

Table: PTMScan® Results, Phospho-AMPK Substrate Motif (LXRXS*/T*), SILAC

Study design: Human non-small cell lung cancer (H1650) cell line; LysC/post-IAP trypsin digest; Antibody: Phospho-AMPK Substrate Motif (LXRXS*/T*), PTMScan® Kit ##5564

Treatments: Untreated (Light), Phenformin-treated (Heavy)

Index	Fold-Change (Phenformin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
1 Adaptor/scaffold									
2	3.89	Abi-1; Abi-1 iso3	323; 296	abl-interactor 1 isoform b	HNsTTSSTSSGGYR	Q8IZP0; Q8IZP0-3	55; 49	2	1.20E+06
3	1.21	atfiphilin	518	atfiphilin protein isoform c	KSsGTGTEPVAK	Q6ULP2	102	5	9.73E+04
4	1.07	AHNAK	210	AHNAK nucleoprotein isoform 1	LPsGSGAASPTGSVAVDIR	Q09666	629	1	2.51E+05
8	1.85	RIAM	528	amyloid beta (A4) prec prot-binding, family B, member 1 interacting prot	SSDlSGSPATPLK	Q7Z5R6	73	1	2.16E+05
9	3.68	CGN	129	cingulin	sHSQASLAGPGVPDPSNR	Q9P2M7	136	1	2.56E+06
11	-1.04	CGN	149	cingulin	SNsMLELAPK	Q9P2M7	136	2	1.94E+06
12	-2.67	CTNND1; CTNND1 iso3, 4	252; 252; 252	catenin, delta 1 isoform 1ABC	APsRDVYVGGPOQVR	O60716; O60716-3; O60716-4	108; 105; 106	2	1.94E+06
13	1.05	SAPAP4; SAPAP4 iso2	711; 714	disks large-associated protein 4 isoform c	RDlSDTDQANDSSCK	Q9Y2H0; Q9Y2H0-2	108; 108	2	1.91E+04
14	3.51	HOMER3	159	Homer, neuronal immediate early gene, 3 isoform 2	SQsADAPGPTER	Q9NSC5	40	2	5.86E+05
15	-1.03	LMO7; LMO7 iso2, 3	1510; 1510; 1176	LIM domain only 7 isoform 1	RGEsLDNLDSPR	Q8WW11; Q8WW11-2; Q8WW11-3	193; 191; 154	1	7.71E+05
16	-1.1	PARD3	144	partitioning-defective protein 3 homolog	RSsDPALIGLSTVSDFSSEEPSR	Q8TEW0	151	2	3.93E+05
17	1.7	LIM; LIM iso3	208; 208	PDZ and LIM domain 5 isoform b	QPVTsVCSETSQELAEQQR	Q96HC4; Q5UW38	64; 64	1	2.64E+05
18	1.18	liprin beta 1; liprin beta 1 iso2	599; 593	PTPRF interacting protein binding protein 1 isoform 1	sQSTTFNDDMSEPEFK	Q86W92; Q86W92-2	114; 113	1	7.49E+05
19	1.52	liprin beta 1; liprin beta 1 iso2	601; 595	PTPRF interacting protein binding protein 1 isoform 1	SQsTTFNDDM#SEPEFK	Q86W92; Q86W92-2	114; 113	1	5.41E+05
20	1.12	NHERF	288	sodium/hydrogen exchanger regulatory factor 1	sASSDTSEELNSQDSPPK	O14745	39	1	7.43E+06
21	1.12	NHERF	290	sodium/hydrogen exchanger regulatory factor 1	SAsSDTSEELNSQDSPPK	O14745	39	2	8.29E+06
22	1.12	NHERF	291	sodium/hydrogen exchanger regulatory factor 1	SASsDTSEELNSQDSPPK	O14745	39	1	8.29E+06
24	-1.37	ZO2	966	tight junction protein 2 (zona occludens 2) isoform 1	KPsPEPR	Q9UDY2	134	1	3.35E+05
25	1.04	ZO2	978	tight junction protein 2 (zona occludens 2) isoform 1	AAsSDQLR	Q9UDY2	134	1	5.44E+06
26	-1.45	ZO2	986	tight junction protein 2 (zona occludens 2) isoform 1	DNsPPPAFKPEPPK	Q9UDY2	134	3	1.53E+06
27	1.05	tensin 3	332	tensin 3	WDsYENLSADGEVLHTQGVPVDSGLYAK	Q68CZ2	155	3	2.18E+06
28	-1.08	TRIP10	296	thyroid hormone receptor interactor 10	APsDSSLGTPSDGRPELR	Q15642	68	1	6.92E+05
29 Adhesion or extracellular matrix protein									
30	-1.11	desmoplakin	22	desmoplakin isoform II	AeSGPDLR	P15924	332	3	1.14E+07
31	3.65	Erbin	1015	ERBB2 interacting protein isoform 7	SEsTENQSYAK	Q96RT1	158	1	9.08E+05
32	1.28	Erbin	485	ERBB2 interacting protein isoform 7	RYPIYPDELK	Q96RT1	158	2	7.14E+05
33	1.29	afadin iso3	1734	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	KLlELENELNTK	P55196-3	198	1	2.35E+05
34	1.52	afadin; afadin iso3	215; 215	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	TlSsNPEVVMK	P55196-1; P55196-3	206; 198	1	3.29E+05
35	-1.18	plakophilin 2; plakophilin 2 iso2	82; 82	plakophilin 2 isoform 2a	TSsVPEVYVNLHLVENDFVGGGR	Q99959; Q99959-2	97; 93	1	1.98E+06
36	1.2	TJAP1	545	tight junction associated protein 1 isoform a	KDsLTAQAEQGNLLN	Q5JTD0	62	4	3.19E+06
37 Apoptosis									
38	-11.66	PRAS40	246	AKT1 substrate 1 (proline-rich)	LNlSDFQK	Q96B36	27	2	8.94E+07
39	1.31	BAD	118	BCL2-associated agonist of cell death	RMsDEFVDSFK	Q92934	18	1	2.23E+05
40 Cell cycle regulation									
41	1.62	AFAP1L2	484	KIAA1914 protein isoform 1	KfSEPNYlDGLPSQDR	Q8N4X5	91	3	1.34E+06
42	-2.36	BAT2D1; BAT2D1 iso8	2695; 2694	HBxAg transactivated protein 2	ATsTSPNSQSSK	Q9Y520; NP_055987	317; 309	1	2.76E+04
43	1.21	CLASP1; CLASP1 iso3	598; 598	CLIP-associating protein 1 isoform 2	sRSSDlDVNAAASAK	Q7Z460; Q7Z460-3	169; 165	1	1.45E+06
44	89.39	CLASP1; CLASP1 iso3	600; 600	CLIP-associating protein 1 isoform 2	SRsDlDVNAAASAK	Q7Z460; Q7Z460-3	169; 165	4	2.68E+06
45	1.41	SPECC1L	832	cytospin A	RSsTSSEPTPTVK	Q69YQ0	125	3	1.11E+06
46	-1.79	TNKS1BP1	1473; 1476	tankyrase 1-binding protein 1	REsAAsGLGLLLEEEGAGAGAAQEEVLEPGR	Q9C0C2	182	1	3.70E+05
47	-1.26	TPX2	147	TPX2, microtubule-associated protein homolog	CAIPVlDEILPSK	Q9ULW0	86	1	3.39E+05
48 Chaperone									
49	1.78	HSP27	82	heat shock protein beta-1	QLsSGVSEIR	P04792	23	2	7.89E+07
50 Chromatin, DNA-binding, DNA repair or DNA replication protein									
51	1.08	GPATCH8	1107	G patch domain containing 8	KPsVSEEVQATPNK	Q8TB99	164	2	2.17E+05
52	-1.18	HIRIP3	370	HIRA interacting protein 3	EvsDSEAGGGPQGER	Q9BW71	62	2	2.16E+05
53	1.03	MCM3	160	minichromosome maintenance complex component 3	RYsDLTLVAFPSVVYPTK	P25205	91	1	3.08E+05
54	-1.38	TMPO; TMPO iso2; TMPO iso6	159; 159; 159	thymopoietin isoform beta	SsTlPLTISSAENTR	P42167; P42167-2; P42166	51; 39; 75	1	5.97E+05
55	-1.38	TMPO; TMPO iso2; TMPO iso6	160; 160; 160	thymopoietin isoform beta	SSlPLTISSAENTR	P42167; P42167-2; P42166	51; 39; 75	1	8.21E+05
56	-1.11	ZNF185; ZNF185 iso1	154; 158; 19; 23	zinc finger protein 185	RSSlSGDlEEEEEEVVPFSSDEQK	NP_009081; O15231	74; 49	1	4.67E+05
57	1.65	ZNF185; ZNF185 iso1	465; 233	zinc finger protein 185	REsCGSSVLTDFEGK	NP_009081; O15231	74; 49	1	3.20E+05

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Index	Fold-Change (Phenformin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
58 Cytoskeletal protein									
59	1.2	ADD1; ADD2; ADD3	726; 713; 693	adducin 1 (alpha) isoform a	TPsFLKK	P35611; P35612; Q9UEY8	81; 81; 79	2	6.01E+06
60	-1.16	IRSp53	366	BAI1-associated protein 2 isoform 4	SSsMAAGLER	Q9UQB8	61	3	8.63E+06
61	1.11	CLASP2; CLASP2 iso3, 6	370; 603; 92	CLIP-associating protein 2	SRsDIDVAAAGAK	O75122; Q8NB74; IP100796485	141; 78; 27	4	1.72E+06
62	-1.55	CTNNA1; CTNNA2	655; 658; 654; 657	catenin, alpha 1	SRTsVQIEDDQLIAGQSAR	P35221; P26232	100; 105	1	6.24E+05
63	3.54	DBNL; DBNL iso2	269; 270	drebrin-like isoform b	AMsTTsISSPPQPK	Q9UJU6; Q9UJU6-2	48; 48	2	2.21E+06
64	3.54	DBNL; DBNL iso2	270; 271	drebrin-like isoform b	AMsITsISSPPQPK	Q9UJU6; Q9UJU6-2	48; 48	1	2.21E+06
65	1.05	FNBP1; FNBP1 iso5	296; 257	formin binding protein 1	TVsDNLSNSR	Q96RU3; Q50P69	71; 66	1	8.05E+05
66	1.15	KIF13A	1698	kinesin family member 13A isoform b	TGsCSELDACPSK	Q9H1H9	202	3	9.44E+05
67	2.55	K19	10	keratin 19	QsSATSFGGLGGGSVR	P08727	44	1	2.25E+06
68	-1.33	K19	35	keratin 19	APsIHGGSGGR	P08727	44	1	5.06E+07
69	2.55	K19	9	keratin 19	QsSATSFGGLGGGSVR	P08727	44	1	8.82E+05
70	-1.28	MAP1B	561	microtubule-associated protein 1B	KEsKEETPEVTK	P46821	271	1	1.44E+06
71	1.71	palladin	893	palladin	IAsDEEIQGTK	Q8WX93	151	2	3.50E+06
72	-1.25	plectin 1 iso11	21	plectin 1 isoform 1	TSsEDNLYLAVLR	Q15149-4	516	1	1.49E+05
73	-1.27	plectin 1; plectin 1 iso2, 6, 10, 11	2886; 2776; 2735; 2753; 2749	plectin 1 isoform 1	RLIVNEAVK	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	3.66E+05
74	-1.39	plectin 1; plectin 1 iso2, 6, 10, 11	4385; 4275; 4234; 4252; 4248	plectin 1 isoform 1	SsSVGSSSSYPISPAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	1.73E+05
75	1.19	plectin 1; plectin 1 iso2, 6, 10, 11	4642; 4532; 4491; 4509; 4505	plectin 1 isoform 1	RGsFDATGSGF	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	22	5.96E+06
76	3.44	SHRM	1441	shroom family member 3 protein	EdsLPEESSAPDFANLK	Q8TF72	217	1	1.81E+05
77	-1.02	SPTBN1 iso2	10	spectrin, beta, non-erythrocytic 1 isoform 1	TSSIsGPLSPAYTGQVPYNNQLEGR	Q01082-3	251	1	2.29E+06
78	7.24	SPTBN1	2328	spectrin, beta, non-erythrocytic 1 isoform 1	AQILPITSVVITSESSPGKR	Q01082	275	2	1.76E+06
79	2.91	SSFA2	270	sperm specific antigen 2 isoform 1	IGsMSSVTSNK	P28290	138	1	3.98E+05
80	1.27	SSFA2	739	sperm specific antigen 2 isoform 1	SQsLPTTLLSPVR	P28290	138	1	2.02E+06
81	-1.13	PSRC2; PSRC2 iso5	352; 361	proline/serine-rich coiled-coil 2	RIsTSDILSEK	O60293; BAA25472	226; 218	1	2.62E+05
82 Enzyme, misc.									
83	5.7	DDX19A; DDX19B	467; 468	DDX19-like protein	LDIDDLDEIEK	Q9NUU7; Q9UMR2	54; 54	1	3.35E+05
84	-1.06	GFAT; GFAT iso2	261; 243	glucosamine-fructose-6-phosphate aminotransferase	VdStTCLFPVEEK	Q06210; Q06210-2	79; 77	3	2.48E+07
85	-1.05	SKI2W	256	superkiller viralicidic activity 2-like homolog	ASsLEDLVLK	Q15477	138	3	1.67E+07
86	1.09	TP1	21	triosephosphate isomerase 1 isoform 1	KQsLGEIIGLNAAK	P60174	27	20	1.59E+08
87 G protein or regulator									
88	1.15	Cdc42EP1	192		RSDsLLSFR	Q00587	40	1	2.47E+05
90	-1.64	RaIGAPA1	798	GTPase activating Rap/RanGAP domain-like 1 isoform 1	SSsSIDILEPFTVER	Q6GYQ0	230	2	1.01E+06
91	1.26	PLEKHG3; PLEKHG3 iso5	618; 176	pleckstrin homology domain containing, family G, member 3	RSsVAQEDSK	A1L390; PLEKHG3	134; 31	1	6.85E+04
93	-1.39	RALBP1	29	ralA binding protein 1	TPsSEESPTK	Q15311	76	2	7.97E+05
94	-1.39	RALBP1	30	ralA binding protein 1	TPsSEESPTK	Q15311	76	2	7.97E+05
95	-1.19	Rap1GAP; Rap1GAP iso5	499; 529	RAP1 GTPase activating protein isoform b	RSsAIGIENIQVEK	P47736; Q5T3S9	73; 77	2	4.99E+05
96	-1.03	SIP1L1	1585	signal-induced proliferation-associated 1 like 1	TLSDESIVNSQR	Q43166	200	1	1.27E+06
97	-1.12	SIP1L3	1544	signal-induced proliferation-associated 1 like 3	TLSDESLSCSR	Q60292	195	1	1.06E+06
98	-1.43	TBC1D1	596	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	ANILSHFPIECDEPPQPAR	Q86T10	133	1	3.61E+05
99	1.1	Tiam1	231	T-cell lymphoma invasion and metastasis 1	ANsLGDLYAQK	Q13009	178	2	6.85E+05
100 Inhibitor protein									
101	1.83	ENSA	109	endosulfine alpha isoform 3	KsSLVTSK	Q43768	13	4	5.73E+05
102	2.42	optineurin	342	optineurin	KNsAIPSELNEK	Q96CV9	66	1	5.54E+05
103	1.33	RKIP	51	prostatic binding protein	NRPSISWDGLDSGK	P30086	21	1	1.97E+05
104 Lipid binding protein									
106	1.04	PLEKHA5	408	pleckstrin homology domain containing, family A member 5 isoform 2	tNSM#QQLQEWIK	Q9HAU0	127	1	4.63E+05
107	-1.22	PLEKHA5	410	pleckstrin homology domain containing, family A member 5 isoform 2	TNSMQQLQEWIK	Q9HAU0	127	1	5.44E+05
108 Mitochondrial protein									
109	-1.37	ETFB	194	electron-transfer-flavoprotein, beta polypeptide isoform 2	YAtLPNIMK	P38117	28	1	1.96E+05
110	-1.07	PKM2; PKM2 iso2	249; 249	pyruvate kinase, muscle isoform M2	KAsDVHEVR	P14618; P14618-2	58; 58	5	1.44E+05

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Index	Fold-Change (Phenformin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
111		Motor or contractile protein							
112	-1.14	MRLC3; MRLC2; MRLC1	18; 19; 19	myosin, light chain 12A, regulatory, non-sarcomeric	AISNVFAM#FDQSQIQEFK	P19105; O14950; P24844	20; 20; 20	2	7.73E+05
113		Phosphatase							
114	1.2	PFKFB3	461	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 isoform 2	RNsVTLPLASPEPTK	Q16875	60	2	8.97E+04
115	-1.45	PPP1CA	320	protein phosphatase 1, catalytic subunit, alpha isoform 3	YGQFSGLNPPGRRIPPR	P62136	38	2	2.26E+06
118	4.43	Spinophilin	100	protein phosphatase 1, regulatory subunit 9B	ASSLNENVDHSALLK	Q96SB3	89	2	1.10E+06
119	1.48	PPP2R5D	573	delta isoform of regulatory subunit B56, protein phosphatase 2A isoform 1	RKsELPQDVYTIK	Q14738	70	2	7.53E+05
120	2.5	PTPN12	435	protein tyrosine phosphatase, non-receptor type 12 isoform 2	NLSFEIK	Q05209	88	1	1.20E+07
121	1.08	PTPN3	359	protein tyrosine phosphatase, non-receptor type 3 isoform 2	SLsVEHLETK	P26045	104	1	3.31E+05
122	1.11	SSH1; SSH1 iso4	515; 203	slingshot homolog 1	RLSDPLLSPEDETGSLVHLEDPER	Q8WYL5; Q8WYL5-4	116; 81	2	4.10E+05
123	1.94	SSH3	37	slingshot homolog 3	RQsFAVLR	Q8TE77	73	1	1.56E+06
124		Protease							
126	-1.35	USP24	2561	ubiquitin specific protease 24	TIsAQDTLAYATALLNEK	Q9UPU5	294	3	1.87E+06
127		Protein kinase, Ser/Thr (non-receptor)							
128	3.28	Bcr	301	breakpoint cluster region isoform 1	SQsTSEQEK	P11274	143	1	5.37E+05
129	-1.11	B-Raf	447	B-Raf	RDSsDDWEIPDQGITVGQR	P15056	84	1	4.54E+05
130	2	CaMK2-gamma; + iso2, 6, 7	287; 287; 287; 287	calcium/calmodulin-dependent protein kinase II gamma isoform 4	QEIVECLR	Q13555; Q13555-2; NP_751913; Q5SWX3	63; 61; 57; 58	1	1.10E+06
131	1.6	CAMKK2; CAMKK2 iso3	495; 495	calcium/calmodulin-dependent protein kinase kinase 2 beta isoform 1	sFGNPFEGSR	Q96RR4; Q96RR4-3	65; 60	1	3.87E+05
132	-1.21	DMPK2	1492	CDC42 binding protein kinase gamma (DMPK-like)	RPA sMGSEGLGGDADPMK	Q6DT37	173	1	2.09E+05
133	-1.14	QSK; QSK iso4	601; 445	KIAA0999 protein	RASDGGANIQLHAQQLLK	Q9Y2K2; A1A5A8	150; 134	6	2.02E+06
134	-1.59	KSR	404	kinase suppressor of ras	TEsVPSDINNPVDR	Q8IVT5	102	1	4.67E+05
135	1.01	MEKK2	239	mitogen-activated protein kinase kinase kinase 2	AQsYPDNHQEFSDYDNPIFEK	Q9Y2U5	70	2	2.04E+06
136	-1.01	PCTAIRE3; PCTAIRE3 iso3	130; 162	PCTAIRE protein kinase 3 isoform b	RAsLSDIGFGK	Q07002; Q07002-3	54; 58	3	1.23E+06
137	-2.38	PKAc + iso2; PKAc + iso2; PKACg	198; 190; 198; 245; 198	cAMP-dependent protein kinase catalytic subunit alpha isoform 1	TWILCGTPEYLAPEILSK	P17612; P17612-2; P22694; P22694-2; P22612	41; 40; 41; 46; 40	2	7.46E+06
140	-2.61	LOK	417	serine/threonine kinase 10	SRPVsM#DAR	Q94804	112	2	4.61E+04
141	-1.22	ZAK	637	MLK-related kinase isoform 1	SSsPTYGLTK	Q9NYL2	91	3	2.99E+05
142		Protein kinase, Tyr (non-receptor)							
143	-1.11	NEK1	1052	NIMA-related kinase 1	TCsLPDLSK	Q96PY6	143	3	1.02E+07
144		Protein kinase, regulatory subunit							
145	-1.2	PHKA2	1015	phosphorylase kinase, alpha 2 (liver)	Rf sADEQFFSVGQAASSAHSSK	P46019	138	3	4.85E+05
146	-1.74	PKAR2A	99	cAMP-dependent protein kinase, regulatory subunit alpha 2	Rv sVCAETYNPDEEEEDTDR	P13861	46	4	3.93E+05
147		RNA processing							
148	1.27	matrin 3; matrin 3 iso3	188; 188	matrin 3	RDSFDDR	P43243; A8MXP9	95; 100	1	1.02E+06
149	1.98	PACT	18	protein kinase, interferon-inducible ds RNA dependent activator isoform 2	EDsGTFSLGK	Q75569	34	1	1.32E+06
150	1.14	PUM1	709	pumilio 1 isoform 1	RDSLTGSSDYLK	Q14671	126	1	5.53E+05
151	-1.7	SART1	448	squamous cell carcinoma antigen recognized by T cells 1	Rv sVEEKEKPPVQPLPSDDTR	Q43290	90	5	1.97E+06
153		Receptor, channel, transporter or cell surface protein							
154	1.01	ALS2CR4	86	amyotrophic lateral sclerosis 2 chromosome region, candidate 4 isoform a	RP sEGNEPSTK	Q96Q45	48	2	2.48E+05
157		Secreted protein							
158	2.8	PDAP1	18	PDGFA associated protein 1	QYsPEEIDAQLQAEK	Q13442	21	1	1.95E+06
159		Transcriptional regulator							
160	-1.08	FLNA	2152	filamin A, alpha isoform 2	RAP sVANVGSCHDLSLK	P21333	281	11	1.82E+06
161	-1.19	TFIIF-alpha	385; 391	general transcription factor IIF, polypeptide 1, 74kDa	GNSRPGTP sAEGGSTSSTLR	P35269	58	1	1.84E+05
162	-1.67	PPARBP	1051	mediator complex subunit 1	SQIPPGVATPIPK	Q15648	168	3	1.04E+06
163	-1.11	MLL2; MLL2 iso2; MLL2 iso4	4463; 4158; 4738	myeloid/lymphoid or mixed-lineage leukemia 2	AL sPVIPLIPR	O14686; O14686-2; NP_003473	564; 532; 593	1	3.77E+05
164	-1.71	SMRT; SMRT iso4	1383; 1374	nuclear receptor co-repressor 2 isoform 2	EGIPPPPPPSK	Q9Y618; NP_001070729	274; 268	1	3.02E+05
165	-1.19	PNN	100	pinin, desmosome associated protein	QEsDPEDDDVK	Q9H307	82	2	1.29E+06
167	1.26	HBXAP	1295	remodeling and spacing factor 1	IEIDEEESCDNAHGDNQPAR	Q96T23	163	2	1.91E+05
168	-1.06	HBXAP	1335	remodeling and spacing factor 1	IEsDEEEDFENVGK	Q96T23	163	2	4.10E+06
169	-1.46	supervillin; supervillin iso2	852; 426	supervillin isoform 1	YQIQPVTLGEVEQVQSGK	O95425; O95425-2	248; 201	1	4.74E+05
170	-1.11	53BP1	1316	tumor protein p53 binding protein 1 isoform 2	TSgTSLSAMHSSGSSGK	Q12888	214	1	5.75E+05

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Table: PTMScan® Results, Phospho-AMPK Substrate Motif (LXRXXS*/T*), SILAC

Study design: Human non-small cell lung cancer (H1650) cell line; LysC/post-IAP trypsin digest; Antibody: Phospho-AMPK Substrate Motif (LXRXXS*/T*), PTMScan® Kit ##5564

Treatments: Untreated (Light), Phenformin-treated (Heavy)

Index	Fold-Change (Phenformin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
171	-1.4	53BP1	1316, 1320	tumor protein p53 binding protein 1 isoform 2	TsSGTslSAMHSSGSSGK	Q12888	214	1	4.71E+05
172	-1.4	53BP1	1319, 1320	tumor protein p53 binding protein 1 isoform 2	TSSGtslSAMHSSGSSGK	Q12888	214	1	6.59E+05
173	1.06	YAP1; YAP1 iso2	109; 109	Yes-associated protein 1, 65kDa isoform 1	QAstDAGTAGALTPQHVR	P46937; Q7Z574	49; 53	3	1.91E+07
174	-1.14	YAP1; YAP1 iso2	164; 164	Yes-associated protein 1, 65kDa isoform 1	QsSFEIPDDVPLPAGWEM#AK	P46937; Q7Z574	49; 53	2	4.77E+06
175 Translation									
176	-1.21	eIF4G2	508	eukaryotic translation initiation factor 4 gamma, 2 isoform 2	TQiPPLGQTPLQLGLK	P78344	102	4	2.48E+06
177 Tumor suppressor									
178	1.59	SASH1	407	SAM and SH3 domain containing 1	TcSFGFDLTNR	O94885	137	1	4.08E+05
180 Ubiquitin conjugating system									
182	2.71	UBE4B	105	ubiquitination factor E4B isoform 1	SQsMDIDGVSCEK	O95155	146	2	9.66E+05
183	-1.07	UBR4; UBR4 iso3	1760; 1760	retinoblastoma-associated factor 600	HAstSSPADK	Q5T4S7; Q5T4S7-3	574; 572	2	1.18E+05
184	4.35	UBXN4	489	UBX domain containing 2	LRiQDDGEDENNTWNGNSTQQM	Q92575	57	2	1.68E+06
185 Unknown function									
186	1.83	ANKS1A	647	ankyrin repeat and sterile alpha motif domain containing 1	SEslSNCSIGK	Q92625	123	1	1.72E+05
187	-1.2	BAIAP2L2; BAIAP2L2 iso2	478; 464	BAI1-associated protein 2-like 2	RSsmGSTAVATDVK	Q6UXY1; Q6UXY1-2	59; 57	2	3.08E+05
188	2.73	C14orf179	78	hypothetical protein LOC112752 isoform 2	KAseEIEDFR	Q96FT9	24	4	2.50E+06
189	-1.05	C19orf21	394	hypothetical protein LOC126353	ALsSDSILSPAPDAR	Q8IVT2	75	2	6.42E+05
190	-1.1	FLJ13137	222, 223	hypothetical protein LOC400793 isoform 2	RAssPSLIER	A1L170	29	1	4.20E+05
191	-1.18	C9orf40	76	hypothetical protein LOC55071	RDsGDNSAPSGQER	Q8IX03	21	4	3.80E+04
192	1.99	CAMSAP1	827	calmodulin regulated spectrin-associated protein 1	LNsCETK	Q5T5Y3	178	2	3.23E+05
193	-1.13	CCNYL1	344	cyclin Y-like 1 isoform 1	SFsADNFIGIOR	Q8N7R7	41	1	3.58E+05
195	1.06	FAM122B; FAM122B iso2	25; 25	hypothetical protein LOC159090	SSsAPLIHGLSDLSQVFQPYTLR	Q7Z309; BAC86380	27; 29	1	2.27E+05
197	-1.11	C5orf6	273	hypothetical protein LOC51307	SRsQPCLDAR	Q9NYF3	43	2	5.12E+05
198	1.02	FCHO2	403	FCH domain only 2 isoform b	NLsNEELTK	Q0JRZ9	89	1	1.93E+06
199	1.09	HN1; HN1 iso2	87; 87	hematological and neurological expressed 1 isoform 2	RNsSEASSGDFLDLK	Q9UK76; Q9UK76-2	16; 20	4	8.22E+06
200	1.09	HN1; HN1 iso2	88; 88	hematological and neurological expressed 1 isoform 2	RNsSEASSGDFLDLK	Q9UK76; Q9UK76-2	16; 20	3	7.55E+06
201	1.02	ARHGAP39	604	KIAA1688 protein	AFsEDEALAQENR	Q9C0H5	125	2	2.64E+05
203	1.53	LUZP1	574	leucine zipper protein 1	RSsSEGLSK	Q86V48	120	2	1.47E+06
204	1.59	LUZP1	575	leucine zipper protein 1	RSSsEGLSK	Q86V48	120	2	1.47E+06
205	-1.41	BPY2-IP1	729	BPY2 interacting protein 1	sASPHVDLCLVSPCFEHR	Q66K74	112	1	4.51E+05
206	-1.41	BPY2-IP1	731	BPY2 interacting protein 1	SAsPHVDLCLVSPCFEHR	Q66K74	112	1	4.51E+05
207	1.07	PLEKHA2	184	pleckstrin homology domain containing, family A member 2	SQsYIPTSGCR	Q9HB19	47	1	2.47E+05
208	-1.82	RBM47	519	RNA binding motif protein 47 isoform a	PIPVYTVAPNVQR	A0AV96	64	2	4.25E+06
209	1.26	SIPA1L2; SIPA1L2 iso2	1488; 1280	signal-induced proliferation-associated 1 like 2	TLsDESICSNR	Q9P2F8; BAA92627	190; 168	2	3.71E+05
210	1.36	TBC1D9B; TBC1D9B iso2	411; 411	TBC1 domain family, member 9B (with GRAM domain) isoform b	KAsVDPSTESSPAPQEGSEQPASPPLSSR	Q66K14; Q66K14-2	141; 139	1	1.19E+05
211	3.54	VPS37B	98	vacuolar protein sorting 37B	QsSSASLETLLALLQAEQAK	Q9H9H4	31	1	1.34E+05
212	-1.79	WDR20	432	WD repeat domain 20 isoform 2	sNSLPHSAVSNAGSK	Q8TB23	63	1	5.01E+05
213	1.34	ZC3H13 iso2	1438	zinc finger CCH-type containing 13	TEsLEAGDDESK	Q5T200-2	185	1	1.47E+05
214 Vesicle protein									
215	-9.76	EHBP1	1058	EH domain binding protein 1 isoform 2	KPsEDEVLNK	Q8NDI1	140	5	9.28E+05
216	-1.13	golgin-245	40	golgi autoantigen, golgin subfamily a, 4	TsSFTEQLDEGTPNR	Q13439	261	1	5.52E+05
217	-1.13	golgin-245	41	golgi autoantigen, golgin subfamily a, 4	TsSFTEQLDEGTPNR	Q13439	261	1	4.91E+05
218	1.04	golgin-245	71	golgi autoantigen, golgin subfamily a, 4	VPsVESLFR	Q13439	261	2	5.30E+06
221	1.33	RABEP1	407	rabaptin, RAB GTPase binding effector protein 1 isoform 2	AQsTDSLGTSGLSQSK	Q15276	99	2	5.90E+05

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