Electronic Supplementary Material (ESI) for Green Chemistry.
This journal is © The Royal Society of Chemistry 2016

Electronic Supplementary Information for:

Lignin depolymerization by fungal secretomes and a microbial sink†

Davinia Salvachúa[a,‡], Rui Katahira[a,‡], Nicholas S. Cleveland[a], Payal Khanna[a], Michael G. Resch[a], Brenna A. Black[a], Samuel O. Purvine[b], Erika M. Zink[b], Alicia Prieto[c], María J. Martínez[c], Angel T. Martínez[c], Blake A. Simmons[d,e], John M. Gladden[d,f], Gregg T. Beckham[a,*]

a. National Bioenergy Center, National Renewable Energy Laboratory (NREL), Golden CO 80401, USA
b. Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory (PNNL), Richland, WA 99352, USA
c. Centro de Investigaciones Biológicas, Consejo Superior de Investigaciones Científicas (CSIC), E-28040 Madrid, Spain
d. Joint BioEnergy Institute (JBEI), Emeryville, CA 94608
e. Biological Systems and Engineering, Lawrence Berkeley National Laboratory, Berkeley CA 94720 USA
f. Sandia National Laboratory, Livermore CA 94550
‡ Equal contribution
* Corresponding author: Gregg.Beckham@nrel.gov

Extension of materials and methods section

Analysis of aromatics by LC-MS/MS

Mass spectrometry was used in the last experiment of the current study to analyze aromatics from the soluble fraction. For this purpose, 14.5 mg of freeze-dried supernatant from 8 different treatments was reconstituted in 1 mL methanol. Analysis of samples was performed on an Agilent 1100 LC system equipped with a diode array detector (DAD) and an Ion Trap SL MS (Agilent Technologies, Palo Alto, CA) with in-line electrospray ionization (ESI). Each sample was injected at a volume of 25 µL into the LC-MS system. Primary degradation compounds were separated using a YMC C30 Carotenoid 0.3 µm, 4.6 x 150 mm column (YMC America, Allentown, PA) at an oven temperature of 30°C. The HPLC solvent gradient was performed using eluents of A) water modified with ammonium hydroxide (pH 7), and eluent B) 9:1 acetonitrile and water also modified with ammonium hydroxide (pH 7). At a flow rate of 0.7 mL min^{-1}, the gradient chromatography was as follows: 0-3 min, 0% B; at 16 min, 7% B; at 21 min, 8.5% B; at 34 min, 10% B; at 46 min, 25% B; and held at 30% B at 51-56 min, for a total run time of 65 min including equilibrium. Flow from the HPLC-DAD was directly routed to the ESI/MS ion trap. The DAD was used to monitor chromatography at 210 nm for a direct comparison to MS data. MS and MS/MS tuned parameters are as follows: smart parameter setting with target mass set to 165 Da, compound stability 70%, trap drive 50%, capillary at 3500 V, fragmentation amplitude of 0.75 V with a 30 to 200% ramped voltage implemented for 50 msec, and an isolation width of 2 m/z (He collision gas). The ESI nebulizer gas was set to 60 psi, with dry gas flow of 11 L min^{-1} held at 350°C. MS scans and precursor isolation-fragmentation scans were performed across the range of 40-350 Da in negative- and positive-ion alternating mode. Vanillin, 4-hydroxybenzaldehyde, PCA, vanillic acid, syringic acid, 4-hydroxybenzoic acid, and FA were the only aromatics detected from an instrument specific in-house database of 70 aromatic compounds. Standards were prepared in the range of 1 – 100 µg/mL and run at the same conditions as the samples. Samples were diluted accordingly to maintain detector response within the linear range of the calibration curves (R^2 value of ≥99.5%).

Proteomic analysis in the secretome of P. eryngii

For proteomic analyses, 50 mL of the *P. eryngii* secretome from 9 days of incubation (used for the depolymerization assays) were taken from 2 biological replicates and flash-frozen. Then, samples were treated and analyzed as described below:

Volume concentration. The volumes of the secretomes from *P. eryngii* were initially reduced prior to isolating the proteins with a chloroform-methanol extraction. To reduce the volumes, centrifugal filters (MilliporeAmicon Ultra-15, 10k MWCO) were used following the vendor protocol for volume concentration. Briefly, the proteins were first denatured by adding 8 M urea and incubating for 1 h at 37°C. The denatured proteins were then added to a spin filter that had been pre-rinsed with 0.1 N NaOH and then 50 mM NH_4HCO_3. The sample was then added to the spin filter and concentrated to less than 0.5 mL by centrifugation (3220 x g, 2 h) at room temperature. The concentrated sample was rinsed three times with 8 M urea in 50 mM NH_4HCO_3 before transferring to a 15-mL Falcon tube that was methanol-chloroform compatible. The volumes were normalized and then the samples were flash frozen and stored at -70°C until ready for extraction.

Methanol-chloroform extraction. Any residual detergents or lipids were removed by performing a methanol-chloroform extraction.[1] Keeping each sample on ice, based on the sample volume (Svol), 4x the Svol of chilled methanol (-20°C) and 1x the Svol of chilled chloroform (-20°C) was added. The samples were vortexed gently before adding 3x Svol of chilled nanopure water (4°C) and vortexed to mix well before chilling on ice for 5 minutes. The layers were separated using centrifugation (8k x g, 4°C, 15 minutes) and the top layer was carefully removed and discarded. An additional 3x Svol was added to the tube, the sample was vortexed to mix well, and the proteins were isolated by centrifugation (8k x g, 4°C, 15 minutes) and removal of the supernatant. The protein pellet was allowed to dry completely under nitrogen before resuspending into 8 M urea in 50 mM NH_4HCO_3 and immediately digested.

Tryptic Digestion. The proteins were tryptically digested following a previously published protocol[2] with the following modifications. The proteins were first denatured with 5 mM dithiotreitol for 30 minutes at 60°C in a thermomixer. After cooling for a few minutes, the samples were diluted 10-fold with 50 mM NH_4HCO_3 and 1 mM $CaCl_2$ was added. A trypsin solution (1 µg/uL in 5 mM acetic acid, UBX) was added at an enzyme-to-protein ratio of 1:50 and the samples were incubated for 3 h at 37°C in a thermomixer. The digested proteins were desalted using a C18 SPE column (Supelco) and the final protein concentration was estimated using a BCA protein assay (Pierce). The concentrations were normalized and a portion was diluted to 0.1 ug/uL to be analyzed by LC-MS.

LC-MS Analysis. Data were acquired using a Velos Pro Orbitrap mass spectrometer (Thermo Scientific, San Jose, CA) outfitted with an electrospray ionization (ESI) interface coupled to custom built constant flow high-performance liquid chromatography (HPLC) system. The LC system consisted of two Agilent 1200 nanoflow pumps (Agilent Technologies, Santa Clara, CA), various Valco valves (Valco Instruments Co., Houston, TX), and a PAL autosampler (Leap Technologies, Carrboro, NC). Software developed in-house allowed for automated event coordination of two parallel reversed-phase analytical columns prepared in-house by slurry packing 3-µm Jupiter C18 (Phenomenex, Torrence, CA) into 40-cm x 360 µm o.d. x 75 µm i.d fused silica (Polymicro Technologies Inc., Phoenix, AZ) using a 1-cm sol-gel frit for media retention.[3] Electrospray emitters were custom made using 150 um o.d. x 20 um i.d. chemically etched fused silica.[4] Mobile phases consisted of 0.1% formic acid in water (A) and 0.1% formic acid acetonitrile (B) with a gradient profile as follows (min:%B); 0:5, 2:8, 20:12, 75:35, 97:60, 100: 85 at a flow rate of 300 nL/min. The gradient start was triggered 20 minutes after injecting a 5 uL sample aliquot with data acquisition beginning 15 minutes into the gradient to account for column dead volume. Ion transfer tube temperature and spray voltage were 350°C and 2.2 kV, respectively. Orbitrap spectra (AGC 1x106) were collected for 100 minutes over the mass (m/z) range of 400-2000 at a resolution of 60K followed by data dependent ion trap CID MS/MS (AGC 3x104) of the 10 most abundant ions using a collision energy of 35% and activation time 10 ms. A dynamic exclusion time of 60 seconds was used to discriminate against previously analyzed ions. The parallel use of two columns, allowed each column to be re-generated off-line at the end of each run.

Data search and protein identification. The MS/MS spectra from 15 LC-MS/MS datasets were converted to ASCII text (.dta format) using DeconMSn[5] which attempts to more precisely assign the charge and parent mass values to an MS/MS spectrum. The data files were then interrogated via target-decoy approach[6] using MSGFPlus[7] using a +/- 20 ppm parent mass tolerance, partially tryptic enzyme settings (one end of each candidate sequence must contain Lysine or Arginine), and a variable posttranslational modification of oxidized Methionine. All MS/MS search results for each dataset were collated into tab separated ASCII text.

Collated search results were further combined into a single result file. These results were imported into a Microsoft SQL Server database. Using decoy identifications (exactly reversed peptide sequences denoted as "XXX_" in their protein references), we determined the PSM level FDR to be less than 1% when using MSGFPlus's Q-value calculation (681 reversed PSMs from a total 71,995 filter passing PSMs using Q-value <= 0.01). Filter passing results were reported in Table S1. Using the protein references as a grouping term, unique peptides belonging to each protein were counted, as were all PSMs belonging to all peptides for that protein (i.e. a protein level observation count value). PSM observation counts were summed across biological replicates, and were also reported in the excel file. Using the pivot function in excel, a cross-tabulation table was created to enumerate protein level PSM observations for each of the five combined replicate samples, allowing low-precision quantitative comparisons to be made between each sample at the protein level.

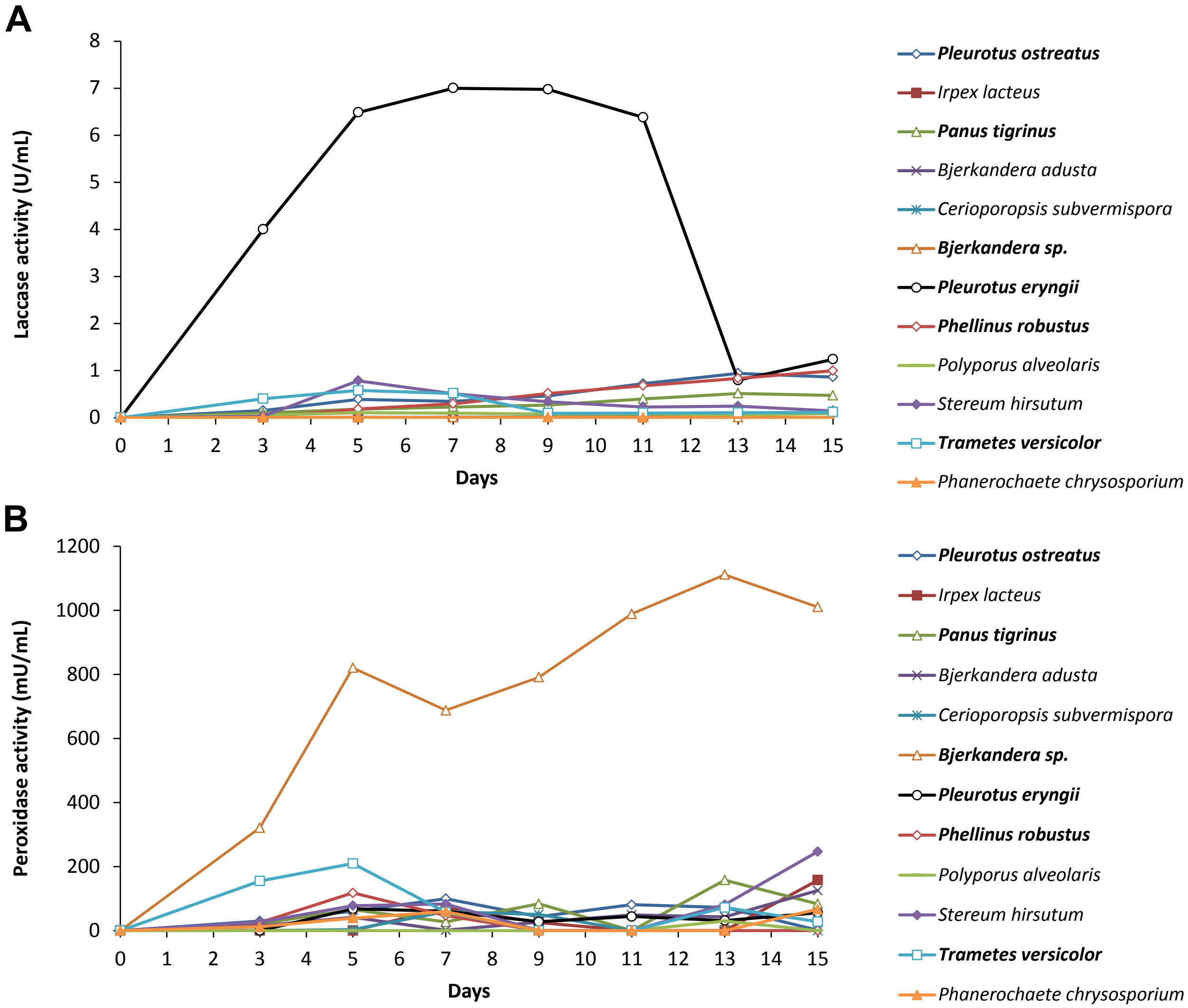
Protein sequences for each reported entry were subjected to BLAST analysis (version 2.2.28) using a combined collection of 2,784,909 fungal proteins reported in the Uniprot knowledgebase and NCBI as of September 2014. Results were imported into SQL Server and the highest-similarity identification (lowest e-value, highest percent similarity) extracted. As many of these matches resulted in an uncharacterized or hypothetical protein reference, the highest similarity non-hypothetical entry (does NOT contain "Uncharacterized", "predicted protein", "hypothetical", or "Unplaced") was also extracted for each query allowing for more useful biological inferences to be made. All BLAST results were imported into the excel file and related to the cross-tabulated results to allow further investigation. SignalP 4.0[8] was finally utilized to predict the presence of signal peptide cleavage sites in the detected proteins.

References

1. D. Wessel and U. I. Flugge, *Anal. Bioochem.*, 1984, 138, 141-143.
2. S. J. Callister, M. A. Domínguez, C. D. Nicora, X. Zeng, C. L. Tavano, S. Kaplan, T. J. Donohue, R. D. Smith and M. S. Lipton, *J. Proteome Res.*, 2006, 5, 1940-1947.
3. A. Maiolica, D. Borsotti and J. Rappsilber, *Proteomics*, 2005, 5, 3847-3850.
4. R. T. Kelly, J. S. Page, Q. Luo, R. J. Moore, D. J. Orton, K. Tang and R. D. Smith, *Anal. Chem.*, 2006, 78, 7796-7801.
5. A. M. Mayampurath, N. Jaitly, S. O. Purvine, M. E. Monroe, K. J. Auberry, J. N. Adkins and R. D. Smith, *Bioinformatics*, 2008, 24, 1021-1023.
6. J. E. Elias and S. P. Gygi, in *Proteome Bioinformatics*, eds. J. S. Hubbard and R. A. Jones, Humana Press, Totowa, NJ, 2010, DOI: 10.1007/978-1-60761-444-9_5, 55-71.
7. S. Kim and P. A. Pevzner, *Nat. Commun.*, 2014, 5.
8. T. N. Petersen, S. Brunak, G. von Heijne and H. Nielsen, *Nat. Meth.*, 2011, 8, 785-786.

Figures

Fig. S1: Detection of oxidoreductases in the secretome of twelve white-rot fungi: (A) Laccase activity tracked by the oxidation of 5 mM 2,2´-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS) at pH 5 and (B) peroxidase (e.g. manganese peroxidase (MnP) and versatile peroxidase (VP)) activity tracked by the oxidation of 0.1 mM $MnSO_4$ in the presence of 0.1 mM H_2O_2 at pH5. Data are the result of biological duplicates. The fungi presented in the manuscript are denoted in bold.



Tables:

Table S1: GPC results (M_p, M_n, M_w, PD) - associated to Fig. 4 in the main manuscript- from DMR-EH lignin before and after the enzyme treatments with the fungal secretomes at 3 and 6 days . Tables show the results from treatments with the *P. eryngii* secretome at **(A)** pH 4.5 and **(B)** pH 7, treatments with **(C)** *Bjerkandera* sp. secretome at pH 4.5 and treatments with **(D)** both fungal secretomes at pH 4.5. Enzyme treatments on DMR-EH lignin were conducted over 3 and 6 days at 30°C and 150 rpm. H_2O_2 and Mn^{2+} were added periodically to treatments containing peroxidases and to the corresponding controls (CTL). Enzyme dosages are expressed as U of enzyme per gram of DMR-EH lignin. Laccase (LA) and peroxidase (PE) activities were calculated following the oxidation of ABTS at the corresponding pH in the absence or the presence of Mn^{2+} and H_2O_2, respectively. The asterisk (*) highlights 3-day treatments.

(A) P. eryngii secretome pH 4.5

	Day	M_p	M_n	M_w	PD
CTL	**6**	4100	1900	12000	6.7
10 U/g	**6**	4100	1700	9600	5.7
50 U/g	**6**	3900	1500	7700	5.2
100 U/g	**6**	3600	1100	5600	4.9
100 U/g*	**3**	3600	1200	5400	4.6

(B) P. eryngii secretome pH 7

	Day	M_p	M_n	M_w	PD
CTL	**6**	3700	1300	6100	4.5
3 U/g	**6**	3800	1400	7400	5.3
15 U/g	**6**	3700	1500	5600	3.8
30 U/g	**6**	3200	840	3200	3.8
30 U/g*	**3**	390	530	2300	4.4

	Day	M_p	M_n	M_w	PD
CTL	**6**	4100	1800	12000	6.5
8 U/g	**6**	4100	2100	15000	7.1
40 U/g	**6**	3900	1900	11000	5.7
80 U/g	**6**	3500	950	5600	5.8
80 U/g*	**3**	4100	1700	11000	6.3

(C) Bjerkandera sp. secretome pH 4.5

	Day	M_p	M_n	M_w	PD
CTL	**6**	4100	1800	12000	6.5
5 U/g LA + 4 U/g PE	**6**	3900	1300	10000	7.9
25 U/g LA + 20 U/g PE	**6**	4100	1500	8800	6.0
50 U/g LA + 40 U/g PE	**6**	3400	620	3500	5.6
50 U/g LA + 40 U/g PE*	**3**	390	700	2000	2.9

(

Table S2: GPC results (M_p, M_n, M_w, PD) - associated to Fig. 4D in the main manuscript- as a function of time from *P. eryngii* secretome treatments at pH 7 over 4 days of incubation. DMR-EH lignin M_p, M_n, and PD by using different laccase dosages (3, 10, 30 U/g LA) from non-dialyzed secretomes. The asterisk (*) at 4 days corresponds to the control that contains boiled secretome.

Control	**M_p**	**M_n**	**PD**
1 d	3450 ± 50	1850 ± 150	3.2 ± 0.0
4 d	3400 ± 0	1800 ± 0	2.9 ± 0.2
4 d*	3450 ± 50	1850 ± 150	3.1 ± 0.0

3 U/g LA	**M_p**	**M_n**	**PD**
1 d	3550 ± 50	1300 ± 0	4.1 ± 0.0
2 d	3600 ± 0	1300 ± 0	4.0 ± 0.3
3 d	3350 ± 50	1250 ± 50	3.5 ± 0.2
4 d	3650 ± 50	1850 ± 50	3.0 ± 0.1

10 U/g LA	**M_p**	**M_n**	**PD**
1 d	3500 ± 100	1300 ± 0	4.2 ± 0.6
2 d	3400 ± 0	1250 ± 50	3.7 ± 0.0
3 d	3300 ± 0	1050 ± 50	3.4 ± 0.2
4 d	3500 ± 0	1500 ± 100	3.1 ± 0.1

30 U/g LA	**M_p**	**M_n**	**PD**
1 d	3350 ± 50	900 ± 100	3.8 ± 0.4
2 d	3250 ± 50	950 ± 50	4.6 ± 1.0
3 d	3200 ± 0	800 ± 0	3.8 ± 0.2
4 d	3350 ± 50	1150 ± 50	3.8 ± 0.1

Table S3: Incubation of DMR-EH lignin, the *P. eryngii* secretome, and *P. putida* KT2440 to demonstrate the microbial sink concept. (A) DMR-EH with fungal secretome and bacteria. **(B)** Bacterial growth after the treatment represented in (B). **(C)** DMR-EH lignin M_w obtained from the different treatments in the insoluble and soluble fractions. **(D)** GPC profiles of DMR-EH lignin and other GPC parameters from the insoluble fraction after the different treatments. **(E)** LC-MS/MS from the soluble fraction at the end point of the different treatments. DMR = DMR-EH with inactivated fungal secretome; DMR+S = DMR-EH with fungal secretome; DMR + B = DMR-EH with bacteria and inactivated secretome; DMR + S + B = DMR-EH with bacteria and fungal secretome; 4-HBA: 4-hydroxybenzoic acid; 4-HB: 4-hydroxybenzaldehyde.

	M_p	M_n	PD
DMR	3550 ± 50	1650 ± 50	5.0 ± 0.2
DMR + B	3567 ± 58	1633 ± 58	4.5 ± 0.1
DMR + S	3350 ± 50	1200 ± 100	4.3 ± 0.2
DMR + B + S	3100 ± 100	920 ± 10	4.0 ± 0.3

Table S4: Proteomic analysis of the secretome of *Pleurotus eryngii* after 9 days of incubation in the presence of DMR-EH lignin. Protein descriptions are based on the most similar fungal proteins found in Uniprot/NCBI databases (whose access numbers and fungal species are indicated) and organized by functional families: (A) oxidoreductases, (B) glycoside hydrolases, (C) proteinases, (D) esterases, (E) proteins with another function, and (F) proteins with unknown function. The analysis is the result of biological duplicates. E-values, identity, and the presence or absence of a signal peptide (predicted by SignalP) from the different proteins are also included. Proteins in each functional group are organized by "spectral mass counts number" in order of abundance.

(A) OXIDOREDUCTASES							
Best BLAST non-hypothetical					**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**	**E-value**	**Identity (%)**	**Average**	**Error**	
A0A0D2N8Y9_9AGAR	GMC oxidoreductase	*Hypholoma sublateritium*	0	53.06	**1890**	103	YES
Q96TR4_PLEOS	Laccase	*Pleurotus ostreatus*	0	98.08	**700**	69	YES
D3YBH4_PLEER	Aryl-alcohol oxidase	*Pleurotus eryngii*	0	99.16	**664**	1	YES
A0A0C2Y131_HEBCY	Copper radical oxidase	*Hebeloma cylindrosporum*	0	76.96	**275**	4	YES
Q9UVY4_PLEOS	Bilirubin oxidase	*Pleurotus ostreatus*	0	98.12	**268**	45	YES
A0A0D2N8Y9_9AGAR	GMC oxidoreductase	*Hypholoma sublateritium*	0	53.06	**259**	11	YES
B6V331_PLEER	Laccase	*Pleurotus eryngii*	0	100	**239**	2	YES
V2WWR3_MONRO	Putative FAD dependent oxidoreductase	*Moniliophthora roreri*	0	64.35	**206**	13	YES
A0AQZ6_PLEOS	POXA3b laccase small subunit	*Pleurotus ostreatus*	2E-124	97.31	**205**	15	YES
A0A067NSZ9_PLEOS	Laccase	*Pleurotus ostreatus*	0	94.55	**155**	1	YES
A0A067N4E7_PLEOS	DyP-type peroxidase	*Pleurotus ostreatus*	0	91.87	**118**	10	NO
A0A067PAG4_PLEOS	Putative GMC-oxidase	*Pleurotus ostreatus*	0	95.15	**113**	12	YES
A0A067NHL8_PLEOS	DyP-type peroxidase	*Pleurotus ostreatus*	0	97.48	**105**	7	YES
Q9P928_PLEPU	Aryl-alcohol oxidase	*Pleurotus pulmonaris*	0	50.17	**59**	5	YES
O94219_PLEER	Aryl-alcohol oxidase	*Pleurotus eryngii*	0	57.82	**50**	4	YES
V2XEX2_MONRO	Copper radical oxidase	*Moniliophthora roreri*	0	60.07	**44**	6	YES
gi|636619781|ref|XP_008041025.1|	Aldo/keto reductase	*Trametes versicolor*	3E-149	68.32	**43**	9	NO
M5BNG8_THACB	Glucose oxidase	*Thanatephorus cucumeris*	8E-173	46.31	**39**	1	YES
A0A0D2N8Y9_9AGAR	GMC oxidoreductase	*Hypholoma sublateritium*	0	53.06	**39**	4	YES
A0A0C3DRC3_9HOMO	Glyoxal oxidase	*Moniliophthora roreri*	0	72.33	**33**	1	YES
A0A0H2RBF2_9HOMO	Alcohol oxidase	*Schizopora paradoxa*	0	55.94	**28**	1	YES
A0A067NPB6_PLEOS	Multi-copper oxidase superfamily	*Pleurotus ostreatus*	0	95.01	**20**	4	YES
V2X5U0_MONRO	Tyrosinase central domain-containing protein	*Moniliophthora roreri*	2E-135	56.25	**18**	1	YES
B0DZR8_LACBS	Glyoxal oxidase	*Laccaria bicolor*	0	73.33	**16**	1	YES
A0A0C3DRC3_9HOMO	Glyoxal oxidase	*Rhizoctonia solani*	0	72.33	**14**	2	YES
gi|636608221|ref|XP_008035245.1|	Glyoxal oxidase precursor	*Trametes versicolor*	0	79.51	**14**	2	NO
V2X162_MONRO	Aryl-alcohol oxidase	*Moniliophthora roreri*	0	52.9	**11**	2	YES
gi|636621931|ref|XP_008042100.1|	Glyoxal oxidase precursor	*Trametes versicolor*	0	75.8	**9**	0	YES
gi|597979803|ref|XP_007363089.1|	GMC oxidoreductase	*Dichomitus squalens*	0	56.44	**7**	1	YES
gi|636621933|ref|XP_008042101.1|	FMN-linked oxidoreductase	*Trametes versicolor*	0	68.46	**7**	1	NO
V2WN23_MONRO	Aryl-alcohol oxidase	*Moniliophthora roreri*	1E-129	49.29	**6**	1	NO
D3YJ58_PLEER	Laccase	*Pleurotus eryngii*	0	99.81	**5**	1	YES
A0A0D7B374_9HOMO	FMN-linked oxidoreductase	*Cylindrobasidium torrendii*	2E-163	61.39	**5**	1	NO
A0A067NL45_PLEOS	Small subunit of laccase POXA3a	*Pleurotus ostreatus*	4E-118	94.57	**5**	2	YES

B5MAF4_PLEOS	Phenol oxidase	*Pleurotus ostreatus*	0	97.89	**5**	2	YES
A0A0D2N8Y9_9AGAR	GMC oxidoreductase	*Hypholoma sublateritium*	0	53.06	**4**	1	YES
A0A0D2N8Y9_9AGAR	GMC oxidoreductase	*Hypholoma sublateritium*	0	53.06	**3**	1	YES
A0A0D2KZY8_9AGAR	Copper radical oxidase	*Hypholoma sublateritium*	0	69.24	**3**	1	YES
A0A0D7B374_9HOMO	FMN-linked oxidoreductase	*Cylindrobasidium torrendii*	2E-163	61.39	**3**	1	NO
gi|597979803|ref|XP_007363089.1|	GMC oxidoreductase	*Dichomitus squalens*	0	56.44	**3**	1	YES
V2WIU4_MONRO	Glutathione-disulfide reductase	*Moniliophthora roreri*	0	77.22	**2**	1	NO
A0A067NUD9_PLEOS	Multi-copper oxidase	*Pleurotus ostreatus*	0	94.8	**2**	1	YES

(B) GLYCOSIDE HYDROLASES							
Best BLAST non-hypothetical			**E-value**	**Identity (%)**	**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**			**Average**	**Error**	
S7QEU8_GLOTA	Cerato-platanin	*Gloeophyllum trabeum*	3E-61	66.2	**971**	78	YES
gi|636609529|ref|XP_008035899.1|	Cerato-platanin	*Trametes versicolor*	2E-66	71.43	**519**	37	YES
G0TES6_PLEOS	Alfa-L-arabinofuranosidase	*Pleurotus ostreatus*	0	96.13	**195**	33	YES
A0A067NJI9_PLEOS	Glucoamylase	*Pleurotus ostreatus*	0	96.2	**140**	24	YES
A0A067NAN6_PLEOS	Glycoside hydrolase family 79 protein	*Pleurotus ostreatus*	0	97.25	**135**	9	YES
A0A067NTS1_PLEOS	1,3-beta-glucanosyltransferase	*Pleurotus ostreatus*	0	98.41	**126**	4	YES
A0A067P251_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	95.88	**75**	12	YES
A0A067NVM1_PLEOS	alpha-1,2-Mannosidase	*Pleurotus ostreatus*	0	97.41	**68**	16	YES
A0A067NV32_PLEOS	Carbohydrate-binding module family 13 protein	*Pleurotus ostreatus*	0	93.7	**60**	8	NO
A0A067NE06_PLEOS	Glycoside hydrolase family 32 protein	*Pleurotus ostreatus*	0	93.05	**60**	4	YES
A0A0D7BL56_9HOMO	Glycoside hydrolase family 30 protein	*Rhizoctonia solani*	0	61.39	**60**	8	YES
S3DB13_GLAL2	Six-hairpin glycosidase	*Glarea lozoyensis*	2E-164	40.32	**57**	27	YES
A0A067NYS5_PLEOS	Glycoside hydrolase family 79 protein	*Pleurotus ostreatus*	0	95.39	**56**	3	YES
A0A067P1A5_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	96.21	**50**	0	YES
A0A067NNN7_PLEOS	Glycoside hydrolase family 43 protein	*Pleurotus ostreatus*	0	88.99	**49**	1	YES
A0A074RMJ0_9HOMO	Putative glycoside hydrolase family 43 protein	*Rhizoctonia solani*	0	61.28	**47**	8	YES
A0A067N9V0_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	98.15	**45**	9	YES
A0A067NAE1_PLEOS	Carbohydrate-binding module family 13 protein	*Pleurotus ostreatus*	0	97.85	**42**	16	YES
A0A067NZH6_PLEOS	Glycoside hydrolase family 105 protein	*Pleurotus ostreatus*	0	94.19	**39**	6	NO
A0A067NZB6_PLEOS	Glycoside hydrolase family 17 protein	*Pleurotus ostreatus*	0	96.76	**31**	0	NO
A0A067NQ10_PLEOS	Alpha-galactosidase	*Pleurotus ostreatus*	0	89.84	**31**	5	YES
A0A067P1X3_PLEOS	Glycoside hydrolase family 16 protein	*Pleurotus ostreatus*	6E-174	96.36	**29**	5	YES
A0A067NLD3_PLEOS	Beta-xylanase	*Pleurotus ostreatus*	0	91.43	**28**	0	YES
A0A067P022_PLEOS	Glycoside hydrolase family 61 protein	*Pleurotus ostreatus*	3E-153	95.78	**28**	6	YES
A0A067NT33_PLEOS	Carbohydrate esterase family 12 protein	*Pleurotus ostreatus*	2E-170	97.64	**25**	1	YES
A0A067P7X8_PLEOS	Glycoside hydrolase family 105 protein	*Pleurotus ostreatus*	0	95.79	**24**	4	YES
V2XER0_MONRO	Alpha beta hydrolase fold family	*Moniliophthora roreri*	7E-155	52.53	**24**	2	NO
V2YA34_MONRO	Arabinofuranosidase	*Moniliophthora roreri*	7E-154	81.85	**20**	3	NO
A0A067NUA1_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	94.59	**18**	2	NO
A0A067NJP3_PLEOS	Glycoside hydrolase family 28 protein	*Pleurotus ostreatus*	0	96.92	**16**	1	YES
A0A067NTX6_PLEOS	Alpha-galactosidase	*Pleurotus ostreatus*	0	87.31	**14**	2	YES
A0A067PBN9_PLEOS	Glycoside hydrolase family 5 protein	*Pleurotus ostreatus*	0	98.76	**13**	3	YES
A0A0D6A8W8_PLEER	Glucanase	*Pleurotus eryngii*	0	96.29	**13**	4	YES
G3JQR4_CORMM	Glycoside hydrolase, family 25	*Cordyceps militaris*	6E-43	52.78	**13**	1	YES

A0A067P815_PLEOS	Glycoside hydrolase family 61 protein	*Pleurotus ostreatus*	4E-174	96.79	**13**	2	YES
A0A067NUL1_PLEOS	alpha-1,2-Mannosidase	*Pleurotus ostreatus*	0	87.94	**12**	1	YES
A0A067NXU0_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	96.06	**12**	3	YES
A0A067P1W9_PLEOS	Glycoside hydrolase family 16 protein	*Pleurotus ostreatus*	0	98.77	**12**	8	NO
A0A067P251_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	95.88	**12**	4	NO
A0A067N637_PLEOS	Glycoside hydrolase family 12 protein	*Pleurotus ostreatus*	4E-171	97.32	**12**	2	YES
A0A067P260_PLEOS	Glycoside hydrolase family 18 protein	*Pleurotus ostreatus*	0	96.61	**10**	1	YES
A0A067P3G0_PLEOS	Glycoside hydrolase family 43 protein	*Pleurotus ostreatus*	0	97.33	**10**	2	YES
A0A067NYF1_PLEOS	Glycoside hydrolase family 16 protein	*Pleurotus ostreatus*	0	92.86	**9**	2	YES
A0A067NUN5_PLEOS	Polysaccharide lyase family 8 protein	*Pleurotus ostreatus*	0	96.44	**9**	1	YES
A0A067N976_PLEOS	Glycoside hydrolase family 18 protein	*Pleurotus ostreatus*	0	95	**8**	4	YES
B0D2X1_LACBS	Cerato-platanin-related secreted protein	*Laccaria bicolor*	2E-45	55.47	**8**	4	YES
A0A067N715_PLEOS	Glycoside hydrolase family 28	*Pleurotus ostreatus*	0	93.01	**7**	3	YES
V2XUY0_MONRO	Glycoside hydrolase family 16 protein	*Moniliophthora roreri*	2E-117	69.41	**7**	3	YES
A0A067NFB3_PLEOS	Beta-galactosidase	*Pleurotus ostreatus*	0	95.38	**7**	4	NO
A0A067P149_PLEOS	Glycoside hydrolase family 31	*Pleurotus ostreatus*	0	95.81	**7**	3	YES
A0A067NPC3_PLEOS	Beta-hexosaminidase	*Pleurotus ostreatus*	0	93.49	**7**	4	YES
A0A067NXA3_PLEOS	Glycoside hydrolase family 28 protein	*Pleurotus ostreatus*	0	82.72	**7**	1	YES
A0A067NYG5_PLEOS	Polysaccharide lyase family 1 protein	*Pleurotus ostreatus*	1E-178	90.38	**7**	1	YES
A0A0D2KN72_9AGAR	Carbohydrate-binding module family 50 protein	*Hypholoma sublateritium*	1E-27	49.56	**6**	0	YES
A0A067NIV2_PLEOS	Glycoside hydrolase family 61 protein	*Pleurotus ostreatus*	5E-116	81.07	**6**	4	YES
A0A067PDP4_9HOMO	Carbohydrate-binding module 1 protein	*Jaapia argillacea*	0	64.91	**6**	1	NO
A0A067P0F8_PLEOS	Glycoside hydrolase family 16 protein	*Pleurotus ostreatus*	0	97.12	**6**	1	YES
A0A067N6T7_PLEOS	Glycoside hydrolase family 3 protein	*Pleurotus ostreatus*	0	94.07	**5**	1	YES
A0A067NXA3_PLEOS	Glycoside hydrolase family 28 protein	*Pleurotus ostreatus*	0	82.72	**5**	2	YES
A0A067NRR9_PLEOS	Polysaccharide lyase family 8 protein	*Pleurotus ostreatus*	0	95.98	**5**	1	YES
A0A067P3Z6_PLEOS	Glycoside hydrolase family 5 protein	*Pleurotus ostreatus*	0	98.48	**5**	1	NO
M5A7J8_GRIFR	Cerato-platanin-like protein 1	*Grifola frondosa*	3E-55	62.67	**5**	1	YES
A0A067NI47_PLEOS	Glycoside hydrolase family 30 protein	*Pleurotus ostreatus*	0	97.18	**4**	0	YES
A0A067P6M4_PLEOS	Carbohydrate-binding module family 13 protein	*Pleurotus ostreatus*	4E-101	92.26	**4**	2	YES
A0A067NX11_PLEOS	Glycoside hydrolase family 92 protein	*Pleurotus ostreatus*	0	93.38	**4**	1	NO
A0A067NUF0_PLEOS	Carbohydrate-binding module family 13 protein	*Pleurotus ostreatus*	2E-104	96.77	**3**	0	YES
A0A067PDE2_PLEOS	Glycoside hydrolase family 55 protein	*Pleurotus ostreatus*	0	97.2	**3**	0	YES
S7S1G5_GLOTA	Glycoside hydrolase	*Gloeophyllum trabeum*	8E-114	48.82	**3**		YES
A0A067NUM1_PLEOS	Glycoside hydrolase family 5 protein	*Pleurotus ostreatus*	0	91.09	**3**	0	YES
G3JQR4_CORMM	Glycoside hydrolase, family 25	*Cordyceps militaris*	6E-43	52.78	**3**	0	NO
A0A067P0T8_PLEOS	Glycoside hydrolase family 88 protein	*Pleurotus ostreatus*	0	93.4	**3**		NO
A0A067NB35_PLEOS	Beta-galactosidase	*Pleurotus ostreatus*	0	90.66	**3**	1	NO
A0A067N6L2_PLEOS	Glycoside hydrolase family 78 protein	*Pleurotus ostreatus*	0	94.12	**3**	1	YES
V2XVB2_MONRO	Glycoside hydrolase family 18 protein	*Moniliophthora roreri*	1E-163	67.47	**3**	1	YES
A0A067NB35_PLEOS	Beta-galactosidase	*Pleurotus ostreatus*	0	90.66	**2**	0	YES
A0A067NHA4_PLEOS	Glycoside hydrolase family 61 protein	*Pleurotus ostreatus*	0	89.46	**2**	0	YES
B0CU10_LACBS	MFS monosaccharide transporter	*Laccaria bicolor*	0	78.8	**2**	0	NO
A0A067NQW1_PLEOS	Trehalase	*Pleurotus ostreatus*	0	95.4	**2**	0	YES
A0A067P685_PLEOS	Arabinogalactan endo-beta-1,4-galactanase	*Pleurotus ostreatus*	0	93.59	**2**	1	YES
A0A067NLV1_PLEOS	Glycoside hydrolase family 79 protein	*Pleurotus ostreatus*	0	96.75	**2**	1	YES
A0A067NL40_PLEOS	Carbohydrate-binding module family 13 protein	*Pleurotus ostreatus*	0	97.31	**2**	1	YES
A0A067P3L9_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	96.9	**2**	0	YES
A0A0C2XGR8_AMAMU	Glycoside hydrolase family 125 protein	*Amanita muscaria*	0	77.38	**2**	1	NO

(C) PROTEINASES							
Best BLAST non-hypothetical			**E-value**	**Identity (%)**	**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**			**Average**	**Error**	
A6P7M6_CHLMY	Peptidyl-Lys metalloendopeptidase	*Chlorophyllum molybdites*	2E-149	61.32	**421**	16	YES
V2X6J0_MONRO	Tripeptidyl peptidase a	*Moniliophthora roreri*	0	60.54	**350**	22	YES
Q6ZYK6_PLEOS	Subtilisin-like protease	*Pleurotus ostreatus*	0	97.31	**183**	21	YES
A0A097IYG6_PLEER	Serine proteinase	*Ashbya gossypii*	2E-178	67.52	**119**	3	YES
K9HY03_AGABB	Carboxypeptidase	*Agaricus bisporus var. bisporus*	0	75	**92**	4	YES
A0A067NYE7_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	96.65	**85**	8	YES
V2XDI6_MONRO	Aspartic peptidase a1	*Moniliophthora roreri*	3E-157	57.27	**51**	7	YES
A0A0D7BN91_9HOMO	Extracellular elastinolytic metallo proteinase	*Rhizoctonia solani*	0	65.85	**48**	12	NO
A0A067N455_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	88.81	**47**	1	NO
A0A097IYG6_PLEER	Serine proteinase	*Pleurotus eryngii*	2E-178	67.52	**31**	4	YES
U6A6W7_PLEOS	Aspartic protease	*Pleurotus ostreatus*	0	98.01	**31**	8	YES
X8IWS6_9HOMO	Peptidase family s41 domain protein, putative	*Rhizoctonia solani*	4E-163	41.69	**28**	1	YES
Q8TGE4_COPCI	Leucine aminopeptidase	*Coprinopsis cinerea*	0	72.95	**27**	6	NO
V2XQK0_MONRO	Tripeptidyl peptidase	*Moniliophthora roreri*	0	69.04	**26**	7	YES
S7QH46_GLOTA	Zn-dependent exopeptidase	*Gloeophyllum trabeum*	0	58.73	**24**	8	NO
gi|597911709|ref|XP_007303153.1|	Zn-dependent exopeptidase	*Stereum hirsutum*	0	61.62	**23**	0	NO
gi|597972679|ref|XP_007361264.1|	Creatinase/aminopeptidase [LYAD-421 SS1]	*Dichomitus squalens*	5E-144	51.47	**18**	1	NO
W4JMJ9_9HOMO	Serine protease S8	*Heterobasidion irregulare*	0	64.26	**18**	1	YES
A0A067N859_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	89.87	**17**	4	YES
B0DCT4_LACBS	Aspartic peptidase A1	*Coprinopsis cinerea*	3E-138	53.37	**14**	1	YES
S7RKM8_GLOTA	Acid protease	*Laccaria bicolor*	0	47.68	**14**	2	NO
W4KN38_9HOMO	Aspartic peptidase	*Heterobasidion irregulare*	0	70.77	**10**	3	YES
A0A067NV51_PLEOS	Dipeptidase	*Pleurotus ostreatus*	0	95.74	**7**	1	NO
gi|636607343|ref|XP_008034806.1|	peptidase S28	*Trametes versicolor*	0	68.33	**7**	1	YES
A0A067N7S5_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	93.12	**6**	0	NO
X8IVN7_9HOMO	IgA peptidase M64	*Rhizoctonia solani*	8E-150	49.03	**6**	1	YES
A8NGX3_COPC7	Leucyl aminopeptidase	*Coprinopsis cinerea*	0	64.71	**6**	1	NO
S7S0P1_GLOTA	Peptidase M18, aminopeptidase	*Gloeophyllum trabeum*	0	78.94	**5**	3	NO
A0A067NXD4_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	95.31	**4**	1	YES
A0A067NID9_PLEOS	Peptide hydrolase	*Pleurotus ostreatus*	0	93.9	**4**	4	YES
V2XZJ8_MONRO	Zinc metalloprotease	*Moniliophthora roreri*	0	69.06	**4**	1	NO
W4JQ52_9HOMO	Metallo peptidase M36	*Heterobasidion irregulare*	0	69.98	**3**	1	YES
S8EK55_FOMPI	Proline iminopeptidase	*Fomitopsis pinicola*	0	82.69	**3**	1	NO
B0D4S6_LACBS	Glutamate carboxypeptidase	*Laccaria bicolor*	0	80.92	**2**	1	NO
A0A077K7X8_PLEER	Serine aminopeptidase	*Pleurotus eryngii*	0	80.34	**2**	1	NO

(D) ESTERASES							
Best BLAST non-hypothetical			**E-value**	**Identity (%)**	**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**			**Average**	**Error**	
A0A067NTY7_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	97.37	**151**	10	YES
A0A067NAF9_PLEOS	Carboxylic ester hydrolase	*Pleurotus ostreatus*	0	91.54	**84**	11	YES
A0A067NUV8_PLEOS	Pectinesterase	*Pleurotus ostreatus*	0	97.01	**80**	5	YES
A0A067NJF8_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	2E-159	91.25	**75**	23	YES
V2YSM2_MONRO	Carbohydrate esterase family 12 protein	*Moniliophthora roreri*	2E-119	67.35	**68**	11	YES
A0A067PBW7_PLEOS	Carboxylic ester hydrolase	*Pleurotus ostreatus*	0	97.14	**54**	4	YES
V6BP73_PLEER	Carboxylic ester hydrolase	*Pleurotus eryngii*	0	99.64	**38**	4	YES
A0A067NPE5_PLEOS	Carbohydrate esterase family 8	*Pleurotus ostreatus*	0	94.12	**37**	0	YES
W4KLA6_9HOMO	Carbohydrate esterase family 4 protein	*Heterobasidion irregulare*	0	75.49	**29**	10	YES
A0A067N5U7_PLEOS	Carbohydrate esterase family 1 protein	*Pleurotus ostreatus*	0	97.56	**28**	4	YES
A0A067NXE9_PLEOS	Carboxylic ester hydrolase	*Pleurotus ostreatus*	0	98.89	**21**	9	YES
A0A067NLL5_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	96.05	**18**	4	YES
S7RRX7_GLOTA	Carbohydrate esterase family 9 protein	*Gloeophyllum trabeum*	0	62.42	**17**	3	NO
A0A0F7VK25_9AGAR	GDSL like lipase	*Pleurotus sapidus*	0	95.27	**12**	3	YES
gi|599118120|ref|XP_007386740.1|	Lipase	*Punctularia strigosozonata*	2E-137	63.12	**12**	1	YES
A0A067NF84_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	97.64	**12**	1	YES
V2YES2_MONRO	Carbohydrate esterase family 16 protein	*Moniliophthora roreri*	3E-136	56.95	**10**	8	YES
A0A067N8C4_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	2E-176	97.96	**7**	4	YES
A0A067NL12_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	96.77	**6**	1	YES
B0D886_LACBS	Carbohydrate esterase family 9 protein	*Laccaria bicolor*	0	65.41	**4**	0	NO
A0A067NGD7_PLEOS	Carbohydrate esterase family 4 protein	*Pleurotus ostreatus*	0	97.58	**4**	1	YES
gi|597968945|ref|XP_007360303.1|	PLC-like phosphodiesterase	*Dichomitus squalens*	2E-143	66.9	**2**	0	YES
A0A067NLJ6_PLEOS	Carboxylic ester hydrolase	*Pleurotus ostreatus*	0	94.61	**2**	0	YES

(E) OTHER FUNCTION							
Best BLAST non-hypothetical			**E-value**	**Identity (%)**	**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**			**Average**	**Error**	
R8BRC1_TOGMI	Putative virulence plasmid b protein	*Togninia minima*	2E-50	23.76	**229**	6	NO
V2WWH5_MONRO	Serine-threonine rich	*Moniliophthora roreri*	2E-21	38.1	**185**	40	YES
V2X6R9_MONRO	Oxalate decarboxylase	*Moniliophthora roreri*	0	74.19	**159**	11	YES
gi|636610047|ref|XP_008036158.1|	Immunomodulatory protein	*Trametes versicolor*	2E-49	65.38	**130**	20	YES
V2XJ06_MONRO	Membrane autotransporter barrel domain protein	*Moniliophthora roreri*	0	62.71	**89**	8	YES
X8J981_9HOMO	Transmembrane protein, putative	*Rhizoctonia solani*	2E-28	36.96	**85**	8	YES
R9AHX0_WALI9	Coiled-coil domain-containing protein	*Wallemia ichthyophaga*	4E-88	64.52	**74**	10	YES
V2YLX4_MONRO	Extracellular dioxygenase	*Moniliophthora roreri*	2E-94	53.44	**72**	8	YES
Q75VR2_PLEER	Ribonuclease T2	*Pleurotus eryngii*	0	91.06	**61**	4	YES
M2PP67_CERS8	CsMn38	*Ceriporiopsis subvermispora*	1E-32	52.67	**59**	13	YES
A0A086T8T8_ACRCH	Mediator of RNA polymerase II transcription subunit-like protein	*Acremonium chrysogenum*	2.3	31.33	**51**	1	NO
A0A0A1UUM1_9HYPO	Ketosteroid isomerase-like protein	*Metarhizium robertsii*	0.0005	28.67	**51**	6	YES
I6UR56_ENCHA	Cyclin-dependent protein	*Encephalitozoon hellem*	0.004	28.07	**48**	18	YES
V2YLU2_MONRO	Nhl repeat-containing protein	*Moniliophthora roreri*	1E-154	55.33	**46**	3	YES

gi|636607513|ref|XP_008034891.1|	Galactose mutarotase-like protein	*Trametes versicolor*	0	71.15	**44**	0	YES
A0A067NZB1_PLEOS	S-adenosylmethionine synthase	*Pleurotus ostreatus*	0	99.48	**40**	4	NO
Q753M7_ASHGO	AFR285Cp	*Ashbya gossypii*	3E-50	100	**40**	2	NO
A0A0D7BTI4_9HOMO	Class I glutamine amidotransferase-like protein	*Rhizoctonia solani*	2E-81	57.01	**39**	2	NO
M5BXC7_THACB	Pathogenesis-related protein 5	*Thanatephorus cucumeris*	8E-143	78.04	**38**	2	YES
B1Q4S7_PLEOS	Ribonuclease T1	*Pleurotus ostreatus*	1E-81	95.24	**35**	3	YES
Q9P356_LENED	Nuclease Le1	*Lentinula edodes*	5E-105	62.18	**35**	1	NO
V2WHJ4_MONRO	Chitin synthase	*Moniliophthora roreri*	4E-11	34.93	**35**	0	NO
V2XER0_MONRO	Alpha beta hydrolase fold family	*Moniliophthora roreri*	7E-155	52.53	**35**	2	NO
G9MD63_PLEOS	Glyceraldehyde-3-phosphate dehydrogenase	*Pleurotus ostreatus*	0	100	**32**	4	NO
A0A074S4Z0_9HOMO	Putative Ran-binding protein	*Rhizoctonia solani*	2E-94	66.05	**31**	4	YES
G4THH4_PIRID	Related to TY3B-TY3B protein	*Piriformospora indica*	0.73	27.27	**28**	6	NO
A0A067P1S4_PLEOS	Aspartate aminotransferase	*Pleurotus ostreatus*	0	97.8	**28**	1	NO
V2XHH7_MONRO	Fad binding domain-containing protein	*Moniliophthora roreri*	5E-150	45.68	**27**	4	YES
A0A067NPM1_PLEOS	Superoxide dismutase	*Pleurotus ostreatus*	1E-118	89.23	**27**	8	NO
V2XBH5_MONRO	Formate dehydrogenase	*Moniliophthora roreri*	0	87.64	**26**	1	NO
A0A0A8IBD8_PLEOS	Lipoxygenase	*Pleurotus ostreatus*	0	97.51	**26**	4	NO
A0A067NEK4_PLEOS	Peptidyl-prolyl cis-trans isomerase	*Pleurotus ostreatus*	3E-110	96.91	**26**	5	NO
gi|595777092|ref|XP_007267089.1|	Alpha/beta-hydrolase	*Fomitiporia mediterranea*	3E-69	44.33	**24**	4	YES
gi|597901894|ref|XP_007298246.1|	Dienelactone hydrolase	*Stereum hirsutum*	2E-168	82.18	**23**	0	NO
gi|628835621|ref|XP_007768114.1|	Alpha beta-hydrolase	*Coniophora puteana*	1E-145	59.52	**23**	4	YES
E2LF87_MONPE	Enolase	*Moniliophthora perniciosa*	0	95.58	**21**	6	NO
A0A067NCD3_PLEOS	Transaldolase	*Pleurotus ostreatus*	0	98.77	**20**	3	NO
gi|597911309|ref|XP_007302953.1|	Cobalamin-independent methionine synthase	*Stereum hirsutum*	0	85.36	**20**	3	NO
V2WXW2_MONRO	Major royal jelly protein	*Moniliophthora roreri*	0	68.3	**20**	7	NO
X8JFA9_9HOMO	Cytochrome b2 (L-lactate ferricytochrome C oxidoreductase)	*Rhizoctonia solani*	2E-121	55.98	**20**	5	YES
V2X4P6_MONRO	Acetyl-hydrolase	*Moniliophthora roreri*	0	82.2	**20**	2	NO
A0A0D7BIU0_9HOMO	Cupredoxin	*Rhizoctonia solani*	2E-98	51.98	**20**	1	YES
S7PXC3_GLOTA	Malate dehydrogenase	*Gloeophyllum trabeum*	5E-71	48.73	**19**	1	YES
X8JM78_9HOMO	GEgh 16 protein, putative	*Rhizoctonia solani*	7E-83	70.97	**17**	1	YES
A0A067NID3_PLEOS	tRNA pseudouridine synthase	*Pleurotus ostreatus*	0	84.28	**17**	1	NO
gi|599119355|ref|XP_007387147.1|	NAD(P)-binding protein	*Punctularia strigosozonata*	1E-104	62.99	**15**	1	NO
V2X1Q4_MONRO	Fumarylacetoacetate hydrolase domain-containing protein 2a	*Moniliophthora roreri*	7E-137	63.37	**15**	6	YES
A8NBU8_COPC7	Carbonic anhydrase	*Coprinopsis cinerea*	3E-50	53.94	**14**	3	NO
S7PXC3_GLOTA	Malate dehydrogenase	*Gloeophyllum trabeum*	5E-71	48.73	**13**	3	YES
V2XER0_MONRO	Alpha beta hydrolase fold family	*Moniliophthora roreri*	7E-155	52.53	**13**	6	YES
Q9C1M8_PLESA	Catalase	*Pleurotus sajor-caju*	0	97.35	**13**	2	NO
gi|595777736|ref|XP_007267411.1|	Amidase signature enzyme	*Fomitiporia mediterranea*	0	77.52	**13**	8	NO
A0A0D7BR14_9HOMO	Aldehyde dehydrogenase	*Cylindrobasidium torrendii*	0	73.19	**11**	1	NO
A0A0C6DUW9_GRIFR	Gf.ODC1 protein	*Polyporus frondosus*	0	72.27	**11**	1	YES
A0A086TGA7_ACRCH	Serine/threonine-protein kinase-like protein	*Acremonium chrysogenum*	0.007	31.31	**11**	4	YES
A0A074S9X6_9HOMO	Putative six-hairpin glycosidase-like protein	*Rhizoctonia solani*	0	54.79	**11**	4	YES
B0DJI3_LACBS	Ectomycorrhiza-regulated small secreted protein	*Laccaria bicolor*	0.37	22.56	**10**	5	YES
M2PP67_CERS8	CsMn38	*Ceriporiopsis subvermispora*	1E-32	52.67	**10**	6	YES
G4THH4_PIRID	Related to TY3B-TY3B protein	*Piriformospora indica*	0.73	27.27	**10**	1	NO
V2WRU0_MONRO	Putative actin filament organization protein App1-like	*Moniliophthora roreri*	1E-115	51.08	**9**	0	YES

B0E0N3_LACBS	NADP-dependent mannitol dehydrogenase MtDH	*Laccaria bicolor*	7E-151	78.24	**9**	4	NO
A0A0C3FTH1_9HOMO	Glucooligosaccharide oxidase	*Rhizoctonia solani*	6E-158	54.77	**9**	1	YES
V2WRN7_MONRO	Macrofage activating glycoprotein	*Moniliophthora roreri*	7E-148	59.83	**9**	1	YES
A0A067NZL3_PLEOS	Transaldolase	*Pleurotus ostreatus*	0	98.77	**8**	1	NO
V2XDY3_MONRO	D-lactonohydrolase-like protein	*Moniliophthora roreri*	0	74.39	**8**	3	NO
A0A074RKL3_9HOMO	Ferritin-like protein	*Rhizoctonia solani*	1E-18	36.9	**8**	3	NO
A0A067NUP7_PLEOS	Aspartate aminotransferase	*Pleurotus ostreatus*	0	99.06	**8**	1	NO
L8WU55_THACA	SKG6 domain-containing protein	*Thanatephorus cucumeris*	7E-47	37.74	**8**	2	YES
A0A067NKD5_PLEOS	Peptidyl-prolyl cis-trans isomerase	*Pleurotus ostreatus*	8E-87	93.94	**8**	1	NO
A0A0A8L9E4_9SACH	Coatomer subunit alpha	*Kluyveromyces dobzhanskii*	5.7	31.08	**8**	1	NO
A0A074RTR7_9HOMO	Protein transporter Sec23	*Rhizoctonia solani*	1E-51	40.43	**8**	1	NO
V2XK68_MONRO	Dj-1 family protein	*Moniliophthora roreri*	2E-97	65.12	**8**	1	YES
X8IX14_9HOMO	Ferritin-like protein	*Rhizoctonia solani*	0.000006	32.09	**8**	2	NO
V2YID8_MONRO	Vacuolar protein	*Moniliophthora roreri*	0	65.38	**7**	3	YES
A0A067NH04_PLEOS	Profilin	*Pleurotus ostreatus*	2E-74	90.48	**7**	1	NO
B6HJZ8_PENCW	Pc21g02480 protein	*Penicillium chrysogenum*	8E-12	35.9	**7**	1	YES
D2JY76_PLEOS	Superoxide dismutase	*Pleurotus ostreatus*	8E-118	97.24	**7**	5	NO
M5G747_DACSP	DUTP diphosphatase	*Dacryopinax sp.*	2E-86	91.97	**7**	4	NO
V2WRN7_MONRO	Macrofage activating glycoprotein	*Moniliophthora roreri*	7E-148	59.83	**7**	1	YES
A0A074S4Z0_9HOMO	Putative Ran-binding protein	*Rhizoctonia solani*	2E-94	66.05	**7**	2	YES
G7XH64_ASPKW	Similar to An15g00620	*Aspergillus kawachii*	5E-09	31.43	**7**	2	NO
A0A0B4GK80_9HYPO	FAD binding domain-containing protein	*Metarhizium brunneum*	2.6	30.28	**7**	1	NO
S7RVM0_GLOTA	Phytase	*Gloeophyllum trabeum*	0	62.78	**7**	1	NO
A0A0D1E1U3_USTMA	Chromosome 5, whole genome shotgun sequence	*Ustilago maydis*	1E-10	28.57	**6**	4	YES
gi|597971127|ref|XP_007360861.1|	Cofactor-independent phosphoglycerate mutase	*Dichomitus squalens*	0	80.46	**6**	3	NO
V2Y6M8_MONRO	Ornithine aminotransferase	*Moniliophthora roreri*	0	80.09	**6**	1	NO
A8NV50_COPC7	WSC domain-containing protein	*Coprinopsis cinerea (*	8E-162	60.7	**6**	1	YES
V2WGW3_MONRO	Aldolase citrate lyase family protein	*Moniliophthora roreri*	6E-117	64.55	**6**	2	NO
gi|599112879|ref|XP_007385021.1|	Eliciting plant response-like protein	*Punctularia strigosozonata*	4E-40	60.19	**6**	1	NO
V2XHB5_MONRO	Hesp-379-like protein	*Moniliophthora roreri*	5E-41	45.24	**6**	2	YES
gi|595786154|ref|XP_007271620.1|	PEBP-like protein	*Fomitiporia mediterranea*	9E-67	56.44	**6**	4	YES
V2XD50_MONRO	Short-chain dehydrogenase reductase sdr	*Moniliophthora roreri*	2E-120	68.38	**6**	1	NO
V2W6S8_MONRO	Epoxide hydrolase	*Moniliophthora roreri*	4E-116	50.61	**6**	2	NO
H1AFL5_PLEOS	Glyceraldehyde-3-phosphate dehydrogenase	*Pleurotus ostreatus*	0	98.98	**5**	3	NO
V2YGF9_MONRO	Chitin binding	*Moniliophthora roreri*	2E-77	63.01	**5**	0	YES
A0A0D7BAF1_9HOMO	Inorganic diphosphatase	*Cylindrobasidium torrendii*	0	88.18	**5**	0	NO
L8WD12_THACA	GPI-anchored domain-containing protein	*Rhizoctonia solani*	2E-27	46.4	**5**	1	YES
A0A0B2X373_9HYPO	Extracellular serine-rich protein	*Metarhizium album*	2E-20	44.6	**5**	0	YES
gi|628838035|ref|XP_007769308.1|	Heat shock protein	*Coniophora puteana*	0	89.32	**5**	2	NO
V2X3A6_MONRO	Serine-threonine protein phosphatase	*Moniliophthora roreri*	6E-178	72.98	**5**	1	YES
gi|636620133|ref|XP_008041201.1|	D-lactonohydrolase-like protein	*Trametes versicolor*	2E-142	54.93	**5**	1	YES
A0A0A1ULS1_9HOMO	Ricin-type beta-trefoil lectin domain protein	*Rhizoctonia solani*	3.1	27.68	**5**	1	NO
B0CU00_LACBS	Phosphoglucomutase	*Laccaria bicolor*	0	84.42	**5**	1	NO
S7Q8D4_GLOTA	Sure-like protein	*Gloeophyllum trabeum*	5E-116	59.79	**5**	4	YES
A0A0H2STW2_9HOMO	Cupredoxin	*Schizopora paradoxa*	2E-95	43.38	**5**	1	YES
gi|597907694|ref|XP_007301146.1|	Heat shock protein 70	*Stereum hirsutum*	0	94.27	**4**	3	NO
A0A067N5Y3_PLEOS	Dihydrolipoyl dehydrogenase	*Pleurotus ostreatus*	0	98.23	**4**	1	NO
V2XB56_MONRO	Neutral ceramidase	*Moniliophthora roreri*	0	70.99	**4**	0	YES
V2X4R1_MONRO	Stomatin family protein	*Moniliophthora roreri*	0	80.74	**4**	1	NO

gi|595777092|ref|XP_007267089.1|	Alpha/beta-hydrolase	*Fomitiporia mediterranea*	3E-69	44.33	**4**	3	YES
gi|628829085|ref|XP_007764846.1|	FAS1 domain-containing protein	*Coniophora puteana*	5E-81	35.28	**4**	0	YES
V2YHR5_MONRO	Abhydrolase domain-containing protein 12	*Moniliophthora roreri*	5E-129	49.23	**4**	1	NO
A0A0D7AGU2_9AGAR	Arginase/deacetylase	*Fistulina hepatica*	0	78.12	**4**	0	YES
A0A099P3U9_PICKU	Serine/threonine-protein kinase	*Pichia kudriavzevii*	2.8	28.3	**4**	3	NO
R7S5S7_PUNST	GroES-like protein	*Punctularia strigosozonata*	0.46	31.36	**4**		NO
B6GW49_PENCW	Pc06g01100 protein	*Penicillium chrysogenum*	2E-22	34.8	**4**		NO
V2XJA5_MONRO	Cellular morphogenesis protein	*Moniliophthora roreri*	0	57.77	**4**	1	YES
V2XIT2_MONRO	Glutamyl-trna amidotransferase subunit a	*Moniliophthora roreri*	0	72.69	**4**		NO
V2WVC1_MONRO	Phosphatidylserine decarboxylase	*Moniliophthora roreri*	0	72.85	**4**	2	NO
A0A067NS53_PLEOS	Pyruvate carboxylase	*Pleurotus ostreatus*	0	99	**4**	2	NO
A0A067NYN3_PLEOS	6,7-dimethyl-8-ribityllumazine synthase	*Pleurotus ostreatus*	2E-151	98.58	**4**	2	NO
X8JFM1_9HOMO	Transmembrane protein, putative	*Rhizoctonia solani*	5E-42	30.1	**4**	1	NO
V2XHI8_MONRO	Phospholipase C/P1 nuclease	*Moniliophthora roreri*	5E-149	54	**4**	1	YES
V2X5R0_MONRO	Immunomodulatory protein	*Pleurotus ostreatus*	8E-09	26.78	**4**	1	YES
A0A067N4P4_PLEOS	OPT superfamily	*Pleurotus ostreatus*	0	97.58	**4**	1	NO
V2XPL7_MONRO	Fumarylacetoacetate hydrolase	*Moniliophthora roreri*	5E-165	74.34	**4**	1	NO
A0A067N7N9_PLEOS	Fet3 ferroxidase	*Pleurotus ostreatus*	0	98.73	**4**	1	YES
V2YRZ7_MONRO	Gpi-anchored small secreted protein	*Moniliophthora roreri*	6E-26	41.13	**4**	1	YES
V2XAL1_MONRO	Guanine nucleotide binding protein beta subunit 2	*Moniliophthora roreri*	0	96.29	**3**	0	NO
V2XDS5_MONRO	Fumarate reductase	*Moniliophthora roreri*	0	84.3	**3**		NO
A0A0D7B1T3_9HOMO	1-Cys peroxiredoxin isozyme	*Cylindrobasidium torrendii*	8E-93	78.36	**3**		NO
V2X374_MONRO	Sub60s ribosomal protein	*Moniliophthora roreri*	7E-117	90.32	**3**		NO
S7QCY4_GLOTA	Sm-like ribonucleo protein	*Gloeophyllum trabeum*	1E-79	95.31	**3**		NO
A0A067NV87_PLEOS	Glucose-6-phosphate isomerase	*Pleurotus ostreatus*	0	99.09	**3**		NO
A0A067TDZ6_9AGAR	3,4-dihydroxy-2-butanone 4-phosphate synthase	*Galerina marginata*	1E-121	66.27	**3**		NO
V2XER0_MONRO	Alpha beta hydrolase fold family	*Moniliophthora roreri*	7E-155	52.53	**3**	0	YES
X8IZK9_9HOMO	Allergen protein	*Rhizoctonia solani*	3E-81	72.62	**3**	0	YES
A0A0C3G6Z6_9HOMO	Imidazoleglycerol-phosphate dehydratase	*Piloderma croceum*	8E-135	91.54	**3**	0	NO
W4JRY9_9HOMO	Lep6-lignin expressed protein 6	*Heterobasidion irregulare*	5E-28	27.58	**3**	0	NO
V2WWY6_MONRO	Hydrophobic surface binding protein	*Moniliophthora roreri*	4E-48	52.46	**3**	3	YES
A0A074S8Y2_9HOMO	Putative transmembrane protein	*Rhizoctonia solani*	1E-76	43.57	**3**	3	YES
A0A0H2S0W7_9HOMO	Gamma-glutamyltranspeptidase	*Schizopora paradoxa*	0	69.31	**3**		NO
V2XWZ3_MONRO	Putative aminotransferase	*Moniliophthora roreri*	0	69.04	**3**		NO
E4ZP67_LEPMJ	Similar to stress responsive alpha-beta barrel domain-containing protein	*Leptosphaeria maculans*	0.00009	29.25	**3**	1	NO
gi|597976059|ref|XP_007362138.1|	4-carboxymuconolactone decarboxylase	*Dichomitus squalens*	2E-83	65.97	**3**	0	YES
V2XVV7_MONRO	Er to golgi transport-related protein	*Moniliophthora roreri*	4E-60	39.41	**3**	1	NO
Q96TU2_PLEOS	Cap64 protein	*Pleurotus ostreatus*	0	97.85	**3**		NO
A0A0H2RUN5_9HOMO	Short-chain dehydrogenase	*Schizopora paradoxa*	4E-168	82.69	**3**		NO
V2Y1X1_MONRO	Mitochondrial protein	*Moniliophthora roreri*	8E-108	65.15	**3**	1	NO
gi|636607613|ref|XP_008034941.1|	Ribosomal protein S25 [Trametes versicolor FP-101664 SS1]	*Trametes versicolor*	7E-41	84.31	**3**	1	NO
Q6L660_PLEOS	Ribonuclease T2	*Pleurotus ostreatus*	0	95.42	**3**	2	YES
K9I1K6_AGABB	XCL-like lectin	*Agaricus bisporus var. bisporus*	2E-22	40.56	**3**	1	NO
gi|597903154|ref|XP_007298876.1|	metal-dependent protein hydrolase	*Stereum hirsutum*	1E-179	73.17	**3**	1	NO
A0A0D7AQF0_9AGAR	Flavocytochrome c	*Fistulina hepatica*	0	63.97	**3**	2	NO

A0A0H2R6D9_9HOMO	PEBP-like protein	*Schizopora paradoxa*	3E-79	56.7	**3**	1	YES
V2XRT0_MONRO	Serine-threonine rich	*Moniliophthora roreri*	8E-43	64.41	**3**	1	YES
A0A0D7B8B9_9HOMO	Acetamidase/Formamidase	*Cylindrobasidium torrendii*	0	86.97	**3**	1	NO
S4S6Z0_HEBCY	L-amino acid oxidase	*Hebeloma cylindrosporum*	3E-175	50.46	**3**	1	NO
gi|599094462|ref|XP_007378965.1|	heparinase II/III family protein	*Punctularia strigosozonata*	0	64.8	**3**	2	NO
X8IZK9_9HOMO	Allergen protein	*Rhizoctonia solani*	3E-81	72.62	**3**	1	YES
S7QKA7_GLOTA	Ribosomal protein S4	*Gloeophyllum trabeum*	1E-122	97.81	**2**		NO
A0A067NHP6_PLEOS	40S ribosomal protein S0	*Pleurotus ostreatus*	0	96.96	**2**		NO
A0A0D7A525_9AGAR	Nucleic acid-binding protein	*Fistulina hepatica*	3E-63	60.81	**2**		NO
NNRD_COPC7	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	*Coprinopsis cinerea*	0	72.43	**2**		NO
A0A067NQ58_PLEOS	Proteasome subunit beta type	*Pleurotus ostreatus*	8E-178	99.59	**2**	0	NO
R7S4L7_PUNST	NAD(P)-binding protein	*Punctularia strigosozonata*	2E-108	71.08	**2**		NO
A0A0C2ZFM7_9HOMO	Transcription elongation factor	*Scleroderma citrinum*	0.52	26.39	**2**	0	NO
V2XWI1_MONRO	NAD-P-binding protein	*Moniliophthora roreri*	4E-120	53.17	**2**		NO
S7RD10_GLOTA	Dioxygenase family protein	*Gloeophyllum trabeum*	3E-154	68.21	**2**	0	NO
S7QCY7_GLOTA	Nonaspanin	*Gloeophyllum trabeum*	0	81.86	**2**	0	YES
A0A074RH65_9HOMO	Putative transmembrane protein	*Rhizoctonia solani*	1	25.88	**2**		NO
X8JNF1_9HOMO	Mucoidy inhibitor A, putative	*Rhizoctonia solani*	1E-54	26.93	**2**		NO
T2HUL2_PLEER	Pe.pleurotolysin A	*Pleurotus eryngii*	1E-96	100	**2**		NO
X8JCL8_9HOMO	Retrotransposon gag protein	*Rhizoctonia solani*	0.4	24.21	**2**	1	NO
W4K568_9HOMO	ABC transporter	*Heterobasidion irregulare*	0	63.43	**2**		NO
V2YXX7_MONRO	Prenylated rab acceptor 1	*Moniliophthora roreri*	3E-86	73.78	**2**	0	NO
R7T2T7_DICSQ	Small GTPase-binding protein	*Dichomitus squalens*	1E-134	94.85	**2**	0	NO
V2XST8_MONRO	Fad binding domain protein	*Moniliophthora roreri*	0	55.74	**2**	1	YES
L8WS14_THACA	KapM protein	*Thanatephorus cucumeris*	5E-16	34.07	**2**		YES
R7SSC4_DICSQ	Anthranilate phosphoribosyltransferase	*Dichomitus squalens*	2E-29	59.48	**2**		YES
V2WVC8_MONRO	Aminoacylase 1-like protein 2	*Moniliophthora roreri*	0	59.92	**2**		NO
B6HJZ8_PENCW	Pc21g02480 protein	*Penicillium chrysogenum*	8E-12	35.9	**2**		YES
S7QJ37_GLOTA	Multidrug efflux transporter AcrB transmembrane domain-containing protein	*Gloeophyllum trabeum*	0	71.6	**2**		NO
A8NPZ1_COPC7	YjgH family protein	*Coprinopsis cinerea*	5E-50	67.86	**2**		NO
gi|636608055|ref|XP_008035162.1|	aflatoxin-detoxifizyme	*Trametes versicolor*	0	77.97	**2**		NO
A0A067P0D5_PLEOS	Glycosyltransferase family 2 protein	*Pleurotus ostreatus*	0	96.74	**2**		NO
gi|597912997|ref|XP_007303797.1|	WD40 repeat-like protein	*Stereum hirsutum*	0	61.21	**2**		NO
gi|628827991|ref|XP_007764299.1|	Carbon-nitrogen hydrolase	*Coniophora puteana*	1E-171	72.85	**2**		NO
B0DW71_LACBS	Ectomycorrhiza-regulated small secreted protein	*Laccaria bicolor*	6E-27	43.97	**2**		YES
V2XHI7_MONRO	2-nitro propane dioxygenase	*Moniliophthora roreri*	4E-112	50	**2**		NO
A0A067NUG5_PLEOS	Non-specific serine/threonine protein kinase	*Pleurotus ostreatus*	0	95.03	**2**		NO
A0A066XCF5_COLSU	Putative RhoGEF domain-containing protein	*Colletotrichum sublineola*	0.32	35.09	**2**		NO
V2WUN4_MONRO	TPR-likeprotein	*Moniliophthora roreri*	7E-87	33.52	**2**		NO
A0A067NN37_PLEOS	Plant-expansin-like protein	*Pleurotus ostreatus*	1E-91	99.22	**2**		YES
S9Q159_SCHOY	BRCT domain-containing protein Brc1	*Schizosaccharomyces octosporus*	0.49	29.85	**2**		NO
V2WU96_MONRO	F-box domain protein	*Moniliophthora roreri*	5E-66	31.31	**2**		NO
A0A0B1PAT4_UNCNE	Putative cyclin-like f-box protein	*Uncinula necator*	3E-86	48.6	**2**	1	NO
V2XG03_MONRO	Short chain type	*Moniliophthora roreri*	2E-72	49.79	**2**	1	NO

(F) UNKNOWN FUNCTION							
Best BLAST non-hypothetical			**E-value**	**Identity (%)**	**Spectral mass counts**		**Signal peptide**
Access number	**Protein description**	**Fungi**			**Average**	**Error**	
D8PY21_SCHCM	Expressed protein	*Schizophyllum commune*	2E-11	35	**152**	31	NO
V2X669_MONRO	Secreted protein	*Moniliophthora roreri*	2E-32	45.56	**55**	7	YES
D8Q129_SCHCM	Expressed protein	*Schizophyllum commune*	2E-17	32.81	**52**	6	YES
A0A067NYR7_PLEOS	Evidence of expression at protein level	*Pleurotus ostreatus*	0	95.16	**38**	3	NO
D8PY21_SCHCM	Expressed protein	*Schizophyllum commune*	2E-11	35	**36**	3	YES
D8PXC2_SCHCM	Expressed protein	*Schizophyllum commune*	0.004	24.02	**29**	1	YES
B0CXV6_LACBS	GPI-anchored small secreted protein	*Laccaria bicolor*	1E-38	53.47	**25**	1	YES
A0A074SC17_9HOMO	DUF4243 family protein 123E	*Rhizoctonia solani*	1E-108	42.58	**15**	1	NO
J4UG46_BEAB2	Putative secreted protein	*Beauveria bassiana*	0.000005	26.35	**14**	4	NO
gi|595769286|ref|XP_007263186.1|	DUF427-domain-containing protein [MF3/22]	*Fomitiporia mediterranea*	3E-109	66.12	**12**	0	NO
gi|636618993|ref|XP_008040631.1|	Sure-like protein	*Trametes versicolor*	2E-106	54.9	**9**	1	YES
D8QIL5_SCHCM	Expressed protein	*Schizophyllum commune*	6E-12	33.62	**9**	3	YES
D8Q6X5_SCHCM	Expressed protein	*Schizophyllum commune*	2E-84	77.33	**8**	1	YES
D8Q1J2_SCHCM	Expressed protein	*Schizophyllum commune*	8E-33	36.29	**8**	0	NO
D8QD03_SCHCM	Expressed protein	*Schizophyllum commune*	2E-07	38.24	**6**	0	YES
K9I8U3_AGABB	Secreted protein	*Agaricus bisporus var. bisporus*	5E-92	47.19	**6**	2	YES
J0WWW8_AURDE	DUF427-domain-containing protein	*Auricularia delicata*	3E-43	69.89	**4**	0	NO
V2XTV0_MONRO	Secreted protein	*Moniliophthora roreri*	1E-75	52.28	**3**	0	NO
W6MS03_9ASCO	Genomic scaffold	*Kuraishia capsulata*	0.00006	25.61	**3**	0	YES
X8JBR9_9HOMO	CHCH domain protein	*Rhizoctonia solani*	2E-56	31.12	**3**	0	NO
W6QVQ8_PENRO	Genomic scaffold, ProqFM164S03	*Penicillium roqueforti*	7E-28	42.86	**3**	1	YES
D8Q6X5_SCHCM	Expressed protein	*Schizophyllum commune*	2E-84	77.33	**2**	1	YES
D8PZF9_SCHCM	Expressed protein	*Schizophyllum commune*	4E-54	54.38	**2**	1	NO
D8PNW9_SCHCM	Expressed protein	*Schizophyllum commune*	7E-164	53.75	**2**	1	YES