

Supplementary Table 5: 125 identified phosphorylation sites from 97 peptides, representing 60 proteins

Peptides are sorted by the number of phosphorylation sites identified for their corresponding proteins. For column information, please see comments by positioning pointer over column headings. The upper set of peptides were derived from candidate or confirmed ubiquitinated proteins; the lower set of peptides are derived from control proteins.

ORF name	Gene Name	#sites	Other names	Peptide Sequence	Modification sites	Codon Bias	Function	MolEnv	SGD process	SGD function	Genbank annotation
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.FNNIDKTLITSP#PVRNRS	S1033	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.S#NHSPTNGLSGANGTYAL	S1037,S1042	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.HSTTAQSGISDQATTT#PRSS#S	S129,S131	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	K.NEES#GGEIDIEAEPYK.V	S552	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.HAS.SS#L.GGAANVSHPAVLNNTI	S58	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.RRPS#VGLGSHK.G	S777	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.TTTSVSGPFGSYDDAGVNVNR	S64	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YBL101C	ECM21	11	ECM21YBL0814/YBL101C	R.SSNT#LQALLGK.K	T89	0.054	str	unk		modular, function unknown	Extra Cellular Mutant
YDR348C	YDR348C	5	YDR348C/D9651.16	K.NPFLDDVSS#ATDPR.R	S116	0.115	oh	unk	biological process unknown	modular, function unknown	
YDR348C	YDR348C	5	YDR348C/D9651.16	R.TNS#FDMRPLQNLRT	S51	0.115	oh	unk	biological process unknown	modular, function unknown	
YDR348C	YDR348C	5	YDR348C/D9651.16	R.TSSQLSTFPNIPEDFQR.N	S63	0.115	oh	unk	biological process unknown	modular, function unknown	
YDR348C	YDR348C	5	YDR348C/D9651.16	R.NADQGFAYGLESF#S#GSL	S93,S95	0.115	oh	unk	biological process unknown	modular, function unknown	
YHR097C	YHR097C	5	YHR097C	K.ANS#ST#LTLLDAKPN#SK.N	S223,T226	0.052	oh	unk	biological process unknown	modular, function unknown	
YHR097C	YHR097C	5	YHR097C	R.ETVDDDBET#LNLQDRA	T207	0.052	oh	unk	biological process unknown	modular, function unknown	
YHR097C	YHR097C	5	YHR097C	R.LPYVEEAAG#PK.Q	T78	0.052	oh	unk	biological process unknown	modular, function unknown	
YHR097C	YHR097C	5	YHR097C	R.T#GPGONGVNTVNFPR.V	T9	0.052	oh	unk	biological process unknown	modular, function unknown	
YML123C	PHO84	5	PHO84/YM056.03/YML123C	K.IHDT#S#DEDAIN#GLERA	S306,T304	0.607	mel,pt	int	phosphate transport	inorganic phosphate transport	inorganic phosphate transport
YML123C	PHO84	5	PHO84/YM056.03/YML123C	R.ASTAAK#S#DNLH#PKA	S324,T319	0.607	mel,pt	int	phosphate transport	inorganic phosphate transport	inorganic phosphate transport
YML123C	PHO84	5	PHO84/YM056.03/YML123C	K.KINDESS#PQLOHEK.-	S381	0.607	mel,pt	int	phosphate transport	inorganic phosphate transport	inorganic phosphate transport
YML103W	MET4	5	MET4/N2177/YNL103W	R.KYSDNDEDEYDDADLHGFKK	S310,T304,S314	-0.013	mel	dna	sulfur amino acid metabolism		member of the leucine zipper
YML103W	MET4	5	MET4/N2177/YNL103W	R.RYSDNDEDEYDDADLHGFKK	S566	-0.013	mel	dna	sulfur amino acid metabolism		member of the leucine zipper
YML103W	MET4	5	MET4/N2177/YNL103W	R.RNIF#L.TSYQDQK.S	T208	-0.013	mel	dna	sulfur amino acid metabolism		member of the leucine zipper
YOR042W	CUE5	4	CUE5/YOR042W/D2762	R.ECHHEDE#SEEDSWG#YEK.D	S222	0.119	unk	unk	biological process unknown	modular, function unknown	Hypothetical ORF
YOR042W	CUE5	4	CUE5/YOR042W/D2762	K.KRNPDEDEFLN#DEM.-	S410	0.119	unk	unk	biological process unknown	modular, function unknown	Hypothetical ORF
YOR042W	CUE5	4	CUE5/YOR042W/D2762	K.WOPL.PEPLDIT#PTK.V	T366	0.119	unk	unk	biological process unknown	modular, function unknown	Hypothetical ORF
YOR042W	CUE5	4	CUE5/YOR042W/D2762	K.SSGIDEDLV#PAEDAK#EEEF	T12	0.119	unk	unk	biological process unknown	modular, function unknown	Hypothetical ORF
YHR025C	PEK2	3	PEK2/YMR325.06/YMR205C	K.NAAS#TKRTPPAPPAE#S#SGLS	S162,S169	0.658	mel	sol	glycolysis	6-phosphofructokinase	phosphofructokinase beta subunit
YMR205C	PEK2	3	PEK2/YMR325.06/YMR205C	K.YHS#YD.LAYR.M	S173	0.658	mel	sol	glycolysis	6-phosphofructokinase	phosphofructokinase beta subunit
YOR153W	PDR5	3	PDR5/STS1.05M/YDR1Y034	K.MLQCS#SEEDSTW#GGLS#K	S851,Y860,S867	0.304	td,tsp	unk	transport	protein kinase	multidrug resistance transporter
YBR059C	ARK1	2	ARK1.YHRO59C/YBR0419	K.DK.DS#N#S#TSTSTPSE#R	S1051,S1055	0.113	unk	unk	biological process unknown	modular, function unknown	Arkt-family kinase-like protein
YOR033W	MRH1	2	MRH1.ID3428Y/DK033W/D967	K.APVAS#PRPAT#PNL.SK.D	S291,T298	0.635	oh	unk	biological process unknown	modular, function unknown	Membrane protein related to
YDR135C	YCF1	2	YCF1.YD9902.11YDR135C	R.RAS#DAT#LGSIDF#GDDENAK.R	S910,T914	0.111	pt	int	bilirubin transport	bilirubin transporter	
YDR508C	GMP1	2	GMP1.D9719.14YDR508C	R.AEGS#ANS#PSSNSG#TPISTH	S114,S116	0.25	mel,pt	int	transport		high-affinity glutamine permease
YGL205W	POX1	2	POX1.YFOX191220/YGL205W	R.RTT#NIPDS#VNLNPK.F	S14,T18	0.122	mel	unk	fatly acid beta-oxidation	acyl-CoA oxidase activity	Defective Cell Wall, N-glycos
YKL046C	DCW1	2	YKL046C/YKL259	R.AIDR#APATYAENG#S#VGDG	S402,S404	0.26	oh	int	cell wall biosynthesis (sensu	modular, function unknown	
YHR018C	GP12	2	YHR018C	K.DSS#S#ED#ED#ED#ED#DGFTLL	S379,S383	0.157	oh	unk	biological process unknown	modular, function unknown	Encodes a Glycerol-3-phosph
YHR067W	GP12	2	GP12/GA11.YHR067W	R.VNS#RGS#L.TDIF#SDAK.Q	S670,S674	0.197	mel	unk	phospholipid biosynthesis	glycerol-3-phosphate O-acytl	
YMR171C	YMR171C	2	YMR171C/YMR0010.01/YMR520	R.NLITDEAS#LDS#VNDNDE#ND	S518,S522	0.113	oh	unk	biological process unknown	modular, function unknown	
YNL321W	YNL321W	2	YNL321W/N0339	K.SHS#V#DLNTATPS#PK.R	S112,S124	0.151	pt	int	biological process unknown	modular, function unknown	
YHR013C	PHO91	2	YHR013C/N2052	R.RINDENS#S#NEEDEDEG#NQE	S313,S315	0.254	pt	int	biological process unknown	modular, function unknown	
YPL019C	YTC3	2	YTC3.YHMA2YPL019C/LPB12	R.HVADL#E#ES#S#DEEG#ALPK	S623,S625	0.15	mel,tm	int	protein biosynthesis*		Low-affinity phosphate transp
Hsmve Ub YEAST	RPL40A	1	Ubiquitin (see RPL40A daaa)	R.LT.SMDVNQK.E	S59	0.788	td,tm,pt	rib	cytokinesis	structural constituent of ribos	Phosphate metabolism; trans
YBR023C	CHS3	1	CHS3/CAL1YCD2D01T01KHT	R.NPSTLLPTS#M#FV#NKA	S608	0.142	str,sp,cdc	int	protein biosynthesis*		Homology to rat L4
YBR114W	RAD16	1	RAD16YBR009Y/YBR114W	K.SV#NCKE#MDDTAK.N	S27	0.127	dna,sp	dna	cytokinesis		Required for chitin synthesis
YBR130C	SHI3	1	SHI3.YBR1005Y/YBR130C	R.Y#NCKE#KDM	Y25	0.078	str,sp	unk	rRNA localization, intracellu	DNA dependent adenosine tri	Nucleotide excision repair, pro
YMR142W	MAK5	1	MAK5/YBR1119Y/YBR142W	K.DADEL#P#SCA#DOFNNV#R.E	S680	0.141	ma	unk	rRNA localization, intracellu	mRNA binding	
YBR223C	YBR273C	1	YBR273C/YBR1741	R.SSTPLSGAASS#COFNNV#R.E	T351	0.117	oh	unk	deficient maintenance of kill	Necessary for maintenance o	Necessary for maintenance o
YHR021C	HSP90	1	HSP90/RO1Y/YHR021C	R.AS#GEI#A#PEPE#EQ#ED#TAJ	T333	0.283	tm,sp,str	int	response to stress*	heat shock protein activity	Protein induced by heat shock
YHR037C	PHO87	1	PHO87/YCR54Y/YHR037C	R.LEIS#GIST#THSS#NPE#HSSNJC	S230	0.168	oh	unk	transport		May collaborate with Prodig
YHR051W	YCR051W	1	YCR051W	R.ROL#QIIT#GDN#NEELER.Y	T185	0.185	oh	pt	biological process unknown	modular, function unknown	
YOR061W	YCR061W	1	YCR061W/YCR061W/YCR04	K.EV#RVDI#PI#NDI.ES#PMV@VNS	S222	0.144	oh	int	biological process unknown	modular, function unknown	
YDL128C	CDG48	1	CDG48/D2228Y/YDL128C	R.KCT#I#EPGL#E#TAALAK.A	T686	0.407	cdc,pm,pt	sol	ubiquitin-dependent protein d	adenosine triphosphatase	Microsomal protein of CDG48
YDL193W	YDL193W	1	YDL193W/D1239	K.OK#FEDL#SK.R	T87	0.204	oh	unk	biological process unknown	modular, function unknown	
YDR119W	YDR119W	1	YDR119W/YD9727.14	K.IEENENS#LTLAS#PK.Q	S64	0.059	pt	int	biological process unknown	modular, function unknown	

YDR171W	HSP42	1	HSP42/YD8395.04/YDR171W	K.S58FAH.OA6SPIDP.LOVSK.P	S216	0.196	tm,ssp	act	stress response	chaperone	Similar to HSP26: expression
YDR211W	GCD6	1	GCD6/YB38.4/2B.03/YDR142.121	R.EEDS#ETEDDED#EKE	S240	0.181	tm	psf	protein synthesis initiation	translation initiation factor	
YDR417W	SNF1	1	SNF1/C611/CCR1/PAS14/HAF3.K	SVSELDITFESQSPPTFQQQSH	S415	0.158	met,na,sp	int	protein phosphorylation	SNF1/AAAMP-activated protein	Guanine nucleotide exchange
YER028C	CHO1	1	CHO1/PSS/PSS1Y/ERO28C	R.DENGYAS#DEVGTL.S#R.R	S36	0.17	met	int	phosphatidylserine biosynthesis		Required for release from glu
YER143W	DDI1	1	DDI1/YER143W	K.SFOGQLPAPTSVTTSSDKPLTHP	T348	0.102	lpt	per	biological process unknown	CDP-diacylglycerol-serine O-2	phosphatidylserine synthase
YFL004W	YTC2	1	YTC2/PHM1/YFL004W	R.SNFNTASERL.S#ASK.F	S189	0.185	met,tm	int	biological process unknown	modular_function unknown	DNA Damage inducible bind
YHR094C	HXT1	1	HXT1/YHR094C	K.GSLAIDEVNMQYFAAGL.PWK	Y331	0.536	met,lpt	int	hexose transport		Phosphate metabolism; trans
YHR120W	MSH1	1	MSH1/YHR120W	R.SJLAIDEVNMQYFAAGL.PWK	S859	0	dna	int	DNA repair	glucose transporter activity*	High-affinity hexose (glucose)
Y.L084C	Y.L084C	1	Y.L084C/D0934	R.SSEFYSGINLSK.D	S902	0.05	oh	unk	biological process unknown	ATP binding activity	mus homolog involved in mit
YKL129C	MYO3	1	MYO3/YKL129C	K.RGS#MYHMLNPVQA.TAVRD	S356	0.067	lpt,ssp,slr	act	cell wall organization and bldg	microfilament motor	
YKL174C	YKL174C	1	YKL174C/YKL639	K.SGVNS#EEGFK.V	S371	0.033	met,ssp	int	biological process unknown	modular_function unknown	myosin I
YKL217W	JEN1	1	JEN1/YKL217W	R.VYSQODGVEYEDED#PNLS	S83	0.186	lpt	int	transport	lactate transporter	Repressed by glucose, induces
YKR097W	PCK1	1	PCK1/PPC1/PPM2/PEP/C/YKR08	K.SHVVDYDSS#IENR.C	S332	0.424	met	sol	gluconeogenesis	phosphoenolpyruvate carbox	phosphoenolpyruvate carbox
YLR024C	UBR2	1	UBR2/YLR024C/L1730	R.KYAS#DNNK1TENDSNK.A	S715	0	plm,plm	unk	protein monoubiquitination*	ubiquitin-protein ligase activity	ubiquitin-protein ligase (E3)
YLR134W	PDC5	1	PDC5/L133/L906/L7LR134W	K.NVETHSLEDHKK	S313	0.828	met	sol	pyruvate metabolism*	pyruvate decarboxylase activity	pyruvate decarboxylase
YLR220W	CCC1	1	CCC1/L8083.6/CLR220W	K.GSGGTFSGSEST#PLL.R.G	T34	0.096	met,cdc,lpt	int	iron homeostasis	modular_function unknown	Thiamine Metabolism
YLR237W	THI7	1	THI7/TH10UPL.3/L8083.2/YLR	R.AYTLGEGYTTGHEVPEGS#DD	S562	0.462	met,lpt	int	thiamin transport	modular_function unknown	Thiamine Metabolism
YML029W	USA1	1	YML029W	R.SQ8#PVSFAFQGR.S	S378	0.058	oh	unk	biological process unknown	modular_function unknown	Identified by its interaction with
YML049C	RSE1	1	RSE1/scsAP130Y/M8627.03/YML	R.DSSIGQLNHVGLENGVMK.F	Y752	0.057	na,lpt,na	ma	mRNA splicing*	U2 snRNA binding activity	RNA splicing and ER to Golgi
YML192W	CHS1	1	CHS1/N1404/YML192W	R.DDEVDDINT#DK.L	T330	0.064	slr	int	cyclohexis	chitin synthase	disrupts mating and sporulate
YNL268W	LYP1	1	LYP1/M0790/YNL268W	R.LQVVS#HEDJEDDEEAHYEDK	T92	0.315	met,lpt	int	transport	lysine permease	
YNL307C	MCK1	1	MCK1/YPK1/N0392/YNL307C	K.KLEHNOBPSY#GSR.F	Y201	0.14	cdc,ssp	sol	protein phosphorylation	protein threonine/tyrosine kin	Disp. for mitosis, required for
YNR016C	ACC1	1	ACC1/FAS3/ACC/BP2/N3175N	R.AVSN#SULSYVANSOSSP.L.R.E	S159	0.441	met,lpt,na	sol	fatty acid biosynthesis	acetyl-CoA carboxylase	acetyl-CoA carboxylase
YOL119C	MGH4	1	YOL119C/MGH4/O0569	R.VLNT#PEASLVDDBR.E	T78	0.067	lpt	int	transport	transporter activity*	monocarboxylate permease T
YOL130W	ALR1	1	ALR1/O0522/YOL130W	R.KSL.VS#PVL.PHESK.S	S190	0.119	lpt	int	di-, tri-valent inorganic cation	di-, tri-valent inorganic cation	aluminum resistance
YOR142W	LSC1	1	LSC1/YOR3352/O3352/YOR144	K.T#KMLLLP.D	T29	0.334	met,met	sol	tricarboxylic acid cycle*	succinate-CoA ligase (ADP-ld	alpha subunit of succinyl-CoA
YDL223C	YDL223C	11	YDL223C/D0843	K.SIS#GTTGR.S	S1038	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.DDQGEETENN#SF.GKPGS#YT	S30.S36	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.GVNSD#NS#RDV/PGSFR.G	S303.S306	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.KDOXSGS#DAOQOQIMEIEK.A	S402	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.DEDMVED#TPEHOQGLDYLD	S497	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.ASYSGSGNQES#DDND	S859	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	K.DINTSSGKPSRGTYPETTSYSA	S945	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	R.KKFS#T#KPTENVL.PK.E	T46	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDL223C	YDL223C	11	YDL223C/D0843	R.I#D1GGADSNAYAAEYGNFPS	T891	0.152	unk		biological process unknown	modular_function unknown	Hypothetical ORF
YDR267C	YDR267C	3	YDR267C/D05420	R.ENSS#NNPOLR.S	S27	0.171	lpt		biological process unknown		Hypothetical ORF
YDR267C	YDR267C	3	YDR267C/D05420	K.SDNKPDVEEETENKEDS#NN	S524.T532	0.171	lpt		biological process unknown		Hypothetical ORF
YCL037C	SRO9	2	SRO9/SY32/YCL037C	K.LAPTEIPVSTIS#EDLDATK	S89	0.38	tm,lpt	rb			Associates with translating rib
YDL025C	YDL025C	2	YDL025C/D2810	K.PHM@SQASTGVSVELQHNSS	S227.S231	0.099	unk		biological process unknown		
YLR371W	ROM2	2	ROM2/L8039.3/YLR371W	R.KPS#L.PQALAGL.K	S195	0.094	ssp,slr		establishment of cell polarity	signal transducer	Hypothetical ORF
YLR371W	ROM2	2	ROM2/L8039.3/YLR371W	R.XTYS#GISTLSRPR.R	S387	0.094	ssp,slr		establishment of cell polarity	signal transducer	Gdp-GTP Exchange Protein (
YJL026W	RNR2	1	RNR2/CRT6/L1271/YJL026W	K.AAADA.LSPDLEK.D	S17	0.641	met		DNA replication	ribonucleoside-diphosphate r	small subunit of ribonucleic