

Table: PTMScan® Results, Phospho-T*PP Motif (T*PP), label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

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	9.77	AHNAK	545	AHNAK nucleoprotein isoform 1	GSRVDIET*PNLEGLTLGPR	Q09666	629	1	1.78E+05	
3	1.22	AKAP1	533	A-kinase anchor protein 1 precursor	AIT*PPLPESTVPFNGVLK	Q92667	97	4	5.83E+05	
4	-1.19	axin 1	75, 77, 79	axin 1 isoform a	RSDLDLGYEPEGS*AS*PT*PPYLK	015169	96	1	2.27E+04	
5	1.12	axin 1	75, 79	axin 1 isoform a	RSDLDLGYEPEGS*ASPT*PPYLK	015169	96	1	5.23E+04	
6	-1.29	axin 1	77, 79	axin 1 isoform a	SDLDLGYEPEGSAS*PT*PPYLK	015169	96	1	3.03E+04	
7	-1.56	axin 1	79	axin 1 isoform a	SDLDLGYEPEGSASPT*PPYLK	015169	96	3	8.40E+04	
8	52.39	BASP1	186, 195	brain abundant, membrane attached signal protein 1	SDGAPASDSKPGSSEAAPSSKET*PAATEAPSS*TPK	P80723	23	1	1.42E+05	
9	15.78	P130Cas	269	breast cancer anti-estrogen resistance 1	GLLPSQYQGEVYDT*PPM#FAVK	P56945	93	7	1.06E+07	
10	1.45	CNKSR1	289, 293, 300	connector enhancer of kinase suppressor of Ras 1	KIPIPET*PPQT*PPQVLDS*PHQR	Q969H4	80	1	2.47E+05	
11	-1.27	DLG1; DLG1 iso2	115; 115	discs, large homolog 1 isoform 1	YQEDT*PQEHIS*PQITNEVIGPELVHVSEK	Q12959; Q12959-2	100; 103	6	9.85E+05	
12	76.63	DLG1; DLG1 iso2	115, 122; 115, 122	discs, large homolog 1 isoform 1	YQEDT*PQEHIS*PQITNEVIGPELVHVSEK	Q12959; Q12959-2	100; 103	8	2.36E+06	
13	1.79	RAMP	508, 512, 516	denticleless homolog	NWVTRT*PSSS*PPIT*PPASETK	Q9NZJ0	79	3	6.27E+05	
14	1.04	RAMP	510, 516	denticleless homolog	TPS*SSPPI*PPASETK	Q9NZJ0	79	1	2.43E+05	
15	13.83	EPS15R	108, 113	epidermal growth factor receptor pathway substrate 15-like 1	FHDTSS*PLM#VT*PPSAEAHWAV	Q9UBC2	94	2	2.63E+06	
16	15.26	EPS15R	113	epidermal growth factor receptor pathway substrate 15-like 1	FHDTSS*PLM#VT*PPSAEAHWAV	Q9UBC2	94	2	2.07E+06	
17	1.89	EPS8L1	182, 187	epidermal growth factor receptor pathway substrate 8-like protein 1 isoform b	DRS*PAAET*PPLQR	Q8TE68	80	3	3.43E+05	
18	-1.60	G3BP-2; G3BP-2 iso2	227; 227	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a	NLEELEEKST*PPAEPVSLPQPEPK	Q9UN86; Q9UN86-2	54; 51	2	7.27E+04	
19	3.61	INADL	335	InaD-like	DPAGDISV*PPAAPALVALPTVASK	Q8NI35	196	1	5.89E+05	
20	-3.20	IRS-1	444, 446	insulin receptor substrate 1	S*VT*PDSLGH*PPARGEEELSNYICM#GGK	P35568	132	1	3.06E+04	
21	-3.56	IRS-1	444, 449, 453	insulin receptor substrate 1	S*VTPDS*LGHT*PPARGEEELSNYICM#GGK	P35568	132	1	1.19E+04	
22	-1.34	IRS-1	446, 449, 453	insulin receptor substrate 1	SVT*PDS*LGHT*PPAR	P35568	132	1	2.24E+04	
23	1.63	IRS-1	446, 453	insulin receptor substrate 1	SVT*PDSLGH*PPAR	P35568	132	1	1.35E+05	
24	-1.02	IRS-1	453	insulin receptor substrate 1	SVTPDSLGH*PPAR	P35568	132	1	3.13E+04	
25	1.69	IRS-2	344, 350	insulin receptor substrate 2	SRT*DSLAA*PPAAK	Q9Y4H2	137	1	2.58E+04	
26	2.93	IRS-2	350	insulin receptor substrate 2	SRTSLAA*PPAAK	Q9Y4H2	137	2	1.80E+05	
27	2.72	IRS-2	515, 518, 520, 527	insulin receptor substrate 2	AFCS*HRS*NT*PESIAET*PPAR	Q9Y4H2	137	1	2.70E+05	
28	2.29	IRS-2	518, 520, 523, 527	insulin receptor substrate 2	AFCSHRS*NT*PES*IAET*PPAR	Q9Y4H2	137	5	1.70E+06	
29	2.95	IRS-2	518, 520, 527	insulin receptor substrate 2	AFCSHRS*NT*PESIAET*PPAR	Q9Y4H2	137	7	5.90E+06	
30	222.16	IRS-2	518, 523, 527	insulin receptor substrate 2	S*NTPES*IAET*PPAR	Q9Y4H2	137	3	3.89E+06	
31	2.05	IRS-2	518, 527	insulin receptor substrate 2	S*NTPESIAET*PPAR	Q9Y4H2	137	6	2.22E+07	
32	114.68	IRS-2	520, 523, 527	insulin receptor substrate 2	SNT*PES*IAET*PPAR	Q9Y4H2	137	9	7.96E+05	
33	2.85	IRS-2	520, 527	insulin receptor substrate 2	SNT*PESIAET*PPAR	Q9Y4H2	137	9	1.10E+07	
34	2.57	IRS-2	523, 527	insulin receptor substrate 2	PES*IAET*PPAR	Q9Y4H2	137	2	1.18E+05	
35	-1.76	IRS-2	527	insulin receptor substrate 2	SNTPESIAET*PPAR	Q9Y4H2	137	15	1.18E+07	
36	9.42	IRS-2	772, 779	insulin receptor substrate 2	LLPNGDYLNVSPS*DAVTTGT*PPDFFSAAALHPGGPEPLR	Q9Y4H2	137	1	8.43E+04	
37	-1.05	IRS-2	779	insulin receptor substrate 2	LLPNGDYLNVSPSDAVTTGT*PPDFFSAAALHPGGPEPLR	Q9Y4H2	137	1	2.19E+04	
38	1.24	KIAA1432	992	connexin 43-interacting protein 150 isoform b	AIGSGESET*PPSTPTAQEPSSSGGFEFF	Q4ADV7	159	6	7.49E+05	
39	1.20	KIAA1432	992, 996	connexin 43-interacting protein 150 isoform b	AIGSGESET*PPSTPTAQEPSSSGGFEFFR	Q4ADV7	159	1	1.69E+05	
40	68.71	TAB3	404, 409	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	NQHSLYTAT*PPSSS*PSR	Q8N5C8	79	3	2.76E+06	
41	-1.52	PPFIA3	714	PTPRF interacting protein alpha 3	GEGPAIPGDT*PPPTPR	Q75145	134	1	1.38E+04	
42	4.98	RanBP2; RGD1; RGD2; RGD3; RGD4; LOC100133510	796, 799; 795, 798; 787, 790; 797, 800; 797, 800; 796, 799	RAN binding protein 2	SYKYS*PKT*PPR	P49792; Q68DN6; P0C839; A6NKT7; Q723J3; XP_001719668	358; 197; 197; 198; 198; 116	4	1.12E+05	
43	-1.01	RAPH1	1057	Ras association and pleckstrin homology domains 1 isoform 3	RPSVDSLVSFKT*PPAESGSPSK	Q70E73	141	1	3.43E+04	
44	20.20	RAPH1	1057, 1064	Ras association and pleckstrin homology domains 1 isoform 3	RPSVDSLVSFKT*PPAESGS*PSKETLPPPAAPPKPGK	Q70E73	141	7	8.20E+05	
45	45.17	RAPH1	1057, 1066	Ras association and pleckstrin homology domains 1 isoform 3	RPSVDSLVSFKT*PPAESGSPS*KETLPPPAAPPKPGK	Q70E73	141	4	1.35E+06	
46	23.71	Tks5; Tks5 iso3	361; 217	SH3 multiple domains 1	ASGDKET*PPAEGEGHEAPIAK	Q5TCZ1; BAA24848	125; 107	3	1.23E+05	
47	6.47	ArgBP2; ArgBP2 iso2; ArgBP2 iso4	921; 487; 512	sorbin and SH3 domain containing 2 isoform 3	VGIFPISYVEKLT*PPEK	Q94875; Q94875-2; Q94875-4	124; 75; 77	6	6.30E+05	
48	10.53	SOS1	1252, 1254, 1263, 1265	son of sevenless homolog 1	KSDHGNAFFPNS*PS*PFTFPPPQT*PS*PHGTR	Q07889	152	1	1.08E+05	
49	-3.88	Z01; Z01 iso2	868; 868	tight junction protein 1 isoform a	NDEVGT*PPESAIR	Q07157; Q07157-2	195; 187	1	6.69E+03	

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

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Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
50		Adhesion or extracellular matrix protein							
51	2.64	Erbin	1116	ERBB2 interacting protein isoform 7	EFHSAGRT*PPM#MPGSQRPLSA	Q96RT1	158	2	4.89E+04
52	6.58	MAP7	277	microtubule-associated protein 7	LFVT*PPEGSSR	Q14244	84	9	3.91E+07
53	14.54	plakophilin 4; plakophilin 4 iso2	406, 412; 406, 412	plakophilin 4 isoform b	SAVS*PDLHT*PIVEGR	Q99569; Q99569-2	134; 130	2	3.29E+05
54	3.21	ROBO1	1240	roundabout 1 isoform c	MYLQDDEEEEEERGP*PPVR	Q9Y6N7	181	17	6.56E+06
55		Apoptosis							
56	6.97	acinus	410, 414	apoptotic chromatin condensation inducer 1	ASLVALPEQTAS*EEET*PPLLTK	Q9UKV3	152	2	2.31E+06
57	3.72	acinus	414	apoptotic chromatin condensation inducer 1	ASLVALPEQTASEEET*PPLLTK	Q9UKV3	152	5	5.03E+06
58	8.32	ANKHD1; MASK-BP3	1553; 1553	ankyrin repeat and KH domain containing 1 isoform 1	TKET*PPTAHLILPEQHMSLAQQK	Q8IWZ3; Q8IWZ2	269; 277	5	2.60E+05
59	33.36	DBC-1	35	p30 DBC protein	NFSGTASTSLGPPGLLT*PPVATELSQNA	Q8N163	103	7	5.70E+06
60		Calcium-binding protein							
61	297.35	ANXA2	18	annexin A2 isoform 2	SLEGDHS*TPPSAYGSVK	P07355	39	2	2.61E+06
62	58.34	ANXA2	19	annexin A2 isoform 2	LSLEGDHST*PPSAYGSVK	P07355	39	17	1.58E+08
63	21.49	ANXA2	19, 26	annexin A2 isoform 2	LSLEGDHST*PPSAYGS*VK	P07355	39	1	1.42E+05
64		Cell cycle regulation							
65	2.73	BAT2D1; BAT2D1 iso8	2673; 2673	HbxAg transactivated protein 2	AFSGSIDIKPGT*PPIAGR	Q9Y520; NP_055987	317; 309	3	1.13E+07
66	8.11	KAB1; KAB1 iso2	914, 920; 816, 822	centrosomal protein 170kDa isoform beta	LREDNKT*DEGPD*PSYNR	Q5SW79; Q5SW79-2	175; 161	1	3.14E+04
67	20.54	KAB1; KAB1 iso2	920; 822	centrosomal protein 170kDa isoform beta	LREDNKTDEGPD*PSYNR	Q5SW79; Q5SW79-2	175; 161	2	1.95E+05
68	7.12	CEP350	878	centrosome-associated protein 350	AVT*PPVKDNDNEVFSA	Q5VT06	351	3	2.75E+05
69	-1.42	CUL4B	31	cullin 4B isoform 2	SATDGNTST*PPTSAAK	Q13620	102	4	4.87E+06
70	6.71	CUL4B	31, 34	cullin 4B isoform 2	SATDGNTST*PPT*SAKK	Q13620	102	1	9.89E+04
71	6.93	CUL4B	31, 35	cullin 4B isoform 2	SATDGNTST*PPTS*AK	Q13620	102	5	6.03E+06
72	2.56	CUL4B	60, 67	cullin 4B isoform 2	KLNSSSSSSSSNSNEREDFDS*TSSSSST*PPLQPR	Q13620	102	1	8.80E+04
73	1.90	CUL4B	67	cullin 4B isoform 2	KLNSSSSSSSSNSNEREDFDS*TSSSSST*PPLQPR	Q13620	102	3	2.70E+05
74	51.68	ZRF1	183	DnaJ (Hsp40) homolog, subfamily C, member 2 isoform 2	DNFFFEVFT*PVFER	Q99543	72	6	3.05E+06
75	-4.03	INCENP	263, 269, 275	inner centromere protein antigens 135/155kDa isoform 1	IAQVS*PGPRDS*PAFPDS*PWRER	Q9NQ57	106	1	3.81E+04
76	-3.93	MDC1	765, 780	mediator of DNA damage checkpoint 1	ESEDSET*QPFDT*HLEAYGPCL*PPR	Q14676	227	1	3.02E+04
77	4.64	Ki-67; Ki-67 iso2	2389, 2406; 2029, 2046	antigen identified by monoclonal antibody Ki-67 isoform 2	AM#DT*PKPAVSDKDNIN*FVET*PVQK	P46013; P46013-2	359; 319	2	1.02E+05
78	25.13	Ki-67; Ki-67 iso2	2395, 2406; 2035, 2046	antigen identified by monoclonal antibody Ki-67 isoform 2	AMDT*PKPAVS*DEKNIN*FVET*PVQK	P46013; P46013-2	359; 319	1	1.31E+05
79	18.83	Ki-67; Ki-67 iso2	2406; 2046	antigen identified by monoclonal antibody Ki-67 isoform 2	NINTFVET*PVQK	P46013; P46013-2	359; 319	4	6.35E+06
80	35.64	Ki-67; Ki-67 iso2	543; 183	antigen identified by monoclonal antibody Ki-67 isoform 2	KSLVMHT*PPVVK	P46013; P46013-2	359; 319	2	1.26E+05
81	27.63	MLF1IP	94, 97, 98	MLF1 interacting protein	HCGLS*LSS*TPPGK	Q71F23	169	1	1.52E+05
82	33.74	NCAPD3	1329, 1331, 1334	non-SMC condensin II complex, subunit D3	ASAGHVAVSS*PT*PET*GPLQR	P42695	168	1	2.21E+06
83	21.26	SAS6	493	spindle assembly abnormal protein 6	KQDVLGPPS*TPPAHSSNTIR	Q6UVJ0	74	1	4.69E+05
84	38.09	SAS6	494	spindle assembly abnormal protein 6	KQDVLGPPS*TPPAHSSNTIR	Q6UVJ0	74	1	2.44E+05
85	57.14	SGO1	423, 425, 436	shugoshin-like 1 isoform A1	YTDEKETEGSKPT*KT*PTTTPPETQQS*PHLSLK	Q5FBB7	64	1	9.12E+05
86	19.75	SGO1	429, 436	shugoshin-like 1 isoform A1	TPTTT*PPETQQS*PHLSLK	Q5FBB7	64	1	4.04E+05
87	11.47	TACC2	2147	transforming, acidic coiled-coil containing protein 2 isoform d	KPTET*PPVK	Q95359	309	1	9.62E+04
88	9.00	TNKS1BP1	131	tankyrase 1-binding protein 1	PAVEASTGGAEQETGKEEAGKEEPPPLT*PPAR	Q9C0C2	182	13	1.58E+06
89		Chaperone							
90	9.26	DNAJC18	28	DnaJ (Hsp40) homolog, subfamily C, member 18	NKYPEDT*PPSHDPCGCCNCMK	Q9H819	42	3	3.10E+04
91	9.96	SGTA	77, 81	small glutamine-rich tetrapeptide	EMPDQLRS*PART*PPEEEDSAEAER	Q43765	34	8	5.86E+05
92	-1.05	SGTA	77, 84	small glutamine-rich tetrapeptide	S*PARTPPS*EEDSAEAER	Q43765	34	1	4.83E+04
93	1.66	SGTA	81	small glutamine-rich tetrapeptide	SPART*PPEEEDSAEAER	Q43765	34	1	3.00E+04
94	2.79	SGTA	81, 84	small glutamine-rich tetrapeptide	EMPDQLRS*PART*PPEEEDSAEAER	Q43765	34	1	6.21E+05
95		Chromatin, DNA-binding, DNA repair or DNA replication protein							
96	17.64	BAZ1A	1547	bromodomain adjacent to zinc finger domain, 1A isoform a	LGLHVTPSNVDQVST*PPAAK	Q9NRL2	179	2	1.99E+06
97	6.10	C14orf43	700, 704, 715	hypothetical protein LOC91748	TNS*AEVT*PPVLSVM#GEAT*PVSIEPR	Q6PJG2	115	1	1.57E+04
98	-4.05	C14orf43	704, 718	hypothetical protein LOC91748	TNSAEVT*PPVLSVM#GEAT*PVSIEPR	Q6PJG2	115	1	2.95E+04
99	3.28	C17orf49; C17orf49 iso3	146, 150, 161; 112, 116, 127	hypothetical protein LOC124944 isoform 1	ALNDS*DANS*DVVDIEGLGET*PPAKK	Q8IXM2; NP_001136271	18; 14	1	2.58E+04
100	9.23	C17orf49; C17orf49 iso3	146, 161; 112, 127	hypothetical protein LOC124944 isoform 1	ALNDS*DANS*DVVDIEGLGET*PPAK	Q8IXM2; NP_001136271	18; 14	2	5.04E+04
101	1.52	C17orf49; C17orf49 iso3	161; 127	hypothetical protein LOC124944 isoform 1	QKADVTLALNDSANS*DVVDIEGLGET*PPAKK	Q8IXM2; NP_001136271	18; 14	1	9.37E+04

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

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102	2.69	CAF-1B	429, 433	chromatin assembly factor 1 subunit B	TQDPSS*PGTT*PPQAR	Q13112	61	14	9.61E+06
103	-1.05	CAF-1B	433	chromatin assembly factor 1 subunit B	TQDPSSPGTT*PPQA	Q13112	61	6	9.90E+05
104	4.54	CHD-7	2551	chromodomain helicase DNA binding protein 7	AFEEDIET*PPTR	Q9P2D1	336	8	4.69E+06
105	1.28	HP1BP3; HP1BP3 iso5	51; 51	HP1-BP74	TVNSTRET*PPK	Q5SSJ5; Q5SSJ5-5	61; 15	3	1.93E+07
106	1.53	HP1BP3; HP1BP3 iso5	85; 85	HP1-BP74	EEQENET*PPATSSEAEQPK	Q5SSJ5; Q5SSJ5-5	61; 15	1	1.97E+04
107	1.90	MSH6	1085	mutS homolog 6	GGDGP#CRP#VILLPEDT*PPFLELK	P52701	153	3	7.53E+04
108	7.24	PRR12	1304, 1308	proline rich 12	HPPLYQAGLT*PPLS*PPK	Q9ULL5	211	4	1.27E+06
109	7.20	PRR12	224	proline rich 12	LAGGGVLGPAGLGAQAT*PPYRPGPPDPPPPPR	Q9ULL5	211	4	1.43E+06
110 Cytoskeletal protein									
111	4.90	restin	140	restin isoform a	KVQAEDEANGLQTT*PASR	P30622	161	2	5.97E+04
112	20.67	cordon-bleu	935	cordon-bleu homolog	DGAQWPCVT*PPNHHGEDLAVGAPPR	O75128	136	2	4.57E+05
113	1.54	KIF1B iso3	1132	kinesin family member 1B isoform b	QTDKPSHCQFVT*PPRM	O60333-3	130	3	3.66E+05
114	2.43	KIF1C	1083	kinesin family member 1C	YPPYTT*PPRM	O43896	123	11	3.39E+06
115	1.59	KIF2A	78	kinesin heavy chain member 2 isoform 2	GKEIDLESIFSLNPDVDEIEIPSPET*PPPPASSAK	O00139	80	1	2.09E+05
116	-1.76	lamin A/C; lamin A/C iso2	22; 22	lamin A/C isoform 2	SGAQASSTPLS*PTRIT	P02545; P02545-2	74; 65	2	3.68E+04
117	2.50	MAP1A	504	microtubule-associated protein 1A	ELSSPEQT*PPAQK	P78559	306	4	2.21E+05
118	1.16	MAP1B	704	microtubule-associated protein 1B	KET*PPKEVK	P46821	271	2	2.24E+06
119	5.02	MAP4 iso4	421, 431	microtubule-associated protein 4 isoform 4	SAGIARPEEGRPVVSGTGNIDIT*TPPNKELPPS*PEKK	P27816-4	91	4	2.01E+05
120	2.15	MAP4 iso4	422	microtubule-associated protein 4 isoform 4	SAGIARPEEGRPVVSGTGNIDIT*TPPNK	P27816-4	91	4	3.29E+05
121	5.88	MAP4	507, 521	microtubule-associated protein 4 isoform 4	DM#S*PLSETEM#ALGKDVT*PPPTEVVLK	P27816	121	2	3.55E+05
122	1.32	MAP4	521	microtubule-associated protein 4 isoform 4	DM#S*PLSETEM#ALGKDVT*PPPTEVVLK	P27816	121	2	1.45E+05
123	5.34	MAP4; MAP4 iso4	686, 696; 421, 431	microtubule-associated protein 4 isoform 4	PEEGRPVVSGTGNIDIT*TPPNKELPPS*PEKK	P27816; P27816-4	121; 91	1	5.11E+04
124	3.37	MAP4; MAP4 iso4	687; 422	microtubule-associated protein 4 isoform 4	PEEGRPVVSGTGNIDIT*TPPNK	P27816; P27816-4	121; 91	1	1.70E+05
125	-11.51	RPRC1	41, 51	MAP7 domain containing 1	TPPEPRSPPEGDPSPPPPPM#S*ALVPDTPDTP*PAM#K	Q3KQU3	93	1	1.97E+04
126	20.76	RPRC1	47, 51	MAP7 domain containing 1	LVPDT*PPDT*PPAMK	Q3KQU3	93	8	4.97E+05
127	2.16	BC060632	258, 263	metastasis suppressor 1-like	GSDYSWSy*QTTPS*SPSSSSSR	Q765P7	80	1	1.75E+05
128	1.09	BC060632	260, 263	metastasis suppressor 1-like	GSDYSWSYQT*PPS*SPSSSSSRK	Q765P7	80	2	8.43E+04
129	10.04	CLIM1	316	PDZ and LIM domain 1	ERVT*PPEGYEYVTVFK	O00151	36	5	2.15E+06
130	18.91	PHACTR2	129	phosphatase and actin regulator 2 isoform 1	SEEGNGSVSEKT*PPLLEEQAEDKK	O75167	70	1	5.90E+04
131	2.40	PHACTR2	16, 23, 25	phosphatase and actin regulator 2 isoform 1	ASIAN#*DGPTAGS*QT*PPFKR	O75167	70	1	7.77E+04
132	-1.91	PHACTR2	16, 25	phosphatase and actin regulator 2 isoform 1	ASIAN#*DGPTAGSQT*PPFK	O75167	70	2	2.25E+05
133	47.34	PHACTR2	25	phosphatase and actin regulator 2 isoform 1	ASIANSDGPTAGSQT*PPFK	O75167	70	9	1.56E+08
134	-3.23	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	9.16E+03
135	-2.59	SHRM	576	shroom family member 3 protein	HLT*PPQGN#PHSNER	Q8TF72	217	1	7.49E+03
136	4.10	SHRM	576, 582	shroom family member 3 protein	HLT*PPQGN#PHSNER	Q8TF72	217	3	6.46E+05
137	164.84	SHRM	576, 582, 585	shroom family member 3 protein	HLT*PPQGN#PHSNER	Q8TF72	217	3	3.13E+05
138	-1.15	talin 2	1843	talin 2	LDEGT*PPEPK	Q9Y4G6	272	9	1.86E+06
139	31.64	WIP	345, 350	WAS/WASL interacting protein family, member 1	NLSLSSST*PPLPS*PGR	O43516	51	5	1.92E+07
140 Endoplasmic reticulum or golgi									
141	4.65	JPH2	484, 486, 490	junctophilin 2 isoform 1	ETPRPEGGS*PS*PAGT*PPQPK	Q9BR39	74	1	6.78E+04
142 Enzyme, misc.									
143	3.64	BRIP1	113	BRCA1 interacting protein C-terminal helicase 1	HFNYPST*PPSER	Q9BX63	141	5	2.73E+06
144	33.72	BRIP1	918, 930	BRCA1 interacting protein C-terminal helicase 1	YST*PPYLAAASHLS*PENFVEDEAK	Q9BX63	141	2	6.73E+05
145	3.16	DUS3L	273, 277	dihydrouridine synthase 3-like	QENCGAQVPAAGTST*PPSS*PVR	Q96G46	73	1	4.93E+05
146	19.19	EHMT2; EHMT2 iso2	555; 521	euchromatic histone-lysine N-methyltransferase 2 isoform a	GDGVT*PPAGTAAPAPPLSQDVVGR	Q96KQ7; Q96KQ7-2	132; 129	2	1.13E+06
147	2.27	EZH2	487	enhancer of zeste 2 isoform a	VKESIIAPAPAEVDVT*PPR	Q15910	85	25	1.74E+07
148	50.84	FTSJ1	262, 271	FtsJ homolog 1 isoform a	SYPLDLEGGSEYKy*TPPTQPPIS*PPYQEAETLK	Q9UET6	36	1	6.10E+05
149	24.34	FTSJ3	573	FtsJ homolog 3	QLLPQT*PPSCLK	Q8Y81	97	1	6.60E+05
150	37.14	METTL2B	154	methyltransferase like 2B	TQT*PPVEENVTKQ	Q6P1Q9	43	4	1.03E+06
151	1.79	WBSR20A	462	NOL1/NOP2/Sun domain family, member 5 isoform 2	AAAGACT*PPCT	Q96P11-2	50	4	6.26E+06
152	21.03	WBSR20A	462, 466	NOL1/NOP2/Sun domain family, member 5 isoform 2	AAAGACT*PPCT*	Q96P11-2	50	6	1.22E+06

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Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
153	17.40	PCF11	535	pre-mRNA cleavage complex II protein Pcf11	QSHMEEFF*PPSREDR	Q94913	173	3	3.55E+06
154	55.44	PDE3A	575, 580	phosphodiesterase 3A	ALTYTQSAAPDL*S*PQLT*PPVICSSCGR	Q14432	125	1	6.54E+05
155	1.16	PPIG	356, 358	peptidylprolyl isomerase G	S*ET*PPHWR	Q13427	89	9	1.07E+06
156	1.62	RRM2	20, 33	ribonucleotide reductase M2 polypeptide	VPLAPITDPOQLQLS*PLKGLSLVDKENT*PPALSGTR	P31350	45	1	6.13E+04
157	15.15	RRM2	20, 33, 40	ribonucleotide reductase M2 polypeptide	VPLAPITDPOQLQLS*PLKGLSLVDKENT*PPALSGT*R	P31350	45	1	1.39E+05
158	2.81	RRM2	33	ribonucleotide reductase M2 polypeptide	GLSLVDKENT*PPALSGT	P31350	45	3	2.20E+06
159	35.25	TKT	287	transketolase isoform 1	ILAT*PPQEDAPSDVIANIR	P29401	68	3	5.91E+06
160	2.04	TRMT1	646	tRNA methyltransferase 1 isoform 1	VSADAAPDCPETSNOT*PPGPGAAAGPGID	Q9NXH9	72	1	7.34E+04
161	-2.81	UNG	60	uracil-DNA glycosylase isoform UNG1 precursor	KAPAGQEEPGT*PPSSPLSAEQLDR	P13051	35	3	3.23E+04
162	1.03	UNG	60, 63	uracil-DNA glycosylase isoform UNG1 precursor	KAPAGQEEPGT*PPS*SPLSAEQLDR	P13051	35	1	2.35E+05
163 G protein or regulator									
164	47.62	ARF GAP1	129, 135	ADP-ribosylation factor GTPase activating protein 1 isoform a	EWSLESS*PAQNW*PPOPR	Q8N6T3	45	2	4.60E+05
165	6.80	ARF GAP1	135	ADP-ribosylation factor GTPase activating protein 1 isoform a	EWSLESSPAQNW*PPOPR	Q8N6T3	45	1	2.46E+05
166	-1.30	ARHGAP17	751, 759, 763	nadrin isoform 1	GLEQPS*HTPPQITP*PPST*PPLGK	Q68EM7	95	2	9.52E+04
167	19.13	ARHGAP17	753, 757, 759, 763	nadrin isoform 1	GLEQPSHT*PPQT*PT*PPST*PPLGK	Q68EM7	95	1	2.69E+05
168	8.25	ARHGEF11	1461, 1462, 1469	Rho guanine nucleotide exchange factor (GEF) 11 isoform 1	SLGGESSGGT*T*PVGSFHT*EAAR	O15085	168	1	5.65E+04
169	-1.22	ARHGEF11	663, 668	Rho guanine nucleotide exchange factor (GEF) 11 isoform 1	S*LENPT*PPFTPK	O15085	168	1	2.62E+05
170	-2.19	FGD1	711	faciogenital dysplasia protein	LLNSTNREDET*PPNSPNVDLKG	P98174	107	4	9.70E+05
171	4.13	FGD1	711, 715	faciogenital dysplasia protein	LLNSTNREDET*PPNS*PNVDLKG	P98174	107	6	5.60E+06
172	20.80	GAPVD1	390	GTPase activating protein and VPS9 domains 1	AVET*PPLSSVNLLELSR	Q9Y4N0	166	10	1.66E+07
173	13.10	HERC1	2701, 2705, 2710	guanine nucleotide exchange factor p532	AQT*PPIS*SLPTS*PSDEVGRR	Q15751	532	1	4.48E+05
174	7.99	NF1; NF1 iso2	2565; 2544	neurofibromin isoform 2	QEMESGITT*PPKM	P21359; P21359-2	319; 317	10	1.36E+06
175	-3.19	PLEKHG2	1257	common-site lymphoma/leukemia guanine nucleotide exchange factor	LESSDLT*PPHSPPSS	Q9H7P9	148	2	1.43E+04
176	2.55	PLEKHG2	1257, 1261	common-site lymphoma/leukemia guanine nucleotide exchange factor	LESSDLT*PPHS*PPSS	Q9H7P9	148	8	6.40E+05
177	2.21	PLEKHG2	445, 450	common-site lymphoma/leukemia guanine nucleotide exchange factor	SKPVLEPT*PPLGS*PRPR	Q9H7P9	148	6	1.29E+07
178	22.49	SEPT2	14	septin 2	QQPTQFINPET*PGYVGFANLPQVH	Q15019	41	2	7.10E+06
179	9.90	SEPT9	38, 41	septin 9 isoform a	SFEVEVET*PNS*TPRR	Q9UHD8	65	3	1.35E+06
180	11.75	SEPT9	38, 42	septin 9 isoform a	SFEVEVET*PNST*PPR	Q9UHD8	65	13	2.06E+06
181	8.05	SEPT9	42	septin 9 isoform a	SFEVEVETPNST*PPR	Q9UHD8	65	3	5.56E+05
182 Kinase (non-protein)									
183	1.24	ITPKB	33	1D-myo-inositol-trisphosphate 3-kinase B	SGGGPGSGSET*PPPPR	P27987	102	6	1.76E+05
184	4.68	PIPSK1A	516	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha isoform 3	AEVEPGVHLGRPDVLPQT*PPLEEI	Q99755	63	1	4.63E+05
185 Mitochondrial protein									
186	4.72	AGPS	155	alkyldihydroxyacetone phosphate synthase precursor	ASLNPSDT*PPSVNEDFLHDLK	O00116	73	1	7.38E+05
187 Motor or contractile protein									
188	34.16	Sec24C	214	SEC24-related protein C	SAPSQASFT*PPASGGPR	P53992	118	3	8.17E+05
189 Phosphatase									
190	-2.11	Cdc25B; Cdc25B iso2; Cdc25B iso3	353, 355; 339, 341; 312, 314	cell division cycle 25B isoform 2	RRS*VT*PPEEQEAEPEK	P30305; P30305-2; P30305-3	65; 63; 61	2	1.71E+04
191	-1.57	Cdc25B; Cdc25B iso2; Cdc25B iso3	355; 341; 314	cell division cycle 25B isoform 2	SVT*PPEEQEAEPEK	P30305; P30305-2; P30305-3	65; 63; 61	1	2.04E+04
192	6.25	INPP5F	261	inositol polyphosphate-5-phosphatase F	SSPET*PPQESTCVDIHPR	Q9Y2H2	128	1	3.36E+05
193	1.35	PHACTR4	28	phosphatase and actin regulator 4 isoform 1	VLDSEVAGDTT*PPTK	Q8I221	78	10	4.54E+06
194	-5.98	PHACTR4	344, 358	phosphatase and actin regulator 4 isoform 1	SPS*PPLPTHIPPEPP*PPFPAK	Q8I221	78	23	7.43E+04
195	15.82	Pnk1	109, 118, 122	polynucleotide kinase 3' phosphatase	WEET*RTPEQPDT*PPGT*PLVSQDEKR	Q9UNF8	57	1	2.37E+05
196	1.76	Pnk1	114, 118, 122	polynucleotide kinase 3' phosphatase	TPES*QPD*PPGT*PLVSQDEKR	Q9UNF8	57	1	3.30E+04
197	1.69	Pnk1	118	polynucleotide kinase 3' phosphatase	TPESQPD*PPGTPLVSQDEKR	Q9UNF8	57	15	4.50E+06
198	33.57	Pnk1	118, 122	polynucleotide kinase 3' phosphatase	TPESQPD*PPGT*PLVSQDEKR	Q9UNF8	57	9	4.36E+06
199	5.47	Pnk1	118, 126	polynucleotide kinase 3' phosphatase	WEETRTPEQPDT*PPGTPLVS*QDEK	Q9UNF8	57	2	4.12E+05
200	9.89	PPP1CB	316	protein phosphatase 1, catalytic subunit, beta isoform 1	YQYGLNSGRVPT*PPR	P62140	37	1	4.60E+05
201	13.77	PPP1R10	256	protein phosphatase 1, regulatory subunit 10	QSNVAAPGDAT*PPAEK	Q96QC0	99	6	3.77E+05
202	6.88	PPP1R11	109	protein phosphatase 1, regulatory (inhibitor) subunit 11	ATLGPPTT*PPQPPDPSQPPPGPM*QH	O60927	14	14	3.00E+06
203	4.54	PTPN12	509, 514	protein tyrosine phosphatase, non-receptor type 12 isoform 2	VSVT*PPEES*QNSDTPPRDRPLDLEK	Q05209	88	5	1.64E+07

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Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
204	7.19	PTPN12	509, 519	protein tyrosine phosphatase, non-receptor type 12 isoform 2	VSVT*PPEESQNSDT*PPRPDR	Q05209	88	6	3.33E+06
205	1.13	PTPN12	519	protein tyrosine phosphatase, non-receptor type 12 isoform 2	VSVTPPEESQNSDT*PPRPDRPLPDEK	Q05209	88	3	2.71E+06
206	18.77	SYNJ1	1282	synaptojanin 1 isoform a	LQELPVPVAPM#PQSGPQPNLET*PPQPPPR	Q43426	173	2	4.45E+05
207	Protease								
208	72.72	ADAM9	758, 761	ADAM metalloproteinase domain 9 isoform 2 precursor	HVS*PVT*PPR	Q13443	91	4	7.41E+05
209	1.54	ADAM9	761	ADAM metalloproteinase domain 9 isoform 2 precursor	HVSPVT*PPR	Q13443	91	2	3.07E+05
210	7.06	SENP6	217, 221	SUMO1/sentrin specific peptidase 6 isoform 2	HCSTYQPT*PPLS*PASKK	Q9GZR1	126	1	3.36E+04
211	Protein kinase, Ser/Thr (non-receptor)								
212	16.72	AAK1; AAK1 iso2	606; 606	AP2 associated kinase 1	VQTT*PPPAVQGGK	Q2M2I8; NP_055726	94; 104	2	1.13E+05
213	2.10	AAK1; AAK1 iso2	620, 623; 620, 623	AP2 associated kinase 1	VGSLT*PPS*SPK	Q2M2I8; NP_055726	94; 104	1	4.30E+05
214	-1.73	Akt1	450	AKT1 kinase	TIT*PPDQDDSM#ECVDSER	P31749	56	1	8.67E+03
215	1.09	ATR	1989	ataxia telangiectasia and Rad3 related protein	GVELCFPENET*PPEGK	Q13535	301	4	3.25E+06
216	-1.56	LATS1	246, 255, 262	LATS homolog 1	SVT*PPPPRRGQT*PPPRGT*PPPPSWEPNSQTK	Q95835	127	2	1.08E+05
217	-3.71	PAK1	230	p21-activated kinase 1 isoform 1	DVATSPISPTENIT*PPDALTR	Q13153	61	2	2.58E+05
218	1.00	PAK2	141, 143	p21-activated kinase 2	YLS*FT*PPEKDGFPSPGTPALNAK	Q13177	58	5	1.63E+06
219	4.03	PAK2	143	p21-activated kinase 2	YLSFT*PPEKDGFPSPGTPALNAK	Q13177	58	4	1.67E+06
220	-1.25	PKN2	958	protein kinase N2	GREDSVNFDEFTSEAPILT*PPREPR	Q16513	112	4	1.52E+06
221	2.59	PKCB iso2	641	protein kinase C, beta isoform 2	HPPVLT*PPDQEVIR	P05771-2	77	1	3.24E+04
222	-1.18	SMG1	3566, 3569	PI-3-kinase-related kinase SMG-1	NLATS*ADT*PPSTVPGTGK	Q96Q15	410	4	1.95E+05
223	3.89	SMG1	3569	PI-3-kinase-related kinase SMG-1	NLATSADT*PPSTVPGTGK	Q96Q15	410	5	6.89E+06
224	-2.30	Wee1	165, 173	WEE1 tyrosine kinase isoform 2	RS*PRPDHPGT*PPHK	P30291	72	1	2.40E+05
225	Protein kinase, Tyr (receptor)								
226	127.38	NPM-ALK; NPM1; NPM1 iso2; NPM1 iso3	95; 95; 95; 95	anaplastic lymphoma kinase	M#SVQPTVSLGGFEIT*PPVVL	AAA58698; P06748; P06748-2; Q9BYG9	75; 33; 29; 28	5	3.95E+06
227	Protein kinase, atypical								
228	50.66	TIF1-beta	752, 757	tripartite motif-containing 28 protein	LQEKLS*PPYSS*PQFAQDQVGR	Q13263	89	2	4.21E+05
229	-3.19	TRIM33	815	tripartite motif-containing 33 protein isoform alpha	SACM#LSSPSSSLT*PPLSTLNHLESELDALASLENHVK	Q9UPN9	123	3	5.72E+05
230	Protein kinase, dual-specificity								
231	24.09	MEK1	286	mitogen-activated protein kinase kinase 1	ELELM#FGCQVEGDAET*PPRPR	Q02750	43	65	9.68E+05
232	Protein kinase, regulatory subunit								
233	15.11	DBF4	553	activator of S phase kinase	APFHT*PPEEPNECDFK	Q9UBU7	77	1	5.39E+05
234	RNA processing								
235	15.28	ataxin-2	660	ataxin 2	GSISSGLEFVSHNPPSEAA*PPVA	Q99700	140	2	8.68E+05
236	5.44	BAT2; BAT2 iso1	597; 609	HLA-B associated transcript-2	EGPEPPEEVPPTT*TPVPVK	P48634-2; P48634	228; 229	3	1.92E+06
237	10.58	BAT2; BAT2 iso1	598; 610	HLA-B associated transcript-2	EGPEPPEEVPPTT*TPVPVK	P48634-2; P48634	228; 229	4	2.70E+06
238	1.44	BAT2; BAT2 iso1	813; 825	HLA-B associated transcript-2	SET*PPVPPPPYLYSYPGFENGAPGPPIS	P48634-2; P48634	228; 229	1	4.79E+05
239	16.07	BAT2; BAT2 iso1	985, 992; 997, 1004	HLA-B associated transcript-2	LGGPKET*PPNGNLS*PAPR	P48634-2; P48634	228; 229	10	1.07E+07
240	5.92	dyskerin	451, 453, 455, 458	dyskerin isoform 2	KRES*ES*ES*DET*PPAAPQLIK	Q60832	58	15	8.80E+05
241	5.52	dyskerin	451, 453, 458	dyskerin isoform 2	KRES*ES*ES*DET*PPAAPQLIK	Q60832	58	5	1.54E+06
242	3.15	dyskerin	451, 455, 458	dyskerin isoform 2	KRES*ESES*DET*PPAAPQLIK	Q60832	58	1	1.14E+05
243	1.41	dyskerin	455, 458	dyskerin isoform 2	KRESESES*DET*PPAAPQLIK	Q60832	58	1	9.90E+04
244	1.68	LARP5	732, 736	La ribonucleoprotein domain family, member 5	EQST*PPKS*PQ	Q92615	81	1	3.20E+05
245	3.48	SKAR	140	DNA polymerase delta interacting protein 3 isoform 1	SSPAAFINPPIGTVI*PALK	Q9BY77	46	1	1.49E+05
246	3.80	SF3B1	235	splicing factor 3b, subunit 1 isoform 2	WDET*PGR	Q75533	146	1	6.41E+04
247	6.22	SF3B1	296, 303, 313	splicing factor 3b, subunit 1 isoform 2	WDET*PKTERDT*PGHSGGWAET*PR	Q75533	146	1	1.17E+05
248	1.21	SF3B1	341, 349	splicing factor 3b, subunit 1 isoform 2	SRWDET*PASQMGG*TPVLTGPK	Q75533	146	1	4.23E+04
249	-2.72	SF3B1	341, 350	splicing factor 3b, subunit 1 isoform 2	SRWDET*PASQMGG*TPVLTGPK	Q75533	146	1	1.88E+04
250	6.87	SF3B3	1200	splicing factor 3b, subunit 3	NVSEELDRTPPEVSK	Q15393	136	2	2.44E+05
251	3.28	SRm300	2090, 2096, 2100, 2104	splicing coactivator subunit SRm300	S*ATPPAT*RNHS*GSRT*PPVALNSSR	Q9UQ35	300	1	3.52E+04
252	-1.72	SRm300	2100, 2102, 2104	splicing coactivator subunit SRm300	NHS*GS*RT*PPVALNSS	Q9UQ35	300	9	7.78E+06
253	42.26	SRm300	2100, 2102, 2104, 2112	splicing coactivator subunit SRm300	NHS*GS*RT*PPVALNSSR	Q9UQ35	300	2	2.73E+06
254	13.72	SRm300	2100, 2104	splicing coactivator subunit SRm300	NHS*GSRT*PPVALNSS	Q9UQ35	300	2	9.35E+05
255	-4.19	SRm300	972, 973, 974, 983	splicing coactivator subunit SRm300	YSHSGS*S*S*PDTKVKPET*PPR	Q9UQ35	300	1	1.27E+04

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Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
256	1.39	SRm300	983	splicing coactivator subunit SRm300	VKPET*PPR	Q9UQ35	300	1	8.32E+06
257	8.36	SRm300	983, 988	splicing coactivator subunit SRm300	VKPET*PPRQS*HSGSISPYPK	Q9UQ35	300	3	2.91E+05
258	10.16	SRm300	983, 990, 992, 994	splicing coactivator subunit SRm300	VKPET*PPRQSHS*GS*IS*PYPK	Q9UQ35	300	4	1.29E+06
259	53.81	SRm300	983, 990, 994	splicing coactivator subunit SRm300	VKPET*PPRQSHS*GSIS*PYPK	Q9UQ35	300	1	6.64E+05
260	3.16	SRm300	983, 990, 996	splicing coactivator subunit SRm300	VKPET*PPRQSHS*GSISPy*PK	Q9UQ35	300	1	5.48E+05
261	1.06	SRm300	983, 994	splicing coactivator subunit SRm300	VKPET*PPRQSHSGSIS*PYPK	Q9UQ35	300	3	4.70E+05
262	2.28	TRA2A	84, 86, 88	transformer-2 alpha	S*RS*YT*PEYR	Q13595	33	1	1.62E+05
263	Receptor, channel, transporter or cell surface protein								
264	-1.57	ataxin-2L	684	ataxin 2 related protein isoform A	STSTPTS*PGPR	Q8WWM7	113	1	2.69E+04
265	12.36	CEPT1	40	choline/ethanolaminephosphotransferase	LFQLPT*PPLS	Q9Y6K0	47	2	8.43E+06
266	7.18	gp130	667, 670	interleukin 6 signal transducer isoform 1 precursor	SHIAQWS*PHT*PPR	P40189	104	1	6.23E+05
267	-1.21	gp130	670	interleukin 6 signal transducer isoform 1 precursor	SHIAQWSPHT*PPR	P40189	104	2	3.92E+04
268	8.25	INTS1	81, 83	integrator complex subunit 1	RPKLS*ST*PPLSALGR	Q8N201	244	1	1.83E+05
269	2.72	INTS1	83	integrator complex subunit 1	LSST*PPLSALGR	Q8N201	244	2	3.83E+05
270	54.98	MAN1B1	21	alpha 1,2-mannosidase	SGALGSSQSDFLT*PPVGGAPWAVATTVM#YPPP PPPPH	Q9UFZ8	80	2	4.49E+05
271	23.23	Notch 2	1802, 1808	notch 2 preproprotein	RT*PSLALT*PPQAEQEVLDVNVNR	Q04721	265	3	4.75E+05
272	8.11	Notch 2	1808	notch 2 preproprotein	TPSLALT*PPQAEQEVLDVNVNR	Q04721	265	6	6.08E+05
273	17.56	NUP214	1312	nucleoporin 214kDa	PVAPSGTALSTSSKLET*PPSK	P35658	214	8	4.46E+06
274	10.25	NUP35	251, 259, 265	nucleoporin 35kDa	SVMS*SDRCALSS*PSLAFT*PIIK	Q8NFH5	35	1	1.15E+05
275	4.73	NUP35	252, 259, 265	nucleoporin 35kDa	SVM#ESS*DRCALSS*PSLAFT*PIIK	Q8NFH5	35	3	9.99E+05
276	11.33	NUP35	258, 259, 265	nucleoporin 35kDa	CALS*S*PSLAFT*PIIK	Q8NFH5	35	7	2.44E+05
277	21.28	NUP35	259, 265	nucleoporin 35kDa	CALSS*PSLAFT*PIIK	Q8NFH5	35	10	3.92E+07
278	1.77	NUP35	265	nucleoporin 35kDa	CALSSPSLAFT*PIIK	Q8NFH5	35	7	6.92E+06
279	-1.03	RTN3	687	reticulon 3 isoform a	MTDFKTT*PPVLEVLHENESGGSEIK	Q95197	113	3	1.13E+05
280	1.46	SLC25A46	32, 35, 45	solute carrier family 25, member 46	S*FST*GSDLGHVWTT*PPDIPGSR	Q96AG3	46	1	5.04E+04
281	10.88	SLC25A46	32, 45	solute carrier family 25, member 46	S*FSTGSDLGHVWTT*PPDIPGSR	Q96AG3	46	2	4.19E+05
282	7.49	SLC25A46	45	solute carrier family 25, member 46	SFSTGSDLGHVWTT*PPDIPGSR	Q96AG3	46	2	3.12E+06
283	18.84	SLC04A1	15, 27	solute carrier organic anion transporter family member 4A1	PLHQLGDKPLTFPS#PNSAMENGLDHT*PPSR	Q96BD0	77	5	1.42E+05
284	-11.02	SLC04A1	27	solute carrier organic anion transporter family member 4A1	PLHQLGDKPLTFPS#PNSAMENGLDHT*PPSR	Q96BD0	77	5	3.82E+04
285	14.64	TMEM131	1490	RW1 protein	EIPTDVKPSSLELPYT*PPLESK	Q92545	205	3	4.59E+06
286	Transcriptional regulator								
287	54.61	ZNF289	331	ADP-ribosylation factor GTPase activating protein 2	SSVSHVLSSEMQIEQET*PVSAK	Q8N6H7	57	5	1.46E+06
288	-1.82	BNC2	543	basonuclin 2	SNLALTSPPGRPPM#GFTT*PPLDVLQNLPLSQLV FSLK	Q6ZN30	122	1	3.26E+04
289	5.60	CC2D1A	118	coiled-coil and C2 domain containing 1A	AS*ETPPPVAQPKPEAPHPGLETTLQER	Q6P1N0	104	1	7.43E+04
290	1.95	DATF1	1256, 1260	death inducer-obliterator 1 isoform a	KPSKYPLCSADAAVSTT*PPGS*PPPPPLPEPVLK	Q9BTC0	244	5	2.55E+06
291	-8.12	ERF	357	Ets2 repressor factor	CPLPPM#APET*PPVSSASSSSSSSSSPFK	P50548	59	3	1.64E+04
292	4.06	FOXK2	484	forkhead box C2	LGIENSTLGEOSVSGNASCOLPYRST*PPLY	Q99958	54	1	1.64E+06
293	21.70	FOXK2	648	forkhead box K2	ALSVDT*PPAAVR	Q01167	69	8	2.16E+06
294	1.69	FOXK1; FOXM1 iso2	627; 612	forkhead box M1 isoform 2	TPESWRLT*PPAK	Q08050; Q08050-2	84; 83	3	9.16E+05
295	3.37	GEMIN5	51	gemin 5	VGPGAGESPGT*PPFR	Q8TEQE	169	3	1.12E+06
296	-1.36	HEXIM2	29, 32	hexamethylene bis-acetamide inducible 2	TSGAPGS*PQT*PPER	Q96MH2	32	2	6.15E+05
297	-1.93	HEXIM2	29, 32, 46	hexamethylene bis-acetamide inducible 2	TSGAPGS*PQT*PPERHDSGSLPLT*PR	Q96MH2	32	2	6.29E+04
298	1.89	HIVEP3	2354	human immunodeficiency virus type I enhancer binding protein 3 b	APTNPESAT*PPLDR	Q9HCL7	260	1	6.98E+04
299	1.07	JAZF1	109, 113	JAZF zinc finger 1	HSSGSLT*PPVT*PPITPSSSF	Q86VZ6	27	3	4.28E+05
300	2.95	JAZF1	109, 113, 117	JAZF zinc finger 1	HSSGSLT*PPVT*PPIT*PSSSFR	Q86VZ6	27	1	3.39E+05
301	51.39	Jun	239, 243	jun oncogene	LOALKEEPQTVPEM#PGET*PPLS*PIDM#ESQER	P05412	36	2	2.40E+06
302	1.56	LIN9; LIN9 iso5	303; 453	lin-9 homolog	LHy*TPPLQSPIDNDPLLGQSPWR	Q5TKA1; Q8IWQ1	62; 60	1	2.36E+04
303	-1.25	LIN9; LIN9 iso5	304; 454	lin-9 homolog	LHYT*PPLQSPIDNDPLLGQSPWR	Q5TKA1; Q8IWQ1	62; 60	1	9.30E+04
304	8.90	LIN9; LIN9 iso5	304, 309; 454, 459	lin-9 homolog	LHYT*PPLQS*PIDNDPLLGQSPWR	Q5TKA1; Q8IWQ1	62; 60	1	7.32E+05
305	500.29	LIN9; LIN9 iso5	304, 309, 321; 454, 459, 471	lin-9 homolog	LHYT*PPLQS*PIIDNDPLLGQSPWR	Q5TKA1; Q8IWQ1	62; 60	3	6.28E+06

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

Table: PTMScan® Results, Phospho-T*PP Motif (T*PP), label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
306	70.71	PPARBP	1051, 1057	mediator complex subunit 1	SQT*PPGVAT*PPIPK	Q15648	168	3	1.02E+06
307	10.00	PPARBP	1207, 1219	mediator complex subunit 1	LAS*PMKVPVGTPTSS*K	Q15648	168	1	1.73E+05
308	8.29	CRSP7	296, 314, 322	mediator complex subunit 26	GS*VPSPPRQALDQVPS*PLPLAQS*TPPV	Q95402	65	1	1.46E+05
309	24.39	MKL1	305	megakaryoblastic leukemia 1 protein	SAGEALGSSGT*PPVR	Q969V6	99	3	3.59E+06
310	8.43	MLL	3053, 3067	myeloid/lymphoid or mixed-lineage leukemia protein	YVPNSTDS*PGSQISNAAVQTT*PPHLKATEK	Q03164	432	1	2.18E+05
311	-2.92	MLL	3067	myeloid/lymphoid or mixed-lineage leukemia protein	YVPNSTDSPGSPQISNAAVQTT*PPHLKATEK	Q03164	432	1	3.66E+04
312	1.85	MLL	337	myeloid/lymphoid or mixed-lineage leukemia protein	DKEGT*PPLTKEDK	Q03164	432	4	2.02E+05
313	-2.28	Myc; N-Myc	58; 58	myc proto-oncogene protein	KFELLPT*PPLSPS	P01106; P04198	49; 50	2	4.83E+04
314	1.16	Myc	58; 62	myc proto-oncogene protein	KFELLPT*PPLS*PSRR	P01106	49	9	1.66E+06
315	1.12	Myc; N-Myc	58, 64; 58, 64	myc proto-oncogene protein	KFELLPT*PPLSPS*R	P01106; P04198	49; 50	1	2.72E+05
316	4.01	N-CoR1	1670	nuclear receptor co-repressor 1	GIIDLTM#PPTILVPHPGGT*STPPM#DR	Q75376	270	5	1.98E+06
317	10.08	NOLC1	607, 610	nucleolar and coiled-body phosphoprotein 1	LQT*PNT*FPK	Q14978	74	1	3.54E+04
318	84.14	NONO	410, 428	non-POU domain containing, octamer-binding isoform 1	GAM#PPAPVPAGT*PAPPGPATM#PDGTLGLT*PPTTER	Q15233	54	2	1.17E+06
319	6.57	NONO	428	non-POU domain containing, octamer-binding isoform 1	GAM#PPAPVPAGT*PAPPGPATM#PDGTLGLT*PPTTER	Q15233	54	25	1.97E+07
320	5.44	NONO	450	non-POU domain containing, octamer-binding isoform 1	FGQAATM#EGIGAIGGT*PPAFNR	Q15233	54	18	7.09E+06
321	4.64	PPRC1	1229, 1233	peroxisome proliferator-activated receptor gamma, coactivator-related 1	LQAPELANVAGLT*PPAT*PPHQLWKPLAAVLLAK	Q5V67	178	1	1.20E+05
322	3.04	Ctip	315	retinoblastoma binding protein 8 isoform a	FSDSTSKT*PQEEELPTR	Q99708	102	1	6.37E+04
323	1.44	RBM14	206	RNA binding motif protein 14	QPT*PPFFGR	Q96PK6	69	2	4.59E+05
324	50.42	NFKB-p65	254	v-rel reticuloendotheliosis viral oncogene homolog A isoform 2	QVAIVFRT*PPYADPSLQAPVR	Q04206	60	1	3.98E+05
325	22.17	PSF	476	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	ERET*PPRFAHQHTEFEYSQR	P23246	76	8	2.49E+06
326	10.29	SIN3A	266, 272	transcriptional co-repressor Sin3A	VSKPSQLQAHTPASQQT*PPLPPY*ASPR	Q96ST3	145	2	2.44E+05
327	4.29	SIN3A	435	transcriptional co-repressor Sin3A	HPTGTT*PPVK	Q96ST3	145	2	3.95E+07
328	-1.99	SHARP	2460	spen homolog, transcriptional regulator	VHSIIESDPVT*PPSDPSIPIPTLPSVTAAK	Q96T58	402	1	2.45E+04
329	1.24	SQSTM1	272	sequestosome 1 isoform 2	LTPVS*PESSSTEK	Q13501	48	1	1.15E+05
330	3.91	SRCAP	2424, 2430	Snf2-related CBP activator protein	STT*TPPRCS*PAR	Q6ZRS2	344	1	6.80E+06
331	137.49	TAF1C	828, 834	TBP-associated factor 1C isoform 1	LPPQRT*PGCATT*PPHSQASSV	Q15572	95	7	8.14E+05
332	1.04	TAF1C	834	TBP-associated factor 1C isoform 1	DTPGCATT*PPHSQASSV	Q15572	95	5	1.50E+06
333	17.35	TCF12; TCF12 iso1	302, 305, 313; 302, 305, 313	transcription factor 12 isoform b	GST*SSS*PYVAASHT*PPINGSDSILGTR	Q86VM2; Q99081	76; 73	2	1.50E+05
334	11.86	TCF12; TCF12 iso1	305, 311; 305, 311	transcription factor 12 isoform b	GSTSSS*PYVAASHT*PPINGSDSILGTR	Q86VM2; Q99081	76; 73	1	9.23E+05
335	-2.12	TCF12; TCF12 iso1	313; 313	transcription factor 12 isoform b	GSTSSSPYVAASHT*PPINGSDSILGTR	Q86VM2; Q99081	76; 73	1	1.85E+05
336	13.64	53BP1	922	tumor protein p53 binding protein 1 isoform 2	EGDIIPPLTGAT*PPLIGHLK	Q12888	214	3	4.13E+06
337	34.30	TRIM25	91	tripartite motif-containing 25	EPPADVWT*PPAR	Q14258	71	19	2.76E+07
338	1.93	ZNF218	639	teashirt zinc finger homeobox 2	KSET*PPEAK	Q4VXM4	115	1	3.28E+04
339	6.58	WHSC2	178	Wolf-Hirschhorn syndrome candidate 2 protein	NALTLLAGPLT*PPVK	Q9H3P2	59	2	3.85E+06
340	14.24	WHSC2	364	Wolf-Hirschhorn syndrome candidate 2 protein	SSYIPSET*PPAPSSR	Q9H3P2	59	1	3.51E+05
341	27.24	RACK7; RACK7 iso6	746, 756, 760; 601, 611, 615	zinc finger, MYND-type containing 8 isoform b	QDVVGKT*PPSTTVGSHS*PPET*PVLTR	Q9ULU4; Q9ULU4-6	132; 113	1	1.29E+06
342	Translation								
343	9.74	eIF3C; eIF3CL	524; 525	eukaryotic translation initiation factor 3, subunit C	QLT*PPEGSSK	Q99613; NP_001093131	105; 105	1	8.74E+04
344	-1.56	eIF4G2	506	eukaryotic translation initiation factor 4 gamma, 2 isoform 2	LQIQITM#PPSAQPPRT*QTPPLGQTPQLGLK	P78344	102	1	1.74E+05
345	1.89	eIF4G2	508	eukaryotic translation initiation factor 4 gamma, 2 isoform 2	TQT*PPLGQTPQLGLK	P78344	102	10	8.43E+07
346	24.17	eIF4G2	508, 514	eukaryotic translation initiation factor 4 gamma, 2 isoform 2	TQT*PPLGQTPQLGLK	P78344	102	3	3.08E+06
347	-1.91	IARS	1047	isoleucine-tRNA synthetase	APLKPYPVS*PSDKVLIQEK	P41252	145	1	1.51E+04
348	Tumor suppressor or oncoprotein								
349	2.35	ALO17; ALO17 iso2	302; 302	hypothetical protein LOC57714	MKQPPAT*TPPFKHCQEAETK	Q9HCF4; Q9HCF4-2	175; 118	9	6.92E+04
350	5.66	ALO17; ALO17 iso2	303; 303	hypothetical protein LOC57714	MKQPPAT*PPFK	Q9HCF4; Q9HCF4-2	175; 118	47	9.93E+06
351	Ubiquitin conjugating system								
352	30.52	FBX46	338, 347	F-box protein 46	ADEASEGDS*PAPARPEDT*PPAPPPPPA	Q6PJ61	69	2	2.46E+05
353	11.63	FZR1	300	Fzr1 protein isoform 3	DIRT*PPLQSER	Q9UM11	55	1	4.07E+04
354	9.85	UBE2Q1; UBE2Q2	416; 369	ubiquitin-conjugating enzyme E2Q	NGWYT*PKKEDG	Q7Z7E8; Q8WVN8	46; 43	4	1.59E+07

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

Table: PTMScan® Results, Phospho-T*PP Motif (T*PP), label-free quantitation

Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
355	Unknown function								
356	19.91	BAT3; BAT3 iso4	350; 447	HLA-B associated transcript-3 isoform b	CNLAET*PPR	P46379; AAD18085	119; 130	1	2.22E+05
357	-1.34	C10orf47	146	hypothetical protein LOC254427	KQDAET*PPPPDPAPETLLAPPPLPSTPDPPIRR	Q86WR7	46	2	2.34E+05
358	3.91	C10orf47	146; 167	hypothetical protein LOC254427	KQDAET*PPPPDPAPETLLAPPPLPST*PDPPIRR	Q86WR7	46	1	1.29E+06
359	2.56	C14orf104	650	kintoun isoform 2	QSM#SLT*PPLIEVLQVTDNK	Q9NVR5	91	4	7.67E+05
360	4.47	C15orf41	114	hypothetical protein LOC84529 isoform 1	FLQEHET*PPSK	Q9Y2V0	32	2	5.18E+05
361	2.67	C15orf42	969	leucine-rich repeat kinase 1	SVAET*PVHK	Q7Z2Z1	211	1	1.51E+06
362	5.44	C1orf103; C1orf103 iso3	732; 702	receptor-interacting factor 1 isoform 2	NYTEDIFPVT*PPELEETIRDEK	Q5T3J3; AA043631	85; 81	5	5.40E+06
363	2.65	TTDN1	10	chromosome 7 open reading frame 11	QNFPRPT*PPYPGGGGWGGSSSF	Q8TAP9	19	1	1.45E+06
364	39.17	TTDN1	45; 51	chromosome 7 open reading frame 11	DGy*GSPHHT*PPYGPR	Q8TAP9	19	2	3.93E+06
365	20.23	TTDN1	47; 51	chromosome 7 open reading frame 11	DGYGS*PHHT*PPYGPR	Q8TAP9	19	1	5.42E+05
366	-1.04	TTDN1	51	chromosome 7 open reading frame 11	DGYGSPHHT*PPYGPR	Q8TAP9	19	2	4.89E+05
367	8.15	CASKIN2	939	casein-interacting protein 2 isoform b	TLSEAPGSEPPGPPAPAGPASDTEEEEGPEGT*PPSR	Q8WXE0	127	1	1.55E+05
368	15.00	CDR2	417; 418	cerebellar degeneration-related protein 2	SVNPEVVSPT*T*PPEYK	Q01850	52	1	1.48E+05
369	1.26	CDR2	418	cerebellar degeneration-related protein 2	SVNPEVVSPT*PPEYK	Q01850	52	1	3.10E+04
370	2.95	CLSTN3	951	calystenien 3	IET*PPHY	Q9BQT9	106	1	2.91E+05
371	11.91	CPNE8	554	copine VIII	GIKPSPAPPYPT*PPTHVLQTOI	Q86Y08	63	2	1.63E+06
372	-1.55	CTAGE5	590; 592; 594	CTAGE family, member 5 isoform 1	LTDPHRAPS*DT*GS*LSPWQDQRR	Q15320	91	2	7.17E+04
373	-1.35	CTAGE5	590; 594; 596	CTAGE family, member 5 isoform 1	LTDPHRAPS*DT*GS*LS*PPWQDQRR	Q15320	91	2	7.47E+04
374	5.32	DENND1B	485	DENN/MADD domain containing 1B isoform 1	HKENEEDYGTCSVVQYT*PVYK	Q6P3S1-5	87	2	2.52E+04
375	-1.05	RAB6I1	1079; 1085	RAB6 interacting protein 1	ILVGLLTSQPEVDERPCRT*PPLQDS*PSVIR	Q6IQ26	147	3	8.27E+05
376	1.05	FBXO42	539; 552	F-box protein 42	HPPEQTNGVHT*PPHVASALAGAVS*PGALR	Q6P3S6	78	1	6.68E+04
377	-1.82	GPBP1L1	301	GC-rich promoter binding protein 1-like 1	ESPSSTT*PPIESSSR	Q9HC44	52	2	8.30E+04
378	2.33	GPR137	356	G protein-coupled receptor 137	CQDQAATTVST*PPHR	Q96N19	46	1	2.54E+04
379	1.05	HOMEZ	427	homeodomain leucine zipper protein	AET*PPLPIPPPPDIQPLER	Q8IX15	59	10	1.11E+06
380	3.55	KIAA0467	1535	hypothetical protein LOC23334	ASTFPPAPVPGPEVT*PPSK	Q5T011	278	1	8.38E+04
381	2.71	KIAA0649	1024	1A6/DRIM (down-regulated in metastasis) interacting protein	DAGAQRDT*PPWSDFAHQS	Q5T8A7	127	2	2.71E+05
382	7.49	KIAA0802; KIAA0802 iso4	1403; 1408; 1412; 418; 423; 427	hypothetical protein LOC23255	GLPSTSS*KEDVT*PPLS*PDDLK	Q9Y4B5; Q9Y4B5-4	209; 109	1	2.54E+05
383	-4.21	KIAA0802; KIAA0802 iso4	1408; 423	hypothetical protein LOC23255	GLPSTSSKEDVT*PPLSPDDLK	Q9Y4B5; Q9Y4B5-4	209; 109	6	4.44E+05
384	2.55	KIAA0802; KIAA0802 iso4	1408; 1412; 423; 427	hypothetical protein LOC23255	GLPSTSSKEDVT*PPLS*PDDLK	Q9Y4B5; Q9Y4B5-4	209; 109	15	1.70E+07
385	5.53	KIAA1211	971; 978	hypothetical protein LOC57482	MPLAQKPALAPKPTST*PPASPLS*K	Q6ZU35	137	1	1.85E+05
386	-1.48	KLF2	173; 177	Kruppel-like factor	GPGGRRPPPPDTP*PPLS*PDGPAR	Q9Y5W3	37	1	5.38E+04
387	1.34	LARP2	454	La ribonucleoprotein domain family member 2 isoform 1	ILVITQT*PPYVK	Q659C4	105	24	1.36E+06
388	22.55	LSM12	143	LSM12 homolog	EEVIT*PPYQVENCK	Q96NL5	22	1	2.20E+05
389	3.71	LSM12	73	LSM12 homolog	NLQYVSEVEINDRT*ETPPPLASLNVS	Q96NL5	22	1	1.52E+05
390	2.32	LSM12	75	LSM12 homolog	NLQYVSEVEINDRT*ETPPPLASLNVS	Q96NL5	22	3	6.75E+05
391	12.24	MON2	1188	MON2 homolog	DSDKPET*PPVNVVPPVLIPIGISM*SRPFV	Q7Z3U7	190	5	9.93E+05
392	-1.56	MORC4	621	zinc finger, CW type with coiled-coil domain 2 isoform b	SSSERST*PPYLFPEYEAASK	Q8TE76	106	1	3.95E+05
393	3.48	MSL1	393; 402	hampin	SS*VDTPPRLST*PQK	Q69Z03	67	1	1.41E+05
394	2.66	MSL1	396	hampin	SSVDT*PPR	Q69Z03	67	1	1.13E+06
395	37.46	MSL1	396; 401; 409	hampin	SSVDT*PPRLS*TPQKGPST*HPK	Q69Z03	67	1	2.31E+05
396	1.80	MSL1	396; 402	hampin	SSVDT*PPRLS*TPQKGPST*HPK	Q69Z03	67	3	1.59E+06
397	2.22	MSL1	401; 402	hampin	SSVDTPPRLS*TPQKGPST*HPK	Q69Z03	67	2	2.43E+06
398	-1.85	MGC3731	124; 134	nucleolar protein 12	LLGLT*PPEGGAGDRS*EEEAASSTKPTK	Q9UGY1	25	1	5.54E+04
399	4.21	OSBP1	356	oxysterol-binding protein-like protein 6 isoform a	LHSSNPNLCADIEFQT*PPSHLTDPLESSTDYTK	Q9BZF3	106	1	1.71E+05
400	2.63	PCNXL3	127; 129	pecanex-like 3	KVS*ST*PPVY	Q9H6A9	222	1	1.62E+05
401	5.69	QSER1	1113	glutamine and serine rich 1	GTDIYLPY*TPPSSCHDGYQHQEK	Q2KHR3	190	1	5.94E+05
402	7.36	QSER1	1114	glutamine and serine rich 1	GTDIYLPY*TPPSSCHDGYQHQEK	Q2KHR3	190	1	1.03E+06
403	73.89	RAB3GAP1	908	RAB3 GTPase-activating protein	AAAMT*PPEELKR	Q15042	111	7	7.83E+05
404	7.19	RAD23B	155; 159	UV excision repair protein RAD23 homolog B	QEKPAEKPAET*PVAT*SPTADTSTGDSSR	P54727	43	1	4.04E+05
405	2.16	RGPD5; RGPD6; RGPD7; RGPD8	796; 799; 796; 799; 799; 796; 799	RANBP2-like and GRIP domain containing 5 isoform 1	SYKYS*PET*PPRWTEDR	Q99666; NP_001116835; Q9H0B2; O14715	199; 199; 103; 199	1	8.49E+05

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Study design: adenocarcinoma (HeLa) cell line; Trypsin digest; Antibody: Phospho-T*PP Motif (T*PP) XP™, PTMScan® Kit #1996, #5567

Treatments: Untreated, nocodazole treated

Index	Fold-Change (Nocodazole/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (nocodazole treated)
406	16.27	SECISBP2L	914	SECIS binding protein 2-like	LPFDY*PPIGK	Q93073	122	7	3.19E+06
407	2.91	SFRS16	92	splicing factor, arginine/serine-rich 16	AHLDHIPDY*TPLLTTISPEQESDER	Q8N2M8	77	1	4.24E+04
408	4.91	SFRS16	93	splicing factor, arginine/serine-rich 16	AHLDHIPDY*TPLLTTISPEQESDER	Q8N2M8	77	1	1.61E+05
409	9.01	SFRS16	93, 101	splicing factor, arginine/serine-rich 16	AHLDHIPDY*TPLLTTIS*PEQESDERK	Q8N2M8	77	1	1.54E+05
410	2.22	SIPA1L2; SIPA1L2 iso2	1520; 1312	signal-induced proliferation-associated 1 like 2	SSVLDQALPNDILFS*TPPYHSTLPPR	Q9P2F8; BAA92627	190; 168	2	4.24E+05
411	49.77	SNAPC2	292	small nuclear RNA activating complex, polypeptide 2, 45kDa	APEET*PPATEK	Q13487	36	3	3.92E+05
412	3.86	SNTB1	205, 214, 219	basic beta 1 syntrophin	KGS*PVSEIGWET*PPPE*PR	Q13884	58	1	1.10E+05
413	2.42	SNTB1	214, 219	basic beta 1 syntrophin	KGSPVSEIGWET*PPPE*PR	Q13884	58	7	8.50E+05
414	8.21	SNX8	452, 456	sorting nexin 8	LSCLFAGPHSTLT*PPCS*PPEDGLCPH	Q9Y5X2	53	2	1.75E+06
415	24.32	ARS2	540, 544	arsenate resistance protein 2 isoform c	TQLWAS*EPGT*PPLPTSLPSQNPILK	Q9BXP5	101	2	2.18E+06
416	2.40	ARS2	544	arsenate resistance protein 2 isoform c	TQLWASEPGT*PPLPTSLPSQNPILK	Q9BXP5	101	5	1.33E+08
417	23.26	TMUB1	71	transmembrane and ubiquitin-like domain containing 1 isoform 2	GEAPGAET*PSLR	Q9BVT8	26	1	1.87E+05
418	21.21	TNS4	168, 173	tensin 4	CHDGPQHCS*SPSVT*PPFGSL	NP_116254	77	1	2.75E+06
419	11.96	TNS4	173	tensin 4	CHDGPQHCS*SPSVT*PPFGSL	NP_116254	77	3	2.90E+06
420	125.44	Tsc22d4	225, 229	TSC22 domain family, member 4	VEAAGGS*GART*PPLS	Q9Y3Q8	41	7	5.09E+06
421	225.53	Tsc22d4	225, 229, 233	TSC22 domain family, member 4	VEAAGGS*GART*PPLS*R	Q9Y3Q8	41	6	2.18E+06
422	-2.66	Tsc22d4	229	TSC22 domain family, member 4	VEAAGSGSGART*PPLS	Q9Y3Q8	41	9	8.15E+06
423	1.32	TWISTNB	316, 322	TWIST neighbor	KHS*EEAEFT*PPLK	Q3B726	37	4	2.67E+05
424	12.54	TWISTNB	316, 322, 328	TWIST neighbor	KHS*EEAEFT*PPLKCS*PK	Q3B726	37	12	1.66E+07
425	-9.00	TWISTNB	322	TWIST neighbor	KHSEAEFT*PPLK	Q3B726	37	7	7.71E+04
426	1.86	TWISTNB	322, 328	TWIST neighbor	HSEAEFT*PPLKCS*PK	Q3B726	37	20	7.53E+06
427	10.02	p37 adaptor	56, 59	UBX domain protein 2B	ATVFKS*PRT*PPQR	Q14CS0	37	2	6.16E+05
428	24.26	UHRF1BP1L	1066, 1070	UHRF1 (ICBP90) binding protein 1-like isoform b	AEDLLPEAASLSENLDIS*KEET*PPVR	AQJNW5	164	3	9.41E+05
429	109.92	WDR24	711	WD repeat domain 24	HEIVDT*PPGPEHLQDK	Q96S15	102	3	1.53E+06
430	2.86	WDR47	522	WD repeat domain 47 isoform 1	GNGSNGSSVTSFTT*PPQDSSQR	Q94967	102	1	1.98E+05
431	-1.09	WWC2	533	WW and C2 domain containing 2	SPSQPGQSGLCGVAAAATGHT*PPLAEAPK	Q6AWC2	134	4	3.36E+05
432	37.30	ZBTB20	685, 690, 695	zinc finger and BTB domain containing 20	HVALHS*ASNGT*PPAGT*PPGAR	Q9HC78	81	1	8.72E+04
433	19.77	ZBTB20	690, 695	zinc finger and BTB domain containing 20	HVALHSASNGT*PPAGT*PPGAR	Q9HC78	81	2	1.20E+05
434	19.38	ZBTB9	376	zinc finger and BTB domain containing 9	LGTT*PPADGK	Q96C00	51	1	3.81E+05
435	-1.14	ZC3H13; ZC3H13 iso2	364; 364	zinc finger CCCH-type containing 13	TLT*PPLR	Q5T200; Q5T200-2	197; 185	4	3.30E+07
436	18.62	ZCCHC8	479, 485	zinc finger, CCH domain containing 8	GT*PPPVFT*PPLPK	Q6NZY4	79	8	1.75E+07
437	2.47	ZNF428	108	zinc finger protein 428	SPLGEAPPGT*PPCR	Q96B54	20	10	5.65E+06
438	155.12	ZNF428	99, 108	zinc finger protein 428	AAQPPAQPCLCGRS*PLGEAPPGT*PPCR	Q96B54	20	11	4.21E+06
439	Vesicle protein								
440	4.42	GORASP2	415	golgi reassembly stacking protein 2	ADAASLTVDVT*PPTAK	Q9H8Y8	47	19	9.40E+05