

TABLE: pTXR MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTXR Motifs; CST #2351

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								
3	-1.1	DOCK1	1772	dedicator of cytokinesis 1	FSVSPSSPSSQQTPPPVT*PR	Q14185	215	1	194,424	
4	1.4	Eps8	§317	epidermal growth factor receptor pathway substrate 8	K ^A GPGEGLVTL ^A	Q12929	92	4	2,618,327	
5	-1.8	LMO7; LMO7 iso2; LMO7 iso3	1588; 1588; 1254	LIM domain only 7	TSTTGVTQSPST*PR	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	2	675,452	
6	4.8	LMO7; LMO7 iso2; LMO7 iso3	§913; §913; §579	LIM domain only 7	LTSVVT*PR ^A PFGSQTR ^A	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	2	4,190,288	
7	9.0	LMO7; LMO7 iso2; LMO7 iso3	§913, §919; §913, §919; §579, §585	LIM domain only 7	LTSVVT*PR ^A PFGS ^A QTR ^A	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	1	1,185,671	
10	9.9	PACS-1	§493, §495, §504	phosphofurin acidic cluster sorting protein 1	TDLQGS ^A AS ^A PSK ^A VEGVHT*PR ^A	Q6VY07	105	1	265,627	
11	1.2	PACS-1	§495, §504	phosphofurin acidic cluster sorting protein 1	TDLQGSAS ^A PSK ^A VEGVHT*PR ^A	Q6VY07	105	2	398,386	
12	1.3	PACS-1	§497, §504	phosphofurin acidic cluster sorting protein 1	TDLQGSASPS ^A K ^A VEGVHT*PR ^A	Q6VY07	105	2	3,617,732	
13	-1.6	PACS-1	§504	phosphofurin acidic cluster sorting protein 1	TDLQGSASPSKVEGVHT*PR	Q6VY07	105	3	2,342,722	
14	-2.8	RanBP2; RGPD1; RGPD4; RanBP2L2; RGPD5; RGPD8	§2450, §2457, 2458; 1467, 1474, 1475; 1475, 1482, 1483; §1474, 1481, 1482; 1474, 1481, 1482; 464, 471, 472	RAN binding protein 2	DSLIT*PHVSRSS ^A T*PR	P49792; NP_001019628; AGNK77; Q53T03; Q99666; Q14715	358; 197; 198; 199; 199; 85	1	393,200	
16	3.3	TANK	§213	TRAF interacting protein TANK isoform a	GAPSITSVT*PR ^A	Q92844	48	1	6,746,865	
17		Adhesion or extracellular matrix protein								
18	3.1	nav1; nav1 iso2	§1000, §1006; §1000, §1006	neuron navigator 1	QGLTNI ^A VS ^A PTAATT*PR ^A	Q8NEY1; Q8NEY1-2	202; 202	1	570,340	
20	7.5	TROAP	§358, §362, §363	tastin isoform 2	TR ^A FT ^A PMPS ^A T*PR ^A	Q8N5B2	84	1	264,947	
27		Cell cycle regulation								
29	6.3	Borealin	185, §189	cell division cycle associated 8	LEVSM ^A VK ^A PT ^A PGLT*PR ^A	Q53HL2	31	2	969,926	
30	4.2	Borealin	§189	cell division cycle associated 8	LEVSM ^A VK ^A PTPGLT*PR ^A	Q53HL2	31	1	340,891	
31	3.5	DLG7	§326, §329	discs large homolog 7	TYQVT*PM ^A T*PR ^A	Q15398	95	2	10,457,631	
32	2.7	DLG7	§329	discs large homolog 7	TYQVTPM ^A T*PR ^A	Q15398	95	3	3,455,822	
33	4.6	MDC1	150	mediator of DNA damage checkpoint 1	GPLTVEET*PR ^A	Q14676	227	2	2,115,637	
37	1.2	NuMA-1	2015	nuclear mitotic apparatus protein 1	ATSCFPRPMT*PR	Q14980	238	1	417,181	
38	3.8	NuMA-1	§2106	nuclear mitotic apparatus protein 1	IATTTASAATAAAIGAT*PR ^A	Q14980	238	17	7,196,831	
39	3.8	PRC1; PRC1 iso2	521, 532, 536; 491, 502, 506	protein regulator of cytokinesis 1 isoform 1	LPPS ^A GSK ^A PVAASTCS ^A GK ^A K ^A T*PR ^A	Q43663; Q43663-2	72; 67	1	306,398	
40	2.0	PRC1; PRC1 iso2	529, 532, 536; 499, 502, 506	protein regulator of cytokinesis 1 isoform 1	LPPSGSKPVAAS ^A TCS ^A GKKT*PR	Q43663; Q43663-2	72; 67	1	140,017	
41	5.1	PRC1; PRC1 iso2	532, 536; 502, 506	protein regulator of cytokinesis 1 isoform 1	LPPSGSK ^A PVAASTCS ^A GK ^A K ^A T*PR ^A	Q43663; Q43663-2	72; 67	1	217,288	
42	5.4	SEPT9	255	septin 9 isoform a	SQEATEAAPS ^A CVGDM ^A ADT*PR	Q9UHD8	65	6	6,202,933	
43		Chromatin, DNA-binding, DNA repair or DNA replication protein								
44	2.4	CAF-1B	485, 496	chromatin assembly factor 1 subunit B	R ^A VT ^A LNTLQAWSK ^A TT*PR ^A	Q13112	61	1	355,533	
45	3.8	CHD-7; CHD-8; CHD-8 iso2	1555; §1119; §1263	chromodomain helicase DNA binding protein 7	NNLVIDT*PR	Q9P2D1; Q9HCK8; Q9HCK8-2	336; 262; 276	2	3,377,629	
46	6.0	MLH1	495	MutL protein homolog 1	EMTAACT*PR ^A	P40692	85	2	54,792	
48	4.6	POLA2	§127, §130, 133	polymerase (DNA directed), alpha 2 (70kD subunit)	AIST ^A PET ^A PLT ^A K ^A R ^A	Q14181	66	1	478,742	
49	1.7	Rad54L	31	RAD54-like protein	SCDDEDWQPGLVT*PR ^A	Q92698	84	2	1,241,805	
51	4.0	Rif1	§402, §409	RAP1 interacting factor 1	GASS ^A PYGAPGT*PR	Q5UIP0	274	1	1,089,468	
52	-1.5	SSBP2	333	single-stranded DNA binding protein 2	NSPNNM ^A SLSNQP ^A GT*PR	P81877	38	1	149,931	
53	-1.8	SSBP3	§360	single stranded DNA binding protein 3 isoform c	NSPNNISGISNPPGT*PR	Q9BWW4	40	2	777,160	
54	6.7	TOP2B	§1581, §1596, 1600	DNA topoisomerase II, beta isozyme	K ^A TSFDQDS ^A DVDIFPSDFPTEPPS ^A LPR ^A T ^A GR ^A	Q02880	183	1	810,337	
55	-1.1	ZNF261	§817, §826	zinc finger protein 261	SAPTAPT ^A PPPPPPAT*PR	Q14202	152	2	449,097	
56	-4.3	ZNF261	§826	zinc finger protein 261	SAPTAPT ^A PPPPPPAT*PR	Q14202	152	1	315,616	

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

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STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTXR Motifs; CST #2351

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
57		Cytoskeletal protein							
59	18.1	claudin 1	195	claudin 1	K^TTSYPT*PR^	095832	23	1	198,570
62	2.7	ezrin; moesin; radixin	\$567; \$557; \$564	ezrin	DK^YK^*LR^	P15311; P26038; P35241	69; 68; 69	1	23,558
63	717.1	KIAA0284 iso2	1247, 1248, 1250	hypothetical protein LOC283638 isoform 1	QPFSR^AR^SGSAR^YTST*^T*QT*PR^	Q9Y4F5-2	168	2	43,818,860
67	2.8	Lamin B1	\$574	lamin B1	TTIEEEEEEEEEAGVVEEELFHQQGT*PR	P20700	66	1	1,635,555
68	-1.4	MAP1B	\$1779, \$1782, \$1788	microtubule-associated protein 1B	VQSLEGEKLS*PKS*DISPLT*PR	P46821	271	3	12,016,201
69	1.0	MAP1B	\$1782, \$1785, \$1788	microtubule-associated protein 1B	S*DIS*PLT*PR^	P46821	271	3	2,478,255
70	1.1	MAP1B	\$1782, \$1788	microtubule-associated protein 1B	S*DISPLT*PR^	P46821	271	1	10,219,799
71	1.1	MAP1B	\$1785, \$1788	microtubule-associated protein 1B	SDIS*PLT*PR^	P46821	271	3	10,219,799
72	-1.0	MAP1B	\$1788	microtubule-associated protein 1B	SDISPLT*PR	P46821	271	4	62,953,868
74	-5.9	EB1	\$155, \$166	microtubule-associated protein, RP/EB family, member 1	KPLTS*SSAAPQRPIS^T*QR	Q15691	30	1	511,009
77	2.0	talin 1	144	talin 1	K^EEITGT*LR^K^	Q9Y490	270	2	219,902
78	1.3	vimentin	\$37, \$47	vimentin	T^YSLGSALR^PS*TSR^	P08670	54	1	916,723
80		Enzyme, misc.							
82	15.1	CRMP-4	75, 85	dihydropyrimidinase-like 3	SGQGSDR^GS^GSR^PGIEGDT*PR^	Q6DEN2	74	2	897,127
83	9.4	CRMP-4	77, 85	dihydropyrimidinase-like 3	GGSG^R^PGIEGDT*PR^	Q6DEN2	74	2	691,238
84	4.3	CRMP-4	85	dihydropyrimidinase-like 3	GGSGR^PGIEGDT*PR^	Q6DEN2	74	10	7,981,700
85	2.1	BAT8; BAT8 iso2	44; 44	euchromatic histone-lysine N-methyltransferase 2 isoform a	VHGLSGDT*PR^	Q96KQ7; Q96KQ7-2	132; 129	2	47,335
86	4.1	GMPS	\$318	guanine monophosphate synthetase	VINAHSFYNGTTLLPISDEDR^T*PR^	P49915	77	4	8,001,535
87	1.4	HMOX1	252	heme oxygenase (decyclizing) 1	VQDSAPVET*PR^	P09601	33	2	4,941,095
88	1.7	LIG1	\$233	DNA ligase I	TLSSFFT*PR^	P18858	102	4	23,216,836
92	-1.0	WHSC1; WHSC1 iso5	\$544; \$544	Wolf-Hirschhorn syndrome candidate 1 protein isoform 1	IQDPTDEAEADT*PR	Q96028; Q96028-5	152; 69	12	10,996,141
93	1.9	ZCCHC6	\$64	zinc finger, CCHC domain containing 6	ITPGNYGNT*PR^	Q5VYS8	171	2	1,014,804
94		G protein or regulator							
95	2.1	ARHGEF12; ARHGEF12 iso2	703; 684	Rho guanine nucleotide exchange factor (GEF) 12	QVGETSAPGDTLDGT*PR^	Q9NZN5; Q9NZN5-2	173; 171	1	1,955,122
97	2.7	DOCK7; DOCK7 iso2; DOCK7 iso3	\$180, 186; \$180, 186; \$180, 186	dedicator of cytokinesis 7	S*MSIDDT*PR^	Q96N67; Q96N67-2; Q96N67-3	243; 241; 239	1	951,497
98	-1.7	EPS8L2	\$303	epidermal growth factor receptor pathway substrate 8-like protein 2	KAPAEGLT*LR	Q9H6S3	81	2	541,917
100	5.4	MgcRacGAP	\$600, \$601, \$606	Rac GTPase activating protein 1	VR^S^*TLTK^*NT*PR^	Q9H0H5	71	5	8,241,254
101	3.9	MgcRacGAP	\$601, \$606	Rac GTPase activating protein 1	VR^S^*TLTK^*NT*PR^	Q9H0H5	71	1	279,581
103	1.2	TBC1D4; TBC1D4 iso3	\$754, 766; \$203, 215	TBC1 domain family, member 4	TSSTCS^NESLSVGGT*SVT*PR^	Q60343; Q5JU47	147; 31	1	244,780
104	2.4	TBC1D4; TBC1D4 iso3	766; 215	TBC1 domain family, member 4	TSSTCSNESLSVGGT*SVT*PR^	Q60343; Q5JU47	147; 31	2	447,934
105		Phosphatase							
106	2.5	CTDSP2	\$86	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	DIDNNLITST*PR^	Q8IY19	53	1	3,404,717
107	2.6	BDP1	391	protein tyrosine phosphatase, non-receptor type 18	SAEEAPLYSK^VT*PR^	Q99952	50	2	1,152,054
109		Protein kinase, Ser/Thr (non-receptor)							
110	1.3	AAK1; DKFZp686K16132 iso2	\$389; 389	AP2 associated kinase 1	AGQTQPNPGLPIQIPAL^T*PR^	Q2M218; NP_055726	94; 104	5	7,860,032
112	-1.4	A-Raf	\$253, \$257	v-raf murine sarcoma 3611 viral oncogene homolog	GGSDGT*PRGS^PSPASVSSGR	P10398	68	3	945,383
113	-1.2	Bcr	693	breakpoint cluster region isoform 1	ISQNFLSSINEEIT*PR^	P11274	143	1	1,980,575
118	4.1	Haspin	108, 112	haspin	AR^PS^*LTV^*PR^	Q8TF76	88	1	1,246,283
119	1.7	ILK	172	integrin-linked kinase	IPYK^DTFWK^GT*TR^	Q13418	51	2	10,274,833

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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
121	5.1	AMPK1	§373	protein kinase, AMP-activated, alpha 1 catalytic subunit isoform 1	VPFLVAET*PR^	Q13131	63	2	11,186,279
123	2.0	MST2	§336	serine/threonine kinase 3 (STE20 homolog, yeast)	TSVESVGT*MR^	Q13188	56	3	613,134
124	1.3	MST1	§340	serine/threonine kinase 4	AVGDEMG*VR^	Q13043	56	1	445,746
125	3.1	ULK1	§450, §456	unc-51-like kinase 1	NLQS*PTQFQT*PR^	Q75385	113	2	1,233,724
128	Protein kinase, dual-specificity								
129	1.8	MKK7	83	mitogen-activated protein kinase kinase 7	HM#LGLPSTLFT*PR^	Q14733	47	2	1,593,044
130	Protein kinase, regulatory subunit								
131	3.3	PKAR2A	§53	cAMP-dependent protein kinase, regulatory subunit alpha 2	APASVLPAAAT*PR^	P13861	45	2	10,973,879
132	RNA processing								
133	2.1	DCP1A	348	DCP1 decapping enzyme homolog A	NSTM#MQAVK^TT*PR^	Q9NPI6	63	1	336,133
136	2.0	LARP; LARP iso3	780, §785, §788; 703, §708, §711	la related protein isoform 1	NT*R^TPR^T*PR^T*PQLK^	Q6PKG0; Q6PKG0-3	124; 116	2	9,411,784
137	1.6	LARP; LARP iso3	782, §785, §788; 705, §708, §711	la related protein isoform 1	NTR^T*PR^T*PR^T*PQLK^	Q6PKG0; Q6PKG0-3	124; 116	3	9,411,784
138	-1.1	LARP; LARP iso3	§785, §788; §708, §711	la related protein isoform 1	TPR^T*PR^T*PQLK^	Q6PKG0; Q6PKG0-3	124; 116	3	1,991,985
141	-2.0	RNUXA	§349, §350	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)	SLNFQEDDDT*S^R^ETFASDTNEALASLDESQEGHAEAK^	Q9H814	44	2	1,450,877
142	-1.6	RNUXA	§349, §350, §356	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)	SLNFQEDDDT*S^RET^FAS^DTNEALASLDESQEGHAEAK	Q9H814	44	2	2,020,828
143	-2.0	RNUXA	§349, §350, 358	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)	SLNFQEDDDT*S^RET^FASDT^NEALASLDESQEGHAEAK	Q9H814	44	1	2,553,818
144	-1.7	PRPF31	§439, §440	pre-mRNA processing factor 31 homolog	QSVVYGGK*S^T^IRDR	Q8WWY3	55	2	5,117,722
147	-1.7	SF3B1	§296, §299	splicing factor 3b, subunit 1 isoform 2	WDET*PKT^ER	Q75533	146	1	190,201
148	-1.9	SF3B1	§296, §299, §303	splicing factor 3b, subunit 1 isoform 2	WDET*PK^T^ER^DT*PGHGSGWAETPR^	Q75533	146	3	3,531,000
149	1.7	SF3B1	§296, §299, §313	splicing factor 3b, subunit 1 isoform 2	WDET*PKT^ERDT^PGHGSGWAET^PR	Q75533	146	1	2,404,093
150	2.1	SF3B1	§296, §303, §313	splicing factor 3b, subunit 1 isoform 2	WDET*PK^TER^DT*PGHGSGWAET^PR^	Q75533	146	2	4,444,628
152	1.4	SF3B1	§303, §313	splicing factor 3b, subunit 1 isoform 2	TER^DT*PGHGSGWAET^PR^	Q75533	146	6	1,187,588
153	-1.3	SF3B1	§313	splicing factor 3b, subunit 1 isoform 2	DTPGHGSGWAET^PR	Q75533	146	4	9,497,941
154	-1.3	SRm300	§1492	splicing coactivator subunit SRm300	ALPQT^PRPR	Q9UQ35	300	3	22,599,558
155	Receptor, channel, transporter or cell surface protein								
159	-1.1	myoferlin	1781	myoferlin isoform a	SLGPPGPPFNIT^PR	Q9NZM1	235	2	3,874,358
161	2.6	NUP107	§37, §46	nucleoporin 107kDa	VLLQAS^QDENFGNTT^PR^	P57740	106	1	174,384
162	3.5	NUP107	§46	nucleoporin 107kDa	VLLQASQDENFGNTT^PR^	P57740	106	11	2,884,853
163	4.0	NUP107	§55, §57, §64	nucleoporin 107kDa	NQVIPR^T^PS^SFR^AQPF^T^PTSR^	P57740	106	1	1,334,999
164	2.5	NUP133	§27, §28	nucleoporin 133kDa	GPLAGLPGGS^T^PR^	Q8WUM0	129	2	1,452,866
165	5.0	NUP133	§27, §28, §31	nucleoporin 133kDa	R^GPLAGLPGGS^T^PR^T^ASR^	Q8WUM0	129	3	450,225
166	-1.2	NUP133	§28	nucleoporin 133kDa	GPLAGLPGGS^T^PR	Q8WUM0	129	1	290,412
167	1.2	NUP210	§1844	nucleoporin 210	DLAVPAALT^PR^	Q8TEM1	205	2	51,469,984
168	3.6	NUP35	§273, §279, §280	nucleoporin 35kDa	TLGT^PTQPGS^T^PR^	Q8NFH5	35	2	4,506,168
169	3.6	NUP35	§275, §279, §280	nucleoporin 35kDa	TLGTPT^QPGS^T^PR	Q8NFH5	35	1	1,260,904
171	4.3	NUP98; NUP98 iso4	§1060, §1070; §1043, §1053	nucleoporin 98kD isoform 3	FTSGAFLS^PSVSVQECR^T^PR^	P52948; NP_624358	188; 187	3	7,385,026
173	4.2	NUP98; NUP98 iso4	§546, 553; §529, 536	nucleoporin 98kD isoform 3	ALTT^PTHYK^LT^PR^	P52948; NP_624358	188; 187	3	1,214,700
176	2.1	SLC4A2	169, §170, §183	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)	T^S^PSSAPALPHQEAT^PR^	P04920	137	1	173,782
177	6.1	TOR1AIP1	20	lamina-associated polypeptide 1B	EGWGVVYT^PR^	Q5JTV8	66	2	4,781,032

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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
178		Secreted protein							
181	2.6	IK	\$42	RED protein	K [*] LLMT*PR [^]	Q13123	66	2	1,550,323
182		Transcriptional regulator							
183	2.3	ELYS; ELYS iso2	\$1817; \$1846	transcription factor ELYS	GLSQNQIQPNQSVT*PR [^]	Q8WYP5; Q8WYP5-2	253; 256	3	6,179,833
185	-1.2	BCLAF1	\$385	BCL2-associated transcription factor 1 isoform 2	AEGEWEDQEALDYFS*DKESGK	Q9NYF8	106	5	2,110,807
186	2.5	BCLAF1; BCLAF1 iso4; LOC731605	\$658, \$660; \$485, \$487; \$483, \$485	BCL2-associated transcription factor 1 isoform 2	R [^] IDIS*PS*TLR [^]	Q9NYF8; Q9NYF8-4; XP_001129341	106; 86; 80	3	4,067,062
187	7.4	BCLAF1; BCLAF1 iso4; LOC731605	\$658, \$661; \$485, \$488; \$483, \$486	BCL2-associated transcription factor 1 isoform 2	IDIS*PST*LRK	Q9NYF8; Q9NYF8-4; XP_001129341	106; 86; 80	3	2,784,133
189	1.7	CDC5L	\$404, \$415, \$424	CDC5-like	QVVQT*PNTVLSTPFR [^] *PSNGAEGLT*PR [^]	Q99459	92	2	1,528,956
190	1.2	CDC5L	\$424	CDC5-like	TPSNGAEGLT*PR [^]	Q99459	92	2	4,941,095
191	5.5	p57Kip2	299, \$310	cyclin-dependent kinase inhibitor 1C isoform a	SSGDVVPAPCPSPS*AAPGVGSVEQT*PR [^]	P49918	32	1	425,329
192	-1.4	ERF	\$526	Ets2 repressor factor	GEGPGEAGGPLT*PR	P50548	59	6	22,814,268
193	-1.6	HEXIM2	\$29, \$32, \$46	hexamethylene bis-acetamide inducible 2	TSGAPGS*PQT*PPER [^] *HDSGGSLPLT*PR [^]	Q96MH2	32	2	491,633
194	-1.3	HEXIM2	\$46	hexamethylene bis-acetamide inducible 2	HDSGGSLPLT*PR	Q96MH2	32	1	1,123,320
195	13.7	BCDIN3	\$254, \$258	bin3, bicoid-interacting 3	DITDPLSLNCTCTDEGHVVLAS*PLK [^] *GR [^]	Q7L2J0	74	1	1,048,326
196	2.4	MKL2	\$367, \$370	megakaryoblastic leukemia 2 protein	NSNSGNSALNNAT*PNT*PR [^]	Q9ULH7	118	1	166,185
197	1.4	MKL2	\$370	megakaryoblastic leukemia 2 protein	NSNSGNSALNNATPNT*PR [^]	Q9ULH7	118	1	275,404
198	-1.3	MLL2; MLL2 iso2	2057; 1752	myeloid/lymphoid or mixed-lineage leukemia 2	TPDVFKAPLT*PR	Q14686; Q14686-2	564; 532	1	383,742
199	4.1	N-CoR1	1300	nuclear receptor co-repressor 1	TVLSGSIM#QGT*PR [^]	Q75376	270	1	984,763
202	2.1	PPP1R13L	241	protein phosphatase 1, regulatory subunit 13 like	AQDDL*LR [^]	Q8WUF5	89	1	1,409,860
203	3.2	RAI1	1476	retinoic acid induced 1	R [^] PYLGALLLT*PR [^]	Q7Z5J4	203	1	2,359,349
204	3.7	Rb	\$249, \$252	retinoblastoma 1	TAVIPINGS*PR [^] *T*PR [^]	P06400	106	2	2,873,089
205	3.4	Rb	\$356	retinoblastoma 1	TLQTDSDISFETQR [^] *T*PR [^]	P06400	106	1	138,788
206	1.8	Rb	\$821, \$826	retinoblastoma 1	ISEGLPT*PTK [^] *MT*PR [^]	P06400	106	3	800,805
208	2.7	RNF4	112	ring finger protein 4	DVYVYTH*PR [^]	P78317	21	1	1,014,804
209	1.7	SHARP	1946	spen homolog, transcriptional regulator	ELQEAAVPT*TPR	Q96T58	402	1	854,981
210	1.7	SHARP	1947	spen homolog, transcriptional regulator	ELQEAAVPTT*PR [^]	Q96T58	402	1	1,442,955
212	2.4	treacle; treacle iso2	\$1350, \$1358; \$1312, \$1320	Treacher Collins-Franceschetti syndrome 1 isoform b	K [*] ALS*GDQPAAR [^] *T*PR [^]	Q13428; AQLJLUO	152; 144	4	5,058,387
214	-1.3	ZNF174	165	zinc finger protein 174 isoform b	TGSQLGEQELPDFQPQT*PR	Q15697	46	2	496,316
215		Translation							
217	7.0	CDA02	\$503, \$517	eukaryotic translation initiation factor 2A	S*DK [*] SPDLAPTAPQS*TPR [^]	Q9BY44	65	1	2,467,832
218	7.0	CDA02	\$503, \$518	eukaryotic translation initiation factor 2A	S*DKSPDLAPTAPQST*PR	Q9BY44	65	1	419,619
219	5.4	CDA02	\$506, \$517	eukaryotic translation initiation factor 2A	SDK [*] S*PDLAPTAPQS*TPR [^]	Q9BY44	65	1	734,031
220	2.5	CDA02	\$517	eukaryotic translation initiation factor 2A	SDK [*] SPDLAPTAPQS*TPR [^]	Q9BY44	65	1	428,434
222	1.8	RPS9	14	ribosomal protein S9	K [^] TYVT*PR [^]	P46781	22	11	26,677
223		Tumor suppressor							
225	1.5	PSRC1; PSRC1 iso2	138, \$140, \$145; 138, \$140, \$145	proline/serine-rich coiled-coil 1 isoform b	ST*PS*PSSLT*PR [^]	Q6PGN9; Q5T2Z1	39; 25	1	384,299
226		Ubiquitin conjugating system							
228	4.2	RNF123	694	ring finger protein 123	FLSTAAVSLMT*PR [^]	Q5XPI4	149	1	17,200,686
229	1.5	USP10	\$205	ubiquitin specific protease 10	DGGDDSISTEALVNGHANSAPVNSVAEDAEFM#GDM#PPSVT*PR	Q14694	87	1	742,871
230	3.5	FAF-X	\$583	ubiquitin specific protease 9, X-linked isoform 3	EICSLFGEAPQNLST*QR [^]	Q93008	290	1	531,301
231	5.5	VPRBP	\$888, 891, \$902	HIV-1 Vpr binding protein	EADLPMTAASHSAFT*PVT*AAASPVSLPR [^] *T*PR [^]	Q9Y4B6	169	1	375,049
232	5.5	VPRBP	\$888, \$895, \$902	HIV-1 Vpr binding protein	EADLPMTAASHSAFT*PVTAAS*PVSLPR [^] *T*PR [^]	Q9Y4B6	169	1	375,049
233		Unknown function							
239	-1.4	C15orf42	1115, 1120	leucine-rich repeat kinase 1	SLS*FSK [*] TT*PR [^]	Q7Z2Z1	211	1	336,660
242	3.1	C9orf167	\$81, \$89	hypothetical protein LOC54863	FFTFDS*PAELPSR [^] *T*PR [^]	Q9NXH8	47	1	526,089

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

TABLE: pTXR MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: pTXR Motifs; CST #2351

Treatments: Nocodazole (Heavy), Untreated (Light)

Index	Fold Change (Nocodazole / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
244	2.9	C9orf5	30, §36	hypothetical protein LOC23731 isoform 2	AVGPS*GGGGET*PR^	Q9H330	101	1	58,084
245	2.7	C9orf5	§36	hypothetical protein LOC23731 isoform 2	AVGPSGGGGET*PR^	Q9H330	101	3	1,786,350
250	3.1	CINP	§10	cyclin-dependent kinase 2-interacting protein	TLGTVT*PR^	Q9BW66	24	1	4,782,054
251	2.5	CIP29	99	cytokine induced protein 29 kDa	ITSEIPQT*ER^	P82979	24	1	174,943
254	3.7	EIF2B4	§86	eukaryotic translation initiation factor 2B, subunit 4 delta isoform 2	ELPESGIQLGT*PR^	Q9UI10	58	2	4,636,740
257	1.1	FBXL19	205	F-box and leucine-rich repeat protein 19	EAGNEPPT*PR	Q6PCT2	74	1	9,318
258	1.4	SOLO	1101	hypothetical protein LOC55701	GPDGPWVGVT*PR^	Q8TER5	168	2	937,430
269	1.8	LRCH1	§568	leucine-rich repeats and calponin homology (CH) domain containing 1	NLESIDPQFT*IR	Q9Y2L9	81	1	757,615
272	1.1	LSM7	22	U6 snRNA-associated Sm-like protein LSm7	YIDK^*IR^	Q9UK45	12	1	387,417
275	3.9	MIRab13	311, §318	molecule interacting with Rab13	K^ASES^TTPAPPT*PR^PR^	Q8N3F8	93	1	357,815
277	10.7	MORC2	§836	MORC family CW-type zinc finger 2	VK^FDYVPTDIT*PR^	Q9Y6X9	118	1	1,122,361
280	2.6	PDCD7	153	programmed cell death 7	QWLEAVFGT*PR^	Q8N8D1	55	1	268,931
282	3.4	PPP4R2	173	protein phosphatase 4, regulatory subunit 2	SNINGPGT*PR^PLNR^PK^	Q9NY27	47	1	383,732
285	7.3	PWP2H	256	PWP2 periodic tryptophan protein homolog	ADLLQR^EEEEEEEDQEGDR^ETT*IR^	Q15269	102	1	353,920
287	3.7	FLJ21908	491	RNA polymerase II associated protein 3	NSSQDDLFPSTSDT*PR	Q9H6T3	76	3	643,193
289	2.2	SMARCAL1	§198, 215	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1	AS^PSGQNISYIHSSSESVT*PR^	Q9NZC9	106	1	391,466
290	-1.1	SSBP4	§341, §355	single stranded DNA binding protein 4 isoform b	S^SPGAVAGLSNAPGT*PR^	Q9BWG4	39	1	749,097
291	-1.1	SSBP4	§342, §355	single stranded DNA binding protein 4 isoform b	SS^PGAVAGLSNAPGT*PR	Q9BWG4	39	1	855,376
292	-1.9	SSBP4	§355	single stranded DNA binding protein 4 isoform b	SSPGAVAGLSNAPGT*PR	Q9BWG4	39	1	436,685
294	5.0	THAP4	154	THAP domain containing 4	QAALQGEAT*PR	Q8WY91	63	2	369,019
295	2.9	TIPIN	233	TIMELESS interacting protein	LLSNSQTLGNM#LM#NT*PR^	Q9BVW5	34	1	595,824
297	7.8	LAP2A; TMPO	§136; §136	thymopoietin isoform beta	YGVNPGPIVGT*TR^	P42166; P42167	75; 51	1	4,871,143
299	4.4	TRMT1	§623, §628	TRM1 tRNA methyltransferase 1	GDQCCYS^HSPPT*PR	Q9NXH9	72	1	871,514
300	4.4	TRMT1	§625, §628	TRM1 tRNA methyltransferase 1	GDQCCYSHS^PPT*PR^	Q9NXH9	72	4	980,532
301	1.8	TRMT1	§628	TRM1 tRNA methyltransferase 1	GDQCCYSHS^PPT*PR^	Q9NXH9	72	2	644,145
302	1.3	Tsc22d4	49, 57	TSC22 domain family, member 4	LPNGEPS^PDPGGK^GT*PR^	Q9Y3Q8	41	1	109,506
303	3.9	STS-1	§23	ubiquitin associated and SH3 domain containing, B	EELYSK^VT*PR^	Q8TF42	73	1	1,012,588
304	2.7	UBP1	194	upstream binding protein 1 (LBP-1a) isoform b	TSAFIQVHCISTEFT*PR^	Q9NZI7	60	2	701,281
305	2.7	USF2	230	upstream stimulatory factor 2 isoform 1	IDGTR^*PR^DER^	Q15853	37	2	50,523
306	2.0	ZC3H7A	210	zinc finger CCCH-type containing 7A	ALNHSVEDIEPDLT*PR	Q8IWR0	111	3	1,517,664
307	1.5	ZNF503	223	zinc finger protein 503	VPSATCQPFT*PR^	Q96E25	63	2	528,730
310	Vesicle protein								
313	3.0	EXOC4	§237	SEC8 protein isoform b	DASVPLIDVTNLPT*PR^	Q96A65	111	4	14,507,494
314	2.7	EXOC5	§122	SEC10 protein	VCHLGDQLQEVNT*PR^	Q00471	82	2	677,799

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