

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

Study design: Human non-small cell lung cancer (H3255) cell line; LysC/post-IAP trypsin digest; Antibody: Phospho-Akt Substrate Motif (RXRXXS*/T*), PTMScan® Kit #1979, #5563

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

Index	Fold-Change (Su11274/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
1 Adaptor/scaffold									
3	1.06	AHNAK	5782	AHNAK nucleoprotein isoform 1	SNsFSDER	Q09666	629	1	2.95E+05
5	8.03	CABLES1	415	Cdk5 and Abl enzyme substrate 1 isoform 2	NHIDSSFSQFR	Q8TDN4	68	2	3.87E+05
6	-2.29	CTNND1; CTNND1 iso3, 4	252; 252; 252	catenin, delta 1 isoform 1ABC	APsRQDVYGPQPQVR	Q60716; Q60716-3; Q60716-4	108; 105; 106	2	2.45E+06
7	-2.16	CTNND1; CTNND1 iso3, 4	321; 321; 321	catenin, delta 1 isoform 1ABC	SY*EDM#IGEEVPSDQYYWAPLAQHER	Q60716; Q60716-3; Q60716-4	108; 105; 106	1	2.87E+05
8	-1.59	EPS8L1	580	epidermal growth factor receptor pathway substrate 8-like prot 1 isoform b	WDSCDSLNGLDPSSEK	Q8TE68	80	1	1.92E+05
9	-1.25	IRS-1	1101	insulin receptor substrate 1	HSSeTFSSPSSATR	P35568	132	2	9.60E+05
10	1.84	LMO7; LMO7 iso2, 3	1510; 1510; 1176	LIM domain only 7 isoform 1	GEsLDNLDSPR	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	4	4.65E+06
11	1.98	LMO7; LMO7 iso2, 3	805; 805; 471	LIM domain only 7 isoform 1	MYsFDDVLEEGK	Q8WWI1; Q8WWI1-2; Q8WWI1-3	193; 191; 154	2	7.57E+06
12	1.54	LMO7; LMO7 iso2, 3	932; 932; 598	LIM domain only 7 isoform 1	SYIMDDAWK	Q8WWI1-3	193; 191; 154	1	1.39E+06
13	10.51	MLPH iso2	336	melanophilin isoform 2	ASsESQGLGAGVR	Q9BV36-2	63	1	1.51E+06
14	1.81	MLPH	337	melanophilin isoform 2	ASsEQIFELNK	Q9BV36	66	2	3.09E+06
15	-1.58	LIM; LIM iso3	208; 208	PDZ and LIM domain 5 isoform b	QPVTVCSETSQELAEQOR	Q96HC4; Q5UW38	64; 64	1	5.58E+05
16	12.13	Rictor	1135	rapamycin-insensitive companion of mTOR	TLtEPSVDFNHSDDFTPISTVQK	Q6R327	192	2	6.02E+06
17	-1.44	ZO2	966	tight junction protein 2 (zona occludens 2) isoform 1	KPsPEPR	Q9UDY2	134	3	2.69E+05
18	-1.24	ZO2	986	tight junction protein 2 (zona occludens 2) isoform 1	DNSPPPAFKPEPPK	Q9UDY2	134	6	3.77E+06
19 Adhesion or extracellular matrix protein									
20	21.36	afadin iso3	1718	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	LFsQGQDVSNK	P55196-3	198	1	1.18E+07
21 Apoptosis									
22	13.92	PRAS40	246	AKT1 substrate 1 (proline-rich)	LNISDFQK	Q96B36	27	2	1.36E+08
23	-1.9	BAD	75	BCL2-associated agonist of cell death	HSSYPAGTEDDEGMGEEPPFR	Q92934	18	1	6.82E+05
24	-1.13	BAD	99	BCL2-associated agonist of cell death	sAPPNLWAAQR	Q92934	18	1	9.91E+05
25 Cell cycle regulation									
26	2.15	SPECC1L	384	cytospin A	KGsSGNASEVSVACLTER	Q69YQ0	125	1	8.89E+05
27	-1.04	ZRF1	47	DnaJ (Hsp40) homolog, subfamily C, member 2 isoform 2	NAsASFQLEDK	Q99543	72	1	1.42E+06
28	1.46	TNKS1BP1	1666	tankyrase 1-binding protein 1	sAEEGSLAESK	Q9COC2	182	5	1.15E+06
29 Cell development/differentiation									
30	2.26	BRD1; BRD1 iso2	852; 983	bromodomain containing protein 1	CAeSSISSNSPLCDSSFNAPK	Q95696; Q86X06	120; 133	1	4.53E+05
31	6.16	COBL1	385	COBL-like 1	AGsLQLSSMSAGNSSLR	Q9Y2I3	132	1	5.64E+05
33 Chaperone									
34	1.06	HSP27	82	heat shock protein beta-1	QLsSGVSEIR	P04792	23	2	1.11E+06
35 Chromatin, DNA-binding, DNA repair or DNA replication protein									
36	1.88	EMSY	209	EMSY protein	TNsSSSPVVLK	Q7Z589	141	1	5.19E+05
37	1.24	C14orf43	461	hypothetical protein LOC91748	RAsQEANLLTLAQK	Q6PJG2	115	3	1.08E+06
38	4.76	NBA1	29	hypothetical protein LOC29086	TRsNPEGAEDR	Q9NWW8	37	3	4.05E+05
39 Cytoskeletal protein									
40	7.03	CCDC6	367	coiled-coil domain containing 6	PlsPGLSYASHTVGFTPTSLTR	Q16204	66	1	1.38E+06
42	3.15	FAM65B	37	hypothetical protein LOC9750 isoform 1	CNsFIENSALK	Q9Y4F9	119	1	8.49E+05
43	2.65	KIAA0284; KIAA0284 iso2	1179; 1179	hypothetical protein LOC283638 isoform 1	AGsFTGTSDPEAAPAR	Q9Y4F5; Q9Y4F5-2	172; 168	2	3.42E+06
44	-1.01	KIF1B	1487	kinesin family member 1B isoform b	GDsLILEHQWELEK	Q60333	204	2	2.24E+06
45	1.16	K19	10	keratin 19	QSSATSSFGGLGGGSVR	P08727	44	1	1.70E+06
47	4.46	lamin A/C; lamin A/C iso2	403; 407; 403; 407	lamin A/C isoform 2	ASsHSsQTGGGGSVTK	P02545; P02545-2	74; 65	1	2.51E+06
48	5.25	lamin A/C; lamin A/C iso2	404; 404	lamin A/C isoform 2	ASsHSSQTGGGGSVTK	P02545; P02545-2	74; 65	7	1.49E+06
49	4.46	lamin A/C; lamin A/C iso2	404; 407; 404; 407	lamin A/C isoform 2	ASsHSsQTGGGGSVTK	P02545; P02545-2	74; 65	1	5.62E+05
50	6.36	lamin A/C; lamin A/C iso2	406; 406	lamin A/C isoform 2	ASsHSsQTGGGGSVTK	P02545; P02545-2	74; 65	1	5.54E+05
51	1.2	lamin A/C; lamin A/C iso2	458; 458	lamin A/C isoform 2	NKSNEOSGMNWQIK	P02545; P02545-2	74; 65	3	1.77E+06
52	-1.14	Lamin B2	296	lamin B2	LeLSYQLSGLQK	Q03252	68	2	3.56E+06
54	4.45	plectin 1; plectin 1 iso2, 6, 10, 11	4384; 4274; 4233; 4251; 4247	plectin 1 isoform 1	sSSVGGSSSYPISPAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	2.43E+06

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

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

Index	Fold-Change (Su11274/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity
55	5.11	plectin 1; plectin 1 iso2, 6, 10, 11	4386, 4389; 4276, 4279; 4235, 4238; 4253, 4256; 4249, 4252	plectin 1 isoform 1	SSsVGsSSSYPIPAVSR	Q15149; Q15149-2; Q6S382; NP_958785; Q15149-4	532; 518; 515; 516; 516	1	3.33E+05
56	1.75	periplakin	887	periplakin	NRPDsGVEEAWK	Q60437	205	2	6.91E+05
57	2.21	SNIP iso6	45	SNAP25-interacting protein	RfSNVGLVHTSER	Q75746	127	1	6.45E+05
58	2.58	SPTBN1	2328	spectrin, beta, non-erythrocytic 1 isoform 1	AQLPSTSVITITSESSPGK	Q01082	275	1	3.81E+05
59 Endoplasmic reticulum or golgi									
60	1.4	ALG3	13	alpha-1,3-mannosyltransferase ALG3 isoform d	SGsAAQAELCK	Q92685	50	2	1.94E+06
61 G protein or regulator									
62	2.8	DDEF2	822	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2 isoform b	SSsDPPAVHPPLPLR	Q43150	112	1	5.31E+05
63	9.76	RaiGAPA2	715	akt substrate AS250	SAITSGAPGVEK	Q2PPJ7	211	1	5.10E+06
64	-1.05	exophilin 5	1821	exophilin 5 isoform b	HFSESTSIDNALS	Q8NEV8	223	1	6.28E+05
65	-1.03	exophilin 5	1851	exophilin 5 isoform b	FRsFSELPCSDGNESWAYR	Q8NEV8	223	1	2.88E+05
66	1.36	RaiGAPA1	754	GTPase activating Rap/RanGAP domain-like 1 isoform 1	tVDIDDAQLPR	Q6GYQ0	230	1	8.82E+05
67	1.17	RaiGAPA1	797	GTPase activating Rap/RanGAP domain-like 1 isoform 1	SSsTSDILEPFTVER	Q6GYQ0	230	2	2.92E+06
68	1.59	GRF-1	1150	glucocorticoid receptor DNA binding factor 1	KVsIVSKPVLYR	Q9NRY4	172	2	1.75E+06
69	1.52	Rap1GAP; Rap1GAP iso5	441; 471	RAP1 GTPase activating protein isoform b	SQsMDAMGLSNK	P47736; Q5T3S9	73; 77	1	3.85E+05
70	1.08	RGS3; RGS3 iso4	943; 662	regulator of G-protein signalling 3 isoform 3	THsEGSLLEPR	P49796; P49796-4	132; 101	2	3.89E+06
71	-1.38	RGS3; RGS3 iso4	943, 946; 662, 665	regulator of G-protein signalling 3 isoform 3	THsEGSLLEPR	P49796; P49796-4	132; 101	2	1.37E+06
73	3.27	AS160	341	TBC1 domain family, member 4	HASAPSHVQPSDSEK	Q60343	147	1	1.26E+06
74	10.49	AS160; AS160 iso3	588; 100	TBC1 domain family, member 4	LGsVDSFER	Q60343; Q5JU47	147; 31	2	8.94E+06
75	9.67	AS160; AS160 iso3	642; 154	TBC1 domain family, member 4	AHfSFHPPSSTK	Q60343; Q5JU47	147; 31	1	1.76E+06
76	8.72	TSC2; TSC2 iso3; TSC2 iso4	1462; 1418; 1439	tuberous sclerosis 2 isoform 1	GYIISDSAPSR	P49815; P49815-3; P49815-4	201; 196; 198	1	5.20E+05
77 Kinase (non-protein)									
78	-2.59	HISPPD1	1006	Histidine acid phosphatase domain containing 1	sGEQITSSPVSPK	Q43314	140	1	4.64E+05
79	1.07	PFKP	386	phosphofructokinase, platelet	GRsFAGLNTYK	Q01813	86	1	1.72E+06
80 Mitochondrial protein									
81	-1.99	ETFB	194	electron-transfer-flavoprotein, beta polypeptide isoform 2	YAlPLNIMK	P38117	28	1	3.13E+05
82 Motor or contractile protein									
83	1.29	MRLC3; MRLC2; MRLC1	18; 19; 19	myosin, light chain 12A, regulatory, non-sarcomeric	AISNVFAMFDQSQIQEFK	P19105; O14950; P24844	20; 20; 20	1	6.11E+05
84	2.92	MRLC3; MRLC2; MRLC1	18, 19; 19, 20; 19, 20	myosin, light chain 12A, regulatory, non-sarcomeric	AtsNVFAMFDQSQIQEFK	P19105; O14950; P24844	20; 20; 20	3	7.62E+06
85	1.7	MRLC3; MRLC2; MRLC1	19, 20; 20	myosin, light chain 12A, regulatory, non-sarcomeric	AtsNVFAMFDQSQIQEFK	P19105; O14950; P24844	20; 20; 20	1	1.03E+06
86 Phosphatase									
87	1.92	CTDSP12	104	CTD (carboxy-term domain, RNA polymerase II, polypep A)	RKsQVNGEAGSYEMTNQHVK	Q8IYI9	53	4	7.92E+05
88	4.37	PFKFB2	466	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 isoform b	RNsFTPLSSNTIR	Q60825	58	1	9.91E+05
89	1.25	DARPP-32	34	protein phosphatase 1, regulatory (inhibitor) subunit 1B isoform 1	RfPAMLFR	Q9UD71	23	1	2.78E+06
90 Protein kinase, Ser/Thr (non-receptor)									
91	-1.05	B-Raf	363	B-Raf	sSAPNVHINTIEPVNIDLLIR	P15056	84	2	1.38E+07
92	1.32	CaMK2-gamma; 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	8.65E+05
93	1.76	DMPK2	1482	CDC42 binding protein kinase gamma (DMPK-like)	GSGPQRPHsFSEALR	Q6DT37	173	1	1.64E+06
94	2.14	Chk1	279	checkpoint kinase 1	VISGGVSESPSGFSK	Q14757	54	1	2.53E+05
95	6.28	GSK3A	19	glycogen synthase kinase 3 alpha	tSFAEPGGGGGGGGPGGSAGSGGTGGGK	P49840	51	1	4.17E+06
96	12.56	GSK3B; GSK3B iso2	9; 9	glycogen synthase kinase 3 beta isoform 2	TtsFAESCKPQQPSAFGSMK	P49841; NP_02084.2	47; 48	8	2.11E+07
97	1.21	PKD1	205	protein kinase D1	RLsNWSLTGVSTIR	Q15139	102	2	2.15E+06
98	2.98	Raf1	232	v-raf-1 murine leukemia viral oncogene homolog 1	Y*sTPHAFTNTSSPSSEGLSQR	P04049	73	1	3.59E+05
99	2.68	SCYL1	754	SCY1-like 1 isoform B	PSTQPRPDSWGEDNWEGLETDSR	Q96KG9	90	2	2.74E+05
100 RNA processing									
101	3.19	LARP; LARP iso3	824; 747	la related protein isoform 1	HsSNPPLESHVGVWMSDR	Q6PKG0; Q6PKG0-3	124; 116	2	1.26E+06
102	6.99	LARP7	300	La ribonucleoprotein domain family, member 7	SSsEDAESLAPR	Q4GQJ3	67	1	4.86E+05
104	-1.6	PUM1	112	pumilio 1 isoform 1	WPIGDNHAEHQVR	Q14671	126	1	1.17E+05
105	1.1	TRA2A	202	transformer-2 alpha	AHPPTGIYMGK	Q13595	33	1	4.52E+05

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106 Receptor, channel, transporter or cell surface protein									
107	1.24	eIF4ENIF1	564	eukaryotic translation initiation factor 4E nuclear import factor 1	APsPPLSQVQFQTR	Q9NRA8	108	2	6.60E+05
108	2.98	APXL	1036, 1039	apical protein of Xenopus-like	AQsPGsPLHAR	Q13796	176	1	2.82E+05
109	3.85	NHE1	703	solute carrier family 9, isoform A1	IGsDPLAYEPK	P19634	91	2	9.71E+06
110 Secreted protein									
111	1.13	PDAP1	18	PDGFA associated protein 1	QYISPEEIDAQLQAEK	Q13442	21	6	7.34E+06
112 Transcriptional regulator									
113	-1.83	ATF7; ATF7 iso2	42; 42	activating transcription factor 7 isoform 1	tDSVIIADQTPTR	P17544; P17544-2	53; 50	1	3.76E+05
114	1.59	FLNA	2152	filamin A, alpha isoform 2	APsVANVGSCHDSLK	P21333	281	8	8.54E+06
115	1.52	FRYL	1959	furry-like	SNLDIMDGR	Q94915	340	2	1.90E+06
116	18.55	TFIIF-alpha	156	general transcription factor IIF, polypeptide 1, 74kDa	TLIAEEAEWEWER	P35269	58	1	1.01E+06
117	-1.15	TFIIF-alpha	385, 389	general transcription factor IIF, polypeptide 1, 74kDa	GNSRPGIPsAEGGSTSSTLR	P35269	58	1	1.73E+05
118	-1.15	TFIIF-alpha	389, 391	general transcription factor IIF, polypeptide 1, 74kDa	GNSRPGIPsAEGGSTSSTLR	P35269	58	1	1.51E+05
120	2.66	RCOR1	257	REST corepressor 1	ERESEDELEEANGNPIDIEVDQNK	Q9UKL0	53	1	3.80E+05
121	6.8	SNURF	30	SNRPN upstream reading frame protein	tASLSNQECQLYPR	Q9Y675	8	1	5.28E+05
122	-1.13	supervillin; supervillin iso2	850; 424	supervillin isoform 1	Y*QTQPVTLGEVEQVQSGK	Q95425; Q95425-2	248; 201	1	1.71E+06
123	-1.13	supervillin; supervillin iso2	852; 426	supervillin isoform 1	YQIQPVTLGEVEQVQSGK	Q95425; Q95425-2	248; 201	1	1.93E+06
125 Translation									
126	3.23	RPS7	123	ribosomal protein S7	SRTLIAVHDAILEDLVFPSEIVGK	P62081	22	1	1.41E+06
127 Ubiquitin conjugating system									
128	4.59	MYCBP2	2833	MYC binding protein 2	SKsDSYTLDPDTRL	Q75592	510	3	2.39E+06
129 Unknown function									
130	2.56	BAT2L; BAT2L iso6	416; 416	HLA-B associated transcript 2-like	QLsMSSADSADAK	Q5JSZ5; Q5H9R5	166; 243	2	8.33E+05
131	8.27	PPDPF	23	hypothetical protein LOC79144	LGsTSSNSSCSSTCEPGEAIPHPPLPK	Q9H3Y8	12	1	6.00E+05
132	1.02	FAM122B; FAM122B iso2	50; 50	hypothetical protein LOC159090	RNsTTIMSR	Q7Z309; BAC86380	27; 29	1	5.33E+05
133	1.02	FKBP15	956	FK506 binding protein 15, 133kDa	RPsQEQSASASSGQPAPLNR	Q5T1M5	134	2	1.73E+06
135	1.96	LUZP1	958	leucine zipper protein 1	SSIDFSELEQPR	Q86V48	120	1	5.68E+05
136	1.4	PLEKHQ1	390	pleckstrin homology domain containing, family O member 2	CSSLGDLLGEGPR	Q8TD55	53	1	3.54E+05
137	5.83	POM121C	368	POM121 membrane glycoprotein (rat)-like	sSSMSSSLTGAYTSGIPSSSR	A8CG34	125	1	3.44E+05
138	1.49	PPP1R3G	86	protein phosphatase 1, regulatory (inhibitor) subunit 3G	SFsLPADPILQAAK	B7ZBB8	38	1	5.34E+05
140	3.42	WDR20	432	WD repeat domain 20 isoform 2	sNSLPHSAVSNAGSK	Q8TBZ3	63	1	1.68E+05
142 Vesicle protein									
143	2.06	AP1AR	228	hypothetical protein LOC55435 isoform b	SKTEEDILR	Q63HQ0	34	1	7.96E+05
144	-1.05	CSP	10	DnaJ (Hsp40) homolog, subfamily C, member 5	SLsTSGESLYHVLGLDK	Q9H3Z4	22	3	1.46E+07
145	1.14	DOPEY1	1247	dopey family member 1	SHsSIQFSFK	Q5TA12	267	2	7.38E+05
146	2.72	golgin-245	41	golgi autoantigen, golgin subfamily a, 4	TSsFTEQLDEGTPNR	Q13439	261	2	3.18E+06
147	2.68	golgin-245	71	golgi autoantigen, golgin subfamily a, 4	VPsVESLFR	Q13439	261	3	3.13E+06
149	2.76	NDRG1	330	N-myc downstream regulated 1	TAsGSSVTSLDGTR	Q92597	43	2	1.63E+06
151	1.23	NECAP2	181	NECAP endocytosis associated 2 isoform 2	VRPASTGGLSLLPPPPGGK	Q9NVZ3	28	2	5.07E+05
152	1.23	NECAP2	182	NECAP endocytosis associated 2 isoform 2	VRPASIGGLSLLPPPPGGK	Q9NVZ3	28	1	5.07E+05
154	1.45	STXBPS; STXBPS iso2	782; 746	syntaxin binding protein 5 (tomosyn) isoform b	SSsVTSIDK	Q5T5C0; Q5T5C0-2	128; 123	1	8.03E+05