

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
1		Adaptor/scaffold							
2	2.98	AHNAK	177	AHNAK nucleoprotein isoform 1	DIDISS*PEFK	Q09666	629	1	6.06E+06
3	<b>22.69</b>	AHNAK	5415	AHNAK nucleoprotein isoform 1	LPOFGIST*PGSDLHVNNAK	Q09666	629	30	1.77E+07
4	1.58	AHNAK	5749, 5763	AHNAK nucleoprotein isoform 1	AS*LGSLEGEAEAEASS*PK	Q09666	629	1	5.86E+04
5	1.69	AHNAK	5763	AHNAK nucleoprotein isoform 1	ASLGSLEGEAEAEASS*PK	Q09666	629	2	8.37E+05
6	1.01	AHNAK	5782, 5793	AHNAK nucleoprotein isoform 1	SNS*FSDEREFSGPS*TPGTLEFEGGEVSLGGKVK	Q09666	629	1	1.04E+05
7	2.62	AHNAK	5790, 5793, 5794	AHNAK nucleoprotein isoform 1	HRSNSFSDEREFSGPS*TPGTLEFEGGEVSLGGK	Q09666	629	1	2.93E+05
8	<b>7.85</b>	AHNAK	5793	AHNAK nucleoprotein isoform 1	EFSGSPS*TPGTLEFEGGEVSLGGK	Q09666	629	4	1.90E+06
9	-0.76	AHNAK	5794	AHNAK nucleoprotein isoform 1	EFSGSPS*TPGTLEFEGGEVSLGGKVK	Q09666	629	17	1.14E+06
10	<b>20.56</b>	AHNAK	637	AHNAK nucleoprotein isoform 1	MKMPTFS*TPGAK	Q09666	629	13	2.18E+06
11	<b>21.02</b>	AHNAK	638	AHNAK nucleoprotein isoform 1	MPTFST*PGAK	Q09666	629	32	9.44E+07
12	<b>5.64</b>	AKAP1	70	A-kinase anchor protein 1 precursor	VVST*PPSVTEPEKELSTVSK	Q92667	97	6	4.66E+06
13	4.13	AKAP13	1226	A-kinase anchor protein 13 isoform 1	ERS*TPSLPCM#VSAQDAPLPK	Q12802	308	2	5.89E+05
14	<b>20.71</b>	BASP1	182, 196	brain abundant, membrane attached signal protein 1	SDGAPASDKPGSSEAAAPS*SKETPAATEAPSST*PK	P80723	23	1	8.10E+05
15	<b>6.55</b>	BASP1	195	brain abundant, membrane attached signal protein 1	ETPAATEAPSS*TPK	P80723	23	3	9.91E+06
16	<b>8.59</b>	BASP1	196	brain abundant, membrane attached signal protein 1	ETPAATEAPSS*PK	P80723	23	4	4.29E+08
17	-0.20	BASP1	31, 36	brain abundant, membrane attached signal protein 1	AEGAAT*EEEGT*PKSEEPQAAAEPAEAK	P80723	23	1	4.55E+04
18	2.47	BASP1	36	brain abundant, membrane attached signal protein 1	AEGAATEEETG*PKSEEPQAAAEPAEAK	P80723	23	4	1.65E+06
19	<b>18.07</b>	BIN1; BIN1 iso2; BIN1 iso7; BIN1 iso10	298, 303, 307; 267, 272, 276; 267, 272, 276; 282, 287, 291	bridging integrator 1 isoform 8	GNKSPS*PPDGS*PAAT*PEIR	000499; 000499-2; 000499-7; 000499-10	65; 57; 48; 47	1	4.60E+05
20	<b>13.92</b>	CTNND1; CTNND1 iso3	906; 906	catenin, delta 1 isoform 1ABC	SLDNNYST*PNER	060716; 060716-3	108; 105	3	3.70E+07
21	-0.41	DAB2	221	disabled homolog 2	SGVDQM#DLFGDM#ST*PPDLNSPTESK	P98082	82	1	2.46E+05
22	4.69	DAB2	328	disabled homolog 2	KENSSSSS*TPLSNGLNGDVFYGGQFDQISNR	P98082	82	1	7.84E+05
23	<b>14.75</b>	DAB2	328, 329	disabled homolog 2	KENSSSSS*TPLSNGLNGDVFYGGQFDQISNR	P98082	82	1	7.80E+05
24	1.87	RAMP	429	denticleless homolog	ESRPLVTVTSSOST*PAKAPR	Q9NZJ0	79	4	6.86E+05
25	3.12	Mena; Mena iso2; Mena iso5	489; 489; 736	enabled homolog isoform a	ASSTST*PEPTR	Q8N8S7; Q8N8S7-2; CAH71475	67; 64; 89	1	2.82E+07
26	<b>6.42</b>	EPB41L1; EPB41L1 iso2	541, 544, 546, 550; 467, 470, 472, 476	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSS*PAS*PS*PKG*PEKANER	Q9H4G0; Q9H4G0-2	99; 88	2	3.28E+05
27	1.23	FRS2	226	fibroblast growth factor receptor substrate 2	VSNASST*PKEEPSIEDRDPQILLEPEGVK	Q8WU20	57	3	4.89E+05
28	<b>16.33</b>	Grb10	418, 422	growth factor receptor-bound protein 10 isoform b	ALLS*PFST*PVR	Q13322	67	3	5.04E+06
29	3.09	INADL	1162	InaD-like	NAGNPVVFVQSLSS*PR	Q8NI35	196	3	7.25E+04
30	1.96	IRS-2	346, 350	insulin receptor substrate 2	TDS*LAAT*PPAAK	Q9Y4H2	137	1	1.01E+05
31	-0.72	IRS-2	350	insulin receptor substrate 2	TDSLAAT*PPAAK	Q9Y4H2	137	1	8.50E+05
32	-0.31	IRS-2	731, 736	insulin receptor substrate 2	ASS*PAESS*PEDSGYMR	Q9Y4H2	137	1	1.13E+05
33	-0.98	LMO7; LMO7 iso2; LMO7 iso3	956, 960; 956, 960; 622, 626	LIM domain only 7 isoform 1	TPNNVVST*PAPS*PDASQLASSLSSQK	Q8WW11; Q8WW11-2; Q8WW11-3	193; 191; 154	1	5.23E+05
34	1.47	TAB3	404, 407	mitogen-activated protein kinase kinase 7 interacting protein 3	NQHSLYTATT*PPS*SSPSR	Q8N5C8	79	1	3.11E+05
35	1.44	THRAP2	398	mediator complex subunit 13-like	SQM#ST*PTLEEPSASNPATWDFVDPQTR	Q71F56	243	1	1.53E+05
36	1.45	THRAP2	762	mediator complex subunit 13-like	DVTPGHS*TPVPDGG	Q71F56	243	1	1.36E+05
37	<b>32.19</b>	Alix	730, 738, 741	programmed cell death 6 interacting protein	EPSAPSIPTPAYQSS*PAGGHAPT*PPT*PAPR	Q8WUM4	96	2	6.04E+06
38	<b>9.44</b>	WDR11	1476, 1480	pleckstrin homology domain interacting protein	SESSTS*AFST*PTR	Q8WWQ0	207	1	1.11E+06
39	2.01	WDR11	1480	pleckstrin homology domain interacting protein	SESSTS*AFST*PTR	Q8WWQ0	207	2	3.41E+06
40	-0.96	RAI14	293, 297	retinoic acid induced 14 isoform a	S*ITST*PLSGK	Q9P0K7	110	1	3.33E+06
41	1.22	RAI14	297	retinoic acid induced 14 isoform a	SITST*PLSGK	Q9P0K7	110	2	7.36E+06
42	<b>19.86</b>	RanBP2	1644, 1703	RAN binding protein 2	QNQTSAVST*PASSETSK	P49792	358	2	1.28E+06
43	<b>31.28</b>	RanBP2	1761	RAN binding protein 2	QNQTTAIST*PASSEISK	P49792	358	3	4.80E+06
44	<b>12.32</b>	RanBP2; LOC100133510	19, 21; 19, 21	RAN binding protein 2	YIASVQGST*PS*PR	P49792; XP_001719668	358; 116	8	1.21E+07
45	1.22	RanBP2; RGD1; RGD2; RGD3; RGD4; RGD5; RGD6; RGD8	2458, 2462; 1475, 1479; 1467, 1471; 1483, 1487; 1483, 1487; 1482, 1486; 1482, 1486; 1482, 1486	RAN binding protein 2	SST*PRES*PCGK	P49792; Q68DN6; POC839; A6NKT7; Q7Z3J3; Q99666; NP_001116835; O14715	358; 197; 197; 198; 198; 199; 199; 199	1	6.87E+06
46	<b>6.41</b>	RanBP2; RGD5	773, 781, 786, 788; 773, 781, 786, 788	RAN binding protein 2	NADS*EIKHSTPS*PTRYS*LS*PSK	P49792; Q99666	358; 199	1	1.43E+06
47	2.00	RanBP2; RGD5	779, 781; 779, 781	RAN binding protein 2	NADSEIKHST*PS*PTR	P49792; Q99666	358; 199	1	4.31E+06
48	-0.10	RANBP3; RANBP3 iso3	101, 108; 33, 40	RAN binding protein 3 isoform RANBP3-a	SAGGSS*PEGGEDS*DREGNYCPVVK	Q9H6Z4; Q9H6Z4-3	60; 53	1	2.55E+04
49	<b>21.62</b>	RAPH1	879, 882	Ras association and pleckstrin homology domains 1 isoform 3	KQPAFPASYIPPS*PPT*PPVPPVPPPTLPK	Q70E73	141	9	2.64E+06
50	<b>11.40</b>	Rictor	1177	rapamycin-insensitive companion of mTOR	HIEDTGSTPS*IGENDLK	Q6R327	192	1	2.91E+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-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
51	-0.43	ArgBP2; ArgBP2 iso2; ArgBP2 iso4	299, 302; 392, 395; 417, 420	sorbin and SH3 domain containing 2 isoform 3	SFTSSS*PSS*PSR	Q94875; Q94875-2; Q94875-4	124; 75; 77	1	3.81E+05
52	2.28	ArgBP2; ArgBP2 iso2; ArgBP2 iso4	301; 394; 419	sorbin and SH3 domain containing 2 isoform 3	SFTSSSPS*SPSR	Q94875; Q94875-2; Q94875-4	124; 75; 77	1	8.11E+04
53	<b>14.40</b>	TANK; TANK iso3	248, 257; 248, 257	TRAF interacting protein TANK isoform a	FPPM#DNDSTFLHS*TPERPGLS*PATSEAVCOEK	Q92844; AAC50681	48; 48	2	9.01E+05
54	<b>9.21</b>	Z01; Z01 iso2	353; 353	tight junction protein 1 isoform a	ISKPGAVS*TPVK	Q07157; Q07157-2	195; 187	8	5.31E+06
55	<b>6.64</b>	Z01; Z01 iso2	354; 354	tight junction protein 1 isoform a	ISKPGAVS*TPVK	Q07157; Q07157-2	195; 187	3	9.73E+06
56	<b>57.62</b>	Z01; Z01 iso2	354, 363; 354, 363	tight junction protein 1 isoform a	ISKPGAVS*PVKHAHDHT*PK	Q07157; Q07157-2	195; 187	1	3.96E+06
57	4.15	Z02	1053, 1068	tight junction protein 2 (zona occludens 2) isoform 1	SILKPS*TPIPPQEGEEVGESS*EEQDNAPK	Q9UDY2	134	1	5.17E+05
58	<b>17.11</b>	TRIP6	162	thyroid receptor-interacting protein 6	SYTTAST*PAGPAFPVQVK	Q15654	50	2	9.89E+05
59	<b>6.58</b>	WAC	456, 471	WW domain-containing adapter with a coiled-coil region isoform 1	IS*TPQNTNVPKPLIST*PPVSSQPK	Q9BTA9	71	1	7.42E+06
60	-0.75	WAC	471	WW domain-containing adapter with a coiled-coil region isoform 1	ISTPQNTNVPKPLIST*PPVSSQPK	Q9BTA9	71	4	1.49E+06
61	<b>7.64</b>	WAC	482	WW domain-containing adapter with a coiled-coil region isoform 1	VST*PVVK	Q9BTA9	71	1	1.84E+07
<b>62</b>	<b>Adhesion or extracellular matrix protein</b>								
63	3.60	DIP2A	155	disco-interacting protein 2A isoform e	LTST*PLQSHSSVEPWLDLDR	Q14689	170	2	6.75E+06
64	<b>111.83</b>	MAP7	673	microtubule-associated protein 7	VTVEST*PDLEK	Q14244	84	1	2.54E+06
65	-0.99	ROBO1	1240	roundabout 1 isoform c	M#YLQQDELEEEEDERGPT*PPVR	Q9Y6N7	181	3	7.94E+05
66	<b>5.12</b>	Scribble; Scribble iso2; Scribble iso3	1342, 1348; 1313, 1319; 1342, 1348	scribble isoform b	AFAAVTSHPPEDAPAQPPT*PGPAAS*PEQLSFR	Q14160; Q14160-2; Q14160-3	175; 171; 178	1	1.10E+06
67	<b>10.79</b>	Scribble; Scribble iso2; Scribble iso3	748; 719; 748	scribble isoform b	GS*TPYKGDDEGIFISR	Q14160; Q14160-2; Q14160-3	175; 171; 178	1	5.86E+06
68	<b>8.40</b>	Scribble; Scribble iso2; Scribble iso3	749; 720; 749	scribble isoform b	GST*PYKGDDEGIFISR	Q14160; Q14160-2; Q14160-3	175; 171; 178	4	1.13E+07
69	4.78	Scribble; Scribble iso2; Scribble iso3	883; 854; 883	scribble isoform b	GLGFSIAGGKGST*PYR	Q14160; Q14160-2; Q14160-3	175; 171; 178	2	1.30E+06
<b>70</b>	<b>Apoptosis</b>								
71	<b>24.17</b>	acinus	115	apoptotic chromatin condensation inducer 1	HS*TPHAAFQPNQSGIEM#SQNSFIK	Q9UKV3	152	5	1.02E+06
72	<b>12.86</b>	acinus	116	apoptotic chromatin condensation inducer 1	HST*PHAAFQPNQSGIEM#SQNSFIK	Q9UKV3	152	10	7.60E+05
73	2.96	acinus	682	apoptotic chromatin condensation inducer 1	DSSTSYTETKDPSSGQEVAT*PPVPQLQVCEPK	Q9UKV3	152	1	9.05E+05
74	-0.56	PRAS40	202, 203, 212	AKT1 substrate 1 (proline-rich)	RTEARS*S*DEENGPPSS*PDLLDR	Q96B36	27	1	1.69E+05
75	-0.15	PRAS40	203, 212	AKT1 substrate 1 (proline-rich)	TEARSS*DEENGPPSS*PDLLDR	Q96B36	27	1	1.90E+05
76	-0.55	PRAS40	212	AKT1 substrate 1 (proline-rich)	SSDEENGPPSS*PDLLDR	Q96B36	27	1	1.54E+05
77	-0.82	BAG3	284, 289	BCL2-associated athanogene 3	SS*TPLHS*PSPIR	Q95817	62	2	9.26E+06
78	<b>22.43</b>	BAG3	284, 289, 291	BCL2-associated athanogene 3	SS*TPLHS*PS*PIR	Q95817	62	4	1.27E+07
79	-0.21	BAG3	285	BCL2-associated athanogene 3	SST*PLHSPSPI	Q95817	62	1	4.30E+06
80	-0.85	BAG3	285, 289	BCL2-associated athanogene 3	SST*PLHS*PSPIR	Q95817	62	4	6.04E+06
81	2.44	CCAR1	627	cell-cycle and apoptosis regulatory protein 1	EIST*PTHWSK	Q8IX12	133	2	1.91E+07
82	3.02	requiem	176	D4, zinc and double PHD fingers family 2	ILEPDDFLDLDDEDEYEDT*PKR	Q92785	44	1	1.37E+05
83	1.56	requiem	244, 248	D4, zinc and double PHD fingers family 2	NRPLGSLYHYAHSHLAEEDGEDKEDS*QPPT*PVSQR	Q92785	44	4	2.01E+05
<b>84</b>	<b>Calcium-binding protein</b>								
85	<b>23.06</b>	ANXA2	19	annexin A2 isoform 2	LSLEGDHST*PPSAYGSVK	P07355	39	28	7.81E+08
<b>86</b>	<b>Cell cycle regulation</b>								
87	-0.64	APC1	529	anaphase promoting complex subunit 1	VFIPGLPAPSLTM#SNTM#PRPS*TPLDGVSTPKPLSK	Q9H1A4	217	2	1.28E+06
88	<b>5.42</b>	APC1	530, 536	anaphase promoting complex subunit 1	VFIPGLPAPSLTM#SNTM#PRPS*TPLDGVSTPKPLSK	Q9H1A4	217	2	1.93E+06
89	1.14	BAT2D1; BAT2D1 iso8	2673; 2673	HBxAg transactivated protein 2	AFGSGIDIKPPT*PPIAGR	Q9Y520; NP_055987	317; 309	1	3.84E+05
90	<b>9.55</b>	CDCA5	107, 111, 115	cell division cycle associated 5	THS*VPAT*PTST*PVPNPEAESSSK	Q96FF9	28	1	7.06E+05
91	4.58	CDCA5	115	cell division cycle associated 5	THSVPATPTST*PVPNPEAESSSK	Q96FF9	28	1	2.03E+05
92	<b>27.56</b>	CDCA5	159	cell division cycle associated 5	LETLGSASTST*PGRR	Q96FF9	28	4	6.45E+06
93	<b>23.14</b>	KAB1; KAB1 iso2	863; 765	centrosomal protein 170kDa isoform beta	QTSST*PSSLALTSASR	Q5SW79; Q5SW79-2	175; 161	1	2.34E+06
94	<b>8.54</b>	CIZ1	573, 583	CDKN1A interacting zinc finger protein 1 isoform 2	AFSTVPLTPVPRPS*DSVSSTPAAT*STPSK	Q9ULV3	100	1	3.83E+05
95	<b>5.57</b>	CIZ1	585	CDKN1A interacting zinc finger protein 1 isoform 2	AFSTVPLTPVPRPS*DSVSSTPAAT*STPSK	Q9ULV3	100	2	1.73E+06
96	<b>17.88</b>	CLASP1; CLASP1 iso3	646, 656; 646, 656	CLIP-associating protein 1 isoform 2	RQS*SGSATNVA*PDNR	Q7Z460; Q7Z460-3	169; 165	1	6.64E+05
97	<b>19.58</b>	CLASP1; CLASP1 iso3	647, 656; 647, 656	CLIP-associating protein 1 isoform 2	RQSS*GSATNVA*PDNR	Q7Z460; Q7Z460-3	169; 165	1	1.53E+06
98	1.17	CLASP1; CLASP1 iso3	656; 656	CLIP-associating protein 1 isoform 2	QSSGSATNVA*PDNR	Q7Z460; Q7Z460-3	169; 165	1	1.57E+05

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Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
99	-0.61	CUL4B	67	cullin 4B isoform 2	KLNSSSSSSSSNNSNEREDFDSTSSSSST*PPLQPR	Q13620	102	1	3.28E+05
100	<b>6.85</b>	B99	489	G-2 and S-phase expressed 1	VTVHST*PVR	Q9NYZ3	77	3	8.31E+06
101	<b>20.21</b>	INCENP	197, 213, 219	inner centromere protein antigens 135/155kDa isoform 1	TLS*PTPASATAPTSQGIPIT*SDDEEST*PKK	Q9NQS7	106	2	2.09E+06
102	1.42	INCENP	197, 219, 223	inner centromere protein antigens 135/155kDa isoform 1	TLS*PTPASATAPTSQGIPIT*SDDEEST*PKKS*K	Q9NQS7	106	1	4.67E+05
103	3.51	INCENP	218	inner centromere protein antigens 135/155kDa isoform 1	TLSPTPASATAPTSQGIPIT*SDDEEST*TPKK	Q9NQS7	106	2	1.47E+06
104	<b>8.33</b>	INCENP	218, 219	inner centromere protein antigens 135/155kDa isoform 1	TLSPTPASATAPTSQGIPIT*SDDEEST*TPKK	Q9NQS7	106	2	6.97E+05
105	<b>7.14</b>	INCENP	292	inner centromere protein antigens 135/155kDa isoform 1	VLAPILPDFNST*PTGSR	Q9NQS7	106	3	5.11E+07
106	3.37	KI-67; KI-67 iso2	1923, 1937; 1563, 1577	antigen identified by monoclonal antibody Ki-67 isoform 2	DINTFVGT*PVEKLDLLGNLPGS*KR	P46013; P46013-2	359; 319	1	2.12E+05
107	<b>5.18</b>	KI-67; KI-67 iso2	2223, 2231; 1863, 1871	antigen identified by monoclonal antibody Ki-67 isoform 2	IACRS*PQDPVGT*PTIFKQSK	P46013; P46013-2	359; 319	1	5.28E+05
108	-0.97	MLF1IP	98	MLF1 interacting protein	HCGLSLST*PPGK	Q71F23	48	4	8.65E+05
109	<b>6.31</b>	NCAPH	49	non-SMC condensin I complex, subunit H	KAPLNIPGT*PVLEDFPQNDDEKER	Q15003	83	6	2.83E+06
110	<b>34.81</b>	NUDE1; NUDE1 iso2	211, 215; 211, 215	nuclear distribution gene E homolog 1	TDTAVQATGS*VPST*PIAHR	Q9NXR1; Q9NXR1-2	39, 38	1	1.36E+06
111	0.00	NUDE1; NUDE1 iso2	240, 243, 246; 240, 243, 246	nuclear distribution gene E homolog 1	GLDDST*GGT*PLT*PAAR	Q9NXR1; Q9NXR1-2	39, 38	1	0.00E+00
112	<b>11.36</b>	NUSAP1	240, 244	nucleolar and spindle associated protein 1 isoform 3	GRLS*VAST*PISQR	Q9BXS6	49	2	5.82E+06
113	<b>45.39</b>	NUSAP1	240, 244, 247	nucleolar and spindle associated protein 1 isoform 3	GRLS*VAST*PIS*QRR	Q9BXS6	49	4	4.35E+06
114	<b>15.41</b>	NUSAP1	244	nucleolar and spindle associated protein 1 isoform 3	LSVAST*PISQR	Q9BXS6	49	3	1.34E+07
115	<b>33.09</b>	NUSAP1	244, 247	nucleolar and spindle associated protein 1 isoform 3	LSVAST*PIS*QR	Q9BXS6	49	2	6.18E+06
116	<b>21.06</b>	NUSAP1	244, 247, 251	nucleolar and spindle associated protein 1 isoform 3	LSVAST*PIS*QRRS*QGR	Q9BXS6	49	1	4.53E+06
117	<b>24.11</b>	securin	43	pituitary tumor-transforming protein 1	SOVST*PR	Q95997	22	1	3.25E+06
118	1.48	SMEK2	840	SMEK homolog 2, suppressor of mek1 isoform 1	GSLVGLVDYDDEEEEEEEESS*PR	Q5MIZ7	97	1	9.20E+04
119	<b>64.39</b>	SPAG5	109	sperm associated antigen 5	WLETQHESEQLDPIPOIS*STPK	Q96R06	134	1	3.53E+06
120	<b>8.71</b>	SUGT1	265	suppressor of G2 allele of SKP1 isoform a	WEKLEGQGDVPT*PK	Q9Y2Z0	41	6	8.51E+06
121	3.09	NIPA	354, 359, 370	zinc finger, C2HC type 1	TRS*WDSSES*PVORPEPEAAS*PTRR	Q86WBO	55	1	3.89E+05
122	<b>Cell development/differentiation</b>								
123	-0.84	COBLL1	297, 301	COBL-like 1	QDTAS*APAT*PLVNK	Q9Y2I3	132	2	2.15E+05
124	2.00	COBLL1	301	COBL-like 1	QDTASAPAT*PLVNK	Q9Y2I3	132	1	4.62E+06
125	<b>Chaperone</b>								
126	<b>5.67</b>	STI1	198	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	LLGVLDLGSMDDEEEIAT*PPPPPPPKK	P31948	63	1	4.36E+05
127	<b>Chromatin, DNA-binding, DNA repair or DNA replication protein</b>								
128	1.02	ATRX	1992, 1996	transcriptional regulator ATRX isoform 1	ATSSS*NPSS*PAPDWKDFVTDADAEVLEHSGK	P46100	283	1	3.89E+06
129	<b>13.44</b>	BAZ1A	1547	bromodomain adjacent to zinc finger domain, 1A isoform a	LGLHVTPSNVDQVST*PPAAK	Q9NRL2	179	6	4.61E+06
130	<b>7.90</b>	C14orf106	1086, 1089	chromosome 14 open reading frame 106	KLVTDFD*TPIT*PR	Q6P0N0	129	1	4.02E+05
131	2.85	C14orf106	1087	chromosome 14 open reading frame 106	LVETDFST*PTPR	Q6P0N0	129	1	1.49E+06
132	<b>21.26</b>	C14orf106	1087, 1089	chromosome 14 open reading frame 106	LVETDFST*PT*PR	Q6P0N0	129	2	1.02E+06
133	<b>12.81</b>	CAF-1A; CAF-1A iso4	291, 298; 309, 316	chromatin assembly factor 1, subunit A (p150)	QHSST*SPFPTST*PLRR	Q13111; Q6NXXG5	105; 107	1	4.14E+06
134	<b>6.15</b>	CAF-1B	429, 433	chromatin assembly factor 1 subunit B	TQDPSS*PGTT*PPQAR	Q13112	61	1	6.22E+05
135	<b>8.38</b>	CHD-3	1705	chromodomain helicase DNA binding protein 3 isoform 3	SATEST*PGERGEEKPLDQGEHR	Q12873	233	4	6.62E+05
136	1.35	CHD-4	1544	chromodomain helicase DNA binding protein 4	TPTPS*TPGDTQNTAPVPPAEDGK	Q14839	218	1	4.49E+05
137	<b>18.96</b>	CHD-9	2013, 2026	chromodomain helicase DNA binding protein 9	TST*PLLQYQVALSAS*PLTSLPR	Q3L8U1	326	1	1.62E+05
138	<b>8.94</b>	TFII-E-beta	19	general transcription factor IIE, polypeptide 2, beta 34kDa	ALST*PVVEKR	P29084	33	3	5.74E+06
139	-0.34	HIVEP1	537	human immunodeficiency virus type I enhancer binding protein 1	SSFTIPSS*PENVIGDFLLQDR	P15822	297	1	1.97E+04
140	<b>36.59</b>	HMG A1	36, 44, 53	high mobility group AT-hook 1 isoform b	KQPPVS*PGTALVGS*QKEPSEVPT*PK	P17096	12	7	1.53E+06
141	<b>31.99</b>	HMG A1	36, 53	high mobility group AT-hook 1 isoform b	KQPPVS*PGTALVGS*QKEPSEVPT*PK	P17096	12	17	2.29E+07
142	<b>6.38</b>	HMG A1 iso2	42	high mobility group AT-hook 1 isoform b	KQPPKEPSEVPT*PK	P17096-2	11	11	1.66E+07
143	<b>5.63</b>	HMG A1; HMG A1 iso2	53; 42	high mobility group AT-hook 1 isoform b	EPSEVPT*PK	P17096; P17096-2	12; 11	12	5.68E+06
144	1.60	MybBP1A	1239, 1244, 1248	MYB binding protein 1a isoform 1	SPAPGAPT*RSPT*PAKS*PK	Q9BQG0	149	1	3.03E+05
145	-0.15	MybBP1A	1241, 1243	MYB binding protein 1a isoform 1	SPAPGAPTRS*PS*TPAKSPK	Q9BQG0	149	1	8.22E+04
146	-0.46	MybBP1A	1244	MYB binding protein 1a isoform 1	SPST*PAKSPK	Q9BQG0	149	2	5.15E+04
147	1.05	NFI-B; NFI-B iso4	328, 333; 328, 333	nuclear factor I/B	KPEKPLFSSAS*PQDSS*PR	Q00712; Q5VW26	47; 63	1	9.44E+04
148	-0.49	NIPBL; NIPBL iso2	592; 592	delangin isoform B	QCNDAPVSVLQEDIVGSLKST*PENHPETPK	Q6KC79; Q6KC79-2	316; 304	1	1.46E+05
149	<b>13.05</b>	NIPBL; NIPBL iso2	592, 599; 592, 599	delangin isoform B	QCNDAPVSVLQEDIVGSLKST*PENHPETPK	Q6KC79; Q6KC79-2	316; 304	1	1.37E+06
150	3.42	ORC1L	373	origin recognition complex, subunit 1	AQNEAT*STPHR	Q13415	97	1	9.57E+03
151	1.05	ORC6L	195	origin recognition complex subunit 6	IGQQVDREFGQVAT*PPR	Q9Y5N6	28	4	9.26E+05

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
152	13.91	polybromo 1	10, 27	polybromo 1 isoform 1	ATS*PSSSVSGDFDDGHHSVS*TPGPSR	Q86U86	193	4	3.41E+06
153	38.91	polybromo 1	10, 28	polybromo 1 isoform 1	ATS*PSSSVSGDFDDGHHSVS*TPGPSR	Q86U86	193	2	5.77E+06
154	14.95	polybromo 1	12, 32	polybromo 1 isoform 1	RATSPS*SSVSGDFDDGHHSVSTPGPS*R	Q86U86	193	1	1.19E+06
155	1.47	polybromo 1	28	polybromo 1 isoform 1	ATSPSSSVSGDFDDGHHSVST*PGPSR	Q86U86	193	1	1.69E+05
156	-0.67	APRIN	1394, 1403	PDS5, regulator of cohesion maintenance, homolog B	AES*PESSAIEST*QSTPQKGR	Q9NTI5	168	1	2.84E+06
157	50.11	APRIN	1394, 1405	PDS5, regulator of cohesion maintenance, homolog B	AES*PESSAIESTOS*TPQK	Q9NTI5	168	1	3.48E+06
158	3.89	APRIN	1398, 1406	PDS5, regulator of cohesion maintenance, homolog B	AESPES*AIESTQST*PQK	Q9NTI5	168	1	3.21E+06
159	1.26	POLA2	127	DNA-directed DNA polymerase alpha 2	AIST*PETPLTK	Q14181	66	3	1.15E+07
160	3.66	POLA2	127, 130	DNA-directed DNA polymerase alpha 2	AIST*PET*PLTKR	Q14181	66	4	9.85E+06
161	23.91	POLA2	141, 147, 152, 156	DNA-directed DNA polymerase alpha 2	S*PHQLLS*PSSFSS*PSAT*PSQK	Q14181	66	6	4.84E+05
162	3.11	POLE	2023	DNA-directed DNA polymerase epsilon	SAPGST*PVR	Q07864	262	1	4.32E+06
163	16.00	PRR12	1192	proline rich 12	IRPLEVPTTAGPASAST*PTDGAK	Q9ULL5	211	1	2.29E+06
164	3.13	RFC1	312	replication factor C large subunit	SSADKIGEVSS*PK	P35251	128	1	2.31E+05
165	18.68	RIF1	401, 409	RAP1 interacting factor 1	GAS*SPYGAPGT*PR	Q5UIPO	274	1	1.55E+06
166	3.22	SMARCC1	328, 330, 337	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1	KHS*PS*PPPTPT*ESR	Q92922	123	1	2.43E+05
167	2.56	SMARCC2; SMARCC2 iso2	322; 322	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform c	KGPST*PYTK	Q8TAQ2; Q8TAQ2-2	133; 125	1	4.56E+07
168	2.21	SMARCC2; SMARCC2 iso2	324; 324	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform c	GPSTPy*TK	Q8TAQ2; Q8TAQ2-2	133; 125	1	4.21E+05
169	29.19	Smc5	10, 12	SMC5 protein	TST*PS*PQPSKR	Q8IY18	129	4	5.71E+05
170	2.62	Smc5	8, 9	SMC5 protein	KT*S*TPSPQPSK	Q8IY18	129	1	4.19E+04
171	3.36	Smc5	9, 12	SMC5 protein	KTS*TPS*PQPSK	Q8IY18	129	1	6.09E+04
172	5.48	SP110	256, 270	SP110 nuclear body protein isoform a	DNS*PEPNDPEEPQEVSS*TPSDKK	Q9HB58	78	1	3.84E+05
173	9.98	TAF9B	193	transcription associated factor 9B	FTVQIPPSQST*PVKVPVATTAVQNLINPSM#IGPK	Q9HBM6	28	1	7.86E+05
174	-0.64	TMPO; TMPO iso2; TMPO iso6	156, 160; 156, 160; 156, 160	thymopoietin isoform beta	EQGTES*RSST*PLPTISSAENTR	P42167; P42167-2; P42166	51; 39; 75	4	6.83E+06
175	12.17	TMPO; TMPO iso2; TMPO iso6	159, 167; 159, 167; 159, 167	thymopoietin isoform beta	SS*PLPTISS*SAENTR	P42167; P42167-2; P42166	51; 39; 75	1	3.95E+06
176	1.12	TMPO; TMPO iso2; TMPO iso6	160; 160; 160	thymopoietin isoform beta	SST*PLPTISSAENTR	P42167; P42167-2; P42166	51; 39; 75	6	2.96E+08
177	36.50	TMPO	278	thymopoietin isoform beta	IDGPVISES*PIAETIM#ASSNESLVVNR	P42167	51	2	8.00E+05
178	121.54	TMPO	279	thymopoietin isoform beta	IDGPVISES*PIAETIM#ASSNESLVVNR	P42167	51	2	3.70E+06
179	26.20	TMPO; TMPO iso2	354; 245	thymopoietin isoform beta	EM#FPYEAS*TPTGISASCR	P42167; P42167-2	51; 39	2	3.37E+06
180	17.37	TMPO; TMPO iso2	355; 246	thymopoietin isoform beta	EM#FPYEAS*PTGISASCR	P42167; P42167-2	51; 39	5	5.33E+06
181	54.68	TMPO; TMPO iso2	355, 362; 246, 253	thymopoietin isoform beta	EM#FPYEAS*PTGISAS*CRRIK	P42167; P42167-2	51; 39	3	4.78E+06
182	5.07	TMPO; TMPO iso2; TMPO iso6	66, 67, 74; 66, 67, 74; 66, 67, 74	thymopoietin isoform beta	GPPDFS*S*DEEREPT*PVLGSGAAAAGR	P42167; P42167-2; P42166	51; 39; 75	5	5.74E+05
183	-0.15	TMPO; TMPO iso2; TMPO iso6	66, 74; 66, 74; 66, 74	thymopoietin isoform beta	GPPDFS*S*DEEREPT*PVLGSGAAAAGR	P42167; P42167-2; P42166	51; 39; 75	2	1.34E+05
184	0.00	TMPO; TMPO iso2; TMPO iso6	67, 74; 67, 74; 67, 74	thymopoietin isoform beta	NRPPLPAGTNSKGGPDFSS*DEEREPT*PVLGSGAA AAGR	P42167; P42167-2; P42166	51; 39; 75	2	0.00E+00
185	18.94	TMPO iso6	671	thymopoietin isoform beta	LAST*PFKGGTLFGGEVCK	P42166	75	8	1.60E+07
186	-0.29	TMPO; TMPO iso2; TMPO iso6	74; 74; 74	thymopoietin isoform beta	GPPDFS*DEEREPT*PVLGSGAAAAGR	P42167; P42167-2; P42166	51; 39; 75	2	9.32E+05
187	2.94	TOPBP1	861	topoisomerase (DNA) II binding protein 1	KPST*PLSEVIVK	Q92547	171	2	1.34E+06
188	22.12	TOPBP1	861, 864	topoisomerase (DNA) II binding protein 1	KPST*PLS*EVIVK	Q92547	171	3	6.56E+06
189	10.19	WHSC1L1	547	WHSC1L1 protein isoform short	LIIST*PNQR	Q9B295	162	3	6.30E+07
190	-0.76	XRCC1	447, 453	X-ray repair cross complementing protein 1	TKPTQAAGPSS*PQKPPT*PEETK	P18887	70	3	2.61E+06
191	5.42	ZNF261	817, 826	zinc finger protein 261	SAPTAPT*PPPPPPAT*PR	Q14202	152	4	1.64E+06
192	1.20	ZNF185; ZNF185 iso1	447; 215	zinc finger protein 185	GGQGDPAVPAQQADPST*PER	NP_009081; O15231	74; 49	2	3.21E+05
193		<b>Cytoskeletal protein</b>							
194	15.92	anillin	472	anillin, actin binding protein	OETHCQST*PLKK	Q9NQW6	124	1	3.54E+05
195	45.15	anillin	621, 628	anillin, actin binding protein	SLLAPLAQTVGVVSPESLVS*TPR	Q9NQW6	124	2	1.27E+06
196	-0.15	Bicd2	329	bicaudal D homolog 2 isoform 1	TSTPKKEGLAPPS*PSLVS*DLLELNISEIQK	Q8TD16	94	1	2.22E+04
197	6.89	Bicd2	329, 334	bicaudal D homolog 2 isoform 1	TSTPKKEGLAPPS*PSLVS*DLLELNISEIQK	Q8TD16	94	1	7.12E+05
198	12.64	caldesmon; caldesmon iso2; caldesmon iso3; caldesmon iso4	724, 730; 495, 501; 489, 495; 469, 475	caldesmon 1 isoform 2	GNVFSS*PTAAGT*PNKETAGLK	Q05682; Q05682-2; Q05682-3; Q05682-4	93; 66; 64; 63	1	5.83E+06
199	33.75	cofilin 1	23	cofilin 1 (non-muscle)	KS*STPEEVKK	P23528	19	1	3.52E+07
200	98.24	cofilin 1	24	cofilin 1 (non-muscle)	KSS*TPPEVKK	P23528	19	7	1.14E+07

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)	
201	<b>22.19</b>	cofilin 1	25	cofilin 1 (non-muscle)	KSST*PEEVK	P23528	19	13	2.63E+07	
202	<b>23.60</b>	restin	45	restin isoform a	ASST*PSSSEQEEFVDDFR	P30622	161	1	4.13E+06	
203	<b>7.41</b>	cordón-bleu	794	cordón-bleu homolog	GPPST*PVPTQTNPESR	O75128	136	2	2.14E+05	
204	<b>17.43</b>	DBN1	336, 344	drebrin 1 isoform a	M#APTPIPTRS*PDSSTAS*TPVAEQIER	Q16643	71	1	7.48E+05	
205	<b>20.08</b>	DBN1	338, 344	drebrin 1 isoform a	MAPTPIPTRS*DSSTAS*TPVAEQIER	Q16643	71	1	5.68E+05	
206	3.34	DBN1	345	drebrin 1 isoform a	SPSDSSTAST*PVAEQIER	Q16643	71	3	1.83E+06	
207	3.48	BPAG1 iso2	421	dystonin isoform 2	LLDPEDVDVSS*PDEK	Q03001	372	1	4.39E+05	
208	<b>9.08</b>	Destrin	24	destrin isoform b	KCS*TPEEIKK	P60981	19	1	3.14E+06	
209	<b>12.13</b>	Destrin	25	destrin isoform b	KCST*PEEIKK	P60981	19	2	8.02E+05	
210	<b>18.94</b>	EPB41L2	658	erythrocyte membrane protein band 4.1-like 2 isoform b	NFM#ES*TPEPRPNEWEKR	O43491	113	1	9.95E+05	
211	<b>8.97</b>	EPB41L2	659	erythrocyte membrane protein band 4.1-like 2 isoform b	NFM#EST*PEPRPNEWEK	O43491	113	3	3.27E+06	
212	2.11	DAL-1; DAL-1 iso2	55; 55	erythrocyte membrane protein band 4.1-like 3	AGAPVPEPPKQQALEQFAAAAAHS*TPVRR	Q9Y2J2; Q9Y2J2-2	121; 97	11	4.30E+06	
213	2.62	DAL-1; DAL-1 iso2	56; 56	erythrocyte membrane protein band 4.1-like 3	AGAPVPEPPKQQALEQFAAAAAHS*TPVRR	Q9Y2J2; Q9Y2J2-2	121; 97	9	2.74E+06	
214	<b>11.62</b>	FLNB	519	filamin B, beta (actin binding protein 278)	QKDFLDGVAIFYEYYPST*PGR	O75369	278	4	1.38E+07	
215	<b>30.84</b>	HPCA; HPCAL1; NCALD	144; 144; 144	hippocalcin	MPEDEST*PEKR	P84074; P37235; P61601	22; 22; 22	1	3.32E+06	
216	<b>5.69</b>	KIF22	462	kinesin family member 22	LLASQGSQGA*PLLS*TPKR	Q14807	73	5	1.09E+07	
217	<b>11.04</b>	KIF22	463	kinesin family member 22	LLASQGSQGA*PLLS*PK	Q14807	73	6	6.86E+06	
218	-0.63	lamin A/C; lamin A/C iso2	19; 19	lamin A/C isoform 2	SGAASST*PLSPTR	P02545; P02545-2	74; 65	2	4.38E+06	
219	<b>145.76</b>	lamin A/C; lamin A/C iso2	19, 22; 19, 22	lamin A/C isoform 2	SGAASST*PLS*PTR	P02545; P02545-2	74; 65	7	2.48E+08	
220	2.03	Lamin B1	575	lamin B1	TTIPEEEEEEEAAGVVEELFHQQGT*PR	P20700	66	3	8.51E+06	
221	<b>11.13</b>	Lamin B2	14, 17	lamin B2	AGGPAT*PLS*PTR	Q03252	68	1	5.28E+06	
222	3.85	MAP1B	1852	microtubule-associated protein 1B	DLS*TPGLEKDSGGK	P46821	271	1	3.52E+05	
223	<b>15.37</b>	MAP1B	1853	microtubule-associated protein 1B	DLST*PGLK	P46821	271	1	1.80E+07	
224	<b>17.83</b>	MAP1B	744	microtubule-associated protein 1B	SST*PLSEAK	P46821	271	1	1.02E+07	
225	-0.33	MAP2; MAP2 iso2; MAP2 iso3; MAP2 iso5	1588, 1592, 1611; 232, 236, 255; 1584, 1588, 1607; 289, 293, 312	microtubule-associated protein 2 isoform 5	AGKS*GTST*PTTPGSTAITGTPPSYSS*R	P11137; P11137-2; P11137-3; Q8IUX2	200; 50; 199; 59	1	9.74E+04	
226	4.14	MAP2; MAP2 iso2; MAP2 iso3; MAP2 iso5	1649, 1653, 1656; 293, 297, 300; 1645, 1649, 1652; 350, 354, 357	microtubule-associated protein 2 isoform 5	KVAIIRT*PPKS*PAT*PK	P11137; P11137-2; P11137-3; Q8IUX2	200; 50; 199; 59	1	1.51E+06	
227	<b>21.00</b>	RP1	209, 217, 223	microtubule-associated protein, RP/EB family, member 2 isoform 2	SS*PAAKPGST*PSRPSS*AKR	Q15555	37	1	2.01E+06	
228	-0.39	RP1	217	microtubule-associated protein, RP/EB family, member 2 isoform 2	SSPAAKPGST*PSRPSSAK	Q15555	37	1	3.75E+05	
229	<b>16.00</b>	MARCKS	143, 150	myristoylated alanine-rich protein kinase C substrate	AEDGAT*PSPSNET*PK	P29966	32	1	2.09E+05	
230	-0.35	ODF2 iso3	6	outer dense fiber of sperm tails 2 isoform 1	SS*TPPLHVHVDENTPVHVIK	Q5BJF6-3	93	1	1.04E+05	
231	<b>8.40</b>	PDLIM7	253	PDZ and LIM domain 7 isoform 1	HSQPATPT*PLQS	Q9NR12	50	2	1.09E+06	
232	4.54	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	1	9.34E+05	
233	1.46	spastin	302	spastin isoform 1	TNKPS*TPPTAT	Q9UBPO	67	2	2.27E+06	
234	<b>22.65</b>	spastin	302, 306	spastin isoform 1	TNKPS*TPPT*ATR	Q9UBPO	67	1	5.86E+05	
235	1.80	spastin	303	spastin isoform 1	TNKPST*PTTATR	Q9UBPO	67	2	7.25E+05	
236	<b>33.83</b>	spastin	305, 306	spastin isoform 1	TNKPSTPT*ATR	Q9UBPO	67	1	7.03E+05	
237	-0.66	SPIRE1; SPIRE1 iso2	509; 495	spire homolog 1 isoform a	FLPISST*PQPER	Q08AE8; Q08AE8-2	86; 84	5	2.46E+06	
238	-0.29	SPTBN1	2161, 2165, 2169	spectrin, beta, non-erythrocytic 1 isoform 1	TSS*KESS*PIPS*PTSDRK	Q01082	275	1	8.96E+04	
239	<b>5.32</b>	SPTBN1	2319	spectrin, beta, non-erythrocytic 1 isoform 1	DDEEM#NTWQAISSAISSDKHEVSASTQS*TPASSR	Q01082	275	2	2.98E+05	
240	-0.75	SPTBN1	2320	spectrin, beta, non-erythrocytic 1 isoform 1	SSAISSDKHEVSASTQST*PASSR	Q01082	275	4	1.33E+05	
241	<b>23.02</b>	TES	214	testin isoform 1	QMINIPGGDRS*TPAAGAMEDK	Q9UGI8	48	1	1.39E+06	
242	<b>27.06</b>	talin 1	941	talin 1	QAAASATQIAAAQAHAAS*PK	Q9Y490	270	3	2.99E+06	
243	1.25	talin 2	2041	talin 2	LLVSGAAS*PDKLAQAQSAATITQLAEVVK	Q9Y466	272	2	3.21E+05	
244	4.81	vimentin	56	vimentin	SLYASS*PGGVYAT	P08670	54	3	4.73E+07	
245	<b>10.78</b>	WIP	345	WAS/WASL interacting protein family, member 1	NLSLSST*PPLSPGR	Q43516	51	2	6.13E+05	
246	<b>35.29</b>	WIP	345, 350	WAS/WASL interacting protein family, member 1	NLSLSST*PPLPS*PGR	Q43516	51	1	1.45E+06	
247	1.47	WIP	398	WAS/WASL interacting protein family, member 1	ALPAT*PQLPSR	Q43516	51	1	2.88E+06	
248	4.35	PSRC2; PSRC2 iso5	949, 953, 958, 962	proline/serine-rich coiled-coil 2	LDSS*PVSS*PR	O60293; BAA25472	226; 218	1	1.04E+06	
249	<b>Endoplasmic reticulum or golgi</b>									
250	0.00	JPH2	486, 490	junctophilin 2 isoform 1	ETPREGGSPS*PAGT*PPQPK	Q9BR39	74	1	0.00E+00	

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Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
251		<b>Enzyme, misc.</b>							
252	-0.48	ACLY	446	ATP citrate lyase isoform 1	LNASGSTS*TPAPSR	P53396	121	2	1.15E+05
253	1.26	ACLY	447	ATP citrate lyase isoform 1	NFLNAGSST*PAPSR	P53396	121	12	6.75E+06
254	-0.81	ATAD2	1149	ATPase family, AAA domain containing 2	T*PSTPVACSTPAQLK	Q6PL18	159	1	1.68E+06
255	-0.94	ATAD2	1152	ATPase family, AAA domain containing 2	LKTPST*PVACSTPAQLK	Q6PL18	159	4	1.45E+06
256	2.39	BRIP1	113	BRCA1 interacting protein C-terminal helicase 1	HFNYPST*PPSR	Q9BX63	141	2	1.50E+06
257	2.09	BRIP1	918	BRCA1 interacting protein C-terminal helicase 1	YST*PPYLLEAASHLSPENFVEDEAK	Q9BX63	141	3	8.41E+05
258	<b>5.11</b>	BRIP1	918, 930	BRCA1 interacting protein C-terminal helicase 1	YST*PPYLLEAASHLS*PENFVEDEAK	Q9BX63	141	2	1.72E+06
259	<b>5.58</b>	coilin	333	coilin	SSST*PECAAGFLK	P38432	63	1	3.16E+05
260	-0.86	DOT1L	900, 902	DOT1-like, histone H3 methyltransferase	ARST*PS*PVLQPR	Q8TEK3	185	1	4.48E+05
261	1.34	CRMP-4	623	dihydropyrimidinase-like 3	GM#YDGPVFDLTT*PK	Q6DEN2	74	3	1.17E+06
262	-0.64	CRMP-4	623, 628	dihydropyrimidinase-like 3	GM#YDGPVFDLTT*PKGPT*PAGSAR	Q6DEN2	74	3	3.98E+06
263	-0.51	DUS3L	273	dihydrouridine synthase 3-like	QENCGAQVPAGPGTST*PPSSPVR	Q96G46	73	1	1.23E+06
264	-0.87	DUS3L	273, 277	dihydrouridine synthase 3-like	QENCGAQVPAGPGTST*PPSS*PVR	Q96G46	73	2	2.54E+06
265	-0.87	EME1	7, 12, 15	essential meiotic endonuclease 1 homolog 1	KSS*PSLDS*GDS*DSEELPTFAFLKK	Q96AY2	63	1	1.03E+05
266	1.48	EZH2	363, 366	enhancer of zeste 2 isoform a	GRLPNNSS*RRS*TPINLVLESK	Q15910	85	2	4.14E+06
267	1.12	EZH2	363, 367	enhancer of zeste 2 isoform a	LPNNS*RPST*PTINLVLESK	Q15910	85	3	1.76E+06
268	-0.93	EZH2	366	enhancer of zeste 2 isoform a	GRLPNNSSRRS*TPINLVLESK	Q15910	85	2	1.09E+06
269	1.12	EZH2	367	enhancer of zeste 2 isoform a	LPNNSRRPST*PTINLVLESK	Q15910	85	5	1.88E+06
270	1.30	EZH2	367, 369	enhancer of zeste 2 isoform a	GRLPNNSSRRPST*PT*INVLESK	Q15910	85	2	1.57E+06
271	<b>13.61</b>	KATNA1	81	katanin p60 subunit A 1	LDST*PLK	O75449	56	6	9.91E+06
272	<b>8.84</b>	KIAA0819	431	microtubule associated monooxygenase, calponin and LIM domain containing 3 isoform 3	TST*PLAPLVQSQSDTK	O94909	127	1	1.88E+05
273	3.83	MYST3	1136, 1142	MYST histone acetyltransferase (monocytic leukemia) 3	DVKNS*PLEPDT*STPLKKK	Q92794	225	1	1.29E+05
274	-0.85	MYST3	1144	MYST histone acetyltransferase (monocytic leukemia) 3	NSPLEPDT*PLKK	Q92794	225	2	2.89E+05
275	1.86	SETD1A	916	SET domain containing 1A	RPRPST*PAEDEDDEPEQEK	O15047	186	1	1.08E+05
276	4.00	SDS3	234, 237, 244	suppressor of defective silencing 3	RPAS*PSS*PEHLPAT*PAESPAQR	Q9H7L9	38	2	1.08E+06
277	<b>9.27</b>	SDS3	234, 237, 244, 248	suppressor of defective silencing 3	RPAS*PSS*PEHLPAT*PAES*PAQR	Q9H7L9	38	1	1.65E+06
278	3.92	TKT	287	transketolase isoform 1	ILAT*PPQEDAPSDIANIR	P29401	68	1	6.79E+05
279	<b>19.95</b>	TRMT1	623, 628	tRNA methyltransferase 1 isoform 1	GDQCCYS*HSPPT*PR	Q9NXH9	72	2	2.12E+06
280	<b>14.70</b>	TRMT1	625, 628	tRNA methyltransferase 1 isoform 1	GDQCCYS*HSPPT*PR	Q9NXH9	72	4	6.00E+05
281	<b>8.07</b>	TRMT1	628	tRNA methyltransferase 1 isoform 1	GDQCCYS*HSPPT*PR	Q9NXH9	72	1	3.03E+05
282	-0.34	UNG	60	uracil-DNA glycosylase isoform UNG1 precursor	KAPAGQEEPGT*PPSSPLSAEQDLR	P13051	35	5	7.24E+05
283	-0.51	UNG	60, 63	uracil-DNA glycosylase isoform UNG1 precursor	KAPAGQEEPGT*PPSS*PLSAEQDLR	P13051	35	1	1.47E+06
284	-0.87	UNG	60, 64	uracil-DNA glycosylase isoform UNG1 precursor	APAGQEEPGT*PPSS*PLSAEQDLR	P13051	35	4	4.56E+05
285	-0.26	WRNIP1	116	Werner helicase interacting protein isoform 1	ESYDAPPT*PSGAR	Q96S55	72	1	8.20E+04
286	1.43	ZDHHC5	345, 348	zinc finger, DHHC domain containing 5	THLGLATNEDSSSLAKDS*PPT*PTM#YK	Q9C0B5	78	1	4.17E+05
287		<b>G protein or regulator</b>							
288	2.24	ARHGAP21	232	Rho GTPase activating protein 21	QQTST*PVLTPQGR	Q575U3	217	1	9.70E+05
289	2.00	ARHGAP21	233	Rho GTPase activating protein 21	QQTST*PVLTPQGR	Q575U3	217	2	4.62E+06
290	<b>18.40</b>	DDEF1	757	development and differentiation enhancing factor 1	LALPGFS*TPR	Q9ULH1	125	1	3.20E+06
291	<b>5.13</b>	ECT2	413	epithelial cell transforming sequence 2 oncogene protein	SST*PVPSK	Q9H8V3	100	1	5.99E+06
292	2.46	GAPVD1	761	GTPase activating protein and VPS9 domains 1	PS*TPGLSVVSGISATSEDPINKIEDLR	Q9Y4N0	166	2	3.90E+05
293	-0.61	GAPVD1	761, 762	GTPase activating protein and VPS9 domains 1	EVSSRPS*TPGLSVVSGISATSEDPINKIEDLR	Q9Y4N0	166	13	1.51E+07
294	2.76	GIT1; GIT1 iso3	480, 493	G protein-coupled receptor kinase interactor 1 isoform 1	QPPGPVPT*PPLPSEK	Q9Y2X7; Q59FC3	84; 86	3	1.18E+06
295	<b>5.63</b>	RIP3; RIP3 iso2	288, 291, 293; 289, 292, 294	myosin phosphatase-Rho interacting protein isoform 1	AEEQQLPPPLS*PPS*PS*PNHRR	Q6WCQ1; Q6WCQ1-2	116; 118	1	3.24E+05
296	<b>19.10</b>	RIP3; RIP3 iso2	288, 291, 294; 289, 292, 295	myosin phosphatase-Rho interacting protein isoform 1	AEEQQLPPPLS*PPS*PST*PNHRR	Q6WCQ1; Q6WCQ1-2	116; 118	6	6.49E+06
297	1.04	RIP3; RIP3 iso2	291, 294; 292, 295	myosin phosphatase-Rho interacting protein isoform 1	AEEQQLPPPLSPPS*PST*PNHRR	Q6WCQ1; Q6WCQ1-2	116; 118	4	2.38E+05
298	<b>10.32</b>	Rab26	13	RAB26, member RAS oncogene family	GAS*TPAASLTPTANGARPA	Q9ULW5	28	1	3.18E+05
299	<b>5.86</b>	RASAL2	878	RAS protein activator like 2 isoform 1	ETQST*POSAPQV	Q2TB22	142	1	1.10E+06
300	<b>9.87</b>	RGS2	54	regulator of G-protein signaling 2, 24kDa	LSYFLQNSST*PGKPK	P41220	24	3	1.12E+06
301	3.29	SEPT9	38, 41	septin 9 isoform a	SFEVEEVE*PNS*TPRR	Q9UHD8	65	1	1.84E+06
302	<b>39.40</b>	SEPT9	38, 42	septin 9 isoform a	SFEVEEVE*PNST*PPR	Q9UHD8	65	9	1.22E+06

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
303	<b>10.68</b>	SEPT9	41	septin 9 isoform a	SFEVEEVETPNS*TPPR	Q9UHD8	65	2	1.31E+07
304	<b>14.84</b>	SEPT9	42	septin 9 isoform a	SFEVEEVETPNS*TPPR	Q9UHD8	65	10	3.42E+07
305	3.07	SIPA1L1	1573	signal-induced proliferation-associated 1 like 1	FHALSSPQSPFPST*PTSR	Q43166	200	1	2.50E+05
306	<b>23.59</b>	SIPA1L1	68	signal-induced proliferation-associated 1 like 1	SEGSHHITST*PGVVK	Q43166	200	2	7.94E+05
307	<b>7.13</b>	TBC1D10B	687, 707, 712	TBC1 domain family, member 10B	RAS*AGPAPGPVWTAEGHLHPSLPS*PTGNS*TPLGSSK	Q4KMP7	87	1	7.15E+05
308	<b>7.61</b>	TBC1D10B	707, 713	TBC1 domain family, member 10B	AEGHLHPSLPS*PTGNST*PLGSSK	Q4KMP7	87	1	3.21E+05
309	-0.36	TBC1D10B	713	TBC1 domain family, member 10B	ASAGPAPGPVWTAEGHLHPSLPSPTGNST*PLGSSK	Q4KMP7	87	1	9.44E+04
310	<b>22.21</b>	TBC1D23	514	TBC1 domain family, member 23	EKVISFIENTST*PVDR	Q9NUY8	78	8	2.41E+06
311	<b>Inhibitor protein</b>								
312	4.66	Daple	1533	DVL-binding protein DAPLE	TCSTSATTAPSNT*PIAR	Q9P219	228	2	5.13E+05
313	<b>Lipid binding protein</b>								
314	3.07	ACBD5 iso3	172	acyl-Coenzyme A binding domain containing 5 isoform 2	SSDITSDLGNLVTST*PNAK	Q5T8D3-3	59	2	1.84E+06
315	<b>Mitochondrial protein</b>								
316	<b>12.83</b>	MFF; MFF iso2; MFF iso4; MFF iso5	105, 115; 79, 89; 79, 89; 79, 89	mitochondrial fission factor	IVVAGNNEVDVFSRPAADLTIQS*TPFKPLALK*TPPR	Q9GZY8; Q9GZY8-2; Q9GZY8-4; Q9GZY8-5	38; 33; 25; 27	2	3.73E+06
317	<b>5.65</b>	MFF; MFF iso2; MFF iso4; MFF iso5	93, 105; 67, 79; 67, 79; 67, 79	mitochondrial fission factor	IVVAGNNEVDV*FSRPAADLTIQS*TPFKPLALK	Q9GZY8; Q9GZY8-2; Q9GZY8-4; Q9GZY8-5	38; 33; 25; 27	1	1.53E+05
318	<b>14.61</b>	MFF; MFF iso2; MFF iso4; MFF iso5	93, 105, 115; 67, 79, 89; 67, 79, 89; 67, 79, 89	mitochondrial fission factor	IVVAGNNEVDV*FSRPAADLTIQS*TPFKPLALK*TPPR	Q9GZY8; Q9GZY8-2; Q9GZY8-4; Q9GZY8-5	38; 33; 25; 27	1	3.28E+06
319	<b>Motor or contractile protein</b>								
320	<b>32.58</b>	DNCI2; DNCI2 iso3	95; 89	dynein, cytoplasmic 1, intermediate chain 2	SVST*PSEAGSQSDSGDVGAVGSR	Q13409; Q13409-3	71; 68	3	4.94E+06
321	<b>8.71</b>	KIF18B	665, 676	kinesin family member 18B	RGS*LPDTQPSQGPS*TPKGER	Q86Y91	93	2	2.97E+06
322	<b>14.83</b>	KIF18B	676	kinesin family member 18B	GSLPDTQPSQGPS*TPKGER	Q86Y91	93	3	7.66E+05
323	2.70	KIF18B	677	kinesin family member 18B	GSLPDTQPSQGPST*PK	Q86Y91	93	1	1.50E+05
324	2.50	KIF18B	714	kinesin family member 18B	SRVPLGPSAM#QNCST*PLALPTR	Q86Y91	93	1	1.95E+05
325	<b>Phosphatase</b>								
326	<b>9.38</b>	CTDSPL2	59	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	FIKGS*TPKEER	Q8IYI9	53	1	2.20E+06
327	<b>16.83</b>	CTDSPL2	86	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	DIDNNLITST*PR	Q8IYI9	53	1	2.75E+07
328	2.16	PPM1H	113	protein phosphatase 1H (PP2C domain containing)	AGAVTST*PNR	Q9ULR3	56	1	9.02E+05
329	4.86	PPP1R10	256	protein phosphatase 1, regulatory subunit 10	QSNVAAPGDAT*PPAEK	Q96QCO	99	1	4.32E+05
330	<b>26.61</b>	PPP2R5D	62	delta isoform of regulatory subunit B56, protein phosphatase 2A isoform 1	RPSNS*TPPPTQLSK	Q14738	70	1	2.44E+06
331	<b>33.31</b>	PPP2R5D	63	delta isoform of regulatory subunit B56, protein phosphatase 2A isoform 1	RPSNST*PPPTQLSK	Q14738	70	6	6.05E+06
332	<b>6.08</b>	PTPN13; PTPN13 iso3	1188; 1169	protein tyrosine phosphatase, non-receptor type 13 isoform 2	VPST*PVHLTNEMK	Q12923; Q12923-3	277; 275	1	3.10E+05
333	4.54	SEC16A; SEC16A iso4	593, 595; 220, 222	SEC16 homolog A	GSVSPST*PS*PKPTGIFQTSANSSFPVK	Q15027; A4QN18	252; 211	2	5.09E+05
334	<b>5.06</b>	SEC16A	65	SEC16 homolog A	QALQST*PLGSSSK	Q15027	252	2	7.48E+06
335	<b>11.51</b>	SSH3	638	slingshot homolog 3	TOAFQEQEQGGGQGGQGEPCISST*PR	Q8TE77	73	1	4.79E+05
336	<b>Protease</b>								
337	-0.76	PSMB5	262	proteasome beta 5 subunit isoform 2	VSSDNVADLHEKYGSGST*P	P28074	28	1	1.29E+06
338	<b>5.04</b>	SEN3	169, 176, 181	SUMO1/sentrin/SMT3 specific protease 3	NHLS*PQQGGAT*POVPS*PCCR	Q9H4L4	65	1	1.79E+05
339	4.97	USP15 iso2	226	ubiquitin specific peptidase 15	GPST*PNVK	Q9Y4E8-2	109	1	1.28E+07
340	3.45	USP19; USP19 iso3	111; 111	ubiquitin specific peptidase 19	EGACEDPHDLLAT*PTPELLLDWR	Q94966; Q94966-3	146; 141	1	1.05E+05
341	<b>19.68</b>	USP19; USP19 iso3	407; 407	ubiquitin specific peptidase 19	VAVPTGPTPLDST*PPGGAPHPLTQGEAR	Q94966; Q94966-3	146; 141	4	1.39E+07
342	<b>8.69</b>	USP37	191	ubiquitin specific peptidase 37	TIPSLTST*PLR	Q86T82	110	1	3.14E+06
343	1.23	USP37	628	ubiquitin specific peptidase 37	ASQMVNSCITS*PSTPSKK	Q86T82	110	1	5.07E+05
344	<b>18.00</b>	USP8	379	ubiquitin specific peptidase 8	M#GPLNIST*PVEPVAASK	P40818	128	2	1.80E+06
345	2.69	USP8	691	ubiquitin specific peptidase 8	YHSPNTVHM#YPPPEMAPSSAPPS*TPPTHK	P40818	128	5	4.64E+05
346	-0.69	USP8	692	ubiquitin specific peptidase 8	YHSPNTVHM#YPPPEMAPSSAPPS*TPPTHK	P40818	128	6	1.06E+05
347	<b>Protein kinase, Ser/Thr (non-receptor)</b>								
348	-0.47	Bcr	459, 463	breakpoint cluster region isoform 1	HQDGLPYIDDS*PSSS*PHLSSK	P11274	143	1	1.23E+05
349	<b>5.07</b>	BubR1	620	budding uninhibited by benzimidazoles 1 beta	FVST*PFHEIM#SLK	Q60566	120	1	3.52E+05

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
350	3.56	CHED; CHED iso2	1147; 1087	cell division cycle 2-like 5 isoform 1	QTDGPST*PQEQSSKPLGGIOPSSQTIQPK	Q14004; Q14004-2	165; 158	2	2.96E+06
351	-0.72	CHED; CHED iso2	1225; 1165	cell division cycle 2-like 5 isoform 1	ENSGGHEASLQLRRPPEPS*TPVSGQDQLIQHDM#R	Q14004; Q14004-2	165; 158	3	3.15E+05
352	<b>5.86</b>	MRCKb	1678, 1690, 1693	CDC42-binding protein kinase beta	HST*PSNNSNPSPGPPS*PNS*PHR	Q9Y5S2	194	1	1.69E+05
353	<b>29.30</b>	CdkL5	813	cyclin-dependent kinase-like 5	SIHSAST*PSSRPK	Q76039	116	1	1.16E+05
354	3.46	CRIK; CRIK iso4	1306; 1348	citron	KATDHPHPST*PATA	Q14578; AAV87216	231; 237	1	2.98E+05
355	<b>43.48</b>	CRIK; CRIK iso4	1345; 1387	citron	ESST*PEEFSR	Q14578; AAV87216	231; 237	3	1.87E+06
356	<b>13.27</b>	CRIK; CRIK iso4	1939, 1955; 1981, 1997	citron	VAS*SPAPPEGSPHPREPST*PHR	Q14578; AAV87216	231; 237	2	3.62E+05
357	<b>18.38</b>	CRIK; CRIK iso4	1940, 1955; 1982, 1997	citron	VASS*PAPPEGSPHPREPST*PHR	Q14578; AAV87216	231; 237	2	9.51E+05
358	<b>29.11</b>	CK1-E	351	casein kinase 1 epsilon	SAAEVAST*PASR	P49674	47	1	6.38E+05
359	<b>25.44</b>	GSK3B; GSK3B iso2	<b>390, 403</b>	glycogen synthase kinase 3 beta isoform 2	IQAAAST*PTNATAASDANTGDR	P49841; NP_002084.2	47; 48	1	1.67E+06
360	2.32	PBK	23	PDZ binding kinase	KSVLCS*PTINIPASPFM#QK	Q96KB5	36	1	2.00E+05
361	<b>51.34</b>	PBK	24	PDZ binding kinase	SVLCST*PTINIPASPFM#QK	Q96KB5	36	1	3.40E+06
362	<b>10.52</b>	PBK	24, 32	PDZ binding kinase	SVLCST*PTINIPAS*PFM#QK	Q96KB5	36	3	1.04E+07
363	<b>17.87</b>	PBK	26	PDZ binding kinase	SVLCSTPT*INIPASPFM#QK	Q96KB5	36	1	5.92E+06
364	1.65	AMPKA1	486, 490	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 1	SIDDETEAKS*GTAT*PQR	Q13131	64	1	3.16E+05
365	<b>15.45</b>	Raf1	<b>259</b>	v-raf-1 murine leukemia viral oncogene homolog 1	STS*TPNVHMVSTTLPVDSR	P04049	73	1	3.76E+05
366	<b>10.62</b>	SCYL2	759	SCY1-like 2 protein	SSASSTFTSVPSM#GIGM#M#FS*TPDNTKR	Q6P3W7	104	1	4.35E+05
367	1.56	Sgk269	809	NKF3 kinase family member	ACSVVELYAIPDADVAKST*PK	Q9H792	193	1	2.98E+05
368	-0.52	LOK	952	serine/threonine kinase 10	LSEEAECNPST*PSK	Q94804	112	2	1.64E+05
369	<b>5.50</b>	TAO2; TAO2 iso2	603; 603	TAO kinase 2 isoform 1	EQLKEELQENPS*TPKR	Q9UL54; Q9UL54-2	138; 119	1	3.13E+05
370	<b>10.44</b>	TAO3	572	TAO kinase 3	IKEEMNEDHS*TPKKEK	Q9H2K8	105	2	8.51E+05
371	-0.21	Trio	2418	triple functional domain (TPRF interacting)	AGAASPLNSLPSAVSLGKPEFPSS*PLQK	Q75962	342	1	7.85E+04
<b>373</b>	<b>Protein kinase, atypical</b>								
374	<b>19.12</b>	ChaK1	1404	transient receptor potential cation channel, subfamily M, member 7	FFVS*TPSQPSCK	Q96QT4	213	1	3.67E+05
375	<b>10.05</b>	ChaK1	555	transient receptor potential cation channel, subfamily M, member 7	NTSSST*PQLR	Q96QT4	213	1	1.33E+06
<b>376</b>	<b>Protein kinase, dual-specificity</b>								
377	<b>5.64</b>	MEK1	385	mitogen-activated protein kinase kinase 1	RSDAEVDFVAGWLCSTIGLNQPS*TPTHAAGV	Q02750	43	3	1.15E+05
378	1.71	MEK1	386	mitogen-activated protein kinase kinase 1	GLNQPST*PTHAAGV	Q02750	43	4	1.63E+07
379	2.12	MKK6	28	mitogen-activated protein kinase kinase 6	EAFEQPQTST*PPRDLDK	P52564	37	2	1.91E+07
<b>381</b>	<b>RNA processing</b>								
382	<b>9.60</b>	RED1	32	RNA-specific adenosine deaminase B1 isoform 2	DGST*PGPGEQSLSNNGGGGPGR	P78563	81	1	1.42E+06
383	<b>70.82</b>	RIP	153	HIV-1 Rev binding protein isoform 1	VVASVHASISGSSASSTSS*TPVVKPLK	P52594	58	3	2.35E+06
384	<b>7.53</b>	ataxin-2	660	ataxin 2	GSISSGLFVSHNPPSEAA*PPVAR	Q99700	140	2	3.55E+05
385	<b>12.26</b>	BAT2; BAT2 iso1	505; 517	HLA-B associated transcript-2	LKAEPAPAAPAST*PAPPPAVPK	P48634-2; P48634	228; 229	2	2.40E+06
386	<b>5.33</b>	BAT2; BAT2 iso1	787, 796; 799, 808	HLA-B associated transcript-2	LAWVGDVFTAT*PAEPRPLTS*PLR	P48634-2; P48634	228; 229	1	1.21E+05
387	<b>79.76</b>	BOP1	106	block of proliferation 1	TTEEQVQAST*PCPR	Q14137	84	5	6.10E+06
388	-0.30	CPSF7	203	pre-mRNA cleavage factor I, 59 kDa subunit isoform 2	DSSDSADGRAT*PSENLVPSAR	Q8N684	52	1	7.78E+04
389	<b>15.06</b>	Dcp1b	363	decapping enzyme Dcp1b	LQST*PGAANK	Q8IZD4	68	1	2.65E+06
390	<b>7.14</b>	DHX38	286	DEAH (Asp-Glu-Ala-His) box polypeptide 38	HLGS*TPR	Q92620	141	2	1.37E+06
391	<b>50.59</b>	HBS1	231	Hsp70 subfamily B suppressor 1-like protein isoform 2	SANPHTIQASEEQSST*PAPVKK	Q9Y450	75	4	3.70E+06
392	<b>39.15</b>	hnRNP 2H9; hnRNP 2H9 iso2	270; 255	heterogeneous nuclear ribonucleoprotein H3 isoform a	YIELFLNST*PGGGSGM#GGSGM#GGYGR	P31942; P31942-2	37; 35	4	4.78E+06
393	<b>32.09</b>	hnRNP L; hnRNP L iso3	456; 487	heterogeneous nuclear ribonucleoprotein L isoform b	FST*PEQAAK	P14866; NP_001524	60; 64	2	7.63E+06
394	<b>26.13</b>	IGF2BP3	249	insulin-like growth factor 2 mRNA binding protein 3	SITILST*PEGTSAACK	Q00425	64	2	2.12E+06
395	<b>8.99</b>	KHSRP	100	KH-type splicing regulatory protein	IGGDAATTVNNST*PDFGFGGQK	Q92945	73	5	1.23E+07
396	<b>8.97</b>	LARP5	701	La ribonucleoprotein domain family, member 5	YREPPALKS*TPGAPR	Q92615	81	1	8.45E+05
397	1.46	LARP5	732, 736	La ribonucleoprotein domain family, member 5	EQST*PPKS*PQ	Q92615	81	1	3.47E+06
398	<b>36.97</b>	METTL3	106	methyltransferase like 3	IST*PDAPATQDQGVESLLQK	Q86U44	64	1	1.14E+06
399	<b>28.51</b>	NOL5A	538	nucleolar protein 5A	KST*PKEETVNDPEEAGHR	Q00567	66	1	8.24E+05
400	<b>20.81</b>	NPM1; NPM1 iso3	217; 217	nucleophosmin 1 isoform 3	SNQNGKDSKPS*STPR	P06748; Q9BYG9	33; 28	2	1.45E+05
401	<b>10.47</b>	NPM1; NPM1 iso3	219; 219	nucleophosmin 1 isoform 3	DSKPSST*PR	P06748; Q9BYG9	33; 28	2	1.13E+05
402	1.67	hnRNP E1	190	poly(rC) binding protein 1	VM#TIPYQPM#PASS*PVICAGGQDR	Q15365	37	1	1.68E+06
403	<b>23.54</b>	PRPF3	164, 167	PRP3 pre-mRNA processing factor 3 homolog	QLSFIS*PPT*PQPK	Q43395	78	2	1.38E+06
404	1.87	RBM15B	232, 238	RNA binding motif protein 15B	RSSSS*AAAAS*PPGPPAPADPLGYPPLHGGYQYK	Q8NDT2	97	1	2.25E+05

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



**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
405	19.77	RBM27	769, 781	RNA binding motif protein 27	LGHAGGNQSDASHLLNQS*GGAGEDCQIFST*PGHPK	Q9P2N5	119	2	7.96E+05
406	17.68	RBM27	884, 888	RNA binding motif protein 27	TSS*AVST*PSKVK	Q9P2N5	119	1	2.63E+06
407	5.96	RBM27	888	RNA binding motif protein 27	TSSAVST*PSKVK	Q9P2N5	119	3	1.45E+07
408	28.64	CSIG	105	ribosomal L1 domain containing 1	SDSEDICLFTKDEPNST*PEKTEOFYR	Q76021	55	3	2.84E+06
409	15.72	CSIG	106	ribosomal L1 domain containing 1	SDSEDICLFTKDEPNST*PEKTEOFY	Q76021	55	4	1.52E+06
410	33.95	CSIG	392, 396, 400	ribosomal L1 domain containing 1	HATGKKS*PAKS*PNPS*TPR	Q76021	55	5	3.96E+05
411	9.16	CSIG	392, 396, 401	ribosomal L1 domain containing 1	KS*PAKS*PNPST*PR	Q76021	55	6	9.26E+05
412	1.90	SF3B1	207, 211	splicing factor 3b, subunit 1 isoform 2	WDQTADQT*PGAT*PK	Q75533	146	4	2.52E+06
413	2.80	SF3B1	211	splicing factor 3b, subunit 1 isoform 2	WDQTADQTPGAT*PK	Q75533	146	1	2.20E+05
414	17.35	SF3B1	261, 267, 273, 278	splicing factor 3b, subunit 1 isoform 2	IWDPTPSHT*PAGAAT*PGRGDT*PGHAT*PGHGGA TSSAR	Q75533	146	2	1.47E+06
415	2.76	SF3B1	261, 278, 287	splicing factor 3b, subunit 1 isoform 2	IWDPTPSHT*PAGAAT*PGRGDT*PGHAT*PGHGGA TSSAR	Q75533	146	1	1.97E+05
416	1.64	SF3B1	267, 273, 278, 287	splicing factor 3b, subunit 1 isoform 2	IWDPTPSHT*PAGAAT*PGRGDT*PGHAT*PGHGGA SS*ARK	Q75533	146	3	1.19E+05
417	10.32	SF3B1	326, 328	splicing factor 3b, subunit 1 isoform 2	GGDSIGET*PT*PGASKR	Q75533	146	1	2.52E+05
418	3.81	SF3B1	326, 332	splicing factor 3b, subunit 1 isoform 2	GGDSIGET*PTPGAS*KR	Q75533	146	1	3.78E+05
419	8.33	SF3B1	328	splicing factor 3b, subunit 1 isoform 2	GGDSIGETPT*PGASK	Q75533	146	1	4.08E+05
420	-0.46	SF3B1	349	splicing factor 3b, subunit 1 isoform 2	SRWDETPASOM#GGST*TVLTPGK	Q75533	146	1	1.35E+05
421	30.43	SF4	116	splicing factor 4	AQTSTADPTSAPSAPPST*PTPSAGK	Q8IWZ8	72	2	1.31E+06
422	3.66	P18SRP	144	P18SRP protein	HS*STPNSEFSR	Q8N9Q2	18	1	5.50E+06
423	2.40	P18SRP	145	P18SRP protein	HSS*TPNSEFSRK	Q8N9Q2	18	2	3.75E+05
424	3.12	P18SRP	146	P18SRP protein	HSST*PNSEFSR	Q8N9Q2	18	2	2.84E+06
425	5.95	P18SRP	146, 150	P18SRP protein	HSST*PNSS*EFSR	Q8N9Q2	18	1	8.11E+05
426	11.90	RNUT1	341	snurportin 1	ASENGHYEHLHST*PK	Q95149	41	7	5.10E+06
427	1.05	SRm160; SRm160 iso3	402, 406; 397, 401	serine/arginine repetitive matrix 1	HRPS*PPAT*PPPK	Q8IYB3; A9Z1X7	102; 103	4	6.19E+06
428	1.44	SRm300	1043	splicing coactivator subunit SRm300	SST*PPGESYFGVSSLQLK	Q9UQ35	300	14	1.02E+08
429	-0.68	SRm300	1453, 1458, 1463	splicing coactivator subunit SRm300	DGSGT*PSRHS*LSGSS*PGMK	Q9UQ35	300	1	4.46E+05
430	-0.48	SRm300	1497, 1499, 1502	splicing coactivator subunit SRm300	S*RS*PSS*PELNK	Q9UQ35	300	1	3.04E+05
431	-0.69	SRm300	1844, 1848	splicing coactivator subunit SRm300	SRT*PPTS*R	Q9UQ35	300	1	3.95E+05
432	1.10	SRm300	367	splicing coactivator subunit SRm300	SSTGPEPPAPT*PLAER	Q9UQ35	300	1	5.20E+05
433	-0.13	SRm300	876	splicing coactivator subunit SRm300	SCFESS*POPELK	Q9UQ35	300	1	4.97E+04
434	-0.48	SRm300	903, 908	splicing coactivator subunit SRm300	SST*PPRQS*PSR	Q9UQ35	300	1	1.88E+07
435	11.13	UPF3B; UPF3B iso2	175; 175	UPF3 regulator of nonsense transcripts homolog B isoform 2	M#T*STPETLLEEIAEK	Q9BZ17; Q9BZ17-2	58; 56	1	2.17E+06
436	9.79	UPF3B; UPF3B iso2	177; 177	UPF3 regulator of nonsense transcripts homolog B isoform 2	M#TST*PETLLEEIAEK	Q9BZ17; Q9BZ17-2	58; 56	3	9.01E+06
437	18.72	ZFR	528	zinc finger RNA binding protein	GTECVKS*TPVSAVQIPEVK	Q96KR1	117	1	2.47E+06
438	<b>Receptor, channel, transporter or cell surface protein</b>								
439	11.76	ATP9B; ATP9B iso2	521; 521	ATPase, class II, type 9B	DSYSQMQSQAGGNTGST*PLRK	Q43861; Q43861-2	129; 128	1	4.76E+05
440	5.23	ataxin-2L	681	ataxin 2 related protein isoform A	STST*PTSPGPR	Q8WWM7	113	1	4.79E+06
441	31.91	ataxin-2L	681, 684	ataxin 2 related protein isoform A	STST*PTS*PGPR	Q8WWM7	113	1	9.02E+06
442	13.61	CELSR2	2776	cadherin EGF LAG seven-pass G-type receptor 2	LPLHS*TPK	Q9HCU4	317	1	1.48E+06
443	13.69	eIF4ENIF1	769	eukaryotic translation initiation factor 4E nuclear import factor 1	SSCST*PLSQANR	Q9NRA8	108	2	3.15E+06
444	1.46	ESYT2; ESYT2 iso2	701, 704; 673, 676	family with sequence similarity 62 (C2 domain containing) member B	SHM#SGSPGPGGSNT*APS*TPVIGGSDKPGMEEK	A0FGR8; A0FGR8-2	102; 99	1	8.18E+04
445	26.90	AHCP	195	family with sequence similarity 8, member A1	TAAGIST*PAPVAGLGPR	Q9UBU6	44	2	4.42E+06
446	3.21	INTS1	83	integrator complex subunit 1	LSST*PPLSALGR	Q8N201	244	3	9.09E+06
447	1.54	NUP133	28	nucleoporin 133kDa	GPLAGLPGST*PR	Q8WUM0	129	2	4.45E+06
448	2.54	NUP133	28, 31	nucleoporin 133kDa	GPLAGLPGST*PRT*ASR	Q8WUM0	129	1	3.30E+05
449	24.08	NUP133	41, 45, 50	nucleoporin 133kDa	KGLPLGS*AVSS*PVLFS*PVGR	Q8WUM0	129	1	9.27E+05
450	6.02	NUP133	45, 50	nucleoporin 133kDa	KGLPLGS*AVSS*PVLFS*PVGR	Q8WUM0	129	1	1.34E+06
451	5.70	NUP210	1848, 1852, 1860, 1862	nucleoporin 210	AS*PGHS*PHYFAASS*PT*SPNALPPAR	Q8TEM1	205	1	2.43E+05
452	19.35	NUP35	100, 106	nucleoporin 35kDa	SIYDDISS*PGLGST*PLTSR	Q8NFH5	35	2	3.19E+06
453	-0.28	NUP35	106	nucleoporin 35kDa	SIYDDISSPGLGST*PLTSR	Q8NFH5	35	1	3.07E+05
454	2.81	NUP35	273, 280	nucleoporin 35kDa	TLGT*PTQPGST*PR	Q8NFH5	35	1	2.82E+05
455	1.10	NUP35	280	nucleoporin 35kDa	TLGTPTQPGST*PR	Q8NFH5	35	2	4.92E+05

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**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
456	<b>11.00</b>	RTN3	396	reticulon 3 isoform a	TPVCSIDGST*PITK	Q95197	113	1	5.28E+05
457	<b>8.85</b>	NKCC1	266	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	LLRPSLAELHDELEKEPFEDGFANGEEST*PTR	P55011	131	8	1.82E+06
458	3.78	SLC25A46	45	solute carrier family 25, member 46	SFSTGSDLGHVWVTP*PPDIPGSR	Q96AG3	46	1	1.27E+05
459	<b>7.63</b>	SLC4A7; SLC4A7 iso3; SLC4A7 iso5	557; 343; 107	solute carrier family 4, sodium bicarbonate cotransporter, member 7	KIPVFHNGST*PTLGETPK	Q9Y6M7; Q9Y6M7-3; Q9Y6M7-5	136; 114; 90	5	2.78E+06
460	<b>17.76</b>	TPR	1676	nuclear pore complex-associated protein TPR	GIASTSDPPTANIKPTPVVVS*TPSK	P12270	266	4	4.04E+06
461	<b>17.35</b>	TPR	1676, 1691	nuclear pore complex-associated protein TPR	GIASTSDPPTANIKPTPVVVS*TPSKVTAAM#AGNKS*TPR	P12270	266	2	1.70E+06
462	<b>40.34</b>	TPR	1682, 1691	nuclear pore complex-associated protein TPR	GIASTSDPPTANIKPTPVVSTPSKVT*AAAMAGNKS*TPR	P12270	266	2	8.38E+05
463	<b>7.46</b>	TPR	1692	nuclear pore complex-associated protein TPR	VTAAMAGNKST*PR	P12270	266	2	3.44E+06
464	<b>6.12</b>	TPR	2102, 2123	nuclear pore complex-associated protein TPR	GLQL*PGIGGM#QQHFFDEEDRTPVST*PTLVVPHR	P12270	266	1	2.65E+05
465	<b>7.07</b>	TPR	2122	nuclear pore complex-associated protein TPR	TVPS*PTLVVPH	P12270	266	4	6.64E+06
466	<b>12.88</b>	TPR	641	nuclear pore complex-associated protein TPR	ILLSQTTGVAIPLHASSLDDVSLAST*PK	P12270	266	13	8.63E+06
467	<b>12.69</b>	TPR	653	nuclear pore complex-associated protein TPR	RPSTSQTVST*PAVVPVIESTEIAEAK	P12270	266	4	3.96E+06
468	2.19	WDFY3	818	WD repeat and FYVE domain containing 3 isoform 1	HAYHSVST*PPVYPYK	Q8LZQ1	395	1	8.21E+05
<b>Secreted protein</b>									
470	<b>13.61</b>	HDFG	200	hepatoma-derived growth factor isoform b	NST*PSEPGSGR	P51858	27	2	2.33E+08
471	<b>20.03</b>	HDFG	200, 202	hepatoma-derived growth factor isoform b	NST*PS*EPGSGR	P51858	27	1	1.04E+06
472	<b>8.04</b>	HDFG	202	hepatoma-derived growth factor isoform b	EAATLEVERPLM#EVEKNSTPS*EPGSGR	P51858	27	1	4.30E+05
<b>Transcriptional regulator</b>									
474	-0.30	ELYS; ELYS iso2	1209, 1222; 1247, 1260	transcription factor ELYS	STLRS*TPLASPSPSGRS*PQR	Q8WYP5; Q8WYP5-2	253; 256	1	3.38E+04
475	-0.31	ELYS; ELYS iso2	1210, 1214, 1218, 1222; 1248, 1252, 1256, 1260	transcription factor ELYS	STLRST*PLAS*PSPS*PGRS*PQR	Q8WYP5; Q8WYP5-2	253; 256	1	1.71E+05
476	1.34	ELYS; ELYS iso2	1210, 1214, 1222; 1248, 1252, 1260	transcription factor ELYS	STLRST*PLAS*PSPS*PGRS*PQR	Q8WYP5; Q8WYP5-2	253; 256	1	8.74E+04
477	<b>53.94</b>	ELYS; ELYS iso2	1764; 1802	transcription factor ELYS	SAQQEASADVAT*PK	Q8WYP5; Q8WYP5-2	253; 256	2	3.03E+06
478	3.00	ATF-2	<b>71</b>	activating transcription factor 2	NDSVIVADQTP*PTR	P15336	55	1	2.31E+05
479	3.77	BMZF-2	1593	bromodomain adjacent to zinc finger domain, 2A	ALLS*TPNGAFEGTTEISYEIYPR	Q9UIF9	208	1	3.91E+05
480	-0.56	Bcl-9	155	B-cell CLL/lymphoma 9	SST*PSHGQTATEPTPAQK	O00512	149	2	6.07E+05
481	<b>56.38</b>	FALZ; FALZ iso2; FALZ iso3; FALZ iso4	1624; 1498; 1637; 1624	bromodomain PHD finger transcription factor isoform 2	LST*PSTGGSDIISVK	Q12830; Q12830-2; NP_872579; Q12830-4	324; 311; 325; 308	1	2.86E+06
482	<b>16.12</b>	FALZ; FALZ iso2; FALZ iso3; FALZ iso4	2100; 1974; 2113; 2100	bromodomain PHD finger transcription factor isoform 2	GQPSTVASPANTVS*STPGQK	Q12830; Q12830-2; NP_872579; Q12830-4	324; 311; 325; 308	1	3.99E+05
483	<b>12.62</b>	FALZ; FALZ iso2; FALZ iso3; FALZ iso4	64; 64; 203; 64	bromodomain PHD finger transcription factor isoform 2	SHSTYSST*PGR	Q12830; Q12830-2; NP_872579; Q12830-4	324; 311; 325; 308	7	1.16E+06
484	2.06	BRCA2	3193	breast cancer 2, early onset	WST*PTKDCSTSGPYTAIIPGTGK	P51587	384	2	3.93E+05
485	1.31	BRCA2	3242	breast cancer 2, early onset	SVST*PVSAQMTSK	P51587	384	1	1.06E+05
486	1.87	ELG	413, 415	ELG protein isoform a	MIST*PS*PKK	Q53F19	71	4	1.02E+07
487	2.50	CASP8AP2	1261	caspase 8 associated protein 2	SLEVHCPST*PK	Q9UKL3	223	1	2.07E+05
488	<b>11.16</b>	CDC5L	411, 415	CDC5-like	QVVTPTNLVST*PFRT*PSNGAEGLTPR	Q99459	92	1	9.33E+05
489	4.62	CDC5L	427, 437, 442	CDC5-like	S*GTTPKPVINS*TPGRT*PLRDK	Q99459	92	1	1.28E+07
490	<b>14.15</b>	CDC5L	429, 430, 438, 442	CDC5-like	SGT*TPKPVINST*PGRT*PLRDK	Q99459	92	1	1.82E+06
491	3.62	CDC5L	430, 438	CDC5-like	SGTT*PKPVINST*PGRT*PLRDK	Q99459	92	1	2.30E+06
492	<b>6.57</b>	CDC5L	430, 438, 442	CDC5-like	SGTT*PKPVINST*PGRT*PLRDK	Q99459	92	3	7.40E+06
493	<b>10.29</b>	CDC5L	437, 442	CDC5-like	SGTTPKPVINS*TPGRT*PLRDK	Q99459	92	2	4.06E+05
494	1.35	CHD-8; CHD-8 iso2	1703; 1847	chromodomain helicase DNA binding protein 8	CST*PLLHQQYTS	Q9HCK8; Q9HCK8-2	262; 276	2	2.33E+06
495	<b>65.13</b>	GEMIN3	688	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	DSEST*PVDDR	Q9UHI6	92	2	1.96E+06
496	-0.25	DATF1	1469	death inducer-oblierator 1 isoform a	NSVERPAEPVAGAAT*PSLVEQQK	Q9BTC0	244	1	6.32E+04
497	<b>8.08</b>	DATF1; DATF1 iso3	502; 502	death inducer-oblierator 1 isoform a	EAACESST*PSWASDHNYNAVKPEK	Q9BTC0; Q9BTC0-3	244; 61	2	3.54E+05
498	2.43	FOXM1; FOXM1 iso2	610; 595	forkhead box M1 isoform 2	ETLPISS*TPSK	Q08050; Q08050-2	84; 83	1	9.50E+05
499	<b>18.14</b>	FBP3	43	far upstream element (FUSE) binding protein 3	IDSIPHLNNST*PLVDPSVYGYGVQK	Q96I24	62	3	8.30E+06
500	-0.55	P66B	120, 129, 135	GATA zinc finger domain containing 2B	GRLT*PSPDIIVLS*DNEASS*PR	Q8WXI9	65	2	3.30E+04
501	-0.68	P66B	120, 135	GATA zinc finger domain containing 2B	GRLT*PSPDIIVLS*DNASS*PR	Q8WXI9	65	1	2.24E+05
502	1.88	TFIIF-alpha	433, 437	general transcription factor IIF, polypeptide 1, 74kDa	LDTGQPSLS*GKST*QPSPSGK	P35269	58	1	2.31E+06
503	0.00	TFIIF-alpha	436	general transcription factor IIF, polypeptide 1, 74kDa	LRLDTGQPSLSGKS*TPQPPSGK	P35269	58	1	0.00E+00

**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-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
504	-0.77	TFIIIC-alpha	514	general transcription factor IIIC, polypeptide 1, alpha 220kDa	TQPHHST*PTKGGWK	Q12789	238	2	2.14E+05
505	<b>11.93</b>	GTF3C2	132, 137	general transcription factor IIIC, polypeptide 2, beta 110kDa	RPOQNPSPAPLVPLGLDQSNPLS*PM#PK	Q8WUA4	101	2	1.09E+06
506	<b>9.26</b>	GTF3C2	136	general transcription factor IIIC, polypeptide 2, beta 110kDa	RPOQNPSPAPLVPLGLDQSNPLS*PM#PK	Q8WUA4	101	1	3.30E+05
507	<b>11.53</b>	GTF3C2	137	general transcription factor IIIC, polypeptide 2, beta 110kDa	RPOQNPSPAPLVPLGLDQSNPLS*PM#PK	Q8WUA4	101	2	4.45E+05
508	<b>12.59</b>	HCFC1	1490, 1507	host cell factor 1	AVTTVTQS*TPVPGSPVPPPEELQVS*PGPR	P51610	209	1	4.77E+05
509	2.91	HGF1	363, 369	heat shock transcription factor 1	GHTDTEGRPPS*PPPTST*PEK	Q00613	577	4	8.30E+06
510	4.18	IFI16	123	interferon, gamma-inducible protein 16	TEGAEAT*PGAQKR	Q16666	88	1	7.32E+04
511	1.89	JAZF1	99	JAZF zinc finger 1	GNVST*PPR	Q86VZ6	27	1	1.48E+06
512	0.00	JunB	255, 259	jun B proto-oncogene	SRDAT*PPVS*PINMEDQER	P17275	36	1	0.00E+00
513	-0.92	ANKRD25	172, 176	ankyrin repeat domain 25	SS*GLST*PVPPSAGHLAIV	Q63ZY3	91	4	1.53E+06
514	1.12	ANKRD25	176	ankyrin repeat domain 25	SSGLST*PVPPSAGHLAIV	Q63ZY3	91	5	7.25E+06
515	2.96	Tip60; Tip60 iso2	155, 158; 103, 106	K(lysine) acetyltransferase 5 isoform 2	KVEVVS*PAT*VPVSTAPASVFPQNGAAR	Q92993; Q92993-2	59, 53	1	9.74E+04
516	1.08	LIN9; LIN9 iso5	95; 245	lin-9 homolog	FTATM#S*TPDKK	Q5TKA1; Q8IWQ1	62; 60	1	6.47E+05
517	2.17	LIN9; LIN9 iso5	96; 246	lin-9 homolog	FIATMST*PDKK	Q5TKA1; Q8IWQ1	62; 60	4	6.21E+06
518	4.52	MCRS1	102	microsphere protein 1 isoform 2	APS*TPVPPSPAPAPGLIK	Q96EZ8	52	1	6.82E+05
519	3.32	PPARBP	1051, 1057	mediator complex subunit 1	SQT*PGVAT*PPIPK	Q15648	168	2	2.24E+06
520	1.88	PPARBP	1431, 1440	mediator complex subunit 1	Ny*GSPISGVS*PKHER	Q15648	168	1	1.77E+05
521	3.01	PPARBP	1433, 1440	mediator complex subunit 1	NYGS*PLISGVS*PK	Q15648	168	2	5.87E+05
522	-0.88	PPARBP	1440	mediator complex subunit 1	NYGSPLISGVS*PK	Q15648	168	3	8.25E+05
523	<b>27.77</b>	MEN1; MEN1 iso2	599; 594	menin isoform 1	VST*PSDYTLISFLK	O00255; O00255-2	68; 67	1	4.45E+06
524	-0.22	MKL1	450	megakaryoblastic leukemia 1 protein	FGSTGVS*PPVSTPSEER	Q969V6	99	1	3.62E+05
525	-0.19	MKL1	450, 454	megakaryoblastic leukemia 1 protein	FGSTGVS*PPVS*PTPSEER	Q969V6	99	2	2.96E+05
526	<b>6.67</b>	MLL	3027, 3036	myeloid/lymphoid or mixed-lineage leukemia protein	NSS*TPGLQVPVS*PTVIQIQNK	Q03164	432	1	2.37E+06
527	<b>5.60</b>	MLL	446	myeloid/lymphoid or mixed-lineage leukemia protein	LEST*PNSR	Q03164	432	1	2.07E+05
528	-0.22	Myc; N-Myc	<b>58; 58</b>	myc proto-oncogene protein	KFELLPT*PPLSPS	P01106; P04198	49; 50	1	1.26E+05
529	-0.42	Myc	<b>58; 62</b>	myc proto-oncogene protein	KFELLPT*PPLS*PSRR	P01106	49	7	5.54E+06
530	<b>8.29</b>	NCL	121	nucleolin	ALVAT*PGKK	P19338	77	2	2.61E+06
531	<b>5.45</b>	N-CoR1	1672	nuclear receptor co-repressor 1	GIIDLTM#PPTLIVPHGGTST*PPM#DR	Q75376	270	2	5.65E+06
532	1.74	SMRT; SMRT iso4	1588; 1579	nuclear receptor co-repressor 2 isoform 2	KLTS*PR	Q9Y618; NP_001070729	274; 268	3	3.86E+05
533	3.63	NFAT5	153	nuclear factor of activated T-cells 5 isoform d	QLTSNTVQHPST*PKR	Q94916	168	2	1.74E+06
534	<b>12.10</b>	NFRKB; NFRKB iso2	1037; 1037	nuclear factor related to kappaB binding protein isoform 1	ASSASAPSTPT*GTTVVK	Q15312; Q6P4R8	139; 139	1	4.60E+05
535	1.05	NONO	450	non-POU domain containing, octamer-binding isoform 1	FGQAATM#EGIGAIGGT*PPAFNR	Q15233	54	1	7.55E+05
536	-0.56	NR2C2	352	nuclear receptor subfamily 2, group C, member 2	DQST*PIIEVEGPLLSDTHVTFK	P49116	65	4	1.85E+06
537	<b>6.41</b>	PML; PML iso2; PML iso3; PML iso4	403, 409; 403, 409; 403, 409; 403, 409	promyelocytic leukemia protein isoform 6	KAS*PEAAS*PRDPIDVLDPEEAER	P29590; P29590-2; P29590-3; P29590-4	98; 67; 90; 62	1	6.45E+05
538	4.80	PML; PML iso2; PML iso3; PML iso4	409; 409; 409; 409	promyelocytic leukemia protein isoform 6	ASPEAAS*PRDPIDVLDPEEAER	P29590; P29590-2; P29590-3; P29590-4	98; 67; 90; 62	1	5.80E+05
539	<b>6.18</b>	PML; PML iso7; LOC652346	867; 847; 283	promyelocytic leukemia protein isoform 6	AEGVST*PLAGR	P29590; Q59FP9; XP_001716158	98; 96; 33	1	3.22E+06
540	-0.96	POGZ	1364, 1368	pogo transposable element with ZNF domain isoform 1	LSGEHS*ESST*PPR	Q723K3	155	1	9.32E+06
541	-0.60	POGZ	1367	pogo transposable element with ZNF domain isoform 1	LSGEHSESS*TPRPR	Q723K3	155	1	5.91E+05
542	<b>17.40</b>	POU2F1	259, 270	POU class 2 homeobox 1	TIAAT*PIQTLQSQSST*PK	P14859	76	1	7.31E+05
543	4.06	POU2F1	270	POU class 2 homeobox 1	TIAATPIQTLQSQSST*PK	P14859	76	2	8.93E+06
544	2.45	PPP1R13L	358	protein phosphatase 1, regulatory subunit 13 like	IPMPSS*PQPR	Q8WUF5	89	1	1.35E+05
545	<b>15.15</b>	FIR	314	poly-U binding splicing factor 60kDa isoform c	AVTPPM#PLLTAT*PGGLPPAAVAAAAATAK	Q9UHX1	60	2	5.58E+06
546	<b>16.09</b>	RAI1	1133, 1136	retinoic acid induced 1	TKETDS*PST*PGKDQR	Q75J4	203	1	1.55E+05
547	1.40	RBM14	571	RNA binding motif protein 14	GQPGNAYDGAGQPSAAYLSM#SQGAVANANS*TPP PYER	Q96PK6	69	4	7.89E+06
548	1.18	RBM14	572	RNA binding motif protein 14	NANST*PPPYER	Q96PK6	69	11	1.77E+06
549	-0.86	RYBP	215	RING1 and YY1 binding protein	SST*PKGDMSAVNDESF	Q8N488	25	2	7.25E+05
550	1.72	SENP1	102	sentrin/SUMO-specific protease 1	NST*PSSSSSLQK	Q9POU3	73	1	2.86E+06
551	<b>7.08</b>	PSF	226	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	MPGGPKPGGGGLST*PGGHPKPPH	P23246	76	22	2.57E+07
552	<b>22.79</b>	SMARCA4	1417, 1423	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4 isoform B	KRDS*DAGSST*PTTSTR	P51532	185	2	8.09E+06

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
553	-0.55	SMARCA4	1423	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4 isoform B	DSDAGSST*PTTSTR	P51532	185	1	2.11E+06
554	-0.52	SHARP	2393	spen homolog, transcriptional regulator	QSEKPHST*PPQSCSTDLSK	Q96T58	402	2	2.93E+05
555	<b>15.70</b>	SHARP	2685	spen homolog, transcriptional regulator	SLVST*PAGPVNWLK	Q96T58	402	1	5.89E+05
556	-0.27	SPT6	1718	suppressor of Ty 6 homolog	AGDAT*PLLEMDMR	Q7KZ85	199	5	4.78E+05
557	4.89	TAF2	1095	TBP-associated factor 2	SALIPQHSAGCDS*TPPTKQWSLELAR	Q6P1X5	137	1	2.95E+05
558	1.05	TAFII31	152, 159	TAF9 RNA polymerase II, TATA box binding protein-associated factor isoform c	LSVGS*VTSRPS*PTLGTPTPQTM#SVSTK	Q16594	29	1	4.85E+05
559	-0.15	TAFII31	158, 159	TAF9 RNA polymerase II, TATA box binding protein-associated factor isoform c	LSVGSVTSRPS*PTLGTPTPQTM#SVSTK	Q16594	29	1	3.34E+04
560	-0.28	TAFII31	159	TAF9 RNA polymerase II, TATA box binding protein-associated factor isoform c	LSVGSVTSRPS*PTLGTPTPQTM#SVSTK	Q16594	29	3	5.43E+05
561	1.39	treacle; treacle iso2	983; 983	Treacher Collins-Franceschetti syndrome 1 isoform b	SPAGPAATPAQAQAAS*PR	Q13428; A0JULU0	152; 144	6	6.00E+06
562	2.79	TLE1	312	transducin-like enhancer protein 1	AST*PVLK	Q04724	83	2	6.20E+06
563	-0.16	TLE3; TLE3 iso3	286, 296; 286, 296	transducin-like enhancer protein 3 isoform b	DAPT*PASVASSSST*PSSK	Q04726; Q04726-3	83; 83	1	4.96E+04
564	1.53	TLE3; TLE3 iso3	311; 311	transducin-like enhancer protein 3 isoform b	DLGHNDKSS*TPGLK	Q04726; Q04726-3	83; 83	1	1.39E+06
565	-0.91	TLE3; TLE3 iso3	312; 312	transducin-like enhancer protein 3 isoform b	DLGHNDKSS*TPGLK	Q04726; Q04726-3	83; 83	3	6.53E+06
566	<b>11.10</b>	TLE3; TLE3 iso3	328, 334; 328, 334	transducin-like enhancer protein 3 isoform b	NDAPT*PGTST*PGLR	Q04726; Q04726-3	83; 83	1	2.11E+06
567	<b>10.43</b>	TMF1	364	TATA element modulatory factor 1	GYALVPIIIVNSST*PK	P82094	123	3	5.17E+06
568	-0.36	53BP1	1114	tumor protein p53 binding protein 1 isoform 2	M#VIQGPSS*PQGEAM#VTDVLEDQKEGR	Q12888	214	2	2.29E+05
569	0.00	53BP1	1640, 1650	tumor protein p53 binding protein 1 isoform 2	SNVSSPATPT*ASSSSSTPT*P	Q12888	214	1	0.00E+00
570	1.18	53BP1	320	tumor protein p53 binding protein 1 isoform 2	TVSSDGCST*TPSREEGGCSLASTPATTLLHLLQLSGQR	Q12888	214	1	6.94E+05
571	1.25	53BP1	323	tumor protein p53 binding protein 1 isoform 2	TVSSDGCST*TPSREEGGCSLASTPATTLLH	Q12888	214	4	9.91E+04
572	<b>9.74</b>	53BP1	373, 380	tumor protein p53 binding protein 1 isoform 2	ST*PFIVPSS*PTEQEGR	Q12888	214	1	1.39E+06
573	-0.46	53BP1	382	tumor protein p53 binding protein 1 isoform 2	STPFIVPSS*PTEQEGR	Q12888	214	1	5.78E+05
574	-0.68	HYD; LOC730429	637; 636	ubiquitin protein ligase E3 component n-recogin 5	RST*PAPKEEKVNEEQWSLR	O95071; XP_001125699	309; 309	2	3.23E+05
575	<b>5.04</b>	UNC45A	4, 8, 20	smooth muscle cell associated protein-1 isoform 3	TVS*GPGT*PEPRPATPGASS*VEQLR	Q9H3U1	103	1	4.03E+05
576	4.09	TCF8	887, 890	zinc finger E-box binding homeobox 1 isoform a	QDTSSEGVSNVEDQNDSD*ST*PPKKK	P37275	124	2	2.48E+05
577	<b>16.06</b>	RACK7; RACK7 iso6	541, 547; 396, 402	zinc finger, MYND-type containing 8 isoform b	ELSESQQGST*PVPLIS*PKR	Q9ULU4; Q9ULU4-6	132; 113	1	8.46E+05
578	-0.40	ZNF295	434	zinc finger protein 295 isoform L	IKTEPS*SPLSDPSDIIR	Q9ULJ3	119	1	2.73E+05
579	1.18	ZNF318	160	zinc finger protein 318	ITVGNDFHFCV*TPER	Q5VUA4	251	1	9.49E+05
580	-0.93	ZNF318	161	zinc finger protein 318	ITVGNDFHFCV*TPER	Q5VUA4	251	2	1.69E+06
581	-0.31	ZNF358	484, 487	zinc finger protein 358	NPDPGSGGPTLPDPSSKPLPGSRS*TPS*TPVESSDPK	Q9NW07	59	1	2.01E+05
582	4.53	ZNF644	165	zinc finger protein 644 isoform 2	VAADLQLST*PQK	Q9H582	150	1	3.93E+06
583	<b>Translation</b>								
584	<b>34.38</b>	eEF1D; eEF1D iso2; eEF1D iso4	147, 162; 513, 528; 416, 431	eukaryotic translation elongation factor 1 delta isoform 1	KPAT*PAEDDEDDIDLFGS*DNEEDKEAAQLR	P29692; P29692-2; Q9BW34	31; 71; 61	70	1.89E+07
585	4.61	CDA02	5	eukaryotic translation initiation factor 2A	APST*PLLTVR	Q9BY44	65	1	1.83E+05
586	<b>93.72</b>	CDA02	506, 517	eukaryotic translation initiation factor 2A	SDKS*PDLAPTAPQSS*TPR	Q9BY44	65	1	4.40E+06
587	<b>85.31</b>	CDA02	506, 518	eukaryotic translation initiation factor 2A	SDKS*PDLAPTAPQST*PR	Q9BY44	65	2	2.03E+07
588	<b>9.83</b>	CDA02	517	eukaryotic translation initiation factor 2A	SDKSPDLAPTAPQSS*TPR	Q9BY44	65	1	6.42E+06
589	<b>8.16</b>	eIF2B4	86	eukaryotic translation initiation factor 2B, subunit 4 delta isoform 2	ELPESGIQLGT*PR	Q9UI10	58	2	3.21E+05
590	-0.57	4E-BP1	37, 46	eukaryotic translation initiation factor 4E binding protein 1	VVLGDGVQLPPGDYSTT*PGGLTFTT*PGGTR	Q13541	13	12	1.11E+06
591	-0.69	4E-BP1	41, 46	eukaryotic translation initiation factor 4E binding protein 1	VVLGDGVQLPPGDYSTT*PGGLTFTT*PGGTR	Q13541	13	3	3.07E+05
592	-0.57	4E-BP2	37, 44	eukaryotic translation initiation factor 4E binding protein 2	TVAISDAAQLPHDYCTT*PGGLTFS*TPGGTR	Q13542	13	1	2.76E+05
593	-0.92	eIF4G; eIF4G iso3	205; 165	eukaryotic translation initiation factor 4 gamma, 1 isoform 4	TAST*PTPQTGGLEPQANGETPQAVIVRPDDR	Q04637; Q04637-3	175; 172	3	1.60E+07
594	3.92	eIF4G; eIF4G iso3	207, 211; 167, 171	eukaryotic translation initiation factor 4 gamma, 1 isoform 4	TASTPT*PPQT*GGLEPQANGETPQAVIVRPDDR	Q04637; Q04637-3	175; 172	1	1.59E+06
595	<b>9.63</b>	eIF4G; eIF4G iso3	301; 261	eukaryotic translation initiation factor 4 gamma, 1 isoform 4	SVEEST*PISR	Q04637; Q04637-3	175; 172	4	5.28E+06
596	<b>Tumor suppressor</b>								
597	<b>7.68</b>	PSRC1 iso2	212, 215	proline/serine-rich coiled-coil 1 isoform b	AAAS*PPT*PIR	Q5T2Z1	25	3	2.35E+06
598	<b>Tumor suppressor or oncoprotein</b>								
599	-0.93	ABC1	643	HEAT repeat containing 6	APAGPSLEETS*VSS*PK	Q6AI08	129	1	1.31E+05

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
600		<b>Ubiquitin conjugating system</b>							
601	<b>51.11</b>	APC7	126	anaphase-promoting complex subunit 7 isoform b	VRPSTGNSAST*PQSQCLPSEIEVK	Q9UJX3	67	4	2.27E+06
602	2.53	FZR1	120	Fzr1 protein isoform 3	LQPS*TPEKK	Q9UM11	55	1	4.71E+06
603	<b>39.32</b>	HUWE1	2887, 2889	HECT, UBA and WWE domain containing 1	AGS*ST*PGDAPPAVAEVOGR	Q7Z6Z7	482	1	9.34E+05
604	<b>8.58</b>	HUWE1	2888, 2889	HECT, UBA and WWE domain containing 1	AGSS*TPGDAPPAVAEVOGR	Q7Z6Z7	482	2	8.21E+05
605	4.82	HUWE1	2889	HECT, UBA and WWE domain containing 1	AGSST*PGDAPPAVAEVOGR	Q7Z6Z7	482	2	1.17E+07
606	-0.71	HUWE1	3919, 3924, 3927	HECT, UBA and WWE domain containing 1	ESQLAHIKDEPPPLS*PAPLT*PAT*PSSLDPPFSR	Q7Z6Z7	482	4	6.83E+05
607	1.54	LONRF3	64	LON peptidase N-terminal domain and ring finger 3 isoform 1	VAEAGPAPLPTREPEQEQSPGTS*PESK	Q496Y0	84	1	1.25E+05
608	-0.69	RKHD2	537, 541, 545	ring finger and KH domain containing 2	RGS*QPST*PRLS*PTFPESIEHPLA	Q5U5Q3	69	1	1.80E+05
609	<b>12.05</b>	RNF169	554	ring finger protein 169	EQFEGLGST*PDAK	Q8NCN4	77	1	9.13E+06
610	-0.26	UBR4; UBR4 iso3	2718, 2722, 2724; 2729, 2733, 2735	retinoblastoma-associated factor 600	HVTLPSS*SPRS*NT*PM*GDKDDDDDDDAEK	Q5T4S7; Q5T4S7-3	574; 572	3	9.86E+04
611	1.76	UBR4; UBR4 iso3	2719; 2730	retinoblastoma-associated factor 600	HVTLPSS*PR	Q5T4S7; Q5T4S7-3	574; 572	1	1.02E+05
612	<b>6.48</b>	UBR4; UBR4 iso3	2719, 2722, 2724; 2730, 2733, 2735	retinoblastoma-associated factor 600	HVTLPSS*SPRS*NT*PM*GDKDDDDDDDAEK	Q5T4S7; Q5T4S7-3	574; 572	4	5.27E+05
613	1.90	WHSC1; WHSC1 iso3; WHSC1 iso5	421; 421; 421	Wolf-Hirschhorn syndrome candidate 1 protein isoform 1	LCSSAETLESHPDIGKS*TPQK	Q96028; Q96028-3; Q96028-5	152; 71; 69	2	1.25E+06
614	1.29	WHSC1; WHSC1 iso3; WHSC1 iso5	422; 422; 422	Wolf-Hirschhorn syndrome candidate 1 protein isoform 1	LCSSAETLESHPDIGKST*PQKTAEDPR	Q96028; Q96028-3; Q96028-5	152; 71; 69	6	1.47E+06
615		<b>Unknown function</b>							
616	<b>15.03</b>	CENTG3	323, 326	centaurin, gamma 3 isoform b	IETIAASS*TPT*PIRK	Q96P47	95	1	2.69E+06
617	1.95	CENTG3	324	centaurin, gamma 3 isoform b	IETIAASS*PTPIR	Q96P47	95	2	8.06E+05
618	<b>22.32</b>	HRBL	163	ArfGAP with FG repeats 2	GSAST*PVQGSIEPGKPL	Q95081	49	2	2.89E+06
619	3.43	ANKLE2	488, 496	ankyrin repeat and LEM domain containing 2	AEETSS*PVIGELWS*PDQTAESHVSR	Q86XL3	104	1	7.75E+04
620	<b>5.13</b>	ATAD5	603	ATPase family, AAA domain containing 5	ISST*PTTETIR	Q96QE3	208	1	2.30E+06
621	2.83	Bcl-9L	1098	B-cell CLL/lymphoma 9-like	YAMPS*STPLYHNAIK	Q86UJ0	157	1	1.42E+05
622	-0.56	Bcl-9L	129	B-cell CLL/lymphoma 9-like	EAGT*PSLDSEAK	Q86UU0	157	1	6.41E+05
623	<b>21.47</b>	FAM44A	1096	biorientation of chromosomes in cell division 1-like	LAANTLST*PSGSSLRPK	Q8NFC6	330	3	3.59E+06
624	-0.34	FAM44A	658	biorientation of chromosomes in cell division 1-like	RT*STPVMIEGVQEETDTR	Q8NFC6	330	1	3.02E+05
625	-0.50	FAM44A	659	biorientation of chromosomes in cell division 1-like	RTS*TPVIM#EGVQEETDTR	Q8NFC6	330	2	2.23E+05
626	1.00	FAM44A	660	biorientation of chromosomes in cell division 1-like	TST*PVIMEGVQEETDTR	Q8NFC6	330	5	2.84E+05
627	<b>5.37</b>	peregrin	879	bromodomain and PHD finger-containing protein 1 isoform 1	GLGPNM#S*STPAHEVGR	P55201	138	1	2.59E+05
628	<b>7.70</b>	peregrin	881	bromodomain and PHD finger-containing protein 1 isoform 1	GLGPNM#S*STPAHEVGR	P55201	138	4	2.51E+06
629	3.65	C10orf47	146, 166	hypothetical protein LOC254427	KQDAET*PPPPDPPAPETLLAPPPLPS*TPDPPRR	Q86WR7	46	2	1.09E+06
630	-0.62	C10orf47	166	hypothetical protein LOC254427	KQDAETPPPPDPPAPETLLAPPPLPS*TPDPPRR	Q86WR7	46	2	6.39E+05
631	<b>5.42</b>	C11orf59	27	hypothetical protein LOC55004	KLLDPSS*PPTK	Q6IAA8	18	1	6.93E+05
632	<b>9.32</b>	C17orf71	657	hypothetical protein LOC55181	LDHINFVFEPEST*PDPAK	Q8ND04	110	1	3.92E+05
633	<b>17.47</b>	C19orf21	178	hypothetical protein LOC126353	TPGPPRS*TPLEENVVDREQIDFLAAR	Q8IVT2	75	5	1.10E+06
634	1.19	C19orf21	377	hypothetical protein LOC126353	AST*PDWVSEGPQPL	Q8IVT2	75	5	1.12E+07
635	-0.30	DKFZP547B1415	151, 163	hypothetical protein LOC126526	M#ITNSLNHDS*PPSTPPRRPDTSTSK	Q8N9M1	45	1	7.48E+04
636	-0.93	DKFZP547B1415	154, 155	hypothetical protein LOC126526	MITNSLNHDSPPS*TPRRPDTSTSK	Q8N9M1	45	1	1.27E+05
637	<b>6.85</b>	SMG9	118	hypothetical protein LOC56006	EEGKGPVAVTGAST*PEGTAPPPAAPAPPKGEK	Q9HOW8	58	5	8.53E+05
638	-0.89	C22orf9	361	hypothetical protein LOC23313 isoform b	VTSFST*PPTPER	Q8IU44	53	1	4.12E+04
639	<b>18.28</b>	C22orf9	361, 364	hypothetical protein LOC23313 isoform b	VTSFST*PPTPER	Q8IU44	53	1	7.67E+05
640	4.24	RAP140; RAP140 iso2	819; 423	retinoblastoma-associated protein 140 isoform a	HEYELNST*PDKK	Q9UK61; Q9UK61-2	189; 140	2	1.65E+05
641	<b>7.97</b>	TTDN1	120	chromosome 7 open reading frame 11	TST*PFGSSR	Q8TAP9	19	1	2.11E+06
642	<b>20.93</b>	CCDC28A	161	coiled-coil domain containing 28A	GAQS*TPIQHSFLTDVSDVQEM#FER	Q8IWP9	30	2	9.28E+05
643	1.56	CENL1	325, 338, 341	cyclin L1	GLNPDGT*PALSTLGGFSPAS*KPS*SPR	Q9UK58	60	2	1.93E+05
644	<b>8.38</b>	FAM120A	991	oxidative stress-associated Src activator	GVIST*PVIR	Q9NZB2	122	2	2.08E+07
645	1.08	Meg-3	679, 683	hypothetical protein LOC64855 isoform 2	AAPEASS*PPAS*PLQHLLPGK	Q96TA1	83	1	5.27E+06
646	<b>8.59</b>	C11orf56 iso3	496, 511	hypothetical protein LOC84067 isoform 2	GPGS*PSVDSSVTTVPRPS*TPSR	NP_115503	107	3	1.06E+06
647	1.46	FBXW9	55, 59	F-box and WD-40 domain protein 9	SGLAFSRPQLST*PAAS*PSASEPR	Q5XUX1	54	3	1.34E+06
648	-0.11	SOLO	1492	hypothetical protein LOC55701	NPSLQPPHGGST*PTLAS	Q8TER5	165	1	4.15E+04
649	4.07	GPBP1L1	354	GC-rich promoter binding protein 1-like 1	DCDKLEDLEDNST*PEPK	Q9HC44	52	2	5.42E+05
650	-0.65	GRAMD1A	11, 14	GRAM domain containing 1A isoform 2	MFDTPHSGRS*TPS*SSPSLR	Q96CP6	81	1	9.89E+04

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
651	17.22	HN1L	76	hematological and neurological expressed 1-like	GSGFDEST*PVQTR	Q9H910	20	3	4.43E+07
652	78.75	INF2; INF2 iso2	420; 420	inverted formin 2 isoform 2	ALEQQAST*PPPPPPPLPGSSAEPPIPPPPPLP SVGAK	Q27J81; Q27J81-2	136; 135	2	3.42E+06
653	1.06	INF2; INF2 iso2	589; 589	inverted formin 2 isoform 2	EHNSM#WASLS*PDAEAVEPFISSIER	Q27J81; Q27J81-2	136; 135	1	1.84E+05
654	12.02	KCNJ12; LOC100131509; LOC100134444	353; 352; 353	potassium inwardly-rectifying channel, subfamily J, member 12	TYEVPS*TPR	Q14500; XP_001718688; XP_001720109	49; 49; 49	1	6.81E+05
655	0.00	KIAA0182	84, 88, 98	genetic suppressor element 1 isoform 2	GSSLSESS*PVSS*PATNHSSPAS*TPK	Q14687	136	1	0.00E+00
656	23.87	KIAA0415	202	hypothetical protein LOC9907	YASLQQGLPHSGGFFST*PR	Q43299	89	2	1.20E+06
657	4.01	KIAA0947	1041	hypothetical protein LOC23379	SGGEALAVANDSTST*PQANGLWK	Q9Y2F5	248	1	3.26E+05
658	1.10	KIAA0947	1642	hypothetical protein LOC23379	IRQEVGPPLPPLAPLIAT*PPR	Q9Y2F5	248	5	1.25E+05
659	12.57	KIAA1211	1202	hypothetical protein LOC57482	FST*PDAAPVSTEPAWLALAK	Q6ZU35	137	1	2.96E+05
660	1.04	LOC284058	1022	hypothetical protein LOC284058	CST*PEGLDEQSVQPWER	Q7Z3B3	121	1	4.66E+05
661	-0.69	KIAA1429	1579	hypothetical protein LOC25962 isoform 1	SFLSEPS*PGR	Q69YN4	202	1	3.00E+05
662	30.37	KIAA1486	469, 476	hypothetical protein LOC57624	SS*PSVPHST*PRVSDQDGAK	Q9P242	71	1	1.56E+06
663	14.64	KIAA1712	346	HBV PreS1-transactivated protein 3 isoform a	SEVERPASILPSSGYSSTASDST*PR	Q9COF1	44	2	1.31E+06
664	1.78	KIAA1826	192	hypothetical protein LOC84437	ENELPDFPHIDEFFTLNST*PSR	Q8NCY6	41	2	7.66E+05
665	6.14	KNTC1	1034	Rough Deal homolog, centromere/kinetochore protein	HKPGS*TPEPIAAEVR	P50748	251	1	9.40E+05
666	13.96	L3MBTL2	67, 73, 76	I(3)mbt-like 2	EAGELPTS*PLHLLS*PGT*PR	Q969R5	79	3	1.13E+06
667	3.95	F25965	135, 137	lin-37 homolog	ERECS*PS*SPLPLPEDEEGSEVTNSK	Q96GY3	28	1	7.17E+05
668	-0.23	F25965	138	lin-37 homolog	ERECS*PS*PLPLPEDEEGSEVTNSK	Q96GY3	28	1	5.36E+04
669	3.87	LOC100133510	779, 781, 786, 788	PREDICTED: similar to nucleoporin	RST*PS*PTRYSL*PSK	XP_001719668	116	2	1.98E+06
670	-0.11	LOC100133510	779, 781, 788	PREDICTED: similar to nucleoporin	RST*PS*PTRYSL*PSK	XP_001719668	116	1	2.84E+04
671	14.46	MORC2	649	MORC family CW-type zinc finger 2	KAPVISS*TPKLPALAA	Q9Y6X9	118	2	1.37E+06
672	6.86	MORC2	725, 730, 735	MORC family CW-type zinc finger 2	KTES*PIKLS*PATPS*R	Q9Y6X9	118	2	4.25E+06
673	6.91	MORC2	836	MORC family CW-type zinc finger 2	FDYVPTDTT*PR	Q9Y6X9	118	1	3.92E+05
674	3.02	MSL1	393, 402	hampin	SS*VDTPPRLST*PQK	Q69Z03	67	1	1.54E+05
675	1.27	MSL1	396, 402	hampin	SSVDT*PPRLST*PQKGPSTHPK	Q69Z03	67	1	3.17E+05
676	-0.76	MSL1	402	hampin	LST*PQKGPSTHPK	Q69Z03	67	2	3.72E+06
677	20.82	N4BP1	426	Nedd4 binding protein 1	GVYSSTNELTIDST*PK	Q75113	100	2	1.20E+06
678	1.30	PCNXL3	129	pecanex-like 3	KVSS*PPVR	Q9H6A9	222	2	1.51E+06
679	2.99	PHF6	145, 154	PHD finger protein 6 isoform 1	TAHNSEADLEES*FNEHELEPS*SPK	Q8IWS0	41	1	1.52E+06
680	2.75	PHF6	145, 155	PHD finger protein 6 isoform 1	TAHNSEADLEES*FNEHELEPS*PK	Q8IWS0	41	1	2.94E+06
681	-0.24	PHF6	154	PHD finger protein 6 isoform 1	TAHNSEADLEESFNEHELEPS*SPK	Q8IWS0	41	3	1.19E+06
682	-0.28	PHF6	155	PHD finger protein 6 isoform 1	KTAHNSEADLEESFNEHELEPS*PK	Q8IWS0	41	5	7.87E+04
683	-0.21	PHF6 iso2	156	PHD finger protein 6 isoform 1	TAHNSEADLEESFNEHELEPS*PK	Q8IWS0-2	35	3	1.27E+05
684	10.87	POM121C	444	POM121 membrane glycoprotein (rat)-like	IREEELCHHSSSS*TPLAADKESQGEK	A8CG34	125	1	1.58E+05
685	0.00	PYG02	302	pygopus homolog 2	GGGT*PDANSLAPPK	Q9BRQ0	41	1	0.00E+00
686	4.95	QSER1	1248	glutamine and serine rich 1	SVST*PLTLTLDATSDKK	Q2KHR3	190	1	2.44E+05
687	9.31	RAVER1	488	RAVER1	DSGLPT*PPGVSLGEPKDYR	Q8Y67-2	78	1	5.72E+05
688	26.30	RP11-74E24.2; ZC3H11A	495, 502; 495, 502		VQQSSESSTSS*PSQHEAT*PGAR	BAG63790; Q75152	89; 89	1	2.56E+05
689	1.11	RPRD2	723	Regulation of nuclear pre-mRNA domain containing 2	GPTSTSIDNIDGT*PVRDER	Q5VT52	156	1	2.35E+05
690	-0.14	RPRD2	762, 769	Regulation of nuclear pre-mRNA domain containing 2	IISPGSS*TPSSTRS*PPGRODESYPR	Q5VT52	156	1	1.08E+05
691	1.19	RPRD2	763	Regulation of nuclear pre-mRNA domain containing 2	IISPGSST*PSSTR	Q5VT52	156	1	5.82E+05
692	1.54	SR-A1	976	SR-related CTD-associated factor 1	VPST*PPPK	Q9H7N4	139	2	2.98E+07
693	22.34	SEC24A	362	SEC24 related gene family, member A	NM#LPST*PLKPPVNLHEDIQK	Q95486	120	3	1.12E+06
694	4.30	SEC24A	363	SEC24 related gene family, member A	NM#LPST*PLKPPVNLHEDIQK	Q95486	120	4	6.61E+05
695	-0.45	ARS2	544	arsenate resistance protein 2 isoform c	TQLWASEPGT*PPLPSTLPSQNPILK	Q9BXP5	101	9	7.14E+07
696	1.05	TBRG4	65	cell cycle progression 2 protein isoform 1	AST*PYIEK	Q969Z0	71	1	7.58E+05
697	0.00	TMUB1	92, 98	transmembrane and ubiquitin-like domain containing 1 isoform 2	GQAAQPEPSTGFTAT*PPAPDS*PQEPVLV	Q9BVT8	26	1	0.00E+00
698	48.92	UBAP2	469, 473	ubiquitin associated protein 2	LREST*PGDS*PSTVNK	Q5T6F2	117	2	6.24E+06
699	13.24	ZC3H18	795	zinc finger CCH-type containing 18	SSQQPS*TPQQAPPQQPQQGTFVAHK	Q86VM9	106	1	6.68E+06
700	-0.17	ZC3H18	95	zinc finger CCH-type containing 18	GPTSS*PCEEEGDEGEDRTSDLR	Q86VM9	106	1	2.60E+04

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

**Table: PTMScan® Results, Phospho-ST\*P Motif (ST\*P), label-free quantitation**

**Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-ST\*P Motif (ST\*P) XP™, PTMScan® Kit #1995, #5566**

*Treatments: Untreated, nocodazole treated*

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
701	<b>Vesicle protein</b>								
702	4.15	CLTA	206	clathrin, light polypeptide A isoform c	AEEEEAVNDIDESS*PGTEWER	P09496	27	1	4.03E+05
703	<b>41.33</b>	COPG	594	coatamer protein complex, subunit gamma 1	TEST*PITAVK	Q9Y678	98	6	1.78E+07
704	<b>18.17</b>	epsin 1; epsin 1 iso3	429, 435, 439; 428, 434, 438	epsin 1 isoform a	GSLAEAVGS*PPPAAT*PTPT*PPTR	Q9Y6I3; Q9Y6I3-3	58; 58	1	2.84E+05
705	<b>8.85</b>	EXOC4	237	SEC8 protein isoform b	DASVPLIDVTLNLT*PR	Q96A65	111	3	3.34E+06
706	<b>24.68</b>	Exoc8	142	exocyst complex 84-kDa subunit	GQAGFFST*PGGASR	Q8IYI6	82	2	3.56E+06
707	<b>5.85</b>	golgin-245	33	golgi autoantigen, golgin subfamily a, 4	ISEEQQLQALAPAQASSNSSTPT*R	Q13439	261	1	1.55E+06
708	<b>11.97</b>	GORASP2	433	golgi reassembly stacking protein 2	VGDST*PVSEKPVSA	Q9H8Y8	47	6	2.43E+06
709	<b>8.92</b>	KIAA0430	687	limkain b1	LVVPTHGNSAAVST*PK	Q9Y4F3	193	2	7.82E+05
710	-0.97	WDR7	926	rabconnectin-3 beta isoform 1	GPTRPPRPST*PDLISK	Q9Y4E6	164	3	7.03E+05
711	<b>c2h2-type zinc finger protein</b>								
712	<b>11.36</b>	ARID2	1726	AT rich interactive domain 2 (ARID, RFX-like)	QPTVGGTSST*PR	Q68CP9	197	2	2.08E+06
713	<b>20.92</b>	TRPS1; TRPS1 iso2	929; 942	zinc finger transcription factor TRPS1	LHST*PRPLNIK	Q9UHF7; Q9UHF7-2	142; 143	1	1.16E+06
714	<b>29.81</b>	ZBTB2	459	zinc finger and BTB domain containing 2	TFST*PNEVVK	Q8N680	57	1	1.73E+06
715	<b>9.11</b>	ZXDC	172	ZXD family zinc finger C isoform 2	APQASGPST*PGYR	Q2QGD7	90	1	5.70E+05
716	<b>nuclear receptor</b>								
717	-0.45	Trap240	554	mediator complex subunit 13	TPST*PQSQHFYQM#PTPDPLVSPKPM#EDR	Q9UHV7	239	1	1.19E+05