

Table S1 Proteins involved in cell wall biogenesis in *Saccharomyces cerevisiae*

Process or protein type	Protein name	Activity or Function	CAZy Family ¹
Precursor supply			
	Ugp1	UDPGlc pyrophosphorylase	
	Pmi40	phosphomannose isomerase	
	Sec53	phosphomannomutase	
	Psa1/Srb1/Vig9	GDP-Man pyrophosphorylase	
	Gfa1	glutamine: Fru-6-P amidotransferase	
	Gna1	GlcN-6-P N-acetylase	
	Agm1/Pcm1	GlcNAc phosphate mutase	
	Uap1/Qri1	UDPGlcNAc pyrophosphorylase	
	Rer2	cis-prenyltransferase (Dol ₁₀₋₁₄)	
	Srt1	cis-prenyltransferase (Dol ₁₉₋₂₂)	
	Dfg10	dehydrodolichol reductase	
	Sec59	Dol-kinase	
	Cwh8/Cax4	Dolichyl pyrophosphate phosphatase	
	Dpm1	GDP-mannose:dolichyl-phosphate Man-T	GT2
	Alg5	UDP-glucose:dolichyl-phosphate Glc-T	GT2
	Yea4	UDP-GlcNAc transporter	
	Vrg4/Vig4	GDP-Man transporter	
	Gda1	GDPase	
	Ynd1	Apyrase	
N-glycosylation			
	Alg7	UDP-GlcNAc: Dol-P GlcNAc-1-P-T	
	Alg13 + Alg14	UDP-GlcNAc: Dol-PP-GlcNAc β 1,4-GlcNAc-T	GT1

Alg1	GDP-Man: Dol-PP-GlcNAc ₂ β1,4-Man-T	GT33
Alg2	GDP-Man: Dol-PP-GlcNAc ₂ Man α1,3-Man-T <i>and</i> GDP-Man: Dol-PP-GlcNAc ₂ Man ₂ α1,6-Man-T	GT4
Alg11	GDP-Man: Dol-PP-GlcNAc ₂ Man ₃ α1,2-Man-T <i>and</i> GDP-Man: Dol-PP-GlcNAc ₂ Man ₄ α1,2-Man-T	GT4
Rft1	Candidate Dol-PP-oligosaccharide flippase	
Alg3	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₅ α1,3-Man-T	GT58
Alg9	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₆ α1,2-Man-T <i>and</i> Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₈ α1,2-Man-T	GT22
Alg12	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₇ α1,6-Man-T	GT22
Alg6	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₉ α1,3-Glc-T	GT57
Alg8	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₉ Glc α1,3-Glc-T	GT57
Alg10	Dol-P-Man: Dol-PP-GlcNAc ₂ Man ₉ Glc ₂ α1,2-Glc-T	GT59
Stt3	OST catalytic subunit	GT66
Wbp1	OST subunit	
Swp1	OST subunit	
Ost1	OST subunit	
Ost2	OST subunit	
Ost3	OST subunit; cysteine oxidoreductase	
Ost6	OST subunit; cysteine oxidoreductase	
Gls1/Cwh41	ER glucosidase I (α1,2 exoglucosidase); indirectly affects β1,6-glucan	GH63
Gls2/Rot2	ER glucosidase II (α1,3 exoglucosidase α-subunit); indirectly affects β1,6-glucan	GH31
Gtb1	ER glucosidase II (regulatory subunit)	
Mns1	ER α-mannosidase I	GH47
Htm1/Mnl1	ER-degradation enhancing α-mannosidase-like protein	GH47
Yos9	Lectin, recognizes α1,6-Man on glucosidase II product, targets misfolded protein for ERAD	
Png1	Cytosolic peptide N-glycanase	
Och1	Initiating α1,6-Man-T	GT32
Mnn9	M-Pol I α1,6-Man-T	GT62

Van1	M-Pol I α 1,6-Man-T	GT62
Mnn9	M-Pol II α 1,6-Man-T	GT62
Anp1	M-Pol II α 1,6-Man-T	GT62
Mnn10	M-Pol II α 1,6-Man-T	GT34
Mnn11	M-Pol II α 1,6-Man-T	GT34
Hoc1	M-Pol II α 1,6-Man-T	GT32
Mnn2	α 1,2-Man-T; Mnn1 subfamily; major role in mannan side chain branching	GT71
Mnn5	α 1,2-Man-T; Mnn1 subfamily; major role in mannan side chain branching	GT71
Mnn4	Positive regulator of Man phosphorylation	
Mnn6/Ktr6	α -Man-P-T; acts on N- and O-glycans in Golgi	GT15
Mnn1	α 1,3-Man-T; acts on N- and O-glycans in Golgi	GT71
Kre2/Mnt1	α 1,2-Man-T; acts on N- and O-glycans in Golgi	GT15
Ktr1	α 1,2-Man-T; acts on N- and O-glycans in Golgi	GT15
Ktr2	α 1,2-Man-T; acts on N-glycans in Golgi	GT15
Ktr3	α 1,2-Man-T; acts on N- and O-glycans in Golgi	GT15
Yur1	α 1,2-Man-T; acts on N-glycans in Golgi	GT15
Ktr4	Putative α -ManT	GT15
Ktr5	Putative α -ManT	GT15
Ktr7	Putative α -ManT	GT15
Gnt1	GlcNAc-T	GT8
Vrg4	GDP-Man transporter	
Gda1	GDPase	
Ynd1	Apyrase	
O-mannosylation		
Pmt1	Dol-P-Man: protein: O-Man-T; Pmt1 family	GT39
Pmt2	Dol-P-Man: protein: O-Man-T; Pmt2 family	GT39

Pmt3	Dol-P-Man: protein: O-Man-T; Pmt2 family	GT39
Pmt4	Dol-P-Man: protein: O-Man-T; specific for membrane proteins	GT39
Pmt5	Dol-P-Man: protein: O-Man-T; Pmt1 family	GT39
Pmt6	Dol-P-Man: protein: O-Man-T; Pmt2 family	GT39
Mnt2	α 1,3-Man-T; Mnn1 subfamily; acts on O-glycans in Golgi	GT71
Mnt3	α 1,3-Man-T; Mnn1 subfamily; acts on O-glycans in Golgi	GT71

GPI anchoring

Gpi1	GPI-Gnt subunit	
Gpi2	GPI-Gnt subunit	
Gpi3	GPI-Gnt subunit, UDP-GlcNAc: Ptd-Ins α 1,6-GlcNAc transferase	GT4
Gpi15	GPI-Gnt subunit	
Gpi19	GPI-Gnt subunit	
Eri1	GPI-Gnt subunit	
Ras2	Negative regulator of GPI-Gnt	
Gpi12	GPI-Ins-deacetylase	
Gwt1	GPI-Ins-acyltransferase	
Gpi14	GPI-ManT-I: Dol-P-Man: GlcN-Ptd-(acyl)Ins α 1,4-Man-T	GT50
Pbn1	Putative subunit of GPI-Man-T-I	
Arv1	Proposed to present GlcN-(acyl)PI to Gpi14	
Mcd4	GPI-Etn-P-T-I	
Gpi18	GPI-ManT-II: Dol-P-Man: Man-GlcN-Ptd-(acyl)Ins α 1,6-Man-T	GT76
Pga1	GPI-ManT-II subunit	
Gpi10	GPI-Man-T-III: Dol-P-Man: Man ₂ -GlcN-Ptd-(acyl)Ins α 1,2-Man-T	GT22
Smp3	GPI-Man-T-IV: Dol-P-Man: Man ₃ -GlcN-Ptd-(acyl)Ins α 1,2-Man-T	GT22
Gpi13	GPI-Etn-P-T-III	
Gpi11	Subunit of GPI-Etn-P-T-II and GPI-Etn-P-T-III	

Gpi7	GPI-Etn-P-T-II
Gpi8	GPI transamidase catalytic subunit
Gaa1	GPI transamidase subunit
Gab1	GPI transamidase subunit
Gpi16	GPI transamidase subunit
Gpi17	GPI transamidase subunit
Bst1	GlcN-(acyl)PI inositol deacylase
Per1	Removes acyl chain at <i>sn</i> -2 position of protein-bound GPIs
Gup1	MBOAT O-acyltransferase, transfers C ₂₆ acyl chain to <i>sn</i> -2 position of protein-bound GPIs
Cwh43	Replaces GPI diacylglycerol with ceramide
Cdc1	Homologue of mammalian PGAP5; possible GPI-Etn-P phosphodiesterase
Ted1	Homologue of mammalian PGAP5; possible GPI-Etn-P phosphodiesterase

Chitin and chitosan synthesis

Chs1	Chitin synthase I catalytic protein	GT2
Chs2	Chitin synthase II catalytic protein	GT2
Chs3	Chitin synthase catalytic subunit	GT2
Cdk1	Mitotic protein kinase, phosphorylates Chs2	
Cdc14	Phosphoprotein phosphatase, dephosphorylates Chs2	
Dbf2	Mitotic exit kinase, phosphorylates Chs2	
Inn1	Localized to mother cell-bud junction with Chs2 and Cyk3, implicated in Chs2 activation	
Cyk3	Localized to mother cell-bud junction with Chs2 and Inn1, implicated in Chs2 activation	
Pfa4	Protein acyltransferase, palmitoylates Chs3	
Chs7	Chaperone required for ER exit of Chs3	
Rcr1	ER protein, small negative effect on Chs3-dependent chitin synthesis	
Yea4	ER protein and UDP-GlcNAc transporter, <i>yea4Δ</i> has 65% of wild type levels of chitin.	
Chs5	Exomer component, involved in Chs3 trafficking	

Chs6	Exomer component, involved in Chs3 trafficking	
Chs4/Skt5	Prenylated protein that interacts with, activates, and anchors Chs3 to septin ring	
Bni4	Scaffold protein, tethers Chs3 and Chs4 to septins	
Shc1	Sporulation-specific Chs4 homologue	
Cda1	Chitin de-N-acetylase	
Cda2	Chitin de-N-acetylase	

β -1,3 glucan synthesis

Fks1/Gsc1/Cwh53/ Etg1/Pbr1	Probable β 1,3-glucan synthase, major role in vegetative cells	GT48
Fks2/Gsc2	Probable β 1,3-glucan synthase, stress-induced, role in sporulation	GT48
Fks3	Probable β 1,3-glucan synthase, role in sporulation	GT48
Rho1	GTPase; activator of Fks1 and Fks2	

β -1,6 glucan formation

Kre5	Diverged UDP-Glc: glycoprotein Glc-T homologue	GT24
Rot1	Fungus-specific ER chaperone	
Big1	Fungus-specific ER chaperone	
Keg1	Fungus-specific ER chaperone	
Kre6	Resembles β -1,6/ β -1,3 glucanases	GH16
Skn1	Sequence and functional Kre6 homologue; additional role in MIPC synthesis	GH16
Kre9	Fungus-specific O-mannosylated protein	
Knh1	Kre9 homologue	
Kre1	GPI-protein, secondary receptor for K1 killer toxin	

Glycosidases, cross-linking enzymes, and proteases

Cts1	Endo-chitinase	GH18
Cts2	Chitinase	GH18
Exg1/Bgl1	Major exo- β -1,3-glucanase of the cell wall; soluble	GH5

Exg2	GPI-anchored plasma membrane exo- β 1,3-glucanase	GH5
Ssg1/Spr1	Sporulation-specific exo- β -1,3-glucanase	GH5
Bgl2	Endo- β 1,3-glucanase; can make β 1,6-linked Glc side branch	GH17
Scw4	Endo- β 1,3-endoglucanase-like	GH17
Scw10	Endo- β 1,3-endoglucanase-like	GH17
Scw11	Endo- β 1,3-endoglucanase-like	GH17
Eng1/Dse4	Endo- β 1,3-endoglucanase	GH81
Eng2/Acf2	Endo- β 1,3-endoglucanase	GH81
Dcw1	GPI-protein, resembles α 1,6-endomannanase	GH76
Dfg5	GPI-protein, resembles α 1,6-endomannanase; Dcw1 homologue	GH76
Crh1	GPI-protein, chitin β -1,6/1,3-glucanosyltransferase	GH16
Crh2/Utr2	GPI-protein, chitin β -1,6/1,3-glucanosyltransferase	GH16
Crr1	GPI-protein, chitin β -1,6/1,3-glucanosyltransferase; sporulation-specific	GH16
Gas1	GPI-protein, β -1,3-glucanosyltransferase	GH72
Gas2	GPI-protein, β -1,3-glucanosyltransferase; sporulation specific	GH72
Gas3	GPI-protein, β -1,3-glucanosyltransferase	GH72
Gas4	GPI-protein, β -1,3-glucanosyltransferase; sporulation specific	GH72
Gas5	GPI-protein, β -1,3-glucanosyltransferase	GH72
Yps1	GPI-protein, yapsin aspartyl protease	
Yps2/Mkc7	GPI-protein, yapsin aspartyl protease	
Yps3	GPI-protein, yapsin aspartyl protease	
Yps6	GPI-protein, yapsin aspartyl protease	
GPI-CWP		
Ecm33	Sps2 family; structural/non-enzymatic	
Pst1	Sps2 family; structural/non-enzymatic	
Sps2	Sps2 family; structural/non-enzymatic; required for ascospore wall formation	

Sps22	Sps2 family; structural/non-enzymatic; required for ascospore wall formation
Cwp1	Tip1 family
Cwp2	Tip1 family
Tip1	Tip1 family; anaerobically induced
Tir1	Tip1 family; anaerobically induced
Tir2	Tip1 family; anaerobically induced
Tir3	Tip1 family; anaerobically induced
Tir4	Tip1 family; anaerobically induced
Dan1/Ccw13	Tip1 family; anaerobically induced
Dan4	Tip1 family; anaerobically induced
Sed1	Induced in stationary phase
Spi1	Induced by stress with weak organic acids; related to Sed1
Ccw12	Major role in stabilizing walls of daughter cells walls and mating projections
Ccw14/Ssr1	Inner cell wall protein
Dse2	Daughter cell specific, role in cell separation
Egt2	Daughter cell specific, role in cell separation
Fit1	Iron binding
Fit2	Iron binding
Fit3	Iron binding
Flo1	Flocculin
Flo5	Flocculin
Flo9	Flocculin
Flo10	Flocculin
Flo11/Muc1	Required for pseudohypha formation by diploids and agar invasion by haploids
Aga1	<i>MATa</i> agglutinin subunit, disulfide-linked to Aga2, which binds <i>MATα</i> agglutinin Sag1
Fig2	Aga1-related adhesin

Sag1	<i>MAT</i> α agglutinin
Non-GPI-CWP	
Pir1/Ccw6	“Protein with internal repeat”, ester-linked via Glu (originally Gln in repeats) to β 1,3-glucan
Pir2/Hsp150/Ccw7	“Protein with internal repeat”, ester-linked via Glu (originally Gln in repeats) to β 1,3-glucan
Pir3/Ccw8	“Protein with internal repeat”, ester-linked via Glu (originally Gln in repeats) to β 1,3-glucan
Pir4/Cis3/ Ccw5/Ccw11	One “internal repeat” sequence”, ester-linked via Glu (originally Gln in repeats) to β 1,3-glucan
Scw3/Sun4	Member of SUN family
Srl1	Acts in parallel with Ccw12 in pathway operative when regulation of Ace2 and polarized morphogenesis are defective

¹CAZy glycosyltransferase (GT) and glycosylhydrolase (GH) families are defined in the Carbohydrate Active Enzymes database (<http://www.cazy.org/>) (Cantarel, B. L., Coutinho, P. M., Rancurel, C., Bernard, T., Lombard, V., et al., 2009 The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. *Nucleic Acids Res.* **37**: D233-238).