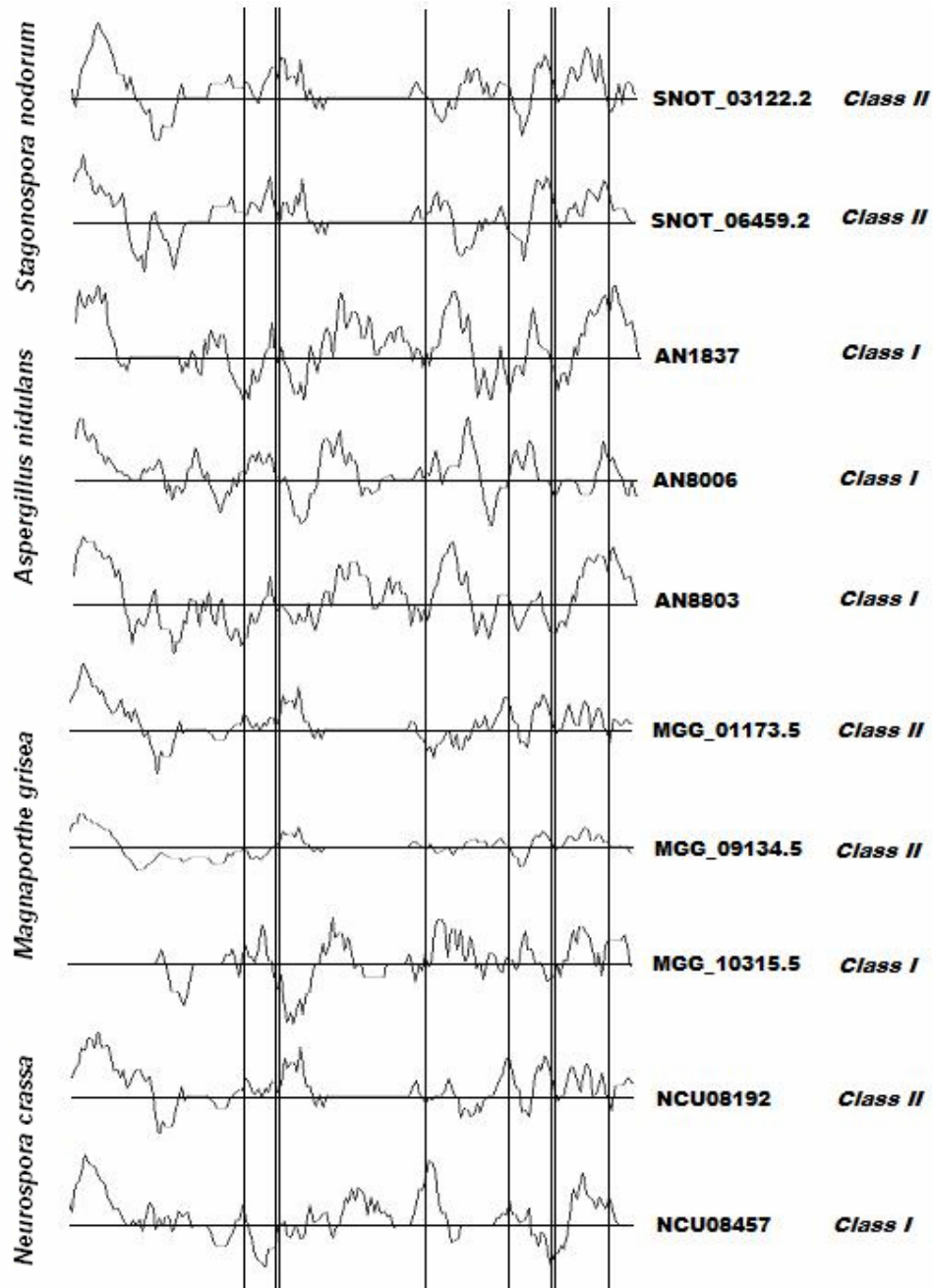


Supplemental Figure 1. Aligned Kyte and Doolittle Hydrophobicity Plots.

Hydrophobins were identified with HMMER v2.0 and classified according to their hydropathy profiles. A multiple alignment generated with CLUSTALW was manually curated to ensure alignment of the 8 cysteine residues typically conserved among fungal hydrophobins (indicated by vertical lines). Hydrophobicity profiles were calculated along the alignment with a 7bp window as per Kyte and Doolittle (1982).

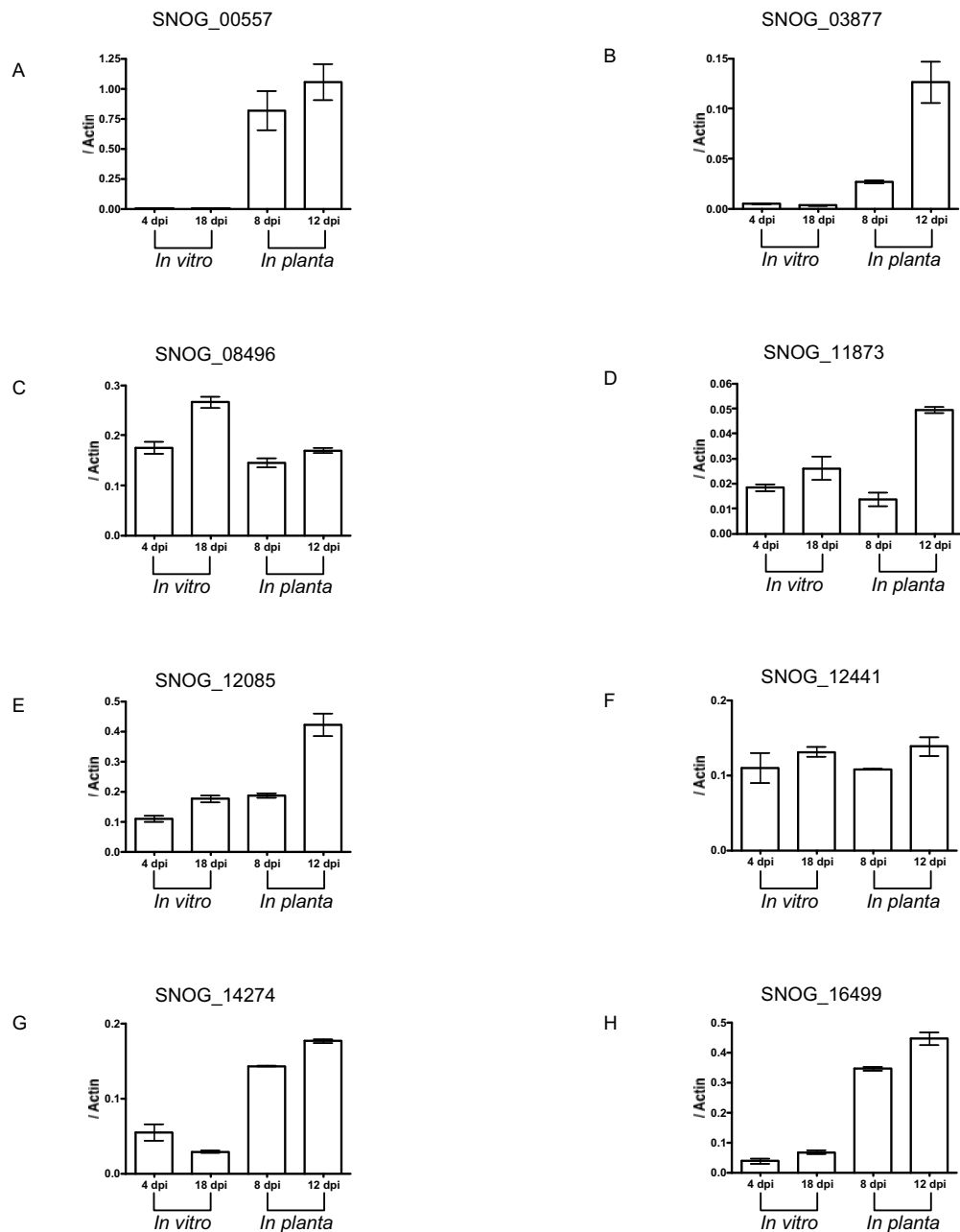
Reference:

Kyte, J. and Doolittle, R. (1982). A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* **157**: 105-132.



Supplemental Figure 2. Quantitative PCR analysis of gene expression from *in planta* associated genes.

Expression of genes abundant in the *in planta* library were determined in four different growth states: In vitro non-sporulating (4 dpi), In vitro sporulating (18 dpi), *In planta* non-sporulating (8 dpi), and *in planta* sporulating (12 dpi). Analysed genes are as follows: (A) SNOG_00557.2, (B) SNOG_03877.2 (C) SNOG_08496.2, (D) SNOG_11873.2, (E) SNOG_12085.2, (F) SNOG_12441.2 (G) SNOG_14274.2, (H) SNOG_16499.2. Transcript levels were calculated as ng/reaction relative to that of actin. Three biological replicate RNAs were pooled prior to cDNA synthesis. n=2, std error bars shown. PCR primers and EST data for these genes are given in Supplemental Tables 2 and 3, respectively.



Supplemental Table 1. Mitochondrial Genes.

Origin	program	group	Start	Stop		frame	name	tRNA
mtDNA	P.nod	tRNA	3207	3277	.	+	tRNA-Thr	T
mtDNA	P.nod	tRNA	3302	3373	.	+	tRNA-Met1	M1
mtDNA	P.nod	tRNA	3375	3447	.	+	tRNA-Met2	M2
mtDNA	P.nod	tRNA	4127	4199	.	+	tRNA-Glu	E
mtDNA	P.nod	tRNA	4230	4301	.	+	tRNA-Ala	A
mtDNA	P.nod	tRNA	5232	5304	.	+	tRNA-Phe	F
mtDNA	P.nod	tRNA	5651	5732	.	+	tRNA-Leu1	L
mtDNA	P.nod	tRNA	5807	5878	.	+	tRNA-Gln	Q
mtDNA	P.nod	tRNA	5884	5956	.	+	tRNA-His	H
mtDNA	P.nod	tRNA	6088	6159	.	+	tRNA-Met3	M3
mtDNA	P.nod	gene	7021	9267	.	+	cytb	
mtDNA	P.nod	exon	7021	7526	.	+	cytb exon 1	
mtDNA	P.nod	gene	(intron)7558	8487	.	+	I-AniI (LAGLIDADG endonuclease)	
mtDNA	P.nod	exon	8574	9267	.	+	cytb exon 2	
mtDNA	P.nod	gene	10215	12723	.	+	atp6	
mtDNA	P.nod	exon	10215	10778	.	+	atp6 exon 1	
mtDNA	P.nod	gene	(intron)11639	12409+	.	.	GIY...YIG endonuclease	
mtDNA	P.nod	gene	12523	12723	.	+	atp6 exon 2	
mtDNA	P.nod	orf	12800	13723	.	+	orf1	
mtDNA	P.nod	orf	15653	17797	.	+	orf2	
mtDNA	P.nod	tRNA	19011	19081	.	+	tRNA-Val1	V
mtDNA	P.nod	tRNA	19112	19181	.	+	tRNA-Cys	C
mtDNA	P.nod	gene	19829	21414	.	+	cox1	
mtDNA	P.nod	gene	21443	22198	.	+	cox2	
mtDNA	P.nod	gene	22535	23787	.	+	S5 rib protein	
mtDNA	P.nod	gene	25603	27070	.	+	nad4	
mtDNA	P.nod	exon	25603	25785	.	+	nad4 exon1	
mtDNA	P.nod	exon	25930	27070	.	+	nad4 exon2	
mtDNA	P.nod	gene	29128	31459	.	-	nad1	
mtDNA	P.nod	exon	30824	31459	.	-	nad1 exon 1	
mtDNA	P.nod	gene	(intron)29637	30347-	.	.	nad1intron protein	
mtDNA	P.nod	exon	29128	29607	.	-	nad1 exon 2	
mtDNA	P.nod	gene	32019	35347	.	-	nad5	
mtDNA	P.nod	exon	35024	35347	.	-	nad5 exon1	
mtDNA	P.nod	gene	(intron)33737	35023-	.	.	nad5 intron protein	
mtDNA	P.nod	exon	32019	33671	.	-	nad5 exon2	
mtDNA	P.nod	orf	35753	36646	.	-	orf3	
mtDNA	P.nod	gene	36821	37105	.	-	nad4L	
mtDNA	P.nod	gene	37612	38058	.	-	nad3	
mtDNA	P.nod	gene	38059	39777	.	-	nad2	
mtDNA	P.nod	gene	39879	41991	.	-	cox3	
mtDNA	P.nod	exon	41773	41991	.	-	cox3 exon1	
mtDNA	P.nod	exon	39879	40469	.	-	cox3 exon2	
mtDNA	P.nod	tRNA	42992	43062	.	+	tRNA-Arg1	R1
mtDNA	P.nod	tRNA	43099	43169	.	+	tRNA-Arg2	R2
mtDNA	P.nod	rRNA	43274	44814	.	+	rns	
mtDNA	P.nod	tRNA	45115	45197	.	+	tRNA-Leu2	L2
mtDNA	P.nod	tRNA	45513	45596	.	+	tRNA-Tyr	Y
mtDNA	P.nod	tRNA	45703	45773	.	+	tRNA-Asn	N
mtDNA	P.nod	gene	46079	46675	.	+	nad6	
mtDNA	P.nod	tRNA	46732	46804	.	+	tRNA-Val2	V
mtDNA	P.nod	tRNA	46837	46908	.	+	tRNA-Lys	K
mtDNA	P.nod	tRNA	47217	47289	.	+	tRNA-Gly	G
mtDNA	P.nod	tRNA	47292	47363	.	+	tRNA-Asp	D
mtDNA	P.nod	tRNA	47638	47717	.	+	tRNA-Ser1	S
mtDNA	P.nod	tRNA	48148	48219	.	+	tRNA-SeC	SC
mtDNA	P.nod	tRNA	48333	48407	.	+	tRNA-Ser2	S2
mtDNA	P.nod	tRNA	48412	48485	.	+	tRNA-Arg3	R3
mtDNA	P.nod	tRNA	48999	49083	.	+	tRNA-Ser3	S3
mtDNA	P.nod	tRNA	49193	49265	.	+	tRNA-Pro	P
mtDNA	P.nod	rRNA	49304	2813	.	+	rnl	

Supplemental Table 2. Summary of PFAM domains used for identification.

Gene family	PFAM models
G-alpha	PF00503.9
Cfem	PF05730.1
Rhodopsin	PF00001.11, PF01036.8
Hydrophobins	PF01185.9, PF06766.1
Feruloyl esterase	PF07519.1
Cutinase	PF01083.12
Subtilisin	PF05922.7, PF00082.11
Transcription factor	PF07716.5, PF00170.11, PF02045.6, PF00808.13, PF06881.1, PF04082.7, PF02200.6, PF00352.12, PF03849.4, PF03850.4, PF00382.9, PF08271.2, PF01096.9, PF07500.3
Cytochrome p450	PF00067.11
PKS and NRPS	PF08415.1, PF00668.9, PF00975.10, PF00550.14, PF08659.1, PF08392.2, PF08545.1, PF00378.9, PF00698.11, PF02801.12

Notes:

all PFAM models derived from the Pfam_Is dataset
domains and families identified via hmmpfam (of HMMER, <http://hmmer.janelia.org>) using PFAM
gathering threshold score cutoffs

Supplemental Table 3. List of species used in this study.

AFTOL no.	Species	Strain/voucher*	nuc-SSU	nuc-LSU	EF-1 α	RPB1	RPB2
54	<i>Cochliobolus heterostrophus</i>	CBS 134.39	AY544727	AY544645	DQ247790	--	DQ497603
59	<i>Botrytis cinerea</i>	OSC 100012	AY544695	AY544651	DQ471045	DQ471116	DQ247786
60	<i>Morchella esculenta</i> cf.	MV3	AY544708	AY544664	DQ471046	DQ471117	DQ470880
87	<i>Teloschistes exilis</i>	--	AY584671	AY584647	DQ883764	DQ883779	DQ883759
134	<i>Peltigera degenii</i>	DUKE 0047504	AY584681	AY584657	DQ782897	DQ782826	AY584688
149	<i>Neofabreae malicorticis</i>	OSC 100036	AY544706	AY544662	DQ847414	DQ471124	DQ470885
161	<i>Fusarium</i> aff. <i>solani</i>	GJS 89-70	AY489697	AY489729	AU489624	AY489660	DQ518180
173	<i>Pyrenophora tritici-repentis</i>	OSC 100066	AY544716	AY544672	--	--	DQ677882
274	<i>Dothidea sambuci</i>	DAOM 231303	AY544722	AY544681	DQ522854	--	DQ497606
277	<i>Leptosphaeria maculans</i>	DAOM 229267	DQ470993	DQ470946	DQ471062	DQ471136	DQ470894
280	<i>Phaeosphaeria avenaria</i>	DAOM 226215	AY544725	AY544684	DQ677941	--	DQ677885
505	<i>Ustilago maydis</i>	PBM 2469	AY854090	AF453938	AY885160	XM_401478	AY487636
507	<i>Peziza vesiculosa</i>	TL-6398	DQ470995	DQ470948	DQ471066	DQ471140	DQ470898
639	<i>Lecanora hybocarpa</i>	DUKE 0047510	DQ782883	DQ782910	DQ782901	DQ782829	DQ782871
657	<i>Capronia pilosella</i>	DAOM 216837	DQ823106	DQ823099	DQ840565	DQ840554	DQ840561
776	<i>Phanerochaete chrysosporium</i>	FPL5175	Genome	Genome	Genome	Genome	Genome
912	<i>Aureobasidium pullulans</i>	CBS 584.75	DQ471004	DQ470956	DQ471075	DQ471148	DQ470906
928	<i>Sclerotinia sclerotiorum</i>	CBS 499.50	DQ471013	DQ470965	DQ471086	--	DQ470916
940	<i>Pleospora herbarum</i>	CBS 191.86	DQ247812	DQ247804	DQ471090	DQ471163	DQ247794
946	<i>Botryosphaeria dothidea</i>	CBS 115476	DQ677998	DQ678051	DQ677944	EU186063	DQ767637
949	<i>Pyronema domesticum</i>	CBS 666.88	DQ247813	DQ247805	DQ471093	DQ471166	DQ247795
1069	<i>Saccharomyces cerevisiae</i>	SGD	SCYLR154C	SCYLR154C	Genome	X96876	SCYOR151C
1072	<i>Eremothecium gossypii</i>	Basel	AE016820	AE016820	Genome	NM_209535	AE016819
1075	<i>Kluyveromyces lactis</i>	Génolevures	Genome	Genome	Genome	XM_455310	XM_451784
1078	<i>Neurospora crassa</i>	Broad	X04971	AF286411	Genome	XM_959004	XM_324476
1079	<i>Aspergillus fumigatus</i>	TIGR	AB008401	AY660917	Genome	XM_747744	XM_741647
1081	<i>Magnaporthe grisea</i>	Broad	AB026819	AB026819	Genome	XM_362207	XM_362269
1083	<i>Histoplasma capsulatum</i>	WUSTL	Genome	Genome	Genome	Genome	Genome
1192	<i>Pneumocystis carinii</i>	PGP	S83267.1	AF047831	--	Genome	AY485631
1199	<i>Schizosaccharomyces pombe</i>	Sanger	X54866	Z19136	Genome	X56564	D13337
1234	<i>Taphrina deformans</i>	CBS 356.35	DQ471024	DQ470973	DQ471097	DQ471170	DQ470927
1289	<i>Cladosporium cladosporioides</i>	CBS 170.54	DQ678004	DQ678057	DQ677952	EU186064	DQ677898
1304	<i>Myriangium duriaei</i>	CBS 260.36	AY016347	DQ678059	DQ677954	--	DQ677900
1575	<i>Phoma herbarum</i>	CBS 276.37	DQ678014	DQ678066	DQ677962	--	DQ677909
1583	<i>Ascochyta pisi</i> var. <i>pisii</i>	CBS 126.54	DQ678018	DQ678070	DQ677967	--	DQ677913
1599	<i>Delitschia winteri</i>	CBS 225.62	DQ678026	DQ678077	DQ677975	--	DQ677922
1610	<i>Alternaria alternata</i>	CBS 916.96	DQ678031	DQ678082	DQ677980	--	DQ677927
1615	<i>Mycosphaerella graminicola</i>	CBS 292.38	DQ678033	DQ678084	DQ677982	--	--
1618	<i>Guignardia bidwellii</i>	CBS 237.48	DQ678034	DQ678085	DQ677983	--	--
1853	<i>Elsinoë veneta</i>	CBS 150.27	DQ767651	DQ767658	DQ767641	--	--
	<i>Stagonospora nodorum</i>	Broad	Genome	Genome	Genome	Genome	Genome

*Source abbreviations:

--Gene absent in alignment

Culture collections and herbaria

ATCC - American Type Culture Collection, Manassas, VA, USA

CBS - Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands

DAOM - National Mycological Herbarium, Department of Agriculture, Ottawa, Ontario, Canada

DUKE - Duke University Herbarium, Durham, NC, USA

FPL - Forest Products Laboratory, Madison, WI, USA

GJS - Collection of Gary Samuels, USDA, Beltsville, MD, USA

MV3 - Collection of Kerry O' Donnell, ARS, Peoria, IL, USA

OSC - Oregon State University Herbarium, Corvallis, OR, USA

TBM - Clark University Herbarium, Worcester, MI, USA

TL - Collection of T. Læssøe, Department of Mycology, University of Copenhagen, Denmark

Genome resources

Basel - University of Basel, Switzerland

Broad - Broad Institute, Cambridge, MA, USA

Génolevures - Collection de Levures d'Intérêt Biotechnologique, Institut National Agronomique,
Thiverval-Grignon, France
PGP - Pneumocystis Genome Project, University of Cincinnati, Cincinnati, OH, USA
SGD - Saccharomyces genome database
Sanger – Wellcome Trust Sanger Institute, Cambridge UK
TIGR - The Institute for Genomic Research Rockville, MD, USA
WUSTL - St. Louis Genome Sequencing Center, Washington University, Seattle, WA, USA

Supplemental Table 4. Quantitative PCR Primers.

Quantitative PCR	
primers	Sequence 5' to 3'
SNOG_00557-Fwd	CAACTGTCCGGAGCATCCCA
SNOG_00557-Rev	AGTTTGCGTTGGAGGGGTCG
SNOG_03877-Fwd	ATGCCGTCCACCAGAAGCAAGAA
SNOG_03877-Rev	CGCGGAGCGTATGTGGCAAGA
SNOG_08496-Fwd	ATCAAGGAGGGTGCCACGTTC
SNOG_08496-Rev	AGGGAGCAGTTTCGGGTTCG
SNOG_11873-Fwd	CGACATCCTCGGCCTCGAAT
SNOG_11873-Rev	ACAATGCCATGCATCCACGTC
SNOG_12085-Fwd	GGTTGGGGAAAGCGGGAGTT
SNOG_12085-Rev	CGTGCTGAGCACCATCAACGT
SNOG_12441-Fwd	ACAAGTCGGACGTCATTGCGA
SNOG_12441-Rev	TGTTCTCGAAGCTGGCTGGG
SNOG_14274-Fwd	CACGAATCCGCTGGCACAGT
SNOG_14274-Rev	TGACGGGTGGTGTGAGAGGA
SNOG_16499-Fwd	GCGCATGGCTGCCAACTATG
SNOG_16499-Rev	TGGCGTTCAAGCTCTGCATCA
Actin-Fwd	AGTCGAAGCGTGGTATCCT
Actin-Rev	ACTTGGGGTTGATGGGAG

Supplemental Table 5. EST data for abundant *in planta* associated genes.

Gene	BlastX annotation	GO classifier	BlastX expect value	EST totals		<i>P Value</i>
				<i>in planta</i>	<i>in vitro</i>	
SNOG_16499	Norsolorinic acid reductase, aldo/keto reductase	GO:0016491; oxidoreductase activity	4.0E-117	26	0	4.60E-10
SNOG_03877	Oxidoreductase	no match	8.0E-27	24	0	2.26E-09
SNOG_00557	Arabinofuranosidase	GO:0046556; alpha-N-arabinofuranosidase activity	2.0E-132	21	0	2.47E-08
SNOG_12085	Aldose epimerase	GO:0004034; aldose 1-epimerase activity	9.0E-108	11	0	7.08E-05
SNOG_08496	rho-gdp dissociation inhibitor	GO:0005094; Rho GDP-dissociation inhibitor activity	7.0E-74	10	0	1.57E-04
SNOG_12441	Alanine transaminase	GO:0008483; transaminase activity	0.0E+00	10	0	1.57E-04
SNOG_14274	Arabitol 4-dehydrogenase	GO:0050019 ;L-arabinitol 4-dehydrogenase activity	5.0E-147	9	0	3.48E-04
SNOG_11873	Dioxygenase, catechol/protocatechuate	GO:0018576, catechol 1,2-dioxygenase activity	4.0E-105	7	0	1.71E-03