

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)	
1		Activator protein								
2	-0.73	NIBP	1051	trafficking protein particle complex 9	M#AIQVDKFNFEFSPES*PGEKGFANPK	Q6ZQT3	139	5	6.13E+05	
3		Adaptor/scaffold								
4	-0.67	ACD	424, 435	adrenocortical dysplasia homolog isoform 1	TPS*SPLQSCPTSL*PR	Q96AP0	58	1	6.45E+05	
5	-0.37	ANK2	3759	ankyrin 2 isoform 3	AM#IVPS*SPSKTPEEVSTPAEEELKYLQPTSSER	Q01484	430	1	1.27E+05	
6	1.37	BIN1 iso7	300	bridging integrator 1 isoform 8	VNHEPEPAGGATPGATLPKS*PSQPAEA	000499-7	48	1	4.80E+05	
7	10.54	BIN1; BIN1 iso2	323, 331; 292, 300	bridging integrator 1 isoform 8	VNHEPEPAGGAT*PGATLPKS*PSQL	000499; 000499-2	65; 57	5	2.32E+06	
8	10.33	BIN1; BIN1 iso2	323, 333; 292, 302	bridging integrator 1 isoform 8	VNHEPEPAGGAT*PGATLPKSPS*QLR	000499; 000499-2	65; 57	1	1.42E+06	
9	-0.24	BIN1; BIN1 iso2	331; 300	bridging integrator 1 isoform 8	VNHEPEPAGGATPGATLPKS*PSQL	000499; 000499-2	65; 57	8	1.59E+07	
10	-0.74	Cbl	483	Cas-Br-M (murine) ecotropic retroviral transforming sequence	VERPPS*PFSM#APQASLPPVPPR	P22681	100	1	2.77E+05	
11	1.88	CD2BP2	194	CD2 antigen (cytoplasmic tail) binding protein 2	GPGQPS*SPQRLDR	Q95400	38	4	1.20E+06	
12	-0.66	CD2BP2	195	CD2 antigen (cytoplasmic tail) binding protein 2	GPGQPS*PQRLDR	Q95400	38	7	4.88E+05	
13	6.89	Crk	74	v-crk sarcoma virus CT10 oncogene homolog isoform b	VSHYIINSSGPRPPVPPS*PAQPPGVSPS	P46108	34	4	7.95E+05	
14	1.56	EPB41L1; EPB41L1 iso2	540, 544, 550; 466, 470, 476	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPS*SPAS*PSPKGT*PEKANER	Q9H4G0; Q9H4G0-2	99; 88	1	1.95E+05	
15	10.25	EPB41L1; EPB41L1 iso2	541, 544, 546, 550; 467, 470, 472, 476	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSS*PAS*PS*PKGT*PEKANER	Q9H4G0; Q9H4G0-2	99; 88	1	2.14E+05	
16	-0.63	EPB41L1; EPB41L1 iso2	541, 546; 467, 472	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSS*PASPS*PK	Q9H4G0; Q9H4G0-2	99; 88	1	9.09E+04	
17	-0.30	EPB41L1; EPB41L1 iso2	544; 470	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSSPAS*PSPK	Q9H4G0; Q9H4G0-2	99; 88	1	2.82E+05	
18	-0.77	FCHSD2	681	FCH and double SH3 domains 2	SSLYFPSS*PSANEK	Q94868	84	2	5.76E+05	
19	-0.19	IRS-1	348	insulin receptor substrate 1	ASSDGEGTMSRPASVDGSPVS*PSTNR	P35568	132	1	4.58E+04	
20	6.93	IRS-2	1148, 1151, 1162	insulin receptor substrate 2	RHS*SET*FSSTTTVTPVS*PSFAHNPK	Q9Y4H2	137	1	8.09E+05	
21	-0.47	IRS-2	1149, 1162	insulin receptor substrate 2	HSS*ETFSSSTTTVTPVS*PSFAHNPK	Q9Y4H2	137	3	1.85E+06	
22	-0.35	IRS-2	1162	insulin receptor substrate 2	HSSETFSSSTTTVTPVS*PSFAHNPK	Q9Y4H2	137	2	3.92E+05	
23	1.16	IRS-2	391	insulin receptor substrate 2	PVSIVAGSPLS*PGVPR	Q9Y4H2	137	3	1.63E+06	
24	1.86	IRS-2	679	insulin receptor substrate 2	SDDYMPM#S*PASVSAPK	Q9Y4H2	137	2	1.44E+06	
25	2.84	MPDZ; MPDZ iso2	790; 790	multiple PDZ domain protein	IGVAKPLPLS*PEEGYVSAK	Q75970; Q75970-2	219; 222	1	7.58E+05	
26	-0.90	AKAP2	383	PALM2-AKAP2 protein isoform 1	DALGDLSLQVPPVS*PSSTSSR	Q9Y2D5-4	122	3	1.37E+07	
27	-0.28	PAR3-beta	364	par-3 partitioning defective 3 homolog B isoform c	LGGKPPSS*PSLSPLMGFGSNK	Q8TEW8	132	1	2.46E+05	
28	2.40	PAR3-beta	366, 368	par-3 partitioning defective 3 homolog B isoform c	LGGKPPSS*LS*PLM#GFGSNK	Q8TEW8	132	1	1.19E+06	
29	-0.18	PARVA	14	parvin, alpha	SPSVPKS*PTPK	Q9NVD7	42	1	5.33E+05	
30	-0.44	PARVA	14, 19	parvin, alpha	SPSVPKS*PTPKS*PPSR	Q9NVD7	42	5	9.48E+06	
31	-0.24	PARVA	14, 22	parvin, alpha	SPSVPKS*PTPKSPPS*RK	Q9NVD7	42	3	3.64E+05	
32	-0.28	PARVA	16	parvin, alpha	SPSVPKSPT*PK	Q9NVD7	42	1	6.62E+05	
33	-0.19	PARVA	19	parvin, alpha	SPTPKS*PPSR	Q9NVD7	42	3	1.62E+07	
34	2.19	PEX14	234	peroxisomal biogenesis factor 14	QFPPSPS*APK	Q75381	41	1	1.44E+06	
35	2.70	RANBP9	477	RAN binding protein 9	SQDSYPVS*PR	Q96S59	78	1	3.63E+05	
36	-0.92	RANBP9	477, 483, 487	RAN binding protein 9	SQDSYPVS*PRPFSS*PSM#S*PSHGMNIHNLASGK	Q96S59	78	1	3.76E+05	
37	-0.14	RANBP9	477, 487	RAN binding protein 9	SQDSYPVS*PRPFSSPSM#S*PSHGMNIHNLASGK	Q96S59	78	1	6.66E+04	
38	2.43	kanadaplin	82	solute carrier family 4 (anion exchanger), member 1, adaptor protein	KPALPVS*PAAR	Q9BWU0	89	7	1.08E+07	
39	-0.18	ArgBP2; ArgBP2 iso2; ArgBP2 iso4	302; 395; 420	sorbin and SH3 domain containing 2 isoform 3	SFTSSSPSS*PSR	Q94875; 094875-2; 094875-4	124; 75; 77	1	3.95E+05	
40	-0.35	vinexin; vinexin iso2	530; 188	sorbin and SH3 domain containing 3 isoform 2	LCDDGQPLQTS*PR	Q60504; Q60504-2	75; 37	2	1.17E+06	
41	-0.34	CHIP	19	STIP1 homology and U-box containing protein 1	LGAGGGS*PEKSPSAQELK	Q9JUN7	35	1	3.14E+05	
42	-0.78	TANC1	1503	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 isoform 2	GRPVS*PQSR	Q9C0D5	202	1	1.39E+07	
43	2.87	TANC1	1564	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 isoform 2	VQISSGNPPPS*PMPGR	Q9C0D5	202	2	9.33E+05	
44	-0.65	TANC1	66	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 isoform 2	GVSMSLPS*SPLLPR	Q9C0D5	202	1	2.57E+05	
45	-0.36	ZO1; ZO1 iso2	899; 899	tight junction protein 1 isoform a	SSEPVREDSGGMHHENQTYPPYS*PQAQPQPIH	Q07157; Q07157-2	195; 187	3	1.34E+05	
46	5.58	tensin 3	844, 850	tensin 3	ESM#CST*PAFPVS*PETPYVK	Q68CZ2	155	1	8.43E+05	
47	4.75	tensin 3	850	tensin 3	ESM#CSTPAFPVS*PETPYVK	Q68CZ2	155	3	3.98E+06	
48		Adhesion or extracellular matrix protein								
49	-0.39	MAP7	209	microtubule-associated protein 7	LSSSSATLLNS*PDRAR	Q14244	84	2	2.46E+06	
50	-0.68	MAP7	365	microtubule-associated protein 7	AAPQVRPPS*PGNIRPVK	Q14244	84	11	1.77E+07	
51	-0.88	MICAL2	649, 658, 660	MICAL-like 2 isoform 1	TPRPAS*PGPSPARP*PS*PPR	Q8IY33	98	2	9.15E+05	

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

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Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
52	-0.35	afadin; afadin iso3	1155, 1165; 1155, 1165	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2	ADHRS*SPNVANQPSP*PGGK	P55196-1; P55196-3	206; 198	1	5.97E+05
53	-0.31	afadin; afadin iso3	1156, 1165; 1156, 1165	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 isoform 2	ADHRSS*PNVANQPSP*PGGK	P55196-1; P55196-3	206; 198	4	9.81E+04
54	-0.08	PCDH7; PCDH7 iso3	1011; 964	protocadherin 7 isoform a precursor	SSSPLPTVQLHPQS*PTAGK	O60245; O60245-3	116; 130	1	7.04E+04
55	1.31	PCDH7; PCDH7 iso3	989; 942	protocadherin 7 isoform a precursor	SVNGGPGS*PDLAR	O60245; O60245-3	116; 130	1	3.01E+06
56	2.12	plakophilin 4; plakophilin 4 iso2	273, 281; 273, 281	plakophilin 4 isoform b	AAS*PYSQRPAS*PTAIR	Q99569; Q99569-2	134; 130	3	3.71E+06
57	1.55	plakophilin 4; plakophilin 4 iso2	275, 281; 275, 281	plakophilin 4 isoform b	AASPY*SQRPAS*PTAIR	Q99569; Q99569-2	134; 130	1	1.71E+06
58	-0.44	plakophilin 4; plakophilin 4 iso2	281; 281	plakophilin 4 isoform b	AASPYSQRPAS*PTAI	Q99569; Q99569-2	134; 130	1	2.76E+06
59	-0.81	liprin alpha 1	708	PTPRF interacting protein alpha 1 isoform b	IPHS*PAR	Q13136	136	1	2.05E+06
60	-0.41	ROBO1	1441	roundabout 1 isoform c	HFHASQCPRPT*SPVSTDSNMSAAVM#QK	Q9Y6N7	181	4	1.67E+05
61	-0.11	ROBO1	1442	roundabout 1 isoform c	HFHASQCPRPTS*PVSTDSNMSAAVMQK	Q9Y6N7	181	3	1.87E+05
62	-0.71	STIM2	523	stromal interaction molecule 2	SIVPSS*PQPQR	Q9P246	84	1	1.58E+06
63 Apoptosis									
64	2.45	BAG3	377, 386	BCL2-associated athanogene 3	VPPAPVPCPPPS*PGSAVPS*PK	Q95817	62	3	2.29E+07
65	-0.13	PDCD4	93	programmed cell death 4 isoform 1	SGLIVPT*SPKGR	Q53EL6	52	2	2.50E+06
66	-0.15	PDCD4	94	programmed cell death 4 isoform 1	SGLTVPTS*PKGR	Q53EL6	52	3	2.83E+06
67 Cell cycle regulation									
68	3.92	ASPM	425	asp (abnormal spindle)-like, microcephaly associated	VPLSNENSVQVQPS*PEDWRK	Q8IZT6	410	3	1.76E+06
69	2.18	CASC5; CASC5 iso6	32; 32	cancer susceptibility candidate 5 isoform 2	HSSILKPPRS*PLQDLR	Q8NG31; Q05C46	265; 48	12	8.16E+06
70	1.01	SPECC1L	868	cytospin A	TPLS*PSPMK	Q69YQ0	125	3	1.43E+06
71	-0.96	DNCL1	207	dynein, cytoplasmic 1, light intermediate chain 1	DFQEVVEPGEDFPAS*PQRR	Q9Y6G9	57	7	4.39E+07
72	-0.20	DNCL1	516	dynein, cytoplasmic 1, light intermediate chain 1	KPVTVSPTTPTS*PTIEGAS	Q9Y6G9	57	2	1.89E+06
73	-0.57	DNCL1	518	dynein, cytoplasmic 1, light intermediate chain 1	KPVTVSPTTPTS*PTIEGAS	Q9Y6G9	57	1	9.69E+05
74	2.02	B99	243	G-2 and S-phase expressed 1	KEIPAS*PSR	Q9NYZ3	77	1	9.92E+05
75	10.96	INCENP	263, 269, 275	inner centromere protein antigens 135/155kDa isoform 1	IAQVS*PGPRDS*PAFPDS*PWRER	Q9NQS7	106	6	2.01E+07
76	-0.86	INCENP	275	inner centromere protein antigens 135/155kDa isoform 1	DSPAFPDS*PWRER	Q9NQS7	106	2	1.08E+06
77	1.55	INCENP	306, 314	inner centromere protein antigens 135/155kDa isoform 1	TDSQSVRHS*PIAPSPS*PQVLAQK	Q9NQS7	106	1	6.50E+05
78	-0.56	INCENP	481	inner centromere protein antigens 135/155kDa isoform 1	SKTPSS*PCPASK	Q9NQS7	106	2	6.79E+05
79	-0.74	MDC1	793	mediator of DNA damage checkpoint 1	AIPGDQHPES*PVHTEPMGIQGR	Q14676	227	6	5.37E+06
80	-0.68	Ki-67	308	antigen identified by monoclonal antibody Ki-67 isoform 2	SGGSGHVAEPAS*PEQLDQNKKG	P46013	359	3	3.15E+05
81	6.74	CNAP1	13	non-SMC condensin I complex, subunit D2	APQM#YEFHPLS*PEELLK	Q15021	157	5	2.25E+06
82	2.37	NuMA-1	76	nuclear mitotic apparatus protein 1	KHPS*SPECLVSAQK	Q14980	238	1	1.84E+06
83	4.56	NuMA-1	77	nuclear mitotic apparatus protein 1	KHPSS*PECLVSAQK	Q14980	238	4	4.31E+05
84	1.24	PCM-1	1103, 1109	pericentriolar material 1	GSSAS*HPPSPS*LFCPF	Q15154	229	1	3.67E+05
85	3.14	PCM-1	1107	pericentriolar material 1	GSSASHPPS*PSLFCPF	Q15154	229	1	5.38E+05
86	3.35	TPX2	186	TPX2, microtubule-associated protein homolog	NASS*PEKAK	Q9ULW0	86	1	8.57E+04
87	4.90	TPX2	486	TPX2, microtubule-associated protein homolog	VLPIVPKS*PAFALK	Q9ULW0	86	9	5.73E+07
88	8.57	TPX2	738	TPX2, microtubule-associated protein homolog	SSDQPLTVPS*PK	Q9ULW0	86	2	3.32E+06
89	8.11	NIPA	161	zinc finger, C3HC type 1	FCFWPDS*PSPDR	Q86WBO	55	1	7.89E+05
90	1.29	NIPA	321	zinc finger, C3HC type 1	LPLVPS*PRR	Q86WBO	55	1	1.56E+06
91	-0.80	NIPA	395	zinc finger, C3HC type 1	SM#GTGDTGGLVPS*PLRK	Q86WBO	55	1	3.71E+05
92 Cell development/differentiation									
93	-0.28	BRD1; BRD1 iso2	18; 18	bromodomain containing protein 1	HPSS*PCSVK	Q95696; Q86X06	120; 133	1	2.89E+05
94 Chaperone									
95	7.15	CRYAB	19	crystallin, alpha B	RPFPPHLS*PSR	P02511	20	1	5.92E+05
96 Chromatin, DNA-binding, DNA repair or DNA replication protein									
97	-0.70	SLX4	1315, 1329	BTB (POZ) domain containing 12	FSVIRPQT*PPQTPSSCLTPVS*PGTSDGRR	Q8IY92	200	1	3.49E+05
98	3.93	CAF-1A iso4	770, 775, 783	chromatin assembly factor 1, subunit A (p150)	GLLSNHT*GSPRS*PSTTYLHT*PTPSEDAIIPSK	Q6NXG5	107	1	8.32E+05
99	-0.39	CAF-1A iso4	775	chromatin assembly factor 1, subunit A (p150)	GLLSNHTGSPRS*PSTTYLHTPTPSEDAIIPSK	Q6NXG5	107	2	4.22E+05
100	-0.76	CHD-4	515	chromodomain helicase DNA binding protein 4	WGQPPS*PTPVPRPPDADPNTSPKPLEGRPER	Q14839	218	4	1.02E+06
101	1.24	CHD-4	515, 529, 531	chromodomain helicase DNA binding protein 4	WGQPPS*PTPVPRPPDADPNT*PS*PKPLEGRPER	Q14839	218	2	1.13E+06
102	-0.63	CHD-4	517	chromodomain helicase DNA binding protein 4	WGQPPSPT*PVPVRPPDADPNTSPK	Q14839	218	3	8.14E+05

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103	-0.41	CHD-4	517, 529	chromodomain helicase DNA binding protein 4	WGQPPSPT*PVPRPPDADPNT*PSPKLEGRPER	Q14839	218	1	1.46E+06
104	-0.32	CHD-4	517, 531	chromodomain helicase DNA binding protein 4	WGQPPSPT*PVPRPPDADPNT*PSPKLEGRPER	Q14839	218	2	3.39E+05
105	1.54	dUTPase iso2	11	deoxyuridine triphosphatase isoform 1 precursor	PCSEETPAIS*PSKR	P33316-2	18	4	1.63E+06
106	1.28	H1E	187	histone cluster 1, H1e	KAPKS*PAK	P10412	22	2	1.98E+07
107	-0.75	HIVEP1	537	human immunodeficiency virus type I enhancer binding protein 1	SSFTPSS*PENVIGDFLLQDR	P15822	297	2	1.71E+06
108	10.86	HMGA1	36	high mobility group AT-hook 1 isoform b	KQPPVS*PGTALVGSQK	P17096	12	7	5.92E+06
109	14.25	HMGA1	36, 53	high mobility group AT-hook 1 isoform b	KQPPVS*PGTALVGSQKPESEVPT*PK	P17096	12	14	7.70E+06
110	1.71	MSH6	14	mutS homolog 6	QSTLYSFFPKS*PALSDANK	P52701	153	4	1.38E+07
111	-0.26	APRN	1202	PDS5, regulator of cohesion maintenance, homolog B	METVSNASSSNPSS*PGRK	Q9NTI5	168	3	1.33E+06
112	-0.86	POLH	687	DNA-directed DNA polymerase eta	NPKS*PLACTNK	Q9Y253	78	1	2.25E+05
113	-0.16	Pur-beta	101	purine-rich element binding protein B	DSLGDFFIEHYAQLGSPSS*PEQLAAGAEAGGGPR	Q96QR8	33	2	4.18E+05
114	-0.43	RAD18	99	postreplication repair protein hRAD18p	NHLLQFALES*PAKSPASSSSK	Q9NS91	56	1	6.98E+04
115	4.36	RAD51C	20	RAD51 homolog C isoform 2	DLVSFPLS*PAVR	Q43502	42	2	2.58E+06
116	1.34	MNAB	808	ring finger and CCH-type zinc finger domains 2 isoform 1	APLVSSTLPVATQSPTPPS*PLFSVDFR	Q9HB01	132	2	1.12E+06
117	-0.30	SP110	244	SP110 nuclear body protein isoform a	DKEDPQEMPHS*PLGSMPEIR	Q9HB58	78	1	6.70E+04
118	-0.36	TDP1	61	tyrosyl-DNA phosphodiesterase 1	KIS*PVKFSNTDSVLPK	Q9NUW8	68	15	4.00E+06
119	-0.84	TEP1	397	telomerase-associated protein 1	RPPRS*PGMEPPFSH	Q99973	290	1	3.67E+05
120	1.20	TRF2	323	telomeric repeat binding factor 2	DLVLPQALPAS*PALK	Q15554	56	3	1.69E+07
121	2.34	TERF2IP	203	telomeric repeat binding factor 2, interacting protein	YLLGDAPVS*PSSQK	Q9NY80	44	2	9.11E+06
122	-0.89	Tsc2d4	264	TSC22 domain family, member 4	M#ELGAPPEM#GQVPLDLSRSPS*PALYFTHDASLVHK	Q9Y308	41	1	1.41E+05
123	10.36	WHSC1L1	1415	WHSC1L1 protein isoform short	LCCSEHDM#APVS*PEYWSK	Q9BZ95	162	1	1.72E+06
124	-0.33	XRCC1	446	X-ray repair cross complementing protein 1	TKPTQAAGPS*SPQKPPTPEETK	P18887	70	2	7.88E+04
125	-0.63	XRCC1	447, 457	X-ray repair cross complementing protein 1	TKPTQAAGPS*PQKPPTEET*K	P18887	70	1	3.35E+05
126	-0.35	ZBED4	624	zinc finger, BED-type containing 4	TEVSETARPPS*PDTR	Q75132	130	2	5.47E+05
127	-0.66	UKp68; UKp68 iso4	620; 455	zinc finger CCH-type containing 14 isoform 5	NGDECAYHHPIPS*PCK	Q6PJ77; Q6PJ77-4	83; 65	7	5.14E+06
128	Cytoskeletal protein								
129	1.33	ACTR8	132	actin-related protein 8	RIPVS*PEQAR	Q9H981	70	4	4.70E+06
130	-0.95	anillin	323	anillin, actin binding protein	TPIS*PLKTGVSKPIVK	Q9NQW6	124	10	2.93E+07
131	1.07	anillin	65	anillin, actin binding protein	SCTKPS*PSKK	Q9NQW6	124	1	2.83E+04
132	4.05	CCDC6	52	coiled-coil domain containing 6	SGGIVS*PFRLEELNTR	Q16204	66	2	1.01E+07
133	1.09	CDK5RAP2	1350	CDK5 regulatory subunit associated protein 2 isoform b	IEEDNLYQHLLPES*PEPSASHALSDYETSEK	Q96SN8	215	1	1.19E+06
134	-0.32	cordón-bleu	260, 271	cordón-bleu homolog	SNS*KGCLTTPNSPS*MHSR	Q75128	136	1	4.69E+05
135	-0.84	cordón-bleu	269	cordón-bleu homolog	GCCLTTPNS*PSMHS	Q75128	136	6	6.50E+06
136	2.78	cordón-bleu	271	cordón-bleu homolog	GCCLTTPNSPS*MHSR	Q75128	136	1	1.27E+06
137	-0.40	cortactin; cortactin iso2	401, 405, 417; 364, 368, 380	cortactin isoform a	AKTQT*PPVS*PAQPTEERLPS*SPVYEDAASF	Q14247; Q96H99	62; 57	1	1.32E+06
138	4.33	cortactin; cortactin iso2	418; 381	cortactin isoform a	LPSS*PVVEDAASF	Q14247; Q96H99	62; 57	2	8.23E+06
139	6.29	EPB41L5; EPB41L5 iso2	418, 436; 418, 436	erythrocyte membrane protein band 4.1 like 5	SALPVS*PSISSAPVVEIENLPQS*PGTDQHDRK	Q9HCM4; Q9HCM4-2	82; 58	1	5.48E+05
140	-0.85	EXOC7	250	exocyst complex component 7 isoform 1	SSSSGVPPYS*PAIPNK	Q9UPT5	83	2	3.45E+06
141	3.83	FLNB	1604	filamin B, beta (actin binding protein 278)	YM#IGVYGGDDIPLSPY*R	Q75369	278	1	5.92E+05
142	26.70	FLNB	730	filamin B, beta (actin binding protein 278)	HTIAVWGGVNIHPS*PYR	Q75369	278	5	3.76E+06
143	54.98	FLNB	983	filamin B, beta (actin binding protein 278)	LDVTILS*PSRK	Q75369	278	2	5.70E+06
144	-0.19	GAS2L1	297, 306	growth arrest-specific 2 like 1 isoform a	VCTFSPQRVS*PTTSPRPAS*PVPGSE	Q99501	73	1	1.46E+05
145	-0.20	GAS2L1	394	growth arrest-specific 2 like 1 isoform a	LTGTGPAS*PR	Q99501	73	1	5.25E+05
146	1.06	eplin	362	LIM domain and actin binding 1 isoform a	SEVQVHPKPLS*PDSR	Q9UHB6	85	6	5.12E+07
147	1.35	eplin	490	LIM domain and actin binding 1 isoform a	ETPHS*PGVEDAPIAK	Q9UHB6	85	5	9.17E+07
148	1.27	lamin A/C; lamin A/C iso2	12, 22; 12, 22	lamin A/C isoform 2	S*GAQASSTPLS*PTR	P02545; P02545-2	74; 65	1	4.20E+05
149	2.32	lamin A/C; lamin A/C iso2	22; 22	lamin A/C isoform 2	SGAQASSTPLS*PTR	P02545; P02545-2	74; 65	4	2.17E+08
150	1.82	Lamin B1	23	lamin B1	AGGPTPLS*PTR	P20700	66	3	5.22E+07
151	2.44	Lamin B2	17	lamin B2	AGGPTPLS*PTR	Q03252	68	1	1.47E+07
152	-0.69	MAP4	358, 384	microtubule-associated protein 4 isoform 4	ETERAS*PIKMDLAPSK	P27816	121	3	2.06E+06
153	-0.10	RPRC1	468, 472, 496	MAP7 domain containing 1	ARPS*SPST*SWHRPASPCSPGPGHTLPPKPPS*PR	Q3KQU3	93	1	8.88E+04
154	-0.16	RPRC1	468, 473, 496	MAP7 domain containing 1	ARPS*SPSTS*WHRPASPCSPGPGHTLPPKPPS*PR	Q3KQU3	93	1	1.26E+05
155	-0.29	RPRC1	469, 496	MAP7 domain containing 1	ARPS*PSTSWHRPASPCSPGPGHTLPPKPPS*PR	Q3KQU3	93	2	8.85E+04

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
156	6.54	RPRC1	473, 479, 483, 496	MAP7 domain containing 1	ARPSSPSTS*WHRPAS*PCPS*PGPGHTLPPKPPS*PR	Q3KQU3	93	1	3.62E+05
157	-0.29	nestin; nestin iso2	471; 470	nestin	QEASTGQSPEDHASLAPPLS*PDHSLSLEAK	P48681; CAA46780	177; 177	2	4.67E+05
158	-0.92	PBXIP1	43	pre-B-cell leukemia homeobox interacting protein 1	ALQAPHS*PSKTDGK	Q96A06	81	1	3.96E+05
159	6.26	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	4386, 4390, 4396; 4276, 4280, 4286; 4235, 4239, 4245; 4253, 4257, 4263; 4249, 4253, 4259	plectin 1 isoform 1	SSS*VGSS*SSYPIS*PAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	4.62E+05
160	1.57	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	4386, 4396; 4276, 4286; 4235, 4245; 4253, 4263; 4249, 4259	plectin 1 isoform 1	SSS*VGSSSSYPIS*PAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	2	5.56E+06
161	9.11	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	4396; 4286; 4245; 4263; 4259	plectin 1 isoform 1	SSSVGSSSSYPIS*PAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	6	2.82E+07
162	-0.44	SPIRE1; SPIRE1 iso2	387; 387	spire homolog 1 isoform a	KLRPVS*PEEIR	Q08AE8; Q08AE8-2	86; 84	1	1.81E+05
163	8.00	SPTBN1 iso2	14	spectrin, beta, non-erythrocytic 1 isoform 1	TSSISGPLS*PAYTGQVPPYNYNQLLEGR	Q01082-3	251	1	8.60E+06
164	-0.34	SPTBN1; SPTBN1 iso2	2102; 2089	spectrin, beta, non-erythrocytic 1 isoform 1	RPPS*PEPSTK	Q01082; Q01082-3	275; 251	2	1.98E+07
165	1.72	STMN1	38	stathmin 1 isoform b	SKESVPEFPLS*PPKKK	P16949	17	51	7.32E+07
166	4.73	SYNE1 iso3	494	spectrin repeat containing, nuclear envelope 1 isoform 4	GAVGLSDVM#IPES*PEAYVK	Q8NF91-3	112	1	3.29E+05
167	-0.34	SYNPO iso2	840	synaptopodin isoform B	SPLPAGPSSCTSPRS*PLPAPPRPFLY	Q8N3V7-2	96	2	3.32E+05
168	29.86	SYNPO; SYNPO iso2	854; 610	synaptopodin isoform B	GALPPS*PALPRPS	Q8N3V7; Q8N3V7-2	99; 96	5	3.80E+07
169	1.18	TRIM3	427	tripartite motif-containing 3	ALRPGDLPPS*PDDVKKR	Q75382	81	7	1.20E+06
170	6.98	WIP	142, 154	WAS/WASL interacting protein family, member 1	STSAKFS*PPSGPGRFPVPS*PGHR	Q43516	51	3	1.27E+06
171 Endoplasmic reticulum or golgi									
172	2.59	SMPD4	130	sphingomyelin phosphodiesterase 4 isoform 1	ASIQECLPDS*PLYHNK	Q9NXE4	93	3	1.01E+07
173 Enzyme, misc.									
174	7.03	ACSL4	447	acyl-CoA synthetase long-chain family member 4 isoform 1	M#MLSGGAPLS*PQTH	Q60488	79	2	4.41E+05
175	3.67	ALDH3A1; ALDH3A1 iso2	446; 563	aldehyde dehydrogenase 3A1	YPPS*PAK	P30838; Q8N9T9	50; 62	11	4.22E+06
176	-0.41	ATAD2	342	ATPase family, AAA domain containing 2	LSSAGPRS*PYCK	Q6PL18	159	1	2.33E+06
177	2.71	BRIP1	1239	BRCA1 interacting protein C-terminal helicase 1	NFKPSPS*KNK	Q9BX63	141	1	2.19E+06
178	-0.74	MRGBP	195	MRG-binding protein	VLANSNPSS*PSAAK	Q9NV56	22	7	5.98E+06
179	1.88	CBR3	192	carbonyl reductase 3	EGWPNPS*PYGVSK	Q75828	31	1	2.93E+05
180	-0.59	DDHD1	11	DDHD domain containing 1	GSPRS*PEHNGR	Q8NEL9	100	1	6.82E+03
181	-0.93	DOT1L	1001, 1009	DOT1-like, histone H3 methyltransferase	NSLPAS*PAHQLSSS*PR	Q8TEK3	185	1	1.02E+06
182	-0.54	DOT1L	997, 1001, 1009	DOT1-like, histone H3 methyltransferase	NS*LPAS*PAHQLSSS*PR	Q8TEK3	185	1	1.53E+05
183	6.95	CRMP-4	586	dihydropyrimidinase-like 3	FIPCS*PFSDYVYK	Q6DEN2	74	1	2.10E+06
184	-0.56	EHMT2; EHMT2 iso2	119; 119	euchromatic histone-lysine N-methyltransferase 2 isoform a	SFPSS*PSKGGSCPS	Q96KQ7; Q96KQ7-2	132; 129	1	3.63E+05
185	-0.32	FASN; FASN iso2	974; 1011	fatty acid synthase	LFDPHPS*PTPNTEPLFLAQAEVYK	P49327; Q4LE83	273; 277	2	9.24E+05
186	2.98	HAT1	361	histone acetyltransferase 1 isoform b	LIS*PYK	Q14929	50	1	3.39E+05
187	3.50	HDAC7	109	histone deacetylase 7 isoform a	TVHPNS*PGIPIYR	Q8WUJ4	103	1	1.73E+06
188	1.83	JARID1C	897	jumonji, AT rich interactive domain 1C isoform 2	EALASLPS*PGLLQSLER	P41229	176	2	6.99E+05
189	-0.79	KIAA0819	546	microtubule associated monooxygenase, calponin and LIM domain containing 3 isoform 3	LGLPKPEGEPLSLTPRS*PSDR	Q94909	127	2	7.83E+05
190	7.60	MOCS2	20	molybdopterin synthase large subunit MOCS2B	LPLS*PPLVEDSAFEPSRK	Q96007	21	2	2.41E+06
191	-0.68	NSUN2	743	NOL1/NOP2/Sun domain family, member 2	AGEPNS*PDAEANS*PDVTAGCDPAGVHPPR	A8K529	86	9	4.77E+06
192	2.34	NSUN2	743, 751	NOL1/NOP2/Sun domain family, member 2	AGEPNS*PDAEANS*PDVTAGCDPAGVHPPR	A8K529	86	6	1.69E+07
193	-0.95	PCYT1A	339, 347	choline phosphate cytidylyltransferase 1 alpha	WPFS*GKTSPPCS*PANLSR	P49585	42	1	3.62E+05
194	2.06	PYCR2	304	pyrroline-5-carboxylate reductase family, member 2	VKLESPTVSTLPPS*PGKLLT	Q96C36	34	3	3.49E+06
195	3.72	senataxin	1663	senataxin	NCSNVLHPQS*PNNNSR	Q72333	303	2	1.93E+06
196	-0.24	SDS3	234	suppressor of defective silencing 3	RPAS*PSSPEHLPATPAESPAQR	Q9H7L9	38	4	7.87E+05
197	5.16	SDS3	234, 236, 248	suppressor of defective silencing 3	RPAS*PS*SPEHLPATPAES*PAQR	Q9H7L9	38	1	3.03E+05
198	-0.55	SDS3	234, 237	suppressor of defective silencing 3	RPAS*PSS*PEHLPATPAESPAQR	Q9H7L9	38	1	1.04E+06
199	2.91	SUV39H1	391	suppressor of variegation 3-9 homolog 1	M#DSNFGLAGLPGS*PK	Q43463	48	2	1.03E+06
200	10.15	TMEM55B	162	transmembrane protein 55B isoform 1	IINLGPVHPGLS*PEPQPM*GVR	Q86T03	29	2	8.98E+05
201	-0.71	ZDHHC18	19	zinc finger, DHHC-type containing 18	MKDCYQQISGAAFLPAS*PGAR	Q9NUE0	42	2	2.00E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
202		G protein or regulator							
203	-0.45	ARHGAP23	1393	Rho GTPase activating protein 23	RPLS*PETR	Q9P227	162	1	1.35E+06
204	5.47	ARPP-19; hCG_18385	23; 23	cyclic AMP phosphoprotein, 19 kD	VTS*PEKAEAAK	P56211; NP_001094866	12; 12	1	1.78E+06
205	1.33	DAB2IP; DAB2IP iso6	995; 802	disabled homolog 2 interacting protein isoform 1	QGPSFVSP*PNALDR	Q5VWQ8; AAM00371	132; 107	1	1.23E+06
206	-0.73	DRP1	616	dynamitin 1-like isoform 3	SKPIPIIM#PAS*PQKHAVNLLDVPVPVA	000429	82	41	1.36E+07
207	2.63	DOCK7; DOCK7 iso2; DOCK7 iso3	896, 909; 896, 909; 896, 909	dedicator of cytokinesis 7	S*LNSNSNDISDGTPT*SPDDEV	Q96N67; Q96N67-2; Q96N67-3	243; 241; 239	1	2.95E+05
208	-0.97	GIT1; GIT1 iso3	570; 583	G protein-coupled receptor kinase interactor 1 isoform 1	GVSASAVPFTPS*SPLLSCSQEGSR	Q9Y2X7; Q59FC3	84; 86	1	8.74E+05
209	1.61	GIT1; GIT1 iso3	570, 577; 583, 590	G protein-coupled receptor kinase interactor 1 isoform 1	KGVSASAVPFTPS*SPLLSCS*QEGSR	Q9Y2X7; Q59FC3	84; 86	1	1.61E+05
210	1.72	PLEKHG3	1028, 1037, 1040	pleckstrin homology domain containing, family G, member 3	TTS*PGGRPSARS*PLS*PTFTFSWPDVR	A1L390	134	1	2.17E+06
211	2.15	Rab3IL1	168	RAB3A interacting protein (rabin3)-like 1	TLVITSTPAS*PNR	Q8TBN0	43	1	1.23E+06
212	4.02	Rab3IL1	168, 179	RAB3A interacting protein (rabin3)-like 1	TLVITSTPAS*PNRELHPQLLS*PTK	Q8TBN0	43	2	7.11E+05
213	-0.38	RanBP10	365	RAN binding protein 10	SQDSYPGS*PSLSR	Q6VN20	67	1	4.52E+05
214	-0.39	RanBP10	365, 369	RAN binding protein 10	SQDSYPGS*PSLS*PR	Q6VN20	67	2	8.72E+05
215	-0.46	RGS12	850	regulator of G-protein signalling 12 isoform 2	ALPDSQQVPS*PASK	Q14924	156	1	3.02E+05
216	14.23	SIPA1L1	1078, 1087	signal-induced proliferation-associated 1 like 1	GPHS*PQVPSQVGS*PMTSR	Q43166	200	1	1.27E+06
217	-0.85	SIPA1L1	161	signal-induced proliferation-associated 1 like 1	FLM#PEAYPS*SPR	Q43166	200	2	9.20E+05
218	-0.87	SIPA1L1	162	signal-induced proliferation-associated 1 like 1	FLMPEAYPS*PR	Q43166	200	3	3.30E+06
219	1.07	SRGAP2; SRGAP2 iso2	206; 206	SLIT-ROBO Rho GTPase activating protein 2 isoform b	QTPRS*PDSTANVR	Q75044; A2RUF3	121; 121	2	2.07E+06
220	3.19	USP6NL	585	USP6 N-terminal like isoform 2	HALYPPS*PR	Q92738	94	4	1.99E+06
222		Kinase (non-protein)							
223	-0.26	PPAT	178	coenzyme A synthase isoform a	TIRPAS*PVAGSPK	Q13057	62	1	8.48E+04
224		Lipid binding protein							
225	-0.95	PLEKHA5	140	pleckstrin homology domain containing, family A member 5 isoform 2	NEASNYNVTSDYAVHPMS*PVGR	Q9HAU0	127	3	1.38E+05
226	4.71	PLEKHA5	543, 557	pleckstrin homology domain containing, family A member 5 isoform 2	TMF#NISDQTM#HSIPT*SPSHGSAAYQGYSPQR	Q9HAU0	127	1	1.92E+06
227	4.34	PLEKHA5	544, 557	pleckstrin homology domain containing, family A member 5 isoform 2	TMF#NISDQTM#HSIPT*PSHGSAAAYQGYSPQR	Q9HAU0	127	1	6.15E+05
228	6.28	PLEKHA5	549, 557	pleckstrin homology domain containing, family A member 5 isoform 2	SIPTSPSHGS*IAAYQGYSPQR	Q9HAU0	127	1	1.11E+06
229		Mitochondrial protein							
230	2.82	NDUFB9	85	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	QHPQYIFPDS*PGGTSYER	Q9Y6M9	22	1	5.60E+05
231		Motor or contractile protein							
232	15.28	KIF18B	825	kinesin family member 18B	RPAGPLVLEPLLS*PLCPSNR	Q86Y91	93	1	1.16E+06
233		Phosphatase							
234	9.82	DULLARD	49	dullard homolog	YDILLPLS*PVSR	Q95476	28	1	3.21E+06
235	1.30	MTMR6	561	myotubularin related protein 6	ELLHSHVPES*PNLK	Q9Y217	72	4	9.82E+06
236	3.74	SEC16A	29	SEC16 homolog A	SFVWASS*PYR	Q15027	252	2	1.81E+06
237		Protease							
238	-0.10	BAP1	521	BRCA1 associated protein-1	SANPTRPSS*PVTS*HISK	Q92560	80	2	1.10E+05
239	-0.75	SEN3	232	SUMO1/sentrin/SMT3 specific protease 3	WTPKS*PLDPSGILLSCTLPNGFGGQSGPEGER	Q9H4L4	65	1	1.23E+06
240	-0.68	SEN3	221	SUMO1/sentrin specific peptidase 6 isoform 2	HCSTYQPTPLLS*PASKK	Q9GZR1	126	1	1.30E+06
241	-0.58	USP31	1323	ubiquitin specific peptidase 31	SSQLDSGVPSS*PGGR	Q70CQ4	147	1	3.38E+05
242	1.16	USP35	980	ubiquitin specific protease 35	AAYISALPT*SPHWGR	Q9P2H5	113	2	5.62E+05
243		Protein kinase, Ser/Thr (non-receptor)							
244	-0.37	CAMKK2; CAMKK2 iso3	129, 133, 136; 129, 133, 136	calcium/calmodulin-dependent protein kinase kinase 2 beta isoform 1	CICPSLPYS*PVSS*POS*SPRLPR	Q96RR4; Q96RR4-3	65; 60	1	4.74E+05
245	-0.69	CHED; CHED iso2	358, 362; 358, 362	cell division cycle 2-like 5 isoform 1	RLPRS*PSPY*SR	Q14004; Q14004-2	165; 158	3	1.09E+06
246	-0.89	MRCCKb	1690	CDC42-binding protein kinase beta	HSTPSNSNIPSGPPS*PNSPHR	Q9Y552	194	1	1.25E+05
247	-0.93	PKR	542	eukaryotic translation initiation factor 2-alpha kinase 2 isoform a	TLTVWKKK*PEKNER	P19525	62	1	6.74E+05
248	-0.66	HIPK1; HIPK1 iso4	1200; 806	homeodomain-interacting protein kinase 1 isoform 2	GSTIYTYGLPS*PTK	Q86Z02; Q86Z02-4	131; 87	1	5.90E+05
249	1.29	MARK2; MARK2 iso3; MARK2 iso4; MARK2 iso13	456; 422; 456, 422	MAP/microtubule affinity-regulating kinase 2 isoform c	VPAS*PLPGLER	Q7KZ17; NP_059672; Q7KZ17-4; A9CP04	88; 83; 81; 78	1	1.25E+06
250	1.78	MARK2; MARK2 iso3; MARK2 iso4; MARK2 iso13	619; 585; 565; 539	MAP/microtubule affinity-regulating kinase 2 isoform c	DQQLNPLYGVTAS*PSGHSQGR	Q7KZ17; NP_059672; Q7KZ17-4; A9CP04	88; 83; 81; 78	1	4.03E+06
251	17.22	MLKL	125	mixed lineage kinase domain-like isoform 2	MPVS*PISQASWAQEDQQDAEDRR	Q8NB16	54	5	2.62E+06
252	-0.95	Nuak1	444, 455	AMPK-related protein kinase 5	TGVLPLS*SPEAEVPGKLS*PK	Q60285	74	1	3.30E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
253	-0.10	PRP4	328	serine/threonine-protein kinase PRP4K	KPKIS*PSKDASSGK	Q13523	117	5	2.69E+05
254	-0.31	p70S6K; p70S6K iso2	441, 444, 447; 418, 421, 424	ribosomal protein S6 kinase, 70kDa, polypeptide 1	FIGS*PRT*PVS*PVKFS*PGDFWGR	P23443; P23443-2	59; 56	1	1.09E+05
255	7.41	p70S6K; p70S6K iso2	441, 444, 447; 452; 418, 421, 424, 429	ribosomal protein S6 kinase, 70kDa, polypeptide 1	FIGS*PRT*PVS*PVKFS*PGDFWGR	P23443; P23443-2	59; 56	3	5.80E+05
256	-0.61	p70S6K; p70S6K iso2	447; 424	ribosomal protein S6 kinase, 70kDa, polypeptide 1	TPVS*PVKFS*PGDFWGR	P23443; P23443-2	59; 56	5	1.48E+07
257	-0.91	p70S6K; p70S6K iso2	447, 452; 424, 429	ribosomal protein S6 kinase, 70kDa, polypeptide 1	TPVS*PVKFS*PGDFWGR	P23443; P23443-2	59; 56	4	1.80E+06
258	2.33	Sgk269	897	NKF3 kinase family member	HFTNWTIKPT*SPTR	Q9H792	193	1	3.90E+05
259	-0.96	SIK	435	SNF1-like kinase	PVS*PSSLLDTAIEEER	P57059	85	3	1.18E+06
260	1.55	SNRK	390	SNF related kinase	IDVQDLEDDLATPLSHATVPQS*PAR	Q9NRH2	84	2	5.56E+05
261	-0.19	TLK1; TLK1 iso1	209; 188	tousled-like kinase 1 isoform 2	SPQNSHSHSTPSSVRPNS*PSPALAFGDHPVQPK	Q9UKI8-2; Q9UKI8	89; 87	3	1.17E+05
262	5.19	Trio	2433, 2442	triple functional domain (PTPRF interacting)	GGSFWSIPAS*PASRPGSFT*FFGSDSLQROTPR	Q75962	342	1	7.45E+05
263	1.53	TRRAP	1628	transformation/transcription domain-associated protein	FITLLPGGAQTAVRPGS*PSTSTM#	Q9Y4A5	438	1	2.38E+06
264 Protein kinase, regulatory subunit									
265	-0.70	Kidins220	1555	kinase D-interacting substrate of 220 kDa	VPKS*PEHSAEPIR	Q9ULH0	197	5	2.84E+06
266	-0.54	PHKA2	1043	phosphorylase kinase, alpha 2 (liver)	SSTPS*SPTGTSSSDSGGHIGWGER	P46019	138	1	4.05E+05
267 RNA processing									
268	1.26	BAT2; BAT2 iso1	1206; 1219	HLA-B associated transcript-2	LIPGPLS*PVAR	P48634-2; P48634	228; 229	1	1.50E+07
269	2.91	hnRNP H1; hnRNP H2	104; 104	heterogeneous nuclear ribonucleoprotein H1	HTGPN*PDTANDGFVR	P31943; P55795	49; 49	15	2.78E+08
270	1.17	LARP; LARP iso3	774; 697	la related protein isoform 1	SLPTTVPS*PNYR	Q6PKG0; Q6PKG0-3	124; 116	2	8.79E+06
271	3.14	CSIG	392, 396, 401	ribosomal L1 domain containing 1	HATGKKS*PAKS*PNPST*PR	Q76021	55	5	2.21E+05
272	-0.72	SF3B1	129	splicing factor 3b, subunit 1 isoform 2	TM#IIS*PERLDPFADGGKTPDPK	Q75533	146	5	2.36E+06
273	1.37	SF3B1	129, 142	splicing factor 3b, subunit 1 isoform 2	TM#IIS*PERLDPFADGGK*PDPK	Q75533	146	4	1.48E+06
274	-0.93	SF2	199	splicing factor, arginine/serine-rich 1 isoform 2	VKVDGPRS*PSYGR	Q07955	28	2	4.92E+07
275	-0.44	SF2	199, 201	splicing factor, arginine/serine-rich 1 isoform 2	VKVDGPRS*PS*YGR	Q07955	28	1	3.35E+05
276	-0.25	SF2	199, 201, 205	splicing factor, arginine/serine-rich 1 isoform 2	VDGPRS*PS*YGRS*R	Q07955	28	1	7.38E+04
277	-0.37	SRp46	273, 281	splicing factor, arginine/serine-rich 2B	SKRPPKS*PEEGQMS*S	Q9BRL6	32	1	1.64E+05
278	-0.84	SFRS2IP	796, 802	splicing factor, arginine/serine-rich 2, interacting protein	FHS*PSTTWS*PNKDTPQEK	Q99590	165	6	1.81E+07
279	12.92	SFRS2IP	796, 802, 807	splicing factor, arginine/serine-rich 2, interacting protein	FHS*PSTTWS*PNKDT*PQEK	Q99590	165	3	5.43E+06
280	-0.36	SFRS2IP	799, 802	splicing factor, arginine/serine-rich 2, interacting protein	SRFHS*PSTTWS*PNKDTPQEK	Q99590	165	1	6.25E+05
281	-0.05	SFRS2IP	816	splicing factor, arginine/serine-rich 2, interacting protein	KRPQS*PSPR	Q99590	165	3	8.59E+04
282	-0.12	SFRS2IP	816, 818	splicing factor, arginine/serine-rich 2, interacting protein	KRPQS*PS*PR	Q99590	165	3	1.90E+04
283	2.06	SRm160; SRm160 iso3	389, 393; 384, 388	serine/arginine repetitive matrix 1	RLS*PSAS*PPR	Q8IYB3; A9Z1X7	102; 103	2	1.06E+06
284	-0.15	SRm160; SRm160 iso3	769, 775; 778, 784	serine/arginine repetitive matrix 1	KPPAPPS*PVQSQS*PSTNWS*PAVPVKK	Q8IYB3; A9Z1X7	102; 103	8	4.88E+05
285	1.17	SRm160; SRm160 iso3	769, 775, 781; 778, 784, 790	serine/arginine repetitive matrix 1	KPPAPPS*PVQSQS*PSTNWS*PAVPVKK	Q8IYB3; A9Z1X7	102; 103	7	6.38E+06
286	-0.20	SRm160; SRm160 iso3	769, 777; 778, 786	serine/arginine repetitive matrix 1	KPPAPPS*PVQSQS*PSTNWS*PAVPVKK	Q8IYB3; A9Z1X7	102; 103	2	9.20E+05
287	1.00	SRm160; SRm160 iso3	769, 777, 778; 778, 786, 787	serine/arginine repetitive matrix 1	KPPAPPS*PVQSQS*PSTNWS*PAVPVKK	Q8IYB3; A9Z1X7	102; 103	2	4.19E+06
288	-0.57	SRm300	2449	splicing coactivator subunit SRm300	M#GOAPSQSLLPADQDPRS*PVPSAFSDQSR	Q9UQ35	300	2	4.33E+05
289	-0.29	SRm300	316, 323	splicing coactivator subunit SRm300	RGGDAPFSEPGTT*STORPSS*PETATK	Q9UQ35	300	1	6.69E+04
290	-0.64	SRm300	322	splicing coactivator subunit SRm300	GEGDAPFSEPGTTSTORPS*SPETATK	Q9UQ35	300	4	1.94E+07
291	-0.08	SRm300	323	splicing coactivator subunit SRm300	RGGDAPFSEPGTTSTORPSS*PETATK	Q9UQ35	300	4	1.01E+06
292	-0.10	SRm300	351, 353	splicing coactivator subunit SRm300	SATRPS*PS*PERSTGPEPPAPTLLAER	Q9UQ35	300	1	7.02E+04
293	-0.46	SRm300	377, 398	splicing coactivator subunit SRm300	HGGS*PQPLATPLSQEPVNPVSEAS*PTR	Q9UQ35	300	2	5.05E+05
294	1.37	ZNF828	204, 214	zinc finger protein 828	LAPVPS*PEPQKAPVS*PESVK	Q96JM3	89	3	3.09E+07
295	-0.40	ZNF828	214	zinc finger protein 828	LAPVPSPEPQKAPVS*PESVK	Q96JM3	89	2	3.05E+06
296	8.12	ZNF828	308, 311, 319	zinc finger protein 828	RPAPAVS*PGS*WKP*GPPGS*PRPWK	Q96JM3	89	4	1.24E+06
297	-0.82	ZNF828	308, 319	zinc finger protein 828	RPAPAVS*PGSWK*GPPGS*PRPWK	Q96JM3	89	5	1.40E+07
298	-0.77	ZNF828	311, 319	zinc finger protein 828	RPAPAVSPGS*WKP*GPPGS*PRPWK	Q96JM3	89	4	7.29E+06
299	-0.19	ZNF828	319	zinc finger protein 828	RPAPAVSPGS*WKP*GPPGS*PRPWK	Q96JM3	89	3	5.15E+05
300	3.18	ZNF828	376, 382, 386	zinc finger protein 828	SSVS*PSSWKS*PPAS*PESWK	Q96JM3	89	3	2.30E+06
301	-0.38	ZNF828	382, 386	zinc finger protein 828	SSVS*PSSWKS*PPAS*PESWK	Q96JM3	89	1	2.63E+06
302	-0.63	ZNF828	386	zinc finger protein 828	SPPAS*PESWK	Q96JM3	89	1	1.56E+06

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
303	-0.42	ZNF828	427	zinc finger protein 828	KPGPPLS*PEIR	Q96JM3	89	4	4.15E+06
304	-0.24	ZNF828	427, 432	zinc finger protein 828	KPGPPLS*PEIRS*PAGSEPELR	Q96JM3	89	2	3.04E+05
305	1.78	ZNF828	427, 432, 436	zinc finger protein 828	KPGPPLS*PEIRS*PAGS*PELR	Q96JM3	89	4	2.29E+07
306	-0.54	ZNF828	87	zinc finger protein 828	HAS*PKWWDKPK	Q96JM3	89	2	8.75E+06
307	Receptor, channel, transporter or cell surface protein								
308	3.68	ataxin-2L	111	ataxin 2 related protein isoform A	GQSTGKGPQPS*PVFEGVYNNR	Q8WWM7	113	3	3.52E+05
309	-0.21	ataxin-2L	680, 684	ataxin 2 related protein isoform A	STS*TPTS*PGPR	Q8WWM7	113	1	8.11E+05
310	-0.48	ataxin-2L	684	ataxin 2 related protein isoform A	STSTPTS*PGPR	Q8WWM7	113	1	4.85E+07
311	-0.82	CELSR3	3175	cadherin EGF LAG seven-pass G-type receptor 3	DLDPQPPPLPS*PQR	Q9NYQ7	358	1	2.03E+05
312	2.16	CEPT1	18	choline/ethanolaminephosphotransferase	CGDHPES*PVGFGHMSTTGCVLNK	Q9Y6K0	47	5	6.69E+05
313	-0.78	FZD6	620	frizzled 6	LREQDCGEPAS*PAASISR	Q60353	79	1	7.14E+05
314	-0.09	KIAA0528	295	hypothetical protein LOC9847	NQTYSFPS*PSKSYS	Q86Y57	110	1	9.43E+04
315	5.45	KPNB1	12	karyopherin beta 1	TVS*PDRLELEAAQK	Q14974	97	3	1.59E+06
316	-0.63	NUP188	1709	nucleoporin 188kDa	GAPSS*PATGVLPSPQGK	Q5SRE5	196	2	7.53E+05
317	5.39	NUP188	1709, 1717	nucleoporin 188kDa	GAPSS*PATGVLPSP*PQGK	Q5SRE5	196	4	7.78E+06
318	7.02	NUP210	1848, 1852, 1860, 1863	nucleoporin 210	AS*PGHS*PHYFAASS*PTS*PNALPPAR	Q8TEM1	205	2	2.28E+06
319	-0.19	NUP214	666, 670, 678	nucleoporin 214kDa	SAQGS SSPVPSMVQKS*PRIT*PPAAKPGS*PQAK	P35658	214	2	1.00E+05
320	-0.20	NUP214	678	nucleoporin 214kDa	ITPPAAKPGS*PQAK	P35658	214	2	3.38E+05
321	3.82	NUP98; NUP98 iso4	839; 822	nucleoporin 98kD isoform 3	CLIKS*PDRLADINYEGR	P52948; NP_624358	188; 187	4	1.96E+07
322	1.37	PTDSS2	16	phosphatidylserine synthase 2	DAGGPRPES*PVPAGR	Q9BVG9	56	1	2.56E+05
323	-0.44	SLC26A6	752	solute carrier family 26, member 6 isoform 4	ALQHPRPVPS*PVSVTR	Q9BX59	83	6	6.25E+05
324	3.58	SLC46A1	458	proton-coupled folate transporter	ADPHLEFQQFQPS*P	Q96NT5	50	2	3.45E+06
325	1.83	SLC04A1	40	solute carrier organic anion transporter family member 4A1	ASPGTPLS*PGSLR	Q96BD0	77	1	7.09E+05
326	1.05	STIM1	575	stromal interaction molecule 1 precursor	LPDS*PALAK	Q13586	77	1	8.82E+05
327	Transcriptional regulator								
328	1.56	AF-4	199, 206, 212	myeloid/lymphoid or mixed-lineage leukemia trithorax homolog 2	ELS*PLISLPS*PVPPLS*PIHSNQQTLPR	P51825	131	1	9.31E+04
329	-0.78	ELYS; ELYS iso2	1214, 1218; 1252, 1256	transcription factor ELYS	STPLAS*PSPS*PGRSPQR	Q8WYP5; Q8WYP5-2	253; 256	1	1.25E+05
330	-0.53	AhRR	458	arylhydrocarbon receptor repressor	NSPIHPPS*PSPSAYSS	A9YTQ3	76	2	3.50E+05
331	-0.19	ARID1A	363	AT rich interactive domain 1A isoform a	SHHAFMS*PGSSGGGQPLA	Q14497	242	1	1.92E+05
332	-0.24	Bright	77	AT rich interactive domain 3A (BRIGHT- like) protein	AAAAGLGH PAS*PGGEDGPPGSEEDAAR	Q99856	63	1	6.47E+04
333	-0.23	Bright	77, 81, 88	AT rich interactive domain 3A (BRIGHT- like) protein	AAAAGLGH PAS*PGGS*EDGPPGS*EEEDAAR	Q99856	63	1	6.75E+04
334	-0.40	ATF-2	328	activating transcription factor 2	TQSESRPQSLQOPATSTTETPAS*PAHITTPQTQSTSGR	P15336	55	1	2.22E+05
335	-0.67	ATF7IP	673	activating transcription factor 7 interacting protein	HEHPNPVPS*PGKTVNDVNSNNMSY	Q6VMQ6	136	3	2.32E+05
336	-0.95	WSTF	374	bromodomain adjacent to zinc finger domain, 1B	MMS*PNKLHTNFHPK	Q9UIG0	171	3	9.24E+05
337	3.19	Bcl-3	448	B-cell CLL/lymphoma 3	GPGRPVPPS*PAPGGS	P20749	48	1	3.50E+05
338	-0.43	Bcl-9	689	B-cell CLL/lymphoma 9	IPVEGPLSPS*RGDFPK	Q00512	149	1	4.95E+05
339	-0.13	BCLAF1; BCLAF1 iso4; LOC731605; LOC731605 iso3	287, 300; 287, 300; 285, 298; 285, 298	BCL2-associated transcription factor 1 isoform 2	YSPS*QNSPIHHIPRRS*PAK	Q9NYF8; Q9NYF8-4; XP_001732863; XP_001129341	106; 86; 100; 80	1	7.98E+04
340	-0.02	BCLAF1; BCLAF1 iso4; LOC731605; LOC731605 iso3	759; 586; 757; 584	BCL2-associated transcription factor 1 isoform 2	SSSSASPS*SPSSREEKESK	Q9NYF8; Q9NYF8-4; XP_001732863; XP_001129341	106; 86; 100; 80	3	5.70E+04
341	-0.45	BCLAF1; BCLAF1 iso4; LOC731605; LOC731605 iso3	760; 587; 758; 585	BCL2-associated transcription factor 1 isoform 2	SSSSASPS*PSSR	Q9NYF8; Q9NYF8-4; XP_001732863; XP_001129341	106; 86; 100; 80	5	3.69E+05
342	-0.97	BCoR	336, 340	BCL-6 interacting corepressor isoform a	AVTSGLPDGTALLLPS*PRPS*PR	Q6W2J9	192	1	1.66E+05
343	-0.15	FALZ; FALZ iso2; FALZ iso3; FALZ iso4	77; 77; 216; 77	bromodomain PHD finger transcription factor isoform 2	VHRPRS*PILEEKDIPPLEFPK	Q12830; Q12830-2; NP_872579; Q12830-4	324; 311; 325; 308	5	1.40E+05
344	1.12	BRD8	284	bromodomain containing 8 isoform 1	KGSLPTS*PR	Q9H0E9-2	103	3	6.27E+06
345	-0.10	ELG	500	ELG protein isoform a	RPHS*PEKAFSSNPVW	Q53F19	71	1	2.94E+05
346	1.16	CDYL; CDYL iso2	201; 147	chromodomain protein, Y chromosome-like isoform d	ILVPS*PKV	Q9Y232; Q9Y232-2	66; 61	2	4.03E+06
347	-0.35	NOT2	165, 170	CCR4-NOT transcription complex, subunit 2	TNSMSSSLGS*PNRSS*PSICM#PK	Q9NZN8	60	3	2.21E+05
348	3.94	CBP	2079	CREB binding protein isoform b	SPSS*PQQQQVNLNLK	Q92793	265	1	7.77E+05
349	1.35	TORC2	433	CREB regulated transcription coactivator 2	RVPLS*PLSLLAGPADAR	Q53ET0	73	3	2.71E+06

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
350	-0.56	Daxx	671	death-domain associated protein isoform a	KICTLPSPPS*PLASLAPVADSSTR	Q9UER7	81	1	4.74E+05
351	2.63	Daxx	695, 702	death-domain associated protein isoform a	VDSPSHGLV*SSLCIPS*PAR	Q9UER7	81	1	1.93E+06
352	12.62	HDJ2	335	DnaJ (Hsp40) homolog, subfamily A, member 1	VNFPENGFLS*PKLALLEK	P31689	45	1	6.05E+06
353	-0.44	ERBP	381	deoxynucleotidyltransferase, terminal, interacting protein 2	WNNKKS*PIKASDLTK	O5QJF6	84	4	7.83E+05
354	-0.20	Eif-1	187	E74-like factor 1 (ets domain transcription factor) isoform b	KTKPPRPDS*PATTPNISVK	P32519	67	3	1.64E+05
355	1.38	ELK1	324	ELK1 protein	DLELPLS*PSLLGGGPER	P19419	45	1	1.22E+06
356	3.29	FLNA	2128	filamin A, alpha isoform 2	FADQHVPGS*PFSVK	P21333	281	2	2.33E+06
357	3.73	FLNA	859	filamin A, alpha isoform 2	GAGSYTIM#VLFADQATPT*SPIRVK	P21333	281	1	2.50E+06
358	6.66	FLNA	860	filamin A, alpha isoform 2	FADQATPTS*PIR	P21333	281	3	4.71E+06
359	3.15	Fra2	83	FOS-like antigen 2	SHPYS*PLPGLASVPGHM#ALPRPGVIK	P15408	35	7	1.74E+06
360	1.17	FOXK1	213, 223	forkhead box K1	IQFTSLYHKEEAPAS*PLRPLYQIS*PLK	P85037	75	5	1.14E+07
361	1.41	FOXK1	219, 223	forkhead box K1	IQFTSLYHKEEAPASPLRPLY*PQIS*PLK	P85037	75	1	1.44E+06
362	-0.36	FOXK1	223	forkhead box K1	IQFTSLYHKEEAPASPLRPLY*PQIS*PLK	P85037	75	1	1.41E+05
363	-0.26	FOXN3	85, 97	checkpoint suppressor 1 isoform 1	SVS*PVQDLDDDTPPS*PAHSDM#PYDAR	O00409	54	1	3.14E+04
364	-0.68	FOXO3A	294	forkhead box O3A	WPGS*PTSR	O43524	71	2	3.27E+06
365	-0.14	HABP4	108	hyaluronan binding protein 4	SLPAPVQRPDS*PGGGLQAPGQK	O5JVS0	46	7	1.21E+06
366	-0.67	ANKRD25	375	ankyrin repeat domain 25	ALAM#PGRPES*PPVF	O632Y3	91	4	1.53E+06
367	-0.72	Tip60; Tip60 iso2	90, 90	K(lysine) acetyltransferase 5 isoform 2	NGLPGRPGS*PER	Q92993; Q92993-2	59; 53	1	3.43E+05
368	-0.46	TIEG2	124	Kruppel-like factor 11	TPVS*POVTDK	O14901	55	1	2.12E+05
369	1.76	Trap170	1112, 1119	mediator complex subunit 14	AGNWPGS*PQVSGPS*PAAR	O60244	161	2	2.17E+06
370	-0.81	MGA; MGA iso1	449; 449	MAX gene associated	WLPSS*PSGVAK	Q9Y4E9; O8IWI9	341; 332	1	6.53E+06
371	-0.87	MGA; MGA iso1	924; 924	MAX gene associated	SILPYVVS*PK	Q9Y4E9; O8IWI9	341; 332	2	4.41E+06
372	-0.16	MLL	3511, 3518	myeloid/lymphoid or mixed-lineage leukemia protein	ALSSAVQASPTS*PGGSPSS*PSSGOR	Q03164	432	1	3.02E+05
373	1.28	MLL2; MLL2 iso2; MLL2 iso4	4547; 4242; 4822	myeloid/lymphoid or mixed-lineage leukemia 2	IPNSYEVLPES*PAR	O14686; O14686-2; NP_003473	564; 532; 593	2	2.67E+06
374	-0.47	Myc	62	myc proto-oncogene protein	KFELLPTPLS*PSRR	P01106	49	3	3.68E+06
375	-0.34	NCL	69	nucleolin	KVVVSP*KK	P19338	77	3	1.88E+06
376	6.52	NFAT5	452	nuclear factor of activated T-cells 5 isoform d	DGSTLTQTQPS*PICTQAPGVEILKK	O94916	168	1	4.80E+05
377	-0.12	NFAT2	261	nuclear factor of activated T-cells, cytosolic component 1 isoform B	SSRPAS*PCNK	O95644	101	1	2.37E+04
378	2.55	NFAT3; NFAT3 iso11	259, 264; 322, 327	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 isoform 1	GPEDSWLLSAPGPTPAS*PRPAS*PCGK	Q14934; Q14934-11	95; 91	1	1.43E+05
379	-0.18	NFAT3; NFAT3 iso11	264; 327	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 isoform 1	GPEDSWLLSAPGPTPAS*PRPAS*PCGK	Q14934; Q14934-11	95; 91	1	1.00E+05
380	3.68	NFkB-p105	893, 907	nuclear factor kappa-B, subunit 1	QM#GYTEAIEVIOAASS*PVKTTQSAHSLPLS*PASTR	P19838	105	1	1.12E+06
381	3.70	NFkB-p105	907	nuclear factor kappa-B, subunit 1	TTQSAHSLPLS*PASTR	P19838	105	1	1.16E+06
382	-0.39	PHF16	566	PHD finger protein 16	NSSTETDQQPHS*PDSSSSVHSI	Q92613	94	1	2.20E+05
383	-0.37	PIAS1	488	protein inhibitor of activated STAT, 1	TCPSLSPTS*PLNNK	O75925	72	1	1.28E+05
384	7.74	PPP1R13L	110, 113	protein phosphatase 1, regulatory subunit 13 like	SESAPTLHPYS*PLS*PK	Q8WUF5	89	2	3.48E+05
385	1.16	PPP1R13L	280	protein phosphatase 1, regulatory subunit 13 like	LDVFARPAS*PSLQLLPWR	Q8WUF5	89	7	2.93E+07
386	1.41	PPP1R13L	282	protein phosphatase 1, regulatory subunit 13 like	LDVFARPAS*PSLQLLPWR	Q8WUF5	89	4	2.88E+06
387	3.09	PPP1R13L	357	protein phosphatase 1, regulatory subunit 13 like	IPM#PPS*SPQPR	Q8WUF5	89	1	4.39E+06
388	1.82	PPP1R13L	358	protein phosphatase 1, regulatory subunit 13 like	IPMPPSS*PQPR	Q8WUF5	89	7	1.75E+07
389	2.52	PPP1R13L	395	protein phosphatase 1, regulatory subunit 13 like	AM#LPGS*PLFT	Q8WUF5	89	3	4.35E+06
390	4.48	FIR	112	poly-U binding splicing factor 60kDa isoform c	QTIHQQLTLNQM#AAVTM#GFGDPLS*PLQS M#AAQR	Q9UHX1	60	2	6.34E+05
391	10.01	RAI1	1352, 1358	retinoic acid induced 1	APGAS*PGNPLS*PSLSDKDR	Q725J4	203	1	1.22E+06
392	-0.29	RERE	594	atrophin-1 like protein isoform a	KKQPAS*PDGR	Q9P2R6	172	1	8.60E+03
393	-0.44	RERE	594, 600	atrophin-1 like protein isoform a	KKQPAS*PDGRS*PINEDIR	Q9P2R6	172	5	1.92E+06
394	-0.54	RLF	41	rearranged L-myc fusion	GHRPVS*PAPGASGLRPCLWQLETEL	Q13129	218	5	5.40E+05
395	-0.29	RLF	632	rearranged L-myc fusion	GICPKS*PSAIEQNHSLNDQAK	Q13129	218	1	2.58E+05
396	-0.29	HBXAP	1349, 1365	remodeling and spacing factor 1	VGS*PLDYSLVLDPLSTNGQS*PGKAIENLIGKPTK	Q96T23	163	2	3.05E+05
397	-0.79	SMARCA1	119	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a1 isoform a	SPTS*PLNMK	P28370	123	1	9.58E+05
398	2.79	SND1	426	staphylococcal nuclease domain containing 1	VNVTVDIYPAS*PATETVPAFSE	Q7KZF4	102	2	1.56E+06
399	-0.45	Skip	224, 232	SKI-interacting protein	GPPS*PPAPVMHS*PSRK	O13573	61	1	4.38E+05
400	-0.72	SOLH	335	small optic lobes	YTPAS*PSSPDFTTWSCAK	O75808	117	1	2.39E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
401	1.28	SP2	78	Sp2 transcription factor	KLVPIKAPLPLS*PGNLSFGLSSK	Q02086	65	9	1.39E+06
402	-0.81	SHARP	736, 740	spen homolog, transcriptional regulator	RPQS*PGAS*PSQAER	Q96T58	402	1	7.34E+04
403	-0.74	SHARP	736, 740, 749	spen homolog, transcriptional regulator	RPQS*PGAS*PSQAERLPS*DSER	Q96T58	402	1	9.84E+05
404	3.66	SQSTM1	269, 272	sequestosome 1 isoform 2	SRLT*PVS*PESSSSTEK	Q13501	48	3	4.36E+06
405	3.33	SQSTM1	272	sequestosome 1 isoform 2	LTPVS*PESSSSTEK	Q13501	48	6	8.98E+07
406	4.28	SQSTM1	272, 276	sequestosome 1 isoform 2	LTPVS*PESS*STEK	Q13501	48	4	2.21E+06
407	1.98	SSB	92	autoantigen La	IRRS*PSKPLPEVTDEYKNDVK	P05455	47	1	2.95E+05
408	3.97	STAT1	727	signal transducer and activator of transcription 1 isoform alpha	LQTTDNLPMF#S*PEEFDEVS	P42224	87	1	1.10E+07
409	1.15	STAT3; STAT3 iso2	727; 726	signal transducer and activator of transcription 3 isoform 2	FICVPTTCSNTIDLPMF#S*PR	P40763; P40763-2	88; 88	1	6.49E+05
410	1.34	supervillin; supervillin iso2	1322; 896	supervillin isoform 1	SVDYNM#PRS*PVEM#DEDFDVFDPYAPK	Q95425; Q95425-2	248; 201	4	1.61E+06
411	2.62	TCF20	1053	transcription factor 20 isoform 1	SSLHTPFS*PNSETLASAYHANT	Q9UGU0	212	1	2.41E+06
412	-0.46	treacle; treacle iso2	233; 233	Treacher Collins-Franceschetti syndrome 1 isoform b	ASSVSTKES*PARK	Q13428; A0JLU0	152; 144	2	4.99E+05
413	2.21	Hic-5	137, 140	transforming growth factor beta 1 induced transcript 1 isoform 1	EDQSEDKRPS*LPS*SPSPGLPK	Q43294	50	6	3.52E+06
414	2.69	Hic-5	137, 140, 143	transforming growth factor beta 1 induced transcript 1 isoform 1	EDQSEDKRPS*LPS*SPS*PGLPK	Q43294	50	1	7.00E+05
415	2.24	Hic-5	137, 141	transforming growth factor beta 1 induced transcript 1 isoform 1	KRPS*LPSS*PSGGLPK	Q43294	50	7	2.63E+07
416	5.35	Hic-5	137, 141, 143	transforming growth factor beta 1 induced transcript 1 isoform 1	KRPS*LPSS*PS*PGLPK	Q43294	50	4	3.77E+06
417	2.50	Hic-5	141	transforming growth factor beta 1 induced transcript 1 isoform 1	KRPSLPSS*PSGGLPK	Q43294	50	2	5.30E+05
418	-0.32	TLE3; TLE3 iso3	286; 286	transducin-like enhancer protein 3 isoform b	DAPTS*PASVASSSTPSSK	Q04726; Q04726-3	83; 83	6	2.30E+06
419	-0.23	TLE3; TLE3 iso3	286, 296; 286, 296	transducin-like enhancer protein 3 isoform b	DAPTS*PASVASSST*PSSK	Q04726; Q04726-3	83; 83	1	1.12E+05
420	-0.16	BCE1	292	transducin-like enhancer protein 4	DAPIS*PASIASSSTPSSK	Q04727	84	2	2.31E+05
421	-0.40	53BP1	1094, 1101	tumor protein p53 binding protein 1 isoform 2	QSQQPMKPIS*PVKDPVS*PASQK	Q12888	214	9	1.39E+07
422	-0.21	53BP1	1101	tumor protein p53 binding protein 1 isoform 2	QSQQPMKPIS*PVKDPVS*PASQK	Q12888	214	2	2.00E+05
423	-0.85	53BP1	1113	tumor protein p53 binding protein 1 isoform 2	M#VIQGPS*SPQGEAM#VTDVLEDKQEGR	Q12888	214	2	9.66E+05
424	-0.32	53BP1	1114	tumor protein p53 binding protein 1 isoform 2	M#VIQGPS*PQGEAM#VTDVLEDKQEGR	Q12888	214	3	1.88E+05
425	1.17	53BP1	380	tumor protein p53 binding protein 1 isoform 2	STPFIVPSS*PTEQEGR	Q12888	214	2	4.51E+06
426	-0.50	53BP1	727	tumor protein p53 binding protein 1 isoform 2	SIDS*PQKLAILDQLEHK	Q12888	214	1	3.23E+05
427	-0.08	53BP2	698	tumor protein p53 binding protein, 2 isoform 1	PLS*PTKLLPFLSNPY	Q13625	126	2	4.69E+04
428	-0.77	TReP-132	491	transcriptional regulating factor 1	AQPGS*PESSGQPK	Q96PN7	132	1	1.87E+05
429	-0.76	TSC22D1	256	TSC22 domain family, member 1 isoform 1	SASITGGPPSS*PVSR	Q15714	110	2	2.50E+05
430	-0.93	ZNF218	332	teashirt zinc finger homeobox 2	VFDVNRPCS*PDSTTGFADFSSQK	Q4VXM4	115	1	6.53E+05
431	2.69	UBE2L	71	ubiquitin-conjugating enzyme E2l	MLFKDDYPSS*PPK	P63279	18	5	1.52E+06
432	1.14	UBF	484	upstream binding transcription factor, RNA polymerase I isoform b	GKLPES*PKRAEEIWQSVIGDYLAR	P17470	89	16	8.73E+06
433	-0.44	VGLL4	52	vestigial like 4 isoform a	TGPPPI*PSKR	Q14135	31	2	2.25E+06
434	-0.72	ZBTB3	549	zinc finger and BTB domain containing 3	SKPDPVGVPLLVQPLPGS*PTADR	Q9H5J0	62	1	2.12E+05
435	1.25	FBI1	511, 525	zinc finger and BTB domain containing 7A	VRGGADPS*PGATATPGAPAQPS*SPDAR	Q95365	61	1	7.27E+05
436	-0.68	FBI1	525	zinc finger and BTB domain containing 7A	GGADPSPGATATPGAPAQPS*SPDARR	Q95365	61	1	7.43E+05
437	-0.33	FBI1	526	zinc finger and BTB domain containing 7A	GGADPSPGATATPGAPAQPS*PDAR	Q95365	61	3	2.01E+06
438	-0.16	RACK7; RACK7 iso6	432, 442; 287, 297	zinc finger, MYND-type containing 8 isoform b	ISLSDMPRS*PMSNTSSVHT*GSDVEQDAEKK	Q9ULU4; Q9ULU4-6	132; 113	1	4.83E+04
439	-0.61	ZNF295	435	zinc finger protein 295 isoform L	IKTEPSS*PLSDPDIIR	Q9ULJ3	119	3	6.45E+05
440	-0.48	ZNF503	102	zinc finger protein 503	TGHILHPEYLQPLPSTPVS*PIELDAK	Q96E25	63	4	4.62E+05
441	-0.40	ZNF687	140	zinc finger protein 687	M#QNGFGSPESPLGTPHS*PAPPSGGTGWK	Q8N1G0	130	3	6.63E+05
442	Translation								
443	1.49	DARS2	242	aspartyl-tRNA synthetase 2, mitochondrial	FYSLPOS*PQQFK	Q6P148	74	1	1.05E+06
444	5.58	eIF3-epsilon	258	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa	TCFS*PNRVIGLSSDDLQVGGASAR	Q00303	38	2	5.39E+06
445	7.19	eIF4B	93	eukaryotic translation initiation factor 4B	SRLPKS*PPYATFLGNLPHYDVTESIK	P23588	69	10	2.88E+06
446	-0.69	eIF4G; eIF4G iso3	1231; 1192	eukaryotic translation initiation factor 4 gamma, 1 isoform 4	EAAALPVVS*PLKAALSEELEKK	Q04637; Q04637-3	175; 172	8	2.38E+07
447	2.44	IARS	1047	isoleucine-tRNA synthetase	APLKPYPVS*PSDKVLIQEK	P41252	145	8	2.95E+07
448	4.93	IARS	1049	isoleucine-tRNA synthetase	APLKPYPVSPS*DK	P41252	145	4	1.41E+07
449	Tumor suppressor								
450	-0.74	PHF17	743	PHD finger protein 17 short isoform	VPTTPAS*PVKNWGGF	Q6IE81	96	5	4.83E+06
451	1.29	PSRC1; PSRC1 iso2	70; 70	proline/serine-rich coiled-coil 1 isoform b	LSLGLPS*PEKLEILDEANR	Q6PGN9; Q5T2Z1	39; 25	2	1.27E+06
452	Ubiquitin conjugating system								
453	1.47	APC2; LOC650621	314; 91	anaphase-promoting complex subunit 2	VFLQDGPAPAS*PEAGNTLR	Q9UJX6; XP_944803	94; 49	1	2.42E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
454	1.35	DRPLA	101	atrophin-1	TEQELPRPQS*PSDLDLSDGR	P54259	125	1	2.81E+05
455	-0.59	DRPLA	168	atrophin-1	PYHPPPLFPSS*PQPPDSTPR	P54259	125	3	9.96E+05
456	-0.79	C14ORF4	662	chromosome 14 open reading frame 4	NSSSPVS*PASVPGQR	Q9H1B7	83	1	1.03E+05
457	-0.40	CCDC86	18	coiled-coil domain containing 86	LGGLRPES*PELTSVS	Q9H6F5	40	14	6.84E+07
458	10.44	CCDC86	18, 24	coiled-coil domain containing 86	LGGLRPES*PELTS*VSR	Q9H6F5	40	2	5.51E+06
459	0.00	CCDC86	58, 66	coiled-coil domain containing 86	AGLGS*PERPPKTS*PGSPR	Q9H6F5	40	1	0.00E+00
460	1.35	CCDC86	58, 66, 69	coiled-coil domain containing 86	AGLGS*PERPPKTS*PGS*PR	Q9H6F5	40	2	1.51E+07
461	-0.83	FBX46	293	F-box protein 46	APDSGLPSGGGRRPGCAYPGS*PGPGAR	Q6PJ61	69	2	1.20E+06
462	-0.23	HDAC6	22	histone deacetylase 6	SRQNQPS*PPQDSSVTSK	Q9UBN7	131	3	1.84E+05
463	4.01	NEDD4L; NEDD4L iso5	479, 483, 487; 459, 463, 467	neural precursor cell expressed, developmentally down-regulated 4-like isoform 2	DTLSNPQS*PQPS*PYNS*PKPQHK	Q96PU5; Q96PU5-5	112; 110	1	8.59E+05
464	11.66	NEDD4L; NEDD4L iso5	479, 487; 459, 467	neural precursor cell expressed, developmentally down-regulated 4-like isoform 2	DTLSNPQS*PQPS*PYNS*PKPQHK	Q96PU5; Q96PU5-5	112; 110	2	3.92E+05
465	-0.50	TRIM11	85	tripartite motif-containing 11	LHPPS*PVQGVCPAHPRELAFCGDELRL	Q96F44	53	5	9.15E+05
466	11.69	TRIM47	463	tripartite motif-containing 47	VLCPINVPLSPT*R	Q96LD4	69	1	6.39E+06
467	1.15	UBE1L2	743	ubiquitin-activating enzyme E1-like 2	RPPS*PIKFDLNEPLHLSFLQNAAK	A0AVT1	118	1	2.19E+05
468	23.76	UBE2S	73	ubiquitin-conjugating enzyme E2S	DFPAS*PPKGYFLTK	Q16763	24	8	2.71E+06
469	-0.83	UBR4; UBR4 iso3	2718; 2729	retinoblastoma-associated factor 600	HVTLPSS*SPR	Q5T4S7; Q5T4S7-3	574; 572	1	4.66E+06
470	-0.94	UBR4; UBR4 iso3	2719, 2722, 2724; 2730, 2733, 2735	retinoblastoma-associated factor 600	HVTLPSS*PRS*NT*PMGDKDDDDDDADEK	Q5T4S7; Q5T4S7-3	574; 572	1	1.96E+05
471	-0.34	UBR4; UBR4 iso3	627; 627	retinoblastoma-associated factor 600	VKSPS*KQAPGKE	Q5T4S7; Q5T4S7-3	574; 572	1	7.41E+03
472	-0.65	ZFPL1	189	zinc finger protein-like 1	SOAPRPPAS*PGRPEQHTVIHMGNPEPLTHAPR	Q95159	34	5	6.55E+05
473	Unknown function								
474	12.77	ANKLE2	259, 268	ankyrin repeat and LEM domain containing 2	GICDYFSS*PSKTSPLS*PVK	Q86XL3	104	2	2.69E+06
475	7.43	ANKLE2	261, 268	ankyrin repeat and LEM domain containing 2	GICDYFSS*PSTSLS*PVKTAFLFSNDR	Q86XL3	104	1	1.90E+06
476	1.21	ANKLE2	268	ankyrin repeat and LEM domain containing 2	TSPLS*PVKTAFLFSNDR	Q86XL3	104	3	5.78E+06
477	5.97	ANKLE2	528	ankyrin repeat and LEM domain containing 2	AFAGPLS*PAKAEDFR	Q86XL3	104	6	8.93E+06
478	-0.30	Bcl-7C	126	B-cell CLL/lymphoma 7C	GTEPSPGGTPQPSRPPVS*PAGPEGVPEEAQPPR	Q8WUZO	23	1	1.93E+05
479	1.84	BEGAIN	385	brain-enriched guanylate kinase-associated protein	FPAS*PGPQALM*PPNLWSL	Q9BUH8	65	1	1.91E+05
480	1.05	BTBD9	599	BTB (POZ) domain containing 9 isoform a	APSGSSLPSS*PGNSNR	Q96007	69	1	2.12E+05
481	-0.60	RAMA1	155	SKA3	SPRS*PQLSDFGLER	Q8IX90	46	1	1.40E+06
482	2.93	C14orf118 iso4	374	hypothetical protein LOC55668 isoform 1	ALASDFPHISACAHEFNPLS*PLYSLDVLADASHR	Q9H3M3	54	1	1.07E+05
483	-0.20	MMTAG2	220	hypothetical protein LOC79169	RPAEATSSPTS*PERPR	Q9BU76	29	1	2.11E+05
484	-0.62	MGC5509	189, 193	ashwin	KSPSGPVKS*PPLS*PVGTTPVK	Q9BV05	26	1	1.84E+05
485	1.59	FLJ37562	121	hypothetical protein LOC134553	AAGFKTS*PGRPLGTTK	Q7Z6I8	20	4	4.30E+06
486	3.18	FLJ37562	137	hypothetical protein LOC134553	AAGYKVS*PGRPPGSIK	Q7Z6I8	20	4	7.46E+06
487	3.13	C7orf27	582	hypothetical protein LOC221927	ASAVTAM#GQLSSQGLHAPTS*PEHAEAR	Q06PJ6	88	2	2.18E+05
488	-0.53	MGC22793	52	hypothetical protein LOC221908	APVPEPGLDLSLSPRDS*PQPR	Q8TAP8	28	3	1.16E+06
489	-0.81	MGC22793	87	hypothetical protein LOC221908	LTPPS*PVRSEPPQAVPQELM#PVLK	Q8TAP8	28	5	1.70E+06
490	-0.67	C9orf30	274	hypothetical protein LOC91283	EWVPSFNRFPNPS*P	Q96H12	32	3	2.68E+06
491	2.57	CCDC99	555	coiled-coil domain containing 99	SGNTPNS*PR	Q96EA4	70	2	1.01E+05
492	1.34	CCNK; CCNK iso3	324, 329; 324, 329	cyclin K isoform 1	KPS*PQPSS*PR	Q75909; NP_001092872	41; 64	1	3.60E+05
493	1.07	CDC37L1	31	cell division cycle 37 homolog (S. cerevisiae)-like 1	AEGEAEEESDFVFPSS*SPR	Q7L3B6	39	2	2.44E+05
494	-0.45	CEP55	430	centrosomal protein 55kDa	VAASPKSPT*AALNESLVECPK	Q53E24	54	2	1.00E+06
495	-0.31	CEP55	430, 436	centrosomal protein 55kDa	VAASPKSPT*AALNES*LVECPK	Q53E24	54	1	3.98E+05
496	1.16	CEP63 iso2	495	centrosomal protein 63 isoform c	LELGLHECSLPS*PLGSIATR	Q96MT8-2	63	1	2.78E+05
497	2.95	CHML	649	choroideremia-like Rab escort protein 2	NLES*PEKHLQN	P26374	74	3	4.70E+06
498	0.00	CIR	365	CBF1 interacting corepressor	THKHS*PEKR	Q86X95	52	2	0.00E+00
499	1.00	CROCC	1451, 1460	ciliary rootlet coiled-coil	APS*PAPRPVPGS*PAR	Q5TZA2	229	2	2.55E+05
500	1.33	CTTNBP2NL	523	CTTNBP2 N-terminal like	FTSQGPIKPVSS*PNSSPFGTDYR	Q9P2B4	70	2	1.05E+06
501	2.66	EFHD2	74	EF-hand domain family, member D2	ADLNGIGEPQS*PSRR	Q96C19	27	5	1.32E+07
502	-0.97	FAM122A	143, 147	hypothetical protein LOC116224	RIDFIPVS*PAPS*PTR	Q96E09	31	1	5.21E+05
503	-0.88	FAM122A	143, 149	hypothetical protein LOC116224	RIDFIPVS*PAPSPT*R	Q96E09	31	1	5.07E+05
504	8.54	FAM122A	158, 173, 179	hypothetical protein LOC116224	QCFS*PSLQSFVSSNGLPPS*PIPSPT*TR	Q96E09	31	1	1.49E+05
505	1.06	FAM122A	76	hypothetical protein LOC116224	HGLLLPAS*PVR	Q96E09	31	3	1.33E+07

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
506	-0.56	FAM122B; FAM122B iso2	115, 119; 134, 138	hypothetical protein LOC159090	RIDFTPVSPAPS*PTR	Q7Z309; BAC86380	27; 29	3	2.94E+06
507	-0.55	FAM122B; FAM122B iso2	115, 121; 134, 140	hypothetical protein LOC159090	RIDFTPVSPAPS*TR	Q7Z309; BAC86380	27; 29	1	2.41E+06
508	-0.39	FAM122B; FAM122B iso2	137; 156	hypothetical protein LOC159090	M#FVSSSGLPPS*VPSPR	Q7Z309; BAC86380	27; 29	7	2.58E+05
509	1.18	FAM122B; FAM122B iso2	137, 141; 156, 160	hypothetical protein LOC159090	M#FVSSSGLPPS*VPVSPR	Q7Z309; BAC86380	27; 29	8	1.04E+06
510	-0.52	TNRC15; TNRC15 iso1	258; 236	GRB10 interacting GYF protein 2 isoform b	WRPHS*PDGPR	Q6Y7W6-3; Q6Y7W6	153; 150	2	3.78E+07
511	2.44	FAM29A	805	HAUS augmin-like complex, subunit 6	LEPNS*PM#HGGTLLEDVVGGR	Q7Z4H7	109	2	1.02E+06
512	-0.63	HEATR5A	2026	HEAT repeat containing 5A	YTKS*PGKNSSIQLK	Q86XA9	222	1	1.30E+05
513	1.78	FLEG1	140	Holliday junction recognition protein	ALAPAVPQS*PLKNELR	Q8NCD3	83	1	7.42E+05
514	4.05	FLEG1	642	Holliday junction recognition protein	LPSS*PLGCR	Q8NCD3	83	2	8.88E+06
515	-0.94	HMG20A	105	high-mobility group 20A	DSNAPKS*PLTGYYR	Q9NP66	40	2	3.73E+05
516	-0.22	INO80C	26	les6-similar protein isoform 1	KRPAS*PSHNGSSGGYGASK	Q6PI98	21	5	2.14E+05
517	-0.71	INO80C	28	les6-similar protein isoform 1	RPASPS*HNGSSGGYGASK	Q6PI98	21	4	9.41E+05
518	1.39	IRF2BP2	460	interferon regulatory factor 2 binding protein 2 isoform B	NSNSPPS*PSSMNQR	Q7Z5L9	61	1	7.98E+05
519	1.40	KHNYN	10	hypothetical protein LOC23351	PAS*PDRFAVSAEAK	O15037	74	4	8.86E+05
520	-0.89	KIAA0947	1890, 1903	hypothetical protein LOC23379	SCS*SPAVSAVSQLPLS*PK	Q9Y2F5	248	4	3.51E+06
521	-0.67	KIAA0947	1891, 1903	hypothetical protein LOC23379	SCSS*PAVSAVSQLPLS*PK	Q9Y2F5	248	4	3.65E+06
522	1.33	KIAA1217; KIAA1217 iso3	361; 79	sickle tail isoform 2	ISSLPVSRPIS*PSPAILER	Q5T5P2; Q5T5P2-3	214; 162	5	5.95E+06
523	-0.30	SI1; SI1 iso3	515; 515	hypothetical protein LOC55683 isoform a	GSRPAS*PAAK	Q9P2N6; Q9P2N6-3	96; 93	1	1.39E+05
524	-0.69	KIAA1429	1579	hypothetical protein LOC25962 isoform 1	SFLSEPPS*PGRTK	Q69YN4	202	1	3.85E+05
525	1.48	KIAA1486	509	hypothetical protein LOC57624	SRTPTS*PLEELTSLFSSGR	Q9P242	71	2	1.51E+06
526	1.37	KIAA1522; KIAA1522 iso2	545; 604	hypothetical protein LOC57648	GLAGPPAS*PGK	Q9P206; NP_065939	107; 113	4	6.09E+06
527	1.07	KIAA1522; KIAA1522 iso2	929; 988	hypothetical protein LOC57648	KLQLERPVS*PETQADLQR	Q9P206; NP_065939	107; 113	6	6.31E+06
528	-0.35	ARHGAP39	366	KIAA1688 protein	QGPSP*PCQQVLTK	Q9C0H5	125	1	7.67E+05
529	1.46	L3MBTL2	66	I(3)mbt-like 2	EAGELPT*SPLHLLSPGTPR	Q969R5	79	1	8.25E+05
530	1.04	L3MBTL2	67, 73	I(3)mbt-like 2	EAGELPTS*PLHLLS*PGTPR	Q969R5	79	1	6.11E+05
531	9.43	L3MBTL2	67, 73, 76	I(3)mbt-like 2	EAGELPTS*PLHLLS*PGT*PR	Q969R5	79	3	2.31E+06
532	3.50	LIMCH1; LIMCH1 iso1	1055, 1066; 670, 681	LIM and calponin homology domains 1 isoform b	CS*PTVAFVEFPSS*PQLKNDVSEEK	Q9UPQ0-3; Q9UPQ0	164; 122	3	5.02E+05
533	2.98	LIMCH1; LIMCH1 iso1	1057, 1065; 672, 680	LIM and calponin homology domains 1 isoform b	CSPT*VAFVEFPSS*SPQLK	Q9UPQ0-3; Q9UPQ0	164; 122	2	6.90E+06
534	1.61	LIMCH1; LIMCH1 iso1	1057, 1066; 672, 681	LIM and calponin homology domains 1 isoform b	CSPT*VAFVEFPSS*PQLK	Q9UPQ0-3; Q9UPQ0	164; 122	6	6.99E+06
535	-0.64	LIMCH1; LIMCH1 iso1	1066; 681	LIM and calponin homology domains 1 isoform b	CSPTVAFVEFPSS*PQLK	Q9UPQ0-3; Q9UPQ0	164; 122	6	7.62E+06
536	18.84	LSM14B	106, 115	LSM14 homolog B	AQHTLPQDPAIVQSSLSGSASAS*PFQPHVPS*PFR	Q9BX40	42	1	1.60E+06
537	3.48	BPY2-IP1	759	BPY2 interacting protein 1	AVPMAPAPAS*PGSSNDSSAR	Q66K74	112	1	3.15E+05
538	-0.38	MAP7D2	290	MAP7 domain containing 2	RPSS*PVISK	Q96T17	82	1	4.38E+05
539	3.16	RP11-535K18.3	524, 533	MAP7 domain containing 3	NCPSP*PLPLISKQS*PQTSFPYK	Q8WIC1	98	1	2.12E+06
540	-0.84	MIOS	766	missing oocyte, meiosis regulator, homolog	GFSQYGVSGS*PTK	Q9NXC5	99	1	2.38E+06
541	-0.39	NOC2L	49, 56	nucleolar complex associated 2 homolog	EAARS*PDKPGGS*PSASR	Q9Y3T9	85	1	3.56E+06
542	5.30	NUBP2	249	nucleotide binding protein 2 (MinD homolog, E. coli)	TLEEGHDFIQEFGPS*PFAALTSIAQK	Q9Y5Y2	29	2	1.79E+05
543	-0.05	OSBP2	765	oxysterol binding protein 2 isoform a	VMHSSPS*SPSDGKQK	Q969R2	101	1	3.13E+04
544	1.45	PHF2	655	PHD finger protein 2	ALRPPTS*PGVFGALQNFK	Q75151	121	4	5.81E+06
545	-0.26	PHF6; PHF6 iso2	199, 204; 200, 205	PHD finger protein 6 isoform 1	DRS*PHRSS*PSDTRPK	Q8IWS0; Q8IWS0-2	41; 35	6	5.65E+05
546	4.96	PHLDA2	42	pleckstrin homology-like domain family A member 2	LSLFPAS*PR	Q53GA4	17	1	3.07E+07
547	-0.52	PHLDB1	324	pleckstrin homology-like domain, family B, member 1 isoform a	KGGHERPPS*PGLR	Q86U11	151	1	4.37E+06
548	-0.73	PHLDB1	404	pleckstrin homology-like domain, family B, member 1 isoform a	IGTLQDRPPS*PFREPPGGER	Q86U11	151	1	1.27E+06
549	6.08	PRR11	344	proline rich 11	FQLAHPRS*PTPLPLSTSSFDEQN	Q96HE9	40	2	9.70E+05
550	2.04	PRR11	346	proline rich 11	KFQLAHPRSPT*PTPLPLSTSSFDEQN	Q96HE9	40	1	2.66E+05
551	5.24	RFX7	314, 321	regulatory factor X domain containing 2	QAPKT*PONVPAS*PGGDR	Q2KHR2	147	2	4.83E+05
552	-0.43	RFX7	321	regulatory factor X domain containing 2	TPONVPAS*PGGDR	Q2KHR2	147	1	3.90E+05
553	-0.49	RPRD2	482, 485	Regulation of nuclear pre-mRNA domain containing 2	NTGVSPASRSPGT*PTS*PSNLTSGLK	Q5VT52	156	1	4.68E+05
554	-0.69	RPRD2	485	Regulation of nuclear pre-mRNA domain containing 2	NTGVSPASRSPGTPPTS*PSNLTSGLK	Q5VT52	156	2	5.38E+06
555	-0.22	RSRC2	17	arginine/serine-rich coiled-coil 2 isoform a	DGLAPEKTS*PDRDK	Q7L4I2	51	1	4.94E+04
556	7.58	SAMD4B	243, 252	sterile alpha motif domain containing 4B	SMSLPIPTS*POVPGEWPS*PEELGAR	Q5PRF9	75	1	1.48E+06
557	1.36	SCML2	495, 511	sex comb on midleg-like 2	QS*TKRSPQQTVPYVPLS*PK	Q9UQRO	77	1	2.08E+06
558	1.89	SCML2	499, 511	sex comb on midleg-like 2	RS*PQQTVPYVPLS*PK	Q9UQRO	77	2	9.62E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-MAPK/CDK (PXS*P and S*PXX/R) Substrate Motif, PTMScan® Kit #1982, #4652

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
559	4.54	SHARPIN	165	shank-interacting protein-like 1	GPPPEADLPRS*PGLTEREELAGSLAR	Q9H0F6	40	2	4.46E+05
560	5.80	SLAIN2	456, 462, 467	SLAIN motif family, member 2	M#OQASAIIPS*PGKFRS*PAAPS*PLALR	Q9P270	63	1	4.28E+05
561	-0.70	SMCR8	498	Smith-Magenis syndrome chromosome region, candidate 8	SDSQASLTVPPLS*PQVVR	Q8TEV9	105	1	7.77E+05
562	1.06	SNFB1	87	basic beta 1 syntrophin	GAGAGHPGAGGAQPPDS*PAGVR	Q13884	58	1	1.08E+05
563	-0.73	SP140L	180	SP140 nuclear body protein-like	QGEVPES*PEAR	Q9H930	50	1	5.56E+05
564	-0.15	TANC2	1564, 1579	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	SQSGSPVRY*QQETSVSQPLGRPKS*PLSK	Q9HCD6	220	1	1.19E+05
565	-0.72	TANC2	1579	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	YQQETSVSQPLGRPKS*PLSK	Q9HCD6	220	4	6.46E+06
566	-0.13	TTC28	2105, 2108	tetratricopeptide repeat domain 28	GSIST*PNS*PVKM#TLIPSPNSPFQK	Q5W189	271	1	9.88E+04
567	-0.98	TTC28	2108	tetratricopeptide repeat domain 28	GSISTPNS*PVK	Q5W189	271	1	2.04E+05
568	7.34	TTC28	2293, 2302	tetratricopeptide repeat domain 28	LKYPSS*PYSAHISKS*PR	Q5W189	271	2	1.10E+06
569	9.98	WDR47	285, 294, 296	WD repeat domain 47 isoform 1	AAYADLLT*PLISKLSPY*PS*SPM#R	Q94967	102	1	3.35E+05
570	5.81	WDR47	292, 296	WD repeat domain 47 isoform 1	AAYADLLT*PLISKLS*PYPS*SPM#R	Q94967	102	2	2.27E+06
571	-0.41	WDR47	296	WD repeat domain 47 isoform 1	LSPYPS*SPMR	Q94967	102	1	6.30E+05
572	3.46	WDR91	272, 277	WD repeat domain 91	KS*PSRLS*PAQGPQQSSAK	A6NK54	83	1	3.26E+05
573	-0.35	WTAP	305	Wilms' tumour 1-associating protein isoform 1	EGNTTDDFPSS*SPGNGNK	Q15007	44	1	1.16E+06
574	-0.12	WTAP	306	Wilms' tumour 1-associating protein isoform 1	EGNTTDDFPSS*PGNGNK	Q15007	44	4	1.67E+06
575	-0.72	ZC3H18	487	zinc finger CCH-type containing 18	GKPKPRS*PQPPSR	Q86VM9	106	2	1.53E+05
576	1.56	ZC3H4	566	zinc finger CCH-type containing 4	HEPLS*PQQLQQDM#YNK	Q9UPT8	140	4	4.07E+05
577	-0.83	ZCCHC11	104	zinc finger, CCH domain containing 11 isoform a	KFPNS*PVKAEK	Q5TAX3	185	2	4.37E+05
578	-0.26	ZCCHC11	134	zinc finger, CCH domain containing 11 isoform a	SPKS*PNSVK	Q5TAX3	185	2	7.93E+04
579	2.80	ZCCHC11	156	zinc finger, CCH domain containing 11 isoform a	SEKVPSS*PAEAKGPSLLLK	Q5TAX3	185	1	1.25E+06
580	-0.13	ZNF768	125, 132	zinc finger protein 768	YEQS*PGYEPRS*PGYEPR	Q9H5H4	60	1	1.79E+05
581	Vesicle protein								
582	1.02	KIAA0430	44	limkain b1	FSNCFSRPEQTLPHS*PQTK	Q9Y4F3	193	1	2.81E+05
583	3.43	TRS85	971	hypothetical protein LOC22878	RPEFTFGGNTAVLTPS*PSASENC SAYK	Q9Y2L5	161	2	9.91E+05
584	1.53	PHLDB2	204	pleckstrin homology-like domain, family B, member 2 isoform b	SGAAMPSS*PK	Q86SQ0	142	2	4.24E+05
585	-0.51	Sec24B	1224	SEC24 (S. cerevisiae) homolog B isoform b	DSRPLS*PILHIVKDESPAK	Q95487	137	3	5.12E+05
586	c2h2-type zinc finger protein								
587	3.54	SUHW4	104	suppressor of hairy wing homolog 4 isoform 2	GITAAFKPTSQHYNTNPTSNPVAS*PINFHPESR	Q6N043	109	4	8.41E+05