

Orthogroup	seed ortholog	evalue	score	eggNOG OGs	max annot lvl	COG category	Description	Preferred name
OG0000027	84751.XP_007881884.1	7.29E-305	909	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	M	Chitin synthase	-
OG0000027	84751.XP_007881884.1	7.29E-305	909	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	M	Chitin synthase	-
OG0000027	84751.XP_007881884.1	7.29E-305	909	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	M	Chitin synthase	-
OG0000027	84751.XP_007881884.1	7.29E-305	909	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	M	Chitin synthase	-
OG0000027	84751.XP_007881884.1	7.29E-305	909	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	M	Chitin synthase	-
OG0000077	84751.XP_007878116.1	4.03E-210	618	KOG5020@1 root,KOG4472@2759 Eukaryota,38C17 4751 Fungi	G	G	Glycolipid 2-alpha-mannosyltransferase	-
OG0000077	84751.XP_007878116.1	4.03E-210	618	KOG5020@1 root,KOG4472@2759 Eukaryota,38C17 4751 Fungi	G	G	Glycolipid 2-alpha-mannosyltransferase	-
OG0000122	430998.XP_007677433.1	1.2E-172	517	2CYIJ@1 root,2S4MX@2759 Eukaryota,3A7PU@331 4751 Fungi	H	H	Glycosyltransferase family 71 protein	-
OG0000126	430998.XP_007672700.1	7.38E-296	866	KOG2204@1 root,KOG2431@1 root,KOG2204@275 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 47 family	-
OG0000126	430998.XP_007672700.1	7.38E-296	866	KOG2204@1 root,KOG2431@1 root,KOG2204@275 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 47 family	-
OG0000140	120017.I2FXD6	1.06E-170	525	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000140	120017.I2FXD6	1.06E-170	525	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000140	120017.I2FXD6	1.06E-170	525	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000144	63405.XP_002849366.1	0	1914	COG3325@1 root,COG5640@1 root,KOG2806@275 4751 Fungi	G	G	Glyco_18	-
OG0000144	63405.XP_002849366.1	0	1914	COG3325@1 root,COG5640@1 root,KOG2806@275 4751 Fungi	G	G	Glyco_18	-
OG0000144	63405.XP_002849366.1	0	1914	COG3325@1 root,COG5640@1 root,KOG2806@275 4751 Fungi	G	G	Glyco_18	-
OG0000160	72558.CBQ70856	1.43E-164	503	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000160	72558.CBQ70856	1.43E-164	503	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000160	72558.CBQ70856	1.43E-164	503	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	KRE6
OG0000170	120017.I2FYB0	0	1752	COG1215@1 root,COG5022@1 root,KOG2571@275 4751 Fungi	MN	MN	Belongs to the TRAFAC class myosin-kinesin ATPase si-	-
OG0000170	120017.I2FYB0	0	1752	COG1215@1 root,COG5022@1 root,KOG2571@275 4751 Fungi	MN	MN	Belongs to the TRAFAC class myosin-kinesin ATPase si-	-
OG0000170	120017.I2FYB0	0	1752	COG1215@1 root,COG5022@1 root,KOG2571@275 4751 Fungi	MN	MN	Belongs to the TRAFAC class myosin-kinesin ATPase si-	-
OG0000170	120017.I2FYB0	0	1752	COG1215@1 root,COG5022@1 root,KOG2571@275 4751 Fungi	MN	MN	Belongs to the TRAFAC class myosin-kinesin ATPase si-	-
OG0000170	120017.I2FYB0	0	1752	COG1215@1 root,COG5022@1 root,KOG2571@275 4751 Fungi	MN	MN	Belongs to the TRAFAC class myosin-kinesin ATPase si-	-
OG0000216	42374.XP_002418592.1	0	989	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@ 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil	-
OG0000216	42374.XP_002418592.1	0	989	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@ 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil	-
OG0000217	42374.XP_002416910.1	1.55E-304	852	COG5309@1 root,2QUSB@2759 Eukaryota,38YVQ@ 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 17 family	-
OG0000217	42374.XP_002416910.1	1.55E-304	852	COG5309@1 root,2QUSB@2759 Eukaryota,38YVQ@ 4751 Fungi	G	G	Belongs to the glycosyl hydrolase 17 family	-
OG0000263	430998.XP_007681000.1	2.52E-255	718	28NTU@1 root,2QVDT@2759 Eukaryota,38E23@33 4751 Fungi	I	I	Glycosyltransferase family 62 protein	ANP1
OG0000263	430998.XP_007681000.1	2.52E-255	718	28NTU@1 root,2QVDT@2759 Eukaryota,38E23@33 4751 Fungi	I	I	Glycosyltransferase family 62 protein	ANP1
OG0000301	310453.XP_007589487.1	5.13E-181	521	28KFK@1 root,2QSWP@2759 Eukaryota,38E1Q@33 4751 Fungi	G	G	Glycosyl hydrolase family 76	-
OG0000301	310453.XP_007589487.1	5.13E-181	521	28KFK@1 root,2QSWP@2759 Eukaryota,38E1Q@33 4751 Fungi	G	G	Glycosyl hydrolase family 76	-
OG0000323	63400.XP_003011537.1	0	962	COG1877@1 root,KOG1050@2759 Eukaryota,38EGS 4751 Fungi	G	G	Alpha,alpha-trehalose-phosphate synthase	-
OG0000323	63400.XP_003011537.1	0	962	COG1877@1 root,KOG1050@2759 Eukaryota,38EGS 4751 Fungi	G	G	Alpha,alpha-trehalose-phosphate synthase	-
OG0000333	5478.XP_449945.1	0	3235	KOG0916@1 root,KOG0916@2759 Eukaryota,38X8A 4751 Fungi	M	M	to Saccharomyces cerevisiae FKS3 (YMR306W)	FKS3
OG0000426	84751.XP_007880919.1	0	910	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	O	MIR domain	PMT2
OG0000426	84751.XP_007880919.1	0	910	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	O	MIR domain	PMT2
OG0000523	5480.68B6K6	0	1727	2AI8K@1 root,2RZ48@2759 Eukaryota,39XBV@331: 4751 Fungi	S	S	Responsible for addition of the terminal mannose res	MNN13
OG0000584	82508.K1VYR6	7.84E-125	384	COG3774@1 root,2QW2I@2759 Eukaryota,39T08@ 4751 Fungi	G	G	to TIGR gene model, INSD accession	-
OG0000584	82508.K1VYR6	7.84E-125	384	COG3774@1 root,2QW2I@2759 Eukaryota,39T08@ 4751 Fungi	G	G	to TIGR gene model, INSD accession	-
OG0000644	430998.XP_007680956.1	4.51E-225	645	COG1087@1 root,KOG1371@2759 Eukaryota,38C46 4751 Fungi	Q	Q	GDP-mannose 4,6 dehydratase	GAL10
OG0000644	430998.XP_007680956.1	4.51E-225	645	COG1087@1 root,KOG1371@2759 Eukaryota,38C46 4751 Fungi	Q	Q	GDP-mannose 4,6 dehydratase	GAL10
OG0000644	430998.XP_007680956.1	4.51E-225	645	COG1087@1 root,KOG1371@2759 Eukaryota,38C46 4751 Fungi	Q	Q	GDP-mannose 4,6 dehydratase	GAL10
OG0000673	327079.R9NZB0	0	1477	COG1215@1 root,KOG2571@2759 Eukaryota,38B4L 4751 Fungi	M	M	Chitin synthase	CHS3
OG0000673	327079.R9NZB0	0	1477	COG1215@1 root,KOG2571@2759 Eukaryota,38B4L 4751 Fungi	M	M	Chitin synthase	CHS3
OG0000688	1392244.V5GG59	0	1089	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	G	Trehalose-phosphatase	-
OG0000688	1392244.V5GG59	0	1089	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	G	Trehalose-phosphatase	-
OG0000688	1392244.V5GG59	0	1089	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	G	Trehalose-phosphatase	-
OG0000769	82508.K1VQA0	0	1549	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	O	MIR domain	PMT1
OG0000769	82508.K1VQA0	0	1549	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	O	MIR domain	PMT1
OG0000769	82508.K1VQA0	0	1549	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	O	MIR domain	PMT1
OG0001006	430998.XP_007677255.1	0	2091	KOG1879@1 root,KOG1879@2759 Eukaryota,38FK5 4751 Fungi	G	G	Glycosyltransferase family 24 protein	KRE5
OG0001006	430998.XP_007677255.1	0	2091	KOG1879@1 root,KOG1879@2759 Eukaryota,38FK5 4751 Fungi	G	G	Glycosyltransferase family 24 protein	KRE5
OG0001006	430998.XP_007677255.1	0	2091	KOG1879@1 root,KOG1879@2759 Eukaryota,38FK5 4751 Fungi	G	G	Glycosyltransferase family 24 protein	KRE5
OG0001209	84751.XP_007878195.1	1.2E-194	593	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	-
OG0001209	84751.XP_007878195.1	1.2E-194	593	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	-
OG0001209	84751.XP_007878195.1	1.2E-194	593	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	G	Beta-glucan synthesis-associated protein (SKN1)	-

OG0001209	84751.XP_007878195.1	1.2E-194	593	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	Beta-glucan synthesis-associated protein (SKN1)	-
OG0001209	84751.XP_007878195.1	1.2E-194	593	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	Beta-glucan synthesis-associated protein (SKN1)	-
OG0001214	82508.K1VDE5	4.49E-303	829	COG0547@1 root,KOG1438@2759 Eukaryota,38E82 4751 Fungi	E	Glycosyl transferase family, a/b domain	TRP4
OG0001214	82508.K1VDE5	4.49E-303	829	COG0547@1 root,KOG1438@2759 Eukaryota,38E82 4751 Fungi	E	Glycosyl transferase family, a/b domain	TRP4
OG0001214	82508.K1VDE5	4.49E-303	829	COG0547@1 root,KOG1438@2759 Eukaryota,38E82 4751 Fungi	E	Glycosyl transferase family, a/b domain	TRP4
OG0001255	82508.K1VV77	0	1218	COG0438@1 root,KOG1387@2759 Eukaryota,38HCl 4751 Fungi	M	ALG11 mannosyltransferase N-terminus	ALG11
OG0001259	63400.XP_003015369.1	0	1479	COG1287@1 root,KOG2292@2759 Eukaryota,38D8E 4751 Fungi	O	Oligosaccharyl transferase STT3 subunit	STT3
OG0001259	63400.XP_003015369.1	0	1479	COG1287@1 root,KOG2292@2759 Eukaryota,38D8E 4751 Fungi	O	Oligosaccharyl transferase STT3 subunit	STT3
OG0001266	430998.XP_007678056.1	1.1E-167	479	COG0627@1 root,KOG3101@2759 Eukaryota,38RFR 4751 Fungi	S	Serine hydrolase involved in the detoxification of forr -	
OG0001266	430998.XP_007678056.1	1.1E-167	479	COG0627@1 root,KOG3101@2759 Eukaryota,38RFR 4751 Fungi	S	Serine hydrolase involved in the detoxification of forr -	
OG0001266	430998.XP_007678056.1	1.1E-167	479	COG0627@1 root,KOG3101@2759 Eukaryota,38RFR 4751 Fungi	S	Serine hydrolase involved in the detoxification of forr -	
OG0001266	430998.XP_007678056.1	1.1E-167	479	COG0627@1 root,KOG3101@2759 Eukaryota,38RFR 4751 Fungi	S	Serine hydrolase involved in the detoxification of forr -	
OG0001315	64363.EME46003	0	1320	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0001315	64363.EME46003	0	1320	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0001315	64363.EME46003	0	1320	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0001464	82508.K1W141	2.52E-223	619	COG0040@1 root,KOG2831@2759 Eukaryota,38BT1 4751 Fungi	E	ATP phosphoribosyltransferase	HIS1
OG0001464	82508.K1W141	2.52E-223	619	COG0040@1 root,KOG2831@2759 Eukaryota,38BT1 4751 Fungi	E	ATP phosphoribosyltransferase	HIS1
OG0001464	82508.K1W141	2.52E-223	619	COG0040@1 root,KOG2831@2759 Eukaryota,38BT1 4751 Fungi	E	ATP phosphoribosyltransferase	HIS1
OG0001489	430998.XP_007679604.1	2.78E-123	357	COG0461@1 root,KOG1377@2759 Eukaryota,39WU 4751 Fungi	F	Phosphoribosyl transferase domain	URA5
OG0001489	430998.XP_007679604.1	2.78E-123	357	COG0461@1 root,KOG1377@2759 Eukaryota,39WU 4751 Fungi	F	Phosphoribosyl transferase domain	URA5
OG0001507	5551.XP_003238320.1	4.99E-198	549	COG0463@1 root,KOG2978@2759 Eukaryota,38E12 4751 Fungi	M	Glycosyltransferase like family 2	DPM1
OG0001507	5551.XP_003238320.1	4.99E-198	549	COG0463@1 root,KOG2978@2759 Eukaryota,38E12 4751 Fungi	M	Glycosyltransferase like family 2	DPM1
OG0001697	84751.XP_007881019.1	1.68E-284	820	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	MIR domain	PMT4
OG0001697	84751.XP_007881019.1	1.68E-284	820	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	MIR domain	PMT4
OG0001697	84751.XP_007881019.1	1.68E-284	820	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	MIR domain	PMT4
OG0001729	327079.R9PDI6	5.49E-186	534	COG0191@1 root,KOG4153@2759 Eukaryota,38EK5 4751 Fungi	G	Fructose-bisphosphate aldolase class-II	FBA1
OG0001729	327079.R9PDI6	5.49E-186	534	COG0191@1 root,KOG4153@2759 Eukaryota,38EK5 4751 Fungi	G	Fructose-bisphosphate aldolase class-II	FBA1
OG0001756	63400.XP_003014316.1	0	1103	COG0034@1 root,KOG0572@2759 Eukaryota,38CJP 4751 Fungi	F	Phosphoribosyl transferase domain	ADE4
OG0001756	63400.XP_003014316.1	0	1103	COG0034@1 root,KOG0572@2759 Eukaryota,38CJP 4751 Fungi	F	Phosphoribosyl transferase domain	ADE4
OG0001756	63400.XP_003014316.1	0	1103	COG0034@1 root,KOG0572@2759 Eukaryota,38CJP 4751 Fungi	F	Phosphoribosyl transferase domain	ADE4
OG0001760	63402.XP_003173730.1	0	1047	COG1171@1 root,KOG2547@2759 Eukaryota,38DAI 4751 Fungi	IM	Glycosyl transferase family 21	HSX11
OG0001760	63402.XP_003173730.1	0	1047	COG1171@1 root,KOG2547@2759 Eukaryota,38DAI 4751 Fungi	IM	Glycosyl transferase family 21	HSX11
OG0001763	1392244.V5GHV5	3.84E-122	379	COG0438@1 root,KOG0853@2759 Eukaryota,38TSN 4751 Fungi	M	Glycosyltransferase Family 4	ALG2
OG0001774	63400.XP_003015159.1	9.87E-153	434	COG0572@1 root,KOG4203@2759 Eukaryota,38HIZ 4751 Fungi	TZ	Uracil phosphoribosyltransferase	FUR1
OG0001774	63400.XP_003015159.1	9.87E-153	434	COG0572@1 root,KOG4203@2759 Eukaryota,38HIZ 4751 Fungi	TZ	Uracil phosphoribosyltransferase	FUR1
OG0001802	63418.F2Q1M4	4.73E-170	477	COG0036@1 root,KOG3111@2759 Eukaryota,38G6J 4751 Fungi	G	Belongs to the ribulose-phosphate 3-epimerase fami	RPE1
OG0001802	63418.F2Q1M4	4.73E-170	477	COG0036@1 root,KOG3111@2759 Eukaryota,38G6J 4751 Fungi	G	Belongs to the ribulose-phosphate 3-epimerase fami	RPE1
OG0001814	82508.K1VSJ4	0	1276	KOG2515@1 root,KOG2515@2759 Eukaryota,38CW 4751 Fungi	G	Alg9-like mannosyltransferase family	ALG9
OG0001997	34349.G7E2Q7	7.44E-76	270	KOG1771@1 root,KOG1771@2759 Eukaryota,38BU1 4751 Fungi	G	Alg9-like mannosyltransferase family	GPI10
OG0001997	34349.G7E2Q7	7.44E-76	270	KOG1771@1 root,KOG1771@2759 Eukaryota,38BU1 4751 Fungi	G	Alg9-like mannosyltransferase family	GPI10
OG0002008	82508.K1WUT2	1.94E-257	738	KOG2516@1 root,KOG2516@2759 Eukaryota,38BV4 4751 Fungi	G	Alg9-like mannosyltransferase family	ECM39
OG0002113	4909.A0A099P155	0	2222	KOG2161@1 root,KOG2504@1 root,KOG2161@275: 4751 Fungi	G	to Saccharomyces cerevisiae CWH41 (YGL027C)	CWH41
OG0002113	4909.A0A099P155	0	2222	KOG2161@1 root,KOG2504@1 root,KOG2161@275: 4751 Fungi	G	to Saccharomyces cerevisiae CWH41 (YGL027C)	CWH41
OG0002113	4909.A0A099P155	0	2222	KOG2161@1 root,KOG2504@1 root,KOG2161@275: 4751 Fungi	G	to Saccharomyces cerevisiae CWH41 (YGL027C)	CWH41
OG0002128	273371.XP_003869670.1	5.54E-243	668	COG0005@1 root,KOG3985@2759 Eukaryota,38GVI 4751 Fungi	F	Catalyzes the reversible phosphorylation of S-methyl- MEU1	
OG0002128	273371.XP_003869670.1	5.54E-243	668	COG0005@1 root,KOG3985@2759 Eukaryota,38GVI 4751 Fungi	F	Catalyzes the reversible phosphorylation of S-methyl- MEU1	
OG0002128	273371.XP_003869670.1	5.54E-243	668	COG0005@1 root,KOG3985@2759 Eukaryota,38GVI 4751 Fungi	F	Catalyzes the reversible phosphorylation of S-methyl- MEU1	
OG0002160	84751.XP_007879353.1	3.25E-126	389	KOG3893@1 root,KOG3893@2759 Eukaryota,38CA7 4751 Fungi	G	Mannosyltransferase (PIG-M)	GPI14
OG0002265	63400.XP_003014617.1	0	2963	COG3408@1 root,KOG3625@2759 Eukaryota,38BR4 4751 Fungi	G	Glycogen debranching enzyme	GDB1
OG0002265	63400.XP_003014617.1	0	2963	COG3408@1 root,KOG3625@2759 Eukaryota,38BR4 4751 Fungi	G	Glycogen debranching enzyme	GDB1
OG0002265	63400.XP_003014617.1	0	2963	COG3408@1 root,KOG3625@2759 Eukaryota,38BR4 4751 Fungi	G	Glycogen debranching enzyme	GDB1
OG0002288	84751.XP_007878940.1	6.74E-161	553	COG0438@1 root,COG5543@1 root,KOG1111@275: 4751 Fungi	DIMO	PIGA (GPI anchor biosynthesis)	SPT14
OG0002340	72558.CBQ71131	3.76E-258	791	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	Trehalose-phosphatase	TPS3
OG0002340	72558.CBQ71131	3.76E-258	791	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	Trehalose-phosphatase	TPS3
OG0002340	72558.CBQ71131	3.76E-258	791	COG1877@1 root,KOG1050@2759 Eukaryota,38CEK 4751 Fungi	G	Trehalose-phosphatase	TPS3
OG0002351	82508.K1WL46	2.68E-155	456	COG3772@1 root,2S6UW@2759 Eukaryota,3A2UF@ 4751 Fungi	O	lysozyme	-
OG0002351	82508.K1WL46	2.68E-155	456	COG3772@1 root,2S6UW@2759 Eukaryota,3A2UF@ 4751 Fungi	O	lysozyme	-
OG0002351	82508.K1WL46	2.68E-155	456	COG3772@1 root,2S6UW@2759 Eukaryota,3A2UF@ 4751 Fungi	O	lysozyme	-
OG0002491	84751.XP_007878012.1	1.7E-115	354	COG0463@1 root,KOG2977@2759 Eukaryota,38DU1 4751 Fungi	M	Glycosyl transferase family 2	ALG5

OG0002507	72558.CBQ72886	1.54E-183	568	KOG2575@1 root,KOG2575@2759 Eukaryota,38F87	4751 Fungi	EG	ALG6, ALG8 glycosyltransferase family	ALG6
OG0002546	4909.A0A099P643	0	2523	COG0323@1 root,COG0438@1 root,COG0665@1 rc	4751 Fungi	H	Transfers the glycosyl residue from UDP-Glc to the nc GSY1	
OG0002546	4909.A0A099P643	0	2523	COG0323@1 root,COG0438@1 root,COG0665@1 rc	4751 Fungi	H	Transfers the glycosyl residue from UDP-Glc to the nc GSY1	
OG0002549	82508.K1VU23	3.49E-279	773	COG0438@1 root,KOG2941@2759 Eukaryota,38CDI	4751 Fungi	O	Glycosyl transferases group 1	ALG1
OG0002601	5480.G8BIF6	0	900	COG0055@1 root,KOG1350@2759 Eukaryota,38CQf	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002601	5480.G8BIF6	0	900	COG0055@1 root,KOG1350@2759 Eukaryota,38CQf	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002601	5480.G8BIF6	0	900	COG0055@1 root,KOG1350@2759 Eukaryota,38CQf	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002601	5480.G8BIF6	0	900	COG0055@1 root,KOG1350@2759 Eukaryota,38CQf	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002616	4932.YFR047C	1.01E-133	389	COG0157@1 root,KOG3008@2759 Eukaryota,38D1f	4751 Fungi	H	Involved in the catabolism of quinolinic acid (QA)	BNAG
OG0002616	4932.YFR047C	1.01E-133	389	COG0157@1 root,KOG3008@2759 Eukaryota,38D1f	4751 Fungi	H	Involved in the catabolism of quinolinic acid (QA)	BNAG
OG0002660	4909.A0A099P7L3	0	1563	KOG2431@1 root,KOG2431@2759 Eukaryota,38CSIf	4751 Fungi	G	Belongs to the glycosyl hydrolase 47 family	MNS1
OG0002660	4909.A0A099P7L3	0	1563	KOG2431@1 root,KOG2431@2759 Eukaryota,38CSIf	4751 Fungi	G	Belongs to the glycosyl hydrolase 47 family	MNS1
OG0002689	82508.K1VPR0	0	1477	KOG1192@1 root,KOG1192@2759 Eukaryota,39TRF	4751 Fungi	CG	Glycosyltransferase family 28 N-terminal domain	-
OG0002782	82508.K1W4X6	0	1339	COG0058@1 root,KOG2099@2759 Eukaryota,38FOlf	4751 Fungi	G	Phosphorylase is an important allosteric enzyme in ca GPH1	
OG0002893	310453.XP_007581512.1	0	1896	COG0055@1 root,COG0296@1 root,KOG0470@275	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002893	310453.XP_007581512.1	0	1896	COG0055@1 root,COG0296@1 root,KOG0470@275	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002893	310453.XP_007581512.1	0	1896	COG0055@1 root,COG0296@1 root,KOG0470@275	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002893	310453.XP_007581512.1	0	1896	COG0055@1 root,COG0296@1 root,KOG0470@275	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002893	310453.XP_007581512.1	0	1896	COG0055@1 root,COG0296@1 root,KOG0470@275	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g ATP2	
OG0002991	5551.XP_003237482.1	0	1083	KOG4748@1 root,KOG4748@2759 Eukaryota,38IOlf	4751 Fungi	GM	galactosyl transferase GMA12/MNN10 family	MNN10
OG0003039	5551.XP_003233463.1	5.15E-203	566	COG0005@1 root,KOG3984@2759 Eukaryota,38BI3f	4751 Fungi	F	Phosphorylase superfamily	PNP1
OG0003039	5551.XP_003233463.1	5.15E-203	566	COG0005@1 root,KOG3984@2759 Eukaryota,38BI3f	4751 Fungi	F	Phosphorylase superfamily	PNP1
OG0003064	5480.G8BJG1	0	1105	KOG2576@1 root,KOG2576@2759 Eukaryota,38DJ6	4751 Fungi	G	Belongs to the ALG6 ALG8 glucosyltransferase family	ALG8
OG0003108	63418.F2Q5S0	0	2057	KOG2429@1 root,KOG2429@2759 Eukaryota,38CUf	4751 Fungi	G	Belongs to the glycosyl hydrolase 47 family	-
OG0003108	63418.F2Q5S0	0	2057	KOG2429@1 root,KOG2429@2759 Eukaryota,38CUf	4751 Fungi	G	Belongs to the glycosyl hydrolase 47 family	-
OG0003151	430998.XP_007671910.1	5.19E-169	491	COG5309@1 root,2QQE6@2759 Eukaryota,38HGUf	4751 Fungi	G	Belongs to the glycosyl hydrolase 17 family	BGL2
OG0003151	430998.XP_007671910.1	5.19E-169	491	COG5309@1 root,2QQE6@2759 Eukaryota,38HGUf	4751 Fungi	G	Belongs to the glycosyl hydrolase 17 family	BGL2
OG0003151	430998.XP_007671910.1	5.19E-169	491	COG5309@1 root,2QQE6@2759 Eukaryota,38HGUf	4751 Fungi	G	Belongs to the glycosyl hydrolase 17 family	BGL2
OG0003154	82508.K1WWK9	0	2000	COG0383@1 root,KOG4342@2759 Eukaryota,38EQf	4751 Fungi	G	Alpha mannosidase, middle domain	AMS1
OG0003154	82508.K1WWK9	0	2000	COG0383@1 root,KOG4342@2759 Eukaryota,38EQf	4751 Fungi	G	Alpha mannosidase, middle domain	AMS1
OG0003154	82508.K1WWK9	0	2000	COG0383@1 root,KOG4342@2759 Eukaryota,38EQf	4751 Fungi	G	Alpha mannosidase, middle domain	AMS1
OG0003206	63402.XP_003174149.1	0	1118	KOG4123@1 root,KOG4123@2759 Eukaryota,38GY4	4751 Fungi	G	Alg9-like mannosyltransferase family	SMP3
OG0003224	1005962.W1Q194	4.98E-113	350	KOG2762@1 root,KOG2762@2759 Eukaryota,38BSJf	4751 Fungi	G	Adds the first Dol-P-Man derived mannose in an alpha: ALG3	
OG0003282	5551.XP_003233785.1	0	907	COG0343@1 root,KOG3908@2759 Eukaryota,38H9f	4751 Fungi	A	Catalytic subunit of the queuine tRNA-ribosyltransfer-	-
OG0003282	5551.XP_003233785.1	0	907	COG0343@1 root,KOG3908@2759 Eukaryota,38H9f	4751 Fungi	A	Catalytic subunit of the queuine tRNA-ribosyltransfer-	-
OG0003299	5551.XP_003231942.1	1.83E-210	582	KOG3339@1 root,KOG3339@2759 Eukaryota,38Z5f	4751 Fungi	S	Involved in protein N-glycosylation. Essential for the s	ALG14
OG0003412	4909.A0A099P6X5	0	909	KOG4748@1 root,KOG4748@2759 Eukaryota,38MC	4751 Fungi	GM	to Saccharomyces cerevisiae MNN11 (YJL183W)	MNN11
OG0003413	82508.K1VB36	0	1285	COG3250@1 root,KOG2230@2759 Eukaryota,38CFf	4751 Fungi	G	Glycosyl hydrolases family 2	-
OG0003413	82508.K1VB36	0	1285	COG3250@1 root,KOG2230@2759 Eukaryota,38CFf	4751 Fungi	G	Glycosyl hydrolases family 2	-
OG0003413	82508.K1VB36	0	1285	COG3250@1 root,KOG2230@2759 Eukaryota,38CFf	4751 Fungi	G	Glycosyl hydrolases family 2	-
OG0003413	82508.K1VB36	0	1285	COG3250@1 root,KOG2230@2759 Eukaryota,38CFf	4751 Fungi	G	Glycosyl hydrolases family 2	-
OG0003413	82508.K1VB36	0	1285	COG3250@1 root,KOG2230@2759 Eukaryota,38CFf	4751 Fungi	G	Glycosyl hydrolases family 2	-
OG0003417	64363.EME49493	2.77E-215	602	28JAZ@1 root,2QRPX@2759 Eukaryota,38HZLf	4751 Fungi	I	Glycosyltransferase family 62 protein	MNN9
OG0003417	64363.EME49493	2.77E-215	602	28JAZ@1 root,2QRPX@2759 Eukaryota,38HZLf	4751 Fungi	I	Glycosyltransferase family 62 protein	MNN9
OG0003505	5480.G8BHR3	0	1155	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0003505	5480.G8BHR3	0	1155	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0003577	5478.XP_448450.1	0	2431	COG1554@1 root,KOG4125@2759 Eukaryota,38G0f	4751 Fungi	G	to Saccharomyces cerevisiae ATH1 (YPR026W)	ATH1
OG0003577	5478.XP_448450.1	0	2431	COG1554@1 root,KOG4125@2759 Eukaryota,38G0f	4751 Fungi	G	to Saccharomyces cerevisiae ATH1 (YPR026W)	ATH1
OG0003606	72558.CBQ72807	1.92E-232	663	COG0318@1 root,KOG1176@2759 Eukaryota,38D1f	4751 Fungi	I	AMP-binding enzyme C-terminal domain	-
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHSf	4751 Fungi	G	Glycosyl hydrolase family 3 N terminal domain	-
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHSf	4751 Fungi	G	Glycosyl hydrolase family 3 N terminal domain	-
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHSf	4751 Fungi	G	Glycosyl hydrolase family 3 N terminal domain	-
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHSf	4751 Fungi	G	Glycosyl hydrolase family 3 N terminal domain	-
OG0003689	5480.G8BIW7	0	1439	COG5309@1 root,2QTKT@2759 Eukaryota,39SDA@	4751 Fungi	I	Belongs to the glycosyl hydrolase 17 family	btgC
OG0003689	5480.G8BIW7	0	1439	COG5309@1 root,2QTKT@2759 Eukaryota,39SDA@	4751 Fungi	I	Belongs to the glycosyl hydrolase 17 family	btgC
OG0003804	63402.XP_003175492.1	0	976	KOG2642@1 root,KOG2642@2759 Eukaryota,39INY	4751 Fungi	IKOT	DIE2/ALG10 family	ALG10
OG0003844	82508.K1VR75	4.8E-136	416	COG0296@1 root,COG0500@1 root,KOG0470@275	4751 Fungi	G	Carbohydrate-binding module 48 (Isoamylase N-term GLC3	
OG0003844	82508.K1VR75	4.8E-136	416	COG0296@1 root,COG0500@1 root,KOG0470@275	4751 Fungi	G	Carbohydrate-binding module 48 (Isoamylase N-term GLC3	
OG0004004	42374.XP_002421104.1	0	1174	28MG1@1 root,2QZG@2759 Eukaryota,39WT5@3	4751 Fungi	S	mannosyltransferase activity	BMT3

OG0004123	63418.F2PQ28	0	1045	KOG1037@1 root,KOG1037@2759 Eukaryota,3887L 4751 Fungi	H	Polymerase	-
OG0004123	63418.F2PQ28	0	1045	KOG1037@1 root,KOG1037@2759 Eukaryota,3887L 4751 Fungi	H	Polymerase	-
OG0004123	63418.F2PQ28	0	1045	KOG1037@1 root,KOG1037@2759 Eukaryota,3887L 4751 Fungi	H	Polymerase	-
OG0004123	63418.F2PQ28	0	1045	KOG1037@1 root,KOG1037@2759 Eukaryota,3887L 4751 Fungi	H	Polymerase	-
OG0004315	63400.XP_003015088.1	0	850	COG0343@1 root,KOG3909@2759 Eukaryota,38D8I 4751 Fungi	A	Non-catalytic subunit of the queuine tRNA- ribosyltra	-
OG0004315	63400.XP_003015088.1	0	850	COG0343@1 root,KOG3909@2759 Eukaryota,38D8I 4751 Fungi	A	Non-catalytic subunit of the queuine tRNA- ribosyltra	-
OG0004315	63400.XP_003015088.1	0	850	COG0343@1 root,KOG3909@2759 Eukaryota,38D8I 4751 Fungi	A	Non-catalytic subunit of the queuine tRNA- ribosyltra	-
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39J2Z@3: 4751 Fungi	E	Glycosyl hydrolase family 3 C-terminal domain	-
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39J2Z@3: 4751 Fungi	E	Glycosyl hydrolase family 3 C-terminal domain	-
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39J2Z@3: 4751 Fungi	E	Glycosyl hydrolase family 3 C-terminal domain	-
OG0004366	63418.F2PQN6	1.23E-153	433	COG0572@1 root,KOG4203@2759 Eukaryota,38H5> 4751 Fungi	TZ	Uracil phosphoribosyltransferase	-
OG0004366	63418.F2PQN6	1.23E-153	433	COG0572@1 root,KOG4203@2759 Eukaryota,38H5> 4751 Fungi	TZ	Uracil phosphoribosyltransferase	-
OG0004435	430998.XP_007681755.1	1.17E-129	395	COG0366@1 root,KOG0471@2759 Eukaryota,38GYC 4751 Fungi	G	Alpha amylase, catalytic domain	-
OG0004476	5551.XP_003235966.1	0	1634	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@ 4751 Fungi	U	to beta-glucosidase 6	exgD
OG0004476	5551.XP_003235966.1	0	1634	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@ 4751 Fungi	U	to beta-glucosidase 6	exgD
OG0004509	5551.XP_003235080.1	0	1470	COG0438@1 root,KOG0853@2759 Eukaryota,39U24 4751 Fungi	M	Glycosyl transferases group 1	-
OG0004509	5551.XP_003235080.1	0	1470	COG0438@1 root,KOG0853@2759 Eukaryota,39U24 4751 Fungi	M	Glycosyl transferases group 1	-
OG0004541	63405.XP_002843167.1	2.9E-237	652	COG1087@1 root,KOG1371@2759 Eukaryota,39JFX 4751 Fungi	M	Aldose 1-epimerase	-
OG0004668	63400.XP_003013510.1	0	3407	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Chitin binding domain	-
OG0004668	63400.XP_003013510.1	0	3407	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Chitin binding domain	-
OG0004668	63400.XP_003013510.1	0	3407	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Chitin binding domain	-
OG0004668	63400.XP_003013510.1	0	3407	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Chitin binding domain	-
OG0004902	84751.XP_007876752.1	0	959	COG1626@1 root,KOG0602@2759 Eukaryota,38CK+ 4751 Fungi	G	Neutral trehalase Ca2+ binding domain	NTH1
OG0004902	84751.XP_007876752.1	0	959	COG1626@1 root,KOG0602@2759 Eukaryota,38CK+ 4751 Fungi	G	Neutral trehalase Ca2+ binding domain	NTH1
OG0004902	84751.XP_007876752.1	0	959	COG1626@1 root,KOG0602@2759 Eukaryota,38CK+ 4751 Fungi	G	Neutral trehalase Ca2+ binding domain	NTH1
OG0005107	5478.XP_445426.1	0	1456	28MG1@1 root,2QZTG@2759 Eukaryota,39W75@3: 4751 Fungi	S	Debaryomyces hansenii and CA4636 IPF1520 Candida BMT1	
OG0005243	552467.XP_003193981.1	5.06E-30	109	KOG3488@1 root,KOG3488@2759 Eukaryota,3A5ZY 4751 Fungi	O	Dolichol phosphate-mannose biosynthesis regulatory dpm2	
OG0005253	430998.XP_007671850.1	8.89E-246	692	COG2730@1 root,2QVVM@2759 Eukaryota,38F6I@ 4751 Fungi	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil EXG3	
OG0005253	430998.XP_007671850.1	8.89E-246	692	COG2730@1 root,2QVVM@2759 Eukaryota,38F6I@ 4751 Fungi	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil EXG3	
OG0005889	5551.XP_003232935.1	1.13E-268	736	COG3325@1 root,KOG2806@2759 Eukaryota,38EFI(4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0005889	5551.XP_003232935.1	1.13E-268	736	COG3325@1 root,KOG2806@2759 Eukaryota,38EFI(4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0005889	5551.XP_003232935.1	1.13E-268	736	COG3325@1 root,KOG2806@2759 Eukaryota,38EFI(4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1> 4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	NAG1
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1> 4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	NAG1
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1> 4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	NAG1
OG0006596	63418.F2PMY8	0	1729	KOG1037@1 root,KOG1037@2759 Eukaryota,38F3B 4751 Fungi	KLO	Vault protein inter-alpha-trypsin domain	-
OG0006624	5551.XP_003239001.1	0	1885	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Glyco_18	-
OG0006624	5551.XP_003239001.1	0	1885	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Glyco_18	-
OG0006624	5551.XP_003239001.1	0	1885	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Glyco_18	-
OG0006813	5270.UM05480P0	0	1058	COG1215@1 root,KOG2571@2759 Eukaryota,38B4L 4751 Fungi	M	Chitin synthase	-
OG0006813	5270.UM05480P0	0	1058	COG1215@1 root,KOG2571@2759 Eukaryota,38B4L 4751 Fungi	M	Chitin synthase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007234	5059.CADAFLAP00003538	0	1286	COG3250@1 root,KOG2024@2759 Eukaryota,39SUC 4751 Fungi	G	beta-galactosidase	-
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007358	710243.XP_007598382.1	0	1043	COG1874@1 root,KOG0496@2759 Eukaryota,38D5C 4751 Fungi	G	Beta-galactosidase, domain 2	lacC
OG0007472	82508.K1VQR4	0	1347	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@ 4751 Fungi	G	PA14 domain	-
OG0007472	82508.K1VQR4	0	1347	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@ 4751 Fungi	G	PA14 domain	-
OG0007472	82508.K1VQR4	0	1347	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@ 4751 Fungi	G	PA14 domain	-
OG0007486	63402.XP_003169260.1	2.42E-143	429	COG3250@1 root,KOG2230@2759 Eukaryota,38JCQ 4751 Fungi	G	Glycosyl hydrolases family 2, sugar binding domain	-
OG0007486	63402.XP_003169260.1	2.42E-143	429	COG3250@1 root,KOG2230@2759 Eukaryota,38JCQ 4751 Fungi	G	Glycosyl hydrolases family 2, sugar binding domain	-
OG0007486	63402.XP_003169260.1	2.42E-143	429	COG3250@1 root,KOG2230@2759 Eukaryota,38JCQ 4751 Fungi	G	Glycosyl hydrolases family 2, sugar binding domain	-

OG0007678	4909.A0A099P3J2	0	1696	COG0572@1 root,KOG2271@1 root,KOG2271@275	4751 Fungi	TZ	to Saccharomyces cerevisiae FUR1 (YHR128W)	FUR1
OG0007947	83344.XP_007926896.1	5.44E-234	669	COG1215@1 root,KOG2571@2759 Eukaryota,38WS	4751 Fungi	M	Chitin synthase	-
OG0007947	83344.XP_007926896.1	5.44E-234	669	COG1215@1 root,KOG2571@2759 Eukaryota,38WS	4751 Fungi	M	Chitin synthase	-
OG0008033	63402.XP_003172026.1	1.38E-209	603	COG1215@1 root,KOG2571@2759 Eukaryota,38HE4	4751 Fungi	M	chitin synthase	CHS3
OG0008040	430998.XP_007673612.1	0	1096	COG3661@1 root,2QWS4@2759 Eukaryota,39ZC0@	4751 Fungi	G	Alpha-glucuronidase involved in the hydrolysis of xyla aguA	-
OG0008040	430998.XP_007673612.1	0	1096	COG3661@1 root,2QWS4@2759 Eukaryota,39ZC0@	4751 Fungi	G	Alpha-glucuronidase involved in the hydrolysis of xyla aguA	-
OG0008063	82508.K1WKG8	0	1068	COG3345@1 root,KOG2571@2759 Eukaryota,39UPE@	4751 Fungi	G	Hydrolyzes a variety of simple alpha-D-galactoside as aglC	-
OG0008063	82508.K1WKG8	0	1068	COG3345@1 root,2QW61@2759 Eukaryota,39UPE@	4751 Fungi	G	Hydrolyzes a variety of simple alpha-D-galactoside as aglC	-
OG0008186	63405.XP_002850856.1	0	840	2EGIF@1 root,2SMG7@2759 Eukaryota,3A4DW@33	4751 Fungi	H	Phosphotransferase enzyme family	-
OG0008186	63405.XP_002850856.1	0	840	2EGIF@1 root,2SMG7@2759 Eukaryota,3A4DW@33	4751 Fungi	H	Phosphotransferase enzyme family	-
OG0008311	82508.K1VH01	0	1102	COG3534@1 root,2QRW4@2759 Eukaryota,38E4X@	4751 Fungi	E	Alpha-L-arabinofuranosidase C-terminus	abfC
OG0008318	82508.K1VV22	0	868	COG2723@1 root,KOG0626@2759 Eukaryota,38CCL	4751 Fungi	G	Glycosyl hydrolase family 1	-
OG0008318	82508.K1VV22	0	868	COG2723@1 root,KOG0626@2759 Eukaryota,38CCL	4751 Fungi	G	Glycosyl hydrolase family 1	-
OG0008327	82508.K1VHA0	0	4382	COG0297@1 root,2QSGC@2759 Eukaryota,38EG4@	4751 Fungi	M	Starch synthase catalytic domain	-
OG0008338	1047171.Mycg:3P110873	1.73E-124	374	28H1@1 root,2QPVV@2759 Eukaryota,39WVW@2	4751 Fungi	H	Glycosyltransferase family 17 protein	-
OG0008397	84751.XP_007877278.1	1.74E-71	238	COG2017@1 root,KOG1604@2759 Eukaryota,3A80E	4751 Fungi	G	Aldose 1-epimerase	-
OG0008414	5270.UM05234P0	8.75E-52	210	COG0438@1 root,COG5543@1 root,KOG1111@275	4751 Fungi	DIMO	PIGA (GPI anchor biosynthesis)	SPT14
OG0008414	5270.UM05234P0	8.75E-52	210	COG0438@1 root,COG5543@1 root,KOG1111@275	4751 Fungi	DIMO	PIGA (GPI anchor biosynthesis)	SPT14
OG0008434	63405.XP_002843360.1	0	1582	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	33154 Opisthokonta	G	Glyco_18	-
OG0008434	63405.XP_002843360.1	0	1582	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	33154 Opisthokonta	G	Glyco_18	-
OG0008434	63405.XP_002843360.1	0	1582	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	33154 Opisthokonta	G	Glyco_18	-
OG0008435	63405.XP_002847004.1	0	2101	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Glyco_18	-
OG0008435	63405.XP_002847004.1	0	2101	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Glyco_18	-
OG0008435	63405.XP_002847004.1	0	2101	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Glyco_18	-
OG0008435	63405.XP_002847004.1	0	2101	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Glyco_18	-
OG0008670	61459.XP_007783006.1	1.67E-276	789	2CMK0@1 root,2QQM5@2759 Eukaryota,39B7E@3	4751 Fungi	G	Pectinolytic enzymes consist of four classes of enzym	rglB
OG0008670	61459.XP_007783006.1	1.67E-276	789	2CMK0@1 root,2QQM5@2759 Eukaryota,39B7E@3	4751 Fungi	G	Pectinolytic enzymes consist of four classes of enzym	rglB
OG0008670	61459.XP_007783006.1	1.67E-276	789	2CMK0@1 root,2QQM5@2759 Eukaryota,39B7E@3	4751 Fungi	G	Pectinolytic enzymes consist of four classes of enzym	rglB
OG0008670	61459.XP_007783006.1	1.67E-276	789	2CMK0@1 root,2QQM5@2759 Eukaryota,39B7E@3	4751 Fungi	G	Pectinolytic enzymes consist of four classes of enzym	rglB
OG0008670	61459.XP_007783006.1	1.67E-276	789	2CMK0@1 root,2QQM5@2759 Eukaryota,39B7E@3	4751 Fungi	G	Pectinolytic enzymes consist of four classes of enzym	rglB
OG0008721	5346.XP_001833722.2	2.65E-109	351	COG2730@1 root,2QVVM@2759 Eukaryota,38F6l@	4751 Fungi	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil	EXG3
OG0008721	5346.XP_001833722.2	2.65E-109	351	COG2730@1 root,2QVVM@2759 Eukaryota,38F6l@	4751 Fungi	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil	EXG3
OG0008775	63405.XP_002843641.1	1.71E-90	296	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Glyco_18	-
OG0008814	82508.K1VQF3	0	987	2CMQJ@1 root,2QRF6@2759 Eukaryota,39RE5@33	4751 Fungi	G	Glycosyl hydrolase family 9	-
OG0008965	42374.XP_002419114.1	1.49E-94	291	COG5020@1 root,KOG4472@2759 Eukaryota,38CI7	4751 Fungi	G	Glycolipid 2-alpha-mannosyltransferase	KRE2
OG0008965	42374.XP_002419114.1	1.49E-94	291	COG5020@1 root,KOG4472@2759 Eukaryota,38CI7	4751 Fungi	G	Glycolipid 2-alpha-mannosyltransferase	KRE2
OG0009536	5480.G8B4W0	8.41E-301	823	2BFNU@1 root,2S17G@2759 Eukaryota,3A5G4@33	4751 Fungi	S	Anp1	-
OG0009719	63402.XP_003171789.1	0	3191	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0009719	63402.XP_003171789.1	0	3191	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0009719	63402.XP_003171789.1	0	3191	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0009719	63402.XP_003171789.1	0	3191	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK	4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0009736	85929.M3BZD8	3.2E-116	352	COG4225@1 root,2RXA5@2759 Eukaryota,39VFD@	4751 Fungi	G	Glycosyl Hydrolase Family 88	-
OG0009736	85929.M3BZD8	3.2E-116	352	COG4225@1 root,2RXA5@2759 Eukaryota,39VFD@	4751 Fungi	G	Glycosyl Hydrolase Family 88	-
OG0009747	92637.XP_007814506.1	7.45E-174	508	COG1621@1 root,KOG0228@2759 Eukaryota,39SNE	4751 Fungi	G	Glycosyl hydrolases family 32	INV1
OG0009747	92637.XP_007814506.1	7.45E-174	508	COG1621@1 root,KOG0228@2759 Eukaryota,39SNE	4751 Fungi	G	Glycosyl hydrolases family 32	INV1
OG0009756	83344.XP_007927422.1	0	1234	COG1501@1 root,KOG1065@2759 Eukaryota,39RGL	4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0009756	83344.XP_007927422.1	0	1234	COG1501@1 root,KOG1065@2759 Eukaryota,39RGL	4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0009756	83344.XP_007927422.1	0	1234	COG1501@1 root,KOG1065@2759 Eukaryota,39RGL	4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0010166	5480.G8B897	1.69E-295	806	COG5333@1 root,KOG0834@2759 Eukaryota,39R02	4751 Fungi	D	Belongs to the cyclin family	CTK2
OG0010166	5480.G8B897	1.69E-295	806	COG5333@1 root,KOG0834@2759 Eukaryota,39R02	4751 Fungi	D	Belongs to the cyclin family	CTK2
OG0010166	5480.G8B897	1.69E-295	806	COG5333@1 root,KOG0834@2759 Eukaryota,39R02	4751 Fungi	D	Belongs to the cyclin family	CTK2
OG0010332	63400.XP_003014495.1	5.32E-28	113	COG0055@1 root,KOG1350@2759 Eukaryota,38CQ	4751 Fungi	C	Produces ATP from ADP in the presence of a proton g	ATP2
OG0010530	1182553.XP_007741283.1	1.08E-81	267	KOG4698@1 root,KOG4698@2759 Eukaryota,38DNI	4751 Fungi	S	Protein of unknown function (DUF563)	-
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQF	4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	-
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQF	4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	-
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQF	4751 Fungi	G	Glycosyl hydrolase family 20, catalytic domain	-
OG0010728	310453.XP_007580829.1	0	919	COG3534@1 root,2QQEX@2759 Eukaryota,38HNC@	4751 Fungi	O	Alpha-L-arabinofuranosidase C-terminal domain	-
OG0010728	310453.XP_007580829.1	0	919	COG3534@1 root,2QQEX@2759 Eukaryota,38HNC@	4751 Fungi	O	Alpha-L-arabinofuranosidase C-terminal domain	-
OG0010745	5062.CADAORAP00001985	8.67E-208	615	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@	4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0010745	5062.CADAORAP00001985	8.67E-208	615	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@	4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-

OG0010745	5062.CADAORAP00001985	8.67E-208	615	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0011019	1392244.V5E607	7.07E-43	160	KOG2575@1 root,KOG2575@2759 Eukaryota,38F87 4751 Fungi	EG	Belongs to the ALG6 ALG8 glucosyltransferase family	ALG6
OG0011107	63405.XP_002842640.1	0	2241	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011107	63405.XP_002842640.1	0	2241	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011107	63405.XP_002842640.1	0	2241	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011107	63405.XP_002842640.1	0	2241	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011201	5551.XP_003233699.1	1.32E-75	251	COG1215@1 root,KOG2571@2759 Eukaryota,38B4L 4751 Fungi	M	Glycosyltransferase like family 2	CHS3
OG0011219	5037.XP_001543537.1	1.09E-122	364	2EGIF@1 root,2SMG7@2759 Eukaryota,3A4DW@33 4751 Fungi	S	Phosphotransferase enzyme family	-
OG0011219	5037.XP_001543537.1	1.09E-122	364	2EGIF@1 root,2SMG7@2759 Eukaryota,3A4DW@33 4751 Fungi	S	Phosphotransferase enzyme family	-
OG0011349	28583.AMAG_0523970	1.28E-179	547	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	Chitin Synthase	-
OG0011349	28583.AMAG_0523970	1.28E-179	547	COG1215@1 root,KOG2571@2759 Eukaryota,38FKC 4751 Fungi	M	Chitin Synthase	-
OG0011444	430998.XP_007673937.1	2.07E-185	546	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0011549	568076.XP_007822163.1	2.05E-220	612	COG0809@1 root,2S12P@2759 Eukaryota,3A58Q@. 4751 Fungi	G	Queuosine biosynthesis protein	-
OG0011549	568076.XP_007822163.1	2.05E-220	612	COG0809@1 root,2S12P@2759 Eukaryota,3A58Q@. 4751 Fungi	G	Queuosine biosynthesis protein	-
OG0011564	63402.XP_003174933.1	0	938	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011564	63402.XP_003174933.1	0	938	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011564	63402.XP_003174933.1	0	938	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0011569	63402.XP_003171789.1	2.84E-184	563	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	-
OG0011618	430998.XP_007681517.1	0	1119	COG1472@1 root,2QR4D@2759 Eukaryota,3AEEV@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0011618	430998.XP_007681517.1	0	1119	COG1472@1 root,2QR4D@2759 Eukaryota,3AEEV@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0011618	430998.XP_007681517.1	0	1119	COG1472@1 root,2QR4D@2759 Eukaryota,3AEEV@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0011618	430998.XP_007681517.1	0	1119	COG1472@1 root,2QR4D@2759 Eukaryota,3AEEV@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	-
OG0011801	64363.EME39063	6.22E-122	356	28PY3@1 root,2QWK@2759 Eukaryota,39DFN@33 4751 Fungi	G	Belongs to the glycosyl hydrolase 12 (cellulase H) fam -	-
OG0011801	64363.EME39063	6.22E-122	356	28PY3@1 root,2QWK@2759 Eukaryota,39DFN@33 4751 Fungi	G	Belongs to the glycosyl hydrolase 12 (cellulase H) fam -	-
OG0011802	69781.S7ZP52	6.62E-183	523	COG5297@1 root,2QWHE@2759 Eukaryota,39RNX@. 4751 Fungi	G	The biological conversion of cellulose to glucose gene cbhC	-
OG0011802	69781.S7ZP52	6.62E-183	523	COG5297@1 root,2QWHE@2759 Eukaryota,39RNX@. 4751 Fungi	G	The biological conversion of cellulose to glucose gene cbhC	-
OG0012058	83344.XP_007919949.1	1.12E-72	232	COG3507@1 root,2QTQG@2759 Eukaryota,39UJW@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	abnA
OG0012058	83344.XP_007919949.1	1.12E-72	232	COG3507@1 root,2QTQG@2759 Eukaryota,39UJW@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	abnA
OG0012194	117187.FVEG_0208370	2.33E-264	746	2D14U@1 root,2SGPV@2759 Eukaryota,39JHS@331 4751 Fungi	G	Belongs to the glycosyl hydrolase 32 family	-
OG0012194	117187.FVEG_0208370	2.33E-264	746	2D14U@1 root,2SGPV@2759 Eukaryota,39JHS@331 4751 Fungi	G	Belongs to the glycosyl hydrolase 32 family	-
OG0012248	82508.K1V1D8	2.04E-162	469	COG0366@1 root,KOG0471@2759 Eukaryota,38EYC 4751 Fungi	G	Domain of unknown function (DUF1966)	-
OG0012308	5270.UM05234P0	7.46E-57	223	COG0438@1 root,KOG5543@1 root,KOG1111@275 4751 Fungi	DIMO	PIGA (GPI anchor biosynthesis)	SPT14
OG0012374	63405.XP_002851156.1	2.33E-82	259	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	LysM domain	-
OG0012577	82508.K1VSV6	1.4E-211	607	2C17J@1 root,2S1N4@2759 Eukaryota,3A48K@331: 4751 Fungi	S	Glycosyltransferase family 18	-
OG0012679	82508.K1V2T3	0	972	2CW4T@1 root,2RTMK@2759 Eukaryota,39X87@33 4751 Fungi	G	Glycosyl hydrolase family 71	-
OG0012700	82508.K1W9Y2	9.35E-282	783	2C17J@1 root,2S1N4@2759 Eukaryota,3A48K@331: 4751 Fungi	S	Glycosyltransferase family 18	-
OG0012895	82508.K1VTI2	0	1316	KOG2204@1 root,KOG2204@2759 Eukaryota,38B69 4751 Fungi	G	Glycosyl hydrolase family 47	-
OG0012895	82508.K1VTI2	0	1316	KOG2204@1 root,KOG2204@2759 Eukaryota,38B69 4751 Fungi	G	Glycosyl hydrolase family 47	-
OG0012992	82508.K1WJ20	7.19E-233	654	29MVY@1 root,2RBAU@2759 Eukaryota,3AXSH@3: 4751 Fungi	S	Protein of unknown function (DUF563)	-
OG0013120	82508.K1V975	0	1221	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@. 4751 Fungi	G	Cellulase (glycosyl hydrolase family 5)	exgD
OG0013120	82508.K1V975	0	1221	COG2730@1 root,2QRG8@2759 Eukaryota,38M6K@. 4751 Fungi	G	Cellulase (glycosyl hydrolase family 5)	exgD
OG0013391	82508.K1VL55	7.92E-253	724	COG0572@1 root,KOG4203@2759 Eukaryota,38HIZ 4751 Fungi	TZ	Uracil phosphoribosyltransferase	-
OG0013410	82508.K1VRU9	0	1016	28J03@1 root,2QRBX@2759 Eukaryota,39SIO@3315 4751 Fungi	G	Cryptococcal mannosyltransferase 1	-
OG0014014	746128.CADAFUBP00002916	7.15E-67	226	COG3507@1 root,2S2VU@2759 Eukaryota,3904B@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	abnB
OG0014014	746128.CADAFUBP00002916	7.15E-67	226	COG3507@1 root,2S2VU@2759 Eukaryota,3904B@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	abnB
OG0014014	746128.CADAFUBP00002916	7.15E-67	226	COG3507@1 root,2S2VU@2759 Eukaryota,3904B@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	abnB
OG0014104	226899.FOXS41	3.79E-134	394	COG5434@1 root,2QW1P@2759 Eukaryota,39DJZ@. 4751 Fungi	G	Glycosyl hydrolases family 28	pgaD
OG0014104	226899.FOXS41	3.79E-134	394	COG5434@1 root,2QW1P@2759 Eukaryota,39DJZ@. 4751 Fungi	G	Glycosyl hydrolases family 28	pgaD
OG0014105	430998.XP_007677087.1	8.21E-107	323	KOG2515@1 root,KOG2515@2759 Eukaryota,38CW 4751 Fungi	MU	Protein of unknown function (DUF3445)	-
OG0014117	85929.M3D2A4	1.37E-128	413	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0014117	85929.M3D2A4	1.37E-128	413	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0014117	85929.M3D2A4	1.37E-128	413	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0014122	430998.XP_007673937.1	0	1158	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0014122	430998.XP_007673937.1	0	1158	COG1501@1 root,KOG1065@2759 Eukaryota,38C0A 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0014142	64363.EME49126	2.01E-294	834	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	bgIA
OG0014142	64363.EME49126	2.01E-294	834	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 3 family	bgIA
OG0014343	64363.EME47659	1.24E-191	543	COG2730@1 root,2S659@2759 Eukaryota,39W75@. 4751 Fungi	G	Belongs to the glycosyl hydrolase 5 (cellulase A) famil -	-
OG0014763	226899.FOXB16	2.71E-80	276	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	Glyco_18	-
OG0014763	226899.FOXB16	2.71E-80	276	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	Glyco_18	-
OG0014763	226899.FOXB16	2.71E-80	276	COG3325@1 root,KOG2806@2759 Eukaryota,38HF2 4751 Fungi	G	Glyco_18	-

OG0014828	5478.XP_448192.1	0	1432	COG1928@1 root,KOG3359@2759 Eukaryota,39UB\ 4751 Fungi	O	Saccharomyces cerevisiae YDR307W	-
OG0014828	5478.XP_448192.1	0	1432	COG1928@1 root,KOG3359@2759 Eukaryota,39UB\ 4751 Fungi	O	Saccharomyces cerevisiae YDR307W	-
OG0015163	5478.XP_449771.1	1.34E-126	374	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0015486	5478.XP_448781.1	0	1367	28MG1@1 root,2QITZG@2759 Eukaryota,39WT5@3: 4751 Fungi	S	Debaryomyces hansenii and CA4636 IPF1520 Candida BMT1	
OG0015606	4909.A0A099P613	8.49E-305	830	COG3774@1 root,2QW2l@2759 Eukaryota,39T08@ 4751 Fungi	G	to Saccharomyces cerevisiae OCH1 (YGL038C)	OCH1
OG0015606	4909.A0A099P613	8.49E-305	830	COG3774@1 root,2QW2l@2759 Eukaryota,39T08@ 4751 Fungi	G	to Saccharomyces cerevisiae OCH1 (YGL038C)	OCH1
OG0015952	82508.K1V2V8	3.41E-238	664	KOG2287@1 root,KOG2287@2759 Eukaryota,3AG4\ 4751 Fungi	G	galactosyltransferase activity	-
OG0016324	5207.AAW46059	0.0000123	52.4	COG2272@1 root,KOG1516@2759 Eukaryota,38D2\ 4751 Fungi	G	Carboxylesterase family	-
OG0016330	552467.XP_003195041.1	1.36E-28	113	COG0366@1 root,KOG0471@2759 Eukaryota,38EZl\ 4751 Fungi	G	Alpha amylase, C-terminal all-beta domain	-
OG0016369	5217.XP_007001966.1	0.00000757	56.6	KOG2287@1 root,KOG2287@2759 Eukaryota,3AG4\ 4751 Fungi	G	galactosyltransferase activity	-
OG0016476	28583.AMAG_12848T0	7.23E-163	464	COG2820@1 root,2RXP@2759 Eukaryota,3A0J6@3: 4751 Fungi	F	purine and uridine phosphorylase	-
OG0016835	42374.XP_002417254.1	0	974	2BX4A@1 root,2RQD2@2759 Eukaryota,38U4M@3: 4751 Fungi	-	-	-
OG0016894	42374.XP_002422471.1	1.82E-69	231	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT3
OG0016948	5480.G8BCG1	1.93E-136	414	COG1626@1 root,KOG0602@2759 Eukaryota,38CK\ 4751 Fungi	G	Alpha-trehalose glucosylhydrolase	NTH1
OG0017120	63402.XP_003172876.1	0.00094	47	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Glycosyl hydrolases family 18	CHT2
OG0017129	63400.XP_003014496.1	4E-86	273	COG0296@1 root,KOG0470@2759 Eukaryota,3AV51 4751 Fungi	G	Alpha amylase, C-terminal all-beta domain	GLC3
OG0017396	1108849.XP_002562974.1	6.58E-53	182	COG3507@1 root,2RADR@2759 Eukaryota,3AWT0@ 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	-
OG0017396	1108849.XP_002562974.1	6.58E-53	182	COG3507@1 root,2RADR@2759 Eukaryota,3AWT0@ 4751 Fungi	G	Belongs to the glycosyl hydrolase 43 family	-
OG0017399	430998.XP_007676388.1	1.28E-210	613	COG1501@1 root,KOG1065@2759 Eukaryota,38C0\ 4751 Fungi	G	Belongs to the glycosyl hydrolase 31 family	-
OG0017922	84751.XP_007878195.1	1.33E-18	87.8	COG2273@1 root,2QR13@2759 Eukaryota,38E3H@ 4751 Fungi	G	Beta-glucan synthesis-associated protein (SKN1)	-
OG0018034	63405.XP_002846368.1	2.88E-33	127	COG3325@1 root,KOG2806@2759 Eukaryota,38BJK 4751 Fungi	G	Glyco_18	-
OG0018066	63405.XP_002846279.1	1.05E-115	355	COG1215@1 root,KOG2571@2759 Eukaryota,38HE4 4751 Fungi	M	chitin synthase	CHS3
OG0018316	4909.A0A099NXN8	4.39E-43	150	COG0676@1 root,KOG1594@2759 Eukaryota,39SA3 4751 Fungi	G	Catalyzes the interconversion between the alpha and YMR099C	
OG0018388	4909.A0A099NXD9	2.23E-35	145	COG0463@1 root,COG0564@1 root,KOG1919@275 4751 Fungi	M	to uniprot P40350 Saccharomyces cerevisiae YPL227C ALG5	
OG0018388	4909.A0A099NXD9	2.23E-35	145	COG0463@1 root,COG0564@1 root,KOG1919@275 4751 Fungi	M	to uniprot P40350 Saccharomyces cerevisiae YPL227C ALG5	
OG0018579	4909.A0A099P720	0	1402	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	C-terminal four TMM region of protein-O-mannosyltr -	
OG0018579	4909.A0A099P720	0	1402	COG1928@1 root,KOG3359@2759 Eukaryota,38DG: 4751 Fungi	O	C-terminal four TMM region of protein-O-mannosyltr -	
OG0018640	4909.A0A099NZR3	3.12E-140	435	COG0584@1 root,COG1626@1 root,KOG0602@275 4751 Fungi	G	Alpha-trehalose glucosylhydrolase	NTH1
OG0018728	4909.A0A099P1T7	6.54E-113	342	2C559@1 root,2QQ16@2759 Eukaryota,38DG6@33 4751 Fungi	G	to Saccharomyces cerevisiae MNN2 (YBR015C)	-
OG0018996	4909.A0A099P1Q4	3.86E-89	271	COG3774@1 root,2QW2l@2759 Eukaryota,39T08@ 4751 Fungi	G	to Saccharomyces cerevisiae OCH1 (YGL038C)	OCH1
OG0019002	4909.A0A099P179	1.41E-67	221	2C559@1 root,2QQ16@2759 Eukaryota,38DG6@33 4751 Fungi	G	to Saccharomyces cerevisiae MNN2 (YBR015C)	-
OG0019003	4909.A0A099P1F8	2.24E-50	172	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G	Belongs to the glycosyl hydrolase 18 family	CHT2
OG0019019	4909.A0A099P1H5	5.42E-38	137	COG3774@1 root,2QW2l@2759 Eukaryota,39T08@ 4751 Fungi	G	to Saccharomyces cerevisiae OCH1 (YGL038C)	OCH1
OG0019300	36080.S2JLC4	0	1232	COG1874@1 root,KOG0496@2759 Eukaryota,38D5\ 4751 Fungi	G	Glycosyl hydrolases family 35	lacA
OG0019300	36080.S2JLC4	0	1232	COG1874@1 root,KOG0496@2759 Eukaryota,38D5\ 4751 Fungi	G	Glycosyl hydrolases family 35	lacA
OG0019300	36080.S2JLC4	0	1232	COG1874@1 root,KOG0496@2759 Eukaryota,38D5\ 4751 Fungi	G	Glycosyl hydrolases family 35	lacA
OG0019300	36080.S2JLC4	0	1232	COG1874@1 root,KOG0496@2759 Eukaryota,38D5\ 4751 Fungi	G	Glycosyl hydrolases family 35	lacA
OG0019315	63400.XP_003017167.1	1.24E-85	272	KOG1037@1 root,KOG1037@2759 Eukaryota,38B7L 4751 Fungi	H	Polymerase	-
OG0019417	5037.XP_001543537.1	6.2E-29	114	2EGIF@1 root,2SMG7@2759 Eukaryota,3A4DW@33 4751 Fungi	S	Phosphotransferase enzyme family	-
OG0019505	82508.K1W084	2.99E-258	717	28J03@1 root,2QRBX@2759 Eukaryota,39S10@3315 4751 Fungi	G	Cryptococcal mannosyltransferase 1	-
OG0019515	5207.AAW41198	3.78E-35	133	28JAD@1 root,2QRP7@2759 Eukaryota,39FS3@331 4751 Fungi	G	Cryptococcal mannosyltransferase 1	-

GOs	EC	KEGG ko	KEGG Pathway	KEGG Module	KEGG Reaction	KEGG rclass	BRTE	KEGG TC
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-	3.2.1.58							

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GO:0000023,GO:0000025,GO:0000272,GO:0003674,ç 3.2.1.20	ko:K01187	ko00052,ko00500,ko01100,map00052,map00500,maj-	-	R00028,R00801,R00802	RC00028,RC00049,R	ko00000,ko00001,ko01000	-
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GO:0000030,GO:0003674,GO:0003824,GO:0004376,ç 2.4.1.259,2.4.	ko:K03846	ko00510,ko00513,ko01100,map00510,map00513,maj	M00055	R06259,R06261	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000030,GO:0003674,GO:0003824,GO:0004584,ç -	ko:K05286	ko00563,ko01100,map00563,map01100	M00065	R05922	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000030,GO:0003674,GO:0003824,GO:0004584,ç -	ko:K05286	ko00563,ko01100,map00563,map01100	M00065	R05922	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000009,GO:0000030,GO:0003674,GO:0003824,ç 2.4.1.260	ko:K03847	ko00510,ko00513,ko01100,map00510,map00513,maj	M00055	R06260	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000271,GO:0000322,GO:0000323,GO:0000324,ç 3.2.1.106	ko:K01228	ko00510,ko01100,ko04141,map00510,map01100,maj	M00073	R05979	-	ko00000,ko00001,ko00002,ko01000,ko04147	-
GO:0000271,GO:0000322,GO:0000323,GO:0000324,ç 3.2.1.106	ko:K01228	ko00510,ko01100,ko04141,map00510,map01100,maj	M00073	R05979	-	ko00000,ko00001,ko00002,ko01000,ko04147	-
GO:0000271,GO:0000322,GO:0000323,GO:0000324,ç 3.2.1.106	ko:K01228	ko00510,ko01100,ko04141,map00510,map01100,maj	M00073	R05979	-	ko00000,ko00001,ko00002,ko01000,ko04147	-
GO:0000096,GO:0000097,GO:0003674,GO:0003676,ç 2.4.2.28	ko:K00772	ko00270,ko01100,map00270,map01100	M00034	R01402	RC00063,RC02819	ko00000,ko00001,ko00002,ko01000	-
GO:0000096,GO:0000097,GO:0003674,GO:0003676,ç 2.4.2.28	ko:K00772	ko00270,ko01100,map00270,map01100	M00034	R01402	RC00063,RC02819	ko00000,ko00001,ko00002,ko01000	-
GO:0000096,GO:0000097,GO:0003674,GO:0003676,ç 2.4.2.28	ko:K00772	ko00270,ko01100,map00270,map01100	M00034	R01402	RC00063,RC02819	ko00000,ko00001,ko00002,ko01000	-
GO:0000030,GO:0003674,GO:0003824,GO:0005575,ç -	ko:K05284	ko00563,ko01100,map00563,map01100	M00065	R05919	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000272,GO:0003674,GO:0003824,GO:0004133,ç 2.4.1.25,3.2.1	ko:K01196	ko00500,ko01100,ko01110,map00500,map01100,maj-	-	R02109,R02111	RC00049	ko00000,ko00001,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004133,ç 2.4.1.25,3.2.1	ko:K01196	ko00500,ko01100,ko01110,map00500,map01100,maj-	-	R02109,R02111	RC00049	ko00000,ko00001,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004133,ç 2.4.1.25,3.2.1	ko:K01196	ko00500,ko01100,ko01110,map00500,map01100,maj-	-	R02109,R02111	RC00049	ko00000,ko00001,ko01000	-
GO:000506,GO:0003674,GO:0003824,GO:0005575,ç 2.4.1.198	ko:K03857	ko00563,ko01100,map00563,map01100	M00065	R05916	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0003825,GO:0005575,ç 2.4.1.15,2.4.1	ko:K00697,ko:K1	ko00500,ko01100,map00500,map01100	-	R02737,R02778	RC00005,RC00017,R	ko00000,ko00001,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0003825,GO:0005575,ç 2.4.1.15,2.4.1	ko:K00697,ko:K1	ko00500,ko01100,map00500,map01100	-	R02737,R02778	RC00005,RC00017,R	ko00000,ko00001,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0003825,GO:0005575,ç 2.4.1.15,2.4.1	ko:K00697,ko:K1	ko00500,ko01100,map00500,map01100	-	R02737,R02778	RC00005,RC00017,R	ko00000,ko00001,ko01000,ko01003	-
-	3.2.1.17	ko:K01185	-	-	-	ko00000,ko01000	-
-	3.2.1.17	ko:K01185	-	-	-	ko00000,ko01000	-
-	3.2.1.17	ko:K01185	-	-	-	ko00000,ko01000	-
GO:0003674,GO:0003824,GO:0004581,GO:0005575,ç 2.4.1.117	ko:K00729	ko00510,ko01100,map00510,map01100	M00055	R01005	RC00005	ko00000,ko00001,ko00002,ko01000,ko01003	-

GO:0003674,GO:0003824,GO:0005575,GO:0005622,Є 2.4.1.267	ko:K03848	ko00510,ko01100,map00510,map01100	M00055	R06262	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000271,GO:0003674,GO:0003824,GO:0004373,Є 2.4.1.11	ko:K00693	ko00500,ko01100,ko04151,ko04152,ko04910,ko0492	-	R00292	RC00005	ko00000,ko00001,ko01000,ko01003	-
GO:0000271,GO:0003674,GO:0003824,GO:0004373,Є 2.4.1.11	ko:K00693	ko00500,ko01100,ko04151,ko04152,ko04910,ko0492	-	R00292	RC00005	ko00000,ko00001,ko01000,ko01003	-
GO:0000030,GO:0003674,GO:0003824,GO:0005575,Є 2.4.1.142	ko:K03842	ko00510,ko00513,ko01100,map00510,map00513,maj	M00055	R05972	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0003674,GO:0003824,GO:0004514,GO:0005575,Є 2.4.2.19	ko:K00767	ko00760,ko01100,map00760,map01100	M00115	R03348	RC02877	ko00000,ko00001,ko00002,ko01000	-
GO:0003674,GO:0003824,GO:0004514,GO:0005575,Є 2.4.2.19	ko:K00767	ko00760,ko01100,map00760,map01100	M00115	R03348	RC02877	ko00000,ko00001,ko00002,ko01000	-
GO:0000139,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.113	ko:K01230	ko00510,ko00513,ko01100,ko04141,map00510,mapC	M00073,M00074	R05982,R06722	-	ko00000,ko00001,ko00002,ko01000,ko04131	-
GO:0000139,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.113	ko:K01230	ko00510,ko00513,ko01100,ko04141,map00510,mapC	M00073,M00074	R05982,R06722	-	ko00000,ko00001,ko00002,ko01000,ko04131	-
- 2.4.1.173	ko:K05841	-	-	-	-	ko00000,ko01000,ko01003	-
GO:0000272,GO:0003674,GO:0003824,GO:0004645,Є 2.4.1.1	ko:K00688	ko00500,ko01100,ko01110,ko02026,ko04217,ko0491	-	R02111	-	ko00000,ko00001,ko01000	-
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
GO:0000009,GO:0000030,GO:0000032,GO:0000136,Є -	ko:K05531	ko00513,ko01100,map00513,map01100	M00074	-	-	ko00000,ko00001,ko00002,ko01000	-
GO:0003674,GO:0003824,GO:0004731,GO:0005575,Є 2.4.2.1	ko:K03783	ko00230,ko00240,ko00760,ko01100,ko01110,map00	-	R01561,R01863,R01969	RC00033,RC00063,R	ko00000,ko00001,ko01000	-
GO:0003674,GO:0003824,GO:0004731,GO:0005575,Є 2.4.2.1	ko:K03783	ko00230,ko00240,ko00760,ko01100,ko01110,map00	-	R01561,R01863,R01969	RC00033,RC00063,R	ko00000,ko00001,ko01000	-
GO:0003674,GO:0003824,GO:0005575,GO:0005622,Є 2.4.1.265	ko:K03849	ko00510,ko01100,map00510,map01100	M00055	R06263	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000139,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.24	ko:K01191,ko:K1	ko00511,ko04141,map00511,map04141	-	-	-	ko00000,ko00001,ko01000,ko04091,ko04131	-
GO:0000139,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.24	ko:K01191,ko:K1	ko00511,ko04141,map00511,map04141	-	-	-	ko00000,ko00001,ko01000,ko04091,ko04131	-
GO:0000322,GO:0000323,GO:0000324,GO:0003674,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000322,GO:0000323,GO:0000324,GO:0003674,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000322,GO:0000323,GO:0000324,GO:0003674,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000322,GO:0000323,GO:0000324,GO:0000329,Є 3.2.1.24	ko:K01191	ko00511,map00511	-	-	-	ko00000,ko00001,ko01000,ko04131	-
GO:0000322,GO:0000323,GO:0000324,GO:0000329,Є 3.2.1.24	ko:K01191	ko00511,map00511	-	-	-	ko00000,ko00001,ko01000,ko04131	-
GO:0000322,GO:0000323,GO:0000324,GO:0000329,Є 3.2.1.24	ko:K01191	ko00511,map00511	-	-	-	ko00000,ko00001,ko01000,ko04131	-
GO:0000026,GO:0000030,GO:0003674,GO:0003824,Є -	ko:K08098	ko00563,map00563	-	R07129	-	ko00000,ko00001,ko01000,ko01003	-
GO:0000030,GO:0000033,GO:0003674,GO:0003824,Є 2.4.1.258	ko:K03845	ko00510,ko00513,ko01100,map00510,map00513,maj	M00055	R06258	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0006139,GO:0006396,Є 2.4.2.29	ko:K00773	-	-	R03789,R10209	RC00063	ko00000,ko01000,ko03016	-
GO:0003674,GO:0003824,GO:0006139,GO:0006396,Є 2.4.2.29	ko:K00773	-	-	R03789,R10209	RC00063	ko00000,ko01000,ko03016	-
GO:0003674,GO:0005488,GO:0005515,GO:0005575,Є 2.4.1.141	ko:K07441	ko00510,ko00513,ko01100,map00510,map00513,maj	M00055	R05970	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000009,GO:0000030,GO:0000136,GO:0000137,Є -	ko:K05532	ko00513,ko01100,map00513,map01100	M00074	-	-	ko00000,ko00001,ko00002,ko01000	-
- 3.2.1.25	ko:K01192	ko00511,ko04142,map00511,map04142	-	-	-	ko00000,ko00001,ko01000	-
- 3.2.1.25	ko:K01192	ko00511,ko04142,map00511,map04142	-	-	-	ko00000,ko00001,ko01000	-
- 3.2.1.25	ko:K01192	ko00511,ko04142,map00511,map04142	-	-	-	ko00000,ko00001,ko01000	-
- 3.2.1.25	ko:K01192	ko00511,ko04142,map00511,map04142	-	-	-	ko00000,ko00001,ko01000	-
- 3.2.1.25	ko:K01192	ko00511,ko04142,map00511,map04142	-	-	-	ko00000,ko00001,ko01000	-
GO:0000030,GO:0000032,GO:0000136,GO:0000137,Є 2.4.1.232	ko:K05529	ko00513,ko01100,map00513,map01100	M00074	-	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000030,GO:0000032,GO:0000136,GO:0000137,Є 2.4.1.232	ko:K05529	ko00513,ko01100,map00513,map01100	M00074	-	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000272,GO:0000322,GO:0000323,GO:0000324,Є 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
GO:0000272,GO:0000322,GO:0000323,GO:0000324,Є 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
GO:0000322,GO:0000323,GO:0000324,GO:0001101,Є 3.2.1.28	ko:K01194	ko00500,ko01100,map00500,map01100	-	R00010	RC00049	ko00000,ko00001,ko00537,ko01000	-
GO:0000322,GO:0000323,GO:0000324,GO:0001101,Є 3.2.1.28	ko:K01194	ko00500,ko01100,map00500,map01100	-	R00010	RC00049	ko00000,ko00001,ko00537,ko01000	-
- 3.2.1.4	ko:K01179	ko00500,ko01100,map00500,map01100	-	R06200,R11307,R11308	-	ko00000,ko00001,ko01000	-
- 3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,mapC	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
- 3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,mapC	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
- 3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,mapC	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
- 3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,mapC	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0003674,GO:0003824,GO:0004583,GO:0005575,Є 2.4.1.256	ko:K03850	ko00510,ko01100,map00510,map01100	M00055	R06264	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000271,GO:0003674,GO:0003824,GO:0003844,Є 2.4.1.18	ko:K00700	ko00500,ko01100,ko01110,map00500,map01100,maj	M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	-
GO:0000271,GO:0003674,GO:0003824,GO:0003844,Є 2.4.1.18	ko:K00700	ko00500,ko01100,ko01110,map00500,map01100,maj	M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	-
GO:0006629,GO:0006643,GO:0006664,GO:0006665,Є -	ko:K13682	-	-	-	-	ko00000,ko01000,ko01003	-

-	2.4.2.30	ko:K10798	ko03410,ko04210,ko04212,ko04214,ko04217,map03-	M00296	-	-	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303	-
-	2.4.2.30	ko:K10798	ko03410,ko04210,ko04212,ko04214,ko04217,map03-	M00296	-	-	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303	-
-	2.4.2.30	ko:K10798	ko03410,ko04210,ko04212,ko04214,ko04217,map03-	M00296	-	-	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303	-
-	2.4.2.30	ko:K10798	ko03410,ko04210,ko04212,ko04214,ko04217,map03-	M00296	-	-	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303	-
GO:0003674,GO:0003824,GO:0006139,GO:0006396,€	2.4.2.29	ko:K00773	-	-	R03789,R10209	RC00063	ko00000,ko01000,ko03016	-
GO:0003674,GO:0003824,GO:0006139,GO:0006396,€	2.4.2.29	ko:K00773	-	-	R03789,R10209	RC00063	ko00000,ko01000,ko03016	-
GO:0003674,GO:0003824,GO:0006139,GO:0006396,€	2.4.2.29	ko:K00773	-	-	R03789,R10209	RC00063	ko00000,ko01000,ko03016	-
-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0	M00628	R00022,R05963,R07809	RC00049	ko00000,ko00001,ko00002,ko01000	-
-	2.4.2.9	ko:K00761	ko00240,ko01100,map00240,map01100	-	R00966	RC00063	ko00000,ko00001,ko01000	-
-	2.4.2.9	ko:K00761	ko00240,ko01100,map00240,map01100	-	R00966	RC00063	ko00000,ko00001,ko01000	-
-	3.2.1.10	ko:K01182	ko0052,ko00500,ko01100,map00052,map00500,maj	-	R00801,R01718,R01791	RC00028,RC00059,R	ko00000,ko00001,ko01000	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,€	3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,€	3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
-	2.4.1.231	ko:K22248	-	-	-	-	ko00000,ko01000	-
-	2.4.1.231	ko:K22248	-	-	-	-	ko00000,ko01000	-
-	5.1.3.3	ko:K01785	ko00010,ko00052,ko01100,ko01110,ko01120,ko0113	M00632	R01602,R10619	RC00563	ko00000,ko00001,ko00002,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
GO:0001101,GO:0003674,GO:0003824,GO:0004553,€	3.2.1.28	ko:K01194	ko00500,ko01100,map00500,map01100	-	R00010	RC00049	ko00000,ko00001,ko00537,ko01000	-
GO:0001101,GO:0003674,GO:0003824,GO:0004553,€	3.2.1.28	ko:K01194	ko00500,ko01100,map00500,map01100	-	R00010	RC00049	ko00000,ko00001,ko00537,ko01000	-
GO:0001101,GO:0003674,GO:0003824,GO:0004553,€	3.2.1.28	ko:K01194	ko00500,ko01100,map00500,map01100	-	R00010	RC00049	ko00000,ko00001,ko00537,ko01000	-
GO:0000030,GO:0000271,GO:0003674,GO:0003824,€	-	ko:K13682	-	-	-	-	ko00000,ko01000,ko01003	-
GO:0003674,GO:0005575,GO:0005622,GO:0005623,€	-	ko:K09658	ko00510,ko00563,ko01100,map00510,map00563,maj	-	R01009,R05916	RC00005	ko00000,ko00001	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,€	3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,€	3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
-	2.4.2.30	ko:K10798	ko03410,ko04210,ko04212,ko04214,ko04217,map03-	M00296	-	-	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
-	2.4.1.16	ko:K00698	ko00520,map00520	-	R02335	RC00005	ko00000,ko00001,ko01000,ko01003	-
-	2.4.1.16	ko:K00698	ko00520,map00520	-	R02335	RC00005	ko00000,ko00001,ko01000,ko01003	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0	-	R01105,R01678,R03355	RC00049,RC00452	ko00000,ko00001,ko01000	-
-	3.2.1.21	ko:K05349	ko00460,ko00500,ko00940,ko01100,ko01110,map00-	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
-	3.2.1.21	ko:K05349	ko00460,ko00500,ko00940,ko01100,ko01110,map00-	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
-	3.2.1.165	ko:K15855	ko00520,ko01100,map00520,map01100	-	R01966	RC00049	ko00000,ko00001,ko01000	-
-	3.2.1.165	ko:K15855	ko00520,ko01100,map00520,map01100	-	R01966	RC00049	ko00000,ko00001,ko01000	-
-	3.2.1.165	ko:K15855	ko00520,ko01100,map00520,map01100	-	R01966	RC00049	ko00000,ko00001,ko01000	-

GO:0003674,GO:0003824,GO:0004845,GO:0004849,Є 2.4.2.9	ko:K00761	ko00240,ko01100,map00240,map01100	-	R00966	RC00063	ko00000,ko00001,ko01000	-
- 2.4.1.16	ko:K00698	ko00520,map00520	-	R02335	RC00005	ko00000,ko00001,ko01000,ko01003	-
- 2.4.1.16	ko:K00698	ko00520,map00520	-	R02335	RC00005	ko00000,ko00001,ko01000,ko01003	-
GO:0000003,GO:0000271,GO:0000278,GO:0000281,Є 2.4.1.16	ko:K00698	ko00520,map00520	-	R02335	RC00005	ko00000,ko00001,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0004553,GO:0016787,Є 3.2.1.139	ko:K01235	-	-	-	-	ko00000,ko01000	-
GO:0003674,GO:0003824,GO:0004553,GO:0016787,Є 3.2.1.139	ko:K01235	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.22	ko:K07407	ko00052,ko00561,ko00600,ko00603,map00052,map0	-	R01101,R01103,R01104	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.22	ko:K07407	ko00052,ko00561,ko00600,ko00603,map00052,map0	-	R01101,R01103,R01104	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
- 3.2.1.99	ko:K06113	-	-	-	-	ko00000,ko01000	-
- 3.2.1.99	ko:K06113	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0004553,Є 3.2.1.55	ko:K01209	ko00520,map00520	-	R01762	-	ko00000,ko00001,ko01000	-
- 3.2.1.21	ko:K01188	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
- 3.2.1.21	ko:K01188	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
- 2.4.1.183	ko:K00749	-	-	-	-	ko00000,ko01000,ko01003	-
- 2.4.1.144	ko:K00737	ko00510,ko01100,map00510,map01100	M00075	R05986	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
- 5.1.3.3	ko:K01785	ko00010,ko00052,ko01100,ko01110,ko01120,ko0113	M00632	R01602,R10619	RC00563	ko00000,ko00001,ko00002,ko01000	-
GO:0000506,GO:0003674,GO:0003824,GO:0005575,Є 2.4.1.198	ko:K03857	ko00563,ko01100,map00563,map01100	M00065	R05916	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000506,GO:0003674,GO:0003824,GO:0005575,Є 2.4.1.198	ko:K03857	ko00563,ko01100,map00563,map01100	M00065	R05916	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0005975,Є 4.2.2.23	ko:K18195	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0005975,Є 4.2.2.23	ko:K18195	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0005975,Є 4.2.2.23	ko:K18195	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0005975,Є 4.2.2.23	ko:K18195	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0003674,GO:0003824,GO:0005975,Є 4.2.2.23	ko:K18195	-	-	-	-	ko00000,ko01000	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
GO:0000003,GO:0000272,GO:0000746,GO:0000747,Є 3.2.1.58	ko:K01210	ko00500,map00500	-	R00308,R03115	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.4	ko:K01179	ko00500,ko01100,map00500,map01100	-	R06200,R11307,R11308	-	ko00000,ko00001,ko01000	-
GO:0000026,GO:0000030,GO:0000032,GO:0000322,Є -	ko:K10967	ko00514,map00514	-	R09300,R09301	-	ko00000,ko00001,ko01000,ko01003	-
GO:0000026,GO:0000030,GO:0000032,GO:0000322,Є -	ko:K10967	ko00514,map00514	-	R09300,R09301	-	ko00000,ko00001,ko01000,ko01003	-
- 2.4.1.232	ko:K05529	ko00513,ko01100,map00513,map01100	M00074	-	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	-	R01206,R02334	RC00467	ko00000,ko00001,ko01000	-
- 3.2.1.172	ko:K15532	-	-	-	-	ko00000,ko01000	-
- 3.2.1.172	ko:K15532	-	-	-	-	ko00000,ko01000	-
GO:0000272,GO:0000322,GO:0000323,GO:0000324,Є 3.2.1.26	ko:K01193	ko00052,ko00500,ko01100,map00052,map00500,maj	-	R00801,R00802,R02410	RC00028,RC00077	ko00000,ko00001,ko01000	-
GO:0000272,GO:0000322,GO:0000323,GO:0000324,Є 3.2.1.26	ko:K01193	ko00052,ko00500,ko01100,map00052,map00500,maj	-	R00801,R00802,R02410	RC00028,RC00077	ko00000,ko00001,ko01000	-
- 3.2.1.177	ko:K01811	-	-	-	-	ko00000,ko01000	-
- 3.2.1.177	ko:K01811	-	-	-	-	ko00000,ko01000	-
- 3.2.1.177	ko:K01811	-	-	-	-	ko00000,ko01000	-
GO:0000079,GO:0000307,GO:0001932,GO:0001934,Є 3.2.1.21	ko:K05349,ko:K1	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000,ko03021	-
GO:0000079,GO:0000307,GO:0001932,GO:0001934,Є 3.2.1.21	ko:K05349,ko:K1	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000,ko03021	-
GO:0000079,GO:0000307,GO:0001932,GO:0001934,Є 3.2.1.21	ko:K05349,ko:K1	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000,ko03021	-
GO:0000166,GO:0000275,GO:0003674,GO:0003824,Є 2.4.1.18,3.6.3	ko:K00700,ko:KC	ko00190,ko00500,ko01100,ko01110,ko04714,ko0501	M00158,M00565	R02110	-	ko00000,ko00001,ko00002,ko01000,ko04147	3.A.2.1
- 2.4.1.255	ko:K18134	ko00514,map00514	-	R09304,R09676	RC00005,RC00059	ko00000,ko00001,ko01000,ko01003	-
- 3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
- 3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
- 3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060	M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-
- 3.2.1.55	ko:K01209	ko00520,map00520	-	R01762	-	ko00000,ko00001,ko01000	-
- 3.2.1.55	ko:K01209	ko00520,map00520	-	R01762	-	ko00000,ko00001,ko01000	-
GO:0008150,GO:0008152,GO:0019748	ko:K05349	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-
GO:0008150,GO:0008152,GO:0019748	ko:K05349	ko00460,ko00500,ko00940,ko01100,ko01110,map00	-	R00026,R02558,R02887	RC00049,RC00059,R	ko00000,ko00001,ko01000	-

GO:0008150,GO:0008152,GO:0019748	3.2.1.21	ko:K05349	ko00460,ko00500,ko00940,ko01100,ko01110,map000460,ko00500,ko00940,ko01100,ko01110,map000460	M00055	R00026,R02558,R02887	RC000049,RC000059,R	ko000000,ko000001,ko010000	-
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-	3.2.1.14	ko:K01183	ko00520,ko01100,ko00520,ko01100	-	R06262	-	ko000000,ko000001,ko000002,ko01000,ko01003	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,ko00520,ko01100	-	R01206,R02334	RC00467	ko000000,ko000001,ko010000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,ko00520,ko01100	-	R01206,R02334	RC00467	ko000000,ko000001,ko010000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,ko00520,ko01100	-	R01206,R02334	RC00467	ko000000,ko000001,ko010000	-
-	3.2.1.14	ko:K01183	ko00520,ko01100,ko00520,ko01100	-	R01206,R02334	RC00467	ko000000,ko000001,ko010000	-
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GO:0000030,GO:0003674,GO:0003824,GO:0004169,Ç 2.4.1.109	ko:K00728	ko00514,ko00515,ko01100,map00514,map00515,maj -	R04072,R07620,R11399 RC00005,RC00059,R ko00000,ko00001,ko01000,ko01003	-	
GO:0000272,GO:0000278,GO:0000281,GO:0000282,Ç 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100 -	R01206,R02334 RC00467	ko00000,ko00001,ko01000	
GO:0000030,GO:0000271,GO:0003674,GO:0003824,Ç -	ko:K13682	-	-	ko00000,ko01000,ko01003	
GO:0000009,GO:0000030,GO:0000032,GO:0000136,Ç 2.4.1.232	ko:K05528	ko00513,ko01100,map00513,map01100 M00074	R08599	ko00000,ko00001,ko00002,ko01000,ko01003	
GO:0000009,GO:0000030,GO:0000032,GO:0000136,Ç 2.4.1.232	ko:K05528	ko00513,ko01100,map00513,map01100 M00074	R08599	ko00000,ko00001,ko00002,ko01000,ko01003	
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-	3.1.1.1,3.1.1.1,Ç	ko00983,map00983	R08220,R08255,R08258 RC00041,RC00475,R ko00000,ko00001,ko01000	-	
-	3.2.1.1	ko00500,ko01100,ko04973,map00500,map01100,maj -	R02108,R02112,R11262	ko00000,ko00001,ko01000	
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-	2.4.2.3	ko00240,ko00983,ko01100,map00240,map00983,maj -	R01876,R02484,R08229 RC00063	ko00000,ko00001,ko01000	
-	3.2.1.3	ko00500,ko01100,map00500,map01100	R01790,R01791,R06199	ko00000,ko00001,ko01000	
GO:0000272,GO:0000278,GO:0000281,GO:0000282,Ç 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	R01206,R02334 RC00467	ko00000,ko00001,ko01000	
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GO:0000272,GO:0000278,GO:0000281,GO:0000282,Ç 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	R01206,R02334 RC00467	ko00000,ko00001,ko01000	
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-	3.2.1.99	ko:K06113	-	ko00000,ko01000	
-	3.2.1.99	ko:K06113	-	ko00000,ko01000	
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-	-	ko:K21850	-	ko00000,ko04131	
-	3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	R01206,R02334 RC00467	ko00000,ko00001,ko01000
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GO:0003674,GO:0003824,GO:0004581,GO:0005575,Ç 2.4.1.117	ko:K00729	ko00510,ko01100,map00510,map01100 M00055	R01005	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0004581,GO:0005575,Ç 2.4.1.117	ko:K00729	ko00510,ko01100,map00510,map01100 M00055	R01005	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0005575,GO:0005623,GO:0005886,GO:0016020,Ç 2.4.1.109	ko:K00728	ko00514,ko00515,ko01100,map00514,map00515,maj -	R04072,R07620,R11399 RC00005,RC00059,R ko00000,ko00001,ko01000,ko01003	-	
GO:0005575,GO:0005623,GO:0005886,GO:0016020,Ç 2.4.1.109	ko:K00728	ko00514,ko00515,ko01100,map00514,map00515,maj -	R04072,R07620,R11399 RC00005,RC00059,R ko00000,ko00001,ko01000,ko01003	-	
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GO:0000009,GO:0000030,GO:0000032,GO:0000136,Ç 2.4.1.232	ko:K05528	ko00513,ko01100,map00513,map01100 M00074	R08599	ko00000,ko00001,ko00002,ko01000,ko01003	-
-	ko:K05535	ko00513,ko01100,map00513,map01100 M00074	-	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0000272,GO:0000278,GO:0000281,GO:0000282,Ç 3.2.1.14	ko:K01183	ko00520,ko01100,map00520,map01100	R01206,R02334 RC00467	ko00000,ko00001,ko01000	-
GO:0000009,GO:0000030,GO:0000032,GO:0000136,Ç 2.4.1.232	ko:K05528	ko00513,ko01100,map00513,map01100 M00074	R08599	ko00000,ko00001,ko00002,ko01000,ko01003	-
GO:0003674,GO:0003824,GO:0004553,GO:0004565,Ç 3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0 -	R01105,R01678,R03355 RC00049,RC00452	ko00000,ko00001,ko01000	-
GO:0003674,GO:0003824,GO:0004553,GO:0004565,Ç 3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0 -	R01105,R01678,R03355 RC00049,RC00452	ko00000,ko00001,ko01000	-
GO:0003674,GO:0003824,GO:0004553,GO:0004565,Ç 3.2.1.23	ko:K01190	ko00052,ko00511,ko00600,ko01100,map00052,map0 -	R01105,R01678,R03355 RC00049,RC00452	ko00000,ko00001,ko01000	-
-	2.4.2.30	ko03410,ko04210,ko04212,ko04214,ko04217,map03 -	M00296	ko00000,ko00001,ko00002,ko01000,ko03032,ko0303 -	-
-	3.2.1.99	ko:K06113	-	ko00000,ko01000	-
-	-	ko:K13690	-	ko00000,ko01000,ko01003	-
-	-	ko:K13690	-	ko00000,ko01000,ko01003	-

CAZy	BiGG Reaction	PFAMs	IPR term	IPR description	Blastocladiella emersonii 22665	Candida dubliniensis 11945	Candida dubliniensis 2747
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR036028	SH3-like domain superfamily	2	2	3
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR029044	Nucleotide-diphospho-sugar transferases	2	2	3
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR036028	SH3-like domain superfamily	2	2	3
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR011992	EF-hand domain pair	2	2	3
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR004835	Chitin synthase	2	2	3
GT15	-	Glyco_transf_15	IPR029044	Nucleotide-diphospho-sugar transferases	0	2	2
GT15	-	Glyco_transf_15	IPR002685	Glycosyl transferase, family 15	0	2	2
GT71	-	Mannosyl_trans3	IPR029044	Nucleotide-diphospho-sugar transferases	0	6	5
GH47	-	Glyco_hydro_47	IPR050749	Glycosyl Hydrolase Family 47	0	0	0
GH47	-	Glyco_hydro_47	IPR036026	Seven-hairpin glycosidases	0	0	0
GH16	-	SKN1	IPR016024	Armadillo-type fold	2	2	1
GH16	-	SKN1	IPR013320	Concanavalin A-like lectin/glucanase domain superfar	2	2	1
GH16	-	SKN1	IPR026739	AP complex subunit beta	2	2	1
GH18	-	Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GH18	-	Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH16	-	SKN1	IPR036638	Helix-loop-helix DNA-binding domain superfamily	0	3	3
GH16	-	SKN1	IPR013320	Concanavalin A-like lectin/glucanase domain superfar	0	3	3
GH16	-	SKN1	IPR005629	Beta-glucan synthesis-associated protein Skn1/Kre6/	0	3	3
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR036236	Zinc finger C2H2 superfamily	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR036322	WD40-repeat-containing domain superfamily	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR004835	Chitin synthase	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR036400	Cytochrome b5-like heme/steroid binding domain su	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR036236	Zinc finger C2H2 superfamily	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR027417	P-loop containing nucleoside triphosphate hydrolase	6	0	0
GT2	-	Chitin_synth_2,Cyt-b5,DEK_C,Myosin_	IPR029044	Nucleotide-diphospho-sugar transferases	6	0	0
-	-	Cellulase	IPR050386	Glycosyl Hydrolase 5 (Cellulase A)	0	3	3
-	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	3	3
-	-	Glyco_hydro_17	IPR050732	Beta-glucan modifying enzymes	0	3	2
-	-	Glyco_hydro_17	IPR017853	Glycoside hydrolase superfamily	0	3	2
GT62	-	Anp1	IPR052086	Mannan Polymerase Complex Subunit	0	2	2
GT62	-	Anp1	IPR029044	Nucleotide-diphospho-sugar transferases	0	2	2
GH76	-	Glyco_hydro_76	IPR014480	Mannan endo-1,6-alpha-mannosidase	0	2	2
GH76	-	Glyco_hydro_76	IPR008928	Six-hairpin glycosidase superfamily	0	2	2
GT20	-	Glyco_transf_20	IPR001830	Glycosyl transferase, family 20	1	1	1
GT20	-	Glyco_transf_20	IPR036291	NAD(P)-binding domain superfamily	1	1	1
GT48	-	FKS1_dom1,Glucan_synthase	IPR017853	Glycoside hydrolase superfamily	1	3	3
GT39	IMM904.YAL023C,iMM MIR,PMT,PMT_4TMC		IPR027005	Glycosyltransferase 39-like	1	2	2
GT39	IMM904.YAL023C,iMM MIR,PMT,PMT_4TMC		IPR036300	Mir domain superfamily	1	2	2
GT71	-	Mannosyl_trans3	IPR029044	Nucleotide-diphospho-sugar transferases	1	4	4
GT32	-	Gly_transf_sug	IPR039367	Initiation-specific alpha-1,6-mannosyltransferase Och	4	2	2
GT32	-	Gly_transf_sug	IPR029044	Nucleotide-diphospho-sugar transferases	4	2	2
-	IMM904.YBR019C,iND: Aldose_epim,Epimerase,GDP_Man_De	IPR050360	Major Facilitator Superfamily Sugar Transporters	2	1	1	
-	IMM904.YBR019C,iND: Aldose_epim,Epimerase,GDP_Man_De	IPR036259	MFS transporter superfamily	2	1	1	
-	IMM904.YBR019C,iND: Aldose_epim,Epimerase,GDP_Man_De	IPR036291	NAD(P)-binding domain superfamily	2	1	1	
GT2	IMM904.YBR023C,iND: Chitin_synth_2	IPR004835	Chitin synthase	2	1	1	
GT2	IMM904.YBR023C,iND: Chitin_synth_2	IPR029044	Nucleotide-diphospho-sugar transferases	2	1	1	
GT20	-	Glyco_transf_20,Trehalose_PPase	IPR036026	Seven-hairpin glycosidases	2	1	1
GT20	-	Glyco_transf_20,Trehalose_PPase	IPR001830	Glycosyl transferase, family 20	2	1	1
GT20	-	Glyco_transf_20,Trehalose_PPase	IPR036412	HAD-like superfamily	2	1	1
GT39	-	MIR,PMT,PMT_4TMC	IPR012340	Nucleic acid-binding, OB-fold	0	2	1
GT39	-	MIR,PMT,PMT_4TMC	IPR036300	Mir domain superfamily	0	2	1
GT39	-	MIR,PMT,PMT_4TMC	IPR027005	Glycosyltransferase 39-like	0	2	1
GT24	-	Glyco_transf_8,UDP-g_GGTase	IPR009448	UDP-glucose:Glycoprotein Glucosyltransferase	1	1	0
GT24	-	Glyco_transf_8,UDP-g_GGTase	IPR029044	Nucleotide-diphospho-sugar transferases	1	1	0
GT24	-	Glyco_transf_8,UDP-g_GGTase	IPR027417	P-loop containing nucleoside triphosphate hydrolase	1	1	0
GH16	-	SKN1	IPR013320	Concanavalin A-like lectin/glucanase domain superfar	2	1	0
GH16	-	SKN1	IPR029060	PIN-like domain superfamily	2	1	0
GH16	-	SKN1	IPR023426	Flap endonuclease 1	2	1	0

GH16	-	SKN1	IPR036279	5'-3' exonuclease, C-terminal domain superfamily	2	1	0
GH16	-	SKN1	IPR005629	Beta-glucan synthesis-associated protein Skn1/Kre6/	2	1	0
-	-	Glycos_trans_3N,Glycos_transf_3	IPR005940	Anthraniolate phosphoribosyl transferase	1	1	1
-	-	Glycos_trans_3N,Glycos_transf_3	IPR005940	Anthraniolate phosphoribosyl transferase	1	1	1
-	-	Glycos_trans_3N,Glycos_transf_3	IPR035902	Nucleoside phosphorylase/phosphoribosyltransferase	1	1	1
GT4	-	ALG11_N,Glycos_transf_1	IPR038013	ALG11 mannosyltransferase	1	1	1
GT66	-	STT3	IPR011009	Protein kinase-like domain superfamily	1	1	1
GT66	-	STT3	IPR003674	Oligosaccharyl transferase, STT3 subunit	1	1	1
CE1	-	Esterase	IPR036161	RPB6/omega subunit-like superfamily	1	1	1
CE1	-	Esterase	IPR029058	Alpha/Beta hydrolase fold	1	1	1
CE1	-	Esterase	IPR006111	Archaeal Rpo6/eukaryotic RPB6 RNA polymerase sub	1	1	1
CE1	-	Esterase	IPR014186	S-formylglutathione hydrolase	1	1	1
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR011013	Galactose mutarotase-like domain superfamily	2	2	2
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR017853	Glycoside hydrolase superfamily	2	2	2
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR029044	Nucleotide-diphospho-sugar transferases	2	2	2
-	-	HisG,HisG_C	IPR001348	ATP phosphoribosyltransferase HisG	1	1	1
-	-	HisG,HisG_C	IPR011322	Nitrogen regulatory PII-like, alpha/beta	1	1	1
-	-	HisG,HisG_C	IPR020621	ATP phosphoribosyltransferase HisG, long form	1	1	1
-	-	Pribosyltran	IPR023031	Orotate phosphoribosyltransferase	1	1	0
-	-	Pribosyltran	IPR029057	Phosphoribosyltransferase-like	1	1	0
GT2	-	Glycos_transf_2	IPR029044	Nucleotide-diphospho-sugar transferases	1	1	1
GT2	-	Glycos_transf_2	IPR039528	DPM1-like	1	1	1
GT39	-	MIR,PMT,PMT_4TMC	IPR016024	Armadillo-type fold	1	1	1
GT39	-	MIR,PMT,PMT_4TMC	IPR027005	Glycosyltransferase 39-like	1	1	1
GT39	-	MIR,PMT,PMT_4TMC	IPR036300	Mir domain superfamily	1	1	1
-	-	F_bp_aldolase	IPR006411	Fructose-bisphosphate aldolase, class II, yeast/E. coli	0	1	1
-	-	F_bp_aldolase	IPR036497	Glycolipid transfer protein superfamily	0	1	1
-	-	GATase_6,Pribosyltran	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	0
-	-	GATase_6,Pribosyltran	IPR029057	Phosphoribosyltransferase-like	1	1	0
-	-	GATase_6,Pribosyltran	IPR005854	Amidophosphoribosyltransferase	1	1	0
GT21	-	Glyco_transf_21	IPR025993	Ceramide glucosyltransferase	2	1	1
GT21	-	Glyco_transf_21	IPR029044	Nucleotide-diphospho-sugar transferases	2	1	1
GT4	-	Glyco_transf_4,Glycos_transf_1	IPR027054	Mannosyltransferase ALG2	1	1	1
-	-	UPRTase	IPR029057	Phosphoribosyltransferase-like	2	1	1
-	-	UPRTase	IPR029057	Phosphoribosyltransferase-like	2	1	1
-	-	Ribul_P_3_epim	IPR000056	Ribulose-phosphate 3-epimerase-like	1	1	1
-	-	Ribul_P_3_epim	IPR011060	Ribulose-phosphate binding barrel	1	1	1
GT22	-	Glyco_transf_22	IPR005599	GPI mannosyltransferase	1	1	0
GT22	-	Glyco_transf_22	IPR011008	Dimeric alpha-beta barrel	1	1	1
GT22	-	Glyco_transf_22	IPR005599	GPI mannosyltransferase	1	1	1
GT22	-	Glyco_transf_22			1	1	1
-	-	Glyco_hydro_63,Glyco_hydro_63N	IPR036259	MFS transporter superfamily	1	0	1
-	-	Glyco_hydro_63,Glyco_hydro_63N	IPR004888	Glycoside hydrolase family 63	1	0	1
-	-	Glyco_hydro_63,Glyco_hydro_63N	IPR008928	Six-hairpin glycosidase superfamily	1	0	1
-	-	PNP_UDP_1	IPR035994	Nucleoside phosphorylase superfamily	1	1	1
-	-	PNP_UDP_1	IPR010044	Methylthioadenosine phosphorylase (MTAP)	1	1	1
-	-	PNP_UDP_1	IPR010044	Methylthioadenosine phosphorylase (MTAP)	1	1	1
GT50	-	Mannosyl_trans	IPR007704	GPI mannosyltransferase 1	1	1	2
GH13	-	GDE_C,hDGE_amylase,hGDE_N,hGDE_	IPR017853	Glycoside hydrolase superfamily	2	2	1
GH13	-	GDE_C,hDGE_amylase,hGDE_N,hGDE_	IPR008928	Six-hairpin glycosidase superfamily	2	2	1
GH13	-	GDE_C,hDGE_amylase,hGDE_N,hGDE_	IPR010401	Glycogen debranching enzyme	2	2	1
GT4	-	Glycos_transf_1,PIGA	IPR016024	Armadillo-type fold	1	1	1
GT20	iMM904.YMR261C,iND	Glyco_transf_20,Trehalose_PPase	IPR036412	HAD-like superfamily	0	1	1
GT20	iMM904.YMR261C,iND	Glyco_transf_20,Trehalose_PPase	IPR011009	Protein kinase-like domain superfamily	0	1	1
GT20	iMM904.YMR261C,iND	Glyco_transf_20,Trehalose_PPase	IPR001830	Glycosyl transferase, family 20	0	1	1
-	-	Phage_lysozyme,SH3_3	IPR051018	Bacteriophage Glycosyl Hydrolase 24	0	0	0
-	-	Phage_lysozyme,SH3_3	IPR034690	Endolysin T4 type	0	0	0
-	-	Phage_lysozyme,SH3_3	IPR023346	Lysozyme-like domain superfamily	0	0	0
GT2	-	Glycos_transf_2	IPR029044	Nucleotide-diphospho-sugar transferases	1	1	1

GT57	-	Alg6_Alg8	IPR004856	Glycosyl transferase, ALG6/ALG8	1	1	1
GT3	-	Glycogen_syn	IPR036890	Histidine kinase/HSP90-like ATPase superfamily	1	1	1
GT3	-	Glycogen_syn	IPR008631	Glycogen synthase	1	1	1
GT33	-	Glyco_trans_1_4,Glyco_trans_4_4,Glyc	IPR026051	Chitobiosyldiphosphodolichol beta-mannosyltransfer:	1	0	0
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR050053	ATPase alpha/beta chains	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR005722	ATP synthase, F1 complex, beta subunit	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR036121	ATPase, F1/V1/A1 complex, alpha/beta subunit, N-tei	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR027417	P-loop containing nucleoside triphosphate hydrolase	1	1	1
-	-	QRPTase_C,QRPTase_N	IPR027277	Nicotinate-nucleotide pyrophosphorylase/Putative py	1	1	1
-	-	QRPTase_C,QRPTase_N	IPR036068	Nicotinate phosphoribosyltransferase-like, C-termina	1	1	1
GH47	-	Glyco_hydro_47	IPR050749	Glycosyl Hydrolase Family 47	0	1	1
GH47	-	Glyco_hydro_47	IPR036026	Seven-hairpin glycosidases	0	1	1
GT1	-	GRAM,Glyco_transf_28,UDPGT	IPR050426	Glycosyltransferase 28	2	1	1
GT35	-	Phosphorylase	IPR000811	Glycosyl transferase, family 35	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR005722	ATP synthase, F1 complex, beta subunit	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR017853	Glycoside hydrolase superfamily	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR036121	ATPase, F1/V1/A1 complex, alpha/beta subunit, N-tei	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR014756	Immunoglobulin E-set	1	1	1
CBM48,GH1:-	-	ATP-synt_ab,ATP-synt_ab_N	IPR027417	P-loop containing nucleoside triphosphate hydrolase	1	1	1
GT34	-	Glyco_transf_34	IPR008630	Glycosyltransferase 34	0	1	1
-	-	PNP_UDP_1	IPR035994	Nucleoside phosphorylase superfamily	1	1	1
-	-	PNP_UDP_1	IPR011268	Purine nucleoside phosphorylase	1	1	1
GT57	-	Alg6_Alg8	IPR004856	Glycosyl transferase, ALG6/ALG8	1	1	0
GH38	-	Glyco_hydro_47,PA	IPR036026	Seven-hairpin glycosidases	1	1	1
GH38	-	Glyco_hydro_47,PA	IPR044674	ER degradation-enhancing alpha-mannosidase-like pr	1	1	1
-	-	Glyco_hydro_17	IPR050732	Beta-glucan modifying enzymes	0	1	1
-	-	Glyco_hydro_17	IPR017853	Glycoside hydrolase superfamily	0	1	1
-	-	Glyco_hydro_17	IPR023395	Mitochondrial carrier domain superfamily	0	1	1
GH38	-	Alpha-mann_mid,Glyco_hydro_38,Glyc	IPR011013	Galactose mutarotase-like domain superfamily	0	1	1
GH38	-	Alpha-mann_mid,Glyco_hydro_38,Glyc	IPR011330	Glycoside hydrolase/deacetylase, beta/alpha-barrel	0	1	1
GH38	-	Alpha-mann_mid,Glyco_hydro_38,Glyc	IPR028995	Glycoside hydrolase families 57/38, central domain su	0	1	1
GT22	-	Glyco_transf_22	IPR005599	GPI mannosyltransferase	1	1	1
GT58	-	ALG3	IPR007873	Glycosyltransferase, ALG3	1	1	0
-	-	TGT	IPR036511	Queuine tRNA-ribosyltransferase-like	1	0	0
-	-	TGT	IPR004803	tRNA-guanine transglycosylase	1	0	0
GT1	-	Alg14	IPR013969	Oligosaccharide biosynthesis protein Alg14-like	1	1	1
GT34	-	Glyco_transf_34	IPR008630	Glycosyltransferase 34	0	1	1
-	-	Glyco_hydro_2	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	1	2
-	-	Glyco_hydro_2	IPR017853	Glycoside hydrolase superfamily	0	1	2
-	-	Glyco_hydro_2	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	1	2
-	-	Glyco_hydro_2	IPR050887	Beta-mannosidase glycosyl hydrolases	0	1	2
-	-	Glyco_hydro_2	IPR008979	Galactose-binding-like domain superfamily	0	1	2
GT62	-	Anp1	IPR052086	Mannan Polymerase Complex Subunit	0	1	1
GT62	-	Anp1	IPR029044	Nucleotide-diphospho-sugar transferases	0	1	1
GH18	-	CBM_1,CBM_19,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	CBM_1,CBM_19,Glyco_hydro_18	IPR050542	Glycosyl Hydrolase 18 Family Chitinases	0	0	0
GH37	-	Glyco_hydro_65C,Glyco_hydro_65N,GI	IPR011013	Galactose mutarotase-like domain superfamily	0	1	1
GH37	-	Glyco_hydro_65C,Glyco_hydro_65N,GI	IPR008928	Six-hairpin glycosidase superfamily	0	1	1
GH5,GH9	-	AMP-binding,AMP-binding_C			0	0	0
-	-	Acetyltransf_1,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain supe	0	1	1
-	-	Acetyltransf_1,Glyco_hydro_3	IPR016181	Acyl-CoA N-acyltransferase	0	1	1
-	-	Acetyltransf_1,Glyco_hydro_3	IPR017853	Glycoside hydrolase superfamily	0	1	1
-	-	Acetyltransf_1,Glyco_hydro_3	IPR050226	NagZ Beta-hexosaminidase	0	1	1
-	-	Glyco_hydro_17	IPR017853	Glycoside hydrolase superfamily	0	0	1
-	-	Glyco_hydro_17	IPR050732	Beta-glucan modifying enzymes	0	0	1
GT59	-	DIE2_ALG10	IPR016900	Alpha-2-glucosyltransferase Alg10	1	1	1
CBM48,GH1:-	-	Alpha-amylase,Alpha-amylase_C,CBM_	IPR052356	Thiol S-methyltransferase	0	0	0
CBM48,GH1:-	-	Alpha-amylase,Alpha-amylase_C,CBM_	IPR029063	S-adenosyl-L-methionine-dependent methyltransfera	0	0	0
GT91	-	DUF3589	IPR036259	MFS transporter superfamily	0	8	7

-	-	BRCT,PARP,PARP_reg,WGR	IPR036420	BRCT domain superfamily	0	0	0
-	-	BRCT,PARP,PARP_reg,WGR	IPR050800	ADP-ribosyltransferase diphtheria toxin-like	0	0	0
-	-	BRCT,PARP,PARP_reg,WGR	IPR036616	Poly(ADP-ribose) polymerase, regulatory domain sup	0	0	0
-	-	BRCT,PARP,PARP_reg,WGR	IPR036930	WGR domain superfamily	0	0	0
-	-	TGT	IPR036511	Queuine tRNA-ribosyltransferase-like	1	0	0
-	-	TGT	IPR050852	Queuine tRNA-ribosyltransferase	1	0	0
-	-	TGT	IPR028592	Queuine tRNA-ribosyltransferase accessory subunit C	1	0	0
-	-	Acetyltransf_1,Acetyltransf_7,Glyco_h	IPR016181	Acyl-CoA N-acyltransferase	0	0	0
-	-	Acetyltransf_1,Acetyltransf_7,Glyco_h	IPR050226	NagZ Beta-hexosaminidase	0	0	0
-	-	Acetyltransf_1,Acetyltransf_7,Glyco_h	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	UPRTase	IPR029057	Phosphoribosyltransferase-like	0	0	0
-	-	UPRTase	IPR050054	Uracil phosphoribosyltransferase/Adenine phosphori	0	0	0
GH13	-	Alpha-amylase	IPR017853	Glycoside hydrolase superfamily	0	2	2
-	-	Cellulase	IPR050386	Glycosyl Hydrolase 5 (Cellulase A)	0	0	0
-	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	0	0
GT4	-	Glycos_transf_1	IPR052078	Trehalose Metabolism Glycosyltransferase	0	0	0
GT4	-	Glycos_transf_1	IPR036322	WD40-repeat-containing domain superfamily	0	0	0
-	-	Aldose_epim	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR053214	Secreted chitinase LysM12-like	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR036861	Endochitinase-like superfamily	0	0	0
GH37	-	Trehalase,Trehalase_Ca-bi	IPR001661	Glycoside hydrolase, family 37	1	0	1
GH37	-	Trehalase,Trehalase_Ca-bi	IPR027534	Large ribosomal subunit protein P1/P2	1	0	1
GH37	-	Trehalase,Trehalase_Ca-bi	IPR008928	Six-hairpin glycosidase superfamily	1	0	1
GT91	-	DUF3589			0	2	1
GT2	-	DPM2	IPR009914	Dolichol phosphate-mannose biosynthesis regulatory	1	0	1
-	-	Cellulase	IPR050386	Glycosyl Hydrolase 5 (Cellulase A)	0	1	1
-	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	1	1
GH18	-	Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GH20	-	Glyco_hydro_20,Glycohydro_20b2	IPR025705	Beta-hexosaminidase	0	0	0
GH20	-	Glyco_hydro_20,Glycohydro_20b2	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH20	-	Glyco_hydro_20,Glycohydro_20b2	IPR029018	Beta-hexosaminidase-like, domain 2	0	0	0
-	-	VIT,VWA_3	IPR036465	von Willebrand factor A-like domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GT2	-	Chitin_synth_2	IPR029044	Nucleotide-diphospho-sugar transferases	0	0	0
GT2	-	Chitin_synth_2	IPR004835	Chitin synthase	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR050347	Bacterial Beta-galactosidase	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR008979	Galactose-binding-like domain superfamily	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	0	0
-	-	Bgal_small_N,DUF4981,Glyco_hydro_2	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR008979	Galactose-binding-like domain superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR027417	P-loop containing nucleoside triphosphate hydrolase	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR001944	Glycoside hydrolase, family 35	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR008979	Galactose-binding-like domain superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR036833	Beta-galactosidase, domain 3 superfamily	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR050288	Cellulose-degrading glycosyl hydrolase 3	0	1	1
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR017853	Glycoside hydrolase superfamily	0	1	1
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain supe	0	1	1
-	-	Glyco_hydro_2,Glyco_hydro_2_C,Glyc	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	0	0
-	-	Glyco_hydro_2,Glyco_hydro_2_C,Glyc	IPR036156	Beta-Galactosidase/glucuronidase domain superfamil	0	0	0
-	-	Glyco_hydro_2,Glyco_hydro_2_C,Glyc	IPR043534	Exo-beta-D-glucosaminidase/Endo-beta-mannosidase	0	0	0

-	-	UPRTase	IPR011502	Nucleoporin Nup85-like	0	1	1
GT2	-	Chitin_synth_2	IPR029044	Nucleotide-diphospho-sugar transferases	9	0	0
GT2	-	Chitin_synth_2	IPR004835	Chitin synthase	9	0	0
GT2	-	Chitin_synth_1,Chitin_synth_1N	IPR004835	Chitin synthase	0	0	0
-	-	Glyco_hydro_67C,Glyco_hydro_67M,G	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	Glyco_hydro_67C,Glyco_hydro_67M,G	IPR029018	Beta-hexosaminidase-like, domain 2	0	0	0
-	-	Glyco_hydro_36C,Glyco_hydro_36N,M	IPR050985	Alpha-glycosidase and related enzymes	0	0	0
-	-	Glyco_hydro_36C,Glyco_hydro_36N,M	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH43	-	APH	IPR011009	Protein kinase-like domain superfamily	0	0	0
GH43	-	APH	IPR051678	Aminoglycoside Phosphotransferase Enzymes	0	0	0
GH51	-	Alpha-L-AF_C	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH1	-	Glyco_hydro_1	IPR001360	Glycoside hydrolase family 1	0	0	0
GH1	-	Glyco_hydro_1	IPR017853	Glycoside hydrolase superfamily	0	0	0
GT5	-	Alpha-amylase,Glyco_transf_5,Glycos_	IPR017853	Glycoside hydrolase superfamily	0	0	0
GT17	-	Glyco_transf_17	IPR006813	Glycosyl transferase, family 17	0	0	0
-	-	Aldose_epim	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
GT4	-	Glycos_transf_1,PIGA	IPR016024	Armadillo-type fold	0	0	0
GT4	-	Glycos_transf_1,PIGA	IPR051954	tRNA (32-2'-O)-methyltransferase regulator THADA	0	0	0
GH18	-	Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GH18	-	Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
PL4	-	CBM-like,fn3_3	IPR008928	Six-hairpin glycosidase superfamily	0	0	0
PL4	-	CBM-like,fn3_3	IPR008979	Galactose-binding-like domain superfamily	0	0	0
PL4	-	CBM-like,fn3_3	IPR052043	Polysaccharide Degradation Enzymes	0	0	0
PL4	-	CBM-like,fn3_3	IPR013784	Carbohydrate-binding-like fold	0	0	0
PL4	-	CBM-like,fn3_3	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
-	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	Cellulase	IPR050386	Glycosyl Hydrolase 5 (Cellulase A)	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18			0	0	0
GH5,GH9	-	Glyco_hydro_9	IPR008928	Six-hairpin glycosidase superfamily	0	0	0
GT15	-	Glyco_transf_15	IPR029044	Nucleotide-diphospho-sugar transferases	0	1	1
GT15	-	Glyco_transf_15	IPR002685	Glycosyl transferase, family 15	0	1	1
GT62	-	Anp1	IPR052086	Mannan Polymerase Complex Subunit	0	1	1
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR050314	Glycosyl Hydrolase Family 18	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18	IPR036861	Endochitinase-like superfamily	0	0	0
GH105	-	Glyco_hydro_88	IPR008928	Six-hairpin glycosidase superfamily	0	0	0
GH105	-	Glyco_hydro_88	IPR052043	Polysaccharide Degradation Enzymes	0	0	0
GH32	-	Glyco_hydro_32C,Glyco_hydro_32N	IPR023296	Glycosyl hydrolase, five-bladed beta-propeller domain	0	0	0
GH32	-	Glyco_hydro_32C,Glyco_hydro_32N	IPR013320	Concanavalin A-like lectin/glucanase domain superfamily	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31	IPR050985	Alpha-glycosidase and related enzymes	0	0	0
GH3	-	Cyclin_N	IPR036915	Cyclin-like superfamily	0	1	0
GH3	-	Cyclin_N	IPR036915	Cyclin-like superfamily	0	1	0
GH3	-	Cyclin_N	IPR043198	Cyclin/Cyclin-like subunit Ssn8	0	1	0
CBM48,GH11	-	ATP-synt_ab,ATP-synt_ab_N			0	0	0
GT41	-	DUF563	IPR007657	Glycosyltransferase 61	0	0	0
GH20	-	Glyco_hydro_20,Glyco_hydro_20b	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH20	-	Glyco_hydro_20,Glyco_hydro_20b	IPR029018	Beta-hexosaminidase-like, domain 2	0	0	0
GH20	-	Glyco_hydro_20,Glyco_hydro_20b	IPR052764	Glycosyl Hydrolase 20 Enzymes	0	0	0
GH51	-	Alpha-L-AF_C,CBM_4_9	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH51	-	Alpha-L-AF_C,CBM_4_9	IPR051563	Glycosyl Hydrolase Family 51	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR050288	Cellulose-degrading glycosyl hydrolase 3	0	0	0

GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain supe	0	0	0
GT57	-	Alg6_Alg8	IPR004856	Glycosyl transferase, ALG6/ALG8	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR053214	Secreted chitinase LysM12-like	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR036779	LysM domain superfamily	0	0	0
GT2	-	iMM904.YBR023C,IND: Chitin_synth_2			0	0	0
GH43	-	APH	IPR011009	Protein kinase-like domain superfamily	0	0	0
GH43	-	APH	IPR051678	Aminoglycoside Phosphotransferase Enzymes	0	0	0
GT2	-	Chitin_synth_1,Chitin_synth_1N,Chitin	IPR029044	Nucleotide-diphospho-sugar transferases	4	0	0
GT2	-	Chitin_synth_1,Chitin_synth_1N,Chitin	IPR004835	Chitin synthase	4	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR017853	Glycoside hydrolase superfamily	0	1	0
-	-	Queuosine_synth	IPR003699	S-adenosylmethionine:tRNA ribosyltransferase-isome	0	0	0
-	-	Queuosine_synth	IPR036100	S-adenosylmethionine:tRNA ribosyltransferase-isome	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR029070	Chitinase insertion domain superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR053214	Secreted chitinase LysM12-like	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18			0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain supe	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR050288	Cellulose-degrading glycosyl hydrolase 3	0	0	0
GH12	-	Glyco_hydro_12	IPR013320	Concanavalin A-like lectin/glucanase domain superfar	0	0	0
GH12	-	Glyco_hydro_12	IPR002594	Glycoside hydrolase family 12	0	0	0
GH6	-	CBM_1,Glyco_hydro_6	IPR016288	1, 4-beta cellobiohydrolase	0	0	0
GH6	-	CBM_1,Glyco_hydro_6	IPR036434	1, 4-beta cellobiohydrolase superfamily	0	0	0
GH43	-	Glyco_hydro_43	IPR023296	Glycosyl hydrolase, five-bladed beta-propeller domai	0	0	0
GH43	-	Glyco_hydro_43	IPR050727	Glycosyl hydrolase 43 family arabinanases	0	0	0
GH32	-	Glyco_hydro_32C,Glyco_hydro_32N	IPR013320	Concanavalin A-like lectin/glucanase domain superfar	0	0	0
GH32	-	Glyco_hydro_32C,Glyco_hydro_32N	IPR023296	Glycosyl hydrolase, five-bladed beta-propeller domai	0	0	0
GH13	-	Alpha-amylase,DUF1966	IPR017853	Glycoside hydrolase superfamily	0	0	0
GT4	-	Glycos_transf_1,PIGA	IPR051954	tRNA (32-2'-O)-methyltransferase regulator THADA	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM			0	0	0
GT18	-	Glyco_transf_18	IPR052105	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglu	0	0	0
-	-	Glyco_hydro_71			0	0	0
GT18	-	Glyco_transf_18	IPR052105	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglu	0	0	0
GH47	-	Glyco_hydro_47	IPR036026	Seven-hairpin glycosidases	0	0	0
GH47	-	Glyco_hydro_47	IPR050749	Glycosyl Hydrolase Family 47	0	0	0
GT41	-	DUF563	IPR007657	Glycosyltransferase 61	0	0	0
-	-	Cellulase	IPR050386	Glycosyl Hydrolase 5 (Cellulase A)	0	0	0
-	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	UPRTase	IPR016024	Armadillo-type fold	0	0	0
GT69	-	CAP59_mtransfer	IPR021047	Mannosyltransferase 1, CMT1	0	0	0
GH43	-	Glyco_hydro_43	IPR036457	PPM-type phosphatase-like domain superfamily	0	0	0
GH43	-	Glyco_hydro_43	IPR050727	Glycosyl hydrolase 43 family arabinanases	0	0	0
GH43	-	Glyco_hydro_43	IPR023296	Glycosyl hydrolase, five-bladed beta-propeller domai	0	0	0
-	-	Glyco_hydro_28	IPR050434	Glycosyl hydrolase family 28	0	0	0
-	-	Glyco_hydro_28	IPR011050	Pectin lyase fold/virulence factor	0	0	0
GT22	-	DUF3445,Glyco_transf_22			0	0	0
GH18	-	CBM_19,Flocculin_t3,Glyco_hydro_18	IPR036861	Endochitinase-like superfamily	0	0	0
GH18	-	CBM_19,Flocculin_t3,Glyco_hydro_18	IPR050542	Glycosyl Hydrolase 18 Family Chitinases	0	0	0
GH18	-	CBM_19,Flocculin_t3,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR011013	Galactose mutarotase-like domain superfamily	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR050288	Cellulose-degrading glycosyl hydrolase 3	0	0	0
GH3	-	Fn3-like,Glyco_hydro_3,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain supe	0	0	0
GH5,GH9	-	Cellulase	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR053214	Secreted chitinase LysM12-like	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18,LysM	IPR029070	Chitinase insertion domain superfamily	0	0	0

GT39	-	MIR,PMT	IPR027005	Glycosyltransferase 39-like	0	0	0
GT39	-	MIR,PMT	IPR036300	Mir domain superfamily	0	0	0
GH18	-	CBM_1,CBM_19,Glyco_hydro_18			0	0	0
GT91	-	DUF3589			0	0	0
GT32	-	Gly_transf_sug	IPR029044	Nucleotide-diphospho-sugar transferases	0	0	0
GT32	-	Gly_transf_sug	IPR039367	Initiation-specific alpha-1,6-mannosyltransferase Och	0	0	0
GT31	-	Galactosyl_T	IPR002659	Glycosyl transferase, family 31	0	0	0
CE10	-	COesterase	IPR029058	Alpha/Beta hydrolase fold	0	0	0
GH13	-	Alpha-amylase,Alpha-amylase_C,DUF1	IPR017853	Glycoside hydrolase superfamily	0	0	0
GT31	-	Galactosyl_T			0	0	0
-	-	PNP_UDP_1	IPR035994	Nucleoside phosphorylase superfamily	1	0	0
GH15	-	-			0	1	0
GH18	-	CBM_1,CBM_19,Glyco_hydro_18			0	0	1
GH37	-	Trehalase,Trehalase_Ca-bi			0	0	0
GH18	-	CBM_19,Flocculin_t3,Glyco_hydro_18			0	0	0
CBM48,GH11	-	Alpha-amylase,Alpha-amylase_C,CBM_1	IPR014756	Immunoglobulin E-set	0	0	0
GH43	-	Glyco_hydro_43	IPR050727	Glycosyl hydrolase 43 family arabinanases	0	0	0
GH43	-	Glyco_hydro_43	IPR023296	Glycosyl hydrolase, five-bladed beta-propeller domain	0	0	0
GH31	-	Gal_mutarotas_2,Glyco_hydro_31,NtC	IPR017853	Glycoside hydrolase superfamily	0	0	0
GH16	-	SKN1			0	0	0
GH18	-	Chitin_bind_1,Glyco_hydro_18			0	0	0
GT2	-	Chitin_synth_1,Chitin_synth_1N			0	0	0
-	-	Aldose_epim			0	0	0
GT2	-	Glycos_transf_2	IPR050188	RluA Pseudouridine Synthase	0	0	0
GT2	-	Glycos_transf_2	IPR020103	Pseudouridine synthase, catalytic domain superfamily	0	0	0
GT39	-	MIR,PMT,PMT_4TMC	IPR027005	Glycosyltransferase 39-like	0	0	0
GT39	-	MIR,PMT,PMT_4TMC	IPR036300	Mir domain superfamily	0	0	0
GH37	-	Trehalase,Trehalase_Ca-bi			0	0	0
GT71	-	Mannosyl_trans3			0	0	0
GT32	-	Gly_transf_sug	IPR039367	Initiation-specific alpha-1,6-mannosyltransferase Och	0	0	0
GT71	-	Mannosyl_trans3			0	0	0
GH18	-	CBM_1,CBM_19,Glyco_hydro_18			0	0	0
GT32	-	Gly_transf_sug			0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR008979	Galactose-binding-like domain superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR017853	Glycoside hydrolase superfamily	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR001944	Glycoside hydrolase, family 35	0	0	0
-	-	BetaGal_dom2,BetaGal_dom3,BetaGal	IPR008979	Galactose-binding-like domain superfamily	0	0	0
-	-	BRCT,PARP,PARP_reg,WGR	IPR050800	ADP-ribosyltransferase diphtheria toxin-like	0	0	0
GH43	-	APH			0	0	0
GT69	-	CAP59_mtransfer	IPR021047	Mannosyltransferase 1, CMT1	0	0	0
GT69	-	CAP59_mtransfer			0	0	0

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[illegible]

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[illegible]

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Trichophyton violaceum 120316	Trichophyton violaceum 51763	Trichophyton violaceum 73088	Trichosporon ovoides 4098	Trichosporon ovoides 7612	Trichosporon ovoides 9430	Total
4	4	4	4	4	9	189
4	4	4	4	4	9	189
4	4	4	4	4	9	189
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4	4	4	4	4	9	189
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3	3	3	1	0	2	122
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2	2	3	0	0	0	116
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1	1	1	1	1	2	61

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