

Phosphopeptides that changed significantly in abundance ($p < 0.05$ (t-test); $|\log_2(500/300 \text{ mOsmol/kg})| > 1$) in response to high NaCl.

Phosphopeptide	m/z	log ₂ (500/300)	Gene symbol	protein ratio (500/300)	Phosphosite	previously reported	Refseq
TAS*LPGYGR	501.227	-1.27	ABLIM1;		S655	Y	NP_002304.3
SSMS*GLHLVK	572.781	-1.64	ACACA;		S117	Y	NP_942131.1
SSDITSDLGNVLTST*PNAK	1003.48	-1.81	ACBD5;		T172	Y	NP_663736.2
AAKLS*EGSQPAEEEEEDQETPSR	828.697	-2.43	ACIN1;		S240	Y	NP_055792.1
TAESQT*PTPSATSFSSGK	965.433	3.18	ADAR;		T601	Y	NP_001102.2
NSYNSQAPS*PGLGSK	853.878	-1.53	AFF4;	0.993	S1043	Y	NP_055238.1
SLLGDSAPTLHLNKGTPSQS*PV	903.112	-1.44	AGFG1;		T177, S181	Y	NP_004495.2
AS*LGSLEGEAEAEASS*PKGK	1045.46	-2.77	AHNAK;	1.022	S5749, S5763	Y	NP_001611.1
S*SKASLGS*LEGEAEAEASSPK	736.324	-2.75	AHNAK;		S5745, S5752	Y	NP_001611.1
SSKAS*LGS*LEGEAEAEASSPK	1103.98	-2.51	AHNAK;		S5749, S5752	Y	NP_001611.1
ASLGS*LEGEAEAEASSPK	909.909	-1.87	AHNAK;		S5752	Y	NP_001611.1
TVIRLPS*GSGAAS*PTGSAVDIR	764.702	1.61	AHNAK;		S210, S216	Y	NP_001611.1
VSMPDVELNLKS*PK	824.925	2.24	AHNAK;		S3426	Y	NP_001611.1
TVIRLPSGS*GAAS*PTGSAVDIR	764.702	3.71	AHNAK;		S212, S216	Y	NP_001611.1
GPAFNM^AS^PESDFGINLK	998.945	4.04	AHNAK;		S5552	Y	NP_001611.1
CDSSPDS*AEDVR	709.251	-4.73	AHSG;	1.082	S138	Y	NP_001613.2
SAESPTS*PVTSETGSTFK	949.922	1.19	AKAP12;	0.988	S188	Y	NP_653080.1
SSDEENGPPSS*PDLDR	896.351	-1.14	AKT1S1;	1.061	S212	Y	NP_001092102.
KSYESSEDCSEAAGS*PAR	670.93	-1.41	ALKBH5;		S384	Y	NP_060228.3
SYESSEDCSEAAGS*PAR	941.844	-1.95	ALKBH5;		S384	Y	NP_060228.3
IM^SS^IGEGIDFSQER	882.88	-2.22	ANKS1A;		S677	Y	NP_056060.2
NKAS*PQSEFM^PSK	779.855	1.36	ANLN;		S792	Y	NP_061155.2
SSS*PELVTHLK	642.321	1.50	ARHGAP1;	0.994	S51	Y	NP_004299.1
SSQGDTPAQAS*PPEEK	912.371	-1.63	ARHGAP27;		S125	Y	NP_954976.1
SLS*PILPGR	510.269	-1.33	ARHGEF18;		S1103	Y	NP_001124427.
GPS*PSPVGSPASVAQSR	830.889	-1.20	ARID1A;		S696	Y	NP_006006.3
GPS*PSPVGS*PASVAQSR	870.872	-1.06	ARID1A;		S696, S702	Y	NP_006006.3
NDSVIVADQT*PT*PTR	887.377	1.76	ATF2;		T69, T71	Y	NP_001871.2
TDSVIIADQT*PT*PTR	892.891	2.64	ATF7;		T51, T53	Y	NP_001123532.
NKQDDDLNCEPLS*PHNIT*PEPV	969.748	2.11	ATF7IP;		S113, T118	Y	NP_060649.3
SLAFEEGS*QSTTISSLSEK	1043.98	2.67	ATM;LOC6516		S1981	Y	NP_000042.3
IEDS*EPHIPLIDDTDAEDDAPTKR	924.747	-1.60	ATP2B1;		S1155	Y	NP_001673.2
SS*TPLHS*PSPIR	724.815	-1.29	BAG3;		S284, S289	Y	NP_004272.2
EGTLTQVPLAPPPGAPPS*PAP	1199.61	-2.27	BAT2;	0.979	S1147	Y	NP_542417.2
DHTVS*GDEDYCPR	815.2923031	1.87	BAZ1B;	0.960	S947	Y	NP_115784.1
GTEPSPGGTPQPSRPVS*PAGPF	1113.86	-4.23	BCL7C;		S126	Y	NP_004756.2
KADTTTPTTAILAPGS*PASPPG	928.136	-2.59	BRD2;		S298	Y	NP_005095.1

KADTTTPTTAILAPGS*PASPPG	954.791	-1.65	BRD2;	S298, S305	Y	NP_005095.1
IPELVGS*PTQSTSSR	876.433	-1.06	BRWD1;	S1475	Y	NP_061836.2
YEYDPDIS*PPR	716.296	-2.52	BUD13;	S325	Y	NP_116114.1
HDT*PDPS*PLR	647.747	-1.61	BUD13;	T159, S163	Y	NP_116114.1
LAVLSS*SLTHWK	714.374	-2.40	C11orf59;	0.943 S97	N	NP_060377.1
SIS*GTPAETPACK	702.813	4.31	C12orf51;	S1075	Y	NP_001103132.
DLFSLDSEDSPAS*PPLR	1011.96	-1.42	C16orf53;	S237	Y	NP_078792.1
RDS*SESQLASTESDKPTTGR	753.344	1.43	C18orf25;	S66	Y	NP_659492.1
WKEPGSGGPQNLS*GPGGR	620.952	-2.04	C19orf61;	S32	Y	NP_061981.2
LS*STDDGYIDLQFK	844.382	2.48	C20orf30;	S23	Y	NP_001009924.
KSPSGPVKS*PPLSPVGTTPVK	740.708	1.94	C2orf49;	S189, T198	Y	NP_076998.1
KSPSGPVKS*PPLS*PVGTTPVK	746.728	2.11	C2orf49;	S189, S193	Y	NP_076998.1
SPSGPVKS*PPLS*PVGTTPVK	702.023	2.59	C2orf49;	S189, S193	Y	NP_076998.1
ST*DSSSVSGSLQQETK	863.878	1.21	C9orf82;	T90	Y	NP_079104.2
S*TDSSSVSGSLQQETK	863.878	1.36	C9orf82;	S89	Y	NP_079104.2
RFS*PSQVPIQTR	748.375	2.54	CAMSAP1L1;	S1008	Y	NP_982284.1
ANS*TSDSVFTETPSPVLK	983.462	1.18	CDC42EP3;	S89	Y	NP_006440.2
KDLSLGLDDS*RTNT*PQGVLPSS	943.786	-2.33	CDK13;	S1054, T1058	Y	NP_112557.2
LGS*LSARS*DSEATISR	915.402	-3.59	CEP170;	S1160, S1165	Y	NP_055627.2
LGEAS*DSELADADK	753.819	-2.46	CEP170;	S1112	Y	NP_055627.2
TQDPSSPGTT*PPQAR	810.357	-2.51	CHAF1B;	T433	Y	NP_005432.1
NSSNTSVGS*PSNTIGR	829.855	-2.21	CLASP1;	S1071	Y	NP_001135745.
VLSTS*TDLEAAVADALK	895.451	-1.35	CLASP1;	S797	Y	NP_056097.1
TASESISNLSEAGS*IK	837.386	-2.19	CLIP1;	S204	Y	NP_002947.1
TTTAAGSSHSRPGVPVEGS*PGF	859.078	-1.70	CNNM3;	S652	Y	NP_951060.1
TDNM^LSDQT*PT*PTR	881.836	2.69	CREB5;	T59, T61	Y	NP_878901.2
TS*M^GGTQQQFVEGVR	860.872	-1.22	CTNNB1;	S552	Y	NP_001895.1
RTS*MGGTQQQFVEGVR	627.625	-1.18	CTNNB1;	S552	Y	NP_001091679.
VGGS*SVDLHR	553.754	-2.98	CTNND1;	S167	Y	NP_001078932.
TQT*PPVSPAPQPTTEER	907.92	-1.59	CTTN;	T401	Y	NP_005222.2
AKTQT*PPVSPAPQPTTEER	677.336	-1.22	CTTN;	T401	Y	NP_005222.2
S*VSSPTSSNTPTPTK	788.864	2.76	CYTSB;	S131	Y	NP_001028725.
KICTLPSPPS*PLASLAPVADSSTI	849.096	-1.63	DAXX;	S683	Y	NP_001135442.
DGEQS*PNVSLM^AQR	778.825	1.33	DCAF6;	S336	Y	NP_060912.2
KASSPS*PLTIGT*PESQR	926.463	-1.62	DCP1A;	S525, T531	Y	NP_060873.3
SLS*YEEPR	535.726	1.76	DCP1B;	S275	Y	NP_689853.3
RSS*LYGIAK	545.786	1.18	DENND4C;	S948	Y	NP_060395.4
YNS*YDISR	554.223	2.25	DENND5B;	S178	N	NP_659410.3
EQM^M^NSSISSGSGS*LR	891.856	-2.61	DLG1;	S575	Y	NP_004078.2
DTIIDVVGAPLT*PNSR	874.436	-1.13	DMAP1;	T445	Y	NP_061973.1

SKPIPI^PAS*PQK	751.399	2.05	DNM1L;	1.011	S616	Y	NP_036192.2
QILACS*PVSSVR	755.379	-1.22	DNTTIP2;		S117	Y	NP_055412.2
QISGQYSGS*PQLLK	793.385	1.94	DOCK7;		S30	Y	NP_212132.2
VDDDS*LGEFPVTNSR	865.868	-1.39	DPF2;		S142	Y	NP_006259.1
VVPSFLPVDQGGG*LVGR	903.962	-1.77	DSG2;		S680	Y	NP_001934.2
KPVTVS*PTTPTS*PTEGEAS	1026.45	1.16	DYNC1LI1;	1.075	S510, S516	Y	NP_057225.2
KPVTVSPTTPT*SPTEGEAS	986.467	1.32	DYNC1LI1;		T515	Y	NP_057225.2
KPVTVSPTTPTS*PTEGEAS	986.467	1.33	DYNC1LI1;		S516	Y	NP_057225.2
ITRKPVTVSPTTPTS*PTEGEAS	784.728	1.64	DYNC1LI1;		S516	Y	NP_057225.2
KPVTVSPTT*PTS*PTEGEAS	1026.45	3.25	DYNC1LI1;		T513, S516	Y	NP_057225.2
SQDVAVS*PQQQCSK	888.883	-1.12	EDC3;		S131	Y	NP_079359.2
RADLNQGIGEPQS*PSR	824.871	-1.56	EFHD2;	0.950	S74	Y	NP_077305.2
ELVEPLT*PSGEAPNQALLR	1057.53	3.46	EGFR;		T693	Y	NP_005219.2
AKPPADPAAAAS*PCR	788.37	-2.25	EGLN1;	0.920	S125	Y	NP_071334.1
SDS*RAQAVSEDAGGNEGR	629.589	-3.08	EIF3B;		S119	Y	NP_001032360.
FLM^ECRNS*PVTK	789.347	-2.57	EIF4EBP1;	0.974	S65	Y	NP_004086.1
TQT*PPLGQTPQLGLK	832.94	-1.31	EIF4G2;		T508	Y	NP_001409.3
GIS*QTNLITVT*PEKK	951.475	-1.59	EPB41L3;	0.995	S460, T469	Y	NP_036439.2
GIS*QTNLITVTPEK	844.435	-1.55	EPB41L3;		S460	Y	NP_036439.2
GIS*QTNLITVTPEKK	911.492	-1.55	EPB41L3;		S460	Y	NP_036439.2
QVS*ASELHTSGILGPETLR	692.344	1.45	EPPK1;	1.022	S2716 or S3250	Y	NP_112598.2
RQVS*ASELHTSGILGPETLR	1126.07	1.51	EPPK1;		S2716 or S3250	Y	NP_112598.2
RQVSAS*ELHTSGILGPETLR	751.05	2.00	EPPK1;		S2718 or S3252	Y	NP_112598.2
SINKLDS*PDPFK	726.863	1.29	EPS15;		S796	Y	NP_001972.1
NGS*PTPAGSLGGGAVATAGGP	1038.97	-1.61	FAM117B;		S10	N	NP_775782.2
RIDFIPVSPAPS*PTR	866.943	-2.94	FAM122A;		S147	Y	NP_612206.3
VSAGEPGSHPS*PAPR	763.344	-1.33	FARP1;		S427	Y	NP_005757.1
GSPTDAEGS*PGLSR	705.799	-1.63	FLJ10357;		S262	Y	NP_060541.3
IQDIKTEN~GTCPS*PPQPLS*PA	1164.54	-2.23	FOXC1;	1.139	S235, S241	Y	NP_001444.2
EGS*PAPLEPEPGAAQPK	880.914	-1.40	FOXK2;		S398	Y	NP_004505.2
LRGQS*TDS*LPQTICR	946.411	-1.63	FRMD6;		S514, S517	N	NP_689543.1
LLDLPAAAAS*SEDIERS	888.919	-1.70	GAL;		S116	Y	NP_057057.2
VS*SPLPSPSAM^TDAANSQAAAI	1099	-2.88	GATAD2B;		S333	Y	NP_065750.1
LQQQAALS*PTTAPAVSSVSK	1035.53	1.01	GATAD2B;		S486	Y	NP_065750.1
ALSSGGSITS*PPLSPALPK	933.49	-1.04	GIGYF2;		S26	Y	NP_056390.2
SQGS*PEDSAPQASPGPSK	903.881	-2.61	GMIP;		S234	Y	NP_057657.2
VGDST*PVSEKPVSAVDANASE	1200.55	2.00	GORASP2;		T433	Y	NP_056345.3
GLGLGANLTEAQALT*PTGPSR	1052.53	1.82	GPKOW;		T216	Y	NP_056513.2
RYDS*DDDLPR	676.276	-1.79	GPR137C;		S357	Y	NP_001093122.
GNSRPGT*PSAEGGSTSSTLR	700.296	-2.60	GTF2F1;	0.994	T389	Y	NP_002087.2

NQIPRT*PENLITEIR	947.489	1.84	HAUS6;		T584	Y	NP_060115.3
M^ETFS*PAVGNR	652.771	3.16	HAUS6;		S715	Y	NP_060115.3
VASS*PVM^VSNPATR	756.35	1.57	HCFC1;	0.972	S598	Y	NP_005325.2
TITLVKS*PISVPGGSALISNLGK	1172.67	2.42	HCFC1;		S666	Y	NP_005325.2
APAGPSLEETSVSS*PK	821.888	-2.09	HEATR6;		S643	Y	NP_071353.4
KAPAGPSLEETSVSS*PK	888.945	-2.00	HEATR6;		S643	Y	NP_071353.4
LSSSGAPPADFPS*PR	783.354	-1.77	HELB;		S967	Y	NP_387467.2
RIS*SSSVQPCSEEVSTPQDSLAC	959.431	1.28	HELZ;		S1763	Y	NP_055692.2
KLEKEEEEGISQES*S*EEEQ	799.648	-1.37	HMGA1;		S91, S92	Y	NP_665912.1
KPAQEETEETS*SQESAEED	1102.42	-1.69	HMGA2;		S101	Y	NP_003474.1
M^GLAM^GGGGGAS*FDR	753.294	4.06	HNRNPM;		S579	Y	NP_112480.2
APQQQPPPQQPPPPQPPQPPF	1136.89	-1.83	HNRNPUL1;		S718	Y	NP_008971.2
SPS*PLVSLQAVK	653.345	-2.09	HPS5;		S420	Y	NP_852609.1
QLS*SGVSEIR	578.275	1.92	HSPB1;		S82	Y	NP_001531.1
LLSPQM^S*GEEEDSDLAAK	1011.44	2.47	HTT;	1.056	S1876	Y	NP_002102.4
LLSPQMS*GEEEDSDLAAK	1003.44	3.34	HTT;		S1876	Y	NP_002102.4
TDSQSVRHS*PIAPSS*PSPQVLA	892.413	-2.23	INCENP;		S306, S312	Y	NP_064623.2
LSST*PPLSALGR	639.827	-1.44	INTS1;		T83	Y	NP_001073922.:
TAS*EGDGGAAAGAAAAGAR	806.342	-2.81	IRS2;		S365	Y	NP_003740.2
LQALKEEPQTVPEM^PGETPPLS	1196.89	-1.86	JUN;		S243	Y	NP_002219.1
NSDLLTS*PDVGLLK	779.398	2.07	JUN;		S63	Y	NP_002219.1
NSDLLT*SPDVGLLK	776.388	2.13	JUN;		T62	Y	NP_002219.1
AKNSDLLTS*PDVGLLK	881.974	2.35	JUN;		S63	Y	NP_002219.1
ALAM^PGRPES*PPVFR	860.916	-1.97	KANK2;		S375	Y	NP_056308.2
SPS*GGAAGPLLTPSQSLDGSR	1017.98	-2.13	KCTD12;	1.079	S187	Y	NP_612453.1
SGS*MDPSGAHPSVR	732.801	-1.04	KHDRBS1;	1.060	S20	Y	NP_006550.1
LGDAS*DTEAADGER	743.789	-1.01	KIAA0284;		S1065	Y	NP_055820.1
HTGM^ASIDSSAPETTSDSS*PTL	844.359	1.13	KIAA0913;		S1161	Y	NP_055852.2
VPGEDGTLPTTQGS*PLR	900.931	-1.18	KIAA0947;		S255	Y	NP_056140.1
RPPS*PPGPEER	649.799	-2.38	KIAA1211;		S1017	N	NP_065773.1
SIS*LSQSAENVPASK	802.388	1.53	KIAA1432;		S938	Y	NP_065880.1
ALS*GRAS*PVPAPSSGLHAAVR	721.016	-1.79	KIAA1522;		S917, S921	Y	NP_065939.2
HPLLSSGGPQS*PLR	509.256	-2.19	KIAA1543;		S395	Y	NP_001073898.
ERPDLAPAGS*PFR	859.899	-3.53	KIF13B;		S1644	Y	NP_056069.2
FDLSHGS*PQM^VR	735.316	-1.57	KSR1;		S197	Y	NP_055053.1
S*LPTTVPES*PNYR	810.84	-3.79	LARP1;	0.968	S689, S697	Y	NP_056130.2
SLPTTVPES*PNYR	770.856	-1.39	LARP1;		S697	Y	NP_056130.2
AS*TASPCNNNINAATAVALQEPF	817.704	-2.41	LARP4;		S600	Y	NP_954658.1
VLGSEGEDEALS*PAK	923.409	-1.53	LIG1;	0.983	S76	Y	NP_000225.1
SPGAGSLGS*PASQR	676.304	-1.72	LIMK1;		S310	Y	NP_002305.1

VTTEIQLPSQS*PVEEQSPASLSS	1382.18	3.00	LMO7;		S533	Y	NP_005349.3
RSS*GFISELPSEEGK	859.903	-1.10	LRRRC16A;		S968	Y	NP_060110.3
RGS*GDTSIDTEASIR	932.932	-1.19	LRRFIP1;		S88	Y	NP_001131023.
LSKS*QGEEEEGPLSDK	870.889	-2.44	MAF1;		S75	Y	NP_115648.2
VQSLEGEKLS*PKS*DISPLT*PR	841.052	-1.77	MAP1B;	0.935	S1779, S1782, T	Y	NP_005900.2
SDIS*PLTPR	533.253	1.22	MAP1B;		S1785	Y	NP_005900.2
SGTSTPTTPGSTAITPGT*PPSYS	830.047	-1.69	MAP2;		T306	Y	NP_001034627.
VGS*LDNVGHLPAAGAVK	835.917	-4.86	MAP4;	0.947	S1073	Y	NP_002366.2
KCS*LPAEEDSVLEK	848.899	-4.01	MAP4;		S636	Y	NP_002366.2
LSSSSATLLNS*PDR	764.357	-1.21	MAP7;		S209	Y	NP_003971.1
LSASTASELS*PK	638.811	-1.28	MAP7D1;	0.854	S460	Y	NP_060537.3
HTDDEMTGY*VATR	788.312	2.87	MAPK14;	0.974	Y182	Y	NP_620582.1
GPVS*PSVSFQPLAR	761.377	1.47	MAVS;	1.034	S222	Y	NP_065797.2
SS*VKTPEPVVPTAPEPHPTTSTL	1039.53	1.42	MDC1;	0.958	S1605	N	NP_055456.2
SSVKT*PEPVVPTAPELQPSTSTL	1302.63	1.55	MDC1;		T1239	N	NP_055456.2
LLSSNEDDANILSS*PTDR	1013.95	-1.26	MED24;		S860	Y	NP_001072986.
LLS*SNEDDANILSSPTDR	1013.95	2.55	MED24;		S849	Y	NP_001072986.
APS*AS*PLALHASR	719.319	-2.85	MICALL1;		S484, S486	Y	NP_203744.1
VEQM^PQAS*PGLAPR	789.356	-1.28	MICALL1;		S578	Y	NP_203744.1
KADT*EEEFALFR	767.8392	1.26	MKI67;		T1764	Y	NP_002408.3
IACKS*PPPESM^DTPPTSTR	690.2959	1.37	MKI67;		S2105	Y	NP_002408.3
TPVQYSQQQNS*PQK	856.3823	2.21	MKI67;		S357	Y	NP_002408.3
IPCES*PPLEVVDTTASTKR	726.677	2.35	MKI67;		S2708	Y	NP_002408.3
M^PCESS*PPESADTPTSTR	681.9278	2.73	MKI67;		S1376	Y	NP_002408.3
TQVLS*PDSLFTAK	746.874	1.29	MLLT4;		S1731	Y	NP_001035090.
S*PSVAAM^ASPQLCR	785.842	-1.90	MPST;		S15	N	NP_066949.2
VAPVINN~GSPT*ILGK	780.906	-3.21	MTA1;		T578	Y	NP_004680.2
VAPVINNGS*PTILGK	780.906	-1.70	MTA1;		S576	Y	NP_004680.2
SY*DNLTTACDNTVPLASR	1039.45	-2.48	MTMR3;		Y614	Y	NP_066576.1
S*DEEVDGKADGAEAKPAE	949.389	1.69	MYH9;	1.022	S1943	Y	NP_002464.1
LDGLVET*PTGYIESLPR	970.475	-2.35	NAP1L1;		T62	Y	NP_631946.1
SPSPGGPQLS*PQLPR	799.391	-2.30	NCKAP5L;		S477	Y	NP_001032895.
ASGLLKS*PASLK	626.34	2.59	NEK4;		S340	Y	NP_003148.2
SPS*PAVPLR	502.253	-2.32	NFRKB;		S253	Y	NP_006156.2
NYSS*PPPCHLSR	747.814	-1.96	NFX1;		S50	Y	NP_667344.1
TPSPKEEDEEPES*PPEK	1002.92	-1.75	NUCKS1;		S214	Y	NP_073568.2
TSQLGDS*PFYPGK	741.835	1.93	NUP153;		S257	Y	NP_005115.2
VQM^TS*PSSTGSPM^FK	851.862	2.65	NUP153;		S516	Y	NP_005115.2
RGAPSS*PATGVLPSP*PQGK	628.299	2.30	NUP188;	1.014	S1709, S1717	Y	NP_056169.1
CALSS*PSLAFTPIIK	837.918	1.95	NUP35;	0.890	S259	Y	NP_612142.2

NSESESNKVAETQS*PSLFGST	830.72	1.88	NUP50;		S221	Y	NP_009103.2
SFSLASSNS*PISQR	824.373	-1.41	OSBPL11;		S181	Y	NP_073613.2
SFSLASS*NSPISQR	829.377	-1.18	OSBPL11;		S179	Y	NP_073613.2
KTEVVMNSQQT*PVGT*PK	1008.47	-2.88	PALM;	1.520	T141, T145	Y	NP_001035224.
KTEVVM*NSQQT*PVGT*PK	677.981	-2.70	PALM;		T141, T145	Y	NP_001035224.
KTEVVMNSQQT*PVGT*PK	645.994	-2.65	PALM;		T145	Y	NP_001035224.
ESVSTASDQPSHS*LER	905.387	-1.57	PARD3;		S973	N	NP_062565.2
SQAN~GAGALSYVS*PNTSK	916.907	-2.08	PARN;	1.016	S102	Y	NP_001127949.
RSTS*PIIGS*PPVR	733.886	-2.15	PATL1;		S179, S184	Y	NP_689929.2
YKSTT*SVSEEDVSSR	590.931	1.95	PAWR;	0.970	T230	N	NP_002574.2
PSSS*PVIFAGGQDR	749.341	1.62	PCBP2;		S189	Y	NP_001122383.
YM^SQM^S*VPEQAELEK	944.397	3.76	PCM1;	0.769	S93	Y	NP_006188.3
YM^SQMS*VPEQAELEK	936.399	3.84	PCM1;		S93	Y	NP_006188.3
AQNEFKDEAQLSHS*PK	669.979	-2.87	PDZD8;		S521	Y	NP_776152.1
TAS*QEGCQELTQEQR	922.878	2.20	PEX1;		S1181	Y	NP_000457.1
AQS*YDIQAWKK	715.35	2.08	PHIP;	1.048	S1315	Y	NP_060404.3
SALLTQNGTGS*LPR	747.87	-1.91	PHLDB1;		S1017	Y	NP_055972.1
AHLTVGQAAAGGS*GNLLTER	1001.99	-2.62	PKP2;	0.882	S329	Y	NP_001005242.:
YARS*EIVGVSR	668.83	-1.87	PKP2;		S197	Y	NP_001005242.:
RLEIS*PDSSPER	743.347	1.42	PKP2;		S151	Y	NP_001005242.:
AGGLDWPEATEVS*PSR	876.386	-2.41	PKP3;		S238	Y	NP_009114.1
AVS*PPHLDGPPS*PR	793.842	-1.69	PML;LOC6526;		S518, S527	Y	NP_150241.2
TPESQPD*PPGT*PLVSQDEKR	813.688	-2.26	PNKP;		T118, T122	Y	NP_009185.2
YSPTS*PTYST*TPK	843.839	-2.46	POLR2A;	1.029	S1878, T1884	Y	NP_000928.1
VGS*GSLDNLGR	577.764	-2.21	PPFIA1;		S666	Y	NP_803172.1
VLS*PTAAKPSPFEGK	804.906	1.05	PPP1R10;	1.087	S313	Y	NP_002705.2
TGS*SGALGPPER	604.77	-1.82	PPP1R12C;		S427	Y	NP_060077.1
SIDDEITEAKS*GTAT*PQR	1047.95	-3.12	PRKAA1;		S501, T505	Y	NP_996790.3
M^PPLIADS*PK	582.773	-3.59	PRKAA2;		S377	Y	NP_006243.2
MPPLIADS*PK	574.775	-3.17	PRKAA2;		S377	Y	NP_006243.2
ITS*PLM^EPSSIEK	767.365	1.01	PSMA5;	1.020	S56	Y	NP_002781.2
TVGT*PIASVPGSTNTGTVPGSEI	1139.52	1.12	PSMD1;		T273	Y	NP_002798.2
ANVSS*PHREFPPATAR	612.961	1.02	PSMF1;	0.956	S153	Y	NP_006805.2
KAPPPPIS*PTQLSDVSSPR	690.692	1.67	RAI14;		S281	N	NP_056392.1
HFSQS*EETGNEVFGALNEEQPL	932.416	-1.94	RALGAPA1;	0.894	S775	Y	NP_055805.1
SAAS*REDLVGPEVGAS*PQSGR	795.367	-1.78	RALGPS2;		S296, S308	Y	NP_689876.2
EALGLGPPAAQLT*PPPAPVGLR	1101.59	-1.17	RAVER1;	0.974	T480	Y	NP_597709.2
TAVIPINGS*PRT*PR	819.892	-2.16	RB1;		S249, T252	Y	NP_000312.2
LEVTEIVKPS*PK	710.379	-1.84	RBBP6;		S1145	Y	NP_061173.1
VIADS*DAES*PAKR	824.372	-1.11	RBL1;		S1037, S1041	N	NP_002886.2

YIKENS*PCVT*PVSTATHSLSR	841.716	-2.69	RBL2;		S413, T417	Y	NP_005602.3
HRHS*PTGPPGFPR	508.241	-1.66	RBM10;		S89	Y	NP_005667.2
LGASNS*PGQPNSVKR	796.876	-1.61	RBM25;	1.083	S677	Y	NP_067062.1
DSYS*SSRSDLYSSGR	589.577	-1.99	RBMX;LOC100		S328	Y	NP_002130.2
SVWGLAVQNS*PK	729.858	-1.34	RDBP;	0.911	S353	Y	NP_002895.3
SIS*ADDDLQESSR	751.805	2.25	RDBP;		S115	Y	NP_002895.3
SLS*EQPVM^DTATATEQAK	996.951	2.80	RDBP;		S51	Y	NP_002895.3
SLS*EQPVM^DTATATEQAK	1004.95	2.98	RDBP;		S51	Y	NP_002895.3
S*LSEQPVM^DTATATEQAK	1004.95	3.10	RDBP;		S49	Y	NP_002895.3
NLS*GSTLYPVSNIPR	849.417	-2.16	RFX7;		S1178	Y	NP_073752.5
ALVVPEPEPDS^SDS*NQER	981.429	-1.65	RNF20;	1.010	S138	Y	NP_062538.5
ILKS*PEIQ~R	590.82	-1.81	RPL4;	0.998	S295	Y	NP_000959.2
KAEAGAGS*ATEFQFR	833.384	-1.80	RPS10;	0.953	S146	Y	NP_001005.1
VLDTSSLTQS*APAS*PTNK	991.945	-1.66	RPTOR;		S859, S863	Y	NP_065812.1
TPTSS*PASS*PLVAK	754.841	-1.72	RRP1B;	0.993	S732, S736	Y	NP_055871.1
TPTSS*PASS*PLVAK	714.858	-1.12	RRP1B;		S732	Y	NP_055871.1
SILVS*PTGPSR	597.301	1.08	RRP1B;		S706	Y	NP_055871.1
DSAPSTPTS*PTEFLTPGLR	1027.48	1.70	SACS;		S4264	Y	NP_055178.3
SVVS*FDKVK	550.794	-1.86	SAFB;		S604	Y	NP_002958.2
KDDVS*PVMQFSSK	780.365	1.76	SCYL3;		S653	N	NP_065156.5
FDS*PRGPPPPR	441.544	-1.47	SENP3;		S188	Y	NP_056485.2
ILEQQNSSRT*LEK	821.413	-1.25	SEPT7;		T425	Y	NP_001011553.:
SSLGQS*AS*ETEEDTVSVSK	1053.93	1.00	SF3B2;	0.994	S307, S309	Y	NP_006833.2
SSLGQS*AS*ETEEDTVSVSKK	1120.98	1.25	SF3B2;		S307, S309	Y	NP_006833.2
SEEKIS*DSEGFK	724.324	1.11	SFPQ;	1.115	S273	Y	NP_005057.1
LTRPAAS*PAVGEK	696.865	-1.55	SFRS16;		S547	Y	NP_008987.2
TLS*SSAQEDIIR	700.327	2.48	SH2D4A;		S315	Y	NP_071354.2
ANS*PSLFGTEGKPK	756.859	-2.37	SH3KBP1;		S587	Y	NP_114098.1
HGS*PEFCGILGER	769.827	-1.87	SHB;		S388	Y	NP_003019.2
S*GSDAGEARPPTPASPR	876.895	2.13	SIPA1;		S53	Y	NP_694985.29
AGAGM^ITQHSSNAS*PINR	954.426	-2.00	SLTM;		S1002	Y	NP_079031.2
AGAGMITQHSSNAS*PINR	631.288	-1.78	SLTM;		S1002	Y	NP_079031.2
GGGGGQDNGLEGLGND^R	870.353	-1.99	SNRNP70;	1.024	S410	Y	NP_003080.2
SAAS*PVVSSM^PER	707.308	-2.05	SON;	0.924	S1769	Y	NP_115571.1
SVESTS*PEPSKIM^LVEPPVAK	774.384	1.67	SON;		S283	Y	NP_115571.1
SRLT*PVSPSSSTEEK	915.429	-3.05	SQSTM1;		T269	Y	NP_003891.1
SGS*SQELDVKPSAS*PQER	661.301	-2.28	SRRM2;	0.992	S1541, S1552	Y	NP_057417.3
TPAAAAAMNLAS*PR	711.335	1.35	SRRM2;		S2272	Y	NP_057417.3
TPAAAAAM^NLAS*PR	719.332	1.43	SRRM2;		S2272	Y	NP_057417.3
M^SCFS*RPSM^SPTPLDR	990.905	1.71	SRRM2;		S2118	Y	NP_057417.3

TAVAPSAVNLADPRT*PTAPAVNI	901.137	2.08	SRRM2;		T2289	Y	NP_057417.3
LQTTDNLLPMS*PEEFDEVSR	1200.532	1.24	STAT1;	0.954	S727	Y	NP_009330.1
LIEGVHPGSLVEKLPDS*PALAK	788.099	-3.24	STIM1;	0.991	S575	Y	NP_003147.2
LPDS*PALAK	499.257	-1.66	STIM1;		S575	Y	NP_003147.2
LTSS*CPDLPSQTDKK	884.916	-2.22	STX17;		S289	Y	NP_060389.2
DVTNFTVGGFAPMS*PR	888.395	-1.32	SUPT5H;		S666	Y	NP_001104490.
M^DSNFGLAGLPGS*PK	793.85	-1.01	SUV39H1;		S391	Y	NP_003164.1
RADNCS*PVAEEETTGSAAESTLP	843.699	-2.77	TANC1;		S270	Y	NP_203752.1
TAANKS*PCETISS*PSSTLESK	763.024	-2.02	TANC1;		S207, S214	Y	NP_203752.1
TEEARPSPAPGPGT*PTGTPTTR	726.343	-2.46	TBC1D10B;		T148	N	NP_056342.3
SQS*LPHSATVTLGGTSDPSTLS	985.132	1.60	TBC1D22A;		S167	N	NP_055161.1
AFSS*PQEEEEAGFTGR	911.371	2.91	TCEB3;		S542	Y	NP_003189.2
SPAGPAATPAQAQAAS*PR	920.435	-1.09	TCOF1;		T983	Y	NP_001008656.
NDAPTPGTSTT*PGLR	782.854	-1.74	TLE3;		T334	Y	NP_005069.2
GPPDFSSDEEREPT*PVLGSGAA	884.065	-2.10	TMPO;	1.008	T74	Y	NP_001027454.
SST*PLPTISSSAENTR	869.401	-1.16	TMPO;		T160	Y	NP_001027454.
LGSQPIRAS*NPDLR	812.41	-1.08	TNIK;		S707	Y	NP_055843.1
HNGSL*PGLEAR	664.798	1.27	TNKS1BP1;		S1385	Y	NP_203754.2
AADRLPNLSS*PSAEGPPGPPSG	859.082	2.82	TOM1;		S462	Y	NP_005479.1
IDEDGENTQIEDTEPM^S*PVLNS	1329.06	-2.09	TP53BP1;		S557	Y	NP_001135451.
VLLS*PSIPSVGQDQTLSPGSK	1098.57	2.90	TP53BP2;		S433	Y	NP_005417.1
N~SATFKS*FEDR	699.8	2.89	TPD52L2;		S189	Y	NP_955392.1
EGVQGPLNV*S*LSEEGK	861.902	-1.87	TPR;	0.988	S1185	Y	NP_003283.2
VPVNULLNS*PDCDVK	828.395	1.21	TTK;		S281	Y	NP_003309.2
RYPSSISS*S*PQKDLTQAK	699.022	-2.33	UBAP2L;	0.984	S608, S609	Y	NP_001120792.
M^EISAELPQT*PQR	798.361	-1.60	UBR1;		T21	Y	NP_777576.1
SESLIDASEDS*QLEAAIR	1007.45	-1.89	UBXN7;	1.050	S288	Y	NP_056377.1
DSALAEAPEGLS*PAPPAR	914.928	-1.55	USP42;		S856	Y	NP_115548.1
STETSDFENIES*PLNER	1024.43	-1.65	USP47;	0.850	S822	Y	NP_060414.3
S*DVSPIIQPVPSIK	783.418	2.22	USP8;		S389	Y	NP_001122082.
SHILEDDENS*VDISM^LK	1023.96	-1.59	WDHD1;	1.012	S260	Y	NP_001008397.
TQSRPGGPPNPPGPS*PK	584.281	-1.80	WIZ;		S249	Y	NP_067064.2
NYQQNYQNS*ESGEKNEGSESA	1118.47	-1.02	YBX1;	1.060	S165	Y	NP_004550.2
QPGQVIGATTPTSTGS*PTNK	960.957	-1.86	YEATS2;		S519	Y	NP_060493.3
SSQQPST*PQQAPPQPQQGTF	904.425	-1.98	ZC3H18;		T796	Y	NP_653205.2
LGVS*VS*PSR	491.243	-1.74	ZC3H18;		S532, S534	Y	NP_653205.2
S*SLGSLQTPEAVTTR	813.891	-3.08	ZC3HAV1;	0.946	S386	Y	NP_078901.3
SCT*PSPDQISHR	732.801	-1.82	ZC3HAV1;		T273	Y	NP_078901.3
IHS*PIPDMSK	605.786	1.35	ZCCHC8;		S658	Y	NP_060082.2
RIS*TSDILSEK	672.841	1.78	ZFC3H1;		S352	Y	NP_659419.3

NEIIQS*PISQVPSVEK	927.472	1.62	ZFYVE16;		S939	Y	NP_055548.3
NQKQPGVDSLS*PVASLPK	653.012	1.77	ZMYM2;		S305	Y	NP_003444.1
TEEPLGS*PHPSGTVESPGEGPC	881.053	-2.45	ZNF446;		S137	Y	NP_060378.1
KLANDFPLDLS*PVK	818.922	-1.92	ZNF462;		S688	Y	NP_067047.4
ATDIPASAS*PPPVAGVPFFK	1025.01	-2.74	ZNF687;		S253	Y	NP_065883.1
S*PGLVPPS*PEFAPR	805.855	-2.36	ZNF768;		S90, S97	Y	NP_078947.3
S*PGAPGPLTLK	562.297	1.16	ZYX;	1.020	S344	Y	NP_003452.1

Protein annotation**Link to known function**

actin-binding LIM protein 1 isoform a [Homo sapiens]
acetyl-Coenzyme A carboxylase alpha isoform 1 [Homo sapiens]
acyl-Coenzyme A binding domain containing 5 isoform 1 [Homo sapiens]
apoptotic chromatin condensation inducer 1 [Homo sapiens]
adenosine deaminase, RNA-specific isoform a [Homo sapiens]
ALL1 fused gene from 5q31 [Homo sapiens]
HIV-1 Rev binding protein isoform 2 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
AHNAK nucleoprotein isoform 1 [Homo sapiens]
alpha-2-HS-glycoprotein [Homo sapiens]
A kinase (PRKA) anchor protein 12 isoform 2 [Homo sapiens]
AKT1 substrate 1 (proline-rich) [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6306&showAllSites=true>
alkB, alkylation repair homolog 5 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=16708&showAllSites=true>
probable alpha-ketoglutarate-dependent dioxygenase ABH5 [Homo sapiens]
ankyrin repeat and sterile alpha motif domain containing 1 [Homo sapiens]
anillin, actin binding protein [Homo sapiens]
Rho GTPase activating protein 1 [Homo sapiens]
Rho GTPase activating protein 27 [Homo sapiens]
Rho-specific guanine nucleotide exchange factor p114 isoform 1 <http://www.phosphosite.org/proteinAction.do?id=13377&showAllSites=true>
AT rich interactive domain 1A isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=7952&showAllSites=true>
AT rich interactive domain 1A isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=7952&showAllSites=true>
activating transcription factor 2 [Homo sapiens]
activating transcription factor 7 isoform 3 [Homo sapiens]
activating transcription factor 7 interacting protein [Homo sapiens]
ataxia telangiectasia mutated protein isoform 1 [Homo sapiens]
plasma membrane calcium ATPase 1 isoform 1b [Homo sapiens]
BCL2-associated athanogene 3 [Homo sapiens]
HLA-B associated transcript-2 [Homo sapiens]
tyrosine-protein kinase BAZ1B [Homo sapiens]
B-cell CLL/lymphoma 7C [Homo sapiens]
bromodomain containing 2 [Homo sapiens]

bromodomain containing 2 [Homo sapiens]
bromodomain and WD repeat domain containing 1 isoform A [Homo sapiens]
BUD13 homolog [Homo sapiens]
BUD13 homolog isoform 1 [Homo sapiens]
hypothetical protein LOC55004 [Homo sapiens]
chromosome 12 open reading frame 51 [Homo sapiens]
PTIP-associated 1 protein [Homo sapiens]
ARKadia-like 1 isoform a [Homo sapiens]
hypothetical protein LOC56006 [Homo sapiens]
hypothetical protein LOC29058 isoform 2 [Homo sapiens]
ashwin [Homo sapiens]
ashwin [Homo sapiens]
ashwin [Homo sapiens]
hypothetical protein LOC79886 [Homo sapiens]
hypothetical protein LOC79886 [Homo sapiens]
calmodulin regulated spectrin-associated protein 1-like 1 [Homo sapiens]
Cdc42 effector protein 3 [Homo sapiens]
cell division cycle 2-like 5 isoform 2 [Homo sapiens]
centrosomal protein 170kDa isoform alpha [Homo sapiens]
centrosomal protein 170kDa isoform alpha [Homo sapiens]
chromatin assembly factor 1 subunit B [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5879&showAllSites=true>
CLIP-associating protein 1 isoform 2 [Homo sapiens]
CLIP-associating protein 1 isoform 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6179&showAllSites=true>
restin isoform a [Homo sapiens]
cyclin M3 isoform 2 [Homo sapiens]
cAMP responsive element binding protein 5 isoform alpha [Homo sapiens]
catenin (cadherin-associated protein), beta 1, 88kDa [Homo sapiens]
catenin beta-1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=454&showAllSites=true>
catenin, delta 1 isoform 3ABC [Homo sapiens]
cortactin isoform a [Homo sapiens]
cortactin isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=1192&showAllSites=true>
spectrin domain with coiled-coils 1 NSP5b3b [Homo sapiens]
death-domain associated protein isoform b [Homo sapiens]
IQ motif and WD repeats 1 isoform a [Homo sapiens]
DCP1 decapping enzyme homolog A [Homo sapiens]
decapping enzyme Dcp1b [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2681&showAllSites=true>
DENN/MADD domain containing 4C [Homo sapiens]
DENN/MADD domain containing 5B [Homo sapiens]
discs, large homolog 1 isoform 2 [Homo sapiens]
DNA methyltransferase 1 associated protein 1 [Homo sapiens]

dynamain 1-like protein isoform 1 [Homo sapiens]
deoxynucleotidyltransferase, terminal, interacting protein 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=9379&showAllSites=true>
dedicator of cytokinesis 7 [Homo sapiens]
zinc finger protein ubi-d4 [Homo sapiens]
desmoglein 2 preproprotein [Homo sapiens]
dynein, cytoplasmic 1, light intermediate chain 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2988&showAllSites=true>
dynein, cytoplasmic 1, light intermediate chain 1 [Homo sapiens]
dynein, cytoplasmic 1, light intermediate chain 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2988&showAllSites=true>
dynein, cytoplasmic 1, light intermediate chain 1 [Homo sapiens]
dynein, cytoplasmic 1, light intermediate chain 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2988&showAllSites=true>
enhancer of mRNA decapping 3 [Homo sapiens]
EF-hand domain-containing protein D2 [Homo sapiens]
epidermal growth factor receptor isoform a precursor [Homo sapiens]
egl nine homolog 1 [Homo sapiens]
eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa [Homo sapiens]
eukaryotic translation initiation factor 4E binding protein 1 [Homo sapiens]
eukaryotic translation initiation factor 4 gamma 2 isoform 1 [Homo sapiens]
erythrocyte membrane protein band 4.1-like 3 [Homo sapiens]
erythrocyte membrane protein band 4.1-like 3 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3467&showAllSites=true>
erythrocyte membrane protein band 4.1-like 3 [Homo sapiens]
epiplakin 1 [Homo sapiens]
epiplakin 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=8674&showAllSites=true>
epiplakin 1 [Homo sapiens]
epidermal growth factor receptor pathway substrate 15 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=4549&showAllSites=true>
amyotrophic lateral sclerosis 2 (juvenile) chromos
hypothetical protein LOC116224 [Homo sapiens]
FERM, RhoGEF and pleckstrin domain-containing protein 1 isoform 1 [Homo sapiens]
hypothetical protein LOC55701 [Homo sapiens]
forkhead box C1 [Homo sapiens]
forkhead box K2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=16478&showAllSites=true>
FERM domain containing 6 [Homo sapiens]
galanin preproprotein [Homo sapiens]
GATA zinc finger domain containing 2B [Homo sapiens]
GATA zinc finger domain containing 2B [Homo sapiens]
GRB10 interacting GYF protein 2 isoform b [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6171&showAllSites=true>
GEM interacting protein [Homo sapiens]
golgi reassembly stacking protein 2 [Homo sapiens]
G patch domain and KOW motifs [Homo sapiens]
G protein-coupled receptor 137C [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=15672287&showAllSites=true>
general transcription factor IIF subunit 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=8665&showAllSites=true>

family with sequence similarity 29, member A [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=13449&showAllSites=true>
family with sequence similarity 29, member A [Homo sapiens]
host cell factor 1 [Homo sapiens]
host cell factor 1 [Homo sapiens]
HEAT repeat containing 6 [Homo sapiens]
HEAT repeat containing 6 [Homo sapiens]
helicase (DNA) B [Homo sapiens]
helicase with zinc finger domain [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5834&showAllSites=true>
high mobility group AT-hook 1 isoform b [Homo sapiens]
high mobility group AT-hook 2 isoform a [Homo sapiens]
heterogeneous nuclear ribonucleoprotein M isoform b [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=8716&showAllSites=true>
heterogeneous nuclear ribonucleoprotein U-like 1 isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2890&showAllSites=true>
Hermansky-Pudlak syndrome 5 isoform b [Homo sapiens]
heat shock protein beta-1 [Homo sapiens]
huntingtin [Homo sapiens]
huntingtin [Homo sapiens]
inner centromere protein isoform 2 [Homo sapiens]
integrator complex subunit 1 [Homo sapiens]
insulin receptor substrate 2 [Homo sapiens]
jun oncogene [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=943&showAllSites=true>
jun oncogene [Homo sapiens]
jun oncogene [Homo sapiens]
jun oncogene [Homo sapiens]
ankyrin repeat domain 25 [Homo sapiens]
potassium channel tetramerisation domain containing 12 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=9130&showAllSites=true>
KH domain containing, RNA binding, signal transduction associated 1 [Homo sapiens]
hypothetical protein LOC283638 isoform 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=16435&showAllSites=true>
hypothetical protein LOC23053 [Homo sapiens]
hypothetical protein LOC23379 [Homo sapiens]
hypothetical protein LOC57482 [Homo sapiens]
connexin 43-interacting protein 150 isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=15964&showAllSites=true>
hypothetical protein LOC57648 [Homo sapiens]
hypothetical protein LOC57662 isoform 1 [Homo sapiens]
kinesin family member 13B [Homo sapiens]
kinase suppressor of ras [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2001&showAllSites=true>
la-related protein 1 isoform 1 [Homo sapiens]
la related protein isoform 1 [Homo sapiens]
c-Mpl binding protein isoform b [Homo sapiens]
DNA ligase I [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=957&showAllSites=true>
LIM domain kinase 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=616&showAllSites=true>

LIM domain only 7 [Homo sapiens]
leucine rich repeat containing 16A [Homo sapiens]
leucine rich repeat (in FLII) interacting protein 1 isoform 2 [Homo sapiens]
MAF1 protein [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=9756&showAllSites=true>
microtubule-associated protein 1B [Homo sapiens]
microtubule-associated protein 1B [Homo sapiens]
microtubule-associated protein 2 isoform 5 [Homo sapiens]
microtubule-associated protein 4 isoform 1 [Homo sapiens]
microtubule-associated protein 4 isoform 1 [Homo sapiens]
microtubule-associated protein 7 [Homo sapiens]
MAP7 domain containing 1 [Homo sapiens]
mitogen-activated protein kinase 14 isoform 3 [Homo sapiens]
virus-induced signaling adapter [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=15129&showAllSites=true>
mediator of DNA damage checkpoint 1 [Homo sapiens]
mediator of DNA damage checkpoint 1 [Homo sapiens]
mediator complex subunit 24 isoform 2 [Homo sapiens]
mediator complex subunit 24 isoform 2 [Homo sapiens]
molecule interacting with Rab13 [Homo sapiens]
molecule interacting with Rab13 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5920&showAllSites=true>
antigen KI-67 isoform 1 [Homo sapiens]
antigen KI-67 isoform 1 [Homo sapiens]
antigen KI-67 isoform 1 [Homo sapiens]
antigen KI-67 isoform 1 [Homo sapiens]
antigen KI-67 isoform 1 [Homo sapiens]
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 1 [Homo sapiens]
mercaptopyruvate sulfurtransferase isoform 1 [Homo sapiens]
metastasis associated protein [Homo sapiens]
metastasis associated protein [Homo sapiens]
myotubularin-related protein 3 isoform c [Homo sapiens]
myosin-9 [Homo sapiens]
nucleosome assembly protein 1-like 1 [Homo sapiens]
hypothetical protein LOC57701 [Homo sapiens]
NIMA (never in mitosis gene a)-related kinase 4 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=766&showAllSites=true>
nuclear factor related to kappaB binding protein [Homo sapiens]
nuclear transcription factor, X-box binding 1 isoform 2 [Homo sapiens]
nuclear casein kinase and cyclin-dependent kinase substrate 1 [Homo sapiens]
nucleoporin 153kDa [Homo sapiens]
nucleoporin 153kDa [Homo sapiens]
nucleoporin 188kDa [Homo sapiens]
nucleoporin 35kDa [Homo sapiens]

nucleoporin 50kDa isoform b [Homo sapiens]
oxysterol binding protein-like 11 [Homo sapiens]
oxysterol binding protein-like 11 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2949&showAllSites=true>
paralemmin isoform 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3843&showAllSites=true>
paralemmin isoform 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3843&showAllSites=true>
paralemmin isoform 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3843&showAllSites=true>
partitioning-defective protein 3 homolog [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2686&showAllSites=true>
poly(A)-specific ribonuclease (deadenylation nuclease) isoform 2 [Homo sapiens]
protein associated with topoisomerase II homolog 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6218&showAllSites=true>
PRKC, apoptosis, WT1, regulator [Homo sapiens]
poly(rC)-binding protein 2 isoform d [Homo sapiens]
pericentriolar material 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3133&showAllSites=true>
pericentriolar material 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3133&showAllSites=true>
PDZ domain containing 8 [Homo sapiens]
peroxin1 [Homo sapiens]
pleckstrin homology domain interacting protein [Homo sapiens]
pleckstrin homology-like domain, family B, member 1 [Homo sapiens]
plakophilin 2 isoform 2a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6853&showAllSites=true>
plakophilin 2 isoform 2a [Homo sapiens]
plakophilin 2 isoform 2a [Homo sapiens]
plakophilin 3 [Homo sapiens]
promyelocytic leukemia protein isoform 1 [Homo sapiens]
polynucleotide kinase 3'-phosphatase [Homo sapiens]
DNA directed RNA polymerase II polypeptide A [Homo sapiens]
PTPRF interacting protein alpha 1 isoform a [Homo sapiens]
protein phosphatase 1, regulatory subunit 10 [Homo sapiens]
protein phosphatase 1, regulatory subunit 12C [Homo sapiens]
protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 2 [Homo sapiens]
AMP-activated protein kinase alpha 2 catalytic subunit [Homo sapiens]
AMP-activated protein kinase alpha 2 catalytic subunit [Homo sapiens]
proteasome alpha 5 subunit [Homo sapiens]
proteasome 26S non-ATPase subunit 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5959&showAllSites=true>
proteasome inhibitor subunit 1 [Homo sapiens]
retinoic acid induced 14 [Homo sapiens]
GTPase activating Rap/RanGAP domain-like 1 isoform 1 [Homo sapiens]
Ral GEF with PH domain and SH3 binding motif 2 [Homo sapiens]
RAVER1 [Homo sapiens]
retinoblastoma 1 [Homo sapiens]
retinoblastoma-binding protein 6 isoform 2 [Homo sapiens]
retinoblastoma-like protein 1 isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=4526&showAllSites=true>

retinoblastoma-like 2 (p130) [Homo sapiens]
RNA binding motif protein 10 isoform 1 [Homo sapiens]
RNA binding motif protein 25 [Homo sapiens]
RNA binding motif protein, X-linked [Homo sapiens]
RD RNA-binding protein [Homo sapiens]
RD RNA-binding protein [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5808&showAllSites=true>
RD RNA-binding protein [Homo sapiens]
RD RNA-binding protein [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5808&showAllSites=true>
RD RNA-binding protein [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5808&showAllSites=true>
regulatory factor X domain containing 2 [Homo sapiens]
ring finger protein 20 [Homo sapiens]
ribosomal protein L4 [Homo sapiens]
ribosomal protein S10 [Homo sapiens]
raptor [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6245&showAllSites=true>
ribosomal RNA processing 1 homolog B [Homo sapiens]
ribosomal RNA processing 1 homolog B [Homo sapiens]
ribosomal RNA processing 1 homolog B [Homo sapiens]
sacsin [Homo sapiens]
scaffold attachment factor B [Homo sapiens]
SCY1-like 3 isoform 1 [Homo sapiens]
SUMO1/sentrin/SMT3 specific protease 3 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6967&showAllSites=true>
cell division cycle 10 isoform 2 [Homo sapiens]
splicing factor 3B subunit 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2959&showAllSites=true>
splicing factor 3B subunit 2 [Homo sapiens]
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens]
Splicing factor, arginine/serine-rich 16 [Homo sapiens]
SH2 domain containing 4A [Homo sapiens]
SH3-domain kinase binding protein 1 isoform a [Homo sapiens]
Src homology 2 domain containing adaptor protein B [Homo sapiens]
signal-induced proliferation-associated protein 1
modulator of estrogen induced transcription isoform a [Homo sapiens]
modulator of estrogen induced transcription isoform a [Homo sapiens]
U1 small nuclear ribonucleoprotein 70 kDa [Homo sapiens]
SON DNA-binding protein isoform B [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5807&showAllSites=true>
SON DNA-binding protein isoform B [Homo sapiens]
sequestosome 1 [Homo sapiens]
splicing coactivator subunit SRm300 [Homo sapiens]
splicing coactivator subunit SRm300 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3140&showAllSites=true>
splicing coactivator subunit SRm300 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3140&showAllSites=true>
splicing coactivator subunit SRm300 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=3140&showAllSites=true>

splicing coactivator subunit SRm300 [Homo sapiens]
signal transducer and activator of transcription 1 isoform alpha [Homo sapiens]
stromal interaction molecule 1 precursor [Homo sapiens]
stromal interaction molecule 1 precursor [Homo sapiens]
syntaxin 17 [Homo sapiens]
suppressor of Ty 5 homolog isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6160&showAllSites=true>
suppressor of variegation 3-9 homolog 1 [Homo sapiens]
tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [Homo sapiens]
tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 [Homo sapiens]
TBC1 domain family member 10B [Homo sapiens]
TBC1 domain family, member 22A [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=20243&showAllSites=true>
elongin A [Homo sapiens]
Treacher Collins-Franceschetti syndrome 1 isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5887&showAllSites=true>
transducin-like enhancer protein 3 isoform a [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2990&showAllSites=true>
thymopoietin isoform beta [Homo sapiens]
thymopoietin isoform beta [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=5144&showAllSites=true>
TRAF2 and NCK interacting kinase [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=2498&showAllSites=true>
tankyrase 1-binding protein 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=4542&showAllSites=true>
target of myb1 isoform 1 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=7770&showAllSites=true>
tumor protein p53 binding protein 1 isoform 2 [Homo sapiens]
tumor protein p53 binding protein, 2 isoform 2 [Homo sapiens]
tumor protein D52-like 2 isoform a [Homo sapiens]
nuclear pore complex-associated protein TPR [Homo sapiens]
TTK protein kinase [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=779&showAllSites=true>
ubiquitin-associated protein 2-like isoform b [
ubiquitin protein ligase E3 component n-recogin 1 [Homo sapiens]
UBX domain containing 7 [Homo sapiens]
ubiquitin specific protease 42 [Homo sapiens]
ubiquitin specific protease 47 [Homo sapiens]
ubiquitin specific peptidase 8 [Homo sapiens]
WD repeat and HMG-box DNA binding protein 1 isoform 2 [Homo sapiens]
widely-interspaced zinc finger motifs [Homo sapiens]
nuclease sensitive element binding protein 1 [Homo sapiens]
YEATS domain containing 2 [Homo sapiens]
zinc finger CCCH-type containing 18 [Homo sapiens]
zinc finger CCCH-type containing 18 [Homo sapiens]
zinc finger antiviral protein isoform 2 [Homo sapiens]
zinc finger antiviral protein isoform 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=6205&showAllSites=true>
zinc finger CCHC domain-containing protein 8 [Homo sapiens]
proline/serine-rich coiled-coil 2 [Homo sapiens] <http://www.phosphosite.org/proteinAction.do?id=13471&showAllSites=true>

zinc finger, FYVE domain containing 16 [Homo sapiens]
zinc finger protein 198 [Homo sapiens]
zinc finger protein 446 [Homo sapiens]
zinc finger protein 462 [Homo sapiens]
zinc finger protein 687 [Homo sapiens]
zinc finger protein 768 [Homo sapiens]
zyxin [Homo sapiens]

<http://www.phosphosite.org/proteinAction.do?id=5439&showAllSites=true>
<http://www.phosphosite.org/proteinAction.do?id=5992&showAllSites=true>

<http://www.phosphosite.org/proteinAction.do?id=6400&showAllSites=true>