

TABLE: MAPK SUBSTRATE MOTIF PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human epithelial carcinoma (HeLa) cell line; Trypsin Digest; Antibody: MAPK Substrate Motif, PXpTP; CST #4391

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	-2.8	DLG5	\$1011	discs large homolog 5	AGPLT*PPKPPR	Q8TDM6	214	1	280,013
3	1.7	FRS2	456, 464	fibroblast growth factor receptor substrate 2	TPT*TPLPQT*RR	Q8WU20	57	1	2,777,547
4	2.7	FRS2	457, 462	fibroblast growth factor receptor substrate 2	TPTT*PLPQT*PTR	Q8WU20	57	1	319,948
5		Adhesion or extracellular matrix protein							
6	3.0	zyxin	\$259, \$267, \$270	zyxin	GPPASS*PAPAPKFS*PVT*PK	Q15942	61	2	1,013,190
7		Cell cycle regulation							
8	1.3	CENPF	\$154	centromere protein F	IFTTPLT*PSQYSGSK	P49454	368	1	6,512,762
9	3.9	INCENP	\$59	inner centromere protein antigens 135/155kDa isoform 1	EFKPELM#PKT*PSQK	Q9NQS7	106	1	1,337,918
10	2.6	MDC1	\$1425	mediator of DNA damage checkpoint 1	LEPSTSDQPV*PEPTSQATR	Q14676	227	4	1,116,425
11	4.2	MDC1	\$1444, \$1466	mediator of DNA damage checkpoint 1	SSVKT*PETVVTAPQLPSTSDQPV*PEPTSQATR	Q14676	227	1	441,373
12	5.1	NUDE1; NUDE1 iso2	\$240, \$243, \$246; \$240, \$243, \$246	nuclear distribution gene E homolog 1	RGLDDST*GGT*PLT*PAAR	Q9NXR1; Q9NXR1-2	39; 38	1	363,039
13	2.2	NUDE1; NUDE1 iso2	\$243, \$246; \$243, \$246	nuclear distribution gene E homolog 1	GLDDSTGGT*PLT*PAAR	Q9NXR1; Q9NXR1-2	39; 38	1	579,989
14	1.7	PRC1; PRC1 iso2	\$470; \$440	protein regulator of cytokinesis 1 isoform 1	QTETEMLYGSAPRT*PSKR	Q43663; Q43663-2	72; 67	3	1,156,145
15	4.6	SEPT2	14	septin 2	QQPTQFINPET*PGYVGFANLPNQVHR	Q15019	41	4	8,185,810
16	2.8	TPX2	\$369	TPX2, microtubule-associated protein homolog	ICRDPQT*PVLQTK	Q9ULW0	86	5	25,922,346
17		Cell development/differentiation							
18	-1.5	COBLL1	\$297, \$301	COBL-like 1	DQTAS*APAT*PLVNK	Q9Y2I3	132	2	1,231,670
19	-1.3	GRIN1	\$877	G protein-regulated inducer of neurite outgrowth 1	SVATGPM#T*PQAAAPAFPEVR	Q7Z2K8	102	2	471,215
20		Chromatin, DNA-binding, DNA repair or DNA replication protein							
21	1.7	FLJ13111; FLJ13111 iso2	27; 27	centromere protein T	VLDTADPRT*PR	Q96BT3; Q96BT3-2	60; 32	1	68,474
22	-1.0	CAF-1A; CAF-1A iso4	\$237, \$241; \$255, \$259	chromatin assembly factor 1, subunit A (p150)	S*LPAT*PQGK	Q13111; Q6NXG5	105; 107	4	875,322
23	-1.1	capicua	\$583	capicua homolog	AQESGGGAGTAGLRPPPPGAGGPAT*PSK	Q96RK0	164	3	681,925
24	2.5	NSBP1	\$31	nucleosomal binding protein 1	LSAM#LVPVT*PEVKPK	P82970	32	1	3,370,839
25		Cytoskeletal protein							
26	2.5	anillin	\$320, \$323	anillin, actin binding protein	SCEGQNPPELLPKT*PIS*PLK	Q9NQW6	124	5	14,889,212
29	2.6	KIF14	81	kinesin family member 14	TADMLPT*PNPVGR	Q15058	186	3	6,344,656
30	3.7	KIF20A	\$857, \$864	kinesin family member 20A	NLLPRT*PTCQSST*DCSPYAR	Q95235	100	1	4,230,949
31	3.7	KIF20A	\$857, \$867	kinesin family member 20A	NLLPRT*PTCQSSTDCS*PYAR	Q95235	100	3	6,776,179
32	-1.6	Lamin B1	\$19	lamin B1	AGGPPT*PLSPTR	P20700	66	1	883,635
33	3.3	Lamin B1	\$19, \$22	lamin B1	AGGPPT*PLS*PTR	P20700	66	3	37,062,696
34	-1.5	Lamin B2	\$14	lamin B2	AGGPAT*PLSPTR	Q03252	68	1	1,921,313
35	3.7	Lamin B2	\$14, \$17	lamin B2	AGGPAT*PLS*PTR	Q03252	68	3	11,317,311
36	-1.3	MAP1B	\$1779, \$1782, \$1788	microtubule-associated protein 1B	VQSLEGEKLS*PKS*DISPLT*PR	P46821	271	4	9,641,526
37	-1.2	MAP1B	\$1782, \$1788	microtubule-associated protein 1B	S*DISPLT*PR	P46821	271	2	3,763,763
38	-1.1	MAP1B	\$1788	microtubule-associated protein 1B	SDISPLT*PR	P46821	271	1	8,211,013
39	1.5	nestin; nestin iso2	\$338; \$337	nestin	LELQFPRT*PEGR	P48681; CAA46780	177; 177	1	1,645,841
40	3.9	PDLIM7	\$247, \$251	PDZ and LIM domain 7 isoform 1	TSTVLTRHS*QPAT*PTPLQSR	Q9NR12	50	2	20,180,930
41	2.9	PDLIM7	\$251	PDZ and LIM domain 7 isoform 1	HSQPAT*PTPLQSR	Q9NR12	50	2	352,519
42	2.8	smoothelin iso4	\$357, \$360	smoothelin isoform c	LQDGTQAALS*PLT*PAR	P53814-4	99	2	1,115,819
43	2.4	VASP	334	vasodilator-stimulated phosphoprotein	SSSVTSETQPCT*PSSSDYDLQR	P50552	40	1	324,513
46		G protein or regulator							
47	-1.5	PLEKHG2	\$445, \$450	common-site lymphoma/leukemia guanine nucleotide exchange factor	SKPVLEPLT*PPLGS*PRPR	Q9H7P9	148	1	737,284
48	-1.9	RALGPS2	\$326, \$329	Ral GEF with PH domain and SH3 binding motif 2	SVAAGALLPQT*PPS*PR	Q86X27	65	2	704,285

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

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49		Motor or contractile protein							
50	1.1	LOC146909	417, 425, §429	kinesin family member 18B	SGPPPEHLPS*PLPPHPPS*QPCT*PELPAGPR	Q86Y91	93	1	553,742
51	2.1	MYO9B	§1267, §1271	myosin IXB isoform 2	VSPAPGS*APET*PEDK	Q13459	244	2	286,076
52		Phosphatase							
53	3.4	PHACTR4	§427, §432	phosphatase and actin regulator 4 isoform 1	IQQALTS*PLPMT*PILEGSHR	Q8IZ21	78	3	5,391,929
54	-1.2	PHACTR4	§432	phosphatase and actin regulator 4 isoform 1	IQQALTSPLPMT*PILEGSHR	Q8IZ21	78	1	632,356,224
55	2.2	PPP1CB	§315	protein phosphatase 1, catalytic subunit, beta isoform 1	YQYGGGLNSGRPVT*PPR	P62140	37	2	6,170,167
56		Protein kinase, Ser/Thr (non-receptor)							
57	1.2	KSR	§268, §272	kinase suppressor of ras	ALHSFIT*PPTT*PQLR	Q8IVT5	102	1	1,104,083
58		Protein kinase, Tyr (non-receptor)							
59	1.7	Abl; Abl iso2	§852; §871	v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a	GSALGTAAAEVPT*PTSK	P00519; P00519-2	123; 125	1	526,975
60		Protein kinase, Tyr (receptor)							
61	-1.8	EGFR	§693	epidermal growth factor receptor isoform a precursor	ELVEPLT*PSGEAPNQALLR	P00533	134	3	222,871,264
62		RNA processing							
63	2.5	hnRNP D0; hnRNP D0 iso3	§193; §193	heterogeneous nuclear ribonucleoprotein D isoform d	IFVGLSPDT*PEEK	Q14103; Q14103-3	38; 33	1	581,633
64	2.0	LARP; LARP iso3	§376; §299	la related protein isoform 1	KFDGVEGPR*PK	Q6PKG0; Q6PKG0-3	124; 116	4	8,690,315
65	1.7	LARP; LARP iso3	780, §785, §788; 703, §708, §711	la related protein isoform 1	NT*RTPT*PRT*PQLK	Q6PKG0; Q6PKG0-3	124; 116	1	126,591
66	1.7	LARP; LARP iso3	782, §785, §788; 705, §708, §711	la related protein isoform 1	NTRT*PRT*PRT*PQLK	Q6PKG0; Q6PKG0-3	124; 116	1	219,621
67	-1.4	SFRS10	§201	splicing factor, arginine/serine-rich 10	RPHT*PTPGIYM#GRPTYGSSR	P62995	34	1	1,771,014
68	-2.4	SFRS10	§203	splicing factor, arginine/serine-rich 10	RPHTPT*PGIYM#GR	P62995	34	1	842,714
69	-1.7	SRm160; SRm160 iso3	§402, §406; §397, §401	serine/arginine repetitive matrix 1	HRPS*PPAT*PPPK	Q8IYB3; A9Z1X7	102; 103	5	514,937
71	-1.4	SRm300	§1434	splicing coactivator subunit SRm300	DGLPRT*PSRR	Q9UQ35	300	1	4,596,490
72	-1.4	SRm300	§1492	splicing coactivator subunit SRm300	ALPQT*PRPR	Q9UQ35	300	1	446,852
73	1.5	SRm300	§2289	splicing coactivator subunit SRm300	TAVAPSAVNLPDPT*PTAPAVNLAGAR	Q9UQ35	300	2	4,046,229
75		Receptor, channel, transporter or cell surface protein							
76	1.2	PMCA4; PMCA4 iso6	1181; 1145	plasma membrane calcium ATPase 4 isoform 4a	SIHSMTHPEFAIEELPRT*PLDEEEENPDKASK	P23634; P23634-6	138; 134	3	1,060,524
77	2.8	IP3R1; IP3R1 iso3	955; 946	inositol 1,4,5-triphosphate receptor, type 1 isoform 1	GGGFLPMT*PM*AAPEGNVK	Q14643; Q14643-3	314; 309	3	1,394,733
78	3.7	NUP107	§55, §58, §64	nucleoporin 107kDa	NQVIPRT*PSS*FRQPFT*PTSR	P57740	106	2	1,704,777
79	3.7	NUP107	§57, §58, §64	nucleoporin 107kDa	NQVIPRTPS*S*FRQPFT*PTSR	P57740	106	1	6,149,160
80	1.1	NUP214	§433, §437	nucleoporin 214kDa	SPGS*TPIT*PTSSQAPQK	P35658	214	2	89,229
81		Transcriptional regulator							
82	-1.0	DMAPI	409	DNA methyltransferase 1 associated protein 1	AGVLGGPAT*PASGPGPASAEPVTEPGLGDPDK	Q9NPF5	53	1	1,529,601
83	-1.1	DMAPI	§445	DNA methyltransferase 1 associated protein 1	DTIIDVVGAPLT*PNR	Q9NPF5	53	4	14,386,767
84	-1.6	ERF	§526	Ets2 repressor factor	GEGPGEAGGPLT*PR	P50548	59	4	4,960,815
86	3.0	FOXC1	68	forkhead box C1	AYGPYT*PQPQPK	Q12948	57	2	1,156,145
87	19.0	NFAT90; NFAT90 iso4; NFAT90 iso5	§592; §596; §592	interleukin enhancer binding factor 3 isoform b	AYAALAALEKLPDPT*PLALDANKK	Q12906; Q12906-4; Q12906-5	95; 76; 75	4	2,538,473
88	3.2	FIR	§60	poly-U binding splicing factor 60KDa	LGLPLPT*PEQAEALQK	Q9UHX1	60	4	6,671,154
89	3.9	SPT5	§1034	suppressor of Ty 5 homolog isoform a	VVSISSEHLEPIT*PTKNNK	O00267	121	2	2,855,990
90		Ubiquitin conjugating system							
92	1.5	UBR1	§21	ubiquitin protein ligase E3 component n-recogin 1	MEISALPQT*PQR	Q8IWW7	200	5	5,847,590
93	-1.3	USP32	1326	ubiquitin specific protease 32	DPALCQHKPLT*PQGDELSEPR	Q8NFA0	182	1	1,272,469

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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
94		Unknown function							
95	2.0	FLJ13144	\$607	ankyrin repeat and zinc finger domain containing 1	AQVPGPLT*PEMEAR	Q9H8Y5	81	2	5,847,590
96	3.5	AUP1	\$433	ancient ubiquitous protein 1	GTQSLPTASASKFPSSGPVT*PQPTALTFAK	Q9Y679	53	3	2,457,190
97	4.0	C12orf52	248, 253	hypothetical protein LOC84934	SVS*ISVPS*TPR	Q96K30	29	1	2,904,683
98	4.9	C19orf21	\$160, \$172	hypothetical protein LOC126353	KSSTVAT*LQGTDPDHGDPRT*PGPPR	Q8IVT2	75	1	475,776
99	5.7	C19orf21	\$164, \$172	hypothetical protein LOC126353	SSTVATLQGT*PDHGDPR*PGPPR	Q8IVT2	75	2	1,933,100
100	-1.6	CCDC9	381, \$385	coiled-coil domain containing 9	EGAASPAPET*PQPT*SPETSPK	Q9Y3X0	60	1	189,690
101	1.0	FLJ13725	\$351, \$355	hypothetical protein LOC79567	FSTYSQS*PPDT*PSLR	Q6ZS17	132	1	1,274,198
102	-1.2	FBXL20	\$417	F-box and leucine-rich repeat protein 20	VHAYFAPVT*PPPSVGGSR	Q96IG2	48	1	474,547
103	2.8	LIMCH1; LIMCH1 iso1	702; 317	LIM and calponin homology domains 1 isoform b	YGPRT*PVSDDAESTSM#FDM#R	Q9UPQ0-3; Q9UPQ0	164; 122	5	1,329,036
104	4.1	PLEKHA2	358	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	APSVASSWQPWT*PVPQAGEK	Q9HB19	47	2	1,653,527
105	1.2	RBM9 iso6	67	RNA binding motif protein 9 isoform 1	TEEAADGGGGMQNEPLT*PGYHGFPAR	Q43251-6	47	4	4,962,586
106	-1.4	KIAA1856	2146	trinucleotide repeat containing 18	GGAVRPLT*PAPR	Q15417	315	3	844,331
107	-1.5	TREP-132	\$743, \$746	transcriptional regulating factor 1	QGSGLFSNVLISGHGPGAHPQLPLT*PLT*PTPR	Q96PN7	132	1	1,324,588
108	-1.5	PYM	\$64, \$72	within bcn homolog	SKPELPPLGLS*PEATAPVT*PSRPEGGEPLSK	Q9BRP8	23	1	448,936
109	8.6	KIAA1064	1153	zinc finger CCCH-type containing 4	VLAAGGLGGGGGGQSSVLSGISLYDPRT*PNAGGK	Q9UPT8	140	1	1,665,591
110	1.5	ZNF609	817, 823	zinc finger protein 609	LENTT*PTQPLT*PLHVVTQNGAEASSVK	Q15014	151	1	4,715,513
111		Vesicle protein							
112	3.3	PHLDB2	\$574	pleckstrin homology-like domain, family B, member 2 isoform b	ASSESSYLSILPKT*PEGISEEQR	Q86SQ0	142	1	832,304

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