

TABLE: CDK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
1		Adaptor/scaffold							
2	1.3	Abi-2; Abi-2 iso2	196; 190	abl interactor 2	GTLGR^HS*PYR^	Q9NYB9; Q9NYB9-2	56; 52	2	806,418
3	6.2	AHNAK	1192, 1986, 2181, 2309, 2832	AHNAK nucleoprotein isoform 1	FK^MPEMHFK^T*PK^	Q09666	629	9	4,275,166
4	1.0	AHNAK	\$2397	AHNAK nucleoprotein isoform 1	ISMPLDLHLK^S*PK^	Q09666	629	1	556,347
5	6.2	AHNAK	3426	AHNAK nucleoprotein isoform 1	VSM^PDVELNLK^S*PK^	Q09666	629	1	6,965,563
6	4.6	AHNAK	4516	AHNAK nucleoprotein isoform 1	FK^M^PDVHFK^S*PQISM^SDIDLNLK^	Q09666	629	19	14,059,313
7	4.0	AHNAK	\$4993	AHNAK nucleoprotein isoform 1	ADIK^S^PSLDVTPAEALNLETPEISVGGK^	Q09666	629	1	1,741,686
8	-1.3	AHNAK2; AHNAK2 iso1	\$3900; \$3408	AHNAK nucleoprotein 2	VDLKS*PQVDIK	Q96EX9; Q8IVF2	668; 617	3	1,286,834
9	4.7	AKAP1	\$169	A-kinase anchor protein 1 precursor	SAEVCK^QDS*PFSR^	Q92667	97	1	7,488,774
10	-1.1	AKAP11	\$422, \$433	A-kinase anchor protein 11	KPES*PYGNLCDAPDS*PRPVK	Q9UKA4	211	2	1,682,318
11	1.1	ANK2	\$3790	ankyrin 2 isoform 3	GGG*PIIQEPEEPSEHRESSPR	Q01484	430	2	312,081
12	-1.6	ANK2	\$3790, \$3806	ankyrin 2 isoform 3	GGG*PIIQEPEEPSEHREES*SPR	Q01484	430	2	841,334
13	-1.1	P130Cas; LOC100133063; LOC646079	\$139; 182; 182	breast cancer anti-estrogen resistance 1	AQQGLYQVPGSPQFQS*PPAK^	P56945; XP_001716809; XP_001716006	93; 46; 29	1	1,746,091
14	2.8	P130Cas	\$269	breast cancer anti-estrogen resistance 1	GLLPSQYGVQEVYDT*PPMAVK^	P56945	93	2	1,918,741
15	-3.8	Mena; Mena iso2; Mena iso5	\$508; \$508; \$755	enabled homolog isoform a	TNTMNGSKS*PVISR	Q8N8S7; Q8N8S7-2; CAH71475	67; 64; 89	19	5,107,028
16	1.0	LMO7; LMO7 iso2; LMO7 iso3	\$988, \$991; \$988, \$991; \$654, \$657	LIM domain only 7	EVAATEEDVTR^LPS*PTS*PFSSLSQDQAATSK^	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	1	2,304,833
17	-1.3	LMO7; LMO7 iso2; LMO7 iso3	\$990; \$990; \$656	LIM domain only 7	EVAATEEDVTR^LPSPT*SFSSLSQDQAATSK^	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	1	717,350
18	1.0	LMO7; LMO7 iso2; LMO7 iso3	\$990, \$991; \$990, \$991; \$656, \$657	LIM domain only 7	EVAATEEDVTRLPSPT*S*PFSSLSQDQAATSK	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	1	2,427,191
19	-1.3	LMO7; LMO7 iso2; LMO7 iso3	\$991; \$991; \$657	LIM domain only 7	EVAATEEDVTRLPSPTS*PFSSLSQDQAATSK	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	2	1,189,070
20	2.0	TAB3	\$60	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	YLYMEYHS*PDDNR^	Q8N5C8	79	1	664,445
21	0.1	MYOZ3	197, 215	myozenin 3	T^PVFPGGPLVGGTFRPRGT*PFIPEPLSGLELLR	Q8TDC0	27	1	1,281,176
22	-1.4	PARVA	\$10, \$19	parvin, alpha	SPS^VPKSPTPKS*PPSR	Q9NVD7	42	1	1,361,369
23	-1.8	PARVA	\$14, \$16	parvin, alpha	SPSVPK^S*PT*PK^SPPSR^K^	Q9NVD7	42	2	1,525,348
24	-1.5	PARVA	\$14, \$19	parvin, alpha	SPSVPKS*PTPKS*PPSR	Q9NVD7	42	5	11,080,020
25	-2.2	PARVA	\$16	parvin, alpha	SPT*PK^SPPSR^	Q9NVD7	42	1	42,390
26	-1.5	PARVA	\$16, \$19	parvin, alpha	SPSVPKSPT*PKS*PPSR	Q9NVD7	42	2	5,628,711
28	-1.5	PARVA	\$19	parvin, alpha	SPTPKS*PPSR	Q9NVD7	42	42	992,337
29	1.4	RanBP2	\$2613	RAN binding protein 2	NLFASFTEESSINYTFK^T*PEK^AK^	P49792	358	1	1,169,550
30	-1.4	vinexin; vinexin iso2	\$348; \$6	sorbin and SH3 domain containing 3 isoform 2	MADGGS*PFLGR	O60504; O60504-2	75; 37	1	11,706,252
31	2.0	SPTAN1	1413	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) isoform 1	AGTFQAFQFQGQLLAHGHYAS*PEIK	Q13813	285	3	2,507,626
33	1.3	WDR62	\$1144	WD repeat domain 62 isoform 1	AGTYGAS^PDR^THVLAAGK^	O43379	166	2	11,378,708
34		Adhesion or extracellular matrix protein							
35	19.9	MAP7	\$219	microtubule-associated protein 7	LQLS*PWESSVNR^	Q14244	84	1	3,650,599
36	-1.6	plakophilin 4; plakophilin 4 iso2	\$273, \$281; \$273, \$281	plakophilin 4 isoform b	AAS^PYSQR^PAS*PTAIR^	Q99569; Q99569-2	134; 130	1	4,112,893
37	9.0	plakophilin 4; plakophilin 4 iso2	\$419, \$427; \$419, \$427	plakophilin 4 isoform b	T^YYSPVYR^S*PNHGTVELQGSQTALYR^	Q99569; Q99569-2	134; 130	1	499,189
38	4.3	TROAP	\$307, \$324	tastin isoform 2	DSHDSHLM#PS*PAFVAQLPGHVVPKPS*PFR^	Q8N5B2	84	2	6,754,980
39		Apoptosis							
40	3.7	ADNP	\$409	activity-dependent neuroprotector	YSLQSANASSLSGQLKS*PSLSQSQASR	Q9H2P0	124	2	3,691,840
41	3.9	Bad	\$91	BCL2-associated agonist of cell death	HSSYPAGTEDDEGM#GEEPS*PFR^GR^	Q92934	18	2	1,707,219
42		Calcium-binding protein							
43	2.9	ANXA1	\$36	annexin I	GGPGSAVS*PYPTFNPSDDVAALHK^	P04083	39	1	4,757,012

LEGEND: § = published site, * - phosphorylation, # = oxidized methionine

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STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

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Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
44		Cell cycle regulation							
45	2.5	BAT2D1 iso8	\$2682, \$2686	HBxAg transactivated protein 2	STT*PTSS*PFR [^]	NP_055987	309	2	11,378,708
46	10.2	Borealin	199, \$204	cell division cycle associated 8	VFK* [^] T*PGLR* [^] T*PAAGER [^]	Q53HL2	31	1	1,310,151
48	1.8	CENPF	\$3094	centromere protein F	GFADIPTGK* [^] TS*PYILR [^]	P49454	368	2	3,086,287
49	3.1	INCENP	\$263, \$269, \$275	inner centromere protein antigens 135/155kDa isoform 1	IAQVS*PGPR* [^] DS*PAFPDS*PWR* [^] ER [^]	Q9NQS7	106	1	9,576,253
50	2.4	INCENP	\$897, \$904	inner centromere protein antigens 135/155kDa isoform 1	T*SSAVWNS*PPLQGAR [^]	Q9NQS7	106	1	394,223
51	3.4	INCENP	\$898, \$899, \$904	inner centromere protein antigens 135/155kDa isoform 1	R* [^] TS* [^] S* [^] AVWNS*PPLQGAR [^]	Q9NQS7	106	3	6,665,322
52	2.3	INCENP	\$904	inner centromere protein antigens 135/155kDa isoform 1	TSSAVWNS*PPLQGAR [^]	Q9NQS7	106	1	584,525
53	4.9	KI-67	235	antigen identified by monoclonal antibody Ki-67	K* [^] NES* [^] PFWK [^]	P46013	359	1	4,884,393
55	2.3	NCAPG	\$931	chromosome condensation protein G	GNK* [^] EFGDQAEAAQDATLTITTTQNEDEK* [^] NK* [^] EVYMT* [^] PLR [^]	Q9BPX3	114	1	344,539
56	-51.4	NCAPH	\$432	non-SMC condensin I complex, subunit H	TMCPLLSM#KPGEYSYFS* [^] PR	Q15003	83	6	156,822,192
57	-54.3	NuMA-1	\$1776	nuclear mitotic apparatus protein 1	LPPK* [^] VESLESLYFT* [^] PIPAR [^]	Q14980	238	1	3,992,116
58	4.4	PRC1; PRC1 iso2	\$513, \$483	protein regulator of cytokinesis 1 isoform 1	LNTTMSNATANSSIR* [^] PIFGTVYHS* [^] PVSR [^]	Q43663; Q43663-2	72; 67	10	17,404,536
59	3.9	SUGT1	\$281	suppressor of G2 allele of SKP1 isoform a	NLYPSSS* [^] PYTR [^]	Q9Y2Z0	41	2	29,292,392
60	6.0	TACC3	59	transforming, acidic coiled-coil containing protein 3	VTFQT* [^] PLR* [^] DPQTHR [^]	Q9Y6A5	90	1	540,327
61	2.4	TPX2	\$486	TPX2, microtubule-associated protein homolog	VLPITPVKS* [^] PAFALK	Q9ULW0	86	2	5,643,604
64		Chaperone							
65	3.0	CRYAB	\$19	crystallin, alpha B	R* [^] PPFFHS* [^] PSR [^]	P02511	20	1	1,819,217
66	8.2	TBCE	\$495	beta-tubulin cofactor E	LLK* [^] VPVSDLLSYES* [^] PK* [^] K* [^] PGR [^]	Q15813	59	1	1,039,634
67		Chromatin, DNA-binding, DNA repair or DNA replication protein							
68	2.7	C14orf106	\$110	chromosome 14 open reading frame 106	ANYES* [^] PGK* [^] IFLR [^]	Q6P0N0	129	1	1,633,414
69	-2.2	CHD-2	1795, \$1801	chromodomain helicase DNA binding protein 2 isoform 2	SPPSQKS* [^] PHDSKS* [^] PLDHR	Q14647	211	1	36,446
70	-1.1	ESCO2	\$75	establishment of cohesion 1 homolog 2	LPSANQGS* [^] PFK	Q56N19	68	4	3,741,257
71	1.4	MSH6	\$14	mutS homolog 6	QSTLYSFFPK* [^] S* [^] PALSDANK [^]	P52701	153	1	719,022
72	-5.7	MybBP1A	\$1290	MYB binding protein 1a isoform 1	K* [^] GVLGK* [^] S* [^] PLSALAR [^]	Q9B0G0	149	1	1,807,423
73	3.3	NIPBL; NIPBL iso2	914; 914	delangin isoform B	SDK* [^] LGFK* [^] SPT* [^] SK [^]	Q6KC79; Q6KC79-2	316; 304	1	1,195,765
74	2.9	POLS	337	DNA polymerase sigma	IATCNGEQTNR* [^] EPES* [^] PYGQR [^]	Q5XG87	60	2	460,536
75	3.9	RBMS1; RBMS1 iso2; RBMS3	\$112; \$112; 111	RNA binding motif, single stranded interacting protein 1 isoform c	GYGFVDFDS* [^] PAAQK [^]	P29558; P29558-2; Q6XE24	45; 44; 48	1	8,967,273
76	1.9	Rif1	\$1616	RAP1 interacting factor 1	ATSEEDVSIK* [^] S* [^] PICEK [^]	Q5UIP0	274	1	297,867
77	3.0	Rif1	\$402, \$409	RAP1 interacting factor 1	GASS* [^] PYGAPGT* [^] PR [^]	Q5UIP0	274	1	1,081,507
78	2.8	TOP2B	\$1236	DNA topoisomerase II, beta isozyme	K* [^] LQLEETMPS* [^] PYGR [^]	Q02880	183	3	386,924
79	2.5	UKp68; UKp68 iso4	\$274; \$240	zinc finger CCHC-type containing 14 isoform 1	LCEPEVLNLSLETYS* [^] PFFR [^]	Q6PJ77; Q6PJ77-4	83; 65	3	4,628,217
80	3.9	ZNF638	\$383	zinc finger protein 638	NYQSQADIPR* [^] S* [^] PFGIVK [^]	Q14966	221	1	993,636
81		Cytoskeletal protein							
82	3.1	abLIM; abLIM iso2	\$640; \$317	actin-binding LIM protein 1 isoform b	YDS* [^] PINSASHIPSSK [^]	Q14639; NP_006711	88; 52	2	3,046,315
83	4.8	caldesmon; caldesmon iso2; caldesmon iso3; caldesmon iso4	\$723, \$730; \$494, \$501; \$488, \$495; \$468, \$475	caldesmon 1 isoform 2	GNVFS* [^] SPTAAGT* [^] PNK* [^] ETAGLK [^]	Q05682; Q05682-2; Q05682-3; Q05682-4	93; 66; 64; 63	1	859,323
84	5.9	CCDC6	395, 410	coiled-coil domain containing 6	AGM# [^] SYYSN* [^] PGLHVQHMGTSHGIT* [^] RPSPR	Q16204	66	1	920,795
85	2.6	CCDC6	395, 413	coiled-coil domain containing 6	AGMSYYSN* [^] PGLHVQHMGTSHGITR* [^] PS* [^] PR [^]	Q16204	66	3	428,130
86	1.6	CCDC6	\$52	coiled-coil domain containing 6	SGGIVIS* [^] PFR* [^] LEELTNR [^]	Q16204	66	4	7,450,797
87	4.2	CLASP2; CLASP2 iso4	\$1029, 1034; \$592, 597	CLIP-associating protein 2	DYNPNYNSDIS* [^] PFNK* [^] S* [^] ALK [^]	Q75122; Q96F87	141; 94	1	339,087
88	1.2	DAG1	888	dystroglycan 1 preproprotein	NMTPYRS* [^] PPYVPP	Q14118	98	1	902,154
89	4.9	DBNL; DBNL iso2	\$275, \$283; \$276, \$284	drebrin-like isoform b	AMSTTSSS* [^] PQPGK* [^] LR* [^] S* [^] PFLQK [^]	Q9UJU6; Q9UJU6-2	48; 48	1	411,134
90	3.3	DBNL; DBNL iso2	\$283; \$284	drebrin-like isoform b	LR* [^] S* [^] PFLQK [^]	Q9UJU6; Q9UJU6-2	48; 48	2	19,664,724
91	-1.1	BPAG1; BPAG1 iso2; BPAG1 iso7	1056; 1606; 1056	dystonin isoform 1e precursor	AMVDSQQKS* [^] PVKR	Q94833; Q03001; Q8WXX8	591; 372; 345	1	107,441

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92	2.8	EPB41; EPB41 iso2; EPB41 iso4	\$712; \$679; \$470	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked) isoform 3	LSTHS*PFR^	P11171; P11171-2; P11171-4	97; 93; 66	2	2,628,432
93	4.4	EPB41L2	908	erythrocyte membrane protein band 4.1-like 2 isoform b	TITYES*PQIDGGAGGDSGLTLTAQTITSESVSTTTTTHITK^	Q43491	113	1	631,313
95	3.6	PLEKHC1	\$159, \$181	fermitin family homolog 2 isoform 2	KLDDQS*EDEALELEGLITPGSGSIYSS*PGLYSK	Q96AC1	78	2	1,143,013
96	4.0	PLEKHC1	\$175, \$181	fermitin family homolog 2 isoform 2	K^LDDQSEDEALELEGLITPGS*GSIYSS*PGLYSK^	Q96AC1	78	1	3,707,715
98	3.0	PLEKHC1	\$181	fermitin family homolog 2 isoform 2	KLDDQSEDEALELEGLITPGSGSIYSS*PGLYSK	Q96AC1	78	2	5,421,859
99	6.6	FLNB	\$1028	filamin B, beta (actin binding protein 278)	EEGLYAVDVTYDGHVPVPGS*PYTVEASLPDPDSK^	Q75369	278	8	3,926,140
100	2.6	FLNB	\$1316	filamin B, beta (actin binding protein 278)	GLHWVEVTYDDVIPNS*PFK^	Q75369	278	3	1,106,371
101	18.2	FLNB	1409	filamin B, beta (actin binding protein 278)	DGSCSAEYIPFAPGDYDVNITYGGAHIPGS*PFR^VPVK^	Q75369	278	1	2,747,865
102	5.1	FLNB	\$1505	filamin B, beta (actin binding protein 278)	YADEEIPR^S*PFK^	Q75369	278	6	35,899,860
103	10.9	FLNB	\$1602	filamin B, beta (actin binding protein 278)	YM#IGVTYGGDDIPLS*PYR^	Q75369	278	2	7,357,317
104	8.4	FLNB	\$2083	filamin B, beta (actin binding protein 278)	FADHVPVGS*PFTVK^	Q75369	278	2	4,571,223
105	6.0	FLNB	2369	filamin B, beta (actin binding protein 278)	FNGSHVVG*PFK^	Q75369	278	3	4,275,736
106	1.9	FLNB	2465	filamin B, beta (actin binding protein 278)	YGGPNHIVGS*PFK^	Q75369	278	3	4,140,463
107	7.8	FLNB	730	filamin B, beta (actin binding protein 278)	HTIAVWGGVNIHPS*PYR^	Q75369	278	4	9,251,700
108	-16.2	FLNB	833	filamin B, beta (actin binding protein 278)	VLFASQEI*PFR	Q75369	278	2	77,356,608
109	7.9	FLNB	\$886	filamin B, beta (actin binding protein 278)	APLNVQFNS*PLPGDAVK^	Q75369	278	2	3,135,923
110	-1.5	KIF1C	\$1083	kinesin family member 1C	YPPYTT*PPR	Q43896	123	3	4,268,986
111	4.6	KIF20A	\$857, \$864	kinesin family member 20A	NLLPRT*PTCQSST*DCSPYAR	Q95235	100	1	2,082,891
112	4.6	KIF20A	\$857, \$867	kinesin family member 20A	NLLPRT*PTCQSSTDCS*PYAR^	Q95235	100	4	6,473,770
113	3.3	KIF20A	\$859, \$867	kinesin family member 20A	TPT*QCSSTDCS*PYAR^	Q95235	100	2	310,771
114	2.6	KIF20A	863, \$867	kinesin family member 20A	TPTCQSS*TDSC*PYAR^	Q95235	100	1	131,473
115	1.9	KIF20A	\$867	kinesin family member 20A	TPTCQSS*TDSC*PYAR^	Q95235	100	3	4,435,237
117	1.0	KIF23	\$738	kinesin family member 23 isoform 2	IPTYNT*PLK	Q02241	110	3	4,884,393
118	10.4	MAP1B	1254, \$1256, \$1260	microtubule-associated protein 1B	DSISAVSSEKVS*KS*PSLS*PSPSPLEK	P46821	271	1	503,074
119	1.2	MAP1B	\$1256, \$1260, \$1265	microtubule-associated protein 1B	VSPSK^S*PSLS*PSPSPLEK^	P46821	271	5	1,357,457
120	-1.2	MAP1B	\$1322, \$1328, \$1339	microtubule-associated protein 1B	TLEVVS*PSQSVT*GSAGHT*PYQ*PTDEK	P46821	271	1	1,626,711
121	-1.2	MAP1B	\$1322, \$1334, \$1341	microtubule-associated protein 1B	TLEVVS*PSQSVTGSAGHT*PYQ*PTDEK^	P46821	271	1	1,269,613
122	-1.2	MAP1B	\$1322, \$1339	microtubule-associated protein 1B	TLEVVS*PSQSVTGSAGHT*PYQ*PTDEK	P46821	271	1	4,181,165
123	-1.2	MAP1B	\$1324, \$1334, \$1339	microtubule-associated protein 1B	TLEVVS*PSQSVTGSAGHT*PYQ*PTDEK	P46821	271	1	1,626,711
124	-1.0	MAP1B	\$1427	microtubule-associated protein 1B	GAES*PFEEK	P46821	271	4	6,900,418
125	-2.8	tau; tau iso2; tau iso3; tau iso5; tau iso6; tau iso8	\$515; \$104; \$140; \$198; \$140; \$199	microtubule-associated protein tau isoform 6	SGYSS*PGSPGTPGSR	P10636; P10636-2; P10636-3; P10636-5; P10636-6; P10636-8	79; 33; 37; 42; 40; 46	1	252,699
126	-5.3	tau; tau iso2; tau iso3; tau iso5; tau iso6; tau iso8	\$712, \$716, \$720, \$270, \$274, \$278; \$306, \$310, \$314; \$364, \$368, \$372; \$337, \$341, \$345; \$396, \$400, \$404	microtubule-associated protein tau isoform 6	AKTDHGAIEVYKS*PVWS*GDT*PR	P10636; P10636-2; P10636-3; P10636-5; P10636-6; P10636-8	79; 33; 37; 42; 40; 46	4	2,195,767
127	-1.1	tau; tau iso2; tau iso3; tau iso5; tau iso6; tau iso8	\$712, \$719; \$270, \$277; \$306, \$313; \$364, \$371; \$337, \$344; \$396, \$403	microtubule-associated protein tau isoform 6	TDHGAIEVYK^S*PVVSGDT*SPR^	P10636; P10636-2; P10636-3; P10636-5; P10636-6; P10636-8	79; 33; 37; 42; 40; 46	1	1,682,318
128	-1.0	tau; tau iso2; tau iso3; tau iso5; tau iso6; tau iso8	\$712, \$720; \$270, \$278; \$306, \$314; \$364, \$372; \$337, \$345; \$396, \$404	microtubule-associated protein tau isoform 6	AKTDHGAIEVYKS*PVVSGDT*PR	P10636; P10636-2; P10636-3; P10636-5; P10636-6; P10636-8	79; 33; 37; 42; 40; 46	2	289,511
129	5.1	PDLIM3 iso2	145	PDZ and LIM domain protein 3 isoform b	QVVSASYNS*PIGLYSTNIQDALHGLR^	Q53G65-2	34	1	1,741,686
130	1.3	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4613; \$4503; \$4462; \$4480; \$4476	plectin 1 isoform 1	GYYS*PYSVSGSGSTAGSR^	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	3	16,489,010

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Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
131	1.1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4613, \$4618; \$4503, \$4508; \$4462, \$4467; \$4480, \$4485; \$4476, \$4481	plectin 1 isoform 1	GYYS*PYSVS*GSGSTAGSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	1,601,152
132	5.7	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4613, \$4620; \$4503, \$4510; \$4462, \$4469; \$4480, \$4487; \$4476, \$4483	plectin 1 isoform 1	GYYS*PYSVSGS*GSTAGSR^TGSRA	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	2	13,317,763
133	1.1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4613, \$4622; \$4503, \$4512; \$4462, \$4471; \$4480, \$4489; \$4476, \$4485	plectin 1 isoform 1	GYYS*PYSVSGSGS*TAGSR^	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	1,517,918
134	1.1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4613, \$4626; \$4503, \$4516; \$4462, \$4475; \$4480, \$4493; \$4476, \$4489	plectin 1 isoform 1	GYYS*PYSVSGSGSTAGS^R	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	1,601,152
135	-1.2	Rab11FIP5	188	RAB11 family interacting protein 5 (class I)	DK^PR^S^PFSK^	Q9BXF6	70	3	564,052
136	0.1	SNIP; SNIP iso6	869, 875; 997, 1003	SNAP25-interacting protein	YRT^EKPSKS^PPPPPPR	Q9C0H9; Q75T46	112; 127	1	3,499,378
137	-1.0	SSFA2	\$1040	sperm specific antigen 2 isoform 1	MPS^PFR^	P28290	138	1	3,258,067
138	3.5	SSFA2	883	sperm specific antigen 2 isoform 1	TLSTHSVPNIGATCSAFAS^PFGCPYSHR^	P28290	138	1	511,120
139	-1.4	talin 1	2162	talin 1	QELAVFCS^PEPPAK	Q9Y490	270	2	27,023,648
140		Enzyme, misc.							
141	1.4	ADSL	434	adenylosuccinate lyase isoform a	IQVDAYFS^PIHSQDLHLLDPSSFTGR	P30566	55	1	748,864
142	-1.7	CHD-1	\$1688	chromodomain helicase DNA binding protein 1	SYGSR^S^PFEHSEVHK^	Q14646	197	2	3,703,493
143	2.2	CRMP-4	586	dihydropyrimidinase-like 3	FIPCS^PFSYVYK^	Q6DEN2	74	2	2,090,536
144	-2.0	CRMP-4	\$628, \$632, \$636	dihydropyrimidinase-like 3	GGT^PAGS^ARGS^PTRNPVPVR	Q6DEN2	74	4	6,439,178
145	1.5	ENO1	\$262	enolase 1	SGKYDLDFKS^PDDPSR	P06733	47	2	1,679,047
146	2.7	JMJD1B	\$647	jumonji domain containing 1B	VEHS^PFSSFASQASGSSSATTVTSK^	Q7LBC6	192	1	1,968,361
147	1.1	PKM2; PKM2 iso2	\$37; \$37	pyruvate kinase, muscle isoform M2	LDIDS^PPITAR^	P14786; P14618-2	58; 58	1	4,433,841
148	-1.4	PPIG	\$687	peptidylprolyl isomerase G	ADRDQS^PFSK	Q13427	89	18	964,687
149	3.7	SETD8	\$100	SET domain-containing protein 8	IYSYMS^PNK^	Q9NQR1	43	1	1,572,905
150		G protein or regulator							
151	4.5	ARHGEF17	418	Rho guanine nucleotide exchange factor (GEF) 17	GSGGWGVYR^S^PSFGAGEGLLR^	Q96PE2	222	1	2,094,796
152	1.5	ARHGEF7; ARHGEF7 iso1	\$257; \$79	PAK-interacting exchange factor beta isoform c	SGTLK^S^PPK^GFDTTAINK^	Q14155; Q14155-1	90; 73	1	5,307,227
153	-1.6	GAPVD1	\$462, \$466	GTPase activating protein and VPS9 domains 1	SSSLEM^TPYNT^PQLS^PATTANKK	Q9Y4N0	166	1	321,169
154	2.5	MgcRacGAP	\$628	Rac GTPase activating protein 1	QGNFFAS^PM^LK^	Q9HOH5	71	4	4,452,201
155	1.2	TBC1D24	480	TBC1 domain family, member 24	HPELTK^PPPLMAAEPTAPLSHSASSDPADR^LS^PFLAAR^	Q9ULP9	63	4	7,358,612
156		Motor or contractile protein							
157	5.3	MYO9B	1926, 1935	myosin IXB isoform 2	LGFSS^PYEGVLNK^S^PK^	Q13459	244	1	908,843
158		Phosphatase							
159	1.8	Cdc25C; Cdc25C iso3	\$214; \$171	cell division cycle 25C protein isoform a	SGLYR^S^PSMPENLNR^PR^	P30307; P30307-3	53; 49	1	750,148
160	1.7	MYPT1	\$299	protein phosphatase 1, regulatory (inhibitor) subunit 12A	DK^K^S^PLIESTANMDNNQSQK^	Q14974	115	3	1,662,363
161	4.2	PPP1R14B	\$32	protein phosphatase 1 regulatory subunit 14B	VYFQS^PPGAAGEGPGGADDEGPVR^R^	Q96C90	16	2	1,958,168
162	-1.1	PTPRK	856	protein tyrosine phosphatase, receptor type, K isoform a	YLCEGTES^PYQTGQLHPAIR	Q15262	162	2	5,023,040
163	1.0	PTPRK	856, 860	protein tyrosine phosphatase, receptor type, K isoform a	YLCEGTES^PYQT^GQLHPAIR	Q15262	162	1	626,100
164		Protease							
165	1.0	PSMD8	13	proteasome 26S non-ATPase subunit 8	GEWNR^K^S^PNLSK^	P48556	30	1	1,735,818
166	-2.0	SEN3	\$232	SUMO1/sentrin/SMT3 specific protease 3	WTPKS^PLDPDSGLLSCTLPNGFGGQSGPEGER	Q9H4L4	65	2	1,135,440
168	-1.6	SEN3	26	SUMO1/sentrin/SMT3 specific protease 3	MKETIQGTGSWGPEPPGPGIPPAYSS^PRR	Q9H4L4	65	7	2,646,047
169	-1.9	USP24; USP24 iso2	\$981; \$1141	ubiquitin specific protease 24	TLLSESSQSSKS^PSLSSK	Q9UPU5; IPI00398505	277; 294	2	473,385

LEGEND: \$ = published site, * - phosphorylation, # = oxidized methionine

TABLE: CDK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
170		Protein kinase, Ser/Thr (non-receptor)							
171	-1.3	BIKE	1014	BMP-2 inducible kinase isoform b	KTLKPTYRT*PER	Q9NSY1	129	1	255,698
172	-1.8	PITSLRE; CDC2L2	\$65; \$65	cell division cycle 2-like 1 (PITSLRE proteins) isoform 2	MEITIR^NS*PYR^	P21127; Q9UQ88	93; 91	2	1,339,557
173	-1.9	CHED; CHED iso2	\$337, \$340, \$348; \$337, \$340, \$348	cell division cycle 2-like 5 isoform 1	S*RKS*PSPAGGGS*SPYSR	Q14004; Q14004-2	165; 158	1	24,391
174	-1.5	CHED; CHED iso2	\$337, \$340, \$349; \$337, \$340, \$349	cell division cycle 2-like 5 isoform 1	S*R^K^S*PSPAGGGS*PYSR^	Q14004; Q14004-2	165; 158	3	77,374
175	-1.6	CHED; CHED iso2	\$337, \$340, 352; \$337, \$340, 352	cell division cycle 2-like 5 isoform 1	S*R^K^S*PSPAGGGS*PYSR^	Q14004; Q14004-2	165; 158	2	609,958
176	-1.6	CHED; CHED iso2	\$337, \$342, \$349; \$337, \$342, \$349	cell division cycle 2-like 5 isoform 1	S*R^K^S*PSPAGGGS*PYSR^	Q14004; Q14004-2	165; 158	1	609,958
177	-1.6	CHED; CHED iso2	\$337, \$342, 352; \$337, \$342, 352	cell division cycle 2-like 5 isoform 1	S*R^K^S*PSPAGGGS*PYSR^	Q14004; Q14004-2	165; 158	3	609,958
178	-1.8	CHED; CHED iso2	\$340, \$342, \$348; \$340, \$342, \$348	cell division cycle 2-like 5 isoform 1	SRKS*PS*PAGGGS*SPYSR	Q14004; Q14004-2	165; 158	4	151,311
179	-1.6	CHED; CHED iso2	\$340, \$342, \$349; \$340, \$342, \$349	cell division cycle 2-like 5 isoform 1	SRKS*PS*PAGGGS*SPYSR	Q14004; Q14004-2	165; 158	22	968,288
180	-1.3	CHED; CHED iso2	\$340, \$342, 352; \$340, \$342, 352	cell division cycle 2-like 5 isoform 1	SRKS*PS*PAGGGS*SPYSR	Q14004; Q14004-2	165; 158	5	56,520
181	-1.8	CHED; CHED iso2	\$340, \$348, \$349; \$340, \$348, \$349	cell division cycle 2-like 5 isoform 1	SR^K^S*PSPAGGGS*SPYSR^	Q14004; Q14004-2	165; 158	3	139,484
182	-2.0	CHED; CHED iso2	\$340, \$349, 352; \$340, \$349, 352	cell division cycle 2-like 5 isoform 1	SR^K^S*PSPAGGGS*SPYSR^	Q14004; Q14004-2	165; 158	1	42,211
183	13.9	CHED; CHED iso2	374, \$383, 390; 374, \$383, 390	cell division cycle 2-like 5 isoform 1	SPSYR^HS*SYER^GGDVS*PSPYSS*SWR^	Q14004; Q14004-2	165; 158	1	458,528
184	1.6	CHED; CHED iso2	\$383, \$385; \$383, \$385	cell division cycle 2-like 5 isoform 1	GGDVS*PS*PSSSSWR^	Q14004; Q14004-2	165; 158	1	797,438
186	-1.6	CRK7; CRK7 iso2	\$318, \$323, \$325; \$318, \$323, \$325	Cdc2-related kinase, arginine/serine-rich isoform 2	SGS*YSGR^S*PS*PYGR^	Q9NYV4; Q9NYV4-2	164; 163	4	3,378,340
187	-1.4	CRK7; CRK7 iso2	\$320, \$323, \$325; \$320, \$323, \$325	Cdc2-related kinase, arginine/serine-rich isoform 2	SGSYS*GR^S*PS*PYGR^	Q9NYV4; Q9NYV4-2	164; 163	1	267,495
188	-1.4	CRK7; CRK7 iso2	\$323, \$325; \$323, \$325	Cdc2-related kinase, arginine/serine-rich isoform 2	SGSYSGRS*PS*PYGR	Q9NYV4; Q9NYV4-2	164; 163	2	535,858
189	-1.7	CRK7; CRK7 iso2	\$332, \$333; \$332, \$333	Cdc2-related kinase, arginine/serine-rich isoform 2	RRS*S*SPFLSK	Q9NYV4; Q9NYV4-2	164; 163	2	1,622,802
190	-1.3	CRK7; CRK7 iso2	\$332, \$333, \$334; \$332, \$333, \$334	Cdc2-related kinase, arginine/serine-rich isoform 2	RRS*S*S*PFLSKR	Q9NYV4; Q9NYV4-2	164; 163	1	474,842
191	-1.7	CRK7; CRK7 iso2	\$332, \$334; \$332, \$334	Cdc2-related kinase, arginine/serine-rich isoform 2	RRS*SS*PFLSKR	Q9NYV4; Q9NYV4-2	164; 163	2	1,591,592
192	2.6	PBK	\$24, \$32	PDZ binding kinase	SVLCST*PTINIPAS*PFM#QK^	Q96KB5	36	2	2,427,191
193	2.5	PBK	\$59	PDZ binding kinase	GLSHS*PWAVK^	Q96KB5	36	2	4,582,125
194	-1.2	PRP4	\$277	serine/threonine-protein kinase PRP4K	KKS*PIINESR	Q13523	117	19	935,330
195	1.3	Sgk269	389	NKF3 kinase family member	IEIPNYES*PSSNNQDK^DSSQASK^	Q9H792	193	2	1,023,331
196	1.9	WNK1	\$19	WNK lysine deficient protein kinase 1	QSSTPGSLFLS*PPAPAPK^	Q9H4A3	251	1	859,944
197	4.0	ZAK	\$599	MLK-related kinase isoform 1	QSQNPILGS*PFFSHFDGQDSYAAVR^	Q9NYL2	91	2	3,286,699
198	1.6	ZAK	700, 703, 706	MLK-related kinase isoform 1	GR^YSKG^S*QHS*TPS*R^GR^	Q9NYL2	91	1	4,416,934
199		Protein kinase, Tyr (non-receptor)							
200	4.8	Nek6; Nek7	215; \$204	putative serine-threonine protein kinase	TTAAHSLVGTYYM#S*PER^IHENGYNFK^	Q9HC98; Q8TDX7	36; 35	5	1,739,510
201		Protein kinase, atypical							
202	-1.4	TIF1-alpha	\$811	transcriptional intermediary factor 1 alpha isoform b	SEWLDPQK^S*PLHVGETR^	Q15164	117	1	2,951,166
203	42.6	TIF1-beta	\$752, \$757	tripartite motif-containing 28 protein	LQEK^LS*PPYSS*PQFAQDVGR^	Q13263	89	2	2,408,282
205	2.7	TIF1-beta	\$757	tripartite motif-containing 28 protein	LSPPYSS*PQFAQDVGR^	Q13263	89	2	2,028,460

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Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
206		Protein kinase, dual-specificity							
207	-1.7	Myt1	\$143	protein kinase Myt1 isoform 1	SMS*PFRGPK	Q99640	55	4	2,234,866
208		Protein kinase, regulatory subunit							
209	1.3	CK2-B	\$209	casein kinase 2, beta polypeptide	IHPM#AYQLQLQAASNFKS*PVK	P67870	25	14	25,701,286
210		RNA processing							
211	1.7	BAT2; BAT2 iso1	\$1293; \$1306	HLA-B associated transcript-2	AAAKS*PDLNQNQSDQANEWEETASESSDFTSER	P48634-2; P48634	228; 229	2	248,920
212	-1.9	CASC3	\$265	metastatic lymph node 51	YGS*PPQRDPNWNNGER	Q15234	76	1	3,790,714
213	3.6	ELAVL1	\$202	ELAV-like 1	NVALLSQLYHS*PAR^R^A	Q15717	36	5	38,986,096
214	2.6	FIP1L1	\$259	FIP1 like 1 isoform 2	AEFTS*PPSLFK^A	Q6UN15	67	2	5,383,335
217	1.4	hnRNP A3; RP11-223F20.1	\$356; \$254	heterogeneous nuclear ribonucleoprotein A3	SS*GSPYGGGYGSGGGSGGYGSR	P51991; Q5T6S7	40; 28	61	23,044,022
218	4.6	hnRNP A3; RP11-223F20.1	\$356, \$358; \$254, \$256	heterogeneous nuclear ribonucleoprotein A3	GGSGFGR^SS*GS*PYGGGYGSGGGSGGYGSR^A	P51991; Q5T6S7	40; 28	1	599,481
219	4.6	hnRNP A3; RP11-223F20.1	\$356, 370; \$254, 268	heterogeneous nuclear ribonucleoprotein A3	SS*GSPYGGGYGSGGGSGGYGSR^A	P51991; Q5T6S7	40; 28	1	311,883
220	1.2	hnRNP A3; RP11-223F20.1	\$358; \$256	heterogeneous nuclear ribonucleoprotein A3	SSGS*PYGGGYGSGGGSGGYGSR	P51991; Q5T6S7	40; 28	67	23,044,022
221	4.0	hnRNP F; hnRNP H1	\$310; \$310	heterogeneous nuclear ribonucleoprotein F	ATENDIYNFFS*PLNPVR^A	P52597; P31943	46; 49	1	1,397,606
222	4.5	hnRNP H2	\$310	heterogeneous nuclear ribonucleoprotein H2	ATENDIYNFFS*PLNPMR^A	P55795	49	2	670,855
223	11.2	hnRNP 2H9; hnRNP 2H9 iso2	\$216; \$201	heterogeneous nuclear ribonucleoprotein H3 isoform a	ATENDIANFFS*PLNPIR^A	P31942; P31942-2	37; 35	1	6,697,233
224	1.3	HNRPU2	\$226	heterogeneous nuclear ribonucleoprotein U-like 2	S*KSPLPPEEEAKEDEEDQTLVNLDTYSDLHFQVSK	Q1KMD3	85	2	2,655,534
225	-1.2	MPHOSPH10	\$163, \$167, \$171	M-phase phosphoprotein 10	SDLRKS*PVFS*DEDS*DLDFDIDLEQSK	Q00566	79	2	1,224,364
226	8.1	PABP 1	\$315	poly(A) binding protein, cytoplasmic 1	K^EFS*PFGTITSAK^A	P11940	71	2	3,475,671
227	1.7	PARN	\$163	poly(A)-specific ribonuclease (deadenylation nuclease) isoform 2	SQANGAGALSYVS*PNTSK^A	Q95453	73	2	5,120,919
228	-1.3	pumilio 2	\$136	pumilio homolog 2	GKAS*PFEEDQNR	Q8TB72	114	2	2,173,077
230	1.0	RBM15	\$128	RNA binding motif protein 15	LHSYSS*PSTK^A	Q96T37	107	7	1,028,148
231	-1.4	RBM15	\$741	RNA binding motif protein 15	TTAPTEGKS*PLKKEDR	Q96T37	107	4	400,095
232	1.0	RBM5	\$59	RNA binding motif protein 5	YDDYRDYDS*PERER	P52756	92	3	5,603,477
233	2.2	RBMS2	\$280, \$285	RNA binding motif, single stranded interacting protein 2	M#LAQSALS*PYLS*PVSSYQR^A	Q15434	44	2	646,533
234	3.4	CSIG	\$445	ribosomal L1 domain containing 1	IK^EEAVK^EK^SPS*LGK^A^K^A	Q76021	55	1	123,975
235	-2.1	SAMD4	\$231	sterile alpha motif domain containing 4	AYSS*PSTTPEAR	Q9UPU9	59	3	327,087
236	-1.3	SFRS10; TRA2A	\$264, \$266; \$260, \$262	splicing factor, arginine/serine-rich 10	S*PS*PYYSR^A	P62995; Q13595	34; 33	8	6,901,102
237	-1.1	SRp46	158, 173	splicing factor, arginine/serine-rich 2B	YSR^S*PYSR^A	Q9BR16	32	1	68,929
238	-1.1	SFRS9	\$211, \$216	splicing factor, arginine/serine-rich 9	GS*PHYFS*PFRPY	Q13242	26	3	29,240,724
239	-1.4	SFRS9	\$216	splicing factor, arginine/serine-rich 9	GSPHYFS*PFRPY	Q13242	26	2	5,810,279
240	-2.0	SRm300	\$1003, \$1012	splicing coactivator subunit SRm300	AQT*PPGSLSGS*KSPCPQEK	Q9UQ35	300	1	1,533,308
241	-2.0	SRm300	\$1003, \$1014	splicing coactivator subunit SRm300	AQT*PPGSLSGSK^A*S*PCPQEK^A	Q9UQ35	300	1	316,881
242	1.6	SRm300	\$1188	splicing coactivator subunit SRm300	DK^FS*PFVQDR^PESSLVFK^A	Q9UQ35	300	4	7,701,215
243	-1.4	SRm300	\$983, \$990, \$994	splicing coactivator subunit SRm300	VKPET*PPRQSHS*GSIS*PYPK	Q9UQ35	300	2	3,849,956
244	-1.4	SRm300	\$983, \$992, \$994	splicing coactivator subunit SRm300	VKPET*PPRQSHSGS*IS*PYPK	Q9UQ35	300	1	290,622
245	-1.5	SRm300	\$983, \$994	splicing coactivator subunit SRm300	VKPET*PPRQSHSGSIS*PYPK	Q9UQ35	300	2	2,318,678
246	-1.4	SRm300	\$992	splicing coactivator subunit SRm300	QSHSGS*ISPYPK	Q9UQ35	300	1	10,549,012
247	-1.3	SRm300	\$992, \$994	splicing coactivator subunit SRm300	QSHSGS*IS*PYPK^A	Q9UQ35	300	1	914,854
248	-1.4	SRm300	\$994	splicing coactivator subunit SRm300	QSHSGSIS*PYPK^A	Q9UQ35	300	1	7,332,409
249	2.4	STAU2	\$440	stau protein homolog 2	VISGTTGLGYS*PK^A	Q9NUL3	63	1	64,033,196
250	-1.1	THOC2	\$1401	THO complex 2 isoform 1	HKSES*PCESPYPNEKDKEK	Q8NI27	170	1	90,459
251	6.2	THOC2	\$1401, 1405	THO complex 2 isoform 1	SES*PCES*PYPNEK^DK^EK^A	Q8NI27	170	1	1,653,731
252	-1.1	THOC2	1405	THO complex 2 isoform 1	SESPCES*PYPNEK^DK^EK^A	Q8NI27	170	2	665,639
253	1.4	KIAA1802	\$108	zinc finger protein 828	ETDPVKs*PPLPEHQK	Q96JM3	89	1	7,366,008
254	-1.4	KIAA1802	\$382, \$386	zinc finger protein 828	SSSVSPSSWKS*PPAS*PESWK	Q96JM3	89	2	699,280

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Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
255		Receptor, channel, transporter or cell surface protein							
256	3.1	AAAS	\$33	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A)	GQVTLYEHNELVTGSSYES*PPPDFR ^Δ	Q9NRG9	60	1	808,187
257	-1.5	DENND4C	\$505	DENN/MADD domain containing 4C	HPTGNSITKS*PPLM#AK	Q5V289	187	5	5,503,587
258	6.9	hnRNP M	\$700	heterogeneous nuclear ribonucleoprotein M isoform a	SK ^Δ GCGVVK ^Δ FES*PEVAER ^Δ	P52272	77	3	1,955,295
260	3.4	GR	394, \$404	nuclear receptor subfamily 3, group C, member 1 isoform alpha	TVFSNGYS*SPSM#R ^Δ PDVSS*PPSSSSTATGPPPK ^Δ	P04150	86	1	305,439
261	2.8	NUP153	\$257	nucleoporin 153kDa	TSQLGDS*PFYPGK ^Δ	P49790	154	1	3,793,029
262	-2.4	POM121; POM121 iso3	\$435; \$412	nuclear pore membrane protein 121	NGPSSS*PFSSPASSR	Q96HA1; A8CG34	128; 125	2	1,496,393
263	2.3	POM121 iso3	95	POM121 membrane glycoprotein (rat)-like	TLFAS*PPAK ^Δ	A8CG34	125	1	18,263,462
264	3.1	STT3B	\$18	source of immunodominant MHC-associated peptides	SSLNSS*PWSGLMALGNSR ^Δ	Q8TCJ2	94	1	3,384,537
265	7.3	TOR1AIP1	20	lamina-associated polypeptide 1B	EGWGVYVT*PR ^Δ	Q5JTV8	66	1	1,602,671
266		Transcriptional regulator							
267	2.3	ARID1A	1599, 1604	AT rich interactive domain 1A isoform a	T*SPSK ^Δ *PFLHSGMK ^Δ	Q14497	242	1	591,420
268	3.1	ARID1A	\$764, \$772	AT rich interactive domain 1A isoform a	NPQMOPYSS*PQPGSALS*PR ^Δ	Q14497	242	1	294,287
269	1.7	BCLAF1 iso4; LOC731605	\$339; \$337	BCL2-associated transcription factor 1 isoform 2	FLK ^Δ *PPLHK ^Δ	Q9NYF8-4; XP_001129341	86; 80	3	3,278,121
270	2.5	BRD7	\$279, 289	bromodomain containing 7	EREDS*GDAEAHAFKS*PSKENK	Q9NP11	74	1	222,439
271	2.5	BRD7	\$279, 291	bromodomain containing 7	ER ^Δ EDS*GDAEAHAFK ^Δ *SPS ^Δ *K ^Δ ENK ^Δ	Q9NP11	74	1	323,036
272	-1.2	BRD7	289	bromodomain containing 7	EREDSGDAEAHAFKS*PSKENK	Q9NP11	74	1	157,433
273	1.1	BRD7	291	bromodomain containing 7	EDSGDAEAHAFK ^Δ *SPS ^Δ *K ^Δ ENK ^Δ	Q9NP11	74	1	76,964
274	1.1	CDYL	\$201	chromodomain protein, Y chromosome-like isoform a	ILVPSK ^Δ *PVK	Q9Y232	66	1	1,047,002
275	1.3	FLI1	241	Friend leukemia virus integration 1	GAWGNM#NSGLNKS*PPLGGAQTISK	Q01543	51	3	586,717
276	16.2	FLNA	\$1338, 1342	filamin A, alpha isoform 2	VEYTPYEGLHSVDVTYDGS*VPVS*SPFQVPVTEGCDPSR ^Δ	P21333	281	1	3,678,266
277	17.5	FLNA	\$1338, \$1343	filamin A, alpha isoform 2	VEYTPYEGLHSVDVTYDGS*VPVS*PFQVPVTEGCDPSR ^Δ	P21333	281	1	2,125,779
278	6.8	FLNA	\$1343	filamin A, alpha isoform 2	VEYTPYEGLHSVDVTYDGSVPVSS*PFQVPVTEGCDPSR ^Δ	P21333	281	1	1,060,177
279	6.2	FLNA	\$1436	filamin A, alpha isoform 2	DGSCSVEIPIYEAAGTYSILNVTYGGHQVPGS*PFK ^Δ	P21333	281	1	567,939
280	18.3	FLNA	1522, \$1533	filamin A, alpha isoform 2	EGPYSIS*VLYGDEEVPR ^Δ *SPK ^Δ	P21333	281	1	1,104,521
281	23.1	FLNA	\$1533	filamin A, alpha isoform 2	EGPYSISVLYGDEEVPR ^Δ *SPK ^Δ	P21333	281	5	19,905,208
282	2.5	FLNA	\$1630	filamin A, alpha isoform 2	YGGDEIPFS*PYR ^Δ VR ^Δ	P21333	281	5	26,018,528
283	1.4	FLNA	1734	filamin A, alpha isoform 2	FGGEHVPNS*PFQVTALAGDQPSVQPPLR ^Δ	P21333	281	1	1,646,387
284	5.6	FLNA	1946	filamin A, alpha isoform 2	YNEQHVPGS*PFTAR ^Δ	P21333	281	2	2,526,510
285	1.6	FLNA	\$2128	filamin A, alpha isoform 2	FADQHVPGS*PFSVK	P21333	281	4	10,442,139
286	1.5	FLNA	\$2414	filamin A, alpha isoform 2	FNGTHIPGS*PFK ^Δ	P21333	281	3	11,902,990
287	1.9	FLNA	\$2510	filamin A, alpha isoform 2	YGGPYHIGGS*PFK ^Δ AK ^Δ	P21333	281	3	8,568,052
288	2.1	FBP3	439	far upstream element (FUSE) binding protein 3	VGGTNLAGPAGFGQS*PFSQPPAPPHQNTFPPR ^Δ	Q96124	62	2	2,266,082
289	-13.2	TFII-I; TFII-I iso2	\$515; \$474	general transcription factor II, i isoform 4	FEAHPNDLYEGLPENIPFR ^Δ *SPSWYGIPR ^Δ	P78347; P78347-2	112; 108	3	1,362,840
290	3.3	TFIIIC-alpha	\$1653	general transcription factor IIIC, polypeptide 1, alpha 220kDa	GYYS*PGIVSTR	Q12789	238	1	547,131
291	1.0	hnRNP U; hnRNP U iso2	\$270; \$252	heterogeneous nuclear ribonucleoprotein U isoform b	AK ^Δ *S*PQPPVEEEDHFDVTWCLDTYNCDLHFK ^Δ	Q00839; Q00839-2	91; 89	2	2,487,595
292	3.2	NFAT90	762	interleukin enhancer binding factor 3 isoform b	KQPHGGQKPSYSGYQSHQGQQSYNQYS*PYSNYGPPQK	Q12906	95	1	441,336
293	2.0	NFAT90	\$792	interleukin enhancer binding factor 3 isoform b	GYNHGQGSYSYNSYNS*PGGGGSDYNYESK ^Δ	Q12906	95	4	2,059,700
294	2.4	NFAT90	860	interleukin enhancer binding factor 3 isoform b	QGGYSQSNYNS*PGSGQNYSGPPSSYQSSQGGYGR ^Δ	Q12906	95	1	1,656,583
295	6.7	MBD1; MBD1 iso4	37; 37	methyl-CpG binding domain protein 1 isoform 4	SDTYQS*PTGDR ^Δ	Q9UIS9; Q9UIS9-4	67; 55	1	1,533,308
296	2.5	MEF2A; MEF2A iso2	\$479, \$494; \$477, \$492	myocyte enhancer factor 2A isoform 2	GDFHS*PIVLGR ^Δ PPNTEDR ^Δ ES*PSVK ^Δ R ^Δ	Q02078; Q02078-2	55; 54	1	752,956
297	2.0	MTA2	\$435	metastasis-associated protein 2	GHLSRPEAQSL*PYTTSANR	Q94776	75	3	4,219,529

LEGEND: \$ = published site, * - phosphorylation, # = oxidized methionine

TABLE: CDK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
298	5.5	NACA	114	nascent polypeptide-associated complex alpha subunit isoform b	NILFVITK^PDVYK^S^PASDTYIVFGAEK^	Q13765	23	3	5,273,773
299	2.4	NFX1; NFX1 iso2; NFX1 iso3	\$310; \$326; \$326	nuclear transcription factor, X-box binding 1 isoform 1	R^QDPQVVS^PFSR^	Q12986; Q12986-2; Q12986-3	123; 114; 93	3	8,283,241
300	-1.7	NFX1 iso2; NFX1 iso3	\$50; \$50	nuclear transcription factor, X-box binding 1 isoform 1	NYSS^PPPCHLSR	Q12986-2; Q12986-3	114; 93	2	2,259,790
301	3.0	NOLC1	\$397	nucleolar and coiled-body phosphoprotein 1	NSSNK^PAVTTK^S^PAVK^PAAAPK^	Q14978	74	3	667,838
302	4.2	NOLC1	\$622, \$623	nucleolar and coiled-body phosphoprotein 1	R^AS^S^PFR^R^	Q14978	74	2	342,785
303	3.7	Rb	\$601, \$612	retinoblastoma 1	DREGPTDHLSEACPLNPLQNNHT^AADM^YLS^PVR^S^PK	P06400	106	1	560,701
304	3.7	Rb	\$608, \$612	retinoblastoma 1	DR^EGPTDHLSEACPLNPLQNNHTAADM^YLS^PVR^S^PK^	P06400	106	2	1,112,425
305	-1.4	RNPC2	\$97	RNA binding motif protein 39 isoform b	YRS^PYSGPK	Q14498	59	7	26,111,994
306	3.8	RDBP	\$281	RD RNA-binding protein	GAFS^PFGNIIDLSM^DPPR^	P18615	43	3	1,563,469
307	1.9	TIF-IA	\$44	RRN3 RNA polymerase I transcription factor homolog	ALENDFNS^PPR^K^	Q9NYV6	74	2	1,850,639
308	3.8	SART3	778	squamous cell carcinoma antigen recognized by T cells 3	PMFVS^PCVDK^	Q15020	110	1	599,238
309	-1.6	PSF	379	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	NLS^PYVSNELLEAFSQFGPIER	P23246	76	1	360,966
310	-2.2	Sin3A	274	transcriptional co-repressor Sin3A	VSKPSQLQAHTPASQQTPLPPYAS^PR	Q96ST3	145	1	300,854
311	5.1	SQSTM1	\$170	sequestosome 1	LAFPS^PFGHLESGFHSR^	Q13501	48	1	647,961
312	3.6	supervillin; supervillin iso2	\$86; \$86	supervillin isoform 1	SR^YCTETSGVHGDS^PYGSGTMDTHSLESK^	O95425; O95425-2	248; 201	1	517,673
313	2.1	TCF12	\$305, \$313	transcription factor 12 isoform b	GSTSS^PYVAASHT^PPINGSDSLGR^	Q99081	73	1	6,330,579
314	2.4	Trap150	\$248, \$253	thyroid hormone receptor associated protein 3	ER^S^PALK^S^PLQSVVVR^	Q9Y2W1	109	3	10,585,348
315	-2.2	Trap150	\$253	thyroid hormone receptor associated protein 3	SPALK^S^PLQSVVVR^	Q9Y2W1	109	1	251,438
316	-1.5	Trap150	\$320	thyroid hormone receptor associated protein 3	SPVGKS^PPSTGTYGSSQKEESAASGGAAYTKR	Q9Y2W1	109	2	296,379
317	-1.4	Trap150	\$698	thyroid hormone receptor associated protein 3	HGLAHDEM^K^S^PR^EPGYK^	Q9Y2W1	109	1	29,623
318	4.4	TMF1	\$102, \$112	TATA element modulatory factor 1	TVVDESENFSAFLS^PTDVQTIQK^S^PVSK^PPAK^	P82094	123	1	245,817
319	4.6	UBA3	399	ubiquitin-activating enzyme 3 isoform 1	LQEVLDYLTNSASLQM^K^S^PAITATLEGK^	Q8TBC4	52	1	441,901
320	1.8	Nice-4; Nice-4 iso2	\$416; \$416	ubiquitin associated protein 2-like isoform b	NPSDSAVHS^PFTK^	Q14157; Q14157-1	115; 104	3	2,370,479
321	2.8	HYD	\$110	ubiquitin protein ligase E3 component n-recogin 5	TSDS^PWFLSGSETLGR^	O95071	309	1	1,684,827
322	2.2	WHSC2	248, \$254, \$256	Wolf-Hirschhorn syndrome candidate 2 protein	QAFPR^SPT^APSVFS^PT^GNR^TPIPPSR^	Q9H3P2	59	1	717,333
323	-1.1	ZNF318	\$214	zinc finger protein 318	YISQEEGLS^PFLGQLDEDYR	Q5VUA4	251	1	239,109
324	Translation								
325	-1.8	CDA02	\$506	eukaryotic translation initiation factor 2A	SDK^S^PDLAPTPAQSTPR^	Q9BY44	65	3	5,603,477
326	7.1	CDA02	\$506, \$518	eukaryotic translation initiation factor 2A	SDK^S^PDLAPTPAQST^PR^	Q9BY44	65	1	444,471
327	-1.3	elf2B-epsilon	\$544	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	GGs^PQMDDIK	Q13144	80	4	5,317,409
328	2.1	elf3-eta	\$239	eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa	GYIFLEYAS^PAHAVDAVK^	P55884	92	2	4,463,192
329	3.0	elf3E	\$399	eukaryotic translation initiation factor 3, subunit 6 48kDa	LGHVVMGNNAVS^PYQQVIEK^	P60228	52	4	2,722,373
330	4.1	elf4B	\$93	eukaryotic translation initiation factor 4B	SR^LPK^S^PPYTAFLGNLPYDVTEESIK^EFFR^	P23588	69	1	608,180
331	-1.2	RPL4	\$295	ribosomal protein L4	ILK^S^PEIQR^	P36578	48	1	1,738,641
332	8.1	RPS17	\$129	ribosomal protein S17	LLDFGSLSNLQVTQPTVGM^NFK^T^PR^	P08708	15	1	4,683,244
333	Tumor suppressor								
334	-1.3	hamartin	\$505	tuberous sclerosis 1 protein isoform 1	GGFDS^PFYR^	Q92574	130	1	2,640,368
335	Ubiquitin conjugating system								
336	-1.6	NEDD4L	\$473, \$479, \$487	neural precursor cell expressed, developmentally down-regulated 4-like	DT^LSNPQS^PQPS^PYN^S^PKPQHK	Q7Z5N3	112	1	2,720,183
337	-1.2	NEDD4L	\$475, \$483, \$487	neural precursor cell expressed, developmentally down-regulated 4-like	DTLS^NPQSPQS^PYN^S^PKPQHK	Q7Z5N3	112	1	226,410

LEGEND: \$ = published site, * - phosphorylation, # = oxidized methionine

TABLE: CDK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
338	-1.5	NEDD4L	\$479, \$483, \$487	neural precursor cell expressed, developmentally down-regulated 4-like	DTLSNPQS*PQPS*PYNS*PKPQHK	Q7Z5N3	112	2	3,399,728
339	-1.1	NEDD4L	\$483, \$487	neural precursor cell expressed, developmentally down-regulated 4-like	DTLSNPQSPQPS*PYNS*PKPQHK	Q7Z5N3	112	1	695,000
340	-2.5	NEDD4L	\$487	neural precursor cell expressed, developmentally down-regulated 4-like	DTLSNPQSPQSPYNS*PKPQHK	Q7Z5N3	112	1	460,536
341		Unknown function							
342	2.9	HRBL	468	ArfGAP with FG repeats 2	LGQR*PLSQPAGISTNPFM#TGPSSS*PFASK*PPTNPFL	Q95081	49	1	516,246
343	2.8	ATAD2	337, \$342	ATPase family, AAA domain containing 2	LSS*AGPRS*PYCK	Q6PL18	159	2	320,634
344	-1.5	ATAD2	\$342	ATPase family, AAA domain containing 2	LSSAGPRS*PYCK	Q6PL18	159	1	1,012,270
345	-1.7	BAT2L	\$776, 792	HLA-B associated transcript 2-like	VRS*PDEALPGGLSGCSSGS*GHSPYALER	Q5JSZ5	166	1	359,735
346	-1.7	BAT2L	\$776, \$795	HLA-B associated transcript 2-like	VRS*PDEALPGGLSGCSSGSHS*PYALER	Q5JSZ5	166	2	359,735
348	0.0	BAZ2B	254, 271	bromodomain adjacent to zinc finger domain, 2B	S*LKKVIAALSNNPKATSSS*PAHPK	Q9UIF8	221	1	19,743,826
349	1.1	BXDC2	\$261	BRIX	IFQGSFGGPTLYENPHYQS*PNM#HR^	Q8TDN6	41	4	4,517,626
350	1.1	C10orf47	\$215	hypothetical protein LOC254427	MAGNEALSPTS*PFR	Q86WR7	46	1	446,722
351	2.0	C15orf39	322	hypothetical protein LOC56905	GTGYQAGGLGS*PYLR^	Q6ZRI6	111	1	883,545
352	-1.5	C15orf42	820	leucine-rich repeat kinase 1	LAGVLPTDFSDDSM#TQENKS*PLLSVPFLSSAR	Q7Z2Z1	211	1	448,254
353	5.1	C19orf21	\$430	hypothetical protein LOC126353	IPPDAYQPYLS*PGTPQLEFSAFGAFGK^PSSLSTAEAK^	Q8IVT2	75	1	1,030,581
354	4.5	C19orf21	\$430, \$433	hypothetical protein LOC126353	IPPDAYQPYLS*PGT*PQLEFSAFGAFGK^PSSLSTAEAK^	Q8IVT2	75	2	1,052,211
355	5.1	C19orf21	\$433	hypothetical protein LOC126353	IPPDAYQPYLSPGT*PQLEFSAFGAFGK^PSSLSTAEAK^	Q8IVT2	75	2	1,030,581
356	-1.7	KIAA0889	\$146	hypothetical protein LOC140710	VYYS*PPVAR	Q94964	56	1	8,338,975
357	-1.4	MGC5509	184	ashwin	K*SPS*GPVK^SPPLSPVGTTPVK^	Q9BVC5	26	1	718,006
358	-1.4	MGC5509	\$189	ashwin	KSPSGPVKS*PPLSPVGTTPVK	Q9BVC5	26	1	2,484,597
359	-2.1	MGC5509	\$189, \$198	ashwin	KSPSGPVKS*PPLSPVGTTPVK	Q9BVC5	26	1	406,046
360	-1.3	RAP140	979	retinoblastoma-associated protein 140 isoform a	SSDYQFPSS*PFTDTLK^	Q9UK61	189	1	962,023
361	1.3	RBM1; RBMX	\$208, \$208	kynurenine aminotransferase III isoform 1	DVYLS*PR^	Q96E39; P38159	42; 42	12	56,054,444
363	1.0	CCNL1	\$352	cyclin L1	AEEKS*PISINVK	Q9UK58	60	3	2,045,372
364	-91.1	CHD1	\$1677, 1683	chromodomain helicase DNA binding protein 1	ASSSGPR^S*PLDQR^S*PYGSR^	NP_001261	197	1	771,764
365	-1.4	CHD1	1687	chromodomain helicase DNA binding protein 1	SPYGS*R^SPFEHSVEHK^	NP_001261	197	1	1,813,533
366	-1.6	CTAGE5	\$517	CTAGE family, member 5 isoform 1	EHS*PYGPSPLGWPSSETR	Q15320	91	1	1,142,728
367	-1.8	CTAGE5	\$517, \$522	CTAGE family, member 5 isoform 1	EHS*PYGPS*PLGWPSSETR	Q15320	91	5	57,649,124
368	3.0	KIAA1433	\$523, \$527	CTTNBP2 N-terminal like	FTSQGQPIK^PVS*PNSS*PFGTDYR^	Q9P2B4	70	1	2,763,627
369	-3.5	KIAA1433	\$568	CTTNBP2 N-terminal like	VSSPLSPLSPGIKS*PTIPR	Q9P2B4	70	1	8,866,493
370	1.4	DCBLD1	602	discoidin, CUB and LCCL domain containing 1	HEYALPLAPPEYAT*PIVER^	Q8N8Z6	78	1	1,982,976
371	1.6	ECE1	\$51	endothelin converting enzyme 1 isoform 3	ATLDEEDLVDSLSEGDYVNGLVQVNFHS*PR^	P42892	87	1	351,258
372	-1.6	ETV3	245, 250	ets variant gene 3	PGMYDPDHS*PFAVS*PIPIGR	P41162	57	1	2,518,546
373	4.8	FAM21A; FAM21B	1091, \$1114; 1003, \$1026	hypothetical protein LOC387680	AASGEDS*TEEALAAAAAPWEGGPVPGVDR^S*PFAK^	A2A3S2; Q5SNT6	147; 137	1	400,332
374	1.4	FAM21A; FAM21B	\$1114; \$1026	hypothetical protein LOC387680	AASGEDSTEALAAAAAPWEGGPVPGVDR^S*PFAK^	A2A3S2; Q5SNT6	147; 137	2	2,571,815
375	2.4	FAM21A; FAM21B; FAM21C	\$352; \$264; \$352	hypothetical protein LOC387680	LTDEDFS*PFGSGGGLFSGGK^	A2A3S2; Q5SNT6; Q9Y4E1	147; 137; 145	2	3,424,137
376	1.9	FAM21A; FAM21B; FAM21C	\$441; \$353; \$441	hypothetical protein LOC387680	KS*PYGPPPTGLFDDDDGDDDDFFSAPHKPSK	A2A3S2; Q5SNT6; Q9Y4E1	147; 137; 145	1	991,583
377	1.6	FAM62A	\$820	family with sequence similarity 62 (C2 domain containing), member A	HLS*PYATLTVGDSSHK^	Q9BSJ8	123	1	1,229,525
378	-1.7	FMNL1	\$1031	formin-like 1	EAAAQEAADTPGKGEPAPKS*PPKAR	Q95466	122	3	538,753
379	-1.9	KIAA0443	512	G protein-coupled receptor associated sorting protein 2	STS*PFGIPEEASEMLEAKPK	Q96D09	94	1	310,236
380	2.4	HEBP2	181	heme binding protein 2	VYYTAGYNS*PVK	Q9Y5Z4	23	1	1,130,086
381	4.7	HEG1	1293	HEG homolog 1	SGDFQM#S*PYAEYK^NPR^	Q9ULI3	147	1	658,462

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STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
382	2.3	HOMER	327	homeodomain leucine zipper protein	VGPTEYLS*PDM#QR^	Q8IX15	59	2	1,787,766
383	3.6	HSPA12A	§23	heat shock 70kDa protein 12A	ETAPTAYSS*PAR	Q43301	75	1	269,651
385	1.5	KIAA0802	§613	hypothetical protein LOC23255	DHAPSIPTS*PFGDSLSESTELRR	Q9Y4B5	209	1	2,165,261
386	1.0	KIAA1602	177	hypothetical protein LOC57701	EVCWEQQLR^PGGPGPPAAPPPALDALS*PFLR^	Q9HCH0	139	2	405,286
387	1.8	KIAA1671	981	Uncharacterized protein KIAA1671	TDYVS*PTASALR^	Q9BY89	197	2	5,081,862
388	1.2	LOC100129899	333	PREDICTED: similar to hCG2040631	VS*PFLGR^	XP_001715056	39	1	2,067,018
389	-1.2	LOC100131017	§112	PREDICTED: similar to zinc finger protein 316	GGDAK^S*PVLQEK^	A6NFI3	108	4	69,187
390	5.1	LSM14B	§106, §115	LSM14 homolog B	AQHRTLQDPAIVQSSLSGSASAS*PFQPHVPYS*PFR^	Q9BX40	42	2	48,545,904
391	-1.3	LY6K	23	lymphocyte antigen 6 complex, locus K	GGR^GS*PYR^PDPGR^	NP_059997	25	1	387,721
392		MGC35274	206	LysM, putative peptidoglycan-binding, domain containing 2	DEES*PYATSLYHS	Q8IV50	23	1	438,170
393	4.0	MBD2; MBD2 iso3	§181; §181	methyl-CpG binding domain protein 2 isoform 1	SDVYFYS*PSGK^K^	Q9UBB5; Q9UBB5-3	43; 32	3	8,496,962
394		MTMR1	§653	myotubularin-related protein 1	GSS*PSHSATSVHTSV	Q13613	75	1	2,067,978
395	2.3	MYO19	685	myosin head domain containing 1 isoform 3	RLHPTSSGPDSP*PYPAK	Q96H55	109	2	797,829
396	-1.5	NFI-C	§333	nuclear factor I/C isoform 1	TEM#DK^S*PFNSPSPQDSPR^	P08651	56	4	4,436,306
397	-1.4	NFI-C	§333, §339	nuclear factor I/C isoform 1	TEM#DK^S*PFNSPS*PQDSPR^	P08651	56	5	2,370,479
398	-1.4	NFI-C	§333, §339, §343	nuclear factor I/C isoform 1	TEMDS*PFNSPS*PQDS*PR	P08651	56	1	1,278,488
399	10.1	NUDCD3	340	NudC domain containing 3	K^GWDAGEGS*PFR^	Q8IVD9	41	2	1,400,777
400	5.7	NUDT9	68	nudix -type motif 9 isoform a	AR^TS*PYPGSK^VER^	Q9BW91	39	1	460,025
402	2.1	PLEKHG3	§76	pleckstrin homology domain containing, family G, member 3	GPLS*PFNSR	A1L390	134	1	3,291,614
403	4.6	RAB3GAP2	§450	rab3 GTPase-activating protein, non-catalytic subunit	ADFS*PFGNSQGFSR^	Q9H2M9	156	3	1,282,624
404	1.9	RBBP6	654	retinoblastoma-binding protein 6 isoform 2	LK^EESK^S*PYSGSSYSR^	NP_061173	197	1	206,573
405	2.1	RBM23; RBM23 iso2	128; 112	RNA binding motif protein 23 isoform 1	VHYR^S*PPLATGYR^	Q86U06; Q86U06-2	49; 47	1	3,841,399
406	3.8	RBMS3	268	RNA binding motif, single stranded interacting protein 3 isoform 3	EGEAGMALTYDPTAAIQNGFYSS*PYSIATNR^	Q6XE24	48	1	1,191,503
407	-1.9	SR-A1	§872	SR-related CTD-associated factor 1	ES*RSPFLKPDER	Q9H7N4	139	2	662,255
408	-1.3	SR-A1	§874	SR-related CTD-associated factor 1	DRESRS*PFLKPDER	Q9H7N4	139	2	4,792,485
409	4.0	KIAA0310	125, 129	SEC16 homolog A	AHASPFS^GALT*PSAPPGPEMNR^	O15027	252	1	4,312,749
410	1.6	KIAA0310	29	SEC16 homolog A	SVFWASS*PYR^	O15027	252	2	4,838,534
411	-2.2	KIAA1732	§744	SET domain containing 2	KSES*PFRETEPLVSPHQDK	Q9BYW2	288	4	2,646,525
412	-1.2	SH2D5	§147	SH2 domain containing 5 isoform 2	LGNPYCS*PTLVR	Q6ZV89	37	2	1,634,938
413	-6.4	SH3BP4	§637	SH3-domain binding protein 4	IILS*PFATTTK	Q9P0V3	107	2	36,851,028
414	1.2	KIAA1458	165	SLAIN motif family, member 2	LSGWEEESWLYSS*PK	Q9P270	66	2	1,641,013
415	7.0	MCT1	§483, §498	solute carrier family 16, member 1	AAES*PDQK^DTEGGPK^EES*PV	P53985	54	2	3,652,795
416	-1.1	MCT1	§498	solute carrier family 16, member 1	DTEGGPK^EES*PV	P53985	54	6	2,173,077
417	3.3	FLJ14803	§222, §228	transmembrane protein 209	YR^SS*PTVYNS*PTDK^EDYMTDLR^	Q49A50	63	2	794,888
418	3.3	LAP2A	§423	thymopoietin isoform beta	FQETFLS*PPR^	P42166	75	4	30,293,714
419	-1.0	KIAA1856	§263	trinucleotide repeat containing 18	LAER^LS*PFLAESK^	O15417	315	2	1,002,285
420	-1.5	TNRC6B	§1322	trinucleotide repeat containing 6B isoform 2	GGG*PYNQFDIIPGDTLGGHTGPAGDSWLPK	Q9UPQ9	183	1	2,669,974
421	-1.1	TNRC6B	§1322, 1345	trinucleotide repeat containing 6B isoform 2	GGG*PYNQFDIIPGDTLGGHTGPAGDS*WLPK^SPPTNK^	Q9UPQ9	183	1	589,308
422	-1.1	TNRC6B	§1322, §1351	trinucleotide repeat containing 6B isoform 2	GGG*PYNQFDIIPGDTLGGHTGPAGDSWLPK^S*PPTNK^	Q9UPQ9	183	1	589,308
423	-1.3	TRPS1	§90	zinc finger transcription factor TRPS1	AGFNYES*PSK^GGNFPSFPHDEVTDR^	Q9UHF7	142	1	379,677
424	-1.3	TRPS1	§92	zinc finger transcription factor TRPS1	AGFNYESPS^KGGNFPSFPHDEVTDR	Q9UHF7	142	1	665,022
425	3.1	UBAP2	1114	ubiquitin associated protein 2	SQASK^PAYGNS*PYWTN	Q5T6F2	117	1	4,384,277
426	1.5	UBAP2	630	ubiquitin associated protein 2	IPYQS*PVSSSESAPGTIMNGHGGGR^	Q5T6F2	117	6	6,605,111
427	4.5	p37 adaptor	§56, §59	UBX domain protein 2B	ATVFK^S*PR^*PPQR^	XP_059929	37	1	707,842

LEGEND: § = published site, * - phosphorylation, # = oxidized methionine

SUMMARY TABLE

TABLE: CDK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CDK Substrate Motif, K/RpSPXK/R; CST #2324
Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
428	1.2	UVRAG	\$518	UV radiation resistance associated	LQYKT*PPPSYNALAQPVTTVPSMGETER	Q9P2Y5	78	4	1,354,188
429	2.8	WDR47	\$289, \$292	WD repeat domain 47	AAYADLLTPLIS*K^LS*PYPSSPM#R^	Q94967	102	1	582,118
430	2.3	HGR8	\$39	high glucose-regulated protein 8	DGLNDDDFEPYLS*PQAR^	Q9Y5A9	62	1	7,358,612
431	-2.4	KIAA0853	\$370, \$372	zinc finger CCCH-type containing 13	S*AS*PYPSHSLSSPQR	Q5T200	197	1	314,947
432	-1.8	KIAA0853	\$370, \$372, \$380	zinc finger CCCH-type containing 13	S*AS*PYPSHSLS*SPQR^	Q5T200	197	1	2,382,931
433	-1.8	KIAA0853	\$370, \$372, \$381	zinc finger CCCH-type containing 13	S*AS*PYPSHSLSS*PQR	Q5T200	197	2	5,441,291
434	-1.1	KIAA1064	\$1265, \$1275	zinc finger CCCH-type containing 4	T*GSGSPFAGNS*PAR^EGEQDAASLK^DVFK^	Q9UPT8	140	1	3,604,441
435	-1.1	KIAA1064	1267, \$1275	zinc finger CCCH-type containing 4	TGS*GSPFAGNS*PAREGEQDAASLK	Q9UPT8	140	1	2,274,178
436	-1.8	KIAA1064	\$1269	zinc finger CCCH-type containing 4	TGSGS*PFAGNSPAR	Q9UPT8	140	2	3,056,060
437	-1.3	KIAA1064	\$1269, \$1275	zinc finger CCCH-type containing 4	TGSGS*PFAGNS*PAREGEQDAASLKDVFK	Q9UPT8	140	7	59,262,116
438	1.2	C10orf56	93	zinc finger, CCHC domain containing 24		Q8N2G6	27	1	997,109
439	-1.9	C10orf56	93, 97	zinc finger, CCHC domain containing 24	GAS*PYGS*LNNIADGLSLTEHFSDLTLTSEAR	Q8N2G6	27	1	327,297
441	-1.6	ZNF609	1311	zinc finger protein 609	S*KSPITSDKTSQER	O15014	151	1	17,123
442	-1.4	ZNF609	758	zinc finger protein 609	AEEGK^S*PFR^ESSGDGMK^	O15014	151	13	1,169,757
443	-1.1	ZRSR2	\$349	U2 small nuclear RNA auxiliary factor 1-like 2	DIYLS*PDRTGSSFGK	Q15696	58	2	1,791,963
444		lipid binding							
445	1.1	OSBPL10	\$223	oxysterol-binding protein-like protein 10	HLSVGAPGVVTITHHSK*PAAAR	Q9BXB5	84	4	5,893,644
446	1.3	SDPR	\$288, \$293	serum deprivation response protein	ISSGKSS*PFKVS*PLTFGR	Q95810	47	4	2,726,903

LEGEND: \$ = published site, * - phosphorylation, # = oxidized methionine