

**TABLE: CK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC**

**STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CK Substrate Motif, pS/pTD/EXD/E; CST #BL4176**

*Treatments: Nocodazole (Heavy), Untreated (Light)*

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity	
1		<b>Adaptor/scaffold</b>								
2	-1.5	DNMBP	1436	dynamins binding protein	CPS*DPDSTSQPR <sup>^</sup>	Q6XZF7	177	5	876,837	
3	1.1	KPNA3	\$60	karyopherin alpha 3	NVPQEESELEDS*DVDADFK <sup>^</sup>	O00505	58	2	1,551,919	
4	1.3	KPNA4	\$60	karyopherin alpha 4	NVPHEDECEDS*DIGDGYR <sup>^</sup>	O00629	58	4	2,546,838	
5	-1.5	LMO7; LMO7 iso2; LMO7 iso3	\$276; \$276; \$276	LIM domain only 7	GGREGFES*DTDESEFTFK	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	3	3,155,504	
6	<b>-4.0</b>	NMD3	\$470	NMD3 homolog	DSAIPVESDT*DDEGAPR	Q9Y2Z6	58	2	3,007,157	
7	-1.9	RanBP2; RGPD1; RGPD4	\$2293; 1310; 1318	RAN binding protein 2	LNQSGTSVGT*DEESDVTQEEER	P49792; NP_001019628; A6NKT7	358; 197; 198	2	1,046,503	
8	-1.1	kanadaplin	\$466	solute carrier family 4 (anion exchanger), member 1, adaptor protein	NWEDEDVYDS*DDDTFLDR	Q9BWU0	89	7	18,247,270	
9	-1.6	SMARCAD1	\$146	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 isoform a	R^NDDIS^ELEDLSELEDLK^DAK <sup>^</sup>	Q9H4L7	117	1	2,559,352	
10	1.0	SMARCAD1	\$146, \$152	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 isoform a	RNDDIS^ELEDLS^ELEDLDAK	Q9H4L7	117	1	4,536,439	
11	-1.1	SMARCAD1	\$152	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 isoform a	RNDISELEDS^ELEDLDAK	Q9H4L7	117	1	4,010,445	
12	2.2	SYNE2	\$6361, 6365	spectrin repeat containing, nuclear envelope 2 isoform 1	LTSCTPGLDEK^EAS^ENET^DMEDPR <sup>^</sup>	Q8WXH0	796	1	683,133	
13	-1.1	ZO2; ZO2 iso6	\$424, \$430, \$431; \$424, \$430, \$431	tight junction protein 2 (zona occludens 2) isoform 1	HQYS*DYDYHS*S^SEKLK	Q9UDY2; NP_963923	134; 118	1	479,176	
14	-1.3	ZO2; ZO2 iso6	\$424, \$430, \$432; \$424, \$430, \$432	tight junction protein 2 (zona occludens 2) isoform 1	RHQYS*DYDYHS*SS^EKLK	Q9UDY2; NP_963923	134; 118	1	1,624,903	
15		<b>Adhesion or extracellular matrix protein</b>								
16	-1.9	CDH6	\$786	cadherin 6, type 2 preproprotein	LADMYGGVDS*DKDS	P55285	88	1	809,944	
17	-1.8	Erbin	\$440	ERBB2 interacting protein isoform 7	TEDVMFIS^DNEFSNPFLWEEQR	Q96RT1	158	3	2,544,717	
18	-1.1	nav1; nav1 iso2	\$391; \$391	neuron navigator 1	SGYM#S^DSDLGK	Q8NEY1; Q8NEY1-2	202; 202	4	1,909,782	
19		<b>Apoptosis</b>								
20	-1.3	p400	\$941, \$945	E1A binding protein p400	KAS^ISLT^DDEVDDEEETIEEEANEGVVDHQTELSNLAK	Q96L91	344	1	2,492,019	
21	-1.5	DBC-1	\$675, \$678, \$681	p30 DBC protein	S^VAS^NQS^EMEFSSLQDMPK <sup>^</sup>	Q8N163	103	1	1,516,290	
22	-1.1	PDCD5	\$118	programmed cell death 5	R^K^VMDS^DEDDDY	O14737	14	2	5,581,027	
23		<b>Cell cycle regulation</b>								
24	1.1	BAT2D1; BAT2D1 iso8	\$1249; \$1249	HBxAg transactivated protein 2	SESS*DFEVVPK <sup>^</sup>	Q9Y520; NP_055987	317; 309	1	3,362,396	
25	-1.4	BAT2D1; BAT2D1 iso8	1263, \$1265, \$1267; 1263, \$1265, \$1267	HBxAg transactivated protein 2	QRGS^ET^DT^DSEIHESASDKDLSK	Q9Y520; NP_055987	317; 309	2	2,438,642	
26	-1.4	BAT2D1; BAT2D1 iso8	1263, \$1265, 1269; 1263, \$1265, 1269	HBxAg transactivated protein 2	QR^GS^ET^DTDS^EIHESASDK^DLSK <sup>^</sup>	Q9Y520; NP_055987	317; 309	1	1,460,983	
27	-2.0	BAT2D1; BAT2D1 iso8	1263, \$1265, 1274; 1263, \$1265, 1274	HBxAg transactivated protein 2	RQRGS^ET^DTDSEIHES^ASDKDLSK	Q9Y520; NP_055987	317; 309	1	574,755	
28	-1.2	BAT2D1; BAT2D1 iso8	\$1265, \$1267; \$1265, \$1267	HBxAg transactivated protein 2	GSET^DT^DSEIHESASDKDLSK	Q9Y520; NP_055987	317; 309	1	691,600	
29	-1.2	BAT2D1; BAT2D1 iso8	\$1265, 1269; \$1265, 1269	HBxAg transactivated protein 2	GSET^DTDS^EIHESASDK^DLSK <sup>^</sup>	Q9Y520; NP_055987	317; 309	1	556,675	
30	1.2	BAT2D1; BAT2D1 iso8	\$1267; \$1267	HBxAg transactivated protein 2	GSETDT^DSEIHESASDKDLSK	Q9Y520; NP_055987	317; 309	2	724,329	
31	-1.1	CCNH	\$315	cyclin H	SKHEEEEW^DDDLVESL	P51946	38	5	16,580,431	
32	1.6	CCNH	\$315, \$322	cyclin H	SK^HEEEEW^DDDLVES^L	P51946	38	1	1,602,251	
33	-1.2	CLASP1; CLASP1 iso3	\$600; \$600	CLIP-associating protein 1	SR^S^DIDVNAASAK <sup>^</sup>	Q7Z460; Q7Z460-3	169; 165	2	9,078,943	
34	-1.7	MDC1	\$299, \$301	mediator of DNA damage checkpoint 1	SQPPGDS^DT^DVDDSRPPGPAEVHLER	Q14676	227	2	1,129,361	
35	-2.0	MDC1	\$329, \$331	mediator of DNA damage checkpoint 1	AQPFQFIDS^DT^DAEEERIPATPVVPMK	Q14676	227	3	2,522,733	
36	-1.1	MDC1	\$448, \$453	mediator of DNA damage checkpoint 1	SQTT^TERDS^DTDVEEEELPVENR	Q14676	227	1	1,626,962	

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

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37	-1.1	MDC1	§453, §455	mediator of DNA damage checkpoint 1	SQTTTTR^DS^DT^DVEEEELPVENR^A	Q14676	227	1	1,174,140
38	2.2	KI-67	§131	antigen identified by monoclonal antibody Ki-67	SSFSS^DPDEK^A^AQDSK^A	P46013	359	1	173,422
39	-1.3	PCM-1	§110	pericentriolar material 1	INFS^DLDQR	Q15154	229	2	8,137,676
40	-1.6	PCM-1	§530, §533, 537	pericentriolar material 1	KDEET^EES^EYDS^EHENSEPVTNIR	Q15154	229	2	653,733
41	-1.2	SEPT7	§228	cell division cycle 10 isoform 2	IYFFPET^DDEEENK^LVK^A	Q16181	51	3	4,354,616
42		<b>Cell development/differentiation</b>							
43		BRD1	§1052, §1055	bromodomain containing protein 1	VHGPTS^DLS^DID	Q95696	120	1	68,355,568
44		<b>Chaperone</b>							
45	1.5	FKBP4	435	FK506 binding protein 52	AEASSGDHPT^DTEMK^EEQK^A	Q02790	52	3	11,266,274
46	-1.2	HSP90B	§225	heat shock 90kDa protein 1, beta	EIS^DDEAEKEEKEEEDKDEEKPK	P08238	83	1	341,814
47	-1.1	NAP1L4	§125	nucleosome assembly protein 1-like 4	EFITGDVEPTDAESEWH^SENEEEELAGDMK	Q99733	43	1	755,750
48	-1.2	TEBP	§113	inactive progesterone receptor, 23 kD	DWEDDS^DEDMSNFR^A	Q15185	19	8	22,986,544
49		<b>Chromatin, DNA-binding, DNA repair or DNA replication protein</b>							
50	-1.3	ALKBH5; ALKBH5 iso2	§64, §69; §64, §69	alkB, alkylation repair homolog 5	K^YQEDS^DPER^S^DYEEQLQK^EEEAR^A	Q6P6C2; Q6P6C2-2	51; 44	2	7,497,092
51	1.0	ARID4B; ARID4B iso2	§790, §793; §704, §707	AT rich interactive domain 4B isoform 1	DIEVLS^EDT^DYEEDEVTKK	Q4LE39; Q4LE39-2	148; 138	3	1,247,601
52	-2.2	ATRX	§788	transcriptional regulator ATRX isoform 1	SSTSGS^DFDTK	P46100	283	2	65,672
53	-1.5	BAZ1A	§731	bromodomain adjacent to zinc finger domain, 1A isoform a	ELDQDMVT^EDEDPGSHK^RA	Q9NRL2	179	4	4,225,549
54	-1.7	CHD-3	383	chromodomain helicase DNA binding protein 3 isoform 3	KGGSYVFSQDEGPEPEAES^DLDSGVSHSASGRPDGPVR	Q12873	233	2	653,547
55	-1.1	CHD-4	§308, §310, §319	chromodomain helicase DNA binding protein 4	KRS^SS^EDDDLDVES^DFDDASINSYSVSDGSTR	Q14839	218	1	1,040,633
56	-1.2	CHD-4	§309, §310, §319	chromodomain helicase DNA binding protein 4	KRSS^S^EDDDLDVES^DFDDASINSYSVSDGSTR	Q14839	218	1	1,040,633
57	-1.2	MCM10	§85	minichromosome maintenance complex component 10 isoform 2	DEK^ENLATLFGDMEDLT^DEEEVPAQSTENR^A	Q7L590	98	1	1,772,365
58	-1.4	MCM2	§139	minichromosome maintenance complex component 2	GLLYDS^DEEDEERPAR	P49736	102	2	4,267,995
59	-1.5	MCM3	§704, §713	minichromosome maintenance complex component 3	DGDS^YDPYDFS^DTEEMPQVHTPK	P25205	91	1	12,449,639
60	-1.3	MCM3	§711	minichromosome maintenance complex component 3	DGDSYDPYDFS^DTEEMPQVHTPK	P25205	91	3	13,200,261
61	-1.5	MCM3	§711, §722	minichromosome maintenance complex component 3	DGDSYDPYDFS^DTEEMPQVHT^PK	P25205	91	5	12,449,639
62	-1.3	MCM3	§713	minichromosome maintenance complex component 3	DGDSYDPYDFS^DTEEMPQVHTPK^A	P25205	91	1	1,600,294
63	1.4	NAP1L1	§10	nucleosome assembly protein 1-like 1	EQS^ELDQDLDDVEVEEETGEETK^A	P55209	45	2	1,821,340
64	-1.5	POLD3	§307	polymerase (DNA directed), delta 3	VALS^DDETKETENMR	Q15054	51	2	740,423
65	-1.6	PRR12	§1561, §1568	proline rich 12	K^QETAAVCGET^DEEAGES^GGGIFR^A	Q9ULL5	211	2	3,307,277
66	1.1	Rad50	§690	RAD50 homolog isoform 1	VFQT^EAELEQVISDLQSK	Q92878	154	3	5,615,997
67	-1.3	EST1A	§479	Smg-6 homolog, nonsense mediated mRNA decay factor	TQTPQLHFLDT^DDEVSPTSWSGDSR	Q86US8	160	2	6,989,852
68	1.7	EST1A	§479, §484	Smg-6 homolog, nonsense mediated mRNA decay factor	TQTPQLHFLDT^DDEVS^PTSWSGDSR	Q86US8	160	2	4,880,879
69	-1.2	TMPO	§183	thymopoietin isoform beta	QNGSNDSDRY^DNEEDSKIELK	P42167	51	1	1,470,178
70	-1.7	TOP2B	§1581	DNA topoisomerase II, beta isozyme	KTSFDQDS^DVDIFPSPFTEPPSLPR	Q02880	183	1	3,990,703
71	1.4	UHRF1	§91	ubiquitin-like with PHD and ring finger domains 1 isoform 1	ERDSLS^DTSGCCCLGQSESDK	Q96T88	90	1	853,914
72	-1.1	WAPL	§77	wings apart-like homolog	VEEESTGDPFGFDS^DDESLPVSSK	Q7Z5K2	133	2	2,348,601
73	-1.3	Ukp68	527, 533	zinc finger CCHC-type containing 14 isoform 1	FIVTLDGVP^PPGYMS^DQEEEDMCFEGMKPVNQTAASNK	Q6PJ7T	83	1	2,001,763
74		<b>Cytoskeletal protein</b>							
75	-1.1	CLASP2; CLASP2 iso3	§370; §603	CLIP-associating protein 2	SRS^DIDVNAAGAK	Q75122; Q8NB74	141; 78	1	7,151,717
76	-1.2	CTNNA1	§641	catenin, alpha 1	TPEELDDS^DFETEDFVDR	P35221	100	11	30,435,712
77	-1.3	cortactin; cortactin iso2	24; 24	cortactin isoform a	ASAGHAVSIQADGAGADDWET^DPDFVNDVSEK^A	Q14247; Q96H99	62; 57	1	748,669
78	-1.6	BPAG1	5106, §5111, §5114	dystonin isoform 1e precursor	AS^SRRGS^DAS^DFDISEIQSVCSVDVTVPQTHRPTPR	Q94833	591	1	4,646,008
79	-1.9	BPAG1	§5111, §5114	dystonin isoform 1e precursor	RGS^DAS^DFDISEIQSVCSVDVTVPQTHRPTPR	Q94833	591	3	3,638,538
80	<b>7.0</b>	PLEKH1	339, 351	fermitin family homolog 2 isoform 2	LSIM^TSENHLNNS^DK^EVDEVAALS^DLEITLEGGK^A	Q96AC1	78	1	1,785,123
81	<b>-2.6</b>	KIF23; KIF23 iso2	§867; §763	kinesin family member 23 isoform 2	YMLTHQLAS^DGEIETK	Q02241; Q02241-2	110; 98	1	533,128
82	<b>-3.4</b>	KIF23; KIF23 iso2	927; 823	kinesin family member 23 isoform 2	SSTVAPAQPDGAESWT^DVETR	Q02241; Q02241-2	110; 98	2	2,430,036
83	-1.9	MYO18A; MYO18A iso4	§2038, §2043; §2023, §2028	myosin 18A isoform a	YSHS^YLSDS^DTEAK	Q92614; Q92614-4	233; 231	1	894,981

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

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84	-1.6	MYO18A; MYO18A iso4	§2041, §2043; §2026, §2028	myosin 18A isoform a	YSHSYLS*DS*DTEAK <sup>A</sup>	Q92614; Q92614-4	233; 231	1	873,776
85	-1.1	NudC	108	nuclear distribution gene C homolog	ELT*DEEAER	Q9Y266	38	2	656,210
86	1.5	palladin	§893	palladin	IAS*DEIQGTK <sup>A</sup>	Q8WX93	151	5	60,857,756
87	<b>3.2</b>	talin 1	§167	talin 1	LHT*DDELNLWDHGR <sup>A</sup>	Q9Y490	270	1	779,188
88		<b>Enzyme, misc.</b>							
89	-1.3	APMAP	19	chromosome 20 open reading frame 3	RPLRPQVVT*DDGQAPPEAK	Q9HDC9	46	1	201,528,512
90	-1.4	FBXL11	§28	F-box and leucine-rich repeat protein 11	RYEDDGIS*DDEIEGKR	Q9Y2K7	133	1	5,469,034
91	1.4	PDE4B; PDE4D; PDE4D iso2; PDE4D iso7	140; §197; §60; §133	phosphodiesterase 4B, cAMP-specific isoform 2	SDS*DYDLSPK <sup>A</sup>	Q07343; Q08499; Q08499-2; Q08499-7	83; 91; 76; 24	2	3,218,416
92	-1.5	PDIA6	§428	protein disulfide isomerase-associated 6	DGELPVEDDIDLS*DVELDDLKDEL	Q15084	48	1	599,821
93	-1.1	PLCD3	§496	phospholipase C delta 3	ALS*DREEEEEDDEEEVEAAQR	Q8TEC1	89	2	3,348,203
94	-1.5	PIPG	§744, §745, §748	peptidylprolyl isomerase G	FDHES*S*PGT*DEDK*SG	Q13427	89	8	8,067,238
95	-1.9	PPIG	§744, §748	peptidylprolyl isomerase G	FDHES*SPGT*DEDKSG	Q13427	89	1	124,421
96	-1.6	PPIG	§744, §748, §753	peptidylprolyl isomerase G	KFDHES*SPGT*DEDKS*G	Q13427	89	1	145,758
97	-1.5	PPIG	§745, §748	peptidylprolyl isomerase G	KFDHES*PGT*DEDKSG	Q13427	89	8	769,075
98	-1.3	PPIG	§745, §748, §753	peptidylprolyl isomerase G	KFDHES*PGT*DEDKS*G	Q13427	89	2	41,447
99	-1.6	PPIG	§748	peptidylprolyl isomerase G	KFDHES*PGT*DEDKSG	Q13427	89	2	84,578
100	1.4	senataxin	§1366	senataxin	R*LS*DCESTDVK <sup>A</sup>	Q7Z333	303	1	532,531
101	<b>3.6</b>	TOP2A; TOP2A iso2	§1374, §1377; §1400, §1403	DNA topoisomerase II, alpha isozyme	ELK*PKK*S*VVS*DLEADDVK <sup>A</sup>	P11388; P11388-2	174; 178	1	6,124,009
102	1.5	TOP2A; TOP2A iso2	§1377; §1403	DNA topoisomerase II, alpha isozyme	SVVS*DLEADDVK <sup>A</sup>	P11388; P11388-2	174; 178	1	25,197,170
103	1.4	TOP2A; TOP2A iso2	§1377, §1393; §1403, §1419	DNA topoisomerase II, alpha isozyme	SVVS*DLEADDVK*GSVPLSS*PPATHFPDETEITNPVK <sup>A</sup>	P11388; P11388-2	174; 178	1	3,274,956
104		<b>G protein or regulator</b>							
105	-1.8	CENTD2	§229	AriGAP with RhoGAP domain, ankyrin repeat and PH domain 1 isoform c	LPFEDDS*DYDEVPEEGPGAPAR	Q96P48-6	162	2	4,772,527
106	-2.3	ARHGEF2	§940	rho/rac guanine nucleotide exchange factor 2	LQDSS*DPDTGSEEEGSSR	Q8TDA3	111	2	201,612
107	-1.4	ARHGEF2	§940, §951, §959	rho/rac guanine nucleotide exchange factor 2	LQDSS*DPDTGSEEEGS*SR*LSPPHS*PR <sup>A</sup>	Q8TDA3	111	1	702,252
108	-1.2	GBF1	§662	golgi-specific brefeldin A resistance factor 1	SGCS*DLEEAVDSGADK* <sup>K</sup>	Q92538	206	2	3,432,485
109	-1.0	RIC8A	§435, §440	resistance to inhibitors of cholinesterase 8 homolog A	GLMAGGRPEGQYS*EDED*TDTEYKEAK	Q9NPQ8	60	5	4,685,826
110	1.1	RIC8A	§435, §442	resistance to inhibitors of cholinesterase 8 homolog A	GLM#AGGR*PEGQYS*EDED*TDTEYKEAK <sup>A</sup>	Q9NPQ8	60	1	1,641,333
111	-1.4	TBC1D23	562, 571	TBC1 domain family, member 23	GVKPVFSIGDEEYDT*DEIDSSMS*DDDRK	Q9NUY8	78	3	3,294,512
112		<b>Mitochondrial protein</b>							
113	-1.7	GPAM	§688, §695	mitochondrial glycerol 3-phosphate acyltransferase	KLPEPLSWRS*DEEEDS*DFGEEQR	Q9HCL2	94	2	4,108,650
114		<b>Motor or contractile protein</b>							
115	-1.2	MRLC2	§133	myosin regulatory light chain MRCL3	ELLTTM#GDRFT*DEEVDELYR	P19105	20	3	1,319,459
116	-1.2	MYH9	§1942	myosin, heavy polypeptide 9, non-muscle	KGAGDGS*DEEVDGKADGAEAKPAE	P35579	226	2	467,363
117	1.0	MYO10	1158	myosin X	FDT*DDELSYR	Q9HD67	237	1	5,070,649
118		<b>Protease</b>							
119	1.1	CPD	§1368	carboxypeptidase D precursor	SLLSHEFQDET*DTEETLYSSK <sup>H</sup>	Q75976	153	1	11,081,869
120	-1.9	CPD	§1368, §1370	carboxypeptidase D precursor	SLLSHEFQDET*DT*EETLYSSK	Q75976	153	1	1,187,031
121	-1.3	PSMA3	§249	proteasome alpha 3 subunit isoform 1	ESLKEEDS*DDDNM	P25788	28	6	20,302,426
122		<b>Protein kinase, Ser/Thr (non-receptor)</b>							
123	-1.4	eEF2K	§470	elongation factor-2 kinase	KYES*DEDSLSSGR	Q00418	82	2	869,011
124		<b>Protein kinase, atypical</b>							
125	1.1	RIOK2	§332, §335, §337	RIO kinase 2	EGS*EFS*FS*DGEVAEK <sup>A</sup>	Q9BVS4	63	5	1,167,664
126		<b>RNA processing</b>							
127	-1.5	BAT2 iso1	§1083, §1089, §1092	HLA-B associated transcript-2	T*ASETRS*EGS*EYEEIPK	P48634	229	3	2,088,997
128	-1.4	BAT2 iso1	§1085, §1089, §1092	HLA-B associated transcript-2	TAS*ETRS*EGS*EYEEIPKR	P48634	229	1	4,225,549
129	-1.5	BAT2 iso1	§1087, §1089, §1092	HLA-B associated transcript-2	TASET*RS*EGS*EYEEIPKR	P48634	229	2	644,888

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130		DDX55	\$594	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	TVDLGIS*DLEDDC	Q8NHQ9	68	2	7,798,137
131	-1.5	FIP1L1	\$492, \$500	FIP1 like 1 isoform 2	DHS*PTPSVFNNS*DEER	Q6UN15	67	4	1,785,218
132	-1.8	FIP1L1	\$496, \$500	FIP1 like 1 isoform 2	ERDHSPTPS*VFNS*DEER	Q6UN15	67	1	7,624,913
133	-1.0	LARP; LARP iso3	\$627, \$631; \$550, \$554	la related protein isoform 1	NTFTAWS*DEES*DYEIDRRDVNK	Q6PKG0; Q6PKG0-3	124; 116	9	7,755,991
134	-1.6	LARP7	\$337, \$338	La ribonucleoprotein domain family, member 7	DIEIS*T*EEEKDTGLDK	Q4GQJ3	67	4	3,810,837
135	1.1	MPHOSPH10	\$163, \$167, \$171	M-phase phosphoprotein 10	KS*PVFS*DEDS*DLDFDISKLEQQSK	O00566	79	3	5,602,253
136	-3.7	MPHOSPH10	\$163, \$171	M-phase phosphoprotein 10	KS*PVFSEDEDS*DLDFDISKLEQQSK	O00566	79	1	2,085,878
137	7.1	NOL5A	\$511, \$520	nucleolar protein 5A	S*FSK^EELM#SS*DLEETAGSTSIPK^	O00567	66	1	541,332
138	-1.4	NOL5A	\$520	nucleolar protein 5A	SFSKEELM#SS*DLEETAGSTSIPK	O00567	66	12	5,284,549
139	-1.3	NOL8	\$365	nucleolar protein 8	VSCHDS*DDDIMR	Q76FK4	132	6	3,023,307
140	1.0	NOL8	\$365, \$378, \$381	nucleolar protein 8	VSCHDS*DDDIRNDRREYDS*GDT*DEIAMK	Q76FK4	132	3	1,912,147
141	-1.3	NOL8	\$888, \$890	nucleolar protein 8	FLET*DS*EEEQEVNEKK	Q76FK4	132	9	15,698,983
142	4.4	NPM; NPM iso2	\$279; \$250	nucleophosmin 1 isoform 3	M#T*DQEAIDLWQWR^	P06748; P06748-2	33; 29	1	1,045,285
143		RALY; RALY iso2	\$286, \$288, \$295; \$270, \$272, \$279	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	DDGDEEGLLT*HS*EEELEHS*QDTDADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	1	157,636
144	1.1	RALY; RALY iso2	\$286, \$288, \$298; \$270, \$272, \$282	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	TRDDGDEEGLLT*HS*EEELEHSQDT*DADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	6	6,471,375
145		RALY; RALY iso2	\$286, \$295, \$298; \$270, \$279, \$282	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	DDGDEEGLLT*HSEEELEHS*QDT*DADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	1	145,816
146	-1.0	RALY; RALY iso2	\$288, \$295, \$298; \$272, \$279, \$282	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	TRDDGDEEGLLTHS*EEELEHS*QDT*DADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	2	3,176,762
147	-1.2	RALY; RALY iso2	\$288, \$298; \$272, \$282	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	TRDDGDEEGLLTHS*EEELEHSQDT*DADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	1	19,910,280
148	-1.0	RALY; RALY iso2	\$298; \$282	RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) short isoform	TRDDGDEEGLLTHSEEELEHSQDT*DADDGALQ	Q9UKM9; Q9UKM9-2	32; 30	1	4,590,044
149	-2.1	RBM12B iso4	839	RNA binding motif protein 12B	SPQEEDFRCPs*DEDFR	NP_976324	118	1	2,359,593
150	1.3	RBM5	\$69, 72, \$78	RNA binding motif protein 5	R*NS*DR*S*EDGYHS*DGDYGEHDYR^	P52756	92	8	20,748,502
151	-1.2	RBM5	\$78	RNA binding motif protein 5	SEDGYHS*DGDYGEHDYR	P52756	92	6	3,191,217
152	1.2	SF3A3	\$475	splicing factor 3a, subunit 3	WQPDY*EEYEDSSGNVWVK^K^	Q12874	59	1	984,572
153	-1.1	SF4	\$485	splicing factor 4	AVQQHQHGYDS*DEEVDSELGTWEHQLR	Q8IWZ8	72	1	1,995,390
154	1.6	UPF3B; UPF3B iso2	\$169; \$169	UPF3 regulator of nonsense transcripts homolog B isoform 2	K^FLESYAT*DNEK^	Q9BZ17; Q9BZ17-2	58; 56	4	8,324,409
155		<b>Receptor, channel, transporter or cell surface protein</b>							
156	-1.3	NUP98; NUP98 iso4	\$1000; \$983	nucleoporin 98kD isoform 3	ASLLT*DEEDVDMALDQR	P52948; NP_624358	188; 187	2	1,677,603
157	-1.4	PGRMC1	\$180	progesterone receptor membrane component 1	EGEPTVYS*DEEFPKDESAR	O00264	22	2	865,621
158	-1.2	PGRMC2	\$208, \$211	progesterone receptor membrane component 2	LLKPGEEPS*EYT*DEEDTKDHNKQD	O15173	24	2	4,353,156
159	-1.5	PGRMC2	\$211	progesterone receptor membrane component 2	LLKPGEEPSEYT*DEEDTKDHNKQD	O15173	24	18	201,528,512
160	-1.8	REEP3	\$201, \$210	receptor accessory protein 3	SKPAPSESAGYIPLKDGDEKT*DEEAEGPYS*DNEMLTHK	Q6NUK4	29	2	2,335,651
161	-1.8	REEP3	\$201, 216	receptor accessory protein 3	SKPAPSESAGYIPLKDGDEKT*DEEAEGPYS*DNEMLTHK	Q6NUK4	29	1	2,335,651
162	1.0	SEC62	\$335, 341, \$343	translocation protein 1	VGPGNHGTEGS*GGER*HS*DT*DSDR^R^	Q99442	46	1	93,738
163	-1.1	SEC62	341, \$343	translocation protein 1	VGPGNHGTEGS*GGER*HS*DT*DSDR	Q99442	46	2	108,478
164	-1.0	SEC62	341, \$343, \$345	translocation protein 1	VGPGNHGTEGS*GGER*HS*DT*DS*DRR	Q99442	46	2	50,294
165	-1.2	SEC62	341, \$345	translocation protein 1	VGPGNHGTEGS*GGER*HS*DT*DS*DR^R^	Q99442	46	1	23,487
166	-1.3	SEC62	\$375	translocation protein 1	EELEQQT*DGDCDEEEENDETGP	Q99442	46	4	16,972,468
167	1.1	SLC19A1	225	solute carrier family 19 member 1	CETSAS*ELER^	P41440	65	1	177,233
168		<b>Transcriptional regulator</b>							
169	1.3	BCLAF1	\$341	BCL2-associated transcription factor 1 isoform 2	R^FT*DEESR^	Q9NYF8	106	4	345,729
170	-2.4	WDR9	1703, 1715, 1720	bromodomain and WD repeat domain containing 1 isoform C	DENQLLPVS*SSHTAQSNVDES*ENRDS*ESESRLRVARK	Q9NS16-2	257	1	689,289

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**STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CK Substrate Motif, pS/pTD/EXD/E; CST #BL4176**

*Treatments: Nocodazole (Heavy), Untreated (Light)*

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity	
171	-1.3	CHD-8; CHD-8 iso2	§1141, §1145, §1285, §1289	chromodomain helicase DNA binding protein 8	HFSTLKKDDDLVEFS*DLSE*EDDERPR	Q9HCK8; Q9HCK8-2	262; 276	4	11,609,433	
172	-1.3	SH2BP1	§925	SH2 domain binding protein 1	GGFEDEFVNDT*DDDLPISK	Q6PD62	134	3	3,823,212	
173	1.3	ERBP	§83, §87	deoxynucleotidyltransferase, terminal, interacting protein 2	GTEPST*DGET*SEAESNYSVSEHHDTLR^	Q5QJE6	84	1	370,394	
174	-1.2	TAT-SF1	§597, §600	HIV-1 Tat specific factor 1	ELHENVLDK^ELEENDS*ENS*EFEDDGSEK^	Q43719	86	1	778,435	
175	-1.3	TAT-SF1	§597, §600, §607	HIV-1 Tat specific factor 1	ELHENVLDKLEENDS*ENS*EFEDDGSEK	Q43719	86	1	2,845,843	
176	-1.4	RbBP2	§1111	retinoblastoma binding protein 2 isoform 1	LLDLEPLS*DLEEGLEETR	P29375	196	2	3,648,422	
177	-1.2	TRIP8	§373, §376, §379	jumonji domain containing 1C isoform b	LRTDNVS*DFS*ESS*DSSESNKR	Q15652	285	1	1,733,809	
178	1.1	LEO1	§171, §179	Leo1, Paf1/RNA polymerase II complex component, homolog	AQGS*DEDKQNS*DDDEK	Q8WVCO	75	2	125,041	
179	-1.0	LEO1	§188, §197	Leo1, Paf1/RNA polymerase II complex component, homolog	MQNT*DDEERPQLS*DDER	Q8WVCO	75	7	9,091,775	
180	-1.5	LEO1	§658	Leo1, Paf1/RNA polymerase II complex component, homolog	KYVIS*DEEEEDDD	Q8WVCO	75	1	1,891,369	
181	-1.2	PHC2	§619	polyhomeotic-like 2 isoform b	YAQQFLPEKLPQQDHTTT*DSEMEEPYLQESK	Q8IXK0	91	1	817,804	
182	-1.4	PSIP1	§106	PC4 and SFRS1 interacting protein 1 isoform 2	QSNASS*DVEVEEK^ETS*VSK^EDTDHEEK^	Q9UER6	60	1	4,384,569	
183	-1.4	PSIP1	§106, §116, §118	PC4 and SFRS1 interacting protein 1 isoform 2	QSNASS*DVEVEEK^ETS*VSK^EDTDHEEK^	Q9UER6	60	1	2,477,690	
184	1.9	PSIP1	§106, §116, §122	PC4 and SFRS1 interacting protein 1 isoform 2	QSNASS*DVEVEEK^ETS*VSK^EDTDHEEK^	Q9UER6	60	1	1,708,673	
185	-1.5	PTMA; PTMA iso2	§106; §106	prothymosin, alpha isoform 1	AAEDDEDDVDTKQKQ*DEDD	P06454; P06454-2	12; 12	8	2,847,416	
186	-1.2	HBXAP	§1295	remodeling and spacing factor 1	LHRIET*DEEESCNDNAHGDNQPAR	Q96T23	163	4	3,543,845	
187	-1.2	Sin3A	§832	transcriptional co-repressor Sin3A	GDLS*DVEEEEEEMDVEATGAVK	Q96ST3	145	4	4,236,106	
188	1.4	SIRT1	§719	sirtuin 1	AGGAGFGT*DGDDQEAINEAISVK^	Q96EB6	82	2	1,509,243	
189	-1.1	SMARCA2	§1564, §1568	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin 2 isoform a	AKPVVS*DFDS*DEEQDR	P51531	181	2	3,703,065	
190	-1.2	SSRP1	§444	structure specific recognition protein 1	EGMNPSYDEYADS*DEDQHDAYLER	Q08945	81	4	14,260,714	
191	-1.3	PC4	§117	activated RNA polymerase II transcription cofactor 4	GISLNPEQWSQLKEQIS*DIDDAVR	P53999	14	2	6,463,117	
192	-1.4	TCF20	1760, §1764	transcription factor 20 isoform 1	SASNGS*KTDT*EEEEQQQQQK	Q9UGU0	212	2	101,913	
193	-1.4	TCF20	1762	transcription factor 20 isoform 1	SASNGSKT*DTEEEEEQQQQK	Q9UGU0	212	1	110,430	
194	-1.4	TCF20	§1764	transcription factor 20 isoform 1	SASNGSK^TDT*EEEEQQQQQK^	Q9UGU0	212	1	97,281	
195	-1.3	PIMT	405, 412	trimethylguanosine synthase homolog	DRPHAS*GTDGDES*EEDPPEHKPSK	Q96RS0	97	1	32,336	
196	-1.0	PIMT	407, 412	trimethylguanosine synthase homolog	DRPHASGT*DGDES*EEDPPEHKPSK	Q96RS0	97	2	129,777	
197	-1.2	PIMT	§85, §89	trimethylguanosine synthase homolog	GIGLDES*ELDS*EAELMR^	Q96RS0	97	1	1,376,134	
198	-1.8	TMF1	§344	TATA element modulatory factor 1	SVSEINS*DDELSGK^	P82094	123	1	1,310,537	
199	<b>Translation</b>									
200	-2.3	eEF1D; eEF1D iso2; eEF1D iso3	§528; §161; §431	eukaryotic translation elongation factor 1 delta isoform 1	KPATPAEDDEDDIDLFGS*DNEEDKEAAQLR	Q96I38; P29692; Q9BW34	71; 31; 61	1	782,769	
201	-1.0	eIF2B	§111	eukaryotic translation initiation factor 2 beta	IESDVQEP*EPEDDLIMLGNK	P20042	38	2	1,105,618	
202	-1.0	eIF3-alpha	§127	eukaryotic translation initiation factor 3, subunit 1 alpha, 35kDa	LQEES*DLELAK	Q75822	29	1	2,717,426	
203	-1.3	eIF5B	§135, §137	eukaryotic translation initiation factor 5B	VEMYS*GS*DDDDDFNKLPK	Q60841	139	2	998,538	
204		MRPS16	§130	mitochondrial ribosomal protein S16	TDAEAT*DTEATET	Q9Y3D3	15	1	995,475	
205	-1.2	RPLP1; RPLP2	§101, §104; §102, §105	ribosomal protein P1 isoform 1	KEES*EES*DDDMGFLFD	P05386; P05387	12; 12	1	123,138	
206	<b>Tumor suppressor</b>									
207	-1.5	ING5	§118	inhibitor of growth family, member 5	MEGS*DFESSGGR	Q8WYH8	28	8	22,117,412	
208	<b>2.6</b>	ING5	§118, 123	inhibitor of growth family, member 5	DK^MEGS*DFESS*GGR^	Q8WYH8	28	1	556,675	
209	<b>Ubiquitin conjugating system</b>									
210	-1.1	PJA1	§277	praja 1 isoform b	IFFDT*DDDDMPHSTSR	Q8NG27	71	4	2,402,128	
211	-1.5	UBL7	§230	ubiquitin-like 7	DMPGGFLFEGLS*DEEDDFHPNTR	Q96S82	41	1	645,942	
212	-1.1	USP13	§122	ubiquitin specific protease 13 (isopeptidase T-3)	IFLDLDT*DDDLNSDDYEDEAK	Q92995	97	2	967,026	
213	-1.2	USP54	442	ubiquitin specific peptidase 54	DTGHLT*DSECNQK^	Q6ZTMO	187	2	98,402	
214	<b>Unknown function</b>									
215	-1.3	ARMCX3	§61	armadillo repeat containing, X-linked 3	YNDWS*DDDDSNESK	Q9UH62	43	2	1,626,591	

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**STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CK Substrate Motif, pS/pTD/EXD/E; CST #BL4176**

*Treatments: Nocodazole (Heavy), Untreated (Light)*

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
216	1.7	BAT2L iso6	§1132, §1136, §1139	HLA-B associated transcript 2-like	VAS*ETHS*EGS*EYEELPK <sup>^</sup>	Q5H9R5	243	1	390,333
217	-1.7	BAT2L iso6	§1134, §1139	HLA-B associated transcript 2-like	VASET*HSEGS*EYEELPK	Q5H9R5	243	1	328,416
218	-1.5	BAT2L iso6	§1136, §1139	HLA-B associated transcript 2-like	VASETHS*EGS*EYEELPKR	Q5H9R5	243	2	1,538,217
219	-1.6	BLOC1S3	§63, §65	biogenesis of lysosomal organelles complex-1, subunit 3	VAGEAAET*DS*EPEPEPEPTAAPR <sup>^</sup>	Q6QNY0	21	3	1,811,301
220	-1.1	DKFZP547B1415	§280	hypothetical protein LOC126526	LGATPETDEDLAWDS*DNDSSSSVLQYAGVLKK	Q8N9M1	45	2	1,833,446
221	-1.5	C9orf25; C9orf25 iso2	§112, §114; §85, §87	hypothetical protein LOC203259	GYSSLDQSPDEKPLVALDT*DS*DDDFDMSR	Q5T595; Q8IW50	20; 17	2	5,156,490
222	1.2	CCDC43	§139	coiled-coil domain containing 43 isoform 2	AALLAQYADV*DEEDEADEK*DDSGATTMNIIGSDK <sup>^</sup>	Q96MW1	25	11	16,977,130
223	1.1	CCDC55	§248	coiled-coil domain containing 55 isoform 1	VEENPDADS*DFDAK	Q9H0G5	66	1	3,432,987
224	-1.1	CCDC55	§248, §254	coiled-coil domain containing 55 isoform 1	VEENPDADS*DFDAK*S*SADDEIEETR <sup>^</sup>	Q9H0G5	66	1	1,753,838
225	-1.6	CCDC55	§248, §254, §255	coiled-coil domain containing 55 isoform 1	VEENPDADS*DFDAK*S*SADDEIEETR	Q9H0G5	66	6	1,894,649
226	-1.1	CCDC55	§248, §255	coiled-coil domain containing 55 isoform 1	VEENPDADS*DFDAK*S*ADDEIEETR	Q9H0G5	66	1	5,681,841
227	-1.1	CHMP2B	§199	chromatin modifying protein 2B	ATIS*DEEIER	Q9UQN3	24	2	2,621,670
228	-1.7	coilin	§122	coilin	AFQLEEGEET*EPDCK <sup>^</sup>	P38432	63	2	1,978,360
229	-1.2	DHX34	§749, §750	DEAH (Asp-Glu-Ala-His) box polypeptide 34	LQEEQDGG*S*S*DEDR	NP_055496	128	1	9,398
230	-1.7	C14orf11	§109, §111	E2F-associated phosphoprotein	YYDDIYFDS*DS*EEDER	Q56P03	33	1	468,713
231	5.1	ESX1L	55, 69	extraembryonic, spermatogenesis, homeobox 1-like	PEYGT*EAENNVGTEGVS*DDQDR <sup>^</sup>	Q8N693	44	1	26,093
232	-1.2	CCDC98	§386, §387, §390	coiled-coil domain containing 98	ASK*MS*S*PET*DEEIEK <sup>^</sup>	Q6UWZ7	47	3	76,109,704
233	1.1	C14orf24	§70, §71	hypothetical protein LOC283635 isoform 2	R*VIHFVSGETMEEYS*T*DEDEVGLK <sup>^</sup> K <sup>^</sup>	Q8N128	24	6	2,581,336
234	-1.6	FBXW9	§18	F-box and WD-40 domain protein 9	TWDDDS*DPESETDPAQAK	Q5XUX1	54	2	1,624,108
235	-1.2	FBXW9	§18, 22	F-box and WD-40 domain protein 9	TWDDDS*DPESETDPAQAK	Q5XUX1	54	1	2,800,828
236	-4.2	p66A	§100, §107, §113	GATA zinc finger domain containing 2A	RPPS*PDVILV*S*DNEQPS*SPR	Q86YP4	68	1	2,853,078
237	-1.4	GNL1	§48, §50, §51	guanine nucleotide binding protein-like 1	EEQT*DT*S*DGESVTHHIR	Q96CT5	69	7	37,537,172
238	1.0	GNL1	§48, §51	guanine nucleotide binding protein-like 1	REEQT*DTS*DGESVTHHIR	Q96CT5	69	5	6,325,533
239	-1.1	GNL1	§48, §51, 55	guanine nucleotide binding protein-like 1	R*EEQT*DTS*DGES*VTHHIR <sup>^</sup>	Q96CT5	69	1	374,605
240	-1.4	GNL1	§50, §51	guanine nucleotide binding protein-like 1	EEQDT*S*DGESVTHHIR <sup>^</sup>	Q96CT5	69	1	9,126,750
241	1.0	GRAMD1B	587	GRAM domain containing 1B	VPHLEEVMSPVTTT*DEDVGH	Q3KR37	85	2	2,615,018
242	-1.6	GRAMD3	242, §252	GRAM domain containing 3	ADRPSS*LPLDFNDEFS*DLDGVVQQR	Q96HH9	48	2	1,599,707
243	-1.4	GRAMD3	§252	GRAM domain containing 3	ADRPSSLPLDFNDEFS*DLDGVVQQR	Q96HH9	48	6	20,057,120
244	1.6	IKBKAP	§867	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	VHELQGNAPS*DPDAVSAEALK	Q95163	150	3	2,252,722
245	1.2	KCTD16	137	potassium channel tetramerisation domain containing 16	QSPDEFCHS*DFEDASQSDTR <sup>^</sup>	Q68DU8	49	3	7,492,364
246	-1.1	KIAA1430	§133, §138, §139	hypothetical protein LOC57587	EGEDDYT*DGEES*S*DDGK*K*YHVK <sup>^</sup>	Q9P2B7	59	1	4,925,510
247	-2.1	KIAA1984	§596, §599	hypothetical protein LOC84960	RADDFPVRDDPS*DVT*DEDEGAEP PPPKLP LPAFR	Q3YEC7	80	11	13,914,348
248	-1.2	LEMD2	§499	LEM domain containing 2	WTK*PSSFS*DSER <sup>^</sup>	Q8NC56	57	2	830,521
249	-1.2	MFAP1	§267	microfibrillar-associated protein 1	SLAALDALNT*DDENDEEYEAWK	P55081	52	8	75,174,864
250	-1.2	RCOR3; RCOR3 iso2	156, 171; 214, 229	REST corepressor 3 isoform a	HNQGDS*DDVEETHPMDGNS*DYDPKK	Q9P2K3; Q9P2K3-2	56; 48	1	506,099
251	-1.3	KIAA0460	§374	Regulation of nuclear pre-mRNA domain containing 2	DVEDMELS*DVEDDGSK	Q5VT52	156	4	4,776,057
252	-1.1	SH3D19	369	SH3 domain containing 19 isoform a	SSS*DMDLQK <sup>^</sup> K <sup>^</sup>	Q5HYK7	87	1	56,820
253	1.3	SPECC1	241	spectrin domain with coiled-coils 1 NSP5b3b	ELS*DLEENR <sup>^</sup>	Q5M775	119	2	1,201,559
254	-1.6	SURF2	§190, §195	surfeit 2	DLGSTEDGGT*DDFLT*DKEDEKAKPPR	Q15527	30	6	11,780,919
255	-1.2	SURF2	§195	surfeit 2	KDLGSTEDGGTDDFLT*DKEDEK	Q15527	30	5	242,675,280
256	-1.2	SYDE1	§231, §235, §244	synapse defective 1, Rho GTPase, homolog 1	AGYLS*DGDS*PERPAGPPS*PTFRPYEVGPAAR	Q6ZW31	80	3	1,455,199
257	-1.2	SYDE1	§231, §235, §247	synapse defective 1, Rho GTPase, homolog 1	AGYLS*DGDS*PERPAGPPS*PTFRPYEVGPAAR	Q6ZW31	80	1	1,455,199
258	-1.3	SYNPO iso2	§856	synaptopodin isoform B	RSPT*DSVSLDSEDSGAK	Q8N3V7-2	96	5	41,993,504
259	-1.7	TACC1	§504	transforming, acidic coiled-coil containing protein 1 isoform 2	DGHAT*DEEKLASTSCGQK	Q75410	88	4	2,296,972
260	1.3	TSGA14	§99	testis specific, 14	LEDNDSAA*DPDAETTR <sup>^</sup>	Q9BYV8	41	2	523,952
261	-1.7	USP42	§1220, §1223, §1227	ubiquitin specific protease 42	HQQDS*DLS*AACS*DADLHR	Q9H9J4	146	3	4,191,638

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**STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: CK Substrate Motif, pS/pTD/EXD/E; CST #BL4176**

*Treatments: Nocodazole (Heavy), Untreated (Light)*

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity	
262	-1.2	SAS10	§362, §368	UTP3, small subunit processome component	TSAAACAVT*DLSDDS*DFDEKAK	Q9NQZ2	55	1	1,462,561	
263	1.0	SAS10	§365, §368	UTP3, small subunit processome component	TSAAACAVTDLSD*DDS*DFDEKAK	Q9NQZ2	55	18	3,164,987	
264	-1.1	VAMP1; VAMP2; VAMP3	§63; §60; §43	vesicle-associated membrane protein 1 isoform 1	DQKLS*ELDDR	P23763; P63027; Q15836	13; 13; 11	2	3,256,509	
265	-2.3	WDR12	221	WD repeat domain 12 protein	IWSTVPT*DEEDEMEESTNR^PR^	Q9GZL7	48	2	11,585,655	
266		WDR43	666, 674	WD repeat domain 43	ELNGDS*DLDPENES*EEE	Q15061	75	1	153,865	
267	1.5	LEREPO4	392	erythropoietin 4 immediate early response	FSTYTS*DKDENK	Q9P079	52	1	712,149	
268	1.1	LEREPO4	§413	erythropoietin 4 immediate early response	AENGER^S*DLEEDNER^	Q9P079	52	5	13,798,555	
269	-1.2	LOC124245	§46	zinc finger CCH-type containing 18	AS*DLEDEESAAR	Q86VM9	106	3	15,964,086	
270	-1.4	KIAA1064	§807, §808	zinc finger CCH-type containing 4	QDRENEEGDTGNWYS*S*DEDEGGSSVTSILK	Q9UPT8	140	1	2,774,995	
271	-1.1	ZC3H8	§32	zinc finger CCH-type containing 8	TATDSERIDDEIDT*EVEETQEEK	Q8N5P1	34	3	4,156,079	
272	-1.4	ZC3H8	§77	zinc finger CCH-type containing 8	SKDYDVYS*DNDICSQESEDNFAK	Q8N5P1	34	2	950,941	
273	1.3	ZFP276	§357, §360, §366	zinc finger protein 276 isoform a	VKDEFS*DLS*EGDVLS*EDENDKK	Q8N554	67	2	1,176,872	
274	-1.4	ZNF609	§358, 361	zinc finger protein 609	FCDS*PTS*DLEMR	O15014	151	3	2,811,106	
275		<b>Vesicle protein</b>								
276	-1.4	AP3B1	§276	adaptor-related protein complex 3, beta 1 subunit	EGDELEDNGKNFYES*DDQKKEK	O00203	121	5	5,029,528	
277	<b>2.6</b>	SNX12	§73	sorting nexin 12	R^YS*DFEWLK^	Q9JMY4	20	4	9,744,422	
278	1.6	SNX3	§71	sorting nexin 3	RYS*DFEWLR	O60493	19	2	14,700,104	
279	1.4	WDR44	§262	WD repeat domain 44 protein	K^R^K^S*ELEFETLK^	Q5JSH3	101	1	329,441	
280	-1.2	WDR44	§403	WD repeat domain 44 protein	EYVSNDAAGS*DDEEK^LQSQPTDGTGGR^	Q5JSH3	101	1	1,770,671	
281		<b>lipid binding</b>								
282	-1.2	PLCL2	§584	phospholipase C-like 2	LSSNCSGVEGDVT*DEDEGAEMSQR	Q9UPR0	126	5	2,427,345	

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