

TABLE: pTPE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTPE Motif; CST #C32G12

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
1		Adaptor/scaffold							
2	4.1	AHNAK	3366	AHNAK nucleoprotein isoform 1	VQT*PEVDVK^	Q09666	629	1	43,541,020
3	1.1	AHNAK	\$490	AHNAK nucleoprotein isoform 1	VK^T*PEMIQK^PK^	Q09666	629	50	63,432,784
4	8.4	AHNAK	\$4993, \$5009	AHNAK nucleoprotein isoform 1	ADIK^S*PSLDVTVPEALNLET*PEISVGGK^	Q09666	629	1	12,335,565
5	3.7	AKAP12	1115	A kinase (PRKA) anchor protein 12 isoform 1	VVGQT*PESFEKAPQVTSIESSELVTTCAETLAGVK	Q02952	191	1	953,282
6	2.4	AKAP12	1116	A kinase (PRKA) anchor protein 12 isoform 1	VVGQT*PESFEK^	Q02952	191	2	8,980,917
8	3.5	AKAP13	1149	A-kinase anchor protein 13 isoform 1	AVTDPQGVGT*PEM#PLDWEK^	Q12802	308	1	1,196,608
9	2.1	AKAP13	813	A-kinase anchor protein 13 isoform 1	GT*ATPELHATDYR	Q12802	308	1	594,646
10	2.1	AKAP13	\$815	A-kinase anchor protein 13 isoform 1	GTAT*PELHATDYR^	Q12802	308	1	1,251,329
11	1.6	BCAR3	130	breast cancer antiestrogen resistance 3	HIMDR^T*PEK^	Q75815	93	5	321,058
12	1.5	SAPAP4; SAPAP4 iso2	\$912, \$915	disks large-associated protein 4 isoform c	ANSWQLVET*PEKR	Q9Y2H0; Q9Y2H0-2	108; 108	3	55,618,280
13	-1.3	RAMP	656	denticleless homolog	ENSS*PENKNWLLAMAAK	Q9NZJ0	79	1	1,988,059
14	-1.5	EPB41L1; EPB41L1 iso2	\$541, \$546, \$550, \$467, \$472, \$476	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSS*PASPS*PKG*PEKANER	Q9H4G0; Q9H4G0-2	99; 88	1	253,717
15	-1.6	EPB41L1; EPB41L1 iso2	\$546, \$550, \$472, \$476	erythrocyte membrane protein band 4.1-like 1 isoform a	RLPSSPASPS*PKG*PEKANER	Q9H4G0; Q9H4G0-2	99; 88	5	10,401,989
16	-1.0	INADL	\$522	InaD-like	VPDS*PENELK	Q8NI35	196	1	1,596,299
18	-1.5	IRS-2	\$518	insulin receptor substrate 2	S*NTPESIAETPPAR	Q9Y4H2	137	1	10,651,498
19	1.7	IRS-2	\$518, \$527	insulin receptor substrate 2	S*NTPESIAET*PPAR^	Q9Y4H2	137	1	5,382,479
20	-1.5	IRS-2	\$520	insulin receptor substrate 2	SNT*PESIAETPPAR^	Q9Y4H2	137	1	6,912,677
21	1.7	IRS-2	\$520, \$527	insulin receptor substrate 2	SNT*PESIAET*PPAR	Q9Y4H2	137	1	3,102,056
23	4.0	RAI14	\$512	retinoic acid induced 14	LGLVS*PESM#DNYSHFHELK^	Q9P0K7	110	1	2,855,073
24	-1.4	RanBP2	1393, \$1400	RAN binding protein 2	ELVGPPLAET*VFTPKTS*PENVQDR	P49792	358	1	26,936,950
25	-1.4	RanBP2	\$1396, \$1399	RAN binding protein 2	ELVGPPLAETVFT*PKT*SPENVQDR	P49792	358	2	2,005,717
26	-1.4	RanBP2	\$1396, \$1400	RAN binding protein 2	ELVGPPLAETVFT*PKTS*PENVQDR	P49792	358	2	26,936,950
27	1.1	RanBP2	\$1399	RAN binding protein 2	ELVGPPLAETVFTPKT*SPENVQDR	P49792	358	2	3,814,553
29	1.3	RanBP2	\$2613	RAN binding protein 2	NLFASFTEESSINVTFTK*PEK	P49792	358	2	4,867,460
30	1.9	SMARCA1	71	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1 isoform a	TESSVPET*PDNER^	Q9H4L7	117	1	77,028
31	-1.5	WAC	62, 64	WW domain-containing adapter with a coiled-coil region isoform 1	R^S*DS*PENK^YSDSTGHSK^	Q9BTA9	71	1	44,256
32	-1.3	WAC	64	WW domain-containing adapter with a coiled-coil region isoform 1	SDS*PENKYSYSTGHSK	Q9BTA9	71	12	435,527
33	1.1	WDR62	\$1048, \$1053	WD repeat domain 62 isoform 1	FATSLPHFGCAGTPEDELSLPEGSPVSS*SLPQT*PEQEK	Q43379	166	1	8,643,037
34	1.1	WDR62	\$1053	WD repeat domain 62 isoform 1	FATSLPHFGCAGTPEDELSLPEGSPVSS*SLPQT*PEQEK	Q43379	166	1	942,202
35		Apoptosis							
36	4.3	PDCD8	\$105	programmed cell death 8 isoform 4	ISGLGLT*PEQK^	Q95831	67	1	5,304,667
37	3.3	p400	\$2814	E1A binding protein p400	AVGKLT*PEHLIK	Q96L91	344	1	2,901,501
38	-1.1	DBC-1	484	p30 DBC protein	RNAET*PEATTQETDLDLPEAPPPLEPAVIAR	Q8N163	103	2	460,867
39	1.5	ARC	114	nucleolar protein 3	SYDPPCPGHWT*PEAPGSGTTCPLPR^	Q60936-2	23	2	2,521,183
40	5.7	SART1	\$392	squamous cell carcinoma antigen recognized by T cells 1	LASEYLT*PEEM#VTFK^K^	Q43290	90	4	6,947,916
41	1.6	TFPT	\$207	TCF3 (E2A) fusion partner (in childhood Leukemia)	AGNALT*PELAPVQIK	POC1Z6	28	1	5,798,343
42		Cell cycle regulation							
43	3.8	AF15q14	438	cancer susceptibility candidate 5 isoform 2	ILAMT*PESISNPSIQGCK^	Q8NG31	265	1	907,758
44	4.7	CENPF	\$3045	centromere protein F	GTPAT*PESFSKK	P49454	368	2	5,576,128
45	1.2	CENPH	68	centromere protein H	SM#VDASEEK^T*PEQMKEK^	Q9H3R5	28	2	4,725,348
46	2.1	KAB1	1376	centrosomal protein 170kDa isoform beta	K^IPLVHVK^T*PEGNNGR^	Q5S79	175	1	1,513,473
47	5.8	CLASP1; CLASP1 iso3	\$646, 655; \$646, 655	CLIP-associated protein 1	R^QS*SGSATNVAS*TPDNR^	Q7Z460; Q7Z460-3	169; 165	6	321,119
48	5.8	CLASP1; CLASP1 iso3	\$646, \$656; \$646, \$656	CLIP-associated protein 1	R^QS*SGSATNVAS*TPDNR^	Q7Z460; Q7Z460-3	169; 165	8	278,788

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

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Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
49	17.1	CLASP1; CLASP1 iso3	\$647, \$656; \$647, \$656	CLIP-associating protein 1	R*QSS*GSATNVA\$T*PDNR^A	Q7Z460; Q7Z460-3	169; 165	1	88,824
50	4.5	CLASP1; CLASP1 iso3	\$649, \$656; \$649, \$656	CLIP-associating protein 1	RQSSGS*ATNVA\$T*PDNR	Q7Z460; Q7Z460-3	169; 165	1	33,474
51	5.8	CLASP1; CLASP1 iso3	\$651, \$656; \$651, \$656	CLIP-associating protein 1	RQSSGSAT*NVAST*PDNR	Q7Z460; Q7Z460-3	169; 165	2	55,029
52	1.9	CLASP1; CLASP1 iso3	\$656; \$656	CLIP-associating protein 1	QSSGSATNVA\$T*PDNR^A	Q7Z460; Q7Z460-3	169; 165	7	30,336
53	1.4	DLG7	\$662	discs large homolog 7	NEMGIPQQTTS*PENAGPQNTK^A	Q15398	95	4	2,712,251
54	3.2	MCPH1	120	microcephalin	DFNFK^A*PENDK^AR^A	Q8NEMO	93	1	1,389,003
55	1.5	MDC1	\$1198	mediator of DNA damage checkpoint 1	SSVKT*PETVVPTALELQ\$PSTSDR\$PVTSEPT\$SQATR	Q14676	227	1	774,406
56	3.7	MDC1	\$1400, \$1403	mediator of DNA damage checkpoint 1	SS*GK^A*PETLVPTAPK^A	Q14676	227	1	1,581,526
57	1.2	MDC1	\$1485	mediator of DNA damage checkpoint 1	SSVKT*PETVVPTAPELQASASTDQ\$PVTSEPT\$SR	Q14676	227	1	1,001,263
58	2.2	MDC1	\$1567	mediator of DNA damage checkpoint 1	SSVKT*PESIVPIAPELQ\$PSTSR	Q14676	227	2	2,750,536
60	-2.9	MDC1	\$1671	mediator of DNA damage checkpoint 1	TPKPVEPAASDL\$EPTDQ\$VST*PEAIAQGGQ\$SK	Q14676	227	1	4,753,203
61	2.0	NCAPH	\$605	non-SMC condensin I complex, subunit H	TAQQNGDT*PEA\$GLDITTYGESNLVAEPQK^AVNK^A	Q15003	83	2	907,932
62	-1.8	Kizuna	283	non-protein coding RNA 153	ERLS*PENR	Q2M2Z5	75	2	44,335
63	1.8	NuMA-1	\$1991, \$2000	nuclear mitotic apparatus protein 1	R^AVS*LPHQGGP\$T*PESK^A	Q14980	238	7	12,066,761
64	-1.1	NuMA-1	\$2000	nuclear mitotic apparatus protein 1	VSLPHQGGP\$T*PESK	Q14980	238	10	34,672,068
65	-1.7	PCM-1	\$65	pericentriolar material 1	VTNDIS*PESSPGVGR^A	Q15154	229	2	14,283,209
Chaperone									
66		DNAJB1							
67	5.5	DNAJB1	307	DnaJ (Hsp40) homolog, subfamily B, member 1	K^AVPGEGLPLPK^A*PEK^AR^A	P25685	38	1	1,938,140
Chromatin, DNA-binding, DNA repair or DNA replication protein									
68									
69	2.0	BAZ1A	\$1363, \$1367, \$1371	bromodomain adjacent to zinc finger domain, 1A isoform a	S^ANNT*PENS*PNFPNFR^A	Q9NRL2	179	1	507,663
70	-2.5	CHD-3	\$1591, 1599, \$1608	chromodomain helicase DNA binding protein 3 isoform 3	AS*SPTK^ATSPT*PEASATNS*PCTSK^APATPAPSEK^A	Q12873	233	1	525,634
71	-2.2	CHD-3	\$1591, 1599, 1611	chromodomain helicase DNA binding protein 3 isoform 3	AS*SPTK^ATSPT*PEASATNSPCT*SK^APATPAPSEK^AGEGIR^A	Q12873	233	1	550,067
72	-2.1	CHD-3	1592, \$1596, 1611	chromodomain helicase DNA binding protein 3 isoform 3	ASS*PTKT^SPTTPEASATNSPCT*SKPATPAPSEK	Q12873	233	1	2,045,145
73	-2.5	CHD-3	1592, 1599, \$1608	chromodomain helicase DNA binding protein 3 isoform 3	ASS*PTKTSPT*PEASATNS*PCTSKPATPAPSEK	Q12873	233	1	1,473,745
74	-1.4	CHD-3	1594, \$1600	chromodomain helicase DNA binding protein 3 isoform 3	ASSPT^KTSPTT*PEASATNSPCT\$K\$PATPAPSEK\$GEGIR	Q12873	233	1	8,098,147
75	-1.1	CHD-3	\$1600, 1604, 1611	chromodomain helicase DNA binding protein 3 isoform 3	TSPTT*PEAS^ATNSPCT*SK^APATPAPSEK^A	Q12873	233	1	423,768
76	-1.6	CHD-3	\$1600, 1606	chromodomain helicase DNA binding protein 3 isoform 3	TSPTT*PEASAT^NSPCT\$K\$PATPAPSEK\$GEGIR	Q12873	233	1	424,001
77	-2.4	CHD-3	\$1600, \$1608	chromodomain helicase DNA binding protein 3 isoform 3	TSPTT*PEASATNS*PCT\$K\$PATPAPSEK	Q12873	233	1	1,880,340
78	-1.1	CHD-3	\$1600, \$1608, \$1616	chromodomain helicase DNA binding protein 3 isoform 3	TSPTT*PEASATNS*PCT\$K\$PATPAPSEK	Q12873	233	1	552,363
79	-1.0	CHD-9	\$550	chromodomain helicase DNA binding protein 9	VMS*PENFP\$TASVEGK^A	Q3L8U1	326	2	1,299,864
80	1.0	HIVEP1	\$537	human immunodeficiency virus type 1 enhancer binding protein 1	SSFTPSS*PENVIDG\$FLLQDR	P15822	297	3	3,246,434
81	2.1	NIPBL; NIPBL iso2	588, 599; 588, 599	delangin isoform B	QCNDAPVSVLQEDIVGS^LK^ASTPENHPET*PK^AK^KA	Q6KC79; Q6KC79-2	316; 304	1	15,454,773
82	2.1	NIPBL; NIPBL iso2	591, 592; 591, 592	delangin isoform B	QCNDAPVSVLQEDIVGS\$K\$S^*PENHPETPKKK	Q6KC79; Q6KC79-2	316; 304	1	1,387,242
83	1.4	NIPBL; NIPBL iso2	591, 599; 591, 599	delangin isoform B	QCNDAPVSVLQEDIVGS\$K\$S^*TPENHPET*PK^A	Q6KC79; Q6KC79-2	316; 304	1	9,126,285
84	4.3	NSBP1	\$20, \$24, \$31	nucleosomal binding protein 1	S^AR^LS^AMLV\$PVT*PEVK^APK^A	P82970	32	1	6,754,920
85	6.6	NSBP1	\$24, \$31	nucleosomal binding protein 1	LS^AM^L\$V\$PVT*PEVK^APK^A	P82970	32	1	9,206,122
86	2.3	NSBP1	\$31	nucleosomal binding protein 1	LSAM^L\$V\$PVT*PEVK^APK^A	P82970	32	11	67,110,616
87	-1.6	APRIN	\$1394	PDS5, regulator of cohesion maintenance, homolog B	AES*PESSAIE\$TQ\$T\$PQK	Q9NTI5	168	1	813,856
88	1.5	APRIN	\$1394, \$1406	PDS5, regulator of cohesion maintenance, homolog B	AES*PESSAIE\$TQ\$T*PQK^A	Q9NTI5	168	1	345,114
89	-1.3	POLA2	\$127	polymerase (DNA directed), alpha 2 (70kD subunit)	AIST*PETPLTK	Q14181	66	1	949,188
90	1.3	PRR12	738	proline rich 12	GGET*PEGLAT\$SVHYGAGAK^A	Q9ULL5	211	3	2,945,868
91	1.0	RAD23A	\$133	UV excision repair protein RAD23 homolog A	EDK^SPSEESAP\$TTS*PESVGS\$V\$PSSGSSGR^A	P54725	40	1	456,505
92	1.3	RECQL	190	RecQ protein-like	LIYVT*PEK^IAK^A	P46063	73	1	1,786,344
93	-2.1	XRCC1	440, \$453	X-ray repair cross complementing protein 1	TKPT^QAAGP\$SSPQK\$PPT*PEETK	P18887	70	1	1,060,475
94	-2.1	XRCC1	\$447, \$453	X-ray repair cross complementing protein 1	TK^PTQAAGP\$SS*PQK^APPT*PEETK^A	P18887	70	1	778,008

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Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
95	-1.1	Ku70	454	ATP-dependent DNA helicase II, 70 kDa subunit	IMAT*PEQVVGK	P12956	70	7	22,410,646
97	4.2	ZAP	§393	zinc finger antiviral protein isoform 1	SSLGSLQQT*PEAVTTR^A	Q7Z2W4	101	3	15,577,585
98	2.3	ZNF262	217	zinc finger protein 262	AANQVEETLHTHLPQT*PETNFR^A	Q5VZL5	173	1	3,019,759
99	-1.3	ZNF185; ZNF185 iso1	446, §453; 214, §221	zinc finger protein 185	GGQGDPAVPAQPADPSP*TPERQSS*PSGSEQLVR	NP_009081; O15231	74; 49	2	2,712,251
100	-1.6	ZNF185; ZNF185 iso1	§447; §215	zinc finger protein 185	GGQGDPAVPAQPADPST*PER	NP_009081; O15231	74; 49	3	7,446,691
101	-1.2	ZNF185; ZNF185 iso1	513, 519; 281, 287	zinc finger protein 185	GGQGDPAVPTQPADPST*PEQQNS*PSGSEQFVR	NP_009081; O15231	74; 49	1	5,763,421
102	Cytoskeletal protein								
103	1.2	CCDC6	§254	coiled-coil domain containing 6	DISMEIDS*PENM#MR	Q16204	66	1	936,130
104	3.7	BPAG1 iso7	1755	dystonin isoform 1e precursor	CHCGEPEHEET*PENR^A	Q8WXX8	345	1	51,931
105	-1.1	DAL-1; DAL-1 iso2	§469; §487	erythrocyte membrane protein band 4.1-like 3	GISQTNLITVT*PEK^A^A	Q9Y2J2; Q9Y2J2-2	121; 97	3	1,711,359
106	4.8	FLNB	§1505	filamin B, beta (actin binding protein 278)	YADEEIPR^A^S*PFK^A	Q75369	278	2	8,150,718
107	4.0	HPCA; HPCAL1; NCALD	144; 143; 144	hippocalcin	MPEDEST*PEK^R^A	P84074; P37235; P61601	22; 22; 22	1	219,964
108	2.8	KIF18A	§706	kinesin family member 18A	ELQPIVVT*PEDCR^A^A	Q8NI77	102	1	887,038
109	-1.3	KIF1B	1650	kinesin family member 1B isoform b	SNSLDQK^A^T*PEANSR^A	Q60333	204	3	324,616
110	1.9	KIF1B	1650, 1655	kinesin family member 1B isoform b	SNSLDQK^A^T*PEANS^R^A	Q60333	204	2	52,555
111	3.0	Lasp-1	§104	LIM and SH3 protein 1	GFVSWADT*PELQR^A	Q14847	30	17	128,877,800
112	4.4	Lasp-1	§68	LIM and SH3 protein 1	QSFTMVADT*PENLR^A	Q14847	30	9	105,487,152
113	2.0	MAP1B	§1932	microtubule-associated protein 1B	TTK^A^T*PEDGDYSYEIEK^A	P46821	271	2	14,929,772
114	8.6	MAP1B	§1932, §1939	microtubule-associated protein 1B	TTK^A^T*PEDGDYS*YEIEK^A	P46821	271	3	12,407,489
115	1.3	MAP1B	§1947	microtubule-associated protein 1B	TT^R^A^TPEEGGYSYDISEK^A	P46821	271	1	34,565,500
116	1.3	MAP1B	§1949	microtubule-associated protein 1B	TTRT*PEEGGYSYDISEK	P46821	271	4	25,994,110
117	6.7	MAP1B	§1949, 1960	microtubule-associated protein 1B	TTT^R^A^TPEEGGYSYDIS*EK^A	P46821	271	1	850,973
118	4.2	MAP1B	§2305	microtubule-associated protein 1B	AAK^A^PTTT*PEVK^A	P46821	271	5	175,186
119	1.2	MAP1B	§908	microtubule-associated protein 1B	GPAESPDEGITTEGECEQT*PEELEPVEK^A	P46821	271	1	654,266
120	1.4	nestin; nestin iso2	§338; §337	nestin	LELQFPR^A^T*PEGR^A	P48681; CAA46780	177; 177	2	6,316,560
121	-1.7	slingshot 2	795	slingshot 2	AQT*PENK^A^PGHM#EQDEDSCTAQPELAK^A	Q76176	158	5	5,574,348
122	1.8	utrophin	§1405	utrophin	SQPLTS*PESR	P46939	395	1	1,369,187
123	1.5	PSRC2; PSRC2 iso5	§766; §775	proline/serine-rich coiled-coil 2	SEK^A^ENDPLR^A^T*PEALPEEK^A	O60293; BAA25472	226; 218	1	677,146
124	Endoplasmic reticulum or golgi								
125	4.0	DSCR2	31	Down syndrome critical region protein 2 isoform a	AGTEDEEEEEER^A^R^A^ET*PEDR^A	Q95456	33	1	184,374
126	Enzyme, misc.								
127	1.3	ACSL3; ACSL4	§688; §679	acyl-CoA synthetase long-chain family member 3	LSPEPWT*PETGLVTDFAK^A	Q95573; Q60488	80; 79	2	3,286,431
128	-1.8	aldolase A	9	aldolase A	PYQYPALT*PEQK	P04075	39	4	22,937,754
129	1.0	BRIP1	§918, §930	BRCA1 interacting protein C-terminal helicase 1	YST*PPYLLEAASHLS*PENFVEDEAK	Q9BX63	141	1	2,243,695
130	-1.4	CHD-1	§1698	chromodomain helicase DNA binding protein 1	SPFEHVSVEHKS*TPHEWTSSR	Q14646	197	2	671,283
131	-1.6	CHD-1	§1699	chromodomain helicase DNA binding protein 1	SPFEHVSVEHKST*PEHTWSSR	Q14646	197	1	11,787,321
132	5.5	EPRS	§898	glutamyl-prolyl tRNA synthetase	NSEPAGELET*PEAK^A	P07814	171	1	5,576,128
133	-1.1	GLUD1; GLUD2	410; 410	glutamate dehydrogenase 1	IIEGANGPTT*PEADKIFLER	P00367; P49448	61; 61	1	5,141,902
134	1.5	HSD17B4	§265	hydroxysteroid (17-beta) dehydrogenase 4	NHPMT*PEAVK	P51659	80	1	439,573
135	-3.6	LIG1	§88, §98	DNA ligase I	GQKPALDCS*QVSPRPATSPENNASLSDTSPMDSSPSGIPK	P18858	102	2	3,471,792
136	-1.8	LIG1	§91, §97	DNA ligase I	GQKPALDCSQVSP*PRPAT*SPENNASLSDTSPMDSSPSGIPK	P18858	102	1	1,026,571
137	7.9	OAS3	365	2'-5'oligoadenylate synthetase 3	AGCSGLGHPIQLDPNQK^A^T*PENSK^A	Q9Y6K5	121	2	6,757,531
138	6.8	PAICS	§237	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase isoform 2	DLK^A^EVT*PEGLQM#VK^A	P22234	47	5	6,686,605
139	-1.1	PPIG	§687	peptidylprolyl isomerase G	ADR^A^DQS*PFK^A	Q13427	89	1	78,436

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140	-1.8	SDS3	§234, §236	suppressor of defective silencing 3	R^PAS^PS^SPEHLPATPAESPAQR^A	Q9H7L9	38	3	5,382,479	
141	-1.8	SDS3	§234, §237	suppressor of defective silencing 3	RPAS^PSS^PEHLPATPAESPAQR	Q9H7L9	38	1	2,901,991	
142	1.1	ZCCHC6	§172	zinc finger, CCHC domain containing 6	DLTSLETTSEMEAGS^PENK^K^A	Q5VYS8	171	2	381,206	
143		G protein or regulator								
144	-1.1	ARFGEF2	§244	ADP-ribosylation factor guanine nucleotide-exchange factor 2	HSQAQSKPTT^PEKDLTNGEHAR	Q9Y6D5	202	1	63,770	
145	2.9	ARHGAP11A	§508	Rho GTPase activating protein 11A isoform 1	SEETLLT^PER^A	Q6P4F7	114	3	5,120,382	
146	1.5	MgcRacGAP	§579, §588	Rac GTPase activating protein 1	VSLLGpvtT^TPEHQLLK^A^T^PSSSSLSQR^A	Q9H0H5	71	1	2,378,264	
147	-1.3	MgcRacGAP	§580	Rac GTPase activating protein 1	VSLLGpvtT^PEHQLLK	Q9H0H5	71	2	5,382,966	
148	4.2	MgcRacGAP	§580, §588, §590	Rac GTPase activating protein 1	VSLLGpvtT^PEHQLLK^A^T^PSSSSLSQR^A	Q9H0H5	71	2	10,659,395	
149	4.2	MgcRacGAP	§580, §588, 593	Rac GTPase activating protein 1	VSLLGpvtT^PEHQLLK^T^PSSSSLSQR	Q9H0H5	71	1	3,254,213	
150	1.5	MgcRacGAP	§580, §590	Rac GTPase activating protein 1	VSLLGpvtT^PEHQLLK^T^PSSSSLSQR	Q9H0H5	71	2	4,474,208	
151	4.2	MgcRacGAP	§580, §590, 593	Rac GTPase activating protein 1	VSLLGpvtT^PEHQLLK^A^T^PSS^SS^LSQR^A	Q9H0H5	71	1	10,659,395	
152	1.2	RanGAP1	§428, §442	Ran GTPase activating protein 1	KILDpntGEPAPVLLSS^PPPADVSTFLAFPS^PEK	P46060	64	2	1,340,194	
153	-5.4	RanGAP1	§442	Ran GTPase activating protein 1	K^ILDpntGEPAPVLLSS^PPPADVSTFLAFPS^PEK^A	P46060	64	2	601,191	
154	-1.1	TBC1D16	99, 103	TBC1 domain family, member 16	YIT^PESS^PVR^A	Q8TBPO	86	1	1,319,697	
155		Kinase (non-protein)								
156	-1.0	B-CK	§35	brain creatine kinase	VLT^PELYAELR^A	P12277	43	1	1,348,042	
157	-3.5	Nedd4-BP2	1210	Nedd4 binding protein 2	AVT^PENHESMTSIFPSAAVGLK^A	Q86UW6	199	1	1,680,583	
158		Motor or contractile protein								
159	1.4	MYO9B	§1267, §1271	myosin IXB isoform 2	VSPAPAGS^APET^PEDK^A	Q13459	244	4	2,055,524	
160		Protease								
161	1.6	PSMD1	§311	proteasome 26S non-ATPase subunit 1	TSSAFVGK^A^T^PEASPEPK^A	Q99460	106	4	11,905,236	
162	-1.3	PSMD1	§311, §315	proteasome 26S non-ATPase subunit 1	TSSAFVGK^T^PEAS^PEPK	Q99460	106	2	2,013,079	
163	2.1	USP24; USP24 iso2	1129; 1289	ubiquitin specific protease 24	QM^SLCGT^PEK^A	Q9UPU5; IPI00398505	277; 294	4	112,255	
164	-1.8	USP34	§3255	ubiquitin specific protease 34	DSSIIDPGTEQDLPS^PENSSVK	Q70CQ2	387	2	1,854,341	
165		Protein kinase, regulatory subunit								
166	-1.2	Kidins220	§1561	kinase D-interacting substrate of 220 kDa	VPKS^PEHSAEPIR	Q9ULH0	197	2	502,623	
167		RNA processing								
168	3.1	DCP1A	422, 433	DCP1 decapping enzyme homolog A	GAMVASFS^PAAGQLATPES^FIEPPSK^A	Q9NPI6	63	1	814,980	
169	-41.8	DCP1A	§522, §531	DCP1 decapping enzyme homolog A	KAS^SPSPLTIGT^PESQR	Q9NPI6	63	1	11,834,112	
170	-1.2	DCP1A	§523, §525, §531	DCP1 decapping enzyme homolog A	K^ASS^PS^PLTIGT^PESQR^A	Q9NPI6	63	3	1,215,187	
171	2.5	DCP1A	§523, §531	DCP1 decapping enzyme homolog A	K^ASS^PS^PLTIGT^PESQR^K^A^PSIILSK^A	Q9NPI6	63	5	3,526,930	
172	-1.9	DCP1A	§525, §531	DCP1 decapping enzyme homolog A	KASSPS^PLTIGT^PESQRKPSIILSK	Q9NPI6	63	5	35,690,840	
173	-1.9	DCP1A	§531	DCP1 decapping enzyme homolog A	ASSPSPLTIGT^PESQR^A	Q9NPI6	63	6	23,996,504	
174	2.7	EDC4	§807, §821	autoantigen RCD8	HNT^PSLLEAALTQEAST^PDSQVWTPADITR^A	Q6P2E9	152	1	376,241	
175	4.3	ELAVL1	§202	ELAV-like 1	NVALLSQLYHS^PAR^A	Q15717	36	1	1,929,503	
176	1.1	hnRNP A3; RP11-223F20.1	§358; §256	heterogeneous nuclear ribonucleoprotein A3	SSGS^PYGGGYSGGGGSGGYGSR^A	P51991; Q5T6S7	40; 28	2	2,027,003	
177	2.9	hnRNP D0; hnRNP D0 iso3	§193; §193	heterogeneous nuclear ribonucleoprotein D isoform d	IFVGGGLSPDT^PEEK^A	Q14103; Q14103-3	38; 33	1	5,899,751	
178	4.9	hnRNP L; hnRNP L iso3	456; 487	heterogeneous nuclear ribonucleoprotein L isoform b	FST^PEQAAK^A	P14866; NP_001524	60; 64	2	807,424	
179	1.8	NIFK	§223	MKI67 (FHA domain) interacting nucleolar phosphoprotein	K^VSGTLDT^PEK^A	Q9BYG3	34	6	626,474	
180	1.0	NOP5	§502, §514	nucleolar protein NOP5/NOP58	HIKEPLS^EEPECTSTAIAS^PEK	Q9Y2X3	60	2	2,772,263	
181	-1.1	RBM6	§1025	RNA binding motif protein 6	EKLQSFDS^PER	P78332	129	2	27,540,942	
182	1.2	SAMD4	§231, 233	sterile alpha motif domain containing 4	AYSS^PS^TTPEAR^A	Q9UPU9	59	1	186,550	
183	1.2	SAMD4	§231, §235	sterile alpha motif domain containing 4	AYSS^PSTT^PEAR^A	Q9UPU9	59	3	186,550	

LEGEND: § = published site, ^ = phosphorylation, # = oxidized methionine

TABLE: pTPE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTPE Motif; CST #C32G12

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity	
185	-1.7	SLBP	§61	stem-loop (histone) binding protein	RPESFT*TPEGPKPR	Q14493	31	1	2,217,904	
186	-1.7	SLBP	§62	stem-loop (histone) binding protein	R^PESFTT*PEGPK^PR^A	Q14493	31	1	1,293,436	
187	3.3	SPF30	§201	survival motor neuron domain containing 1	SIFAS*PESVTGK	Q75940	27	2	7,189,969	
188	1.5	THOC2	1173	THO complex 2 isoform 1	EK^TPAT*TPEAR^A	Q8NI27	170	14	23,962	
189	1.9	THOC2	§1174	THO complex 2 isoform 1	EK^TPATT*PEAR^A	Q8NI27	170	4	18,315	
190	3.4	UPF3B; UPF3B iso2	176; 176	UPF3 regulator of nonsense transcripts homolog B isoform 2	MTS*TPETLLEEIAK^A	Q9BZ17; Q9BZ17-2	58; 56	1	1,127,306	
191	2.8	UPF3B; UPF3B iso2	§177; §177	UPF3 regulator of nonsense transcripts homolog B isoform 2	M^TST*PETLLEEIAK^A	Q9BZ17; Q9BZ17-2	58; 56	1	3,736,905	
192	-1.8	KIAA1802	§204, §214	zinc finger protein 828	LAPVPS*PEPQKPAPVS*PESVK	Q96JM3	89	4	8,150,718	
193	-2.4	KIAA1802	§214	zinc finger protein 828	LAPVPSPEPQKPAPVS*PESVK	Q96JM3	89	1	1,079,599	
194	-1.1	KIAA1802	§405	zinc finger protein 828	TAPTLS*PEHWK	Q96JM3	89	3	12,011,136	
195		Receptor, channel, transporter or cell surface protein								
196	-5.0	NUP214	§416	nucleoporin 214kDa	SLIKT*PER	P35658	214	2	21,673,464	
197	4.8	NUP50	246	nucleoporin 50kDa isoform b	LQESTFLFHGNK^TEDT*PDK^K^A	Q9UKX7	50	1	1,062,992	
198	-1.1	NUP98; NUP98 iso4	670; 653	nucleoporin 98kD isoform 3	PIPQT*PESAGNK	P52948; NP_624358	188; 187	4	1,422,503	
199	4.1	OSMR	§889	oncostatin M receptor	APSMGLMTS*PENVLK^A	Q99650	111	1	901,906	
200	1.4	PSEN1	§353	presenilin 1 isoform I-467	DSHLGPHR^A*TPESR^A	P49768	53	4	1,152,008	
201	1.6	PSEN1	§354	presenilin 1 isoform I-467	DSHLGPHR^A*TPESR^A	P49768	53	1	211,891	
202		SLC16A3	§460	solute carrier family 16, member 3	NGEVVHT*PETS	Q15427	49	3	8,882,079	
203	1.7	SLC16A3	§460, 463	solute carrier family 16, member 3	AEPEK^NGEVVHT*PET*SV	Q15427	49	1	1,833,379	
204		SLC16A3	§460, §464	solute carrier family 16, member 3	NGEVVHT*PETS*V	Q15427	49	2	3,469,868	
205	-1.2	TOMM70A	§85, §91	translocase of outer mitochondrial membrane 70 homolog A	NSERKT*PEGRAS*PAPGSGHPEPGAHLDMNSLDR	Q94826	67	1	819,352	
206	-1.9	TOMM70A	§85, §96	translocase of outer mitochondrial membrane 70 homolog A	NSERKT*PEGRASPAGS*GHPEPGAHLDM#NSLDR	Q94826	67	1	7,119,218	
209		Transcriptional regulator								
210	-1.5	BCLAF1; BCLAF1 iso4; LOC731605	§259, §268; §259, §268; 257, 266	BCL2-associated transcription factor 1 isoform 2	NTPS*QHSHSIQHS*PER	Q9NYF8; Q9NYF8-4; XP_001129341	106; 86; 80	1	33,622	
211	-1.9	BCLAF1; BCLAF1 iso4; LOC731605	§268; §268; 266	BCL2-associated transcription factor 1 isoform 2	NTPSQHSHSIQHS*PER	Q9NYF8; Q9NYF8-4; XP_001129341	106; 86; 80	1	192,729	
212	1.4	BRCA2	2035	breast cancer 2, early onset	EENTAIRT*PEHLISQK	P51587	384	1	415,590	
213	6.7	FLNA	1055	filamin A, alpha isoform 2	EEGPYEVEVTDGVPVPGS*PFPEAVATK^PSK^A	P21333	281	1	1,340,194	
214	-1.5	FOXK1	431, §441, §445	forkhead box K1	S*GGLQTPCELS*REGS*PIPHDPEFGSK	P85037	75	3	44,225,668	
215	1.1	FOXK1	§436	forkhead box K1	SGGLQT*PECLSR	P85037	75	2	5,477,708	
216	-1.4	FOXK1	§436, §441	forkhead box K1	SGGLQT*PECLS*R	P85037	75	2	15,370,549	
217	-1.5	FOXK1	§436, §441, §445	forkhead box K1	SGGLQT*PECLS*REGS*PIPHDPEFGSK	P85037	75	7	44,225,668	
218	1.1	FOXK2	§373, 385, §394	forkhead box K2	SAPAS*PNHAGVLSAHSS*GAQTPELSL*R	Q01167	69	1	1,341,775	
219	1.3	FOXK2	§373, §389	forkhead box K2	SAPAS*PNHAGVLSAHSSGAQT*PELSR^A	Q01167	69	1	487,020	
220	2.6	FBP1	§153	far upstream element-binding protein	SCMLTGT*PESVQSAK^A	Q96AE4	68	8	23,541,430	
221	3.6	FBP1	318	far upstream element-binding protein	IQFK^PDDGTT*PER^A	Q96AE4	68	2	4,997,833	
222	3.8	FBP3	130	far upstream element (FUSE) binding protein 3	IQIASSESSGIPER^PCVLTGT*PESIEQAK^A	Q96I24	62	2	1,122,889	
223	-1.4	HSF1	§363, §369	heat shock transcription factor 1	GHTDTEGRPPS*PPPTST*PEK	Q00613	57	11	12,997,874	
224	2.0	JDP-2	§148	Jun dimerization protein 2 isoform a	TDSVKT*PESEGNPLLEQLEKK	Q8WYK2	19	3	4,117,434	
225	1.1	LIN9; LIN9 iso5	§96; §246	lin-9 homolog	FTATMST*PDK^K^A	Q5TKA1; Q8IWQ1	62; 60	1	304,871	
226	1.6	MLL	§506, §518	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	SDT*PEVHPPLPISQS*PENESNDR^R^A	Q03164	432	1	443,957	
227	-1.0	NCOA7	500	nuclear receptor coactivator 7 isoform 2	QDIMPEVDKQS*GSPESR	Q5TF95	106	1	838,230	
229	-14.5	N-CoR1	§2120	nuclear receptor co-repressor 1	YSPESAQSQSVHHQRPGSRVRS*PENLVDK	Q75376	270	1	6,912,677	
230	-3.0	NFAT3	221, 226	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 isoform 1	AS*PRPW*PEDPWSLYGSPGGRR	Q14934	95	1	885,655	

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

TABLE: pTPE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTPE Motif; CST #C32G12

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
231	1.4	NFAT3	226	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 isoform 1	ASRPWWT*PEDPWSLYGSPSPGGR	Q14934	95	1	1,109,961
232	3.2	FIR	§60	poly-U binding splicing factor 60KDa	LGLPPLT*PEQQEALQK^	Q9UHX1	60	4	11,191,136
233	1.4	RAI1	470	retinoic acid induced 1	NLVS*RA^TPEQHK^	Q7Z5J4	203	2	904,608
234	1.5	RAI1	472	retinoic acid induced 1	NLVSRT*PEQHK	Q7Z5J4	203	1	259,642
235	-1.8	RNPC2	§97	RNA binding motif protein 39 isoform b	YRS*PYSGPK	Q14498	59	1	243,294
236	1.9	SMARCE1	363	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin e1	KDDENIPM#ETEETHLEETTESQQNGEEST*PEDK	Q969G3	47	2	516,054
237	-1.1	SHARP	§1619	spen homolog, transcriptional regulator	EVEKQEDTENHPKT*PESAPENK	Q96T58	402	4	2,663,437
239	-1.3	SQSTM1	§269	sequestosome 1	SRLT*PVSPESSSTEELK	Q13501	48	1	2,044,052
240	1.7	SQSTM1	§269, §272	sequestosome 1	SR^LT*PVS*PESSSTEELK^	Q13501	48	2	6,255,401
241	-1.3	SQSTM1	§272	sequestosome 1	LTPVS*PESSSTEELK	Q13501	48	4	27,424,876
242	2.4	TAF12	§43, §51	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20 kD	IPGT*PGAGGR^LS*PENNVQLTK^	Q16514	18	1	9,062,255
243	-1.3	TAF12	§51	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20 kD	IPGTPGAGGRSL*PENNVQLTK	Q16514	18	4	16,811,010
244	-1.0	AP-4	37	transcription factor AP-4 (activating enhancer binding protein 4)	EVIGGLCSLANIPLT*PETQRDQER	Q01664	39	1	1,230,159
245	-2.4	TCF8	151	zinc finger E-box binding homeobox 1 isoform a	QGT*PEASGHDENGTDFAFSLLTTPCYCDR	P37275	124	1	1,107,566
246	2.1	ZFP161	225	zinc finger protein 161 homolog	K^VNCYGQVEVSM#ET*PESK^	Q43829	51	1	2,596,712
247	Translation								
248	-1.8	EEF1G	§45	eukaryotic translation elongation factor 1 gamma	VLSAPPHFHGQTNRT*PEFLR	P26641	50	1	32,063,184
249	4.6	eIF3-alpha	§109	eukaryotic translation initiation factor 3, subunit 1 alpha, 35kDa	R^LEEPEEPK^VLT*PEEQADK^LR^	Q75822	29	5	7,365,462
250	Tumor suppressor								
251	1.3	BARD1	§299	BRCA1 associated RING domain 1	SR^NEVWT*PEK^VCK^	Q99728	87	7	1,942,366
252	Ubiquitin conjugating system								
253	-1.3	CCDC86	§18	coiled-coil domain containing 86	LGGLRPES*PELTSVSR	Q9H6F5	40	4	32,011,866
254	3.4	CCDC86	§18, §24	coiled-coil domain containing 86	LGGLR^PES*PELTS*VSR^	Q9H6F5	40	1	7,189,969
256	2.8	RNF40	556	ring finger protein 40	AQASGSAHSTPNLGHPEDSGVSAPAPGK^EEGGPGV*TPDNR^	Q75150	114	2	831,053
257	5.3	RNF40	557	ring finger protein 40	AQASGSAHSTPNLGHPEDSGVSAPAPGK^EEGGPGV*TPDNR^K^	Q75150	114	2	396,947
258	Unknown function								
259	-1.3	ANKRD40	199	ankyrin repeat domain 40	DHTSLALVQNGDVSAPSAILRT*PESTKPGPVCQPPVQSQR	Q6A112	41	1	2,425,561
260	2.3	FLJ13144	§607	ankyrin repeat and zinc finger domain containing 1	AQVPGPLT*PEMEAR^	Q9H8Y5	81	4	6,480,461
261	1.0	A2LP	§557	ataxin 2 related protein isoform A	LQPS*SSPENSLDPFPPR^	Q8WWM7	113	1	4,408,219
262	1.1	A2LP	§559	ataxin 2 related protein isoform A	LQPS*SSPENSLDPFPPR^	Q8WWM7	113	9	12,625,057
263	-1.2	BAT3; BAT3 iso4	§1081; §1178	HLA-B associated transcript-3 isoform b	PLTS*PELSR	P46379; AAD18085	119; 130	3	4,488,941
264		BAZ2B	254, 270	bromodomain adjacent to zinc finger domain, 2B	S*LKVKVIAALSNPATSS*SPAHPK	Q9UIF8	221	1	18,194,328
265	4.2	Bcl-9L	514	B-cell CLL/lymphoma 9-like	LGQDSL*PEQVAWR^	Q86UU0	157	1	1,688,288
266	3.1	C10orf12	1218	hypothetical protein LOC26148	AR^PSTK^T*PESSAAQR^	Q8N655	137	1	65,201
267	2.0	C12orf41	131	hypothetical protein LOC54934	TELGST*PESSR^	Q9H9L4	55	2	973,976
268	5.0	C12orf43	§79	hypothetical protein LOC64897	HK^VNEHQDGNELQTT*PEFR^	Q96C57	28	2	2,546,611
269	-2.0	C15orf42	§1134	leucine-rich repeat kinase 1	ISHTQTPPLYT*PER	Q7Z2Z1	211	1	1,382,863
270	-1.1	MGC4606	§138, §143, §148	PTIP-associated 1 protein	RPPT*PEAQS*EEERS*DEEPEAK	Q9BTK6	28	1	732,413
271	2.1	FLJ12886	§118	hypothetical protein LOC56006	EEGKGPVAVTGAST*PEGTAPPPAAPPAPKGEK	Q9HOW8	58	2	1,154,865
272	-1.2	C22orf9	360, §364	hypothetical protein LOC23313 isoform b	VTSFS*TPPT*PER	Q8IU4Y	53	1	966,328
273	1.2	CCDC55	§275	coiled-coil domain containing 55 isoform 1	VIET*PENDFK^	Q9H0G5	66	7	11,834,112
274	5.6	FLJ23518	219, 220, 227	coiled-coil domain containing 82	R^VVEDEGS*S^VMEQK^T*PEK^	Q8N4S0	64	1	283,915

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

TABLE: pTPE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTPE Motif; CST #C32G12

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
275	2.1	FLJ23518	227	coiled-coil domain containing 82	R^VVEDEGSSVEMEQK^*T^PEK^A	Q8N4S0	64	1	663,758
276	1.5	CENPC1	§126, §130	centromere protein C 1	ILATDVS^*SK^*NT^*PDSK^A	Q03188	107	1	900,501
277	-1.3	CENPC1	§130	centromere protein C 1	ILATDVSSK^*NT^*PDSK^A	Q03188	107	3	1,385,335
278	1.5	CEP4	488	centrosome protein 4	SSIFR^*T^PEK^*GDYNEIHQITR^A	Q66GS9	134	1	3,477,226
279	-1.3	CHD1	§1689, §1699	chromodomain helicase DNA binding protein 1	SPYGSRS^*PFEHSEVHK^*TPEHTWSSR	NP_001261	197	1	6,299,397
280	1.4	CKAP2L	§742	cytoskeleton associated protein 2-like	R^NEALPVTLGFQT^*PES	Q8IYA6	84	1	1,272,356
281	2.5	CKAP2L	§742, §745	cytoskeleton associated protein 2-like	R^NEALPVTLGFQT^*PES^*	Q8IYA6	84	1	813,752
282	2.5	CNNM3	§661	cyclin M3 isoform 1	AQNL PQS^*PENTDLQVIPGSQTR^A	Q8NE01	76	1	2,322,156
283	-33.4	COL18A1	1170	alpha 1 type XVIII collagen isoform 1 precursor	GS^*PGKGEK	P39060	178	1	2,625,729
284	-1.8	CXorf38	§314	hypothetical protein LOC159013	LDSQEPGRQT^*PDR	Q8TB03	37	2	406,474
285	1.2	DTNA; DTNB; DTNB iso5	§504; §468; §468	dystrobrein alpha isoform 9	LRLEHQASQPT^*PEK	Q9Y4J8; O60941; Q110L3	84; 71; 68	1	42,576,652
286	6.6	ELP4	151	elongation protein 4 homolog	EFDEDVYNHK^*T^PESNIK^A	Q96EB1	47	1	712,613
287	2.1	EME1	§150	essential meiotic endonuclease 1 homolog 1	IPEVPLHDT^*PER^A	Q96AY2	63	3	3,966,555
288	2.4	FAM29A	§584	family with sequence similarity 29, member A	NQIPR^*T^PENLITEIR^A	Q7Z4H7	109	1	3,450,460
289	1.1	FAM29A	§823	family with sequence similarity 29, member A	QTT^*PESDFNLQALR^A	Q7Z4H7	109	1	833,563
290	10.0	FAM29A	854, §858	family with sequence similarity 29, member A	K^R^EESYLS^*NSQT^*PER^A	Q7Z4H7	109	1	470,085
291	4.2	FAM29A	§858	family with sequence similarity 29, member A	K^R^EESYLSNSQT^*PER^A	Q7Z4H7	109	2	2,102,008
292	3.4	FBLIM1	51, 64	filamin-binding LIM protein-1 isoform b	GR^*PWEAPAPMK^*T^PEAGLAGR^*PSPWT^*TPGR^A	Q8WUP2	41	1	1,939,669
293	1.6	FBLIM1	61	filamin-binding LIM protein-1 isoform b	GR^*PWEAPAPMK^*T^PEAGLAGR^*PS^*PWTTPGR^A	Q8WUP2	41	1	432,006
294	-1.2	FNBP4	§479	formin binding protein 4	TGR^*DT^*PENGETAIGAENSEK^A	Q8N3X1	110	4	46,537,240
295	-1.4	FNBP4	§479, 492	formin binding protein 4	TGRDT^*PENGETAIGAENS^*EKIDENS DKEM#EVEESPEK	Q8N3X1	110	1	862,070
296	1.1	FNBP4	§479, §499	formin binding protein 4	TGRDT^*PENGETAIGAENSEKIDENS^*DKEMEVEESPEK	Q8N3X1	110	3	1,866,773
297	-1.1	FOXC2	§232, §240	forkhead box C2	VETLS^*PESALQGS^*PR	Q99958	54	2	1,507,996
298	-1.3	GRAMD1B	53	GRAM domain containing 1B	GSDHSSDK^*S^*PSTPEQGVQR^A	Q3KR37	85	1	15,615
299	3.0	GRAMD1B	53, 56	GRAM domain containing 1B	GSDHSSDK^*S^*PST^*PEQGVQR^A	Q3KR37	85	3	72,145
300	-1.2	GRAMD1B	56	GRAM domain containing 1B	GSDHSSDKSPST^*PEQGVQR	Q3KR37	85	3	206,368
301	2.3	GULP1	§16	GULP, engulfment adaptor PTB domain containing 1	TWMHT^*PEALSK^A	Q9UBP9	34	3	15,997,562
302	3.2	Hn1	§54	hematological and neurological expressed 1 isoform 2	MASNFGT^*PEENQASWAK^A	Q9UJ76	16	11	40,438,544
303	1.4	IMPA1	168	inositol(myo)-1(or 4)-monophosphatase 1	SLLVTEL GSSR^*T^*PETVR^A	P29218	30	1	1,200,724
304	1.0	KIAA0947	958	hypothetical protein LOC23379	LS^*FSPENILIQNDIVR	Q9Y2F5	248	1	1,230,969
305	-1.0	KIAA0947	§960	hypothetical protein LOC23379	LSFS^*PENILIQNDIVR^A	Q9Y2F5	248	2	3,216,638
306	5.0	KIAA1217	1633	sickle tail isoform 2	SQPEDT^*PENTVR^A	Q5T5P2	214	1	527,057
307	-1.0	LOC284058	1021	hypothetical protein LOC284058	CS^*TPELGLDEQSVQPWER	Q7Z3B3	121	1	834,434
308	-1.1	KIAA1671	600	Uncharacterized protein KIAA1671	GGSSVEAPCPSDVT^*PEDDR^*SFQTVWATVFEHHVER^A	Q9BY89	197	2	947,388
309	11.2	KIAA1949	§195, §199	phostensin	WRLS^*PGET^*PER	Q6NYC8	68	1	2,015,658
310	1.0	LEMD2	§138, §139, 147	LEM domain containing 2	ASVR^*GS^*S^*EDEDAR^*T^*PDR^A	Q8NC56	57	2	180,553
311	1.5	LRRC16	§1228	leucine rich repeat containing 16A	FGLGT^*PEK^A	Q5VZK9	152	2	2,764,390
312	2.3	MAGE-D2	§70	melanoma antigen family D, 2	ATEVS^*K^*T^PEAR^A	Q9UNF1	65	4	96,501
313	1.7	MAGE-D2	§72	melanoma antigen family D, 2	ATEVSK^*T^PEAR^A	Q9UNF1	65	43	192,729
314	1.9	RPRC1	§811	MAP7 domain containing 1	SLS^*RTPETLLPFAEAEFLK	Q3KQU3	93	1	22,052,736
315	1.5	RPRC1	§813	MAP7 domain containing 1	SLSR^*T^PETLLPFAEAEFLK^*K^A	Q3KQU3	93	3	4,735,150
316	2.6	RP11-535K18.3	499, 509	MAP7 domain containing 3	WSS^*SPENACGLPS^*PISTNR^A	Q8IWC1	98	2	1,209,505
317	1.1	MLP	§148	MARCKS-like 1	AAAT^*PESQEPQAK^A	P49006	20	28	382,672
318	3.4	NOSIP	§168	nitric oxide synthase interacting protein	VLPSPFWIPSLT^*PEAK^A	Q9Y314	33	2	14,184,311
319	2.7	NVL	§134, §138	nuclear VCP-like isoform 1	K^GNPDS^*VSNT^*PEMEQR^A	O15381	95	1	289,545

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

TABLE: pTPE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTPE Motif; CST #C32G12

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	
								Intensity	
320	4.3	PCNT	191	pericentrin	GMFTVSDHT*PEQR ^A	Q95613	378	2	1,790,378
321	5.7	RBM41; RBM41 iso3	113; 113	RNA binding motif protein 41	LR ^A AT*PEAIQNR ^A	Q96IZ5; Q96IZ5-3	47; 36	1	660,320
322	3.3	RBM7; RBM7 iso2	§137; §144	RNA binding motif protein 7	SFSS*PENFQR ^A	Q9Y580; Q59EQ8	31; 17	1	8,698,275
323	1.3	KIAA1991	§554	ring finger protein 169	EQFEGLGST*PDAK ^A	Q8NCN4	77	2	6,264,443
324	3.5	KIAA0460	§517	Regulation of nuclear pre-mRNA domain containing 2	VEIT*PESILSLSK ^A	Q5VT52	156	1	2,958,668
325	5.2	CGI-115	§104	ribosomal RNA processing 15 homolog	VLNK ^A K ^A T*PESK ^A PTILVK ^A	Q9Y3B9	31	5	19,044,046
326	1.7	SAPLa	§631	SAPS domain family, member 3	HIAFT*PESQRR	Q5H9R7	98	2	18,401,220
327	-1.2	SR-A1	§989, §1001	SR-related CTD-associated factor 1	AAPPPALT*PDSQTVDSCK ^A T*PEVSFLPEEATEEAGVR ^A	Q9H7N4	139	1	2,363,649
328	19.7	LOC435684	101	Src homology 2 domain containing F	VIK ^A DLWPPVPGQLDSS*PSLPDGR ^A	Q8N9I8	23	1	160,713
329	2.2	SNRPD2	§12	small nuclear ribonucleoprotein polypeptide D2	SEMT*PEELQK ^A R ^A	P62316	14	3	4,022,545
330	5.3	SNX4	367	sorting nexin 4	LFQGET*PEQR ^A	Q95219	52	1	1,009,694
331	3.3	SURF6	184	surfeit 6	K ^A AEEATEAQEVVEAT*PEGACTEPR ^A	Q75683	41	1	2,332,498
332	2.7	SYNPO; SYNPO iso2	§746; §502	synaptopodin isoform B	YVIESSHT*PELAR	Q8N3V7; Q8N3V7-2	99; 96	1	690,483
333	-2.9	TANC2	425, §434	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	ELPLTPPPSAHSS*ITSGSCPGT*PEM#R	Q9HCD6	220	1	1,574,759
334	-1.8	TANC2	§434	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	ELPLTPPPSAHSSITSGSCPGT*PEMR	Q9HCD6	220	4	20,318,704
335	1.8	TRPS1	751	zinc finger transcription factor TRPS1	VYNLLT*PDSK ^A	Q9UHF7	142	1	1,135,487
336	-1.1	KIAA0853	§370, §372, §381	zinc finger CCCH-type containing 13	S*AS*PYPSHSLSS*PQR	Q5T200	197	1	242,032
337	Vesicle protein								
338	-1.3	EHBP1L1	§964	tangerin	VLES*PENK	Q8N3D4	162	15	870,691
339	5.1	PHLDB2	§574	pleckstrin homology-like domain, family B, member 2 isoform b	ASSESSYLSILPK ^A T*PEGISEEQR ^A	Q86SQ0	142	3	5,838,500
340	-1.2	SYNJ1	§1220	synaptojanin 1 isoform a	ASAGRLT*PESQSK	Q43426	173	3	254,093
341	inhibitor								
342	-1.5	PINX1	§164	PIN2-interacting protein 1	KTPEGDASPST*PEENETTTTSAFTIQEYFAK	Q96BK5	37	2	2,423,007