TABLE: TYROSINE PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human non-small cell lung cancer (H3255) cell line; Trypsin Digest; Antibody: pY; CST #9411

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
1		**Actin binding proteins**						
2	-1.6	CTNNA1	177	Catenin alpha-1 (Cadherin-associated protein)	NAGNEQDLGIQyK	P35221	100	4
3	**-14.5**	CTNND1	248	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	YRPSMEGyR	O60716	108	2
4	**-3.9**	CTNND1	865	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	SQSSHSyDDSTLPLIDR	O60716	108	1
5	**-5.5**	CTNND1	904	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	SLDNNySTPNERGDHNR	O60716	108	1
6	**-3**	CTNND1	904	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	SLDNNySTPNER	O60716	108	4
7	-1.8	CTNND1	§228	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	HYEDGYPGGSDNyGsLSR	O60716	108	4
8	-1.8	CTNND1	§228	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	HYEDGYPGGSDNyGSLSR	O60716	108	6
9	-1.1	CTNND1	§257	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	QDVyGPQPQVR	O60716	108	1
10	**-6.1**	CTNND1	§280	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	FHPEPyGLEDDQR	O60716	108	3
11	**-3**	CTNND1	§96	Catenin delta-1 (Cadherin-associated Src substrate) (p120(cas))	LNGPQDHSHLLySTIPR	O60716	108	1
12	**-11.1**	DBNL	§162	Drebrin-like protein (SH3 domain-containing protein 7) (HIP-55)	FQDVGPQAPVGSVyQK	Q9UJU6	48	2
13		**Adaptor/scaffold proteins**						
14	-0.7	ANK3	533	Ankyrin-3 (ANK-3) (Ankyrin-G)	ADIVQQLLQQGASPNAATTSGyTPLHLSAR	Q12955	480	3
15	-1.2	NEDD9	§166	Enhancer of filamentation 1 (CRK-associated substrate-related protein)(CasL)	TGHGYVyEYPSR	Q14511	93	4
16	**-9.9**	CRK	136	Proto-oncogene C-crk (p38) (Adapter molecule crk)	QGSGVILRQEEAEyVR	P46108	34	1
17	**>-8.4**	CRK	136	Proto-oncogene C-crk (p38) (Adapter molecule crk)	QEEAEyVR	P46108	34	1
18	**>-58.4**	DLG3	673	Disks large homolog 3 (Synapse-associated protein 102) (SAP102)	RDNEVDGQDyHFVVSR	Q92796	90	7
19	**-25.5**	DLG3	673	Disks large homolog 3 (Synapse-associated protein 102) (SAP102)	DNEVDGQDyHFVVSR	Q92796	90	3
20	**-19.9**	EPS8	§485	Epidermal growth factor receptor kinase substrate 8	LSTEHSSVSEyHPADGYAFSSNIYTR	Q12929	92	2
21	-1.3	FLOT1	203	Flotillin-1	VSAQyLSEIEMAK	O75955	47	3
22	**-13.9**	GAB1	§406	GRB2-associated-binding protein 1 (GRB2-associated binder 1)	DASSQDCyDIPR	Q13480	77	2
23	**>-11.0**	GAB1	§627	GRB2-associated-binding protein 1 (GRB2-associated binder 1)	GDKQVEyLDLDLDSGK	Q13480	77	4
24	**>-22.0**	GAB1	§659	GRB2-associated-binding protein 1 (GRB2-associated binder 1)	SSGSGSSVADERVDyVVVDQQK	Q13480	77	3
25	**-8.7**	ITSN2	§552	Intersectin-2 (SH3 domain-containing protein 1B) (SH3P18)	LIyLVPEK	Q9NZM3	193	2
26	-1	WASL	§256	Neural Wiskott-Aldrich syndrome protein (N-WASP)	VIyDFIEK	O00401	55	2
27	-1.6	PAG1	§227	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	AEFAEyASVDR	Q9NWQ8	47	4
28	**-3.2**	PAG1	§341	Phosphoprotein associated with glycosphingolipid-enriched microdomains 2	SGQSLTVPESTyTSIQGDPQR	Q9NWQ8	47	1
29	**-2.6**	PAG1	§359	Phosphoprotein associated with glycosphingolipid-enriched microdomains 3	SPSSCNDLyATVK	Q9NWQ8	47	4
30	**>-10.4**	PAG1	§417	Phosphoprotein associated with glycosphingolipid-enriched microdomains 4	ATLGTNGHHGLVPKENDyESISDLQQGR	Q9NWQ8	47	4
31	**-3.2**	PAG1	§417	Phosphoprotein associated with glycosphingolipid-enriched microdomains 5	ENDyESISDLQQGR	Q9NWQ8	47	4
32	-1.7	PARD3	388	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	FSPDSQyIDNR	Q8TEW0	151	2
33	-1.3	PARD3	489	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	DVTIGGSAPIyVK	Q8TEW0	151	4
34	-1.4	PARD3	719	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	RISHSLySGIEGLDESPSR	Q8TEW0	151	1
35	-0.9	PARD3	719	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	ISHSLySGIEGLDESPSR	Q8TEW0	151	5
36	**-0.3**	PARD3	719	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	RIsHSLySGIEGLDESPSR	Q8TEW0	151	2
37	-0.8	PARD3	§1127	Partitioning-defective 3 homolog (Atypical PKC isotype-specific-interacting prot)	EGHMMDALyAQVK	Q8TEW0	151	1
38	-2.1	MPZL1	§263	Myelin protein zero-like protein 1	SESVVyADIR	O95297	29	3
39	-1.5	DLG1	760	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg)	DyHFVTSR	Q12959	100	1
40	-1.2	DLG1	760	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg)	DYEVDGRDyHFVTSR	Q12959	100	3
41	-1.1	DLG1	760	Disks large homolog 1 (Synapse-associated protein 97) (SAP-97) (hDlg)	RDYEVDGRDyHFVTSR	Q12959	100	1
42	-1	SHB	§201	SH2 domain-containing adapter protein B	LDyCGGSGEPGGVQR	Q15464	55	2
43	-1.3	SHB	§333	SH2 domain-containing adapter protein B	DKVTIADDySDPFDAK	Q15464	55	4
44	-1.1	SHB	§333	SH2 domain-containing adapter protein B	DKVTIADDySDPFDAKNDLK	Q15464	55	5
45	-1.1	SHB	355	SH2 domain-containing adapter protein B	AGKGESAGyMEPYEAQR	Q15464	55	6
46	-1.1	SHB	355	SH2 domain-containing adapter protein B	GESAGyMEPYEAQR	Q15464	55	3
47	**>-18.1**	SHC1	§427	SHC-transforming protein 1 (SH2 domain protein C1)	ELFDDPSyVNVQNLDK	P29353	63	7

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STUDY DESIGN: Human non-small cell lung cancer (H3255) cell line; Trypsin Digest; Antibody: pY; CST #9411

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
48	>-13.9	SPRY1	53	Sprouty homolog 1	GSNEyTEGPSVVK	O43609	35	1
49	>-11.1	SPRY1	89	Sprouty homolog 1	THEIIPINVNNNyEHR	O43609	35	2
50	>-15.8	SPRY4	§75	Sprouty homolog 4	TSHVENDyIDNPSLALTTGPKR	Q6QIX2	35	1
51	>-11.3	TNS3	§780	Tumor endothelial marker 6	KLsLGQyDNDAGGQLPFSK	Q8IZW7	155	2
52	-8.7	TNS3	§780	Tumor endothelial marker 6	LSLGQyDNDAGGQLPFSK	Q8IZW7	155	1
53	-7.4	TNS3	§780	Tumor endothelial marker 6	KLSLGQyDNDAGGQLPFSK	Q8IZW7	155	5
54	-1.1	TNS1	1404	Tensin-1	AGSLPNyATINGK	Q9HBL0	186	2
55	-1.9	TJP2	§1118	Tight junction protein ZO-2 (Zonula occludens protein 2)	IEIAQKHPDIyAVPIK	Q9UDY2	134	3
56		**Adhesion proteins**						
57	>-11.8	CTNNB1	30	Catenin beta-1	AAVSHWQQQSyLDSGIHSGATTTAPSLSGK	P35222	86	2
58	-2.6	CDH1	§753	Epithelial cadherin	DNVyYYDEEGGGEEDQDFDLSQLHR	P12830	98	2
59	-2.1	ERBB2IP	§1104	Protein LAP2 (Erbb2-interacting protein) (Erbin) (Densin-180-like protein)	AQIPEGDyLSYR	Q96RT1	158	6
60	-3.1	ERBB2IP	§1104	Protein LAP2 (Erbb2-interacting protein) (Erbin) (Densin-180-like protein)	RAQIPEGDyLSYR	Q96RT1	158	8
61	-17.8	ERBB2IP	1164	Protein LAP2 (Erbb2-interacting protein) (Erbin) (Densin-180-like protein)	TMSVSDFNySR	Q96RT1	158	2
62	-3	F11R	280	Junctional adhesion molecule A	KVIySQPSAR	Q9Y624	33	4
63	-2.1	F11R	280	Junctional adhesion molecule A	VIySQPSAR	Q9Y624	33	2
64	-33.7	ITGB1	§783	Integrin beta-1	WDTGENPIyKSAVTTVVNPK	P05556	89	1
65	-2.4	ITGB1	§783	Integrin beta-1	WDTGENPIyK	P05556	89	4
66	-103.9	ITGB1	§795	Integrin beta-1	SAVTTVVNPKyEGK	P05556	89	1
67	-1.7	MUC1	§1203	Mucin-1	DTyHPMSEYPTYHTHGR	P15941	122	2
68	-0.8	MUC1	1209	Mucin-1	DTYHPMSEyPtYHTHGR	P15941	122	1
69	-0.9	MUC1	1209, §1212	Mucin-1	DTYHPMSEyPTyHTHGR	P15941	122	1
70	-1.6	MUC1	§1212	Mucin-1	DTYHPMSEYPTyHTHGR	P15941	122	2
71	-1.9	MUC1	§1229	Mucin-1	YVPPSSTDRSPyEK	P15941	122	3
72	-1.8	PVRL1	468	Poliovirus receptor-related protein 1	YDEDAKRPyFTVDEAEAR	Q15223	57	4
73	-0.7	PVRL4	445	Poliovirus receptor-related protein 4	SySTLTTVR	Q96K15	55	1
74	-0.9	PVRL4	502	Poliovirus receptor-related protein 4	AKPTGNGIyINGR	Q96K15	55	4
75	>-7.9	OCLN	287	Occludin	SNILWDKEHIyDEQPPNVEEWVK	Q16625	59	1
76	-6.3	PKP2	166	Plakophilin-2	AHYTHSDyQYSQR	Q99959	97	4
77	-5.1	PKP2	631	Plakophilin-2	YSQNIyIQNR	Q99959	97	1
78	-6.8	PKP3	§84	Plakophilin-3	GQyHTLQAGFSSR	Q9Y446	87	9
79	-2.7	PKP3	176	Plakophilin-3	ADyDTLSLR	Q9Y446	87	7
80	-1	PKP3	176	Plakophilin-3	GGVGSRADyDTLSLR	Q9Y446	87	2
81	-1.1	PKP3	390	Plakophilin-3	NLIyDNADNK	Q9Y446	87	1
82	-4.5	PKP4	157	Plakophilin-4 (p0071)	SSTQMNSYSDSGyQEAGSFHNSQNVSK	Q99569	134	1
83	-0.8	PKP4	372	Plakophilin-4 (p0071)	TVHDMEQFGQQQYDIyER	Q99569	134	4
84	-0.7	PKP4	§415	Plakophilin-4 (p0071)	SAVSPDLHITPIyEGR	Q99569	134	3
85	-1.6	PKP4	470	Plakophilin-4 (p0071)	NNyALNTTAtYAEPYRPIQYR	Q99569	134	1
86	-1.5	PKP4	470, §478	Plakophilin-4 (p0071)	NNyALNTTATyAEPYRPIQYR	Q99569	134	2
87	-1.1	PKP4	§478	Plakophilin-4 (p0071)	NNYALNTTATyAEPYRPIQYR	Q99569	134	2
88	-1.3	PKP4	1168	Plakophilin-4 (p0071)	STTNyVDFYSTK	Q99569	134	7
89	-1.7	SDC4	197	Syndecan-4	KAPTNEFyA	P31431	22	2
90	-0.7	VCL	§821	Vinculin (Metavinculin)	SFLDSGyR	P18206	124	4
91		**Cytoskeletal proteins**						
92	-1	KRT7	39	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (Sarcolectin)	LSSARPGGLGSSsLyGLGASRPR	P08729	51	2
93	-0.7	KRT7	39	Keratin, type II cytoskeletal 7 (Cytokeratin-7) (Sarcolectin)	LSSARPGGLGSSSLyGLGASRPR	P08729	51	4
94	-8.4	CLDN3	214	Claudin-3 (CPE-receptor 2) (HRVP1)	STGPGASLGTGyDR	O15551	23	1

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
95	-9.3	CLDN3	219	Claudin-3 (CPE-receptor 2) (HRVP1)	STGPGASLGTGYDRKDyV	O15551	23	3
96	-5.8	CFL1	§139	Cofilin-1 (Cofilin, non-muscle)	LTGIKHELQANCyEEVKDR	P23528	19	2
97	-4.3	CFL1	§139	Cofilin-1 (Cofilin, non-muscle)	HELQANCyEEVKDR	P23528	19	3
98	-1.2	CTTN	§421	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	LPSSPVyEDAASFK	Q14247	62	2
99	-1.8	CTTN	§446	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	GPVSGTEPEPVySMEAADYR	Q14247	62	6
100	-159.2	JUP	§19	Junction plakoglobin (Desmoplakin-3) (Desmoplakin III) (Catenin gamma)	VTEWQQTyTYDSGIHSGANTCVPSVSSK	P14923	82	2
101	-34.3	EPB41L4B	479	Band 4.1-like protein 4B (Protein EHM2) (FERM-containing protein CG1)	ASASGDDSHFDyVHDQNQK	Q9H329-2	57	2
102	>-6.3	VIL2	423	Ezrin (p81) (Cytovillin) (Villin-2)	SQEQLAAELAEyTAK	P15311	69	2
103	-1.6	PXN	§88	Paxillin	FIHQQPQSSsPVyGSSAK	P49023	65	3
104	-1.5	PXN	§88	Paxillin	FIHQQPQSsSPVyGSSAK	P49023	65	2
105	-0.7	PXN	§88	Paxillin	FIHQQPQSSSPVyGSSAK	P49023	65	5
106	-1	PXN	§118	Paxillin	VGEEEHVySFPNK	P49023	65	7
107	-0.9	PXN	§118	Paxillin	VGEEEHVySFPNKQK	P49023	65	9
108	-0.5	SNIP	136	p130Cas-associated protein (p140Cap) (SNAP-25-interacting protein) (SNIP)	KEPLyAAFPGSHLTNGDLR	Q9C0H9	113	3
109	-0.8	SNIP	268	p130Cas-associated protein (p140Cap) (SNAP-25-interacting protein) (SNIP)	GEGLyADPYGLLHEGR	Q9C0H9	113	3
110	-3.9	TAGLN2; TAGLN3	191; 192	Transgelin-2 (SM22-alpha homolog)	GASQAGMTGyGMPR	P37802	22	2
111	-0.9	TLN1	70	Talin-1	ALDyYMLR	Q9Y490	270	11
112	-9.6	TLN1	127	Talin-1	IGITNHDEySLVR	Q9Y490	270	2
113	-1.1	TUBB4; TUBB; TUBB2C; TUBB3	340; 340; 340; 340	Tubulin beta-4 chain (Tubulin 5 beta)	NSSyFVEWIPNNVK	P04350; P07437; P68371; Q13509	50	1
114		**Enzyme, misc.**						
115	-1	ALDH9A1	476	4-trimethylaminobutyraldehyde dehydrogenase	VTIEyYSQLK	P49189	54	2
116	-1.3	ALDOA	2	Fructose-bisphosphate aldolase A (Lung cancer antigen NY-LU-1)	PyQYPALTPEQK	P04075	39	3
117	-2	CALM1; CALM2; CALM3	§99	Calmodulin (CaM)	VFDKDGNGyISAAELR	P62158	17	4
118	-0.3	CTPS	473	CTP synthase 1 (UTP--ammonia ligase 1) (CTP synthetase 1)	KLYGDADyLEER	P17812	67	2
119	-5.4	DDX3X	§103	ATP-dependent RNA helicase DDX3X (DEAD box protein 3, X-chromosomal)	GRSDyDGIGSR	O00571	73	1
120	-1	ENO1; ENO2; ENO3	§43; 43; §43	Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase)	AAVPSGASTGIyEALELR	P06733; P09104; P13929	47	2
121	-0.7	G6PD	§400	Glucose-6-phosphate 1-dehydrogenase (G6PD)	VQPNEAVyTK	P11413	59	1
122	-1.5	G6PD	502	Glucose-6-phosphate 1-dehydrogenase (G6PD)	VGFQyEGTYK	P11413	59	2
123	-1.5	G6PD	502	Glucose-6-phosphate 1-dehydrogenase (G6PD)	RVGFQyEGTYK	P11413	59	3
124	-5	G6PD	§506	Glucose-6-phosphate 1-dehydrogenase (G6PD)	VGFQYEGTyK	P11413	59	5
125	-1.5	G6PD	§506	Glucose-6-phosphate 1-dehydrogenase (G6PD)	RVGFQYEGTyK	P11413	59	2
126	-1	LDHA	§238	L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	QVVESAyEVIK	P00338	37	1
127	-1	LDHB	§239	L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)	MVVESAyEVIK	P07195	37	4
128	-2	ATP1A1	260	Sodium/potassium-transporting ATPase subunit alpha-1	GIVVyTGDR	P05023	113	4
129	-30.9	PLCG1	§771	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1	IGTAEPDyGALYEGR	P19174	149	1
130	-44.5	PLCG1	§783	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2	NPGFyVEANPMPTFK	P19174	149	2
131		**GTP binding protein or regulator**						
132	>-8.5	ARHGEF5	710	FLJ00261 protein	SGRDySTVSASPTALSTLK	Q6ZML7	182	2
133	-0.4	ARHGEF5	1424	FLJ00261 protein	RTEELIyLSQK	Q6ZML7	182	1
134	-13.4	GNAI3	60	Guanine nucleotide-binding protein G(k) subunit alpha (G(i) alpha-3)	IIHEDGySEDECKQYK	P08754	41	1
135	-11.1	GNAI3	60	Guanine nucleotide-binding protein G(k) subunit alpha (G(i) alpha-3)	IIHEDGySEDECK	P08754	41	2
136	-1	IQGAP1	§1510	Ras GTPase-activating-like protein IQGAP1 (p195)	LQQTyAALNSK	P46940	189	2
137	-21.4	RAB34	247	Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah)	INSDDSNLyLTASK	Q9BZG1	29	2
138		**Kinase (non-protein)**						
139	>-9.6	GUK1	53	Guanylate kinase (GMP kinase)	NPRPGEENGKDYyFVTR	Q16774	22	1
140	-1.1	PIK3R1	467	Phosphatidylinositol 3-kinase regulatory subunit alpha	SREYDRLyEEYTR	P27986	84	2
141	-1	PIK3R2	§464	Phosphatidylinositol 3-kinase regulatory subunit beta	SREYDQLyEEYTR	O00459	82	3

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142	-1	PIK3R2	§464	Phosphatidylinositol 3-kinase regulatory subunit beta	EYDQLyEEYTR	O00459	82	2
143	-1.2	PIK3R2	§467	Phosphatidylinositol 3-kinase regulatory subunit beta	EYDQLYEEyTR	O00459	82	3
144	-17.6	PIK3R2	605	Phosphatidylinositol 3-kinase regulatory subunit beta	NETEDQyALMEDEDDLPHHEER	O00459	82	1
145	-0.9	PI4KA	973	Phosphatidylinositol 4-kinase alpha (PI4-kinase alpha)	DQPyYDIPDAPYR	P42356	231	3
146		**Lipid binding proteins**						
147	>-4.9	ANXA1	§20	Annexin A1 (Lipocortin I) (Phospholipase A2 inhibitory protein)	QAWFIENEEQEyVQTVK	P04083	39	2
148	-4.3	ANXA1	38	Annexin A1 (Lipocortin I) (Phospholipase A2 inhibitory protein)	GGPGSAVSPyPTFNPSSDVAALHK	P04083	39	2
149	-1.6	ANXA2	§23	Annexin A2 (Lipocortin II) (Calpactin I heavy chain)	LSLEGDHSTPPSAyGSVK	P07355	39	4
150	-38.1	ANXA2	§29	Annexin A2 (Lipocortin II) (Calpactin I heavy chain)	AyTNFDAERDALNIETAIK	P07355	39	3
151	-6.7	ANXA2	§29	Annexin A2 (Lipocortin II) (Calpactin I heavy chain)	AyTNFDAER	P07355	39	3
152	-3.4	ANXA2	§237	Annexin A2 (Lipocortin II) (Calpactin I heavy chain)	SYSPyDMLESIRK	P07355	39	4
153	-2.2	ANXA2	§237	Annexin A2 (Lipocortin II) (Calpactin I heavy chain)	SYSPyDMLESIR	P07355	39	1
154	-0.8	PLEKHA6	§492	Pleckstrin homology domain-containing family A member 6 (PEPP-3)	SEDIyADPAAYVMR	Q9Y2H5	117	3
155		**Other**						
156	-2	AP2B1	276	AP-2 complex subunit beta-1 (Beta-adaptin)	DSDyYNMLLK	P63010	105	2
157	-1.9	CSTB	97	Cystatin-B (Stefin-B) (Liver thiol proteinase inhibitor) (CPI-B)	AKHDELTyF	P04080	11	2
158	-1.2	EFNB2	§304	Ephrin-B2	TADSVFCPHyEK	P52799	37	3
159	-10.7	DNAJA1	§381	DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4)	HYNGEAyEDDEHHPR	P31689	45	2
160	-27.3	ERRFI1	394	ERBB receptor feedback inhibitor 1 (Mitogen-inducible gene 6 protein) (Mig-6)	VSSTHyYLLPERPPYLDKYEK	Q9UJM3	51	2
161	>-57.0	ERRFI1	395	ERBB receptor feedback inhibitor 1 (Mitogen-inducible gene 6 protein) (Mig-6)	VSSTHYyLLPERPPYLDKYEK	Q9UJM3	51	1
162	-13.7	MYO6	1114	myosin VI	SVTDyAQQNPAAQIPAR	CAI19522	145	2
163	-6.9	STX4	251	Syntaxin-4 (Renal carcinoma antigen NY-REN-31)	NILSSADyVER	Q12846	34	2
164	-2.6	HDLBP	§437	Vigilin (High density lipoprotein-binding protein) (HDL-binding protein)	MDyVEINIDHK	Q00341	141	7
165	-5	VTI1B	115	Vesicle transport through interaction with t-SNAREs homolog 1B	YGIyAVENEHMNR	Q9UEU0	27	1
166		**Phosphatase**						
167	-1.4	PTPRA	§798	Receptor-type tyrosine-protein phosphatase alpha precursor (R-PTP-alpha)	VVQEYIDAFSDyANFK	P18433	91	5
168	-0.7	INPPL1	§886	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2 (SHIP-2)	ERLyEWISIDKDEAGAK	O15357	139	1
169	-4.2	INPPL1	§1135	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2 (SHIP-2)	TLSEVDyAPAGPAR	O15357	139	2
170	-0.9	PTPN11	§62	Tyrosine-protein phosphatase non-receptor type 11 (PTP-2C)(SHP-2)	IQNTGDyYDLYGGEK	Q06124	68	4
171	-7.3	PTPN11	§580	Tyrosine-protein phosphatase non-receptor type 11 (PTP-2C)(SHP-2)	VyENVGLMQQQK	Q06124	68	2
172		**Protease**						
173	-2.9	CPD	1376	Carboxypeptidase D	SLLSHEFQDETDTEEETLySSKH	O75976	153	4
174	-4.1	CPD	1344	Carboxypeptidase D	LRQHHDEyEDEIR	O75976	153	2
175	-0.7	PSMA2	56	Proteasome subunit alpha type-2 (Proteasome component C3)	SILyDER	P25787	26	1
176	-0.6	PSMA2	75	Proteasome subunit alpha type-2 (Proteasome component C3)	HIGLVySGMGPDYR	P25787	26	2
177		**Protein kinase, dual-specificity**						
178	-0.9	DYRK1A; DYRK1B	§321; §273	Dual specificity tyrosine-phosphorylation-regulated kinase 1A	IYQyIQSR	Q13627; Q9Y463	86	8
179	-1.3	DYRK2; DYRK4	§309; 286	Dual specificity tyrosine-phosphorylation-regulated kinase 2	VYTyIQSR	Q92630; Q9NR20	60	2
180		**Protein kinase, Ser/Thr (non-receptor)**						
181	-1.5	CDC2	§15	Cell division control protein 2 homolog (CDK1)	IEKIGEGTyGVVYK	P06493	34	5
182	-0.8	CDC2	§15	Cell division control protein 2 homolog (CDK1)	IGEGtyGVVYKGR	P06493	34	3
183	-0.7	CDC2	§15	Cell division control protein 2 homolog (CDK1)	IEKIGEGtyGVVYK	P06493	34	6
184	-0.8	CDC2	§19	Cell division control protein 2 homolog (CDK1)	IGEGTYGVVyKGR	P06493	34	1
185	-1.2	CDC2; CDK2; CDK3	§15; §15; 15	Cell division control protein 2 homolog (CDK1)	IGEGTyGVVYK	P06493; P24941; Q00526	34	6
186	-0.8	CDC2; CDK2; CDK3	§15; §15; 15	Cell division control protein 2 homolog (CDK1)	IGEGtyGVVYK	P06493; P24941; Q00526	34	8
187	-0.8	CDC2; CDK2; CDK3	§19; 19; 19	Cell division control protein 2 homolog (CDK1)	IGEGTYGVVyK	P06493; P24941; Q00526	34	2
188	-0.6	CDK2; CDK3	§15; 15	Cell division protein kinase 2 (p33 protein kinase)	VEKIGEGtyGVVYK	P24941; Q00526	34	1

TABLE: TYROSINE PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human non-small cell lung cancer (H3255) cell line; Trypsin Digest; Antibody: pY; CST #9411

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
189	-1	CDK2; CDK3	§15; 15	Cell division protein kinase 2 (p33 protein kinase)	VEKIGEGTyGVVYK	P24941; Q00526	34	4
190	-1	CDK5	§15	Cell division protein kinase 5	IGEGTyGTVFK	Q00535	33	3
191	-1.2	CDKL5	§171	Cyclin-dependent kinase-like 5 (Serine/threonine-protein kinase 9)	NLSEGNNANYTEyVATR	O76039	116	3
192	-8.7	MAPK3	§204	Mitogen-activated protein kinase 3 (ERK-1) (MAPK 1)	IADPEHDHTGFLtEyVATR	P27361	43	1
193	-6.9	MAPK3	§204	Mitogen-activated protein kinase 3 (ERK-1) (MAPK 1)	IADPEHDHTGFLTEyVATR	P27361	43	5
194	-10.7	MAPK1	§186	Mitogen-activated protein kinase 1 (ERK-2) (MAPK 2)	VADPDHDHTGFLtEyVATR	P28482	41	6
195	-8.2	MAPK1	§186	Mitogen-activated protein kinase 1 (ERK-2) (MAPK 2)	VADPDHDHTGFLTEyVATR	P28482	41	9
196	-6.8	MAPK7	§220	Mitogen-activated protein kinase 7 (ERK-5)	GLCTSPAEHQYFMTEyVATR	Q13164	89	2
197	-0.9	GSK3A; GSK3B	§279; §216	Glycogen synthase kinase-3 alpha (GSK-3 alpha)	GEPNVSyICSR	P49840; P49841	51	19
198	-0.9	GSK3A; GSK3B	§279; §216	Glycogen synthase kinase-3 alpha (GSK-3 alpha)	GEPNVSyICsR	P49840; P49841	51	8
199	-1.2	HIPK1; HIPK2	§352; §361	Homeodomain-interacting protein kinase 1	AVCSTyLQSR	Q86Z02; Q9H2X6	131	3
200	-4.8	HIPK3	§359	Homeodomain-interacting protein kinase 3 (FIST) (ANPK)	TVCSTyLQSR	Q9H422	134	1
201	-0.9	ICK	§159	Serine/threonine-protein kinase ICK (MRK) (LCK2)	SKPPYtDyVSTR	Q9UPZ9	71	2
202	>-8.4	MINK1	906	Misshapen-like kinase 1 (MAPK/ERK kinase kinase kinase 6) (MEKKK 6)	NLLHADSNGyTNLPDVVQPSHSPTENSK	Q8N4C8	150	2
203	-0.8	MAPK14	§181	Mitogen-activated protein kinase 14 (MAP kinase p38 alpha)	HTDDEMTGyVATR	Q16539	41	9
204	-0.8	MAPK14	§181	Mitogen-activated protein kinase 14 (MAP kinase p38 alpha)	HTDDEMtGyVATR	Q16539	41	3
205	-0.5	MAPK13	182	Mitogen-activated protein kinase 13 (MAP kinase p38 delta)	HADAEMTGyVVTR	O15264	42	5
206	-1.1	PRKCD	§313	Protein kinase C delta type (nPKC-delta)	RSDSASSEPVGIyQGFEKK	Q05655	78	1
207	-1.4	PRPF4B	§849	Serine/threonine-protein kinase PRP4 homolog (PRP4 kinase)	LCDFGSASHVADNDITPyLVSR	Q13523	117	6
208		**Protein kinase, tyrosine (non-receptor)**						
209	-1.2	PTK2	§397	Focal adhesion kinase 1 (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2)	THAVSVSETDDyAEIIDEEDTYTMPSTR	Q05397	119	1
210	-1.3	PTK2	§397, §407	Focal adhesion kinase 1 (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2)	THAVSVSETDDyAEIIDEEDTyTMPSTR	Q05397	119	1
211	-0.9	PTK2	§576	Focal adhesion kinase 1 (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2)	YMEDSTyYK	Q05397	119	7
212	-0.5	PTK2	§576, §577	Focal adhesion kinase 1 (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2)	YMEDSTyyKASK	Q05397	119	2
213	-0.9	PTK2	§577	Focal adhesion kinase 1 (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2)	YMEDSTYyK	Q05397	119	1
214	-0.9	FRK	46	Tyrosine-protein kinase FRK (FYN-related kinase)	HGHyFVALFDYQAR	P42685	58	5
215	-0.6	LCK; FYN; YES1; SRC	§393; §419; §425; §418	Proto-oncogene tyrosine-protein kinase LCK (LSK)	LIEDNEyTAR	P06239; P06241; P07947; P12931	61	2
216	-0.7	FYN; YES1	212; 221	Proto-oncogene tyrosine-protein kinase Fyn (SLK)	KLDNGGyYITTR	P06241; P07947	61	2
217	-0.9	LYN; HCK	§396; §410	Tyrosine-protein kinase Lyn	VIEDNEyTAR	P07948; P08631	59	2
218	-0.6	LYN	§192	Tyrosine-protein kinase Lyn	SLDNGGyYISPR	P07948	59	2
219	-1.1	PTK2B	§579, §580	Protein tyrosine kinase 2 beta (Focal adhesion kinase 2) (FADK 2)	YIEDEDyyKASVTRLPIK	Q14289	116	2
220	-1.3	TYK2	§292	Non-receptor tyrosine-protein kinase TYK2	LLAQAEGEPCyIR	P29597	134	3
221		**Protein kinase, tyrosine (receptor)**						
222	-11.2	EGFR	§869	Epidermal growth factor receptor	LLGAEEKEyHAEGGKVPIK	P00533	134	3
223	-52.1	EGFR	§998	Epidermal growth factor receptor	MHLPSPtDSNFyR	P00533	134	1
224	-4.7	EGFR	§998	Epidermal growth factor receptor	MHLPSPTDSNFyR	P00533	134	10
225	-42	EGFR	§1110	Epidermal growth factor receptor	RPAGSVQNPVyHNQPLNPAPSR	P00533	134	7
226	-39	EGFR	§1172	Epidermal growth factor receptor	GSHQIsLDNPDyQQDFFPK	P00533	134	14
227	-38.2	EGFR	§1172	Epidermal growth factor receptor	GSHQISLDNPDyQQDFFPK	P00533	134	17
228	-36.4	EGFR	§1172	Epidermal growth factor receptor	GsHQISLDNPDyQQDFFPK	P00533	134	1
229	>-25.3	EGFR	§1197	Epidermal growth factor receptor	EAKPNGIFKGSTAENAEyLR	P00533	134	2
230	>-10.4	EGFR	§1197	Epidermal growth factor receptor	GStAENAEyLR	P00533	134	1
231	-11.5	EGFR	§1197	Epidermal growth factor receptor	GSTAENAEyLR	P00533	134	4
232	-0.9	EGFR; ERBB2; ERBB4	§727; 735; 733	Epidermal growth factor receptor	VLGSGAFGTVyK	P00533; P04626; Q15303	134	3
233	-1.3	EPHA1	§781	Ephrin type-A receptor 1	LLDDFDGTyETQGGKIPIR	P21709	108	3
234	-1	EPHA2	575	Ephrin type-A receptor 2	QSPEDVyFSKSEQLKPLK	P29317	108	2
235	-0.8	EPHA2	575	Ephrin type-A receptor 2	QSPEDVyFSK	P29317	108	2

TABLE: TYROSINE PHOSPHOSCAN® FINAL RESULTS, SILAC

STUDY DESIGN: Human non-small cell lung cancer (H3255) cell line; Trypsin Digest; Antibody: pY; CST #9411

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
236	-1.4	EPHA2	§588	Ephrin type-A receptor 2	SEQLKPLKTyVDPHTYEDPNQAVLK	P29317	108	2
237	-1.5	EPHA2	§588, §594	Ephrin type-A receptor 2	SEQLKPLKTyVDPHTyEDPNQAVLK	P29317	108	3
238	-0.8	EPHA2	§588, §594	Ephrin type-A receptor 2	TyVDPHTyEDPNQAVLK	P29317	108	3
239	-1	EPHA2	§594	Ephrin type-A receptor 2	TYVDPHTyEDPNQAVLK	P29317	108	5
240	-1	EPHA2	§772	Ephrin type-A receptor 2	VLEDDPEATyTTSGGKIPIR	P29317	108	6
241	-1	EPHA2	§772	Ephrin type-A receptor 2	VLEDDPEATyTTSGGK	P29317	108	5
242	-1.2	EPHA2	§921	Ephrin type-A receptor 2	MQQyTEHFMAAGYTAIEK	P29317	108	2
243	-0.9	EPHA2	§921, §930	Ephrin type-A receptor 2	MQQyTEHFMAAGyTAIEK	P29317	108	1
244	-3.2	EPHA2	§930	Ephrin type-A receptor 2	MQQYTEHFMAAGyTAIEK	P29317	108	2
245	-1	EPHA3; EPHA5; EPHA4	§779; 833; 779	Ephrin type-A receptor 3	VLEDDPEAAyTTR	P29320; P54756; P54764	110	2
246	-0.9	EPHA4	§596, §602	Ephrin type-A receptor 4	TyVDPFTyEDPNQAVR	P54764	110	2
247	-1.4	EPHB3; EPHB4	§614; 596	Ephrin type-B receptor 3	VYIDPFTyEDPNEAVR	P54753; P54760	110	1
248	-2.2	EPHB4	574	Ephrin type-B receptor 4	EAEySDKHGQYLIGHGTK	P54760	108	2
249	-2.4	EPHB4	774	Ephrin type-B receptor 4	FLEENSSDPTyTSSLGGKIPIR	P54760	108	3
250	-1.7	EPHB4	774	Ephrin type-B receptor 4	FLEENSSDPTyTSSLGGK	P54760	108	4
251	-1	EPHB4	987	Ephrin type-B receptor 4	SQAKPGTPGGTGGPAPQy	P54760	108	3
252	-1.1	ERBB2	§877	Receptor tyrosine-protein kinase erbB-2	LLDIDETEyHADGGKVPIK	P04626	138	3
253	>-17.7	ERBB3	1328	Receptor tyrosine-protein kinase erbB-3	SLEATDSAFDNPDyWHSR	P21860	148	1
254	-1.3	TYRO3; MERTK	686; §754	Tyrosine-protein kinase receptor TYRO3	IYSGDYyR	Q06418; Q12866	97	1
255	-1.3	TYRO3; MERTK	685; §753	Tyrosine-protein kinase receptor TYRO3	IYSGDyYR	Q06418; Q12866	97	1
256	-1.5	TYRO3; MERTK	685; §753	Tyrosine-protein kinase receptor TYRO3	KIYSGDyYR	Q06418; Q12866	97	1
257	-1.4	MET	§1003	Hepatocyte growth factor receptor	SVSPTTEMVSNESVDyR	P08581	156	4
258	-2.7	MET	§1234	Hepatocyte growth factor receptor	DMYDKEyYSVHNK	P08581	156	11
259	-8.9	MET	§1234, §1235	Hepatocyte growth factor receptor	DMYDKEyySVHNK	P08581	156	4
260	-2.8	MET	§1235	Hepatocyte growth factor receptor	DMYDKEYySVHNK	P08581	156	1
261		**Receptor, channel, or other cell surface protein**						
262	-1.6	APP	§757	Amyloid beta A4 protein precursor (APP) (Alzheimer disease amyloid protein)	MQQNGyENPTYK	P05067	87	1
263	-1.1	APLP2	750	Amyloid-like protein 2	MQNHGyENPTYK	Q06481	87	2
264	-0.6	APLP2	755	Amyloid-like protein 2	MQNHGYENPTyK	Q06481	87	1
265	-3.9	CD46	§354	Membrane cofactor protein	GKADGGAEyATYQTK	P15529-4	41	2
266	-3.8	CD46	§354	Membrane cofactor protein	ADGGAEyATYQTK	P15529-4	41	3
267	-3.9	CD46	§357	Membrane cofactor protein	GKADGGAEYATyQTK	P15529-4	41	2
268	-3.7	CD46	§357	Membrane cofactor protein	ADGGAEYATyQTK	P15529-4	41	4
269	>-9.1	CD46	378	Membrane cofactor protein	GTyLTDETHR	P15529	44	2
270	>-6.8	GJA1	§246	Gap junction alpha-1 protein (Connexin-43)	SDPyHATSGALSPAK	P17302	43	2
271	-1.4	GPRC5C	387	G-protein coupled receptor family C group 5 member C	VPSEGAyDIILPR	Q9NQ84	48	2
272	-1	GPRC5C	414	G-protein coupled receptor family C group 5 member C	AEDMySAQSHQAATPPKDGK	Q9NQ84	48	2
273	-3.8	LDLR	§845	Low-density lipoprotein receptor	TTEDEVHICHNQDGySYPSR	P01130	95	2
274	-0.7	GPRC5A	§347	Retinoic acid-induced protein 3 (Orphan G-protein-coupling receptor PEIG-1)	AHAWPSPyKDYEVK	Q8NFJ5	40	2
275	-0.6	GPRC5A	§347, §350	Retinoic acid-induced protein 3 (Orphan G-protein-coupling receptor PEIG-1)	AHAWPSPyKDyEVKK	Q8NFJ5	40	2
276	-0.5	GPRC5A	§347, §350	Retinoic acid-induced protein 3 (Orphan G-protein-coupling receptor PEIG-1)	AHAWPSPyKDyEVKKEGS	Q8NFJ5	40	1
277	-0.6	GPRC5A	§350	Retinoic acid-induced protein 3 (Orphan G-protein-coupling receptor PEIG-1)	AHAWPsPYKDyEVKKEGS	Q8NFJ5	40	1
278	-29.7	SLITRK6	801	SLIT and NTRK-like protein 6	KVLVEQTKNEyFELK	Q9H5Y7	95	2
279	-2	TFRC	§20	Transferrin receptor protein 1 (CD71 antigen) (T9) (p90)	SAFSNLFGGEPLSyTR	P02786	85	4
280		**Transcriptional regulation**						
281	-28.8	S100A11	30	Protein S100-A11 (S100 calcium-binding protein A11) (Calgizzarin) (MLN 70)	YAGKDGyNYTLSK	P31949	12	1
282	>-8.6	SND1	304	Staphylococcal nuclease domain-containing protein 1	IWRDyVAPTANLDQKDK	Q13122	102	1

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STUDY DESIGN: Human non-small cell lung cancer (H3255) cell line; Trypsin Digest; Antibody: pY; CST #9411

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

Index	Fold-Change (Iressa / Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study
283	>-10.4	SND1	304	Staphylococcal nuclease domain-containing protein 1	IWRDyVAPTANLDQK	Q13122	102	2
284	-37.6	SND1	§883	Staphylococcal nuclease domain-containing protein 1	ADDADEFGySR	Q13122	102	1
285	-1.6	GRLF1	§1087	Glucocorticoid receptor DNA-binding factor 1 (GRF-1) (Rho GAP p190A)	SVSSSPWLPQDGFDPSDyAEPMDAVVKPR	Q9NRY4	172	1
286	-1.9	GRLF1	§1105	Glucocorticoid receptor DNA-binding factor 1 (GRF-1) (Rho GAP p190A)	NEEENIySVPHDSTQGK	Q9NRY4	172	11
287	-0.7	STAT3	§705	Signal transducer and activator of transcription 3	YCRPESQEHPEADPGSAAPyLK	P40763	88	4
288	-0.7	STAT3	§704	Signal transducer and activator of transcription 4	YCRPESQEHPEADPGAAPyLK	P40763-2	88	3
289	>-44.7	STAT5A; STAT5B	§694; §699	Signal transducer and activator of transcription 5A	AVDGyVKPQIK	P42229; P51692	91	2
290		**Translation initiation complex**						
291	-0.9	EEF1A1; EEF1A2	§29; §29	Elongation factor 1-alpha 1 (Elongation factor Tu)	STTTGHLIyK	P68104; Q05639	50	2
292	-0.8	EEF1A1; EEF1A2	§141; §141	Elongation factor 1-alpha 1 (Elongation factor Tu)	EHALLAyTLGVK	P68104; Q05639	50	2
293	-0.9	RPS27	30	40S ribosomal protein S27 (Metallopan-stimulin 1) (MPS-1)	LVQSPNSyFMDVK	P42677	10	10
294		Transporter						
295	-0.7	PITPNA	139	Phosphatidylinositol transfer protein alpha isoform	HVEAVyIDIADR	Q00169	32	3
296	-7.3	SLC38A2	41	Amino acid transporter system A	SHyADVDPENQNFLLESNLGK	Q9HAV3	56	1
297	-4	SLC38A2	41	Amino acid transporter system A	SHyADVDPENQNFLLESNLGKK	Q9HAV3	56	3
298		**Unknown function**						
299	>-5.8	TANC2	1793	Amino acid transporter system A	TNNAQNGHLLEDDyYSPHGMLANGSR	Q9HCD6	206	1
300	-18.6	TANC2	1794	Amino acid transporter system A	TNNAQNGHLLEDDYySPHGMLANGSR	Q9HCD6	206	1
301	>-9.0	C21orf13	98	Uncharacterized protein C21orf13	yNVSKIsQSK	O95447	77	1
302	>-29.5	CRIP2	196	Cysteine-rich protein 2 (CRP2) (Protein ESP1)	GVNTGAVGSyIYDRDPEGK	P52943	23	5
303	-5.6	CRIP2	198	Cysteine-rich protein 2 (CRP2) (Protein ESP1)	GVNTGAVGSYIyDRDPEGK	P52943	23	3
304	>-6.6	CRIP2	196, 198	Cysteine-rich protein 2 (CRP2) (Protein ESP1)	GVNTGAVGSyIyDRDPEGK	P52943	23	1
305	-2.9	TMEM106B	90	TMEM106B	NGDVSQFPyVEFTGR	Q8N353	35	2
306	-0.8	FAM62A	§822	Protein FAM62A (Membrane-bound C2 domain-containing protein)	HLSPyATLTVGDSSHK	Q9BSJ8	123	6
307	-10.2	BAIAP2L1	163	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	EIEyVETVTSR	Q9UHR4	57	2
308	-1.2	KIAA1217	239	Sickle tail protein	NVyYELNDVR	Q9ULK3	146	6
309	-0.9	KIAA1217	§388	Sickle tail protein	NEGFyADPYLYHEGR	Q9ULK3	146	6
310	-7.1	LSR	324	Lipolysis-stimulated lipoprotein receptor	SSSAGGQGSyVPLLR	Q86X29	71	2
311	>-7.6	LSR	487	Lipolysis-stimulated lipoprotein receptor	SRDDLyDQDDSRDFPR	Q86X29	71	1
312	-5.4	LSR	503	Lipolysis-stimulated lipoprotein receptor	SRDPHyDDFR	Q86X29	71	2
313	-6.3	LSR	304	LSR protein	NSSAGGQGSyVPLLR	Q9BWS2	64	2
314	-4.1	LLGL1	509	Lethal(2) giant larvae protein homolog 1	KVGCFDPySDDPR	O00188	112	2
315	-2.5	LLGL1	509	Lethal(2) giant larvae protein homolog 1	VGCFDPySDDPR	O00188	112	4
316	>-5.2	LMBRD2	290	LMBR1 domain-containing protein 2	NMDDyEDFDEK	Q68DH5	81	1
317	-0.9	PLEKHA7	282	Pleckstrin homology domain-containing family A member 7	SADDTyLQLKK	Q86VZ7	85	2
318	>-6.0	LRBA	1110	Lipopolysaccharide-responsive and beige-like anchor protein	SIVEEEEDDDyVELK	P50851	319	2
319	-7.5	MPP7	417	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	SQESDGVEyIFISK	Q8IY28	66	2
320	-23.2	MPP7	417	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	RSQESDGVEyIFISK	Q8IY28	66	1
321	-4.8	NAALADL2	106	N-acetylated alpha-linked acidic dipeptidase-like protein 2	LQEESDyITHYTR	Q58DX5	89	4
322	-34.5	NAALADL2	106, 110	N-acetylated alpha-linked acidic dipeptidase-like protein 2	LQEESDyITHyTR	Q58DX5	89	1
323	-0.8	PROSC	69	Proline synthetase co-transcribed bacterial homolog protein	TFGENyVQELLEK	O94903	30	4
324	-1.3	PTTG1IP	174	Pituitary tumor-transforming gene 1 protein-interacting protein	KYGLFKEENPyAR	P53801	20	1
325	-1.3	PTTG1IP	174	Pituitary tumor-transforming gene 1 protein-interacting protein	YGLFKEENPyAR	P53801	20	7
326	>-12.6	SLITRK5	945	SLIT and NTRK-like protein 5	LNVEPDyLEVLEK	O94991	108	2
327	-368.9	STEAP1	27	Metalloreductase STEAP1 (Six-transmembrane epithelial antigen of prostate 1)	NLEEDDyLHKDTGETSMLK	Q9UHE8	40	1
328	>-13.8	STEAP1	27	Metalloreductase STEAP1 (Six-transmembrane epithelial antigen of prostate 1)	RNLEEDDyLHKDTGETSMLK	Q9UHE8	40	3