

Orthogroup	seed ortholog	evalue	score	eggNOG OGs	max annot lvl	COG category	Description	Preferred name
OG0005714	63402.XP_003172339.1	8.99E-60	206	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG 4751 Fungi	S		biological adhesion	-
OG0006735	82508.K1VM76	2.08E-112	365	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG 4751 Fungi	S		biological adhesion	-
OG0009836	1392244.V5EU92	0.000000444	63.5	KOG1836@1 root,KOG1836@2759 Eukaryota,3AA1F 4751 Fungi	S		biological adhesion	-
OG0011053	1392244.V5EU92	0.000378	53.5	KOG1836@1 root,KOG1836@2759 Eukaryota,3AA1F 4751 Fungi	S		biological adhesion	-
OG0012131	430998.XP_007678228.1	3.56E-102	354	KOG1836@1 root,KOG1836@2759 Eukaryota,39UPC 4751 Fungi	S		biological adhesion	-
OG0012757	82508.K1WDK1	5.55E-225	668	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG 4751 Fungi	S		biological adhesion	-
OG0015998	82508.K1VVS8	4.6E-156	502	KOG1836@1 root,KOG1836@2759 Eukaryota,39QB1 4751 Fungi	W		biological adhesion	-
OG0016064	82508.K1WOG1	3.23E-60	225	KOG1836@1 root,KOG1836@2759 Eukaryota,3AA1F 4751 Fungi	S		biological adhesion	-
OG0014954	5478.XP_446542.1	2.53E-251	706	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		to Saccharomyces cerevisiae SAG1 (YJR004C)	-
OG0014954	5478.XP_446542.1	2.53E-251	706	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		to Saccharomyces cerevisiae SAG1 (YJR004C)	-
OG0011484	42374.XP_002421133.1	2.05E-199	593	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		Agglutinin-like protein	-
OG0013855	42374.XP_002419518.1	2.03E-296	908	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		Agglutinin-like protein	-
OG0017091	5480.G8BJ60	7.22E-154	501	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		Agglutinin-like protein	ALS3
OG0017106	5482.XP_002547996.1	1.4E-42	154	299AS@1 root,2RGCG@2759 Eukaryota,39WNJ@33 4751 Fungi	S		Cell-wall agglutinin N-terminal ligand-sugar binding	-
OG0018270	4909.A0A099NZM2	1.07E-237	654	2BJT2@1 root,2S1H2@2759 Eukaryota,3A55M@331 4751 Fungi	S		Some similarities with uniprot P08640 Saccharomyces	-
OG0018270	4909.A0A099NZM2	1.07E-237	654	2BJT2@1 root,2S1H2@2759 Eukaryota,3A55M@331 4751 Fungi	S		Some similarities with uniprot P08640 Saccharomyces	-
OG0018619	4909.A0A099NW14	3.29E-126	381	2BJT2@1 root,2S1H2@2759 Eukaryota,3A55M@331 4751 Fungi	S		cfem domain-containing protein	-
OG0018932	4909.A0A099NW14	7.83E-20	89	2BJT2@1 root,2S1H2@2759 Eukaryota,3A55M@331 4751 Fungi	S		cfem domain-containing protein	-
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
OG0017120	63402.XP_003172876.1	0.00094	47	KOG4701@1 root,KOG4701@2759 Eukaryota,38GW 4751 Fungi	G		Glycosyl hydrolases family 18	CHT2
OG0015866	82508.K1WUU1	0.00000176	54.3	2E9CW@1 root,2SFRC@2759 Eukaryota,3A7JQ@331 4751 Fungi	O		Ricin-type beta-trefoil	-
OG0016085	82508.K1WUU1	0.00000481	52.4	2E9CW@1 root,2SFRC@2759 Eukaryota,3A7JQ@331 4751 Fungi	O		Ricin-type beta-trefoil	-
OG0019618	82508.K1WUU1	4.22E-67	212	2E9CW@1 root,2SFRC@2759 Eukaryota,3A7JQ@331 4751 Fungi	O		Ricin-type beta-trefoil	-
OG0009008	5037.XP_001544598.1	9.01E-22	109	2CMXB@1 root,2QSI5@2759 Eukaryota,3ADD7@33 4751 Fungi	S		structural molecule activity	RBT1
OG0013961	63418.F2Q268	2.44E-77	251	2CMXB@1 root,2QSI5@2759 Eukaryota,3ADD7@33 4751 Fungi	S		structural molecule activity	RBT1
OG0018148	5478.XP_002999571.1	0	1023	2CMXB@1 root,2QSI5@2759 Eukaryota,3ADD7@33 4751 Fungi	S		structural molecule activity	RBT1
OG0006811	82508.K1VI73	0	1615	COG2335@1 root,KOG1437@2759 Eukaryota,39KPA 4751 Fungi	MW		Four repeated domains in the Fasciclin I family of pro-	-
OG0007702	5480.G8B8X6	0	1913	COG2335@1 root,KOG1437@2759 Eukaryota,38HGI 4751 Fungi	MW		Four repeated domains in the Fasciclin I family of pro-	-
OG0012888	82508.K1VXF6	4.63E-220	621	2BCVV@1 root,2S1OZ@2759 Eukaryota,39KFH@331 4751 Fungi	S		Four repeated domains in the Fasciclin I family of pro-	-
OG0009588	5482.XP_002545368.1	3.08E-243	688	2CMI8@1 root,2QQEE@2759 Eukaryota,38YNS@33: 4751 Fungi	S		Flocculin type 3 repeat	-
OG0010210	42374.XP_002419233.1	5.66E-109	352	28HR7@1 root,2QQI@2759 Eukaryota,38V02@331 4751 Fungi	S		Flocculin type 3 repeat	-
OG0010239	42374.XP_002419233.1	7.94E-133	423	28HR7@1 root,2QQI@2759 Eukaryota,38V02@331 4751 Fungi	S		Flocculin type 3 repeat	-
OG0013770	5479.M3J535	6.93E-50	185	2CYJH@1 root,2S4SV@2759 Eukaryota,3A7MH@33: 4751 Fungi	S		Flocculin type 3 repeat	YWP1
OG0018124	5478.XP_449851.1	1.07E-29	109	2CPDS@1 root,2S42T@2759 Eukaryota,3A77B@331 4751 Fungi	S		to Saccharomyces cerevisiae YDR134C (Scer_YGOB_Y: CCW12	-
OG0012469	4909.A0A099NWA7	0	1655	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
OG0018324	4909.A0A099NWW7	1.38E-75	240	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
OG0018325	4909.A0A099NWW7	1.8E-145	436	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
OG0018673	4909.A0A099NXQ4	1.15E-189	555	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
OG0018702	4909.A0A099P0F8	5.83E-71	240	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
OG0012458	5478.XP_002999584.1	2.89E-205	617	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015320	5478.XP_445192.1	0	1085	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015386	5478.XP_449203.2	3.76E-295	853	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015485	5478.XP_002999534.1	1.11E-85	310	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015525	5478.XP_002999597.1	0	938	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015556	5478.XP_002999584.1	3.24E-112	367	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015561	5478.XP_002999534.1	0	1095	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015577	5478.XP_445761.1	6.8E-21	105	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0015582	5478.XP_446805.1	2.71E-167	494	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0018151	5478.XP_002999534.1	6.51E-37	139	2D0UM@1 root,2SFJJ@2759 Eukaryota,39VPT@331 4751 Fungi	S		some similarities with uniprot	-
OG0014969	5478.XP_447567.2	1.96E-280	820	2CM9P@1 root,2QPQC@2759 Eukaryota,39SM9@3: 4751 Fungi	S		some similarities with uniprot	-
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	-
OG0012211	83344.XP_007926532.1	0	1113	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@: 4751 Fungi	G		Glycoside hydrolase family 3 protein	-
OG0012211	83344.XP_007926532.1	0	1113	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@: 4751 Fungi	G		Glycoside hydrolase family 3 protein	-
OG0012211	83344.XP_007926532.1	0	1113	COG1472@1 root,2QR4D@2759 Eukaryota,38FS1@: 4751 Fungi	G		Glycoside hydrolase family 3 protein	-
OG0015562	5478.XP_445700.1	6.86E-257	726	2E17R@1 root,2S8JT@2759 Eukaryota,3AA98@331: 33154 Opisthok S	S		some similarities with uniprot	-

OG0015572	5478.XP_445189.1	3.09E-18	90.9	2E17R@1 root,2S8JT@2759 Eukaryota,3AA98@33154751 Fungi	O	Pfam:PA14_2	-
OG0014482	430998.XP_007681652.1	0.000108	52.4	2B92N@1 root,2S0T3@2759 Eukaryota,3A9YN@3314751 Fungi	S	Pheromone	-
OG0015591	5478.XP_447815.1	7.82E-47	177	KOG3544@1 root,KOG3544@2759 Eukaryota,39M1:33154 Opisthokc	W	Hyphally regulated cell wall protein N-terminal	-
OG0017424	430998.XP_007681652.1	0.000102	52.4	2B92N@1 root,2S0T3@2759 Eukaryota,3A9YN@3314751 Fungi	S	Pheromone	-
OG0018144	5478.XP_447816.1	2.57E-204	602	KOG3544@1 root,KOG3544@2759 Eukaryota,39M1:33154 Opisthokc	W	Hyphally regulated cell wall protein N-terminal	-
OG0018145	5478.XP_447815.1	5.13E-12	75.1	KOG3544@1 root,KOG3544@2759 Eukaryota,39M1:33154 Opisthokc	W	Hyphally regulated cell wall protein N-terminal	-
OG0002832	42374.XP_002421668.1	0	1985	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG4751 Fungi	S	cell wall protein	-
OG0010295	42374.XP_002421505.1	3.33E-155	495	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG4751 Fungi	S	Hyphally regulated cell wall protein N-terminal	-
OG0013748	42374.XP_002421505.1	1.48E-115	406	KOG1216@1 root,KOG1216@2759 Eukaryota,38BYG4751 Fungi	S	Hyphally regulated cell wall protein N-terminal	-
OG0009674	5480.G8B4Z6	0	1389	28VHC@1 root,2R28W@2759 Eukaryota,38D9E@334751 Fungi	S	Lisencephaly type-1-like homology motif	FLO8
OG0010320	5478.XP_446512.1	0	1764	28VHC@1 root,2R28W@2759 Eukaryota,38D9E@334751 Fungi	K	to Saccharomyces cerevisiae FLO8 (YER109C)	FLO8
OG0018967	4909.A0A099P5I1	1.13E-77	257	28VHC@1 root,2R28W@2759 Eukaryota,38D9E@334751 Fungi	S	Lisencephaly type-1-like homology motif	FLO8
OG0015139	113608.XP_003684663.1	1.6E-10	60.1	2E1M7@1 root,2S8XT@2759 Eukaryota,3AAZX@3314751 Fungi	K	to Saccharomyces cerevisiae RPA14 (YDR156W)	-
OG0003454							

PFAMs	IPR term	IPR description	Blastocladiella emersonii 22665	Candida dubliniensis 11945	Candida dubliniensis 2747	Candida dubliniensis 8501
-			0	0	0	0
-	IPR039295	Signaling mucin MSB2	0	0	0	0
-			0	0	0	0
-			0	0	0	0
-			0	0	0	0
-			0	0	0	0
-			0	0	0	0
-			0	0	0	0
-			0	0	0	0
Candida_ALS_N,Flocculin	IPR033504	Agglutinin-like protein	0	0	0	0
Candida_ALS_N,Flocculin	IPR008966	Adhesion domain superfamily	0	0	0	0
Candida_ALS,Candida_ALS_N	IPR033504	Agglutinin-like protein	0	1	1	1
Candida_ALS,Candida_ALS_N	IPR033504	Agglutinin-like protein	0	1	1	1
Candida_ALS,Candida_ALS_N	IPR033504	Agglutinin-like protein	0	0	0	0
Candida_ALS,Candida_ALS_N	IPR033504	Agglutinin-like protein	0	0	0	0
Candida_ALS,Candida_ALS_N,Flo11	IPR035971	Cellulose-binding domain superfamily	0	0	0	0
Candida_ALS,Candida_ALS_N,Flo11	IPR035971	Cellulose-binding domain superfamily	0	0	0	0
Candida_ALS,Candida_ALS_N,Flo11			0	0	0	0
Candida_ALS,Candida_ALS_N,Flo11			0	0	0	0
CBM_19,Flocculin_t3,Glyco_hydro_18	IPR036861	Endochitinase-like superfamily	0	0	0	0
CBM_19,Flocculin_t3,Glyco_hydro_18	IPR050542	Glycosyl Hydrolase 18 Family Chitinases	0	0	0	0
CBM_19,Flocculin_t3,Glyco_hydro_18	IPR017853	Glycoside hydrolase superfamily	0	0	0	0
CBM_19,Flocculin_t3,Glyco_hydro_18			0	0	0	0
Cellulase,GLEYA,Ricin_B_lectin	IPR035992	Ricin B-like lectins	0	0	0	0
Cellulase,GLEYA,Ricin_B_lectin	IPR035992	Ricin B-like lectins	0	0	0	0
Cellulase,GLEYA,Ricin_B_lectin	IPR035992	Ricin B-like lectins	0	0	0	0
Cyt-b5,Flocculin_t3			0	0	0	0
Cyt-b5,Flocculin_t3			0	0	0	0
Cyt-b5,Flocculin_t3			0	0	0	0
Fasciclin	IPR050904	Cell adhesion and biosynthesis-related protein	0	0	0	0
Fasciclin	IPR050904	Cell adhesion and biosynthesis-related protein	0	1	1	1
Fasciclin	IPR050904	Cell adhesion and biosynthesis-related protein	0	0	0	0
Flocculin_t3			0	1	1	1
Flocculin_t3			0	2	1	1
Flocculin_t3	IPR052479	GPI-anchored Adhesion Regulator	0	1	0	1
Flocculin_t3			0	1	1	1
Flocculin_t3			0	0	0	0
Flocculin,GLEYA			0	0	0	0
Flocculin,GLEYA			0	0	0	0
Flocculin,GLEYA			0	0	0	0
Flocculin,GLEYA			0	0	0	0
Flocculin,GLEYA			0	0	0	0
Flocculin,GLEYA,Hyphal_reg_CWP			0	0	0	0
Flocculin,GLEYA,Hyphal_reg_CWP			0	0	0	0
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Flocculin,GLEYA,Hyphal_reg_CWP			0	0	0	0
Flocculin,Hyphal_reg_CWP			0	0	0	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR050288		Cellulose-degrading glycosyl hydrolase 3	0	1	1	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR017853		Glycoside hydrolase superfamily	0	1	1	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR036881		Glycoside hydrolase family 3 C-terminal domain su	0	1	1	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR017853		Glycoside hydrolase superfamily	0	0	0	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR036881		Glycoside hydrolase family 3 C-terminal domain su	0	0	0	0
Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C,P IPR051915		Cellulose Degradation Glycosyl Hydrolase 3	0	0	0	0
GLEYA			0	0	0	0

GLEYA			0	0	0	0
Hyphal_reg_CWP			0	0	0	0
Hyphal_reg_CWP			0	0	0	0
Hyphal_reg_CWP			0	0	0	0
Hyphal_reg_CWP			0	0	0	0
Hyphal_reg_CWP			0	0	0	0
Hyphal_reg_CWP,Hyr1			0	5	4	7
Hyphal_reg_CWP,Hyr1			0	0	1	0
Hyphal_reg_CWP,Hyr1			0	1	1	1
LisH			0	1	1	1
LisH	IPR044716	Transcriptional corepressor LEUNIG-like	0	0	0	0
LisH			0	0	0	0
RNA_poll_A14			0	0	0	0
	IPR050904	Cell adhesion and biosynthesis-related protein	2	0	0	0

[illegible]

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[illegible]

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[illegible]

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[illegible]

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0	0	1	1	1	0	0
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[illegible]

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[illegible]

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0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	1

[illegible]

0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
1	1	1	1	1	1	1	0

Trichosporon ovoides 7612	Trichosporon ovoides 9430	Total	Predicted secreted
0	0	28	FALSE
2	2	19	FALSE
0	0	6	FALSE
0	0	5	FALSE
0	0	4	FALSE
1	2	4	FALSE
1	1	3	FALSE
1	1	3	FALSE
0	0	3	TRUE
0	0	3	TRUE
0	0	4	FALSE
0	0	3	FALSE
0	0	2	FALSE
0	0	2	TRUE
0	0	2	TRUE
0	0	2	TRUE
0	0	2	FALSE
0	0	3	FALSE
0	0	3	FALSE
0	0	3	FALSE
0	0	2	FALSE
1	1	3	TRUE
1	1	3	TRUE
0	1	2	TRUE
0	0	7	FALSE
0	0	3	FALSE
0	0	2	TRUE
1	2	18	FALSE
0	0	11	FALSE
1	2	4	TRUE
0	0	6	FALSE
0	0	5	FALSE
0	0	5	TRUE
0	0	3	FALSE
0	0	2	FALSE
0	0	4	FALSE
0	0	2	FALSE
0	0	2	TRUE
0	0	2	FALSE
0	0	2	FALSE
0	0	4	TRUE
0	0	3	TRUE
0	0	3	TRUE
0	0	3	FALSE
0	0	3	TRUE
0	0	3	TRUE
0	0	3	TRUE
0	0	3	TRUE
0	0	3	TRUE
0	0	2	FALSE
0	0	3	FALSE
1	2	12	FALSE
1	2	12	FALSE
1	2	12	FALSE
0	0	4	TRUE
0	0	4	TRUE
0	0	4	TRUE
0	0	3	FALSE

0	0	3	TRUE
0	0	3	TRUE
0	0	3	TRUE
0	0	2	TRUE
0	0	2	FALSE
0	0	2	TRUE
0	0	52	FALSE
0	0	5	FALSE
0	0	3	FALSE
0	0	6	FALSE
0	0	5	FALSE
0	0	2	FALSE
0	0	3	FALSE
0	0	44	FALSE