1037	IPI00135443	DNA topoisomerase 2	Top2b	Y1358	1	1	YTFDFSEEDDDAAAADI	Y(0.594)T(0.371)FDFS	Y(ph)TFDFSEEDDDAAAADD	NDLEELK	1.1	0.49057		No
1011	IPI00762273	Lamina-associated poly	Tor1aip1;Lap1B;Tor1ai	S94	1	5	FRPASAGEEVR	FRPAS(1)AGEEVR	FRPAS(ph)AGEEVR	CAMK2	1.1	0.48123		Yes
260	IPI00755183	Tumor protein D52-like	Tpd52l2;RP23-33L3.2-0	S189	1	7	NSATFKSFEDR	NSATFKS(1)FEDR	NSATFKS(ph)FEDR	FHA KAPP	0.9	0.10071		Yes
1315	IPI00755183	Tumor protein D52-like	Tpd52l2;RP23-33L3.2-0	T186	1	4	NSATFKSFEDR	NS(0.279)AT(0.361)FKS	(ca)NSATFKS(ph)FKS	FEDR				No
30	IPI0080644	Tpr protein;Putative un	Tpr;Tpr;Tpr;C77892	S2149	1	10	TDGFAEIHSPOVAGVPI	TDGFAEIHS(1)POVAG	TDGFAEIHS(ph)POVAG	PR	6.3	4.991E-24	Up	Yes
1094	IPI00340806	TRAF3-interacting prot	Traf3ip1;Mipt3	S409	1	4	RQESTETLVVDR	RQES(0.924)T(0.07)ET	RQES(ph)TETLVVDR	PKA				Yes
1111	IPI00131130	Transcription intermed	Trim24;Tif1;Tif1a;Trim	S806	1	4	SEWSDASQKSPVHVGET	S(0.025)EWS(0.325)DA	SEWS(ph)DASQKSPVH	CK1				No
1114	IPI00131130	Transcription intermed	Trim24;Tif1;Tif1a;Trim	S809	1	7	SEWSDASQKSPVHVGET	S(0.025)EWS(0.325)DA	SEWS(ph)DASQKSPVH	CK1				No
149	IPI00131130	Transcription intermed	Trim24;Tif1;Tif1a;Trim	S812	1	10	SEWSDASQKSPVHVGET	SEWS(0.005)DAS(0.005)	SEWSDASQKS(ph)PVH	CK1	0.8	0.017897	Down	Yes
1125	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S40	1	5	RPAASAAAAAASSP	RPAAS(0.239)S(0.239)A	RPAAS(ph)AAAAAASSP	AGGGGEEAQLLEHCGVCR				No
1128	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S41	1	6	RPAASAAAAAASSP	RPAAS(0.239)S(0.239)A	RPAAS(ph)AAAAAASSP	AGGGGEEAQLLEHCGVCR				No
1131	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S46	1	11	RPAASAAAAAASSP	RPAAS(0.239)S(0.239)A	RPAAS(ph)AAAAAASSP	GSK3				No
153	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S473	1	3	SRSGEVSGLLR	S(0.12)RS(0.88)GEGEV	SRS(ph)GEGEVSGLLR	PKA	1.5	0.024199	Up	Yes
1135	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S50	1	15	RPAASAAAAAASSP	RPAAS(0.001)S(0.001)A	RPAASAAAAAASSP	CK1				No
872	IPI00312128	Transcription intermed	Trim28;Krip1;Tif1b;Trim	S51	1	16	RPAASAAAAAASSP	RPAASAAAAAASS(0.0)	RPAASAAAAAASS	Polo box	1.1	0.42651		Yes



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
237	IPI00480235	Tripartite motif-contain	Trim47;Trim47;Trim47	S393	1	4	GLGSNEDGLQK	GLGS(1)NEDGLQK	_GLGS(ph)NEDGLQK		0.9	0.082599		Yes
32	IPI00828306	Triple functional doma	Trio;Trio;Trio	S2575	2	7	TRPGAVSPNSPLSTTFPS	T(0.004)RPGAVS(0.994)	TRPGAVS(ph)PLNS(ph)GSK3		5.0	7.477E-19	Up	Yes
33	IPI00828306	Triple functional doma	Trio;Trio;Trio	S2579	2	11	TRPGAVSPNSPLSTTFPS	T(0.004)RPGAVS(0.994)	TRPGAVS(ph)PLNS(ph)CK1		5.0	7.477E-19	Up	Yes
760	IPI00828306	Triple functional doma	Trio;Trio;Trio;Trio	S1935	1	11	KSADAGSQKDSDDSAAT	KS(0.001)ADAGS(0.038)	KSADAGSQKDS(ph)DDCK1		1.0	0.37546		Yes
1103	IPI00828306	Triple functional doma	Trio;Trio;Trio;Trio	S1938	2	5	DSDDSAATPQDETIIEER	DS(0.445)DDS(0.445)AA	DS(ph)DDSAATPQDET	CK1				No
1107	IPI00828306	Triple functional doma	Trio;Trio;Trio;Trio	T1946	2	13	DSDDSAATPQDETIIEER	DS(0.445)DDS(0.445)AA	DS(ph)DDSAATPQDET	PLK				Yes
429	IPI00622738	TRIO and F-actin-bindin	Triobbp;Kiaa1662;Tara	S1607	1	20	KADGPRPSLDYVELSPLA	KADGPRPSLDYVELSPLA	KADGPRPSLDYVELSPL	NEK6	1.0	0.22435		No
430	IPI00622738	TRIO and F-actin-bindin	Triobbp;Kiaa1662;Tara	S1608	1	21	KADGPRPSLDYVELSPLA	KADGPRPSLDYVELSPLA	KADGPRPSLDYVELSPL	WW GroupIV	1.0	0.22435		No
867	IPI00380829	Thyroid hormone rece	Trip11	S1879	1	2	LSVHGLKPLDSPGR	LS(0.707)VHGLKPLDS(0	LS(ph)VHGLKPLDSPGR	AURORA	1.1	0.4225		No
546	IPI00380829	Thyroid hormone rece	Trip11	S1888	1	11	LSVHGLKPLDSPGR	LSVHGLKPLDS(1)PGR	LSVHGLKPLDS(ph)PGR	CDK2	1.2	0.2745		Yes
406	IPI00623570	Cbp37	Trip12;Gtl6;cbp37	S312	1	3	SESPPAELPSLR	S(0.103)ES(0.897)PPAE	SES(ph)PPAELPSLR	14-3-3 binding	1.0	0.21072		Yes
1150	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S267	1	6	SEDRPSSQVSAVAETK	S(0.006)EDRPS(0.496)S	SEDRPS(ph)SPQVSAVA	PKA				No
506	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S268	1	7	SEDRPSSQVSAVAETK	SEDRPS(0.006)S(0.994)	SEDRPS(ph)SPQVSAVA	WW GroupIV	1.2	0.25971		Yes
1155	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S381	1	8	STPFIVPSSPTEQGG	STPFIVPS(0.333)S(0.333)	STPFIVPS(ph)SPTQGG					No
347	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S382	1	9	STPFIVPSSPTEQGG	STPFIVPS(0.098)S(0.804)	STPFIVPS(ph)PTEQGG	WW GroupIV	1.3	0.16586		Yes
1012	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S530	1	3	MESLGS	MES(0.5)LGS(0.5)PR	M(ox)ES(ph)LGSPR	CK1	1.1	0.48147		Yes
495	IPI00229801	Transformation related	Trp53bp1;RP23-43711	S533	1	6	MESLGS	MESLGS(1)PR	M(ox)ESLGS(ph)PR	CDK1	1.0	0.25454		Yes
1160	IPI00229801	Transformation related	Trp53bp1;RP23-43711	T384	1	11	STPFIVPSSPTEQGG	STPFIVPS(0.333)S(0.333)	STPFIVPS(ph)SPTQGG	CK1				No
89	IPI00620969	Tuberin;Tuberous scler	Tsc2;Tsc2;Tsc2;Tsc2	S937	1	1	STSLNERPK	S(0.566)T(0.283)S(0.15)	S(ph)TSLNERPK	CAMK2	1.9	0.006194	Up	No
619	IPI00113746	Splicing factor U2AF 65	U2af2;U2af65	S79	1	12	GAKEEHGGLIRSPR	GAKEEHGGLIRS(1)PR	(ca)GAKEEHGGLIRS(ph)	CDK1	1.2	0.30983		Yes
1099	IPI00407835	Ubiquitin-associated pr	Ubap2l;Ubap2l;Ubap2l	S633	1	8	RYPSSISSPQKDLTQAK	RY(0.001)PS(0.001)S(0	RYPSSISS(ph)SPQKDLT	CK1				No
520	IPI00407835	Ubiquitin-associated pr	Ubap2l;Ubap2l;Ubap2l	S634	1	9	RYPSSISSPQKDLTQAK	RYPS(0.012)S(0.012)S(1	RYPSSISS(ph)PQK	Polo box	1.2	0.26382		Yes
31	IPI00331539	Ubiquitin-associated ar	Ubash3b;Sts1;Ubash3b	S542	1	1	SFQVTKIIESECK	S(1)FQVTKIIESECK	S(ph)FQVTKIIESECK		0.2	1.274E-23	Down	Yes
333	IPI00399869	Ubiquitin-like protein 7	Ubl7	S230	1	12	DMPGGFLFDGLSDEDD	DMPGGFLFDGLS(0.997)	DMPGGFLFDGLS(ph)DCK2		0.9	0.15539		Yes
1104	IPI00399869	Ubiquitin-like protein 7	Ubl7	S239	1	21	DMPGGFLFDGLSDEDD	DMPGGFLFDGLS(0.365)	DMPGGFLFDGLS(ph)DDEDDHPSTR					No
246	IPI00648709	E3 ubiquitin-protein lig	Ubr4;Kiaa0462;Zubr1	S2743	1	6	HVTLPSSPR	HVTLPS(0.951)S(0.049)	HVTLPS(ph)SPR	GSK3	0.9	0.092862		Yes
207	IPI00648709	E3 ubiquitin-protein lig	Ubr4;Kiaa0462;Zubr1	S2744	1	7	HVTLPSSPR	HVTLPS(0.06)S(0.94)PR	HVTLPS(ph)PR	WW GroupIV	0.8	0.060875		Yes
510	IPI00169767	E3 ubiquitin-protein lig	Uhrf2;Nirf	S668	1	4	RPASDDECPGDSK	RPAS(1)DDECPGDSK	RPAS(ph)DDECPGDSK	PKA	1.2	0.26158		Yes
812	IPI00128071	General vesicular trans	Uso1;Vdp;Uso1;Vdp;Uso	S940	1	14	LKDLGHPVEEDESDDQ	LKDLGHPVEEDES(1)G	LKDLGHPVEEDES(ph)GQ	QEDDDDEIDDDGDKD	1.0	0.39724		Yes
37	IPI00420601	Ubiquitin carboxyl-term	Usp10;Ode-1;Uchpr	S223	2	19	TCDSQNPVDFISGVPV	T(0.505)CDS(0.466)PQ	T(ph)CDSQNPVDFIS	WW GroupIV	3.8	2.762E-13	Up	Yes
316	IPI00420601	Ubiquitin carboxyl-term	Usp10;Ode-1;Uchpr	T205	1	1	TCDSQNPVDFISGVPV	T(0.61)CDS(0.39)PQNP	T(ph)CDSQNPVDFIS	FHA KAPP	0.9	0.14117		No
508	IPI00123410	Ubiquitin carboxyl-term	Usp24	S2044	1	6	VSDQNSPVLPK	VSDQNS(1)PVLPK	VSDQNS(ph)PVLPK	CK1	1.0	0.26087		Yes
1333	IPI00226889	U3 small nucleolar RNA	Utp15	S517	1	21	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK(ph)	ESPTQPSDTDKNS				No
1336	IPI00226889	U3 small nucleolar RNA	Utp15	S522	1	26	NSDSPVPEHVAELPEEK	NDS(0.001)DPVPEHVA	NSDSPVPEHVAELPEEKTES(ph)	PTQPSDTDKNS				No
1339	IPI00226889	U3 small nucleolar RNA	Utp15	S528	1	32	NSDSPVPEHVAELPEEK	NDS(0.001)DPVPEHVA	NSDSPVPEHVAELPEEK	CK1				No
1343	IPI00226889	U3 small nucleolar RNA	Utp15	T515	1	19	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK(ph)	ESPTQPSDTDKNS				No
1347	IPI00226889	U3 small nucleolar RNA	Utp15	T519	1	23	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK	NSDSPVPEHVAELPEEK	FHA KAPP				No
1350	IPI00226889	U3 small nucleolar RNA	Utp15	T524	1	28	NSDSPVPEHVAELPEEK	NDS(0.001)DPVPEHVA	NSDSPVPEHVAELPEEKTES(ph)	PTQPSDTDKNS				No
285	IPI00353420	Cytoskeletal protein	Utrn;utrophin	S933	1	5	AAQASLNLALNDPIAVEQ	AAQAS(1)NLALNDPIAVE	AAQAS(ph)NLALNDPIAVE	EQALQEK	0.9	0.11334		Yes
653	IPI00118372	Vesicle-associated men	Vamp4;Vamp4;mCG 2	S30	1	7	NLLEDDSDDEEDFFLR	NLLEDDSD(1)DEEDFFLR	NLLEDDSD(ph)DEEDFF	CK2	1.0	0.33003		Yes
541	IPI00453589	Vesicle-associated men	Vamp8	T54	1	3	NKTEDLEATSEHF	NKT(0.039)EDLEAT(0.9)	NKTEDLEAT(ph)SEHF	NEK6	1.0	0.27197		Yes
64	IPI00624876	Vasodilator-stimulated	Vasp	S317	1	9	MKSSSVTTSEAHPTSP	MKS(0.877)JS(0.053)S(0	M(ox)KS(ph)SSSVTTSE	CHK1/2	0.5	1.73E-05	Down	Yes
1206	IPI00624876	Vasodilator-stimulated	Vasp	S318	1	4	MKSSSVTTSEAHPTSP	MKS(0.317)S(0.317)S(0	M(ox)KS(ph)SSSVTTSE	AHPSTPCSSDDSDLER				No
1212	IPI00624876	Vasodilator-stimulated	Vasp	S319	1	5	MKSSSVTTSEAHPTSP	MKS(0.317)S(0.317)S(0	M(ox)KS(ph)SSSVTTSE	AHPSTPCSSDDSDLER				No
823	IPI00126834	Vascular cell adhesion	Vcam1;Vcam-1;Vcam1	S165	1	4	QEFSSSEEMTK	QEFSS(0.5)S(0.5)EEMTK	QEFSS(ph)SEEMTK	CK2	1.1	0.40126		Yes
970	IPI00126834	Vascular cell adhesion	Vcam1;Vcam-1;Vcam1	S166	1	5	QEFSSSEEMTK	QEFSS(0.005)S(0.995)E	(ca)QEFSS(ph)EEMTK		1.1	0.46401		Yes
528	IPI00875672	versican core protein is	Vcan	S2281	1	5	MEDVSNNEVR	MEDVS(1)NEVR	M(ox)EDVS(ph)NEVR		1.0	0.26744		Yes
362	IPI00405227	Vinculin;Metavinculin	Vcl	S721	1	1	SLLDASEAIAIK	S(0.999)LLDASEAIAIK	S(ph)LLDASEAIAIK		0.9	0.17814		Yes
455	IPI00122549	Voltage-dependent ani	Vdac1;Vdac5;Vdac1;Vd	S117	1	8	LTFDSSFPNTGKK	LTFDSS(0.011)S(0.011)F	LTFDSS(ph)PNTGKK	CK1	1.2	0.23545		Yes
139	IPI00227299	Vimentin	Vim	S419	1	9	ISLPLPTFSSLNLR	ISLPLPT(0.064)FS(0.872	ISLPLPTFS(ph)LSNLR		0.8	0.014883	Down	Yes
329	IPI00227299	Vimentin	Vim	S420	1	10	ISLPLPTFSSLNLR	ISLPLPT(0.001)FS(0.008	ISLPLPTFS(ph)LSNLR		0.9	0.1495		Yes
119	IPI00227299	Vimentin	Vim	T417	1	7	ISLPLPTFSSLNLR	IS(0.036)LP(0.607)F	ISLPLPT(ph)FSSLNLR	FHA KAPP	0.7	0.0047223	Down	No
1243	IPI00227299	Vimentin;Vimentin	Vim;Vim;RP23-185P20	S54	1	4	SLYSSSPGGAYVTR	S(0.128)LY(0.131)S(0.1	SLYS(ph)SPGGAYVTR	CK1	1.0	0.22766		Yes
1246	IPI00227299	Vimentin;Vimentin	Vim;Vim;RP23-185P20	S55	1	5	SLYSSSPGGAYVTR	S(0.128)LY(0.131)S(0.1	SLYS(ph)SPGGAYVTR	NEK6				No
436	IPI00227299	Vimentin;Vimentin	Vim;Vim;RP23-185P20	S56	1	6	SLYSSSPGGAYVTR	SLYSSS(1)PGGAYVTR	SLYSSS(ph)PGGAYVTR	Polo box	1.0	0.22766		Yes
731	IPI00923704	Wings apart-like homo	Wapal;Wapal;Kiaa0261	S77	1	14	VEEEDTGDPFGFSDDE	VEEEDTGDPFGFDS(1)D	VEEEDTGDPFGFDS(ph)	CK2	1.0	0.36255		Yes
1268	IPI00923704	Wings apart-like homo	Wapal;Wapal;Kiaa0261	S81	1	18	VEEEDTGDPFGFSDDE	VEEEDT(0.001)GDPFGF	VEEEDTGDPFGFDS(ph)	PLK1				No
475	IPI00123333	WW domain-binding pr	Wbp11	S237	1	9	RRDEDMLYSPELAQR	RRDEDMLY(0.031)S(0.9	RRDEDM(ox)LYS(ph)PELAQR		1.0	0.24495		Yes
244	IPI00123333	WW domain-binding pr	Wbp11	Y236	1	8	RRDEDMLYSPELAQR	RRDEDMLY(0.86)S(0.14	RRDEDMLY(ph)SPELAQR	SRC	1.4	0.08766		Yes
908	IPI00229856	WD repeat-containing 1	Wdr42a;D1Ucla4;H326	S100	1	2	GHGHSDEDEEQPR	GHGHS(1)DEDEEQPR	GHGHS(ph)DEDEEQPR	CK2	1.1	0.44341		Yes
894	IPI00459468	ATPase WRNIP1;Werne	Wrnrip1;Whip;Wrnrip1	S153	1	15	RPAAAAAGSASPR	RPAAAAAGSAS(0.021)AS	RPAAAAAGSAS(ph)SP	CDK1	1.1	0.43515		Yes
380	IPI00121100	Protein WWC2;WW do	Wwc2;D8ErtD594e;MN	T999	1	3	SQTFSPGER	SQT(1)FSPGER	SQT(ph)FSPGER	PKA/AKT	0.9	0.18891		Yes
768	IPI00120046	5'-3' exoribonuclease 2	Xrn2;Dhm1;Xrn2;Dhm1	S499	2	5	KAEDSDSEPEPEDNVR	KAEDS(1)DS(1)EPEPEDN	KAEDS(ph)DS(ph)EPE	CK2	1.2	0.37809		Yes
769	IPI00120046	5'-3' exoribonuclease 2	Xrn2;Dhm1;Xrn2;Dhm1	S501	2	7	KAEDSDSEPEPEDNVR	KAEDS(1)DS(1)EPEPEDN	KAEDS(ph)DS(ph)EPE	CK2	1.2	0.37809		Yes
906	IPI00108989	Yap1 protein;Yes-assoc	Yap1;mCG 9891;Yap1	S46	1	3	GDSSETDLEALFNAMVNP	GDS(0.5)ET(0.5)DLEALF	GDS(ph)ETDLEALFNAM	CAMK2	1.1	0.44246		No
258	IPI00108989	Yap1 protein;Yes-assoc	Yap1;mCG 9891;Yap1	T48	1	5	GDSSETDLEALFNAMVNP	GDS(0.195)ET(0.805)D	GDS(ph)ETDLEALFNAM	CK2	1.4	0.099744		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signif	Up-/Down-r	Localized phosphosite?
1153	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nse	S166	1	9	NYQQNYQNSSEGEKNE	NY(0.029)QQNY(0.029)	_NYQQNYQNS(ph)ESGKNEGSESPEGQAQQR				No	
1158	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nse	S168	1	11	NYQQNYQNSSEGEKNE	NY(0.029)QQNY(0.029)	_NYQQNYQNS(ph)ESGKNEGSESPEGQAQQR				No	
611	IPI00849786	Nuclease-sensitive elen	Ybx1;Msy-1;Msy1;Nse	S177	1	20	NYQQNYQNSSEGEKNE	NY(0.001)QQNY(0.003)	_NYQQNYQNSSEGEKNE	CK2	1.0	0.30582	No	
324	IPI00222801	Proto-oncogene tyrosin	Yes1;Yes;Fyn;Fyn;Lck;L	T425	1	8	LIEDNEYTAR	LIEDNEY(0.5)TI(0.5)AR	LIEDNEY(ph)TAR		0.9	0.14459	No	
267	IPI00222801	Proto-oncogene tyrosin	Yes1;Yes;Fyn;Fyn;Lck;L	Y424	1	7	LIEDNEYTAR	LIEDNEY(0.997)TI(0.003)	LIEDNEY(ph)TAR		0.9	0.10517	Yes	
967	IPI00515528	Zinc finger CCCH type c	Zc3h13	S1273	1	3	LRSPNSNDSAHR	LR(0.999)PS(0.001)ND	LR(ph)PSNDSAHR	CAMK2	1.1	0.46224	Yes	
482	IPI00673693	Zinc finger CCCH doma	Zc3h18;Nhn1	S552	2	4	LGVSVSPSR	LGVS(0.999)VS(0.997)P	LGVS(ph)VS(ph)PSR	NEK6	1.0	0.24903	Yes	
761	IPI00673693	Zinc finger CCCH doma	Zc3h18;Nhn1	S554	1	6	LGVSVSPSR	LGVSVS(1)PSR	LGVSVS(ph)PSR	CDK2	1.2	0.37569	Yes	
1305	IPI00673693	Zinc finger CCCH doma	Zc3h18;Nhn1	S556	1	8	LGVSVSPSR	LGVS(0.006)VS(0.497)P	(ca)LGVSVS(ph)PSR	CK1			No	
645	IPI00673693	Zinc finger CCCH doma	Zc3h18;Nhn1	S871	1	4	ANLSPDRGSR	ANLS(1)PDRGSR	ANLS(ph)PDRGSR	CDK2	1.2	0.32577	Yes	
266	IPI00673693	Zinc finger CCCH doma	Zc3h18;Nhn1;Zc3h18;N	S58	1	3	VQSQEETRSDEDRASEF	VQS(0.82)QEET(0.17)RS	VQS(ph)QEETRSDEED	CAMK2	1.4	0.10396	Yes	
627	IPI00136572	Zinc finger CCCH-type a	Zc3hav1;Zc3hav1;Zc3h	S324	1	2	ASQEFLEDGDPDGLFSR	AS(1)QEFLEDGDPDGLFS	AS(ph)QEFLEDGDPDG	PKA	1.0	0.31513	Yes	
49	IPI00465879	Nuclear-interacting par	Zc3hc1;Nipa;Zc3hc1;Ni	S406	1	3	LCSSSSSDTSR	LCS(0.923)S(0.07)S(0.0)	LCS(ph)SSSSSDTSR	PKA/AKT	2.6	4.931E-07	Up	Yes
1276	IPI00124064	Probable palmitoyltran	Zdhc5;Kiaa1748;Zdhh	S376	1	2	LSRGDSLKEPTSIADSSR	LS(0.499)RGDS(0.499)L	LS(ph)RGDSLKEPTSIAC	GSK3			No	
883	IPI00124064	Probable palmitoyltran	Zdhc5;Kiaa1748;Zdhh	S380	1	6	LSRGDSLKEPTSIADSSR	LS(0.002)RGDS(0.998)L	LSRGDS(ph)LKEPTSIAC	CHK1/2	1.1	0.43033	Yes	
293	IPI00131810	Zinc finger RNA-binding	Zfr	S1054	1	4	RRDSGVDGDFEAEAGK	RRDS(1)DGVDFEAEAGK	RRDS(ph)DGVDFEAE	PKA	1.3	0.1228	Yes	
1000	IPI00126804	Zinc finger Ran-binding	Zranb2;Zfp265;Zis;Znf2	S130	1	11	ENVEYIEREESDGEYDEF	ENVEY(0.001)IEREES(0.	_ENVEYIEREES(ph)DGE	PKD	1.1	0.47786	Yes	
539	IPI00126804	Zinc finger Ran-binding	Zranb2;Zfp265;Zis;Znf2	S163	1	7	EVEDKESGEEDEDEDL	EVEDKES(1)EGEEDEDE	EVEDKES(ph)EGEEDE	CK2	1.2	0.27081	Yes	
801	IPI00126804	Zinc finger Ran-binding	Zranb2;Zfp265;Zis;Znf2	S198	1	22	YKLDEDEDEDDADLSKYN	YKLDEDEDEDDADLS(0.0	YKLDEDEDEDDADLSKYN	CK2	1.1	0.39263	Yes	
1331	IPI00126804	Zinc finger Ran-binding	Zranb2;Zfp265;Zis;Znf2	S203	1	27	YKLDEDEDEDDADLSKYN	Y(0.16)KLDEDEDEDDAD	YKLDEDEDEDDADLSKYNLDAS(ph)EEDSNK				No	
102	IPI00387422	Putative uncharacteriz	Zyx;Zyx;Zyx	S336	1	1	SPGGPGPLTLK	S(1)PGGPGPLTLK	_S(ph)PGGPGPLTLK	ERK/MAPK	1.8	0.0014985	Up	Yes
501	IPI00132478	Uncharacterized protein	C6orf203 homolog	S106	1	7	EAEDEESDEETSYPERS	EAEDEES(0.997)DEET(0	EAEDEES(ph)DEETSYP	CK2	1.2	0.25801	Yes	
839	IPI00224561	UPF0550 protein C7orf28	homolog	S264	1	11	HIEPELAGRDSPVRAEM	HIEPELAGRDS(0.999)PV	HIEPELAGRDS(ph)PVR	CDK2	1.1	0.40914	Yes	
The End														

<sup>1</sup> The ratios are normalized to correct for unequal amounts of "light" and "heavy" protein in the assay. For the peptides where a value for ""Ratio of Phosphorylations (+GH/-GH), Normalized"" is not listed, one or both peptide signals in the corresponding peptide pair (light and heavy) were below the threshold for quantification.



No	IPI Numbers	Protein Names	Gene Names	pAA	Number of	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Phosphosites Localized?
99	IPI00119618	Calnexin	Canx	S582	1	10	AEDEILNRSR	AEDEILNRS(ph)PR	AEDEILNRS(1)PR	CDK1	0.9	0.17936		Yes
176	IPI00133349	Calcium-regulated heat	Carhsp1	S42	1	6	GNVVPSPLPTRR	(ca)GNVVPSP(ph)PLPTR	GNVVPSP(0.999)PLPTO	ERK/MAPK	1.1	0.33687		Yes
55	IPI00133349	Calcium-regulated heat	Carhsp1	S53	1	3	TFSATVR	TFS(ph)ATVR	TFS(1)ATVR	PKA/AKT	1.5	0.062937		Yes
96	IPI00551498	Girdin;Girders of actin	Ccdc88a;Grdn;Kiaa121	S1704	1	3	SSSQENLLDEVK	SSS(ph)QENLLDEVK	S(0.098)S(0.054)S(0.848)QENLLDEVK		0.9	0.17468		Yes
183	IPI00170037	Malcaverin;Cerebral c	Ccm2;Osm;Ccm2;Osm	S393	1	6	GIITDSFGR	GIITDS(ph)FGR	GIIT(0.001)DS(0.999)FGR		1.1	0.34547		Yes
267	IPI00308149	Cyclin-Y;Cyclin fold pro	Ccny;Cfp1;Ccny;Cfp1	S326	1	3	SASADNLILPR	SAS(ph)ADNLILPR	S(0.103)AS(0.897)ADNL	PKA/AKT	1.1	0.46047		No
207	IPI00753875	Putative uncharacterize	Ccny1	S350	1	1	SLSADNFIGIQR	S(ph)LSADNFIGIQR	S(0.755)LS(0.245)ADNF	NIMA	1.1	0.39447		Yes
211	IPI00410802	CD44 antigen;Phagocyt	Cd44;Ly-24;Cd44;Ly-2	T728	1	9	LVINGGNGTVEDR	LVINGGNGT(ph)VEDR	LVINGGNGT(1)VEDR	FHA1 Rad53p	1.1	0.39966		Yes
129	IPI00464128	Cell division cycle 2-like	Cdc2l5;Kiaa1791;Cdc2l	T1245	1	5	IILETPEDRPR	IILELT(ph)PEPDRPR	IILELT(1)PEPDRPR	NEK6	0.9	0.23988		Yes
157	IPI00138190	Cadherin-11;Osteoblas	Cdh11;Cad-11	S788	1	7	LADLYGSKDTFDDDS	LADLYGS(ph)KDTFDD	LADLY(0.102)GS(0.797)	NEK6	1.2	0.30396		Yes
414	IPI00124240	Cell division protein kin	Cdk2;Cdk3;Cdk2;Cdc2	Y15	1	6	IGEGTYGVVYK	IGEGTY(ph)GVVYK	IGEGT(0.071)Y(0.929)G	ALK				No
347	IPI00399663	Centromere-associated	Centpe	S451	2	2	TSVTSLRENSLMK	(ca)T(ph)S(ph)VTSLRE	T(1)S(1)VTSLRENSLMK	PKA/AKT				Yes
398	IPI00399663	Centromere-associated	Centpe	T450	2	1	TSVTSLRENSLMK	(ca)T(ph)S(ph)VTSLRE	T(1)S(1)VTSLRENSLMK	PKA				No
109	IPI00890117	Cofilin-1;Cofilin, non-m	Cfl1;Cfl1	S3	1	2	ASGVAVSDGVK	(ca)AS(ph)GVAVSDGV	AS(1)GVAVSDGVK		0.9	0.20239		Yes
142	IPI00222386	Charged multivesicular	Chmp2b	S199	1	4	ATISDEEIER	ATIS(ph)DEEIER	ATIS(1)DEEIER	CK2	1.2	0.27722		No
247	IPI00467854	CAP-Gly domain-contai	Clip2;Cyln2;Kiaa0291;C	S924	1	10	VLLLEANRHSPPGER	VLLLEANRHS(ph)PGPE	VLLLEANRHS(1)PGPER	PKA	1.1	0.44697		Yes
356	IPI00762331	Cordon-bleu protein-lik	Cobl1;Cobl1;Kiaa0977	S364	1	1	STSVDDTDKSSSEAIMVR	S(ph)TSDVDDTDKSSSEAI	S(0.438)T(0.281)S(0.281)S(0.281)VDDTDKSSSEAIMVR					No
50	IPI00928004	Putative uncharacterize	Copa;Copa	S173	1	3	NLSPGAVESDVR	NLS(ph)PGAVESDVR	NLS(1)PGAVESDVR		1.5	0.053828		No
311	IPI00123891	Cysteine and glycine-ric	Csrp1;Crp1;Csrp	S192	1	14	GFGFGQGAGALVHSE	GFGFGQGAGALVHS(ph)	GFGFGQGAGALVHS(1)E	NEK6				Yes
236	IPI00112963	Catenin alpha-1;102 kD	Ctnn1;Catna1	S641	1	8	TPPELDDSFETEDFVR	TPPELDDS(ph)DFETED	TPPELDDS(1)DFETEDF	CK2	1.1	0.43413		Yes
69	IPI00128975	Death-associated prote	Dap	S51	1	11	DKDDQEWESTSPPKPTV	DKDDQEWESTS(ph)PH	DKDDQEWES(0.013)T(0.013)C	CDK2	1.4	0.10649		No
378	IPI00761729	Serine/threonine-prote	Dck1;Dcamk1;Dck1;Dc	S352	1	7	DLYRPLSDDLDSVGDV	DLYRPLS(ph)SDDLDSV	DLYRPLS(0.499)S(0.499)S	CHK1/2				No
379	IPI00761729	Serine/threonine-prote	Dck1;Dcamk1;Dck1;Dc	S353	1	8	DLYRPLSDDLDSVGDV	DLYRPLS(ph)SDDLDSV	DLYRPLS(0.499)S(0.499)S	DDLDS(0.002)VGDSV				Yes
380	IPI00761729	Serine/threonine-prote	Dck1;Dcamk1;Dck1;Dc	S362	1	17	DLYRPLSDDLDSVGDV	DLYRPLSDDLDSVGDV	DLY(0.158)RPLS(0.146)	CK1				No
191	IPI00896604	Probable ATP-depende	Ddx10	T587	1	14	LASGDGDEEQDEETE	LASGDGDEEQDEE(ph)	LASGDGDEEQDEE(1)E	CK2	1.0	0.35681		No
100	IPI00120691	Nucleolar RNA helicase	Ddx21;Ddx21;mcG	S118	1	15	QADSETKEIITEPSEEA	QADSETKEIITEPSE(ph)	QADSETKEIT(0.005)EE	CK2	0.9	0.18436		Yes
89	IPI00113576	ATP-dependent RNA he	Ddx24;Ddx24	S126	1	5	AQAVSEEEEEEGSSP	AQAVS(ph)EEEEEEGSS	AQAVS(1)EEEEEEGSS	CK2	1.3	0.1578		No
246	IPI00113635	H/ACA ribonucleoprote	Dkc1;Dkc1;BC068171	S508	1	8	VKVVEEMSE	VKVVEEMS(ph)E	VKVVEEMS(1)E		1.0	0.4466		Yes
76	IPI00125861	Disks large homolog 1;	Dlg1;Dlgh1;Dlg1;Dlgh1	S575	1	14	EQMMNNSVSSGSGSLR	EQMMNNSVSSGSGS(ph)	EQMMNNSVSSGSGS(0.013)	GSK3	1.4	0.12241		No
66	IPI00816914	Dedicator of cytokines	Dock7;Gm430;Kiaa177	S900	1	5	SLSNSNPDISGTPSPDDI	SLSNS(ph)NPDISGTPPT	S(0.107)LS(0.064)NS(0.0)	NEK6	0.8	0.090241		Yes
14	IPI00882020	Putative uncharacterize	Dpf2;Dpf2;Req;Ubid4	S142	1	5	VDDDSLGEFVPSNSR	VDDDS(ph)LGEFVPSNS	VDDDS(1)LGEFVPSNSR	PLK	0.6	6.61E-05	Down	No
65	IPI00114375	Dihydropyrimidinase-re	Dpysl2;Crmp2;Ulip2	T509	1	13	GLYDGPVCEVSTPK	GLYDGPVCEVST(ph)	GLYDGPVCEVS(0.001)Y	CDK1	0.8	0.078542		Yes
107	IPI00406447	Collapsin response me	Dpysl3;Dpysl3;Drp3;Uli	T622	1	13	GMVDGVPFDLTTTPK	GMVDGVPFDLTTT(ph)	GMVDGVPFDLTT(0.004)	CDK1	0.9	0.20093		Yes
156	IPI00127942	Destrin;Actin-depolyme	Dstn;Dsn;Sid23	S3	1	2	ASGVQVADEVCR	(ca)AS(ph)GVQVADEV	AS(1)GVQVADEVCR		1.2	0.29601		Yes
181	IPI00380332	Dual specificity phosph	Dusp9;RP23-329M9.2	S393	1	1	SNISPNFNFMGQLLDFE	S(ph)SNISPNFNFMGQVL	S(0.61)NIS(0.39)PNFNF	PKA	1.1	0.3442		Yes
21	IPI00118849	Dual specificity tyrosine	Dyrk1a;Dyrk;Dyrk1a;RP	Y321	1	2	IYQYIQSR	IYQY(ph)IQSR	IYQY(1)IQSR		0.7	0.0030188	Down	No
365	IPI00848728	Enhanced at puberty p	Eap1;Kiaa1865	S694	1	2	NSSSPVSPASVPGQR	NS(ph)SSPVSPASVPGQ	NS(0.332)S(0.332)S(0.3)	PKA/AKT				No
366	IPI00848728	Enhanced at puberty p	Eap1;Kiaa1865	S695	1	3	NSSSPVSPASVPGQR	NS(ph)SSPVSPASVPGQ	NS(0.332)S(0.332)S(0.3)	CAMK2				Yes
13	IPI00848728	Enhanced at puberty p	Eap1;Kiaa1865	S696	1	4	NSSSPVSPASVPGQR	NSSS(ph)PVSPASVPGQ	NS(0.08)S(0.08)S(0.832)	Polo box	0.5	1.19E-05	Down	No
264	IPI00330066	Enhancer of mRNA-dec	Edc4;Edc4	S727	1	28	GPGQVSTAASALDLQ	GPGQVSTAASALDLQ	GPGQVSTAASALDLQ	CDK2	1.1	0.45692		No
36	IPI00320208	Elongation factor 1-bet	Eef1b;Eef1b2	S106	1	28	YGPSSVEDTTGSGAADA	YGPSSVEDTTGSGAAD	YGPSSVEDTTGSGAADA	CK2	0.8	0.032437	Down	Yes
221	IPI00944009	Elongation factor 1-del	Eef1d;Eef1d;Eef1d;Eef	S541	1	18	GATPAEDEDKIDIDLF	GATPAEDEDKIDIDLF	GATPAEDEDKIDIDLF	CK2	1.1	0.41713		Yes
93	IPI00402968	EH domain-containing	Ehd2	S438	1	13	GPDEAIEDGEGESDFAI	GPDEAIEDGEGES(ph)	GPDEAIEDGEGES(1)EDDAE	VWVTK	0.9	0.16562		Yes
235	IPI00261239	Translation initiation fa	Eif2b5	S540	1	3	AGSPQLDDIR	AGS(ph)PQLDDIR	AGS(1)PQLDDIR	CAMK2	1.1	0.43344		Yes
357	IPI00417155	Eukaryotic translation	Eif4g3;Eif4g3;Eif4g3;Eif	S277	1	22	EQAGQMPETAAGEPTPI	EQAGQMPETAAGEPTP	EQAGQMPETAAGEPTP	PKA				Yes
358	IPI00417155	Eukaryotic translation	Eif4g3;Eif4g3;Eif4g3;Eif	S278	1	23	EQAGQMPETAAGEPTPI	EQAGQMPETAAGEPTP	EQAGQMPETAAGEPTP	PKA/AKT				Yes
359	IPI00417155	Eukaryotic translation	Eif4g3;Eif4g3;Eif4g3;Eif	S281	1	26	EQAGQMPETAAGEPTPI	EQAGQMPETAAGEPTP	EQAGQMPETAAGEPTP	CK1				Yes
404	IPI00417155	Eukaryotic translation	Eif4g3;Eif4g3;Eif4g3;Eif	T280	1	25	EQAGQMPETAAGEPTPI	EQAGQMPETAAGEPTP	EQAGQMPETAAGEPTP	CK1				Yes
174	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S114	1	8	TSFDENDEELEDKDKSK	TSFDENDS(ph)ELEDK	TSFDENDS(1)ELEDKDKSK		1.1	0.3356		Yes
184	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S137	1	11	TARPNSEAPLSGSEDADL	TARPNSEAPLS(ph)GSE	TARPNSEAPLS(0.982)G	CK2	1.1	0.34552		Yes
209	IPI00756424	Eukaryotic translation	Eif5b;Iif2;Eif5b;Iif2	S215	1	7	SVPTVDSGNEDDSSFK	SVPTVDS(ph)GNEDDD	SVPTVDS(1)GNEDDSS	CK2	1.1	0.39881		Yes
336	IPI00403406	Epb4.112 protein;Eryth	Epb4.112;Epb4.112	S596	1	11	ATPLPAEGKSSHETLN	ATPLPAEGKSS(ph)HET	ATPLPAEGKS(0.097)S(0.451)HET	(0.451)LN				No
364	IPI00464296	Band 4.1-like protein 3	Epb4113;Dal1;Epb4.113	S962	1	10	VESTSVSGISPGGAK	VESTSVSGIS(ph)PGGA	VESTS(0.001)VGS(0.113)S(0.886)PGGAK		0.9	0.15866		Yes
90	IPI00464280	Epsin 2;Epsin-2;EPS-15	Epn2;RP23-15513.7-004	S172	1	2	GSSQPNLSTSYSEYQY	GS(ph)SQPNLSTSYSEY	GS(0.5)S(0.5)QPNLSTSY	PKA	1.2	0.28147		Yes
145	IPI00464280	Epsin 2;Epsin-2;EPS-15	Epn2;RP23-15513.7-004	S173	1	3	GSSQPNLSTSYSEYQY	GS(ph)QPNLSTSYSEY	GS(0.119)S(0.881)QPN	CAMK2	1.2	0.28147		Yes
37	IPI00420185	Epidermal growth fact	Eps15l1;Eps15-rs;Eps1	S255	1	18	STPHSGVSSLNSTGSL	STPHSGVSSLNSTGSL	STPHSGVSSLNSTGSL	CDK1	0.8	0.033532	Down	Yes
169	IPI00896710	Protein LAP2;ErbB2-int	ErbB2ip;Erbin;Kiaa122	S849	1	12	ASSADVGISKSTEDLSP	ASSADVGISKSTEDLSP	ASSADVGISKSTEDLSP	(0.997)T(0.003)EDLSPQR	1.1	0.32815		Yes
405	IPI00896710	Protein LAP2;ErbB2-int	ErbB2ip;Erbin;Kiaa122	T850	1	13	ASSADVGISKSTEDLSP	ASSADVGISKSTEDLSP	ASSADVGISKSTEDLSP	AS(0.035)S(0.094)S(0.0)	CK1			Yes
131	IPI00223670	Protein FAM40A;Prote	Fam40a;Kiaa1761;Fam	S335	1	3	AASPPASADLIEQQQK	AAASPPASADLIEQQQ	AAAS(0.863)PPAS(0.132)	CAMK2	0.9	0.24666		Yes
54	IPI00874398	Protein FAM65A	Fam65a;Kiaa1930	S417	1	7	FSTYSQSPDPDTPSLR	FSTYSQSP(ph)PDPDTP	F(0.018)T(0.018)Y(0.0)	CK1	0.8	0.059528		Yes
376	IPI00678532	Regulator of microtubu	Fam82a2;Fam82c;120C	S46	1	3	SHSLPNSLDYAQASER	SHS(ph)LPNSLDYQAAS	S(0.055)HS(0.473)LPNS	14-3-3 binding				Yes
377	IPI00678532	Regulator of microtubu	Fam82a2;Fam82c;120C	S50	1	7	SHSLPNSLDYAQASER	SHS(ph)LPNSLDYQAAS	S(0.055)HS(0.473)LPNS	NEK6				Yes
59	IPI00378206	F-box/WD repeat-cont	Fbxw8;Fbxw8	S86	1	3	SRSPPPDRDATEPEPLV	SRS(ph)PPDRDATEPEP	S(0.193)RS(0.805)PPDR	14-3-3 binding	1.5	0.067597		Yes
81	IPI00921658	Filamin, alpha;Filamin	Flna;RP23-436K3.1-003	S968	1	10	SPFSVGVSPSLDLSK	SPFSVGVSPSLDLSK	SPFSVGVSPSLDLSK	(0.087)PS(0.0)	1.4	0.1306		No
31	IPI00664670	Filamin-C;Gamma-filam	Flncc;Abpl;Flnc2;Flncc	S2234	1	3	LGSFGSITR	LGS(ph)FGSITR	LGS(1)FGSITR	PKA/AKT	1.7	0.017833	Up	Yes
308	IPI00119242	Formin-binding protein	Fmnp4;Fbp30;Kiaa1014	S486	1	13	ALEEGDGSVSGSSPR	ALEEGDGSVSGSS(ph)	ALEEGDGS(0.003)VS(0)	Polo box				Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-r	Phosphosites Localized?
68	IPI00130455	Phospholemman;FXD	Fxyd1;Plm	S83	1	14	TGPEDEEETFRSSIR	TGPEDEEETFRSSIR(ph)	TGPEDEEETFRSSIR(1)IR	AURORA	0.8	0.10333		No
175	IPI00130455	Phospholemman;FXD	Fxyd1;Plm	T79	1	10	TGPEDEEETFRSSIR	TGPEDEEETFRSSIR(ph)	TGPEDEEETFRSSIR(0.778)FR	PLK1	1.1	0.33565		No
126	IPI00130095	Ras GTPase-activating	G3bp1;G3bp;G3bp1;G3	S229	1	1	STSPAPADVAPAQEDLR	S(ph)TSPAPADVAPAQ	S(0.97)T(0.015)S(0.015)PAPADVAPAQEDLR		1.2	0.23413	Yes	
73	IPI00124245	Ras GTPase-activating	G3bp2;G3bp2	S225	1	1	SATPPPAEPASLPQPEPK	S(ph)ATPPPAEPASLPQ	S(0.578)AT(0.422)PPPAEPASLPQPEPK		0.9	0.11808	Yes	
72	IPI00124245	Ras GTPase-activating	G3bp2;G3bp2	T227	1	11	HLEELLESKATPPPAEPAS	HLEELLESKAT(ph)PPP	HLEELLESK(0.009)AT(0.991)PPPAEPASLPQPEPK		0.9	0.11659	Yes	
296	IPI00114226	Endothelial transcriptid	Gata2	S425	3	16	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
297	IPI00114226	Endothelial transcriptid	Gata2	S429	3	20	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
298	IPI00114226	Endothelial transcriptid	Gata2	S447	3	38	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
299	IPI00114226	Endothelial transcriptid	Gata2	S449	3	40	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
300	IPI00114226	Endothelial transcriptid	Gata2	S462	3	53	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
301	IPI00114226	Endothelial transcriptid	Gata2	S463	3	54	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
302	IPI00114226	Endothelial transcriptid	Gata2	S464	3	55	GAEFFEELSKCMQEKSP	GAEFFEELSKCMQEK(S)	GAEFFEELSKCMQEK(S)	GSK3			Yes	
130	IPI00128615	Transcriptional repress	Gatad2b;Gatad2b	S136	1	17	LTPSPDIIVLSDNEASSPR	LTPSPDIIVLSDNEASSPR	LTPSPDIIVLSDNEASSPR	Polo box	0.9	0.24144	Yes	
153	IPI00323179	Rab GDP dissociation in	Gdi1;Rabgdia	S65	1	10	FQILEGPPESMGR	FQILEGPPES(ph)MGR	FQILEGPPES(1)MGR		1.2	0.29154	No	
216	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	S259	1	3	VDSSTCLFPVEEK	VDS(ph)TCLFPVEEK	VDS(0.953)T(0.045)T(0.0)	CHK1/2	1.1	0.40526	Yes	
401	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	T260	1	4	VDSSTCLFPVEEK	VDS(ph)TCLFPVEEK	VDS(0.333)T(0.333)T(0.0)	FHA2 Rad53p			No	
402	IPI00406371	Glucosamine-fructose	Gfpt1;Gfpt;Gfpt1;Gfpt	T261	1	5	VDSSTCLFPVEEK	VDS(ph)TCLFPVEEK	VDS(0.333)T(0.333)T(0.333)	CLFPVEEK			Yes	
243	IPI00473912	PERQ amino acid-rich v	Gigyf2;Kiaa0642;Perq2	T383	1	21	AGAEAESEVPTQLSSAR	AGAEAESEVPTQLSSAR	AGAEAESEVPTQLSSAR	ERK/MAPK	1.0	0.44565	Yes	
419	IPI00177243	GTPase, IMAP family m	Gimap9	Y126	1	1	Y(M)ILFTHK	Y(ph)MILFTHK	Y(1)MILFTHK	ALK			No	
295	IPI00112024	similar to QM protein	GM4892	S116	2	6	LQTGMSGAVGKPKQGTV	(ca)LQT(ph)GMS(ph)G	LQT(1)GMS(1)GAVGKPKQGTVAR				Yes	
427	IPI00458227	similar to spermidine/s	Gm552	Y27	1	1	YEYEDQVILTEK	(ca)Y(ph)EYEDQVILTE	Y(0.939)EY(0.061)IEDQ	EGFR			Yes	
188	IPI00222461	Guanine nucleotide-bir	Gnl3;Ns	S505	1	17	NAEISDVAPVEETRELS	NAEISDVAPVEETRELS	NAEISDVAPVEET(0.006)	CAMK2	1.1	0.3522	Yes	
172	IPI00131457	Probable G-protein cou	Gpr124;Tem5	S1104	1	10	ALPTATEDGSPVLGEGPA	ALPTATEDGSP(ph)VLG	ALPTAT(0.001)EDG(S)0.0	CK1	1.0	0.33359	Yes	
154	IPI00461962	Probable G-protein cou	Gpr126;Dreg;Gm222	S480	1	7	LMTNNSASLEDGLR	(ca)LMTNNSAS(ph)LED	LMT(0.002)NNSAS(0.998)	CK1	1.2	0.29154	No	
232	IPI00480321	Glucocorticoid recepto	Grff1;Kiaa1722	S1179	1	7	TFSVSGSDDDELGP	TFSVSGS(ph)DDELGPI	TFSVSGS(1)DDELGPIR	CK2	1.0	0.43069	Yes	
313	IPI00648141	Glycogen synthase kina	Gsk3a;Gsk3b	S278	1	6	GEPNVSYICSR	GEPNVS(ph)YICSR	GEPNVS(0.491)Y(0.491)	GSK3			Yes	
102	IPI00648141	Glycogen synthase kina	Gsk3a;Gsk3b	Y279	1	11	GEPNVSYICSR	GEPNVS(ph)YICSR	GEPNVS(0.002)Y(0.998)	ICSR	0.9	0.18639	Yes	
29	IPI00331241	Glutathione S-transfer	Gsta3;Gstyc	T68	2	4	LVQTKAILNYIASKYNYL	(ca)LVQTK(ph)KAILNYI	LVQTK(1)KAILNY(0.886)	NEK6	1.7	0.015555	Up	Yes
30	IPI00331241	Glutathione S-transfer	Gsta3;Gstyc	Y74	2	10	LVQTKAILNYIASKYNYL	(ca)LVQTK(ph)KAILNYI	LVQTK(1)KAILNY(0.957)	IAS(0.033)KY(0.002)NLY	1.7	0.015555	Up	Yes
198	IPI00313817	Hepatoma-derived gro	Hdgf;Tdrn1	S165	1	8	AGDVLDSPKRPK	AGDVLDS(ph)PKRPK	AGDVLDS(1)PKRPK	CDK2	1.1	0.36576	No	
110	IPI00331612	High mobility group pr	Hmga2;Hmgic	S100	1	10	KPAQETEETSSQESAED	KPAQETEETSS(ph)SQE	KPAQETE(0.003)EET(0.1)	CK2	0.9	0.20442	No	
337	IPI00331612	High mobility group pr	Hmga2;Hmgic	S101	1	11	KPAQETEETSSQESAED	KPAQETEETSS(ph)SQE	KPAQETEET(0.001)S(0.245)S(0.377)QES(0.377)	AED			No	
212	IPI00331612	High mobility group pr	Hmga2;Hmgic	S104	1	14	KPAQETEETSSQESAED	KPAQETEETSSQES(ph)	KPAQETEETSSQES(1)A	CK2	1.0	0.40118	Yes	
338	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S584	1	25	GKQADVADQQTTELP	GKQADVADQQTTELP	GKQADVADQQT(0.031)	CK1			No	
193	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S587	1	26	QADVADQQTTELP	QADVADQQTTELP	QADVADQQTTELP	CK2	1.0	0.36042	Yes	
339	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	S595	1	34	QADVADQQTTELP	QADVADQQTTELP	QADVADQQTTELP	CK2			No	
16	IPI00338745	Non-histone chromoso	Hmgn1;Hmg-14;Hmg14	T80	1	21	GKQADVADQQTTELP	GKQADVADQQTTELP	GKQADVADQQTTELP	CK2			No	
149	IPI00853914	Heterogeneous nuclear	Hnrnpa2b1;Hnrpa2b1;	S720	1	21	GFGDGYNGYGGGPGGG	GFGDGYNGYGGGPGGG	GFGDGYNGYGGGPGGG	CK2	0.9	0.28897	Yes	
106	IPI00853914	Heterogeneous nuclear	Hnrnpa2b1;Hnrpa2b1;	Y723	1	24	GFGDGYNGYGGGPGGG	GFGDGYNGYGGGPGGG	GFGDGY(0.128)NGY(0.068)GGGPGGGNFGGS(0.0)	CK2	0.9	0.20032	Yes	
329	IPI00269661	Heterogeneous nuclear	Hnrnpa3;Hnrpa3;Hnrn	S356	1	1	SSGSPYGGYGGGSGGSG	S(ph)SSGSPYGGYGGSG	S(0.424)S(0.273)GS(0.273)PY(0.028)GGY(0.003)SSGSGGSGY				Yes	
253	IPI00269661	Heterogeneous nuclear	Hnrnpa3;Hnrpa3;Hnrn	S359	1	4	SSGSPYGGYGGGSGGSG	SSGS(ph)PYGGYGGSG	S(0.094)S(0.051)GS(0.8)CK1		1.1	0.44856	Yes	
268	IPI00330958	Heterogeneous nuclear	Hnrnpd;Auf1;Hnrpd;Hr	S82	1	15	IDASKNEEDEGHNSNSP	IDASKNEEDEGHNSNS(p)	IDASKNEEDEGHNS(0.005)INS(0.928)S(0.066)PR		1.0	0.46332	Yes	
322	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrnpk;	S116	1	13	IIPTEEGQLQSPATSQ	IIPTEEGQLQPS(ph)PT	IIPTEEGQLQPS(0.444)PT(0.444)AT(0.092)S(0.02)QLPLESDAVECLNYQHYK				Yes	
393	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrnpk;	T118	1	15	IIPTEEGQLQSPATSQ	IIPTEEGQLQPS(ph)PT	IIPTEEGQLQPS(0.444)P	FHA KAPP			Yes	
135	IPI00224575	Heterogeneous nuclear	Hnrnpk;Hnrpk;Hnrnpk;	S284	1	6	DYDDMSR	DYDDMS(ph)PR	DYDDMS(1)PR	CDK2	0.9	0.25642	Yes	
159	IPI00554929	Heat shock protein HSP	Hsp90ab1;Hsp84;Hsp8	S255	1	6	IEDVGSDEEDDSGKDK	IEDVGS(ph)DEEDDSG	IEDVGS(1)DEEDDSGDK	CK2	1.2	0.30825	Yes	
78	IPI00331556	Heat shock 70 kDa prot	Hspa4;Apg2;Hsp110	S76	1	3	AFSDPFVFAEK	AFS(ph)DPFVFAEK	AFS(1)DPFVFAEK	CAMK2	1.4	0.1278	Yes	
202	IPI00463909	E3 ubiquitin-protein lig	Huwe1;Kiaa0312;Ureb	S1907	1	6	GSGTASDDEFENLR	GSGTAS(ph)DDEFENLR	GS(0.001)GT(0.006)AS	CK2	1.1	0.37789	Yes	
150	IPI00332321	Interferon-gamma rece	Ifngr1;Ifngr;Ifngr1;Ifngr	T373	1	18	ALEAGGSTSAMTPDSP	ALEAGGSTSAMTPDSP	ALEAGGSTSAMTPDSP	WW GroupIV	0.9	0.28961	Yes	
392	IPI00332321	Interferon-gamma rece	Ifngr1;Ifngr;Ifngr1;Ifngr	T375	1	20	ALEAGGSTSAMTPDSP	ALEAGGSTSAMTPDSP	ALEAGGSTSAMTPDS(0.012)PPT(0.494)PT(0.494)QRR				No	
84	IPI00131056	Insulin-like growth fact	Igf2bp1;Vickz1	S181	1	3	QGS(ph)PVAAGAPAK	QGS(ph)PVAAGAPAK	QGS(1)PVAAGAPAK	CAMK2	0.9	0.14192	Yes	
269	IPI00761863	Insulin-like growth fact	Igf2bp2;Imp2;Vickz2;I	S164	1	13	ISYIPDEEVSSPPPHR	ISYIPDEEVSSPP(ph)PP	ISYIPDEEVSSPP(0.002)S(0.0)	CK1	1.0	0.46408	Yes	
282	IPI00331315	Insulin-like growth fact	Igf2bp3;Vickz3	S165	1	15	VAVYIPDEETAQQNPSPQ	VAVYIPDEETAQQNP(S)P	VAVYIPDEETAQQNP(S)1)PQLR		1.0	0.48364	Yes	
324	IPI00229522	Interleukin-28 receptor	Il28a;Ifnlr1	S17	1	11	WAPLFLFLQSLALGR	WAPLFLFLQSL(ph)ALG	WAPLFLFLQSL(1)ALGR	NEK6			No	
180	IPI00319956	Protein IMPACT;Imprin	Impact	S137	1	9	KTEEVESVEEEDPILEPH	KTEEVESVEEEDPI	KT(0.005)EEVES(0.995)EEDPILEHPENPVK		1.0	0.34157	Yes	
276	IPI00410790	Iroquois-class homeod	Irx1;Irx1a;Irx1	S267	1	4	DQSSS(ph)PLSAEATLK	DQSSS(ph)PLSAEATLK	DQSSS(0.085)S(0.83)PLS(	Polo box	1.0	0.47597	Yes	
74	IPI00122143	Tyrosine-protein kinase	Lak2	S523	1	10	TNGISDVQISPTLQR	TNGISDVQIS(ph)PTLQ	TNGISDVQIS(0.992)PT(0.008)LQR		0.9	0.11977	Yes	
360	IPI00421009	Kinesin-like protein KIF	Kifc3	S15	1	9	TWNLGATPSLR	TWNLGATPS(ph)LR	TWNLGAT(0.01)PS(0.99)LR				No	
312	IPI00653162	Klotho;Klotho peptide;	Kl;Kl	S485	1	10	RGLFYVDLSDQDK	(ca)RGLFYVDLSDQDK	RGLFYVDLSDQDK				Yes	
421	IPI00317465	Kinetochore-associated	Knl2;Kiaa1903;M18bp1	Y107	1	5	NEMIVISPKGIFKFR	(ca)NEMIVIS(ph)ESPK	NEMIVIS(0.989)ES(0.011)	ABL			No	
249	IPI00230429	Importin subunit alpha	Kpna3;Qip2;Kpna3	S60	1	11	NVPOEESLSDVDADDF	NVPOEESLSDS(ph)DV	NVPOEESLSDS(1)DVDA	NEK6	1.1	0.44797	Yes	
186	IPI00134106	Protein KTI12 homolog	Kti12	S157	1	3	ATSPVANGVGLAAVSK	AT(ph)SPVANGVGLAA	AT(0.5)S(0.5)PVANGGV	CAMK2	1.0	0.34946	Yes	
187	IPI00134106	Protein KTI12 homolog	Kti12	T156	1	2	ATSPVANGVGLAAVSK	AT(ph)SPVANGVGLAA	AT(0.5)S(0.5)PVANGGV	PKA	1.0	0.34946	No	
286	IPI00929786	La-related protein 1;La	Larp1;Kiaa0731;Larp	T626	1	7	ILIVTQTPPYMR	ILIVTQ(ph)PPYMR	ILIVTQ(1)PPYMR		1.0	0.49011	Yes	
104	IPI00474486	RNA polymerase-assoc	Leo1;Gm185	S659	1	5	KYVISDEEEEDD	KYVIS(ph)DEEEEDD	KYVIS(1)DEEEEDD	CK2	0.9	0.19202	Yes	
123	IPI00112339	LIM domain and actin	Lima1;D15Erd366e;Ep	S488	1	22	SDNEETLGRPAQPPNAG	SDNEETLGRPAQPPNA	SDNEETLGRPAQPPNAG	WW GroupIV	1.2	0.23083	Yes	

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signific	Up-/Down-r	Phosphosites Localized?
182	IPI00620256	Lamin-A/C	Lmna;Lmn1	S637	1	9	SVGGSGGGSGFDNLVTR	SVGGSGGGG(ph)FGDN	S(0.003)VGGS(0.015)G	CK1	1.1	0.3454		Yes
238	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S390	1	4	LRLSPSPTSQR	(ca)LRLS(ph)PSPTSQR	LRLS(0.949)PS(0.05)PTS	PKA	1.1	0.43499		No
371	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S392	1	6	LRLSPSPTSQR	LRLS(ph)PSPTSQR_	LRLS(0.483)PS(0.483)P	NEK6				Yes
372	IPI00620256	Lamin-A/C;Lamin-A/C;L	Lmna;Lmn1;Lmna;Lmn	S395	1	9	LRLSPSPTSQR	LRLSPSPTS(ph)QR_	LRLS(0.105)PS(0.018)P	CK1				Yes
168	IPI00676243	Microtubule-associated	Map1a;Mtap1;Mtap1a	S2027	1	9	VPSAPGQESVPVPTDK	VPSAPGQES(ph)VPVD	VPSAPGQES(1)VPVPTDK		1.1	0.32584		Yes
417	IPI00124786	Mitogen-activated prot	Map3k14;Nik	Y671	1	16	ALQEVGGLKSPWKGEYK	ALQEVGGLKSPWKGEYK	ALQEVGGLKS(0.001)PWKG	Y(0.999)K				No
287	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S506	1	11	VAEFNNVTPLEEEVTSV	VAEFNNVTPLS(ph)EEE	VAEFNNVT(0.158)PLS(D	CK2	1.0	0.49348		No
92	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S517	1	22	VAEFNNVTPLEEEVTSV	VAEFNNVTPLEEEVTS	VAEFNNVTPLEEEVTS(0.001	VKDMS(0.932)PS(	1.0	0.16426		Yes
240	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S667	1	21	AAVGVGTNDITTPPNKEI	AAVGVGTNDITTPPNKE	AAVGVGTNDITTPPNKE(WW	GroupIV	1.1	0.43692		Yes
355	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	S785	1	3	ATSPSTLVSTGSPSSR	AT(ph)SPSTLVSTGSPSS	AT(0.498)S(0.498)PS(0.	PKD				No
403	IPI00408119	Microtubule-associated	Map4;Mtap4;Map4;M	T784	1	2	ATSPSTLVSTGSPSSR	AT(ph)SPSTLVSTGSPSS	AT(0.498)S(0.498)PS(0.	CK1				No
330	IPI00281011	MARCKS-related protei	Marcks1;Mlp;Mrp	S182	1	16	EGDTEEEAGPQAAEPSTI	EGDTEEEAGPQAAEPSTI	EGDTEEEAGPQAAEPSTI(0.425	JT(0.425)PS(0.126)GPES	(0.014)GPT(0.005)PAS(0.005)AEQ			Yes
396	IPI00281011	MARCKS-related protei	Marcks1;Mlp;Mrp	T183	1	17	EGDTEEEAGPQAAEPSTI	EGDTEEEAGPQAAEPSTI	EGDTEEEAGPQAAEPSTI(WW	GroupIV				No
164	IPI00453826	Matrin-3	Matr3	S596	1	1	SYPDGKESPSDKK	S(ph)YSPDGKESPSDKK	S(0.591)Y(0.372)S(0.03	PKA	1.2	0.31959		Yes
88	IPI00453826	Matrin-3	Matr3	S598	1	3	SYPDGKESPSDKK	SYS(ph)PDGKESPSDKK	SY(0.001)S(0.999)PDGK	PKA/AKT	0.9	0.15631		No
220	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S139	1	6	GLLYDSSEDEERPAR	GLLYDS(ph)SEDEERPAR	GLLY(0.004)DS(0.936)S	CK2	1.0	0.41576		No
290	IPI00323820	DNA replication licensi	Mcm2;Bm28;Ccd1;Kia	S27	1	8	ISDPLTSSPGR	ISDPLTSS(ph)JGDR	ISDPLTS(0.002)S(0.998)	Polo box	1.0	0.49617		Yes
141	IPI00123881	DNA replication licensi	Mcm6;Mcm6;Mis5	S689	1	31	VETPVNLDQEEIQQME	VETPVNLDQEEIQQME	VETPVNLDQEEIQQMET(0.006	DEGGGGVGNH	0.9	0.27487		Yes
134	IPI00753701	Mediator of DNA dama	Mdc1;Kia0170	S168	1	7	VLLAADSEEEGDFPSGR	VLLAADSEEEGDFPSGR	VLLAADS(1)EEEGDFPSG	CK2	0.9	0.25613		No
34	IPI00222037	Melanoma inhibitory a	Mia3;Kia0268;Mia3;K	S1916	1	15	DSLPSGPRREEAKPASPS	DSLPSGPRREEAKPAS	DSLPSGPRREEAKPAS(0.9	WW GroupIV	1.7	0.02448	Up	No
215	IPI00116372	Myeloid leukemia fact	Mlf2	S237	1	9	LAIQGPEDSPSR	LAIQGPEDS(ph)PSR	LAIQGPEDS(0.988)PS(0.	CDK2	1.1	0.40472		Yes
194	IPI00757871	MLI2 protein	MLI2	S4475	1	3	ALSPVPIPIPR	ALS(ph)PVPIPIPR	ALS(1)PVPIPIPR	CAMK2	1.1	0.36111		Yes
412	IPI00858168	Mitochondrial ribosom	Mrpl39;RP24-120H1.1	T308	1	4	AQFTIWDKLVRSR	(ca)AQFT(ph)IWDKLVRS	AQFT(1)IWDKLVRSR	FHA1 Rad53p				No
382	IPI00882333	Putative uncharacterize	Ms4a15	S13	4	13	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	Yes		Yes
383	IPI00882333	Putative uncharacterize	Ms4a15	S25	4	25	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	No		No
384	IPI00882333	Putative uncharacterize	Ms4a15	S30	4	30	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	No		No
385	IPI00882333	Putative uncharacterize	Ms4a15	S35	4	35	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	Yes		Yes
386	IPI00882333	Putative uncharacterize	Ms4a15	S45	4	45	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	No		No
387	IPI00882333	Putative uncharacterize	Ms4a15	S48	4	48	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAG	CK1				No
388	IPI00882333	Putative uncharacterize	Ms4a15	S60	4	60	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAG	NEK6				No
381	IPI00882333	Putative uncharacterize	Ms4a15	S7	4	7	MMCECGSAEAEAGSQQP	MMCECGS(ph)AEAG	MMCECGS(0.592)AEAGS(0.554)	QQPVQPPWQAGS(0.308)	LNT(0.308)MS(0.308)APPAS	No		No
38	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	S1793	1	7	ESSPLYSYPGFSDSTSAK	ESSPLYS(ph)PGFSDST	ES(0.032)S(0.023)PLY(D	GSK3	1.6	0.035943	Up	Yes
49	IPI00896700	Mtap1b protein;Microt	Mtap1b;Map1b;Mtap1	T1945	1	4	TRTRPEEGGYSYSEIK	TRTR(ph)PEEGGYSYSEI	TT(0.001)RT(0.999)PEE	CK2	1.5	0.051147		Yes
40	IPI00128196	Myotubularin-related p	Mtmr2;Mtmr2;RP23-1	S126	1	18	SASAISSDSISADNFSPI	SASAISSDSISADNFS	SASAISSDSISADNFS(0.999)	PDLR	0.8	0.037036	Down	No
43	IPI00226263	Matrix-remodeling-ass	Mxra7;Tmap1;Mxra7;R	S79	1	7	VAEPEESEAEPAEAKC	VAEPEES(ph)EEPEPAE	VAEPEES(1)EAEEPAEAKC	CK2	0.8	0.039173	Down	No
158	IPI00123181	Myosin-9;Myosin heav	Myl9	S1943	1	7	KGTGDCSDEEVDGKADG	KGTGDCS(ph)DEEVDG	KGTGDCS(1)DEEVDGKA	CK2	1.0	0.30824		No
139	IPI00123181	Myosin-9;Myosin heav	Myl9	T1939	1	3	KGTGDCSDEEVDGKADG	KGT(ph)GDCSDEEVDG	KGT(0.5)GDCS(0.5)DEE	PKA	0.9	0.26527		Yes
121	IPI00849670	Myof protein;Myoferli	Myof;Myof;Frl13;Kia	S175	1	7	GPSGTVSEAEQLAR	GPSGTVSEAEQLAR	GPSGTV(0.002)VS(0.998)	CK1	0.9	0.22734		Yes
275	IPI00896637	Nek1 protein;Nek1 pro	Nek1;Nek1;Nek1	S1069	1	3	TCSLPDLK	TCS(ph)LPDLK	TCS(1)LPDLK	CHK1	1.0	0.47533		No
239	IPI00844655	Serine/threonine-prote	Nek10;Gm282	S448	1	4	FLFSMER	(ca)FLFS(ph)MER	FLFS(1)MER		1.0	0.43541		Yes
348	IPI00400168	Nexilin;F-actin binding	Nexn	S281	1	1	SMVLDDDSPEYK	S(ph)MVLDDDSPEYK	S(1)MVLDDDSPEYK	PKA	0.7			No
23	IPI00131415	Nuclear factor 1 A-type	Nfia;Nfia;Nfia;Nfia;Nfia	S310	1	8	SVEDEMDSPGEEPPFYG	SVEDEMDS(ph)PGEEP	SVEDEMDS(1)PGEEP	CK2	0.7	0.0038577	Down	Yes
229	IPI00421052	Nipped-B-like protein;	Nipbl;Nipbl	S2652	1	10	AITSLGGGSPK	AITSLGGGS(ph)PK	AITSLGGGS(1)PK	CDK1	1.1	0.42771		Yes
271	IPI00720058	MKIAA0035 protein;Pu	Nolc1;MKIAA0035;Nolc	S563	1	5	AAKESEEEEEETEKE	AAKES(ph)EEEEEEETE	AAKES(1)EEEEEEETE	CK2	1.0	0.46441		Yes
258	IPI00720058	MKIAA0035 protein;Pu	Nolc1;MKIAA0035;Nolc	S701	1	15	GGJSISQVNSVKFDS	GGJSISQVNSVKFDS	GGJSISQVNSVKFDS(1)E		1.0	0.45267		Yes
231	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S536	1	9	SSPKEEVASEPEEAASPT	SSPKEEVAS(ph)EPEEA	SSPKEEVAS(0.999)EPEE	CK2	1.1	0.42806		Yes
332	IPI00318048	Nucleolar protein 56;N	Nop56;Nol5a;Nol5a;RP	S543	1	12	EEVASEPEEAASPTPK	EEVAS(ph)EPEEAASPT	EEVAS(0.452)EPEEAAS(0.452)	PT(0.08)T(0.017)PK				No
319	IPI00129186	Epididymal secretory p	Npc2	S108	1	3	VYSYLNK	VYSYLNK	VY(0.002)S(0.499)Y(0.499)	LNK				No
418	IPI00129186	Epididymal secretory p	Npc2	Y109	1	4	VYSYLNK	VYSYLNK	VY(0.002)S(0.499)Y(0.499)	LNK				Yes
1	IPI00125992	Neuronal pentraxin-1;	Nptx1	S203	2	5	AKIESALTSLHQR	AKIES(ph)ALTS(ph)LH	AKIES(0.911)ALT(0.178)	GSK3	0.04	5.81E-95	Down	No
2	IPI00125992	Neuronal pentraxin-1;	Nptx1	S207	2	9	AKIESALTSLHQR	AKIES(ph)ALTS(ph)LH	AKIES(0.911)ALT(0.178)	CK1	0.04	5.81E-95	Down	Yes
314	IPI00856881	Glucocorticoid recepto	Nr3c1;Nr3c1;Gr1;Gr1;N	S283	1	10	IQDTGDTILSSPSSVALPQ	IQDTGDTILS(ph)SPSS	IQDT(0.001)GDT(0.001)	GSK3				No
315	IPI00856881	Glucocorticoid recepto	Nr3c1;Nr3c1;Gr1;Gr1;N	S284	1	11	IQDTGDTILSSPSSVALPQ	IQDTGDTILS(ph)SPSS	IQDT(0.001)GDT(0.001)	Polo box				No
234	IPI00664246	Putative uncharacterize	Nrbp1;Nrbp;Nrbp1;Ma	T441	1	3	TPTPEPAEVETR	TPT(ph)PEPAEVETR	T(0.103)PT(0.897)PEPAE	VETR	1.1	0.43322		Yes
144	IPI00132314	Nucleobindin-1;CALNU	Nucb1;Nuc;Nucb;Nucb	S368	1	5	AQRLSQETEALGR	AQRLS(ph)QETEALGR	AQRLS(0.991)QET(0.00)	PKA	0.9	0.28145		Yes
94	IPI00341869	Nuclear ubiquitous cas	Nucks1;Nucks	S19	1	10	VVDYSQFQESDDADEDY	VVDYSQFQES(ph)DDA	VVDYSQFQES(1)DDADEDY	GR	0.9	0.16696		Yes
423	IPI00341869	Nuclear ubiquitous cas	Nucks1;Nucks	Y26	1	17	VVDYSQFQESDDADEDY	VVDYSQFQESDDADEDY	VVDY(0.133)S(0.134)Q	SRC				No
85	IPI00263048	Putative uncharacterize	Numa1	S1739	1	14	TQPDGTVSPGEPASIPQ	TQPDGTVSPGEPAS(ph)	TQPDGTVSPGEPAS(1)P	WW GroupIV	1.3	0.1454		Yes
288	IPI00918049	Oxysterol-binding prot	Osbp11	S192	1	10	SFSLASSGNSPISQR	SFSLASSGNS(ph)PISQ	SFSLASSGNS(0.001)GNS(0.	CK1	1.0	0.494		Yes
79	IPI00116202	PAXIP1-associated prot	Pa1	S236	1	14	DLFSLDSEGSPSPPLR	DLFSLDSEGSPS(ph)	DLFSLDSEGSPS(0.102)P	WW GroupIV	0.9	0.1285		Yes
206	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S65	1	6	VTNAISPSSPGVGR	VTNAIS(ph)PESSPGVGR	VTNAIS(1)PESSPGVGR	GSK3	1.0	0.38966		Yes
318	IPI00828325	Pericentriolar material	Pcm1;Pcm1	S68	1	9	VTNAISPSSPGVGR	VTNAIS(ph)PESSPGVGR	VT(0.001)NAIS(0.49)PE	CK1				Yes
112	IPI00337893	Pyruvate dehydrogenas	Pdha1;Pdha-1	S232	1	6	YMGMTSVR	YMGMTS(ph)VER	YMGMT(0.06)S(0.94)VER		0.9	0.20874		Yes
320	IPI00153375	PDZ and LIM domain p	Pdlim2;Pdlim2	S199	1	5	VLLHSPGRPSSPR	VLLHS(ph)PGRPSSPR	VLLHS(0.333)PGRPS(0.	CDK2				Yes
321	IPI00153375	PDZ and LIM domain p	Pdlim2;Pdlim2	S204	1	10	VLLHSPGRPSSPR	VLLHS(ph)PGRPSSPR	VLLHS(0.333)PGRPS(0.	PKA				Yes
197	IPI00153375	PDZ and LIM domain p	Pdlim2;Pdlim2	S205	1	11	VLLHSPGRPSSPR	VLLHSPGRPS(ph)PR	VLLHSPGRPS(0.009)S(0.	PKC	1.0	0.36413		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Phosphosites Localized?
254	IPI00845638	Sister chromatid cohes	Pds5b;Aprin;As3;Kiaa0	S1358	1	3	AESPETAVESTQSTPKQ	AES(ph)PETAVESTQ	AES(1)PETAVESTQSTPK	CAMK2	1.1	0.44892		Yes
77	IPI00856504	Pyridoxal-dependent d	Pdxcd1;Pdxcd1;Pdxcd1	T6877	1	7	VQGTGVTPTPLGTR	VQGTGVT(ph)PPPTPL	VQGT(0.01)GVT(0.99)PPPTPLGTR		1.4	0.12541		Yes
41	IPI00321597	Proline-, glutamic acid-	Pelp1;Mnar	T751	1	14	AGSGEDPVLAPSGTPPP	AGSGEDPVLAPSGT(ph)	AGSGEDPVLAPSG(0.003)GT(0.996)PPPS(0.001)PP		0.8	0.038607	Down	No
179	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	S181	1	12	LLKEGEEPTVYSDEEPEK	LLKEGEEPTVYS(ph)DD	LLKEGEEPTVYS(1)DDEE	CK2	1.0	0.34071		Yes
397	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	T178	1	9	LLKEGEEPTVYSDEEPEK	LLKEGEEPT(ph)YSSD	LLKEGEEPT(0.331)VY(0	PLK1				No
422	IPI00319973	Membrane-associated	Pgrmc1;Pgrmc	Y180	1	11	LLKEGEEPTVYSDEEPEK	LLKEGEEPT(ph)YSSD	LLKEGEEPT(0.331)VY(0.331)DDEEPEK(0.006)AR					Yes
352	IPI00648030	Phosphatase and actin	Phactr4;Kiaa4120;Phac	S126	1	1	SSSPVLVEEPEER	S(ph)SSPVLVEEPEER	S(0.423)S(0.288)S(0.28	CK1				No
195	IPI00648030	Phosphatase and actin	Phactr4;Kiaa4120;Phac	S128	1	3	SSSPVLVEEPEER	SSS(ph)PVLVEEPEER	S(0.006)S(0.003)S(0.99	Polo box	1.0	0.36204		No
19	IPI00121277	Phosphatidylinositol 4-	Pi4k2a	S460	1	1	SASESYTQSFQSR	S(ph)ASESYTQSFQSR	S(0.642)AS(0.355)ES(0	CK2	2.3	0.0004387	Up	No
119	IPI00474711	Putative uncharacterize	Pkn1;Pkn1;Pkn;Prk1;Pr	S925	1	18	TDVSNFDEEFTGEAPTLS	TDVSNFDEEFTGEAPT(L	TDVSNFDEEFTGEAPT(0	CDK2	0.9	0.21843		Yes
408	IPI00474711	Putative uncharacterize	Pkn1;Pkn1;Pkn;Prk1;Pr	T781	1	1	TSTFCGTPFLAPEVLDTI	T(ph)STFCGTPFLAPEV	T(0.379)S(0.287)T(0.287)FCGT(0.047)PEFLAPEVLDTSTVTR					Yes
44	IPI00312414	Serine/threonine-prote	Pkn2;Prkcl2;Pkn2;Prkcl	T957	1	20	GREDSVNFDEEFTSEAPI	GREDSVNFDEEFTSEAPI	GREDSVNFDEEFTSEAPI	CDK2	1.6	0.039879	Up	Yes
367	IPI00473693	Plakophilin-4;Armadillo	Pkp4;Armrp;Pkp4;Armr	S958	1	5	ALADSGGIEK	ALADS(ph)GGIEK	ALADS(1)GGIEK	NEK6				No
170	IPI00400215	Plectin-1;Plectin-6	Plec1	S21	1	3	TSSEDNLVLAVALR	TSS(ph)EDNLVLAVALR	T(0.083)S(0.035)S(0.88	PKA	1.1	0.32949		Yes
47	IPI00400215	Plectin-1;Plectin-6	Plec1	T19	1	1	TSSEDNLVLAVALR	T(ph)SSEDNLVLAVALR	T(0.692)S(0.014)S(0.29	CK2	1.6	0.047001	Up	Yes
351	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4243	1	1	SSSVGSSSYPISSAGPR	(ca)S(ph)SSSVGSSSYPI	S(0.266)S(0.219)S(0.21	PKA/AKT				Yes
83	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4245	1	3	SSSVGSSSYPISSAGPR	SSS(ph)YVSSSVGSSSYPI	S(0.087)S(0.04)S(0.873	PKA/AKT	1.3	0.13901		Yes
9	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4472	1	4	GYSPYSPVSGSGTAGSR	(ca)GYSPY(ph)PYSVSGS	GY(0.006)Y(0.006)S(0.988)PY(0.001)SVSGSGST	0.4	1.59E-10	Down	Yes	
349	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4475	1	7	GYSPYSPVSGSGTAGSR	GYSPY(ph)SVSGSGST	GY(0.006)PY(0.331)S	CK1				Yes
350	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	S4477	1	9	GYSPYSPVSGSGTAGSR	GYSPY(ph)SVSGSGST	GY(0.006)PY(0.331)S	GSK3				No
399	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	T4261	1	1	TQLASWSDPTEETGPVA	T(ph)QLASWSDPTEET	T(0.423)QLAS(0.288)W	FHA KAPP				Yes
424	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	Y4470	1	2	GYSPYSPVSGSGTAGSR	(ca)GYSPYSPVSGSGS	GY(0.135)Y(0.135)S(0.135)PY(0.135)S(0.135)VS(0.069)GS(0.069)GS(0.069)T(0.069)AGS	No				No
425	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	Y4471	1	3	GYSPYSPVSGSGTAGSR	(ca)GYSPYSPVSGSGS	GY(0.135)Y(0.135)S(0.135)PY(0.135)S(0.135)VS(0.069)GS(0.069)GS(0.069)T(0.069)AGS	No				No
426	IPI00400215	Plectin-1;Plectin-6;Plec	Plec1;Plec1;Plec1;Plec1	Y4474	1	6	GYSPYSPVSGSGTAGSR	GYSPY(ph)SVSGSGST	GY(0.006)PY(0.331)S(0.331)VS(0.331)GSGTAGSR					Yes
132	IPI00403031	Pleckstrin homology do	Plekho2;Plekho1	S395	1	3	SSSLGDLR	SSS(ph)LGDLR	S(0.011)S(0.005)S(0.985	CAMK2	1.2	0.24746		Yes
57	IPI00896602	Ppfi1 protein;Ppfi1 a	Ppfi1;Ppfi1	S717	1	17	SMSSIPPYPASSLAGSPP	SMSSIPPYPASSLAGS	SMSSIPPYPASSLAGS(0	Polo box	0.8	0.066111		Yes
368	IPI00480372	Liprin-beta-1;Protein ty	Ppfi1b;Ppfi1;Kiaa1230;Ppfi	S968	1	1	SPSASITDEDSNV	S(ph)SPSASITDEDSNV	S(0.661)T(0.464)AS(0	GSK3				Yes
369	IPI00480372	Liprin-beta-1;Protein ty	Ppfi1b;Ppfi1;Kiaa1230;Ppfi	S972	1	5	SPSASITDEDSNV	SPSAS(ph)TDEDSNV	S(0.026)PS(0.12)AS(0	CK1				No
413	IPI00890946	Protein phosphatase 2c	ppm1m	T47	1	12	FLRGSGLSPGATDASRR	(ca)FLRGSGLSPGAT(ph)	FLRGSGLS(0.085)S(0.085	FHA KAPP				Yes
80	IPI00230005	cAMP-dependent prote	Prkaca;Prkaca;Prkaca;P	S539	1	21	FKGPGDTSNFDDYEEEL	FKGPGDTSNFDDYEEEL	FKGPGDTSNFDDYEEEL	AURORA	0.9	0.12886		No
420	IPI00230005	cAMP-dependent prote	Prkaca;Prkaca;Prkaca;P	Y331	1	13	FKGPGDTSNFDDYEEEL	FKGPGDTSNFDDYEEEL	FKGPGDTSNFDDYEEEL	EGFR				Yes
46	IPI00230005	cAMP-dependent prote	Prkaca;Prkaca;Prkaca;P	T196	1	1	TWTLGCTPEYLAPEILSK	T(ph)TWTLGCTPEYLAPE	T(0.761)WT(0.198)LCG	FHA2 Rad53p	0.8	0.043057	Down	Yes
146	IPI00119575	Putative uncharacterize	Prkar1a;Prkar1a;Prkar1	S212	1	9	TDSREDEISPPPPNPVVK	TDSREDEIS(ph)PPPPNP	TDSREDEIS(1)PPPPNPVVK		0.9	0.28158		Yes
225	IPI00224570	cAMP-dependent prote	Prkar2b	S112	1	3	RASVCAEAYNPDEEEDD	RAS(ph)VCAEAYNPDEE	RAS(1)VCAEAYNPDEEEL	AURORA-A	1.0	0.42244		No
316	IPI00227880	Protein kinase C delta t	Prkcd;Prkcd;Prkcd;Prkcd	S530	1	2	ASTFCGTPDYIAPEILQGL	AS(ph)TFCGTPDYIAPE	AS(0.464)T(0.464)FCGT	PKA				Yes
391	IPI00227880	Protein kinase C delta t	Prkcd;Prkcd;Prkcd;Prkcd	T531	1	3	ASTFCGTPDYIAPEILQGL	AS(ph)TFCGTPDYIAPE	AS(0.464)T(0.464)FCGT	CAMK2				Yes
262	IPI00227880	Protein kinase C delta t	Prkcd;Prkcd;Prkcd;Prkcd	T535	1	7	ASTFCGTPDYIAPEILQGL	ASTFCGTPDYIAPE	AS(0.126)T(0.126)FCGT(0.623)PDY(0.126)IAPEI	1.1	0.45455		Yes	
125	IPI00122069	Protein kinase C gamm	Prkcg;Prkcg;Prkcg;Prkcg	T514	1	1	TFCGTPDYIAPEIAYQPY	T(ph)TFCGTPDYIAPEI	T(0.906)FCGT(0.094)PDY(0.001)IAPEIAYQPY	0.9	0.23243		Yes	
115	IPI00896672	PRP4 pre-mRNA proces	Prpf4b;mCG_22253;Pr	Y849	1	18	LCDFGSASHVADNDITPY	LCDFGSASHVADNDIT	LCDFGSASHVADNDIT(0.003)PY(0.824)LV(0.17)	0.9	0.21526		Yes	
305	IPI00117124	Presenilin-1;Protein S1	Psen1;Ad3h;Psn1	S365	1	7	AAVQELSGILTSDEPEER	AAVQELS(ph)GILTSE	AAVQELS(0.467)GS(0.467)ILT(0.065)S(0.002)EDPEER					Yes
306	IPI00117124	Presenilin-1;Protein S1	Psen1;Ad3h;Psn1	S367	1	9	AAVQELSGILTSDEPEER	AAVQELS(ph)GILTSE	AAVQELS(0.467)GS(0.4	NEK6				Yes
98	IPI00224784	Prothymosin alpha;Thy	Ptma	S2	1	1	SDAAVDTSSSEITTK	(ca)S(ph)DAAVDTSSSE	S(1)DAAVDTSSSEITTK		0.9	0.17808		No
67	IPI00322145	Protein tyrosine phosph	Ptlad1	S114	1	5	WLDESDAEMELR	WLDES(ph)DAEMELR	WLDES(1)DAEMELR	CK2	0.8	0.097036		Yes
307	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	S38	1	6	ATEEPPSGTGSDLEIKSDQ	ATEEPPSGTGSDLEI	AT(0.045)EPPS(0.276)G	GSK3				Yes
227	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	S42	1	10	ATEEPPSGTGSDLEIKSDQ	ATEEPPSGTGSDLEI	ATEEPPSGTGSDLEI(0.068)GS(0	CK1	1.0	0.42704		No
390	IPI00117689	Polymerase I and trans	Ptrf;Ptrf;Ptrf	T40	1	8	ATEEPPSGTGSDLEIKSDQ	ATEEPPSGTGSDLEI	AT(0.045)EPPS(0.276)G	FHA1 Rad53p				No
285	IPI00416731	R3H domain-containing	R3hdm2;Kiaa1002;R3h	S381	1	3	ASSFSGISILTR	ASS(ph)FGSILTR	AS(0.031)S(0.969)FGS	PKD	1.0	0.48969		Yes
259	IPI00480432	MKIAA0857 protein;Ra	Rab11fip5;mKIAA0857	S307	1	3	TYSDEASQLR	TYS(ph)DEASQLR	TYS(1)DEASQLR	PKA	1.0	0.45312		Yes
304	IPI00116031	RNA-binding protein 1c	Rbm10;Kiaa0122;Rbm	S718	1	3	LASDDRRSPPR	LAS(ph)DDRRSPPR	LAS(0.88)DDRRPS(0.12)	PKD				Yes
140	IPI00116031	RNA-binding protein 1c	Rbm10;Kiaa0122;Rbm	S723	1	3	LASDDRRSPPR	LASDDRRSPPR	LASDDRRPS(1)PPR	CDK2	0.9	0.27123		Yes
266	IPI00340815	Rbm15 protein	Rbm15	S293	1	8	SLSPGGAAALGYR	SLS(ph)PGGAAALGYR	S(0.111)LS(0.889)PGGA	CAMK2	1.1	0.45957		No
208	IPI00170394	Splicing factor 45;45 kD	Rbm17;Spf45	S155	1	6	RPDPDSDEDEDYERER	RPDPDS(ph)DEDEDYER	RPDPDS(1)DEDEDYERER		1.0	0.39748		Yes
103	IPI00223371	RNA-binding protein 39	Rbm39;Caper;Rnpc2;R	S136	1	3	DKSPVREPIDNLTPEER	DKS(ph)PVREPIDNLTPE	DKS(0.999)PVREPIDNLT	CDK2	0.9	0.18712		Yes
138	IPI00130160	RNA-binding protein 5	Rbm5;Luca15;Rbm5;Lu	S624	1	10	GLVAAVYSGDSNDEEELV	GLVAAVYSGDS(ph)DNE	GLVAAVYSGDS(1)DNEE	CK2	0.9	0.26369		Yes
244	IPI00124979	Heterogeneous nuclear	Rbmrx;RP23-372E6.2-0	S208	1	5	DVYLSPRDDGYSTK	DVYLS(ph)PRDDGYSTK	DVYLS(1)PRDDGYSTK	CDK1	1.0	0.44582		Yes
361	IPI00453982	REST corepressor 3;RES	Rcor3;Rcor3	S15	1	15	MPGMMEKGPPELLGSKR	MPGMMEKGPPELLGSK	MPGMMEKGPPELLGSKS(	NEK6				Yes
6	IPI00269129	RING finger protein 22c	Rnf220;Rnf220;Rnf220	T474	1	1	TCKNSDIEK	(ca)T(ph)CKNSDIEK	T(1)CKNSDIEK		5.6	2.90E-12	Up	No
120	IPI00453849	mRNA cap guanine-N7	Rnmt;Kiaa0398;Rnmt;K	S15	1	9	ASVADSPESPGGNEPA	ASVADSPES(ph)PPGGNE	ASVADSPES(1)PPGGNE	ERK/MAPK	0.9	0.22051		Yes
160	IPI00869441	Uncharacterized protei	RP23-263M10.5;12000	S25	1	13	AEAPAGPALGLPSPEVES	AEAPAGPALGLPS(ph)	AEAPAGPALGLPS(1)PEVESGLER		1.0	0.30886		Yes
294	IPI00110724	60S ribosomal protein	Rpl22l1;Rpl22l1	S118	1	11	YFQISQDEEDGSESD	YFQISQDEEDG(ph)ESE	YFQISQDEEDG(0.986)E	CK2				Yes
163	IPI00113377	60S acidic ribosomal pr	Rplp1	S101	1	4	KEESESEDDMGFLGFD	KEES(ph)EESEDDMGFL	KEES(1)EESEDDMGFLG		1.2	0.31714		No
241	IPI00755495	40S ribosomal protein	Rps17	S133	1	6	LLDFGSLSNLQVQTPTVG	LLDFGSL(ph)LSNLQVTC	LLDFGSL(0.855)LS(0.144)NLQVQTPTVGMNFK	1.1	0.43868		No	
185	IPI00134599	40S ribosomal protein	Rps3	T221	1	7	DEILPTTPISEQK	DEILPTT(ph)PISEQK	DEILPT(0.001)T(0.999)	WW Group I	1.1	0.34688		Yes
293	IPI00113655	40S ribosomal protein	Rps6;Rps6;Dcd5;RP23	S236	1	4	RLSLSL	RLS(ph)LSL	RLS(0.044)S(0.956)LR	PKA/AKT				Yes
274	IPI00849948	40S ribosomal protein	Rps8;Rps8;OTTMUSG0	S172	1	2	ISLLLEEFQFQQGK	IS(ph)SLLLEEFQFQQGK	IS(0.5)S(0.5)SLLLEEFQFQQGK		1.0	0.4739		No
70	IPI00849948	40S ribosomal protein	Rps8;Rps8;OTTMUSG0	S173	1	3	ISLLLEEFQFQQGK	ISS(ph)SLLLEEFQFQQGK	IS(0.007)S(0.993)SLLLEEFQFQQGK	CK2	1.4	0.1125		Yes

No	IPI Numbers	Protein Names	Gene Names	pAA	Number of P	Position in p	Peptide Sequence	Phospho (STY) Probabi	Modified Sequence	Best Motif	Ratio <sup>1</sup> of Phd	Ratio Signifid	Up-/Down-r	Phosphosites Localized?
25	IPI00411051	Regulatory-associated	Rptor;Raptor;Raptor;R	S863	1	14	ILDTSLLTQASAPASPTNK	ILDTSLLTQASAPAS(ph)	ILDTSLLTQASAPAS(0.898)	WW GroupIV	1.9	0.0063455	Up	Yes
214	IPI00605227	MKIAA0138 protein;Sc	Safb2;mkIAA0138;Safb	S459	1	7	APTAALSPEPQDSKEDVK	APTAALS(ph)PEPQDS	APTAALS(1)PEPQDSKE	CK1	1.1	0.40438	Yes	Yes
309	IPI00605227	MKIAA0138 protein;Sc	Safb2;mkIAA0138;Safb	S465	1	13	APTAALSPEPQDSKEDVK	APTAALS(ph)PEPQDS	APT(0.008)AALS(0.496)PEPQDS(0.496)KEDVKK				Yes	Yes
218	IPI00338954	SAM and SH3 domain-c	Sash1	S400	1	3	TCSFGGFDLTNR	TCS(ph)FGGFDLTNR	T(0.011)CS(0.989)FGGF	CAMK2	1.1	0.41305	No	No
52	IPI00133030	Protein transport prote	Sec61b	S14	1	13	PGPTPSGTNVGSSGRSP	PGPTPSGTNVGSS(ph)	PGPTPSGT(0.005)NVGS(0.123)S(0.727)GRS(0.1		0.8	0.055439	Yes	Yes
86	IPI00114945	Septin-2;Neural precu	Sept2;Nedd-5;Nedd5	S218	1	9	IYHLPDAESEDEDFKFEQ	IYHLPDAESE(ph)DEDE	IYHLPDAESE(1)DEDEDFKFEQ		0.9	0.15135	Yes	Yes
389	IPI00114945	Septin-2;Neural precu	Sept2;Nedd-5;Nedd5	T228	1	19	IYHLPDAESEDEDFKFEQ	IYHLPDAESEDEDFKE	IY(0.001)HLPDAESE(0.2)FHA2 Rad53p				No	No
91	IPI00923056	Sept5 protein;Septin-5	Sept5;Sept5;Pnut1;Se	S225	1	13	FGIHVYQFPECDSDEDED	FGIHVYQFPECDS(ph)	FGIHVY(0.004)QFPECDS(0.996)DEDED	FKQDDR	1.3	0.15866	Yes	Yes
97	IPI00923056	Sept5 protein;Septin-5	Sept5;Sept5;Pnut1;Se	Y218	1	6	FGIHVYQFPECDSDEDED	FGIHVYQFPECDSDEDED	FGIHVY(0.712)QFPECDS	ABL	0.9	0.17799	Yes	Yes
279	IPI00457611	Septin-9;SL3-3 integrat	Sept9;Kiaa0991;Sint1;S	S585	1	9	LVDSLSQRSQPKPSLR	LVDSLSQRS(ph)PKPSL	LVDSLS(0.001)QRS(0.99)CDK1		1.0	0.47803	Yes	Yes
335	IPI00903371	Alpha-1 antitrypsin 1-6	Serpina1f;Serpina1f;Se	S376	1	4	KLGDMDMGR	(ca)KLGS(ph)TDMGR	KLGS(0.887)T(0.113)DMGR				No	No
178	IPI00420807	Splicing factor, arginine	Sfrs1	S199	1	8	VKVDGPRSPSYGR	VKVDGPRSP(ph)PSYGR	VKVDGPRSP(0.999)PS(0.1	WW GroupIV	1.0	0.33939	Yes	Yes
24	IPI00848672	Putative uncharacterize	Sfrs11;mcCG_11658;Sfr	S477	1	7	RPTAEVAVPK	RPTAEVAVS(ph)PK	RPT(0.001)EAVS(0.999)CDK1		0.7	0.0053942	Down	Yes
331	IPI00310880	Putative uncharacterize	Sfrs6;mcCG_1675	S303	1	3	SHSLPAPPSK	SHS(ph)PLPAPPSK	S(0.014)HS(0.986)PLPA	CAMK2			Yes	Yes
233	IPI00120052	Sphingosine-1-phospha	Sgpp1;Spp1;Spph1	S101	1	3	RNSLTGEEGELVK	RNS(ph)LTGEEGELVK	RNS(0.997)LT(0.003)GE	PKA/AKT	1.0	0.43083	Yes	Yes
203	IPI00116331	Small glutamine-rich te	Sgta;Sgt;Sgta;Sgt	T82	1	5	APDRTPPSEEDSAEAEER	APDRTP(ph)PSEEDSAE	APDRTP(0.996)PSPS(0.00	FHA GroupIV	1.0	0.38459	Yes	Yes
45	IPI00673176	Signal-induced prolifer	Sipa12;Kiaa0545;Sipa1	S1461	1	6	LMLPDSPLVEEGR	LMLPDS(ph)PLVEEGR	LMLPDS(1)PLVEEGR	WW GroupIV	1.6	0.04032	Up	Yes
166	IPI00454140	MCG15924, isoform CR	Skiv2l;Sk1;Stk19;mcG	S253	1	3	ASSLELDLVK	ASS(ph)LELDLVK	AS(0.003)S(0.997)LELD	CHK1/2	1.1	0.32536	Yes	Yes
341	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S697	1	3	LDSPTLSR	LDS(ph)PTLSR	LDS(0.999)PT(0.001)LS	GSK3			Yes	Yes
12	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S707	1	3	IGSDPLAYEYK	IGS(ph)DPLAYEYK	IGS(1)DPLAYEYK	PKA/AKT	3.3	1.18E-06	Up	Yes
51	IPI00622815	Sodium/hydrogen exch	Slc9a1;Slc9a1;Nhe1	S790	1	20	SKEPSSPGTDDVFTPGSS	SKEPSSPGTDDVFTPGS	SKEPSSPGTDDVFTPGS(CK1		0.8	0.053925	No	No
87	IPI00109311	Na(+)/H(+) exchange re	Slc9a3r1;Nherf;Nherf1	S283	1	1	SASSDTSEELNSQDSPK	S(ph)ASSDTSEELNSQD	S(0.526)AS(0.237)S(0.2	NEK6	1.3	0.15281	No	No
200	IPI00127941	Small acidic protein;Sid	Smap;Sid2057	S15	1	1	SASPDDDLGSSNWEAAD	S(ph)ASPPDDDLGSSNW	S(0.69)AS(0.31)PDDDLGSSNWEAAD	ADLNGNEER	1.1	0.37245	No	No
428	IPI00467181	SWI/SNF-related matrix	Smarcd3;Baf60c	Y419	1	2	GYVQDLLR	GY(ph)VQDLLR	GY(1)VQDLLR				No	No
133	IPI00922961	Sntb2 protein;Beta-2-s	Sntb2;Sntb2;Sntb2	S373	1	1	SPSLGSDLTFATR	S(ph)PSLGSDDLTFATR	S(0.627)PS(0.373)LGSD	CK1	0.9	0.25377	Yes	Yes
4	IPI00922961	Sntb2 protein;Beta-2-s	Sntb2;Sntb2;Sntb2	S88	1	7	GPAGEASASPPVR	GPAGEAS(ph)ASPPVR	GPAGEAS(0.5)AS(0.5)PPVR		0.2	1.21E-26	Down	Yes
5	IPI00922961	Sntb2 protein;Beta-2-s	Sntb2;Sntb2;Sntb2	S90	1	9	GPAGEASASPPVR	GPAGEAS(ph)ASPPVR	GPAGEAS(0.5)AS(0.5)PPVR		0.2	1.21E-26	Down	Yes
373	IPI00620743	Putative uncharacterize	Srcap	S1178	2	2	LSSPTLTGTR	LS(ph)SPTLTGTR(ph)R	LS(0.921)S(0.079)PTLG	PKA			Yes	Yes
201	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S915	1	5	KETESAEDDNLDDL	KETES(ph)EAEDDNL	KETES(1)EAEDDNL	CK2	1.1	0.37576	Yes	Yes
283	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	T913	1	3	KETESAEDDNLDDL	KET(ph)EAEEDDNL	KET(0.999)ES(0.001)EA	PKA	1.0	0.48444	Yes	Yes
277	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S260	1	14	APKPEPVEPKEPSPK	APKPEPVEPKEPSPS(ph)	APKPEPVEPKEPSPS(1)PE	CDK2	1.0	0.47699	Yes	Yes
64	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	S463	1	7	KVELSEEDKGSK	KVELS(ph)EEDKGSK	KVELS(0.069)ES(0.931)	NEK6	1.5	0.074988	No	Yes
410	IPI00605037	Serine/arginine repetit	Srrm1;Pop101;Srrm1;R	T633	1	1	TASPPPPPK	T(ph)ASPPPPPK	T(0.957)AS(0.043)PPPP	PKA			Yes	Yes
222	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1068	1	3	SSSPVTELTAR	SSS(ph)PVTELTAR	S(0.097)S(0.054)S(0.84	CHK1/2	1.1	0.41764	Yes	Yes
242	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1151	1	4	DKFSPQDRPESSTLVK	DKFS(ph)PQDRPESST	DKFS(0.103)PT(0.113)QDRPESSTLVK		1.1	0.44274	Yes	Yes
32	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1305	1	13	NSGPNVSEVNTGFSPEVK	NSGPNVSEVNTGFS(ph)	NSGPNVSEVNTGFS(1)PEVK		0.7	0.018453	Down	No
323	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1338	1	2	RSSSELSPEVVEK	RS(ph)SSELSPEVVEK	RS(0.479)S(0.479)S(0.0	PKA			Yes	Yes
111	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1339	1	3	RSSSELSPEVVEK	RSS(ph)SSELSPEVVEK	RS(0.065)S(0.87)S(0.06	PKA	1.3	0.2066	No	Yes
101	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1359	1	2	VSSPVLETVQQR	(ca)VS(ph)SPVLETVQ	VS(0.893)S(0.095)PVLE	CK1	0.9	0.18575	No	Yes
228	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S1360	1	3	VSSPVLETVQQR	VSS(ph)PVLETVQQR	VS(0.003)S(0.997)PVLE	ERK/MAPK	1.1	0.42719	Yes	Yes
230	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S2351	1	6	VSGRTSPLMLDR	VSGRTS(ph)PLMLDR	VSGRT(0.003)S(0.997)P	PKA	1.0	0.42785	No	No
280	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	S2404	1	19	MVQASSQSLLPPAQDRP	MVQASSQSLLPPAQDR	MVQASSQSLLPPAQDR(ph)WW	GroupIV	1.0	0.48084	No	No
177	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	T1153	1	6	DKFSPQDRPESSTLVK	DKFSPT(ph)QDRPESST	DKFS(0.103)PT(0.673)QDRPES(0.103)T		1.0	0.33787	No	No
273	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	T2350	1	1	TSPLMLDR	T(ph)SPLMLDR	T(0.668)S(0.332)PLML	CK1	1.0	0.46977	Yes	Yes
217	IPI00874854	Srrm2 protein;Serine/a	Srrm2;Srrm2;Kiaa0324	T973	1	5	SMLQTPPDQNLGSGSK	SMLQT(ph)PPDQNLGSG	SMLQT(0.999)PPDQNL	FHA1 Rad53p	1.1	0.41149	No	No
248	IPI00830670	Sperm-specific antigen	Ssfa2;Kiaa1927;Krap;S	S736	1	1	SQSLPTLLSPVR	S(ph)QSLPTLLSPVR	S(0.681)QS(0.319)LP	NIMA	1.1	0.44748	No	No
289	IPI00830670	Sperm-specific antigen	Ssfa2;Kiaa1927;Krap;S	S90	1	6	TPLGASLDEQSSGTPK	TPLGAS(ph)LDEQSSG	TPLGAS(1)LDEQSSGTPK	CK2	1.0	0.49506	Yes	Yes
415	IPI00114979	Signal transducer and a	Stat5a;Mgf;Mpf	Y694	1	5	AVDGYVVKPQIK	AVDGY(ph)VKPQIK	AVDGY(1)VKPQIK	EGFR			No	No
416	IPI00114982	Signal transducer and a	Stat5b	Y699	1	5	AADGYVVKPQIK	AADGY(ph)VKPQIK	AADGY(1)VKPQIK	EGFR			Yes	Yes
58	IPI00330941	Metalloenductase STEA	Steap3;Tsap6;Steap3;T	S58	1	8	RLVSDSGSLAEVVK	RLVSDSGS(ph)LAEVVK	RLVSDSGS(1)LAEVVK	PLK	0.8	0.067213	No	No
20	IPI00831595	Serine/threonine kinas	Stk10;Stk10;Lok	T950	1	11	LSEAEPRPTTPSK	LSEAEPRPTT(ph)PSK	LSEAEPRPTT(0.002)T(0	WW GroupIV	2.3	0.0005873	Up	No
151	IPI00662157	Synaptotaxin;Synapto	Synpo;Kiaa1029;Synpo	S535	1	6	LLGQRSPLVLR	LLGQRS(ph)PLVLR	LLGQRS(1)PLVLR		1.2	0.28975	No	No
35	IPI00110247	TBC1 domain family me	Tbc1d15	S201	1	1	SLSQSFENLLDEPAYGLIQ	S(ph)LSQSFENLLDEPA	S(0.672)LS(0.163)QS(0	GSK3	1.6	0.031244	Up	Yes
127	IPI00453842	TBC1 domain family me	Tbc1d2b;Kiaa1055	S959	1	11	DTSPDKGELVSDSEEDT	DTSPDKGELVS(ph)DEE	DTSPDKGELVS(0.999)D	CK2	0.9	0.23432	Yes	No
53	IPI00930819	Transcription elongatio	Tcea1;Tceat;Tcea1;Tce	S111	1	11	KKEPAISSQNSPEAR	KKEPAISSQNS(ph)PEA	KKEPAISSQNS(1)PEAR	CK1	1.0	0.055527	No	No
226	IPI00828809	Transcription factor E3	Tcfe3;RP23-109E24.7-0	S553	1	11	AASDPLSSVSPAVSK	AASDPLSSVSPAVS(ph)PAV	AASDPLSSVSPAVS(0.013)VS(0	CK1	0.8	0.42565	No	No
173	IPI00115660	Treacle protein;Treach	Tcof1;Tcof1	S169	1	12	SAEPLANTVLASETEEDI	SAEPLANTVLAS(ph)ET	SAEPLANTVLAS(0.889)E	CK2	1.1	0.33435	Yes	Yes
255	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S243	1	7	ASVSDLSR	ASVSDLS(ph)PR	ASVSDLS(1)PR	CDK1	1.1	0.44928	Yes	Yes
284	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S679	1	4	IDISPSTFR	IDIS(ph)PSTFR	IDIS(1)PSTFR		1.0	0.48535	Yes	Yes
370	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	S681	1	7	RIDISPSTFR	RIDIS(ph)PSTFR	RIDIS(0.5)S(0.5)T(0.001)FR				No	No
409	IPI00556768	Thyroid hormone rece	Thrap3;Trap150;Thrap	T682	1	7	IDISPSTFRK	IDIS(ph)PSTFRK	IDIS(0.472)PS(0.056)T(CK1				Yes	Yes
374	IPI00674926	Toll-like receptor 5	Tlr5	S862	2	2	SSSIQLRTIATIS	(ca)SSS(ph)SIQLRTIATIS	S(0.124)S(0.789)S(0.08	PKA			No	No
375	IPI00674926	Toll-like receptor 5	Tlr5	S873	2	13	SSSIQLRTIATIS	(ca)SSS(ph)SIQLRTIATIS	S(0.124)S(0.789)S(0.087)IQLRT(0.014)IAT(0.014)IS(0.971)				Yes	Yes
317	IPI00896574	Thymopietin;Thymop	Tmpo;mcG_10339;Tm	S157	1	1	SSTPLPTVSSSAENR	S(ph)STPLPTVSSSAEN	S(0.477)S(0.262)T(0.26	CK1			Yes	Yes
292	IPI00121341	Thioredoxin-related tra	Tmx1;Txndc;Txndc1	S245	1	13	VEEQEAEEDVSEEEAE	VEEQEAEEDVSE(ph)E	VEEQEAEEDVSE(1)EE	CK2	1.0	0.5	Yes	Yes
27	IPI00459443	182 kDa tankyrase-1-b	Tnks1bp1;Kiaa1741;Ta	S1375	1	6	SSGSLSPGLETEDEPLEAR	SSGSLS(ph)PGLTEDEP	S(0.129)S(0.098)S(0.0	CK1	1.8	0.010412	Up	Yes



