

Orthogroup	seed ortholog	evalue	score	eggNOG OGs	max annot lvl	COG category
OG0000159	746128.CADAFUBP00004876	2.9E-130	418	KOG1325@1 root,KOG1325@2759 Eukaryota,38GBY 4751 Fungi	I	I
OG0000159	746128.CADAFUBP00004876	2.9E-130	418	KOG1325@1 root,KOG1325@2759 Eukaryota,38GBY 4751 Fungi	I	I
OG0000760	430998.XP_007673420.1	2.08E-121	353	COG0400@1 root,KOG2112@2759 Eukaryota,3AGRF 4751 Fungi	I	I
OG0000760	430998.XP_007673420.1	2.08E-121	353	COG0400@1 root,KOG2112@2759 Eukaryota,3AGRF 4751 Fungi	I	I
OG0000857	83344.XP_007926496.1	0	2025	COG1502@1 root,KOG1329@2759 Eukaryota,38G6H 4751 Fungi	I	I
OG0000857	83344.XP_007926496.1	0	2025	COG1502@1 root,KOG1329@2759 Eukaryota,38G6H 4751 Fungi	I	I
OG0001218	1392244.V5EUT2	1.88E-166	493	COG0654@1 root,KOG1298@2759 Eukaryota,38HUH 4751 Fungi	I	I
OG0001218	1392244.V5EUT2	1.88E-166	493	COG0654@1 root,KOG1298@2759 Eukaryota,38HUH 4751 Fungi	I	I
OG0001670	63400.XP_003017629.1	1.09E-72	223	KOG1772@1 root,KOG1772@2759 Eukaryota,3A6AE 4751 Fungi	U	U
OG0001779	63402.XP_003172162.1	5.78E-269	753	KOG4569@1 root,KOG4569@2759 Eukaryota,39S2Q 4751 Fungi	G	G
OG0001779	63402.XP_003172162.1	5.78E-269	753	KOG4569@1 root,KOG4569@2759 Eukaryota,39S2Q 4751 Fungi	G	G
OG0001779	63402.XP_003172162.1	5.78E-269	753	KOG4569@1 root,KOG4569@2759 Eukaryota,39S2Q 4751 Fungi	G	G
OG0002258	5551.XP_003239251.1	2.99E-195	544	COG1024@1 root,KOG0016@2759 Eukaryota,38F2P 4751 Fungi	I	I
OG0002258	5551.XP_003239251.1	2.99E-195	544	COG1024@1 root,KOG0016@2759 Eukaryota,38F2P 4751 Fungi	I	I
OG0002779	5270.UM04973P0	1.44E-133	388	COG1024@1 root,KOG1680@2759 Eukaryota,38F58 4751 Fungi	I	I
OG0003129	84751.XP_007878317.1	1.29E-178	555	KOG1325@1 root,KOG1325@2759 Eukaryota,38CVD 4751 Fungi	I	I
OG0003129	84751.XP_007878317.1	1.29E-178	555	KOG1325@1 root,KOG1325@2759 Eukaryota,38CVD 4751 Fungi	I	I
OG0003398	430998.XP_007675208.1	2.96E-301	827	COG3173@1 root,KOG1469@2759 Eukaryota,38BW 4751 Fungi	E	E
OG0003398	430998.XP_007675208.1	2.96E-301	827	COG3173@1 root,KOG1469@2759 Eukaryota,38BW 4751 Fungi	E	E
OG0003398	430998.XP_007675208.1	2.96E-301	827	COG3173@1 root,KOG1469@2759 Eukaryota,38BW 4751 Fungi	E	E
OG0003425	430998.XP_007676682.1	0	1443	COG1502@1 root,KOG1329@2759 Eukaryota,38G6H 4751 Fungi	I	I
OG0003501	5501.XP_001241297.1	0	1457	COG5277@1 root,KOG3871@1 root,KOG0676@275 4751 Fungi	Z	Z
OG0003501	5501.XP_001241297.1	0	1457	COG5277@1 root,KOG3871@1 root,KOG0676@275 4751 Fungi	Z	Z
OG0003501	5501.XP_001241297.1	0	1457	COG5277@1 root,KOG3871@1 root,KOG0676@275 4751 Fungi	Z	Z
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHS@ 4751 Fungi	G	G
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHS@ 4751 Fungi	G	G
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHS@ 4751 Fungi	G	G
OG0003673	5551.XP_003236178.1	0	1697	COG1472@1 root,2QTNX@2759 Eukaryota,39UHS@ 4751 Fungi	G	G
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39JZ2@3 4751 Fungi	E	E
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39JZ2@3 4751 Fungi	E	E
OG0004344	63402.XP_003172744.1	0	1355	COG1472@1 root,2R6JK@2759 Eukaryota,39JZ2@3 4751 Fungi	E	E
OG0005366	63418.F2PHA1	0	1176	COG2272@1 root,KOG4389@2759 Eukaryota,397KR 4751 Fungi	G	G
OG0005366	63418.F2PHA1	0	1176	COG2272@1 root,KOG4389@2759 Eukaryota,397KR 4751 Fungi	G	G
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1Y 4751 Fungi	G	G
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1Y 4751 Fungi	G	G
OG0006099	63402.XP_003169254.1	0	1089	COG3525@1 root,KOG2499@2759 Eukaryota,38D1Y 4751 Fungi	G	G
OG0006297	63418.F2PYI5	2.86E-102	308	COG1960@1 root,KOG0139@2759 Eukaryota,38HBF 4751 Fungi	I	I
OG0006946	82508.K1VK85	2.68E-253	706	COG1960@1 root,KOG0140@2759 Eukaryota,38BNR 4751 Fungi	I	I
OG0006946	82508.K1VK85	2.68E-253	706	COG1960@1 root,KOG0140@2759 Eukaryota,38BNR 4751 Fungi	I	I
OG0006950	42374.XP_002419767.1	0	1219	COG1752@1 root,KOG2214@2759 Eukaryota,38H5V 4751 Fungi	I	I
OG0006950	42374.XP_002419767.1	0	1219	COG1752@1 root,KOG2214@2759 Eukaryota,38H5V 4751 Fungi	I	I
OG0008676	83344.XP_007921008.1	2.98E-63	226	COG3509@1 root,2SBTI@2759 Eukaryota,39SMX@3 4751 Fungi	Q	Q
OG0008676	83344.XP_007921008.1	2.98E-63	226	COG3509@1 root,2SBTI@2759 Eukaryota,39SMX@3 4751 Fungi	Q	Q
OG0008676	83344.XP_007921008.1	2.98E-63	226	COG3509@1 root,2SBTI@2759 Eukaryota,39SMX@3 4751 Fungi	Q	Q
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQR 4751 Fungi	G	G
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQR 4751 Fungi	G	G
OG0010693	83344.XP_007926155.1	4.39E-228	663	COG3525@1 root,KOG2499@2759 Eukaryota,38TQR 4751 Fungi	G	G
OG0013923	5551.XP_003239348.1	6.39E-52	169	COG0400@1 root,KOG2112@2759 Eukaryota,38RN5 4751 Fungi	I	I
OG0013923	5551.XP_003239348.1	6.39E-52	169	COG0400@1 root,KOG2112@2759 Eukaryota,38RN5 4751 Fungi	I	I

Description	Preferred name	GOs	EC	KEGG ko	KEGG Pathway
Cytoplasmic phospholipase A2, catalytic subunit	PLB1	GO:0000003,GO:0000322,GO:0000323,GO:0000324,G	3.1.1.5	ko:K13333	ko00564,map00564
Cytoplasmic phospholipase A2, catalytic subunit	PLB1	GO:0000003,GO:0000322,GO:0000323,GO:0000324,G	3.1.1.5	ko:K13333	ko00564,map00564
Phospholipase/Carboxylesterase	-	-	3.1.1.5	ko:K06128,ko:K06130	ko00564,ko05231,map00564,map05231
Phospholipase/Carboxylesterase	-	-	3.1.1.5	ko:K06128,ko:K06130	ko00564,ko05231,map00564,map05231
Phospholipase D. Active site motifs.	SPO14	GO:0000003,GO:0000746,GO:0000747,GO:0000753,G	3.1.4.4	ko:K01115	ko00564,ko00565,ko01100,ko01110,ko04014,ko0402
Phospholipase D. Active site motifs.	SPO14	GO:0000003,GO:0000746,GO:0000747,GO:0000753,G	3.1.4.4	ko:K01115	ko00564,ko00565,ko01100,ko01110,ko04014,ko0402
Squalene epoxidase	ERG1	GO:0003674,GO:0003824,GO:0004497,GO:0004506,G	1.14.14.17	ko:K00511	ko00100,ko00909,ko01100,ko01110,ko01130,map001
Squalene epoxidase	ERG1	GO:0003674,GO:0003824,GO:0004497,GO:0004506,G	1.14.14.17	ko:K00511	ko00100,ko00909,ko01100,ko01110,ko01130,map001
Catalytic subunit of the peripheral V1 complex of vacu	-	GO:0000166,GO:0000221,GO:0000322,GO:0000323,G	3.1.1.3	ko:K01046,ko:K02152	ko00190,ko00561,ko01100,ko04145,ko04150,ko0472
Lipase (class 3)	-	-	3.1.1.73	ko:K21016	-
Lipase (class 3)	-	-	3.1.1.73	ko:K21016	-
Lipase (class 3)	-	-	3.1.1.73	ko:K21016	-
Enoyl-CoA hydratase/isomerase	ECI1	GO:0003674,GO:0003824,GO:0004165,GO:0005575,G	5.3.3.8	ko:K13239	ko00071,ko04146,map00071,map04146
Enoyl-CoA hydratase/isomerase	ECI1	GO:0003674,GO:0003824,GO:0004165,GO:0005575,G	5.3.3.8	ko:K13239	ko00071,ko04146,map00071,map04146
Belongs to the enoyl-CoA hydratase isomerase family	-	-	4.2.1.17	ko:K07511	ko00062,ko00071,ko00280,ko00310,ko00380,ko00410
4'-phosphopantetheinyl transferase superfamily	-	-	3.1.1.4	ko:K16342	ko00564,ko00565,ko00590,ko00591,ko00592,ko01100
4'-phosphopantetheinyl transferase superfamily	-	-	3.1.1.4	ko:K16342	ko00564,ko00565,ko00590,ko00591,ko00592,ko01100
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Phospholipase D. Active site motifs.	-	-	3.1.4.4	ko:K01115	ko00564,ko00565,ko01100,ko01110,ko04014,ko0402
Belongs to the actin family	ARP9	GO:0000228,GO:0000785,GO:0000790,GO:0000988,G	3.1.1.73	ko:K09252,ko:K11768	-
Belongs to the actin family	ARP9	GO:0000228,GO:0000785,GO:0000790,GO:0000988,G	3.1.1.73	ko:K09252,ko:K11768	-
Belongs to the actin family	ARP9	GO:0000228,GO:0000785,GO:0000790,GO:0000988,G	3.1.1.73	ko:K09252,ko:K11768	-
Glycosyl hydrolase family 3 N terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 N terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 N terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 N terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 C-terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 C-terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Glycosyl hydrolase family 3 C-terminal domain	-	-	3.2.1.52	ko:K01207	ko00520,ko00531,ko01100,ko01501,map00520,map0
Belongs to the type-B carboxylesterase lipase family	-	-	3.1.1.8	ko:K01050	-
Belongs to the type-B carboxylesterase lipase family	-	-	3.1.1.8	ko:K01050	-
Glycosyl hydrolase family 20, catalytic domain	NAG1	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Glycosyl hydrolase family 20, catalytic domain	NAG1	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Glycosyl hydrolase family 20, catalytic domain	NAG1	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Acyl-CoA dehydrogenase, C-terminal domain	-	-	1.3.8.7	ko:K00249	ko00071,ko00280,ko00410,ko00640,ko01100,ko01110
Domain of unknown function (DUF3336)	TGL3	GO:0000003,GO:0003674,GO:0003824,GO:0004806,G	3.1.1.3	ko:K14675	ko00561,ko01100,map00561,map01100
Domain of unknown function (DUF3336)	TGL3	GO:0000003,GO:0003674,GO:0003824,GO:0004806,G	3.1.1.3	ko:K14675	ko00561,ko01100,map00561,map01100
ferulic acid esterase	-	-	3.1.1.73	ko:K09252	-
ferulic acid esterase	-	-	3.1.1.73	ko:K09252	-
ferulic acid esterase	-	-	3.1.1.73	ko:K09252	-
Glycosyl hydrolase family 20, catalytic domain	-	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Glycosyl hydrolase family 20, catalytic domain	-	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Glycosyl hydrolase family 20, catalytic domain	-	-	3.2.1.52	ko:K12373	ko00511,ko00513,ko00520,ko00531,ko00603,ko0060
Dienelactone hydrolase family	-	GO:0002084,GO:0003674,GO:0003824,GO:0005575,G	3.1.1.5	ko:K06128,ko:K06130,ko:K01	ko00564,ko05231,map00564,map05231
Dienelactone hydrolase family	-	GO:0002084,GO:0003674,GO:0003824,GO:0005575,G	3.1.1.5	ko:K06128,ko:K06130,ko:K01	ko00564,ko05231,map00564,map05231

KEGG Module	KEGG Reaction	KEGG rclass	BRITE	KEGG TC	CAZy
-	-	-	ko00000,ko00001,ko01000	-	-
-	-	-	ko00000,ko00001,ko01000	-	-
-	R02746,R02747,R03416,R03417	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko01000	-	-
-	R02746,R02747,R03416,R03417	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko01000	-	-
-	R01310,R02051,R07385	RC00017,RC00425	ko00000,ko00001,ko01000,ko04131	-	-
-	R01310,R02051,R07385	RC00017,RC00425	ko00000,ko00001,ko01000,ko04131	-	-
-	R02874	RC00201	ko00000,ko00001,ko01000	-	-
-	R02874	RC00201	ko00000,ko00001,ko01000	-	-
M00098,M00160	R02250,R02687	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko00002,ko01000	3.A.2.2	-
-	-	-	ko00000,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
-	R04756	RC01078	ko00000,ko00001,ko01000	-	-
-	R04756	RC01078	ko00000,ko00001,ko01000	-	-
M00013,M00032,M00085,M00087	R02685,R03026,R03045,R04137,R04170,R04204,R042	RC00077,RC000831,RC000834,RC01086,RC01095,RC010	ko00000,ko00001,ko00002,ko01000	-	-
-	R01315,R01317,R02053,R07064,R07379,R07387,R078	RC00037,RC00094	ko00000,ko00001,ko01000	-	-
-	R01315,R01317,R02053,R07064,R07379,R07387,R078	RC00037,RC00094	ko00000,ko00001,ko01000	-	-
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
-	R01310,R02051,R07385	RC00017,RC00425	ko00000,ko00001,ko01000,ko04131	-	-
-	-	-	ko00000,ko01000,ko03021,ko03036	-	-
-	-	-	ko00000,ko01000,ko03021,ko03036	-	-
-	-	-	ko00000,ko01000,ko03021,ko03036	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
M00628	R00022,R05963,R07809,R07810,R10831	RC00049	ko00000,ko00001,ko00002,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
M00013,M00036,M00087	R00924,R01175,R01279,R02661,R03172,R03777,R038	RC00052,RC00068,RC00076,RC00095,RC00148,RC002	ko00000,ko00001,ko00002,ko01000	-	-
M00098	R02250,R02687	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko00002,ko01000	-	-
M00098	R02250,R02687	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko00002,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
-	-	-	ko00000,ko01000	-	-
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
M00079	R00022,R06004,R11316	RC00049	ko00000,ko00001,ko00002,ko01000,ko03110	-	GH20
-	R02746,R02747,R03416,R03417	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko01000	-	-
-	R02746,R02747,R03416,R03417	RC00020,RC00037,RC00041,RC00094	ko00000,ko00001,ko01000	-	-

BiGG Reaction	PFAMs	IPR term	IPR description	Blastocladiella emersonii 22665	Candida dubliniensis 11945
iMM904.YMR006C	PLA2_B	IPR029033	Histidine phosphatase superfamily	0	6
iMM904.YMR006C	PLA2_B	IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	0	6
-	Abhydrolase_2	IPR050565	Acyl-protein thioesterase 1-2/Carboxylesterase-like	1	1
-	Abhydrolase_2	IPR029058	Alpha/Beta hydrolase fold	1	1
iMM904.YKR031C	PLDc,PLDc_2,PX	IPR015679	Phospholipase D family	1	1
iMM904.YKR031C	PLDc,PLDc_2,PX	IPR036871	PX domain superfamily	1	1
-	DAO,FAD_binding_3,SE	IPR036188	FAD/NAD(P)-binding domain superfamily	1	1
-	DAO,FAD_binding_3,SE	IPR040125	Squalene monooxygenase	1	1
-	V-ATPase_G	IPR005124	Vacuolar (H+)-ATPase G subunit	1	1
-	Lipase_3	IPR029058	Alpha/Beta hydrolase fold	1	1
-	Lipase_3	IPR017383	Actin-related protein 2/3 complex subunit 1	1	1
-	Lipase_3	IPR036322	WD40-repeat-containing domain superfamily	1	1
iMM904.YOR180C	ECH_1	IPR029045	ClpP/crotonase-like domain superfamily	1	2
iMM904.YOR180C	ECH_1	IPR051053	Enoyl-CoA hydratase/isomerase and chromodomain-c	1	2
-	ECH_1	IPR029045	ClpP/crotonase-like domain superfamily	4	0
-	ACPS,PLA2_B	IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	1	0
-	ACPS,PLA2_B	IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	1	0
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR009100	Acyl-CoA dehydrogenase/oxidase, N-terminal and mic	1	1
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR036250	Acyl-CoA dehydrogenase-like, C-terminal	1	1
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR050741	Acyl-CoA dehydrogenase	1	1
-	PLDc,PLDc_2	IPR015679	Phospholipase D family	0	0
-	Actin	IPR043129	ATPase, nucleotide binding domain	0	1
-	Actin	IPR007955	Bystin	0	1
-	Actin	IPR043129	ATPase, nucleotide binding domain	0	1
-	Acetyltransf_1,Glyco_hydro_3	IPR036881	Glycoside hydrolase family 3 C-terminal domain super	0	1
-	Acetyltransf_1,Glyco_hydro_3	IPR016181	Acyl-CoA N-acyltransferase	0	1
-	Acetyltransf_1,Glyco_hydro_3	IPR017853	Glycoside hydrolase superfamily	0	1
-	Acetyltransf_1,Glyco_hydro_3	IPR050226	NagZ Beta-hexosaminidase	0	1
-	Acetyltransf_1,Acetyltransf_7,Glyco_hydro_3,Glyco_t	IPR016181	Acyl-CoA N-acyltransferase	0	0
-	Acetyltransf_1,Acetyltransf_7,Glyco_hydro_3,Glyco_t	IPR050226	NagZ Beta-hexosaminidase	0	0
-	Acetyltransf_1,Acetyltransf_7,Glyco_hydro_3,Glyco_t	IPR017853	Glycoside hydrolase superfamily	0	0
-	COesterase	IPR050309	Type-B Carboxylesterase/Lipase	0	0
-	COesterase	IPR029058	Alpha/Beta hydrolase fold	0	0
-	Glyco_hydro_20,Glycohydro_20b2	IPR025705	Beta-hexosaminidase	0	0
-	Glyco_hydro_20,Glycohydro_20b2	IPR017853	Glycoside hydrolase superfamily	0	0
-	Glyco_hydro_20,Glycohydro_20b2	IPR029018	Beta-hexosaminidase-like, domain 2	0	0
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR009100	Acyl-CoA dehydrogenase/oxidase, N-terminal and mic	0	0
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR009100	Acyl-CoA dehydrogenase/oxidase, N-terminal and mic	1	0
-	Acyl-CoA_dh_1,Acyl-CoA_dh_M,Acyl-CoA_dh_N	IPR036250	Acyl-CoA dehydrogenase-like, C-terminal	1	0
-	DUF3336,Patatin	IPR016035	Acyl transferase/acyl hydrolase/lysophospholipase	1	1
-	DUF3336,Patatin	IPR050301	Neuropathy target esterase	1	1
-	Esterase_phd	IPR029058	Alpha/Beta hydrolase fold	0	0
-	Esterase_phd	IPR036861	Endochitinase-like superfamily	0	0
-	Esterase_phd	IPR043595	Feruloyl esterase B/C/D	0	0
-	Glyco_hydro_20,Glyco_hydro_20b	IPR017853	Glycoside hydrolase superfamily	0	0
-	Glyco_hydro_20,Glyco_hydro_20b	IPR029018	Beta-hexosaminidase-like, domain 2	0	0
-	Glyco_hydro_20,Glyco_hydro_20b	IPR052764	Glycosyl Hydrolase 20 Enzymes	0	0
-	Abhydrolase_2	IPR029058	Alpha/Beta hydrolase fold	0	0
-	Abhydrolase_2	IPR050565	Acyl-protein thioesterase 1-2/Carboxylesterase-like	0	0

[illegible]

Epidermophyton floccosum 10867	Epidermophyton floccosum 130802	Hortaea werneckii 100455	Hortaea werneckii 1163	Hortaea werneckii 41051	Malassezia furfur 14140-1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	3	2	3	1
1	1	3	2	3	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	1
1	1	2	1	2	1
1	1	2	1	1	0
1	1	2	1	1	0
1	1	2	1	1	0
1	1	4	2	4	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	0	0	0	0
1	1	0	0	0	0
1	1	0	0	0	0
0	0	2	1	2	0
0	0	2	1	2	0
1	1	2	1	2	0
1	1	2	1	2	0
1	1	0	0	0	0
0	0	0	0	0	1
0	0	0	0	0	1
0	0	2	1	2	0
0	0	2	1	2	0
0	0	4	2	2	0
0	0	4	2	2	0
0	0	4	2	2	0
0	0	2	1	2	0
0	0	2	1	2	0
0	0	2	1	2	0
0	1	0	0	0	0
0	1	0	0	0	0

[illegible]

[illegible]

[illegible]

Nakaseomyces glabratus 15698	Nannizzia gypsea 17164	Pichia kudriavzevii 573-1	Pichia kudriavzevii 573-2	Radiomyces spectabilis	Trichophyton concentricum 109405
4	1	2	2	0	1
4	1	2	2	0	1
1	1	1	1	1	1
1	1	1	1	1	1
1	1	1	1	4	1
1	1	1	1	4	1
1	1	1	1	2	1
1	1	1	1	2	1
1	1	1	1	1	1
1	1	1	1	1	1
1	1	1	1	1	1
1	1	1	0	2	1
1	1	1	0	2	1
0	1	0	0	3	1
0	1	0	0	2	1
0	1	0	0	2	1
0	1	0	0	1	1
0	1	0	0	1	1
0	1	0	0	1	1
0	1	0	0	3	1
1	1	1	1	0	1
1	1	1	1	0	1
1	1	1	1	0	1
0	1	2	1	0	1
0	1	2	1	0	1
0	1	2	1	0	1
0	1	2	1	1	1
0	1	2	1	1	1
0	1	0	0	0	1
0	1	0	0	0	1
0	1	0	0	0	1
0	1	0	0	0	1
0	0	0	0	0	0
0	0	0	0	0	0
1	0	1	1	1	0
1	0	1	1	1	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
0	0	0	0	0	1

[illegible]

[illegible]

[illegible]

Trichophyton violaceum 73088	Trichosporon ovoides 4098	Trichosporon ovoides 7612	Trichosporon ovoides 9430	Total
1	2	2	4	112
1	2	2	4	112
2	1	1	2	66
2	1	1	2	66
1	1	1	2	64
1	1	1	2	64
1	1	1	2	61
1	1	1	2	61
1	1	1	2	60
1	1	1	1	59
1	1	1	1	59
1	1	1	1	59
1	1	1	2	57
1	1	1	2	57
1	1	1	3	52
1	0	0	0	48
1	0	0	0	48
1	1	1	2	45
1	1	1	2	45
1	1	1	2	45
1	1	1	2	45
1	0	0	0	44
1	0	0	0	44
1	0	0	0	44
1	0	0	0	42
1	0	0	0	42
1	0	0	0	42
1	0	0	0	42
1	0	0	0	42
1	0	1	2	35
1	0	1	2	35
1	0	1	2	35
1	0	0	0	30
1	0	0	0	30
1	0	0	1	27
1	0	0	1	27
1	0	0	1	27
1	0	0	0	25
0	1	1	2	16
0	1	1	2	16
0	0	0	0	16
0	0	0	0	16
0	0	0	0	8
0	0	0	0	8
0	0	0	0	8
0	0	0	0	5
0	0	0	0	5
0	0	0	0	5
0	0	0	0	3
0	0	0	0	3