

Supplementary Table 3: 110 identified ubiquitination sites from 107 peptides, representing 72 proteins

Peptides are sorted by the number of ubiquitination sites identified for their corresponding proteins. For column information, please see comments by positioning pointer over column headings.

ORF name	Gene Name	#sites	Other names	Peptide Sequence	Modification sites	Codon Bias	Function	MoEnvy	SGD process	SGD function	Genbank annotation
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	KIQDK*EGIPDDQRL	33	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	KLISEEDIGM*QIFVK*TLTGK.T	6	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	KSK*IQDK*EGIPDDQRL	29,33	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	K*TLTEVSSSDIDNVK*SK.I	27	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	K*TLTGK*TLTEVSSDIDNVK.S	11	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	R.LIFGK*QLDGR.T	48	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
Hismyc Ub YEAST	RPL40A	7	Ubiquitin (use Ubi1 data)	R.TLSDVNIQK*ESTLHVLR.L	63	0.788	trn,pjm	nb	protein biosynthesis*	structural constituent of	Homology to ral L4
YBL101C	ECM21	6	ECM21/YBL1081/4YBL10	K.FHQTIK*NSGLPVK.T	807	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YBL101C	ECM21	6	ECM21/YBL1081/4YBL10	K.GYEYEDQIDPVAK*DPYNPYLDFA	651	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YBL101C	ECM21	6	ECM21/YBL1081/4YBL10	K.SHEENFNNDLLSVSPFDDSDSK*G	794	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YBL101C	ECM21	6	ECM21/YBL1081/4YBL10	R.FNNLDK*LLSTPSPVNR.S	712	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YBL101C	ECM21	6	ECM21/YBL1081/4YBL10	R.FNNLDK*LLSTPSPVNR.S	1024	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YBL101C	SAM2	4	SAM2/ETH2/D9719.8/YTR.DTK*IGYDSAK.G	EDYK.T	577	0.054	str	unk		modular function unkn	ExtraCellular Mutant
YDR502C	SAM2	4	SAM2/ETH2/D9719.8/YTR.DTK*IGYDSAK.G	EDYK.T	77,78	0.642	met	unk	methionine metabolism	methionine adenosyltran	methionine biosynthesis
YDR508C	GNP1	3	GNP1/D9719.14/YDR50	K.EK*QIGSEIENEVEVEK.T	41	0.25	met,pt	int	transport		high-affinity glutamine p
YDR508C	GNP1	3	GNP1/D9719.14/YDR50	K.SSVITVDGK*QSPQDEQK.Q	132	0.25	met,pt	int	transport		high-affinity glutamine p
YDR508C	GNP1	3	GNP1/D9719.14/YDR50	R.NDLDDVSHYMK*EIQPK.E	34	0.25	met,pt	int	transport		Hexose transporter
YDR342C	HXT7	3	HXT7/D9651.11/YDR34	K.LAGNASWGF.LSSK*TK.V	318	0.666	met,pt	int	transport		Hexose transporter
YDR342C	HXT7	3	HXT7/D9651.11/YDR34	R.DEGYDWLIMPVGVLGDLK.GDALGQC	560	0.666	met,pt	int	transport		Hexose transporter
YEL021W	URA3	3	URA3/YEL021W	R.KAFAWGYLR.R	253	0.206	met	unk			Hexose transporter
YEL021W	URA3	3	URA3/YEL021W	R.DEGYDWLIMPVGVLGDLK.GDALGQC	209	0.206	met	unk			Hexose transporter
YEL021W	URA3	3	URA3/YEL021W	R.KAFAWGYLR.R	93	0.206	met	unk			Hexose transporter
YHR097C	YHR097C	3	YHR097C	K.KSTLDEYFGR.E	187	0.052	oh	unk	biological process unkn	modular function unkn	
YHR097C	YHR097C	3	YHR097C	K.NITQDSK*MK.T	242	0.052	oh	unk	biological process unkn	modular function unkn	
YHR097C	YHR097C	3	YHR097C	R.LPSYEEAAGTPK*QOAPYK.E	78	0.052	oh	unk	biological process unkn	modular function unkn	
YBR059C	AKL1	2	AKL1/YBR059C/YBR04	R.VSPHASTATENK.R.H	1046	0.113	unk	unk	biological process unkn	modular function unkn	Ark-family kinase-like pr
YBR059C	AKL1	2	AKL1/YBR059C/YBR04	R.VSPHASTATENK.R.H	1008	0.113	unk	unk	biological process unkn	modular function unkn	Ark-family kinase-like pr
YDL126C	CDC48	2	CDC48/D2228/YDL126C	R.AAPTAVFDELDIAK*AR.G	594	0.407	cdc,pjm,pt	sol	ubiquitin-dependent prot	adenosinetriphosphatase	Microsomal protein of CI
YCR005C	CIT2	2	CIT2/YCR043/YCR005C	R.YMAQRK*FAMDHPDYELFK.L	673	0.407	cdc,pjm,pt	sol	ubiquitin-dependent prot	adenosinetriphosphatase	Microsomal protein of CI
YCR005C	CIT2	2	CIT2/YCR043/YCR005C	K.LVSVIYEVAPGV.LTEHGK*TK.N	385	0.163	met	sol	glutamate biosynthesis	citrate (SI)-synthase	non-mitochondrial citrate
YCR042W	CUE5	2	CUE5/YOR042W/O2762	K.KKNPDEDEFLNSHDDM-	396	0.119	unk	unk	biological process unkn	modular function unkn	Hydrophobic ORF
YOR042W	CUE5	2	CUE5/YOR042W/O2762	K.KKNPDEDEFLNSHDDM-	76	0.119	unk	unk	biological process unkn	modular function unkn	Hydrophobic ORF
YLR056W	ERG3	2	ERG3/SYR1L2150/YLR	K.EVHEIK.FVEGDNDRI.	344	0.32	met,pt,isp	int	ergosterol biosynthesis	C-5 sterol desaturase	C-5 sterol desaturase
YLR056W	ERG3	2	ERG3/SYR1L2150/YLR	R.RPDDSLFEPGCLRD	324	0.32	met,pt,isp	int	ergosterol biosynthesis	C-5 sterol desaturase	C-5 sterol desaturase
YMR015C	ERG5	2	ERG5/CYP61/YMR711	R.K*SL.NGLFTK.Q	164	0.435	met,pt	unk	ergosterol biosynthesis	C-22 sterol desaturase	Cyclochrome P45 Involved
YMR015C	ERG5	2	ERG5/CYP61/YMR711	R.LSK*ENNVERPOL/FHEMR.E	198	0.435	met,pt	unk	ergosterol biosynthesis	C-22 sterol desaturase	Cyclochrome P45 Involved
YOR375C	GDH1	2	GDH1/URE1/GDHA/O6	K.VDIALPCATQNEVSSSEAK*ALVAGV	325	0.746	met	sol		glutamate dehydrogenase	NADP-specific glutamate
YGR268C	HUA1	2	YGR268C/G9352	K.DTHDELPSYEDVYK*TEER.L	18	0.162	oh	unk	biological process unkn	modular function unkn	NADP-specific glutamate
YGR268C	HUA1	2	YGR268C/G9352	K.LKSDYAK*ANGGEPLPK.A	338	0.186	pt	int	transport	lactate transporter	Repressed by glucose, it
YK1217W	JEN1	2	JEN1/YK1217W	M.AC*SSITIDK*IGEOQOPAGR.K	9	0.186	pt	int	transport	lactate transporter	Repressed by glucose, it
YGR136W	LSB1	2	LSB1/G6409/YGR136W	K.LPEK*WIDGNOR.S	41	0.027	str	unk	biological process unkn	modular function unkn	Las17 Binding protein
YGR136W	LSB1	2	LSB1/G6409/YGR136W	K.TGDK*IQVLEK.I	79	0.027	str	unk	biological process unkn	modular function unkn	Las17 Binding protein

YML123C	PHO84	2	PHO84/YMT056.03/YML	K KIHDTSDDEMANGLERA	288	0.607	met,pt	int	phosphate transport	inorganic phosphate tran	inorganic phosphate tran
YML123C	PHO84	2	PHO84/YMT056.03/YML	M.SVNAEK'DTHIAERS	6	0.607	met,pt	int	phosphate transport	inorganic phosphate tran	inorganic phosphate tran
YAL005C	SSA1	2	SSA1/YG100/YAL005C	K.MVAEAEK'KEEDEESQR.I	521	0.833	tm,pt	sol	protein folding	adenosinephosphatase	Stress-seventy subfamily
YAL005C	SSA1	2	SSA1/YG100/YAL005C	R.IASK'NOLIESAYSL.K.N	536	0.833	tm,pt	sol	protein folding	adenosinephosphatase	Stress-seventy subfamily
YAR027W	UIP3	2	YAR027W/FUN55	-MOTPSENTDVK'LTLDLEPSAHL	11	-0.011	oh	unk	biological process unkn	biological function unkn	Ulp1 Interacting Protein
YAR027W	UIP3	2	YAR027W/FUN55	K.AAEIHK'EAEEFYVYR.K	218	-0.011	oh	unk	biological process unkn	biological function unkn	Ulp1 Interacting Protein
YHL010C	YHL010C	2	YHL010C	K.K'DGEI'LAAMF.R.H	410	0.019	pt	unk	biological process unkn	nuclear localization sequ	
YHL010C	YHL010C	2	YHL010C	R.LVONEVDGK'LVIEVGSDDNDNIG	369	0.019	pt	unk	biological process unkn	nuclear localization sequ	
YHL041W	YHL041W	2	YHL041W/Y9905.07	K.EFLSNSFAEPEPAK'PEVAEEK'PQT	305,313	0.361	cdc	unk	biological process unkn	biological function unkn	
YMR295C	YMR295C	2	YMR295C	R.ASVPK'ISEDDK'AR.L	26,32	0.347	oh	unk	biological process unkn	biological function unkn	
YOL109W	YOL109W	2	ZEO1/OO738/YOL109W	K.EQAEASIDNLK'NEATPEAEQVK.K	45	0.724	oh	unk	biological process unkn	biological function unkn	
YOL109W	YOL109W	2	ZEO1/OO738/YOL109W	K.K'EQUADVGEQK.K	57	0.724	oh	unk	biological process unkn	biological function unkn	
YLR153C	ACS2	1	ACS2/L9634.10/L3333/Y	Y.MDTYK'PYPGHYFT'GDGA.GR.D	506	0.469	met	int	biological process unkn	acetyl-CoA ligase	one of 2 acetyl-CoA synt
YLR359W	ADE13	1	ADE13/BRA1/BRA8/YLR	R.NDIG.RGVK'GTTGTQASFLA.FHGNH	196	0.418	met	unk	carbohydrate metabolist	adenylosuccinate lyase	Adenylosuccinate Lyase
YPL061W	ALD6	1	ALD6/LPE9/YPL061W	M.TK'LFHDTAEPVK.I	3	0.664	met	sol	leucine catabolism	aldehyde dehydrogenase	Utilizes NADP+ as the p
YDR380W	ARO10	1	ARO10/D9481.3/YDR38	K.YTNSTLQOC@PSK'LAL.K.L	588	0.113	met	unk	transport	carboxy-lyase activity*	
YBR290W	BSD2	1	BSD2/YBR203/YBR290	K.K'Y.LNQSQA-	312	-0.033	pt,rsp	int	transport	chaperone	metal homeostasis prote
YJL008C	CCT8	1	CCT8/J1374/YJL008C	R.LPONPAAGLF.K'QGVNSYNADGQIHK	15	0.271	tm,sir	unk	protein folding	chaperone	Required for assembly o
YER164W	CHD1	1	CHD1/SYGP-ORF4/YER	K.YLK'NLNSNYK.D	1144	0.138	ma,sp	dna	transcription	chitin synthase	Required for chitin synth
YBR023C	CHS3	1	CHS3/GAL1/CSD2/DIT	K.ISDEGVAEEDFK'DGDV/DNFESSTG	136	0.142	sir,sp,cdc	int	cytokinesis	molucular function unkn	Protein with strong simle
YEL062W	COS4	1	COS4/YEL062W	K.LENSEK'SWSPVGLADAK.L	205	0.064	unk	unk	biological process unkn	molucular function unkn	
YPR030W	CSR2	1	CSR2/MR019/YPR367	K.IPQDK'NHNEVNDNGNSNTSLQTSST	841	0.065	oh	unk	cell wall organization and	molucular function unkn	chrs sp2 rescue, overe
YOL145C	CTR9	1	CTR9/D91/AO41045/G	K.LTYOK'ENVM@ASLK.I	196	0.16	cdc,ma,dna	dna	cell wall organization and	molucular function unkn	CTR9 is required for por
YER143W	DDI1	1	DDI1/YER143W	R.LMANPDDPDK*K.R.I.	171	0.102	pt	per	biological process unkn	molucular function unkn	DNA Damage inducible,
YEL071W	DL3	1	DL3/YEL071W	M.TAHPA/LJL.PG22/YPL	17	0.245	met,met	sol	regulation of transcrip	D-lactate dehydrogenase	D-lactate dehydrogenase
YJL086C	ELP3	1	ELP3/HPA1/L.PG22/YPL	K.K'DIILGLRL	453	0.234	ma,ptm,dna	dna	regulation of transcrip	Pcl1 transcription elong	Squalene monooxygena
YGR175C	ERG1	1	ERG1/G129/YGR175C	K.SLSPSP'DEASQGR.FRA	311	0.574	met	int	ergosterol biosynthesis	molucular function unkn	exocyst complex compo
YBR102C	EXO84	1	EXO84/YBR102C/YBR1	L.OVQEEV/K'LNNK.S	219	0.053	pt,sir	sol	mRNA splicing*	general amino acid perm	
YKR039W	GAP1	1	GAP1/YKR039W	R.VKPEEVDNPLSEAEK'YAITQTPLK.H	76	0.434	met,pt	int	amino acid transport	general amino acid perm	
YPR039W	GLN1	1	GLN1/YP3085.01/YPR0	R.SVAK'EGYGFEDR.R	324	0.676	met	sol	glutamine aldolase	threonine aldolase	Threonine Aldolase
YEL046C	GLY1	1	GLY1/SYGP-ORF34/YE	K.SMAGPAGSLVGNLK'FYVK.K	228	0.516	met	unk	cell wall organization and	1,3-beta-glucan synthase	Highly similar to FKS1 (G
YGR032W	GSC2	1	GLS2/YK52/GSC2/G40	K.LLYHQV'PSEIE.GKR.T	806	0.224	sir	int	transport		Member of superfamily c
YHR096C	HXT5	1	HXT5/YHR096C	K.PYSSYAEDEPK'DELELOK.E	61	0.269	met,pt	int	transport		Repression of HXT6 exp
YDR434C	HXT6	1	HXT6/D9651.12/YDR34	R.GANYDAEEMAHDDK'PLYK.R	560	0.666	met,pt	int	transport		Member of sugar transp
YDR497C	ITR1	1	ITR1/D9719.3/YDR497C	R.VHELK'YEPTEHIEDI.-	573	0.27	met,pt	int	transport		putative partner of Rpb8
YGR089W	NNF2	1	YGR089W/G4630	K.K'YVSHLOSL.MNTR.K	10	0.095	oh	unk	biological process unkn	molucular function unkn	
YPL058C	PDR12	1	PDR12/PE14/YPL058C	R.TLDIKPGYEDK'VPK.S	426	0.364	pt	int	transport	transporter	similar to Pdr5p
YOR153W	PDR5	1	PDR5/STS1/LEM1/YDR	R.GVLT.EK'YANDENEN.GERS	825	0.304	pt,rsp	int		transporter	mutidoxine resistance tran
YBR036C	PDX3	1	PDX3/YBR0321/YBR03	K.FTLNEK'Q.LTDDPIDL.FTK.W	29	0.358	met	unk	transport	pyridoxamine-phosphate	pyridoxamine (pyridoxamin
YCR037C	PHO87	1	PHO87/YCR624/YCR03	R.GDSDEK'AIDGNINNEIETLDEL.SPQC	102	0.168	met,pt	int			May collaborate with Ptk
YPR154W	PLN3	1	PLN3/YPR154W/P9584.4	R.NASPA.SL.EYVEAL.YORFDPQDDGDL.GI	80	0.167	sir	unk	biological process unkn	molucular function unkn	
YHL015W	RPS20	1	RPS20/URP2/YHL015W	K.EK'VEEQEQQQQI.K.I	8	0.963	tm	nb	protein biosynthesis	structural protein of ribos	Homology to rat S2, hun
YNL178W	RPS3	1	RPS3/PT13/SUF14/N16	K.K'ALPDATLIEPK'EEEP.LAPSVK.D	212	0.805	tm	nb	protein biosynthesis	structural protein of ribos	Homology to rat S4 and
YHR203C	RPS4B	1	RPS4B/RPS21A/YHR20	K.ID.LASGKTTDK.F	168	0.804	tm	nb	protein biosynthesis	structural protein of ribos	Homology to rat S4 and
YDR389W	RVS167	1	RVS167/D9509.8/YDR3	R.YNGQOAPGPGVNVQLN'N.-	481	0.221	pt,sir	act	endocytosis	cytoskeletal protein bind	Involved in endocytosis
YJL151C	SNA3	1	SNA3/J0630/YJL151C	R.D.IEAHPAESQAOPAYNDEDEAGAI	125	0.173	oh	unk	biological process unkn	molucular function unkn	Homology to PIMF3/SNA
YAL030W	SNC1	1	SNC1/YAL030W	R.LT.SIEDK'ADNLV.ASAGGFR.R	63	0.157	pt	int	endocytosis	v-SNARE	Involved in mediating tar
YOR327C	SNC2	1	SNC2/O6223/YOR327C	R.LT.SIEDK'ADNLV.ASAGGFR.R	62	0.281	pt	int	endocytosis	v-SNARE	Involved in mediating tar
YJL024C	SSA2	1	SSA2/O6223/YOR327C	R.LT.SIEDK'ADNLV.ASAGGFR.R	556	0.883	tm,pt	sol	protein folding	chaperone	mediate the targeting an
YKL200C	STE6	1	STE6/CEP1/YKL209C	K.NTISEAGDK'LEQADKDAVTK.K	1022	0.054	pt,rsp	int	a-factor export	ATP-binding cassette (A	member of 7 kDa head s
YGR260W	TNA1	1	TNA1/G93838/YGR260W	K.NLED.SWFFNK'EEK.E	283	0.284	pt	int	nicotinamide mononucle	nicotinamide mononucle	Transporter of Nicotinic
YLR024C	UBR2	1	UBR2/YLR024C/L1730	R.K'PAISH#DNASTENDSN.A	709	0	ptm,ptm	unk	protein monoubiquitinatio	ubiquitin-protein ligase a	Ubiquitin-protein ligase (f
YBL039C	URAT	1	URAT/YBL0410/YBL1039	R.K'DSHSA#EPPIDIEK.N	422	0.394	met	unk	biological process unkn	CTP synthase	Last step in pyrimidine b
YDL203C	YDL203C	1	YDL203C/D1066	R.LI.QEK'YVYR.T	184	0.038	oh	unk	biological process unkn	molucular function unkn	
YER067W	YER067W	1	YER067W	K.LNLYPFPVLIHSHEDPEK'ISDAANSH	68	0.118	oh	unk	biological process unkn	molucular function unkn	

YKL187C	1	YKL187C	R.FGDHNLGDDDDADFEKQVNR.N	697	0.112	oth	unk	biological process unkn	
YKR041W	1	YKR041W	-M@SDDDYNSDDNDNDNAEK.R.Y	17	0.085	oth	unk	biological process unkn	
YLR413W	1	YLR413W/L9931.4	R.IIEEHESPDIAEK*NFAR.-	671	0.282	oth	unk	biological process unkn	
YPL207W	1	R.HGTNPVSK*WNR.W		496	0.085	oth	unk	biological process unkn	
YBR054W	1	YKR02YBR0507YBR05	R.LGLIFDEEPAEHGVPVIAEK*K.M	286	0.616	tm	unk	biological process unkn	Homolog to HSP3 heat