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Developmental stage-specific gene expression profiling for a medicinal fungus *Cordyceps militaris*

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The caterpillar fungus *Cordyceps militaris* is a well-known traditional Chinese medicine that has been shown to have immunostimulatory and anticancer activities. Molecular and genetic studies of *Cordyceps* spp. are still limited. In this study, we sequenced >5000 clones from four cDNA libraries representing different asexual and sexual developmental stages of *C. militaris*. The resulting 1341 unigenes were assembled into 454 contigs and 887 singletons. Transcriptional differences were considerable with only 2.1% of unigenes being detected in all libraries. Gene ontology mapping revealed divergent transcriptional patterns among the libraries. Thus, the fungus differentially upregulated more genes for cell metabolism, energy metabolism and stress responses during asexual compared to sexual development. In particular, the transcriptional profiles were found to be different between fruit-bodies produced on rice medium and silkworm pupae. However, both libraries were enriched in transcripts for cell wall structures, i.e. 38.72 and 26.35% of unigenes transcribed by rice medium and pupae induced fruit-bodies, respectively. This is consistent with the morphological changes associated with sexual development. Our data will provide a starting point for future molecular studies of this promising resource of medicinal products. Further study with high-throughput sequencing techniques is still required for whole-genome transcriptome analysis of this fungus.

Keywords: *Cordyceps militaris*; expressed sequence tag; developmental control; fruit-body; sexuality

Introduction

The fungal pathogens of caterpillars, *Cordyceps militaris* and *C. sinensis,* are well known traditional Chinese medicines (TCMs) with immunostimulatory and anti-cancer activities resulting from an array of active metabolites, e.g. the deoxyadenosine analogue cordycepin, cordycepic acid and polysaccharides (Ng and Wang, 2005; Xiao and Zhong, 2007; Paterson, 2008; Cheung et al., 2009; Zhou et al., 2009). The annual market for *C. militaris*- and *C. sinensis*-related products has been growing steadily, especially in Asian countries (Li et al., 2006). A combination of fungal stromata and mycosed insect is the "natural" medicinal product of *Cordyceps* spp. However, most commercial products are mycelial powders of *C. militaris* or *C. sinensis* produced by liquid fermentation or fruiting bodies of *C. militaris* produced on artificial media. Even though growth conditions in artificial media are completely different from those *in insecta*, these products are usually claimed to be substantially similar to those of naturally harvested *Cordyceps* in terms of their contents of cordycepin, cordycepic acid, polysaccharides, ergosterol and mannitol (Li et al., 2006). Nevertheless, most consumers remain unconvinced by these claims and prefer the natural products. Both the natural and artificially grown fungi are believed to have many undetermined compounds with pharmacological properties. To date molecular studies on *Cordyceps* have been largely limited to obtaining sequences for phylogenetic trees, and analysis of the genetic resources of this fungus is required to facilitate the exploration of its medicinal potential.

More than 400 species of *Cordyceps* have been isolated from different insect hosts (Sung et al., 2007). Apart from their medicinal implications, *Cordyceps* taxa also play important roles as natural regulators of insect populations. For example, in some years in Japan *C. militaris* infects more than 90% of the overwintering pupae of beech caterpillar, *Syntipistis punctatella* (Sato et al., 2002). The anamorphs of *Cordyceps* spp., include well known insect biocontrol fungi such as *Beauveria* spp., *Metarhizium* spp. and *Paecilomyces* spp., among others (Li et al., 2001; Huang et al., 2005; Rehner and Buckley, 2005; Wang and St. Leger, 2007; de Faria and Wraight, 2007). Differing from *C. sinensis,* which does not produce sexual structures outside an insect host (Stone, 2008), *C. militaris* exhibits asexual and sexual stages in artificial media (e.g. the rice medium) or on the pupae of lepidopteran insects. *C. militaris* can, therefore, be used as a model to explore the complexities of sexuality in this genus.

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The technique of expressed sequence tag (EST) analysis is frequently employed to study fungal development and pathogenicity (e.g. Nugent et al., 2004; Wang et al., 2005; Cho et al., 2006a). In this study, we explored the transcriptomes of *C. militaris* during asexual and sexual development, by constructing four cDNA libraries representing the fungus growing in liquid culture, on solid rice medium before and after the formation of fruit bodies and on silkworm (*Bombyx mori*) pupae (to induce stromata). Gene ontology analysis of more than 5000 sequenced clones indicated that the gene expression patterns were very different between libraries, including that between the transcriptomes of fungal sexual structures produced *in insecta* and in artificial medium.

Methods

Strain and cultural conditions

C. militaris strain Pm36 from the Research Center of Entomopathogenic Fungi (Anhui Agricultural University, Hefei, China) was used in this study. To evaluate gene expression profiles, the fungus was grown in conditions required to induce different developmental stages and the resulting RNA was used for cDNA library constructions. For the first library, designated as the liquid mycelium (LM) library, conidia of Pm36 were inoculated in Sabouraud dextrose broth (SDB; Difco) and incubated for 3 days in a rotory shaker at 170 rpm and 25 °C. The mycelia were harvested, washed twice with sterile distilled water and used for RNA isolation.

For the second library, mycelial inoculum from SDB culture (5 ml) was used to inoculate rice medium (25 g rice plus 40 ml nutrient solution: 1% *Bombyx mori* pupae homogenate, 1% peptone, 1% yeast extract) in canned bottles (10 cm × 16 cm^2, height × bottom square centimeters). Fungal cultures turned yellowish orange when incubated at 22 °C for 14 days in the dark and then for 6 days with a 16:8-h dark/light cycle. This just precedes formation of stromata. The mycelial mats at this stage were collected for RNA isolation (to construct the rice mycelia, RM library). For the third library, additional rice cultures were continuously incubated at 22 °C for up to 20 days with a 16:8-h dark/light cycle to induce fruit-bodies (perithecia) (Kanauchi and Futatsu, 1999). The fresh fruit-bodies were collected for RNA isolation to construct the rice fruit-body (RF) library. The fourth library was constructed by injecting the silkworm pupae with fungal spores. Briefly, 10 μl of a conidial suspension of Pm36 (5×10^6 spores/ml, 10 μl) was used to inject 5-day-old pupae of *B. mori*, which were then maintained in >95% relative humidity. The fruit bodies were induced under the same light conditions as used for rice medium cultures and the mature stromata used for RNA isolation to generate the fourth library for pupae fruit-body formation (PF library). Microscopic images for different developmental stages were taken using an Olympus B51 microscope equipped with a DP71 CCD camera.

Construction of cDNA libraries and sequencing

Total RNA was extracted using an RNeasy Plant mini kit (Qiagen, Valencia, CA, USA). The cDNA libraries were constructed using a SMART™ cDNA Library construction kit (Clonetech, Palo Alto, CA, USA) without normalization, following the manufacturer's instructions. Individual clones were randomly picked up and the cDNA inserts sequenced from the 5′-end. Vector sequences from each clone were manually removed after analysis with the program VecScreen (http://www.ncbi.nlm.nih.gov/VecScreen/VecScreen.html). All sequences were submitted to GenBank under the accession numbers: GR224073–GR228668. The contigs were assembled using the program CAP3 (Huang and Madan, 1999). The contigs and singletons obtained from four libraries were compared with non-redundant protein databases using BLASTx searches. A hit with an *E*-value less than 10^{-5} was considered to be significant (Anderson and Brass, 1998). Functional categorization was conducted according to our previous study (Wang et al., 2005) as well as by reference against the UniProt Knowledgebase (http://www.uniprot.org/uniprot/). Differences in transcript accumulation between libraries were assessed with the algorithm developed by Audic and Claveric (1997).

Analysis of the relative transcript level using semi-quantitative RT-PCR

To verify differentially expressed genes detected in EST analysis, semi-quantitative reverse transcription PCR (RT-PCR) was conducted for 13 selected genes (Table 2). The amount of 0.5 μg total RNA was used for cDNA synthesis for each sample using the ReverTra Ace-α^{TM} kit (Toyobo, Osaka, Japan) according to the manufacturer's instructions. PCR amplification was conducted in a 20-μl reaction system with the specific primers for each selected gene (Table 2) and the diluted (10×) cDNA templates. The PCR products (5 μl each) were analyzed on 1.5% agarose gels and the images documented with a UVP EC3 imaging system.

Results

Phenotypic pleomorphism of Cordyceps militaris

Cordyceps militaris demonstrates highly pleomorphic phenotypes when grown under different culture conditions. After growth in nutrient-rich liquid broth (SDB) for 3 days, cultures became cloudy as bar-shaped blastospores budded off from the tips of branched mycelia (Figure 1A). When grown on rice medium for up to 3 weeks, i.e. before the formation of stromata, fungal cultures produced fluffy mycelia and turned yellowish orange with the production of round to ovoid conidia (Figure 1B and C). About 50 days post-inoculation of the fungus on rice medium or silkworm pupae, mature fruit bodies (ca. 3–5 cm) were formed with protruding spindle or pear-shaped perithecia (Figure 1D and 1E), containing asci that discharged long linear ascospores (400–600 µm) (Figure 1F).

Characterization of the EST libraries

To profile gene expression patterns that correlate with different developmental stages of *C. militaris*, four cDNA libraries were constructed and clones were sequenced from each library. In total, 5088 clones were randomly selected from four libraries and 4596 valid sequences were acquired after vector screening analyses. After assembly, 547 unigenes (of 1324 valid sequences) were obtained from the LM library, 447 unigenes (of 860 sequences) from the RM library, 258 unigenes (of 545 sequences) from the RF library and 513 unigenes (of 1867 sequences) from the PF library. The frequency of contig numbers was approximately the same (ca. 10%), while the unigene ratio in the PF library was almost 2-fold less than that of other libraries (Figure 2A). The frequency of total unigenes from the four libraries was 26% (1341 of 4596). The distribution of overlapping unigenes between libraries differed considerably with only 28 of 1341 genes (2.1%) being detected in all four libraries. The LM and PF libraries shared 49 common unigenes, while the LM, RM and RF libraries only shared eight common unigenes. Significantly, only 65 unigenes were shared between fruit-bodies from rice medium and silkworm pupae (Figure 2B).

Gene ontology

To obtain insight into the putative functions of ESTs, the genes were classified into nine functionally associated groups based on gene ontology assignments (Table 1 and Appendix Table 1). There were high frequencies of ESTs with hypothetical or unknown functions in all four libraries, i.e. 47.51% in LM, 48.26% in RM, 39.27% in RF and 52.54% in the PF library. However, less than 0.2 % of the transcripts in the four libraries encoded transposable

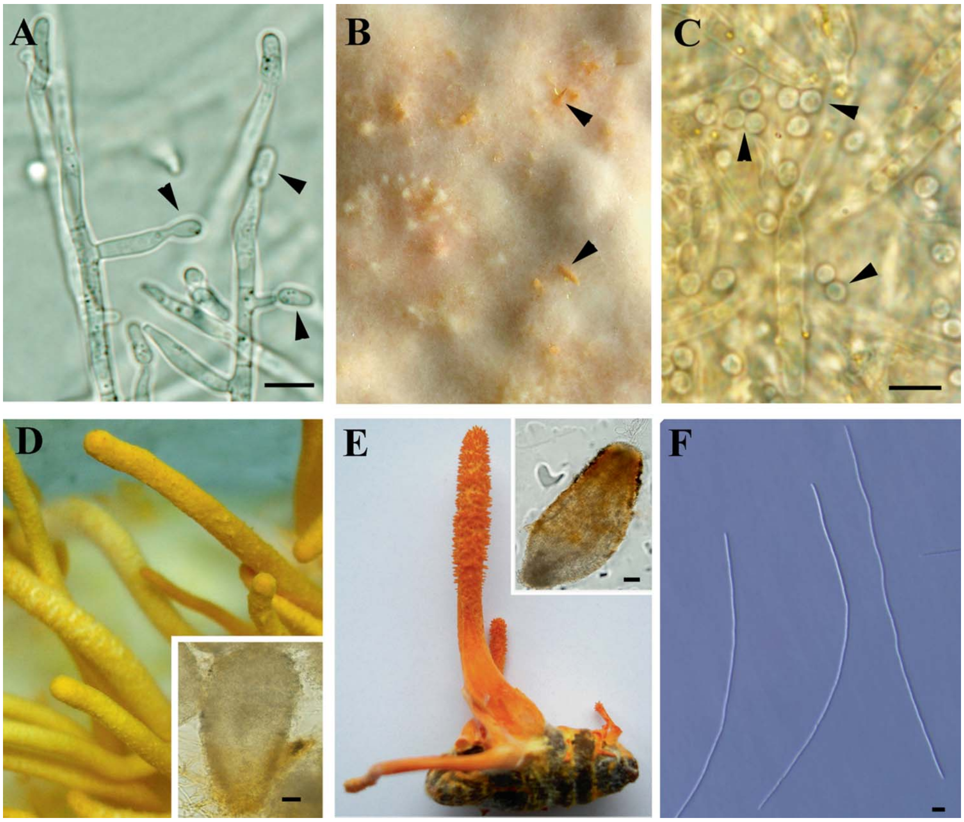

Figure 1. Morphological characteristics of *Cordyceps militaris*. (A) Production of blastospores (indicated by arrows) by *C. militaris* grown in Sabouraud dextrose broth for 3 days. (B) Formation of stromata (indicated by arrows) from the yellowish-orange mycelial mat produced 2 weeks post-inoculation on rice medium. (C) Microscopic examination showing the production of conidia (indicated by arrows) before fruit-body differentiation, as shown at panel (D). (D) Mature fruit-body with perithecia (inset on the lower right), 5 weeks post-inoculation on rice medium. (E) Mature fruit-body with perithecia (inset on the upper right) formed 5 weeks post-inoculation on silkworm pupae. (F) Linear ascospores on agar discharged from mature fruit bodies. Bar: 10 µm.

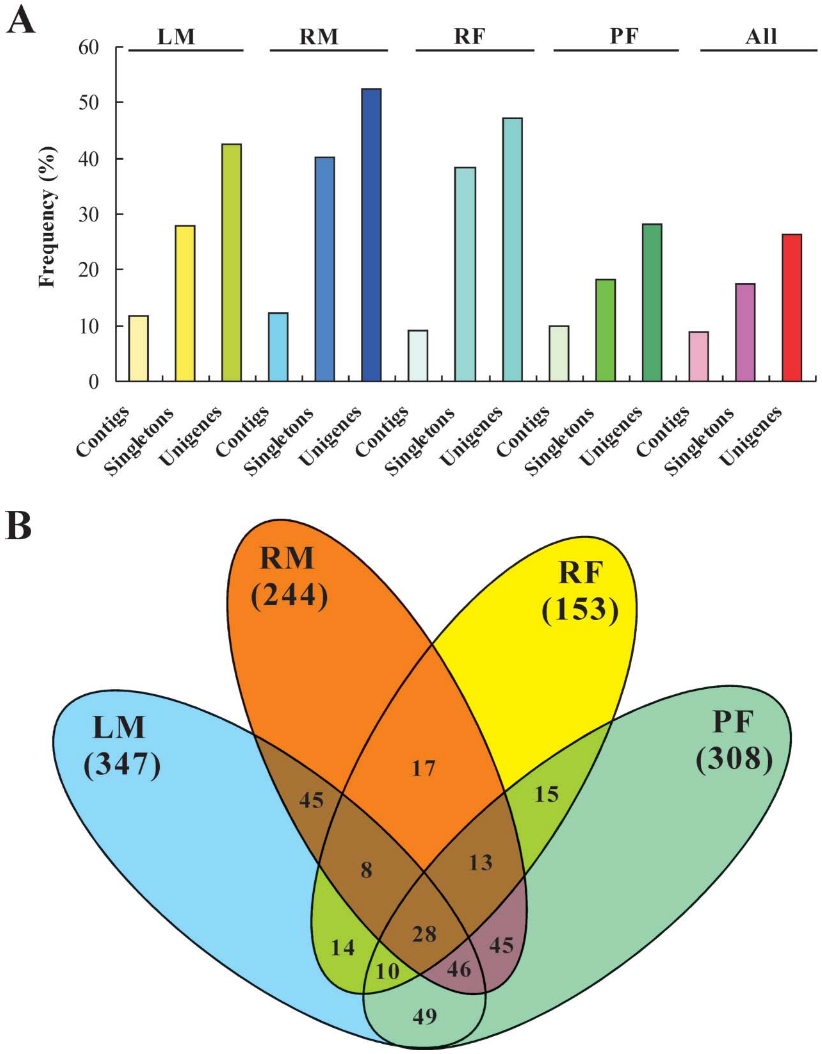

Figure 2. Transcriptional profiling of expressed sequence tags. (A) Contig, singleton and unigene distribution in each library. (B) Overlap of unigenes among libraries, the numbers in parenthesis showing library specific unigenes. LM, liquid mycelium library; RM, rice mycelium library; RF, rice medium fruit-body library; PF, pupae fruit-body library.

elements. Beside these, the transcriptomes varied considerably between libraries, consistent with fungal phenotypic switches at different developmental stages (Figure 1).

During growth in SDB liquid medium or on rice medium preceding formation of fruit-bodies, *C. militaris* transcribed many more ($p < 0.01$) genes involved in cell metabolism, particularly of lipids, compared to other growth conditions. For example, the transcription of a C-4 sterol methyl oxidase (GenBank accession no. GR225276) was upregulated (11/1324) by the fungus grown in liquid broth (LM library) (Table 1, Appendix Table 1). The fungus also expressed more genes involved in energy metabolism, protein metabolism and stress responses during growth in liquid medium and on rice medium. These included an ATP synthase (GR224260, 19 of 1324 ESTs) for energy synthesis, protein genes for ribosomal subunits (including GR224311 for ribosomal protein subunit L39, 19/1324; GR226008, 22/1324 for L30; GR228503 for L33, 25/1324; GR227381 for S25, 18/1324), DnaJ domain protein (GR225925, 11/1324) and thioredoxins (GR224602, 2/1324) involved in cell stress responses. Before fruit-body differentiation on rice medium, i.e. represented by the RM library, *C. militaris* demonstrated particularly high expression of proteins involved in RNA metabolism, e.g. an RNA-dependent RNA polymerase (GR225730, $E = 2.0 \times 10^{-42}$, 63 of 860 ESTs) and RNA binding proteins (GR226855, 5/860). However, during fruit-body formation either on rice medium or on caterpillar pupae the fungus was characterized by high level expression of homologs ($E < 10^{-15}$) of cell wall proteins, e.g. GR224929 (284/1867) in the PF library and GR227979 (157/545) in the RF library. Finally, fewer genes putatively involved in cell cycle

Table 1. Distribution of EST functional category of four libraries.

No.	Functional category	% ESTs in library LM	RM	RF	PF
1	**Cell metabolism**	**5.51A**	**4.30AB**	**2.39BC**	**1.98C**
1.a	Amino acid metabolism	0.38a	0.58a	0.55a	0.64a
1.b	Carbohydrate metabolism	1.44A	1.16A	0.92ABb	0.16Bc
1.c	Lipid metabolism	2.11Aa	1.05ab	0.55Bb	0.43Bb
1.d	Nucleotide metabolism	0.91a	0.81a	0.18a	0.48a
1.e	N-, P-, S-metabolism	0.15a	0.35a	0a	0.05a
1.f	Cofactor and vitamins	0.53a	0.35a	0.18a	0.21a
2	**Energy metabolism**	**5.89A**	**2.44B**	**1.83B**	**2.68B**
3	**Protein metabolism**	**21.98**	**13.49**	**10.64**	**9.53**
3.a	Ribosomal proteins	14.65Aa	6.16Bb	3.85Bb	4.87Bb
3.b	Translation	0.98Bb	2.56Aa	1.47ab	1.18Bb
3.c	Proteolysis	4.68Aa	3.02Ab	4.40Aa	2.62Bb
3.d	Protein modification and targeting	1.66a	1.74a	0.92ab	0.86b
4	**RNA metabolism**	**2.95**	**12.79**	**4.40**	**5.36**
4.a	RNA synthesis	0.53Bb	7.56A	0.55Bb	0.37Bb
4.b	RNA modification	0.68b	1.74a	0.55b	0.91ab
4.c	Transcription	1.74Bb	3.49ABa	3.30ABa	4.07Aa
5	**Cell structure and function**	**11.03**	**14.88**	**38.72**	**26.35**
5.a	Cell wall	0.45a	0.35a	1.1a	0.54a
5.b	Cytoskeleton	3.02a	2.79ab	1.65b	1.66b
5.c	Extracellular matrix, cell wall protein	1.28	1.98	**29.91**	**18.16**
5.d	Transport proteins	1.74ab	3.02Aa	2.02ab	1.45Bb
5.e	Cellular transportation	1.81a	2.91a	1.65a	1.93a
5.f	Signaling	2.72a	3.84a	2.39a	2.62a
6	**Cell cycle and division**	**2.34A**	**3.14A**	**1.10AB**	**0.59B**
6.a	Cell cycle	0.68Aa	0.47a	0.18b	0.11Bb
6.b	Chromosome structure	0.76Aa	0.93Aa	0.18ab	0.05Bb
6.c	DNA synthesis	0.30a	0.12ab	0b	0b
6.d	Cell polarity, budding and septation	0.38Aa	0.35Aa	0.73Aa	0.05Bb
6.e	Sexual cycle	0a	0.23a	0a	0.11a
6.f	Clock control and light response	0.23a	0.12a	0a	0.16a
6.g	Cell death	0a	0a	0a	0.11a
7	**Stress response and defense**	**2.79A**	**1.63AB**	**1.47AB**	**0.96B**
7.a	Stress response	2.49Aa	1.63ab	1.47ab	0.75Bb
7.b	Detoxification	0.23a	0a	0a	0.05a
7.c	Synthesis of secondary metabolites	0.08a	0a	0a	0.16a
8	**Transposable elements**	**0a**	**0a**	**0.18a**	**0a**
9	**Hypothetical or unknown proteins**	**47.51**	**48.26**	**39.27**	**52.54**

Note: *Values in the same row having a letter not in common are significantly different at $P < 0.01$ for upper case and $P < 0.05$ for lower case letter. The tests for the category percentage >10% become ambiguous and are, thus, not evaluated and compared (Audic and Claveric, 1997).

and division were expressed by the fungus during sexual stages (Table 1, Appendix Table 1).

Reverse transcription PCR analysis of differentially transcribed genes

To verify differential expression of genes identified by EST analysis, 13 genes were selected for semi-quantitative RT-PCR analysis. The results of RT-PCR patterns generally agreed with the transcript accumulation profiles of EST analysis (Table 2, Figure 3). For example, the transcription frequencies of an RNA binding protein (g1 in Figure 3, GR227007, $E = 1.0 \times 10^{-60}$) were detected with the percentiles of 0.15, 023, 0.73 and 2.3 in LM, RM, RF and PF libraries, respectively, showing similar PCR band densities using the corresponding cDNA samples as templates (Figure 3). A spermatogenesis associated protein (g3, GR225674, $E = 1.0 \times 10^{-33}$) only detected in RM library (0.12%) and a LysM domain protein (g8, GR226742, $E = 5.0 \times 10^{-27}$) only detected in RF library (0.18%) in EST analysis were similarly verified by RT-PCR. Multiple bands of g5 detected in RT-PCR analysis were consistent with the identifications of cell-wall protein isoforms GR226746, GR226864, GR227054 and GR 227979 (Figure 3; Appendix Table 1).

Table 2. Selected transcripts with altered expression ratios in different libraries for RT-PCR analysis.

			Transcript frequency (%)				
Genes	Acc. No.	Description ($E < 10^{-5}$)	LM	RM	RF	PF	Primers (F, forward; R, reverse)
Gene1	GR227007	RBP (RNA binding protein)	0.15	0.23	0.73	2.30	F: ACTTCCCATGCACAACCTTC R: GACTTGGTCTCGTCGTGCTT
Gene2	GR225263	16 kDa allergen	0.08	0.12	0.55	0.64	F: CACCGTCAAGCCTGGCGAGTA R: AGCCGCCTTGGCTGTAGCA
Gene3	GR225674	Spermatogenesis associated CRA_b	—	0.12	—	—	F: TTTATTCCCGTTCTTATTGACC R: AACTTCGGTGGCTTCCCT
Gene4	GR227833	Unknown	0.45	6.86	9.36	7.61	F: TTGATGATGATAGACGCCTGAC R: GCTGAACCAAACCGAACC
Gene5	GR227979	Plasmin-sensitive surface protein (cell-wall protein)	0.38	1.74	29.17	17.57	F: GTTCTTGCTGCCACTGCC R: AGCATCCGAGCGCTTATC
Gene6	GR226824	Cyanovirin-N family protein	5.29	0.93	0.37	1.12	F: AATGTCTTTCAACACCAGC R: TCAAGCAAAGGAAAGGCTAC
Gene7	GR225435	Nuclear transport factor 2	0.68	0.12	0.37	0.37	F: CTGACCGCAAGGCACTTT R: CGCGACCTCATCATTATCCA
Gene8	GR226742	Lys M domain protein	—	—	0.18	—	F: ACATCTCCACCACCGCAAGT R: GGCACGAAGCGATTAGGC
Gene9	GR226855	Shwachman–Bodian–Diamond syndrome (SBDS) domain containing protein	0.15	0.35	1.10	0.32	F: ACCAAGTGCCACTACAAGGG R: GTCGTTCTTTTGTCCTTGGC
Gene10	GR226225	Calmodulin	0.23	0.12	—	0.21	F: CCAGAACCCTTCCGAGTC R: AGCTCACCAGCCAAACCC
Gene11	GR225094	Snodprot2	0.08	—	—	0.11	F: AAGACTCGTCGTCAAGCG R: ACCCTGTCTCCGATAATGT
Gene12	GR224905	GPI-anchored cell wall organization protein Ecm33	0.15	0.23	0.18	0.11	F: CTCGGCTGCCAACCTTAC R: TTGACCTTGCCCTGAACG
Gene13	GR224296	L-PSP endoribonuclease family protein	0.15	0.58	0.18	0.64	F: GCGTTGGTGACCGCATTA R: GCTTGACACCTTCGGCTC
18S RNA	AB070375	18S RNA	NA	NA	NA	NA	F: GACCCAGGCACATCAGCA R: CCCAGCACGACGGAGTTT

Note: (—) Means not detected in EST analysis of different libraries; NA, not available. 18S RNA gene was amplified as positive control in Figure 3.

Discussion

Due to the increasingly widespread use of caterpillar infecting fungi as alternative medicines, we investigated the transcriptional profiles of *C. militaris* to identify genes associated with different developmental stages and cultural conditions. From four non-normalized libraries, we sequenced more than 5000 clones and obtained 4496 valid sequences. Gene ontology analysis indicated that like many genomic studies, a large number of sequenced clones (>45%) could not be annotated due to either a lack of BLAST matches or because hits were limited to hypothetical fungal sequences (e.g. Nugent et al., 2004; Wang et al., 2005; Cho et al., 2006a,b). Different transcripts were abundant in each of the four *Cordyceps* libraries consistent with previous EST projects that show that fungi express very different transcriptomes when grown in different media (Freimosier et al., 2003; Wang et al., 2005) or producing different developmental stages (Cho et al., 2006a,b; Bluhm et al., 2008). However, surprisingly few overlapping genes were expressed by the fungus producing sexual structures on artificial rice medium and insect host pupae (Figure 2B), although these structures looked very much alike. Thus, in terms of the transcriptome-determining metabolome (ter Kuile and Westerhoff, 2001), our data would strongly argue that the capsules or tablets made from the liquid-fermented mycelia or artificially cultured fruit-body would not have similar health effects as those made with insect host originated fruit-bodies. In support of this, a previous study has shown that the water-soluble constituents are different between natural and cultured *Cordyceps* (Li et al., 2004).

Similar to the insect pathogenic fungus *Beauveria bassiana* (Bidochka et al., 1987; Cho et al., 2006a), *C. militaris* quickly accumulated biomass in SDB liquid medium and produced large numbers of blastospores or submerged conidia upon nutrient deprivation. *Cordyceps* highly transcribed genes involved in cell metabolism, protein metabolism, energy metabolism and stress responses in SDB (Table 1). A high level of a C-4 sterol methyl oxidase (GR225276) would be required for ergosterol biosynthesis

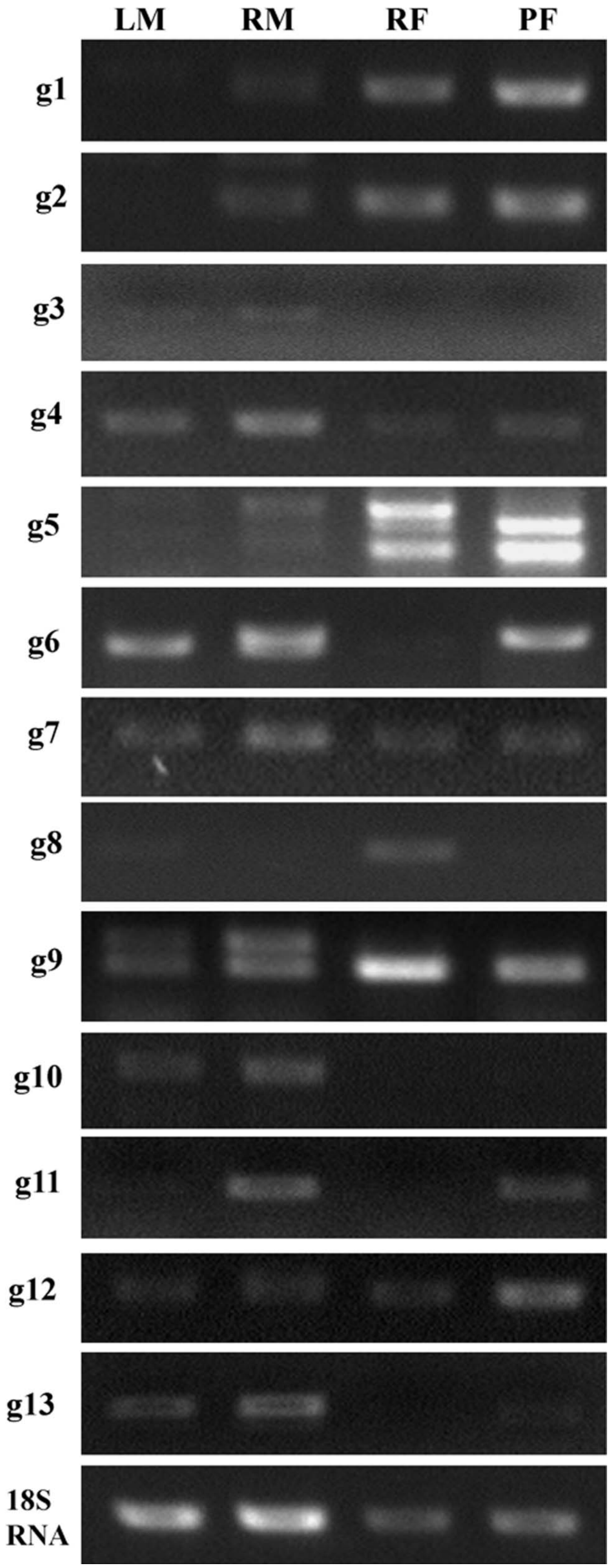

Figure 3. Reverse transcription PCR analysis of selected transcripts. Genes g1–g13 are as shown in Table 2.

for cell membrane components (Bard et al., 1996). The upregulation of ubiquitin (GR228448, 27/1324), ubiquitin conjucating enzyme (GR224654, 4/1324) and ubiquitin activating enzyme (GR224807, 2/1324) (Appendix Table 1) for proteolysis is consistent with rapid cell division during fungal growth in liquid culture (Sprague et al., 2004). Following rapid growth, the upregulation of heat shock proteins (GR225003, GR225211), DNAJ-like protein (GR226209) and thioredoxins (GR224602, GR224629) would suggest cell stress responses upon nutrient deprivation in stationary cultures.

After growing the medicinal fungus on rice medium for 20 days, the culture turned yellowish orange with the production of aerial conidia and then switched to sexual reproductive growth (Figure 1BC). We generated a cDNA library, i.e. the rice medium (RM) library, to investigate the *C. militaris* transcriptome at this stage. Unlike the EST analysis of a library generated with pure conidial spores of *B. bassiana* that showed upregulation of hydrophobins, proteases, glycosidase and lipases etc. (Cho et al., 2006a), the *C. militaris* RM library was characterized by greater upregulation of genes associated with RNA metabolism and the cell cycle and division (Table 1). These included RNA-dependent RNA polymerase (RdRP, GR225730, $E = 2 \times 10^{-42}$), RNA binding protein (GR226855, GR227007) and cell division control protein (GR225617), etc. Unlike typical RNA polymerases that catalyze the transcription of RNA from a DNA template, RdRP replicates RNA from an RNA template (reviewed in Kok and McMinn, 2009). The identification of RdRP in eukaryotes has been associated with RNA interference for antiviral immunity (reviewed in by Aliyari and Ding, 2009) or epigenetic control of differentiation and development (Verdel et al., 2009). The RNAi machinery has been characterized in fission yeast (White and Allshire, 2008), ascomycetes (Nolan et al., 2005; Wang et al., 2008) and basidomycetes (Feldbrügge et al., 2008). Thus, it is possible that epigenetic controls are employed by *C. militaris* to switch from asexual to sexual development.

The mating-type genes have been cloned from *Cordyceps takaomontana* (Yokoyama et al., 2003) and its sexuality may be heterothallic (Yokoyama et al., 2005). No homolog of a mating-type locus was identified during our EST survey of *C. militaris*. However, many transcription factors were found to be upregulated in the RM library, including the homologs of C6 transcription factors (GR225862, $E = 4 \times 10^{-88}$; GR226082, $E = 7 \times 10^{-17}$), C2H2 finger domain proteins (GR225860, $E = 2 \times 10^{-14}$; GR226013, $E = 4 \times 10^{-46}$), zinc finger proteins (GR225433, $E = 3 \times 10^{-37}$; GR226212, $E = 2 \times 10^{-25}$; GR224394, $E = 2 \times 10^{-33}$ and GR225819, $E = 4 \times 10^{-96}$) and MYB DNA-binding protein (GR226114, $E = 2 \times 10^{-8}$) (Appendix Table 1), suggesting that like other fungi, initiation of sexual differentiation in *C. militaris* involves a large-scale change in the pattern of gene expression (Coppin et al., 1997).

The most surprising aspect of our data was the transcriptional differences between fruit-body development on artificial rice medium (i.e. for RF library) and on insect host (silkworm) pupae (i.e. for PF library). However, in terms of the EST numbers from gene ontology assignments for each functional class, there were no statistical variations between RF and PF libraries (Table 1). Thus, during sexual development, the fungus transcribed more genes associated with the extracellular matrix and cell wall structure than did during asexual growth. This was largely due to the upregulation of bacterial-like plasmin-sensitive surface (Pls) protein isoforms, i.e. 15.2% of GR224929 ($E = 5 \times 10^{-30}$) in PF library and 28.8% of GR227979 ($E = 8 \times 10^{-28}$) in the RF library. The Pls protein present on the cell wall of *Staphylococcus aureus* strains is involved in cell adherence and biofilm formation (Hildén et al., 1996; Corrigan et al., 2007). The function of Pls-like proteins in fungi remains to be determined. Blast searches reveal that, besides bacteria, Pls ($E \leq 10^{-5}$) can only be detected in four other ascomycete fungal species, i.e. *Paracoccidioides brasiliensis*, *Ajellomyces dermatitidis*, *A. capsulatus* and *Chaetomium globosum*.

Consistent with previous studies RT-PCR or microarray analysis data generally agreed with gene transcriptional profiles derived from EST analysis (e.g. Freimoser et al., 2003; Wang et al., 2005). In this study our RT-PCR analysis of 13 selected genes showed that the genes with varied transcript numbers among libraries usually followed PCR profiling patterns (Table 2, Figure 3). As mentioned above, no mating-type transcripts nor other well-documented genes involved in fungal sexuality were found in our EST survey of *C. militaris* (Table 1, Appendix Table 1). Recently, high-throughput sequencing techniques utilizing 454 and Illumina/Solexa have been used in transcriptome analyses of different organisms (e.g. Morozova and Marra, 2008; Wall et al., 2009), and would be better suited for detection of rare transcripts than an EST study. In addition, more time points correlated with fruit body development should be surveyed in future studies to fine tune our knowledge of transcriptional changes, e.g. before the formation of perithecia and before the maturation of asci.

Cordycepin (3′-deoxyadenosine) is a well known product of *Cordyceps* spp. that blocks polyadenylation and thus interferes with processing of RNA. It inhibits the growth of cancer cells, bacteria or yeasts (reviewed by Ng and Wang, 2005), and is now under Phase II antitumor clinical trials by the National Cancer Institute (http://www.cancer.gov/drugdictionary/?CdrID=42667). Cordycepin is also toxic to *Cordyceps* itself but is regulated by feedback inhibition (Das et al., 2008). The exact synthetic pathway for cordycepin is still unclear. Both adenine and adenosine could be the precursor of cordycepin (Masuda et al., 2006); thus, the cellular accumulation of adenine or adenosine would lead to an increased yield of cordycepin. Cordycepin can be produced by *C. militaris* grown either in liquid culture or on solid media (e.g. Xie et al., 2009; Ni et al., 2009). Our EST survey identified a few transcripts involved in nucleotide metabolism, including an adenosine (cytosine) deaminase ($E = 6 \times 10^{-58}$, GR226685) in the RF and PR libraries, an adenine phosphoribosyltransferase ($E = 6 \times 10^{-58}$, GR224460) in the LM library, an inosine triphosphate pyrophosphatase ($E = 3 \times 10^{-27}$, GR224569) in the LM and PF libraries, an ATP phosphoribosyltransferase ($E = 6 \times 10^{-102}$, GR224183) in the LM and RM libraries and a 5′-nucleotidase ($E = 9 \times 10^{-50}$, GR228442) in the PF library (Appendix Table 1). Connected with cytosolic adenosine concentration, adenosine deaminase converts adenosine into inosine during RNA editing (Jaikaran et al., 2002). Inosine triphosphate pyrophosphatase controls the cellular level of ITP and dITP by pyrophosphorylation or stepwise phosphorylation of IMP, a precursor of both AMP and GMP (Lin et al., 2001). A substrate cycle between AMP and adenosine occurs in many eukaryotic cells through the action of a 5′-nucleotidase (Bontemps et al., 1983). Adenine phosphoribosyltransferase (APRTase) is the sole catalyst for adenine recycling in most eukaryotes and a deficiency of APRTase can result in the accumulation of 2,8-dihydroxyadenine (reviewed in by Moriwaki et al., 1999). Further studies will be required to determine how these proteins are involved in cordycepin production.

In conclusion, we identified a plethora of genes involved in the development of *C. militaris* under different cultural conditions, providing some useful starting points for further molecular biology studies of this increasingly widely used medicinal fungus. Particular interest will be paid, for example, in investigating the metabolic pathways involved with the production of pharmaceutical compounds, including cordycepin. Taken together with our ongoing genome project for this fungus (GenBank project ID 41129), *C. militaris* can now be explored as a genetically tractable model for studies on fungal sexuality.

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References

Aliyari R, Ding SW. 2009. RNA-based viral immunity initiated by the Dicer family of host immune receptors. Immunol Rev. 227: 176–188.

Anderson I, Brass A. 1998. Searching DNA databases for similarities to DNA sequences: when is a match significant? Bioinformatics 14: 349–356.

Audic S, Claverie JM, 1997. The significance of digital gene expression profiles. Genome Res. 7: 986–995.

Bard M, Bruner DA, Pierson CA, Lees ND, Biermann B, Frye L, Koegel C, Barbuch R. 1996. Cloning and characterization of ERG25, the *Saccharomyces cerevisiae* gene encoding C-4 sterol methyl oxidase. Proc Natl Acad Sci USA 93: 186–190.

Bidochka MJ, Pfeifer TA, Khachatourians GG. 1987. Development of the entomopathogenic fungus *Beauveria bassiana* in liquid cultures. Mycopathologia 99: 77–83.

Bluhm BH, Dhillon B, Lindquist EA, Kema GH, Goodwin SB, Dunkle LD. 2008. Analyses of expressed sequence tags from the maize foliar pathogen *Cercospora zeae-maydis* identify novel genes expressed during vegetative, infectious, and reproductive growth. BMC Genomics 9: 523.

Bontemps F, van den Berghe G, Hers HG. 1983. Evidence for a substrate cycle between AMP and adenosine in isolated hepatocytes. Proc Natl Acad Sci USA 80: 2829–2833.

Cheung JK, Li J, Cheung AW, Zhu Y, Zheng KY, Bi CW, Duan R, Choi RC, Lau DT, Dong TT, Lau BW, Tsim KW. 2009. Cordysinocan, a polysaccharide isolated from cultured *Cordyceps*, activates immune responses in cultured T-lymphocytes and macrophages: signaling cascade and induction of cytokines. J Ethnopharmacol. 124: 61–68.

Cho EM, Liu L, Farmerie W, Keyhani NO. 2006a. EST analysis of cDNA libraries from the entomopathogenic fungus *Beauveria* (*Cordyceps*) *bassiana*. I. Evidence for stage-specific gene expression in aerial conidia, *in vitro* blastospores and submerged conidia. Microbiology 152: 2843–2854.

Cho EM, Boucias D, Keyhani NO. 2006b. EST analysis of cDNA libraries from the entomopathogenic fungus *Beauveria* (*Cordyceps*) *bassiana*. II. Fungal cells sporulating on chitin and producing oosporein. Microbiology 152: 2855–2864.

Coppin E, Debuchy R, Arnaise S, Picard M. 1997. Mating types and sexual development in filamentous ascomycetes. Microbiol Mol Biol Rev. 61: 411–428.

Corrigan RM, Rigby D, Handley P, Foster TJ. 2007. The role of *Staphylococcus aureus* surface protein SasG in adherence and biofilm formation. Microbiology 153: 2435–2446.

Das SK, Masuda M, Hatashita M, Sakurai A, Sakakibara M. 2008. A new approach for improving cordycepin productivity in surface liquid culture of *Cordyceps militaris* using high-energy ion beam irradiation. Lett Appl Microbiol. 47: 534–538.

de Faria MR, Wraight SP. 2007. Mycoinsecticides and Mycoacaricides: A comprehensive list with worldwide coverage and international classification of formulation types. Biol Control 43: 237–256.

Feldbrügge M, Zarnack K, Vollmeister E, Baumann S, Koepke J, König J, Münsterkötter M, Mannhaupt G. 2008. The post-transcriptional machinery of *Ustilago maydis*. Fungal Genet Biol. 45: S40–S46.

Freimoser FM, Screen S, Bagga S, Hu G, St. Leger RJ. 2003. Expressed sequence tag (EST) analysis of two subspecies of *Metarhizium anisopliae* reveals a plethora of secreted proteins with potential activity in insect hosts. Microbiology 149: 239–247.

Hildén P, Savolainen K, Tyynelä J, Vuento M, Kuusela P. 1996. Purification and characterisation of a plasmin-sensitive surface protein of *Staphylococcus aureus*. Eur J Biochem. 236: 904–910.

Huang B, Li CR, Humber RA, Hodge KT, Fan MZ, Li ZZ. 2005. Molecular evidence for the taxonomic status of *Metarhizium taii* and its teleomorph, *Cordyceps taii* (Hypocreales, Clavicipitaceae). Mycotaxon 94: 137–147.

Huang X, Madan A. 1999. CAP3: a DNA sequence assembly program. Genome Res. 9: 868–877.

Jaikaran DC, Collins CH, MacMillan AM. 2002. Adenosine to inosine editing by ADAR2 requires formation of a ternary complex on the GluR-B R/G site. J Biol Chem. 277: 37624–37629.

Kanauchi A, Futatsu T. 1999. Light-induced fruit-body formation of an entomogenous fungus *Paecilomyces tenuipes*. Mycoscience 40: 349–351.

Kok CC, McMinn PC. 2009. Picornavirus RNA-dependent RNA polymerase. Int J Biochem Cell Biol. 41: 498–502.

Li SP, Song ZH, Dong TT, Ji ZN, Lo CK, Zhu SQ, Tsim KW. 2004. Distinction of water-soluble constituents between natural and cultured *Cordyceps* by capillary electrophoresis. Phytomedicine 11: 684–690.

Li SP, Yang FQ, Tsim KWK. 2006. Quality control of *Cordyceps sinensis*, a valued traditional Chinese medicine. J Pharm Biomed Anal. 41: 1571–1584.

Li ZZ, Li CR, Huang B, Fan MZ. 2001. Discovery and demonstration of the teleomorph of *Beauveria bassiana* (Bals.) Vuill., an important entomogenous fungus. Chinese Sci Bull. 46: 751–753.

Lin S, McLennan AG, Ying K, Wang Z, Gu S, Jin H, Wu C, Liu W, Yuan Y, Tang R, Xie Y, Mao Y. 2001. Cloning, expression, and characterization of a human inosine triphosphate pyrophosphatase encoded by the itpa gene. J Biol Chem. 276: 18695–18701.

Masuda M, Urabe E, Sakurai A, Sakakibara M. 2006. Production of cordycepin by surface culture using the medicinal mushroom *Cordyceps militaris*. Enzyme Microb Technol. 39: 641–646.

Morozova O, Marra MA. 2008. Applications of next-generation sequencing technologies in functional genomics. Genomics 92: 255–264.

Moriwaki Y, Yamamoto T, Higashino K. 1999. Enzymes involved in purine metabolism–a review of histochemical localization and functional implications. Histol Histopathol. 14: 1321–1340.

Ng TB, Wang HX. 2005. Pharmacological actions of *Cordyceps*, a prized folk medicine. J Pharm Pharmacol. 57: 1509–1519.

Ni H, Zhou XH, Li HH, Huang WF. 2009. Column chromatographic extraction and preparation of cordycepin from *Cordyceps militaris* waster medium. J Chromatogr B 877: 2135–2141.

Nolan T, Braccini L, Azzalin G, de Toni A, Macino G, Cogoni C. 2005. The post-transcriptional gene silencing machinery functions independently of DNA methylation to repress a LINE1-like retrotransposon in *Neurospora crassa*. Nucleic Acids Res. 33: 1564–1573.

Nugent KG, Choffe K, Saville BJ. 2004. Gene expression during *Ustilago maydis* diploid filamentous growth: EST library creation and analyses. Fungal Genet Biol. 41: 349–360.

Paterson RR. 2008 Cordyceps: a traditional Chinese medicine and another fungal therapeutic biofactory? Phytochemistry 69: 1469–1495.

Rehner SA, Buckley E. 2005. A *Beauveria* phylogeny inferred from nuclear ITS and EF1-alpha sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. Mycologia 97: 84–98.

Sato H, Shimazu M. 2002. Stromata production for *Cordyceps militaris* (Clavicipitales: Clavicipitaceae) by injection of hyphal bodies to alternative host insects. Appl Entomol Zool. 37: 85–92.

Sprague GF, Cullen PJ, Goehring AS.. 2004. Yeast signal transduction: regulation and interface with cell biology. Adv Exp Med Biol. 547: 91–105.

Stone R. 2008. Mycology: Last Stand for the body snatcher of the Himalayas? Science 322: 1182.

Sung GH, Hywel-Jones NL, Sung JM, Luangsa-Ard JJ, Shrestha B, Spatafora JW. 2007. Phylogenetic classification of

Cordyceps and the clavicipitaceous fungi. Stud Mycol. 57: 5–59.

ter Kuile BH, Westerhoff HV. 2001. Transcriptome meets metabolome: hierarchical and metabolic regulation of the glycolytic pathway. FEBS Lett. 500: 169–171.

Verdel A, Vavasseur A, Le Gorrec M, Touat-Todeschini L. 2009. Common themes in siRNA-mediated epigenetic silencing pathways. Int J Dev Biol. 53: 245–257.

Wall PK, Leebens-Mack J, Chanderbali AS, Barakat A, Wolcott E, Liang H, Landherr L, Tomsho LP, Hu Y, Carlson JE, Ma H, Schuster SC, Soltis DE, Soltis PS, Altman N, de Pamphilis CW. 2009. Comparison of next generation sequencing technologies for transcriptome characterization. BMC Genomics 10: 347.

Wang CS, St. Leger RJ. 2007. A scorpion neurotoxin increases the potency of a fungal insecticide. Nat Biotechnol. 25: 1455–1456.

Wang CS, Hu G, St. Leger RJ. 2005. Differential gene expression by *Metarhizium anisopliae* growing in root exudate and host (*Manduca sexta*) cuticle or hemolymph reveals mechanisms of physiological adaptation. Fungal Genet Biol. 42: 704–718.

Wang CS, Duan ZB, St. Leger RJ. 2008. The MOS1 osmosensor of *Metarhizium anisopliae* is required for adaptation to insect host hemolymph. Eukaryot Cell 7: 302–309.

White SA, Allshire RC. 2008. RNAi-mediated chromatin silencing in fission yeast. Curr Top Microbiol Immunol. 320: 157–183.

Xiao JH, Zhong JJ. 2007. Secondary metabolites from *Cordyceps* species and their antitumor activity studies. Recent Pat Biotechnol. 1: 123–137.

Xie CY, Gu ZX, Fan GJ, Gu FR, Han YB, Chen ZG. 2009. Production of cordycepin and mycelia by submerged fermentation of *Cordyceps militaris* in mixture natural culture. Appl Biochem Biotechnol. 158: 483–492.

Yokoyama E, Yamagishi K, Hara A. 2003. Structures of the mating-type loci of *Cordyceps takaomontana*. Appl Environ Microbiol. 69: 5019–5022.

Yokoyama E, Yamagishi K, Hara A. 2005. Heterothallism in *Cordyceps takaomontana*. FEMS Microbiol Lett. 250: 145–150.

Zhou X, Gong Z, Su Y, Lin J, Tang K. 2009. *Cordyceps* fungi: natural products, pharmacological functions and developmental products. J Pharm Pharmacol. 61: 279–291.

Appendix

Appendix Table 1. Unique ESTs from four libraries of *Cordyceps militaris*. LM, for liquid mycelium library; RM, for rice medium culture library; RM, rice medium fruit body library; PF, insect pupae fruit body library. The data are presented in the order of functional category. No., indicates identified trancript numbers.

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224452	LM	1	1.a	XP_001258037	1.0E-43	xaa-pro dipeptidase app (*E.coli*)	*Neosartorya fischeri*
GR224518	LM/PF	2	1.a	BAB40769	6.0E-122	argininosuccinate lyase	*Fusarium oxysporum*
GR224846	LM	1	1.a	XP_001273386	2.0E-39	glutathione S-transferase, putative	*Aspergillus clavatus*
GR224980	LM/PF	3	1.a	XP_001933414	7.0E-120	aspartate aminotransferase	*Pyrenophora tritici-repentis*
GR225111	LM	1	1.a	XP_001276018	2.0E-43	GNAT family acetyltransferase, putative	*Aspergillus clavatus*
GR225444	RM	1	1.a	ABB47829	5.0E-08	lanthionine synthetase C-like protein, expressed	*Oryza sativa Japonica*
GR225933	RM	1	1.a	XP_960754	1.0E-82	N-acetyltransferase 5	*Neurospora crassa*
GR226607	RF	2	1.a	XP_001264010	7.0E-06	tyrosinase central domain protein	*Neosartorya fischeri*
GR226647	RF	1	1.a	EDP56958	2.0E-16	tyrosinase	*Aspergillus fumigatus*
GR227378	PF	1	1.a	XP_001248336	6.0E-45	cystathionine gamma-synthase	*Coccidioides immitis*
GR227613	PF	3	1.a	XP_962367	9.0E-76	cysteine dioxygenase	*Neurospora crassa*
GR227659	RM/PF	2	1.a	XP_001263041	9.0E-74	indoleamine 2,3-dioxygenase subfamily	*Neosartorya fischeri*
GR228019	RM/PF	3	1.a	ABU48597	1.0E-51	Xaa-Pro dipeptidase	*Trichophyton tonsurans*
GR228241	PF	1	1.a	XP_386466	7.0E-59	GLYC_NEUCR Serine hydroxymethyltransferase, cytosolic	*Gibberella zeae*
GR228378	PF	1	1.a	XP_750969	7.0E-45	homogentisate 1,2-dioxygenase	*Aspergillus fumigatus*
GR228619	PF	1	1.a	CAD70964	2.0E-53	related to 3-phosphoserine aminotransferase	*Neurospora crassa*
GR224254	LM	1	1.b	XP_001248603	6.0E-57	acetamidase	*Coccidioides immitis*
GR224277	LM	1	1.b	XP_962166	1.0E-94	glycogen phosphorylase	*Neurospora crassa*
GR224334	LM	1	1.b	XP_001262762	2.0E-94	phytase, putative	*Neosartorya fischeri*
GR224372	LM	1	1.b	XP_001228267	2.0E-14	citrate synthase, mitochondrial precursor	*Chaetomium globosum*
GR224513	LM/PF	4	1.b	ABH10639	2.0E-111	fructose biphosphate aldolase	*Coccidioides posadasii*
GR224831	LM	1	1.b	NP_741808	3.0E-08	beta carbonic anhydrase family member (bca-1)	*Caenorhabditis elegans*
GR224869	LM	1	1.b	XP_001262948	4.0E-57	alpha/beta hydrolase, putative	*Neosartorya fischeri*
GR224889	LM	1	1.b	XP_366548	3.0E-45	transaldolase	*Magnaporthe grisea*
GR225165	LM	3	1.b	XP_001219658	1.0E-107	pyruvate decarboxylase	*Chaetomium globosum*
GR225216	LM	1	1.b	YP_001173410	2.0E-33	hydrolase, alpha/beta fold family	*Pseudomonas stutzeri*
GR225327	LM/RM	2	1.b	BAF98892	1.0E-52	formate oxidase 2	*Debaryomyces vanrijiae*
GR225333	LM	1	1.b	XP_001548578	1.0E-12	fumarate hydratase	*Botryotinia fuckeliana*
GR225379	LM	1	1.b	XP_366548	2.0E-83	transaldolase	*Magnaporthe grisea*
GR225408	RM	1	1.b	XP_961145	4.0E-60	protein kinase gsk3	*Neurospora crassa*
GR225496	RM	1	1.b	ZP_02121510	2.0E-10	ethyl tert-butyl ether degradation EthD	*Methylobacterium nodulans*
GR225510	RM	1	1.b	XP_001274982	2.0E-36	glucose-methanol-choline (gmc) oxidoreductase	*Aspergillus clavatus*
GR225647	RM	1	1.b	XP_001938825	8.0E-69	cyclopentanone 1,2-monooxygenase	*Pyrenophora tritici-repentis*
GR225777	RM	1	1.b	XP_962927	3.0E-129	malate dehydrogenase, mitochondrial precursor	*Neurospora crassa*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225910	LM/RM	3	1.b	XP_962283	1.0E-166	isocitrate dehydrogenase subunit 2, mitochondrial precursor	*Neurospora crassa*
GR225992	RM	1	1.b	XP_001259634	1.0E-111	1,4-alpha-glucan branching enzyme	*Neosartorya fischeri*
GR226197	RM	1	1.b	AAG32629	1.0E-123	mannose phospho-dolichol synthase	*Hypocrea jecorina*
GR226313	RF	1	1.b	XP_001246410	2.0E-08	1,3-b-glucanosyltransferase	*Coccidioides immitis*
GR226373	RF	1	1.b	XP_751328	2.0E-27	endo-1,3(4)-beta-glucanase	*Aspergillus fumigatus*
GR226546	RF	1	1.b	XP_750969	8.0E-43	homogentisate 1,2-dioxygenase	*Aspergillus fumigatus*
GR226556	RF	1	1.b	XP_001939469	3.0E-83	molybdopterin binding domain containing protein	*Pyrenophora tritici-repentis*
GR226678	RF	1	1.b	XP_001939425	7.0E-71	alpha-1,3-mannosyltransferase CMT1	*Pyrenophora tritici-repentis*
GR227412	RM/PF	2	1.b	XP_961145	3.0E-57	glycogen synthase kinase	*Neurospora crassa*
GR228571	PF	1	1.b	XP_001382922	4.0E-07	alcohol dehydrogenase	*Pichia stipitis*
GR224134	LM	1	1.c	XP_001265779	2.0E-32	fatty acid desaturase, putative	*Neosartorya fischeri*
GR224176	LM	2	1.c	ACB12561	7.0E-84	Fum16, long-chain acyl-CoA synthetases (AMP-forming)	*Fusarium oxysporum*
GR224258	LM	1	1.c	CAA04820	2.0E-32	phenylacetyl-CoA ligase	*Penicillium chrysogenum*
GR224288	LM	2	1.c	AAX07629	2.0E-59	cell lysis protein-like protein	*Magnaporthe grisea*
GR224400	LM	1	1.c	ABF84060	2.0E-34	C-4 sterol methyl oxidase	*Chaetomium globosum*
GR224594	LM	1	1.c	BAC67175	1.0E-34	phospholipase D	*Emericella nidulans*
GR224777	LM	1	1.c	XP_001273259	2.0E-50	cyclopropane-fatty-acyl-phospholipid synthase, putative	*Aspergillus clavatus*
GR224820	PF/LM	2	1.c	XP_001940316	2.0E-53	phospholipase A2	*Pyrenophora tritici-repentis*
GR225137	LM	1	1.c	EDU48549	2.0E-51	phosphoglycerate mutase family protein	*Pyrenophora tritici-repentis*
GR225206	LM	1	1.c	XP_958250	8.0E-60	lathosterol oxidase	*Neurospora crassa*
GR225208	LM/RM	2	1.c	XP_961824	3.0E-153	acyl-CoA desaturase 1	*Neurospora crassa*
GR225276	LM	11	1.c	ABF84060	3.0E-89	C-4 sterol methyl oxidase	*Chaetomium globosum*
GR225281	LM	1	1.c	XP_001276142	2.0E-32	alkaline phosphatase family protein	*Aspergillus clavatus*
GR225376	LM	1	1.c	AAP47107	4.0E-58	serine paLMitoyl transferase subunit; SPT subunit; LCBB	*Emericella nidulans*
GR225450	RM	1	1.c	NP_214355	1.0E-18	enolase-phosphatase E-1	*Aquifex aeolicus*
GR225565	RM	1	1.c	XP_001932331	8.0E-10	sterol O-acyltransferase 1	*Pyrenophora tritici-repentis*
GR225632	RM	1	1.c	XP_001273303	2.0E-49	BEM46 family protein	*Aspergillus clavatus*
GR225706	RM	1	1.c	NP_587790	3.0E-35	steroid oxidoreductase superfamily protein	*Schizosaccharomyces pombe*
GR226153	RM	2	1.c	XP_753885	2.0E-73	steroid monooxygenase (CpmA)	*Aspergillus fumigatus*
GR226173	RM	1	1.c	XP_752948	4.0E-129	fatty acid hydroxylase	*Aspergillus fumigatus*
GR226391	RF	1	1.c	XP_753491	3.0E-40	glycerophosphocholine phosphodiesterase Gde1	*Aspergillus fumigatus*
GR226517	RF	1	1.c	XP_001264979	3.0E-17	protein phophatase 2C family protein	*Neosartorya fischeri*
GR226727	RF	1	1.c	XP_753885	9.0E-67	steroid monooxygenase (CpmA)	*Aspergillus fumigatus*
GR227476	RM/PF	2	1.c	XP_001547762	3.0E-27	acyl-CoA desaturase	*Botryotinia fuckeliana*
GR227506	PF	1	1.c	XP_001547868	6.0E-24	oleate-induced peroxisomal protein	*Botryotinia fuckeliana*
GR228255	PF	1	1.c	XP_001263009	1.0E-25	lipase/esterase family protein, putative	*Neosartorya fischeri*
GR228535	LM/PF	3	1.c	XP_955999	4.0E-125	D-3-phosphoglycerate dehydrogenase 1	*Neurospora crassa*
GR228540	PF	1	1.c	EDU50261	3.0E-49	ethanolaminephosphotransferase	*Pyrenophora tritici-repentis*
GR228575	PF	1	1.c	XP_001267686	6.0E-52	DDHD domain protein	*Aspergillus clavatus*
GR228592	PF	1	1.c	EDU43602	4.0E-64	arylsulfatase precursor	*Pyrenophora tritici-repentis*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224183	LM/RM	2	1.d	XP_001561243	6.0E-102	ATP phosphoribosyltransferase	*Botryotinia fuckeliana*
GR224306	LM	1	1.d	AAK13589	1.0E-06	rRNA intron-encoded homing endonuclease	*Oryza sativa (rice)*
GR224309	LM/RM	7	1.d	YP_002213592	5.0E-12	GIY-YIG endonuclease	*Cordyceps brongniartii*
GR224460	LM	1	1.d	XP_963727	6.0E-58	adenine phosphoribosyltransferase	*Neurospora crassa*
GR224515	LM	1	1.d	XP_753417	1.0E-79	ribonucleotide reductase small subunit RnrA	*Aspergillus fumigatus*
GR224569	PF/LM	3	1.d	XP_001273892	3.0E-27	inosine triphosphate pyrophosphatase (itpase)	*Aspergillus clavatus*
GR224757	LM	1	1.d	XP_754074	9.0E-65	predicted nucleotide kinase	*Aspergillus fumigatus*
GR224973	LM/PF	3	1.d	P32761	3.0E-11	DNA endonuclease I-CeuI (23S rRNA intron 1 protein	*chloroplast Chlamydomonas eugametos*
GR225995	RM	2	1.d	XP_001263831	3.0E-68	phosphoribosyl-aminoimidazole-succinocarboxamide synthase	*Neosartorya fischeri*
GR226201	RM	1	1.d	YP_810411	3.0E-11	nucleotidyltransferase	*Oenococcus oeni*
GR226685	RF/PF	3	1.d	XP_570103	8.00E-60	nucleoside/cytosine deaminase	*Cryptococcus neoformans*
GR226872	PF	1	1.d	XP_964453	3.0E-133	UTP-glucose-1-phosphate uridylyltransferase	*Verticillium albo-atrum*
GR228018	RM/PF	2	1.d	XP_955968	8.0E-105	uracil phosphoribosyltransferase	*Neurospora crassa*
GR228442	PF	1	1.d	XP_749865	9.0E-50	5′-nucleotidase	*Aspergillus fumigatus*
GR224294	LM/RM	2	1.e	CAD71132	6.0E-41	related to DCG1 protein	*Neurospora crassa*
GR225213	LM	1	1.e	XP_001262166	5.0E-43	isoflavone reductase family protein	*Neosartorya fischeri*
GR225487	RM	1	1.e	AAL77224	4.0E-27	thioredoxin II	*Podospora anserina*
GR225544	RM	1	1.e	XP_001939670	4.0E-19	glutation S-transferase	*Pyrenophora tritici-repentis*
GR226897	PF	1	1.e	P13998	4.0E-58	Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase)	*Kluyveromyces lactis*
GR225246	LM	7	1.f	ACB56643	5.0E-73	coproporphyrinogen III oxidase	*Trichoderma aureoviride*
GR226569	RM/RF	4	1.f	XP_751220	2.0E-51	choline sulfatase	*Aspergillus fumigatus*
GR227819	PF	2	1.f	EDL80237	5.0E-07	pantothenate kinase 2	*Rattus norvegicus*
GR227840	PF	1	1.f	XP_001543015	4.0E-59	riboflavin synthase alpha chain	*Ajellomyces capsulatus*
GR228219	PF	1	1.f	XP_962504	3.0E-67	ferrochelatase, mitochondrial precursor	*Neurospora crassa*
GR224080	LM	2	2	NP_775409	1.0E-32	cytochrome oxidase subunit III	*Lecanicillium muscarium*
GR224113	LM	1	2	EDP53376	2.0E-17	FAD binding domain protein	*Aspergillus fumigatus*
GR224206	LM/RM	2	2	XP_001225654	2.0E-106	adenylate kinase	*Chaetomium globosum*
GR224260	LM	19	2	XP_386224	1.0E-36	ATP9_NEUCR ATP synthase protein 9, mitochondrial precursor (Lipid-binding protein)	*Gibberella zeae*
GR224281	LM	1	2	Q5K8S8	1.0E-14	vacuolar ATP synthase subunit e (V-ATPase subunit e) (Vacuolar proton pump subunit e).	*Cryptococcus neoformans*
GR224301	LM/RF	2	2	XP_362271	3.0E-28	vacuolar ATPase	*Magnaporthe grisea*
GR224302	LM	1	2	XP_001276002	4.0E-05	AAA family ATPase, putative	*Aspergillus clavatus*
GR224320	LM	1	2	NP_570156	5.0E-81	NADH-ubiquinone oxidoreductase chain 5	*Hypocrea jecorina*
GR224359	LM	1	2	YP_001876510	3.0E-77	NADH dehydrogenase subunit 6	*Beauveria bassiana*
GR224390	LM	1	2	XP_965776	1.0E-70	ATP synthase D chain, mitochondrial	*Neurospora crassa*
GR224444	LM	1	2	XP_965645	1.0E-92	ATP synthase alpha chain, mitochondrial precursor	*Neurospora crassa*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224490	LM	1	2	XP_001228192	3.0E-55	cytochrome *c* oxidase polypeptide V, mitochondrial precursor	*Chaetomium globosum*
GR224508	LM	1	2	XP_956673	4.0E-16	NADH:ubiquinone oxidoreductase 6.6kD subunit	*Neurospora crassa*
GR224553	LM	1	2	XP_001216003	2.0E-86	monothiol glutaredoxin-5, mitochondrial precursor	*Aspergillus terreus*
GR224674	LM	1	2	Q12664	4.0E-72	cytochrome P450 51	*Penicillium italicum*
GR224722	LM/PF/RF	12	2	XP_389763	2.0E-58	VATF_NEUCR Vacuolar ATP synthase subunit F (V-ATPase F subunit)	*Gibberella zeae*
GR224723	LM	1	2	YP_001876509	6.0E-94	cytochrome oxidase subunit III	*Beauveria bassiana*
GR224731	LM	1	2	EDP53461	5.0E-35	cytochrome P450 monooxygenase, putative	*Aspergillus fumigatus*
GR224744	LM/RM/RF	3	2	NP_010609	2.0E-06	subunit e of mitochondrial F1F0-ATPase, which is a large,evolutionarily conserved enzyme complex required for ATP synthesis;essential for the dimeric and oligomeric state of ATP synthase;Tim11p	*Saccharomyces cerevisiae*
GR224745	LM	1	2	YP_001876504	2.0E-56	cytochrome oxidase subunit I	*Beauveria bassiana*
GR224796	LM	1	2	EDU48156	2.0E-53	NADPH:adrenodoxin oxidoreductase, mitochondrial precursor	*Pyrenophora tritici-repentis*
GR224867	LM	1	2	YP_001876509	1.0E-102	cytochrome oxidase subunit III	*Beauveria bassiana*
GR224916	LM	1	2	XP_001276795	7.0E-05	FAD binding domain protein	*Aspergillus clavatus*
GR224927	LM	1	2	YP_001876502	2.0E-42	NADH dehydrogenase subunit 5	*Beauveria bassiana*
GR224991	LM	1	2	XP_001269706	4.0E-30	NADH-cytochrome b5 reductase, putative	*Aspergillus clavatus*
GR225163	LM	1	2	NP_780573	2.0E-07	LYR motif containing 2	*Mus musculus*
GR225179	LM	1	2	XP_001219268	7.0E-31	NADH-ubiquinone oxidoreductase 23 kDa subunit	*Chaetomium globosum*
GR225210	LM/PF	2	2	XP_001262839	2.0E-15	cytochrome c oxidase assembly protein	*Neosartorya fischeri*
GR225226	LM	2	2	XP_001267960	1.0E-10	UQCRX/QCR9 like ubiquinol-cytochrome C reductase family protein	*Aspergillus clavatus*
GR225242	LM	2	2	XP_963863	3.0E-31	NADH: ubiquinone oxidoreductase 12.3kD subunit	*Neurospora crassa*
GR225254	LM/PF	2	2	XP_956673	2.0E-15	NADH:ubiquinone oxidoreductase 6.6kD subunit	*Neurospora crassa*
GR225394	LM/PF	2	2	XP_965807	1.0E-61	vacuolar ATP synthase 16 kDa proteolipid subunit 2	*Neurospora crassa*
GR225492	RM/RF	2	2	XP_001546681	2.0E-20	cytochrome *c* oxidase chain VIIc	*Botryotinia fuckeliana*
GR225504	RM	1	2	XP_960814	2.0E-26	ubiquinol-cytochrome *c* oxidoreductase complex III subunit VIII, 11kD protein of the UcrQ family	*Neurospora crassa*
GR225705	RM	1	2	XP_961585	4.0E-24	glutaredoxin	*Neurospora crassa*
GR226010	RM/LM	5	2	YP_002213610	3.0E-89	cytochrome oxidase subunit III	*mitochondrion Cordyceps brongniartii*
GR226026	RM	2	2	EDP49959	9.0E-15	F1F0-ATP synthase regulatory factor Stf2, putative	*Aspergillus fumigatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226042	RM/RF	3	2	XP_960712	5.0E-24	NADH:ubiquinone oxidoreductase 11.5kD subunit	*Neurospora crassa*
GR226169	RM	1	2	XP_753017	6.0E-48	heme/steroid binding domain protein	*Aspergillus fumigatus*
GR226178	RM	1	2	XP_001554426	1.0E-164	plasma membrane ATPase	*Botryotinia fuckeliana*
GR226184	RM	1	2	XP_747154	2.0E-61	cytochrome P450 oxidoreductase OrdA-like	*Aspergillus fumigatus*
GR226235	RM	1	2	NP_775409	7.0E-31	cytochrome oxidase subunit III	*Lecanicillium muscarium*
GR226284	RF	1	2	XP_965645	4.0E-100	ATP synthase alpha chain, mitochondrial precursor	*Neurospora crassa*
GR226620	RF	1	2	XP_001942298	1.0E-40	cytochrome P450 3A17	*Pyrenophora tritici-repentis*
GR226684	LM/RF	7	2	AAW69350	5.0E-108	NADH-ubiquinone oxidoreductase 40 kDa subunit-like protein	*Magnaporthe grisea*
GR226733	RF	1	2	XP_001552446	2.0E-91	H+ ATPase C subunit	*Botryotinia fuckeliana*
GR227099	PF	27	2	CAB65297	6.0E-08	P-type ATPase	*Neurospora crassa*
GR227147	RM/PF/LM	6	2	XP_390178	5.0E-67	VATL_NEUCR Vacuolar ATP synthase 16 kDa proteolipid subunit	*Gibberella zeae*
GR227229	LM/PF/RM	7	2	XP_002151699	7.0E-09	mitochondrial F1F0 ATP synthase subunit Atp18, putative	*Penicillium marneffei*
GR227372	LM/PF	6	2	ACI68759	5.0E-29	NADH dehydrogenase 1 beta subcomplex subunit 9	*Salmo salar*
GR227643	PF	1	2	EDP53517	9.0E-15	DUF341 domain oxidoreductase, putative	*Aspergillus fumigatus*
GR227968	PF	1	2	XP_961915	6.0E-84	cytochrome P450 61	*Neurospora crassa*
GR228053	RM/PF	3	2	YP_001424457	2.0E-24	oxidoreductase, short chain dehydrogenase/reductase family	*Coxiella burnetii*
GR228223	LM/RM/PF	8	2	XP_001936487	8.0E-40	cytochrome *c* oxidase polypeptide vib	*Pyrenophora tritici-repentis*
GR228492	PF	1	2	XP_001481718	1.0E-13	cytochrome *c* oxidase assembly protein Cox19	*Aspergillus fumigatus*
GR224149	LM/RM	2	3.a	XP_001932197	4.0E-28	60S ribosomal protein L30	*Pyrenophora tritici-repentis*
GR224282	LM/PF	15	3.a	XP_370455	2.0E-21	ribosomal protein L38e	*Magnaporthe grisea*
GR224311	LM/PF/RM	31	3.a	XP_359800	2.0E-19	ribosomal protein L39	*Magnaporthe grisea*
GR224450	LM/PF	2	3.a	XP_390544	1.0E-22	60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).	*Gibberella zea*
GR224461	LM	1	3.a	XP_370161	5.0E-96	40S ribosomal protein S5	*Magnaporthe grisea*
GR224465	LM	1	3.a	XP_749362	1.0E-54	40S ribosomal protein S14	*Aspergillus fumigatus*
GR224470	LM	1	3.a	XP_386763	7.0E-97	RS7_NEUCR 40S ribosomal protein S7	*Gibberella zeae*
GR224478	LM/RM/PF	4	3.a	XP_002153254	5.0E-34	60S ribosomal protein L28	*Penicillium marneffei*
GR224524	LM	1	3.a	XP_001271667	5.0E-91	60S ribosomal protein L11	*Aspergillus clavatus*
GR224599	LM	2	3.a	XP_388032	7.0E-76	RL2A_ERYGR 60S ribosomal protein L27a (L29)	*Gibberella zeae*
GR224774	LM	2	3.a	XP_390357	4.0E-55	60S RIBOSOMAL PROTEIN L44	*Gibberella zeae*
GR224813	LM	1	3.a	XP_001560156	8.0E-78	40S ribosomal protein S11	*Botryotinia fuckeliana*
GR224876	LM/RF	4	3.a	XP_965758	8.0E-40	40S ribosomal protein S27	*Neurospora crassa*
GR224984	LM	1	3.a	XP_001229121	2.0E-80	60S ribosomal protein L12	*Chaetomium globosum*
GR225012	LM/RM	2	3.a	ABU50146	1.0E-86	ribosomal protein S3	*Cordyceps bassiana*
GR225065	LM	1	3.a	XP_001595641	1.0E-69	60S ribosomal protein L19	*Sclerotinia sclerotiorum*
GR225070	PF/LM	11	3.a	XP_965640	7.0E-78	60S ribosomal protein L11	*Neurospora crassa*
GR225116	LM	1	3.a	XP_001227903	9.0E-33	40S ribosomal protein S26	*Chaetomium globosum*
GR225126	LM/PF	5	3.a	XP_387224	1.0E-73	RS13_XENLA 40S RIBOSOMAL PROTEIN S13	*Gibberella zeae*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225151	LM	1	3.a	XP_001549932	2.0E-21	mitochondrial ribosomal protein L44	*Botryotinia fuckeliana*
GR225154	LM/PF/RM	6	3.a	XP_001550019	6.0E-26	60S ribosomal protein L29	*Botryotinia fuckeliana*
GR225227	LM	1	3.a	XP_001224493	1.0E-46	40S ribosomal protein S24	*Chaetomium globosum*
GR225231	LM/PF	2	3.a	ACI69241	2.0E-49	mitochondrial ribosomal protein of the small subunit; Mrps17p	*Salmo salar*
GR225239	LM	1	3.a	XP_001553621	6.0E-78	60S ribosomal protein L11	*Botryotinia fuckeliana*
GR225244	LM	1	3.a	EDU40024	3.0E-31	mitochondrial ribosomal protein S19	*Pyrenophora tritici-repentis*
GR225304	LM/RM	4	3.a	XP_001551610	6.0E-31	60S ribosomal protein L14	*Botryotinia fuckeliana*
GR225384	LM/PF/RF	6	3.a	XP_001229209	2.0E-31	60S ribosomal protein L22	*Chaetomium globosum*
GR225385	LM	1	3.a	XP_961514	2.0E-21	40S ribosomal protein S29	*Neurospora crassa*
GR225704	LM/RM/PF	8	3.a	ABE68883	2.0E-76	ribosomal protein S28	*Stachybotrys elegans*
GR225736	LM/RM	3	3.a	XP_749081	5.0E-36	small nuclear ribonucleoprotein (LSM5)	*Aspergillus fumigatus*
GR225778	RM/RF	3	3.a	XP_002146425	5.0E-53	60S ribosomal protein L18	*Penicillium marneffei*
GR225870	RM/RF	2	3.a	XP_001221626	6.0E-105	60S ribosomal protein L7	*Chaetomium globosum*
GR225904	RM	1	3.a	XP_001937290	1.0E-45	mitochondrial 40S ribosomal protein MRP2	*Pyrenophora tritici-repentis*
GR225934	RM/LM/PF	21	3.a	XP_001561242	1.0E-12	40S ribosomal protein S28	*Botryotinia fuckeliana*
GR225985	RM	1	3.a	XP_001546444	5.0E-56	60S ribosomal protein L21	*Botryotinia fuckeliana*
GR226008	RM/PF/LM	30	3.a	XP_001551813	2.0E-44	60S ribosomal protein L30	*Botryotinia fuckeliana*
GR226028	RM/PF	5	3.a	XP_001248452	1.0E-64	40S ribosomal protein S15	*Coccidioides immitis*
GR226085	LM/RM	4	3.a	ACG48268	1.0E-88	60S ribosomal protein L9	*Zea mays*
GR226089	RM/RF	2	3.a	XP_001265242	2.0E-17	50S ribosomal protein YmL27	*Neosartorya fischeri*
GR226095	LM/RF/RM	4	3.a	XP_001229578	2.0E-58	60S ribosomal protein L32	*Chaetomium globosum*
GR226126	RM	1	3.a	XP_963540	2.0E-68	60S ribosomal protein L16, mitochondrial precursor	*Neurospora crassa*
GR226181	LM/RM/PF	8	3.a	XP_957322	1.0E-63	40S ribosomal protein S22	*Neurospora crassa*
GR226187	LM/RM/PF	16	3.a	XP_001218480	5.0E-41	60S ribosomal protein L30-2	*Aspergillus terreus*
GR226255	RM/RF/PF	4	3.a	XP_001555389	3.0E-119	40S ribosomal protein S3	*Botryotinia fuckeliana*
GR226778	RF	2	3.a	NP_596108	1.0E-05	mitochondrial ribosomal protein subunit L39	*Schizosaccharomyces pombe*
GR226884	PF	1	3.a	XP_963118	7.0E-45	60S ribosomal protein L34	*Neurospora crassa*
GR227083	LM/RF/RM/PF	20	3.a	XP_964906	5.0E-25	40S ribosomal protein S30	*Neurospora crassa*
GR227301	PF/LM/RM	5	3.a	XP_001227903	3.0E-36	40S ribosomal protein S26	*Chaetomium globosum*
GR227381	LM/RM/RF/PF	37	3.a	XP_963231	2.0E-24	40S ribosomal protein S25	*Neurospora crassa*
GR227676	RM/PF	2	3.a	XP_965247	4.0E-59	60S ribosomal protein L31	*Neurospora crassa*
GR227700	PF	1	3.a	XP_001597937	8.0E-54	60S ribosomal protein L25	*Sclerotinia sclerotiorum*
GR227806	PF	1	3.a	NP_011731	9.0E-10	mitochondrial ribosomal protein of the small subunit	*Saccharomyces cerevisiae*
GR228060	PF	1	3.a	XP_382047	2.0E-84	RL17_NEUCR 60S ribosomal protein L17	*Gibberella zeae*
GR228124	LM/RM/PF	15	3.a	XP_001560156	1.0E-77	40S ribosomal protein S11	*Botryotinia fuckeliana*
GR228503	LM/PF/RF/RM	50	3.a	XP_958318	5.0E-50	60S ribosomal protein L33	*Neurospora crassa*
GR224251	LM	1	3.b	XP_961513	2.0E-105	elongation factor Tu, mitochondrial precursor	*Neurospora crassa*
GR224283	LM/RM	8	3.b	XP_001212985	9.0E-69	eukaryotic translation initiation factor 5A	*Aspergillus terreus*
GR224296	LM/RM/RF/PF	20	3.b	XP_746529	2.0E-27	L-PSP endoribonuclease family protein	*Aspergillus fumigatus*
GR224405	LM/RM/PF	3	3.b	XP_001209019	4.0E-178	eukaryotic initiation factor 4A	*Aspergillus terreus*
GR224551	RF/LM	2	3.b	XP_361098	3.0E-28	elongation factor 1-alpha	*Magnaporthe grisea*
GR224979	LM/RM/PF	7	3.b	XP_754980	3.0E-42	translation initiation factor SUI1	*Aspergillus fumigatus*
GR225030	LM	1	3.b	XP_957252	5.0E-37	eukaryotic translation initiation factor 5	*Neurospora crassa*
GR225375	LM/RM/RF/PF	6	3.b	XP_001262870	2.0E-33	L-PSP endoribonuclease family protein (Hmf1), putative	*Neosartorya fischeri*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225509	RM	1	3.b	XP_001937483	3.0E-106	eukaryotic translation initiation factor 3 110 kDa subunit	*Pyrenophora tritici-repentis*
GR225662	RM	1	3.b	XP_957296	8.0E-126	eukaryotic peptide chain release factor subunit 1	*Neurospora crassa*
GR225693	RM	1	3.b	CAE76428	2.0E-11	probable ribosomal elongation factor EF-2	*Neurospora crassa*
GR225708	RM	1	3.b	XP_001930631	1.0E-92	elongation factor 1-alpha	*Pyrenophora tritici-repentis*
GR225829	RM	1	3.b	XP_001941716	3.0E-80	tRNA ligase	*Pyrenophora tritici-repentis*
GR226132	RM	1	3.b	XP_001260399	7.0E-29	eukaryotic translation initiation factor 5, putative	*Neosartorya fischeri*
GR226493	RF	1	3.b	ABG37118	3.0E-57	elongation factor 2	*Glomerella graminicola*
GR226574	RF	1	3.b	XP_961215	2.0E-45	elongation factor 1-gamma	*Neurospora crassa*
GR227357	LM/PF	3	3.b	XP_959625	2.0E-82	elongation factor 1-beta	*Neurospora crassa*
GR227437	RF/PF	4	3.b	XP_002148934	2.0E-26	eukaryotic translation initiation factor 3 subunit EifCj, putative	*Penicillium marneffei*
GR227992	PF	1	3.b	T51896	2.0E-101	probable translation release factor erf3 [imported]	*Neurospora crassa*
GR228275	PF	1	3.b	XP_001273105	5.0E-27	nonribosomal peptide synthase, putative	*Aspergillus clavatus*
GR224078	LM/RM	2	3.c	XP_001937344	9.0E-96	26S proteasome non-ATPase regulatory subunit 12	*Pyrenophora tritici-repentis*
GR224350	LM	4	3.c	XP_001263333	2.0E-09	proteasome subunit alpha type	*Neosartorya fischeri*
GR224353	LM	1	3.c	XP_001276207	2.0E-65	ubiquitin C-terminal hydrolase (HAUSP), putative	*Aspergillus clavatus*
GR224374	LM	1	3.c	XP_001268325	3.0E-24	ubiquitin C-terminal hydrolase Ubp8, putative	*Aspergillus clavatus*
GR224415	LM/RM/RF	4	3.c	XP_957331	2.0E-100	proteasome component PRE6	*Neurospora crassa*
GR224416	LM	1	3.c	CAE76523	2.0E-61	related to ubiquitin-conjugating enzyme	*Neurospora crassa*
GR224468	LM	1	3.c	CAD21393	1.0E-53	probable ubiquitin-conjugating enzyme CDC34	*Neurospora crassa*
GR224654	LM	4	3.c	XP_001270622	5.0E-82	ubiquitin conjugating enzyme (UbcD), putative	*Aspergillus clavatus*
GR224695	LM	1	3.c	XP_001547757	7.0E-31	20S proteasome alpha subunit E	*Botryotinia fuckeliana*
GR224807	LM	2	3.c	XP_750948	3.0E-44	ubiquitin-like activating enzyme (UlaA)	*Aspergillus fumigatus*
GR224849	RM/LM	3	3.c	AAT85970	4.0E-73	SCF complex subunit Skp1	*Fusarium oxysporum*
GR224852	LM	1	3.c	AAC16012	3.0E-115	polyubiquitin	*Elaeagnus umbellata*
GR224893	LM	1	3.c	XP_959792	5.0E-64	rhomboid protein 2	*Neurospora crassa*
GR224953	LM	1	3.c	XP_001258419	3.0E-41	proteasome regulatory particle subunit (RpnI), putative	*Neosartorya fischeri*
GR225054	LM	1	3.c	XP_001597677	2.0E-66	ubiquitin fusion protein	*Sclerotinia sclerotiorum*
GR225073	LM	1	3.c	XP_365068	5.0E-54	ubiquitin conjugating enzyme	*Magnaporthe grisea*
GR225144	LM	1	3.c	NP_001007844	2.0E-19	ubiquitin related modifier 1 homolog	*Gallus gallus (chicken)*
GR225243	LM	1	3.c	XP_001259989	4.0E-43	dipeptidyl peptidase III	*Neosartorya fischeri*
GR225306	LM/PF	7	3.c	XP_958786	2.0E-110	proteasome component Y13	*Neurospora crassa*
GR225323	LM	1	3.c	EDU49040	2.0E-51	cullin binding protein CanA	*Pyrenophora tritici-repentis*
GR225414	RM	1	3.c	XP_001939353	2.0E-96	seprase	*Pyrenophora tritici-repentis*
GR225517	RM/RF/PF	8	3.c	XP_001597677	4.0E-67	ubiquitin fusion protein	*Sclerotinia sclerotiorum*
GR225783	RM	1	3.c	XP_001259989	5.0E-60	dipeptidyl peptidase III	*Neosartorya fischeri*
GR225906	RM	1	3.c	XP_751155	1.0E-84	proteasome regulatory particle subunit (RpnI)	*Aspergillus fumigatus*
GR225957	RM/RF	2	3.c	XP_752450	1.0E-33	ubiquitin-like modifier SUMO	*Aspergillus fumigatus*
GR226004	RM	1	3.c	XP_755213	4.0E-42	zinc carboxypeptidase	*Aspergillus fumigatus*
GR226007	RM	1	3.c	ACB30123	1.0E-19	subtilisin-like protease	*Epichloe festucae*
GR226027	RM	1	3.c	XP_001259989	2.0E-49	dipeptidyl peptidase III	*Neosartorya fischer*
GR226570	RF	1	3.c	XP_750213	2.0E-43	ubiquitin-protein ligase (Hul4)	*Aspergillus fumigatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226636	RF	1	3.c	CAE76125	5.0E-74	related to non-canonical ubiquitin conjugating enzyme 1	*Neurospora crassa*
GR226837	PF	1	3.c	XP_964107	5.0E-63	ubiquitin-conjugating enzyme E2 13	*Neurospora crassa*
GR226965	PF	1	3.c	AAB84057	1.0E-97	proteasome regulatory subunit 12	*Hypocrea jecorina*
GR227026	PF	1	3.c	CAE84597	1.0E-09	aspartic proteinase precursor	*Botryotinia fuckeliana*
GR227130	RM/PF	3	3.c	XP_750948	6.0E-64	ubiquitin-like activating enzyme (UlaA)	*Aspergillus fumigatus*
GR227175	PF	1	3.c	CAD21393	9.0E-59	probable ubiquitin-conjugating enzyme CDC34	*Neurospora crassa*
GR227206	PF	1	3.c	CAA51679	4.0E-113	ubiquitin	*Solanum lycopersicum*
GR227278	PF	10	3.c	AAY41882	3.0E-10	ubiquitin	*Gracilaria lemaneiformis*
GR227695	PF	1	3.c	XP_001403458	1.0E-74	proteasome regulatory particle subunit Rpt5	*Magnaporthe grisea*
GR227803	PF	1	3.c	XP_001486573	9.0E-110	ubiquitin	*Pichia guilliermondii*
GR227825	PF	2	3.c	ABG57251	7.0E-119	vacuolar protease A	*Trichoderma atroviride*
GR228034	PF	1	3.c	XP_001258419	1.0E-49	proteasome regulatory particle subunit (RpnI), putative	*Neosartorya fischeri*
GR228171	PF	1	3.c	XP_001247866	2.0E-53	ubiquitin-conjugating enzyme	*Coccidioides immitis*
GR228195	LM/RM/RF/PF	7	3.c	NP_588156.1|	2.0E-07	protease inhibitor (predicted)	*Schizosaccharomyces pombe*
GR228330	PF/LM	4	3.c	XP_001931304	1.0E-48	ring-box 1	*Pyrenophora tritici-repentis*
GR228374	PF	2	3.c	XP_751155	9.0E-68	proteasome regulatory particle subunit (RpnI)	*Aspergillus fumigatus*
GR228448	LM/RM/RF/PF	67	3.c	XP_001210780	4.0E-162	ubiquitin	*Aspergillus terreus*
GR224130	LM/PF	2	3.d	XP_752303	5.0E-20	S-adenosylmethionine-dependent methyltransferase	*Aspergillus fumigatus*
GR224135	LM	1	3.d	XP_001391905	2.0E-85	cyclophilin-like peptidyl prolyl cis-trans isomerase cypA	*Aspergillus niger*
GR224186	LM	1	3.d	AAT77151	7.0E-20	mitochondrial cytochrome c oxidase assembly factor	*Paracoccidioides brasiliensis*
GR224199	LM/PF	2	3.d	NP_001134344	4.0E-06	p8 MTCP-1, enhances the phosphorylation and activation of AKT1 and AKT	*Salmo salar*
GR224236	LM/RM	2	3.d	XP_959599	3.0E-74	L-A virus GAG protein N-acetyltransferase	*Neurospora crassa*
GR224298	LM/RM	2	3.d	AAC49417	1.0E-179	kinase	*Colletotrichum trifolii*
GR224386	LM	1	3.d	XP_751767	3.0E-44	geranylgeranyl transferae type II alpha subunit	*Aspergillus fumigatus*
GR224497	LM	1	3.d	NP_013749	5.0E-11	catalytic subunit of the mitochondrial inner membrane peptidase complex, required for maturation of mitochondrial proteins of the intermembrane space; complex contains Imp1p and Imp2p	*Saccharomyces cerevisiae*
GR224543	LM	1	3.d	AAK77607	5.0E-131	protein O-mannosyl transferase	*Aspergillus awamori*
GR224676	LM	1	3.d	XP_001556929	4.0E-29	dolichyl-phosphate mannosyltransferase polypeptide 2	*Botryotinia fuckeliana*
GR224760	LM	1	3.d	XP_001556929	3.0E-28	dolichyl-phosphate mannosyltransferase polypeptide 2	*Botryotinia fuckeliana*
GR224864	LM	1	3.d	XP_749371	3.0E-118	UDP-glucose:glycoprotein glucosyltransferase	*Aspergillus fumigatus*
GR225078	LM	1	3.d	XP_001561084	5.0E-11	dolichyl-phosphate mannosyltransferase polypeptide 3	*Botryotinia fuckeliana*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225110	LM	1	3.d	XP_001268279	2.0E-57	phosphotransferase enzyme family protein	*Aspergillus clavatus*
GR225267	LM	1	3.d	EDU45804	7.0E-53	dihydrolipoamide succinyltransferase	*Pyrenophora tritici-repentis*
GR225500	LM/RM	3	3.d	S71849	2.0E-78	peptidylprolyl isomerase (EC 5.2.1.8) A precursor, mitochondrial -cyclosporin fungus	*Elaphocordyceps subsessilis*
GR225609	RM	1	3.d	XP_001931420	1.0E-80	GPI ethanolamine phosphate transferase 2	*Pyrenophora tritici-repentis*
GR225636	RM	1	3.d	XP_752295	5.0E-125	protein phosphatase 2C	*Aspergillus fumigatus*
GR225806	RM	1	3.d	XP_001275202	6.0E-74	oligosaccharyl transferase subunit (gamma), putative	*Aspergillus clavatus*
GR225810	RM/PF	3	3.d	XP_750133	4.0E-41	prefoldin subunit 2	*Aspergillus fumigatus*
GR225866	RM	1	3.d	XP_749298	9.0E-48	MSF1 domain protein	*Aspergillus fumigatus*
GR225872	RM	2	3.d	XP_001728304	5.0E-81	peptidyl-prolyl cis-trans isomerase B precursor	*Neurospora crassa*
GR225895	RM	1	3.d	XP_751595	2.0E-22	prefoldin subunit 1	*Aspergillus fumigatus*
GR225961	RM	2	3.d	XP_001938168	1.0E-48	di-trans,poly-cis-decaprenylcistransferase	*Pyrenophora tritici-repentis*
GR226032	RM/PF	4	3.d	XP_956973	5.0E-60	ribosome biogenesis protein BRX1	*Neurospora crassa*
GR226272	RF	1	3.d	XP_001936409	1.0E-24	defective in cullin neddylation protein 1	*Pyrenophora tritici-repentis*
GR226320	RF	1	3.d	XP_752633	9.0E-17	mannosylphosphate transferase (Mnn4)	*Aspergillus fumigatus*
GR226612	RF	1	3.d	XP_001595013	4.0E-79	T-complex protein 1, beta subunit	*Sclerotinia sclerotiorum*
GR226632	RF	1	3.d	XP_955906	6.0E-123	T-complex protein 1 subunit alpha	*Neurospora crassa*
GR226924	PF	1	3.d	XP_959535	6.0E-85	dihydrolipoyl dehydrogenase, mitochondrial precursor	*Neurospora crassa*
GR226933	PF	3	3.d	XP_001267508	1.0E-35	2OG-Fe(II) oxygenase family oxidoreductase	*Neosartorya fischeri*
GR227254	PF	1	3.d	XP_958274	2.0E-138	negative regulator of the PHO system	*Neurospora crassa*
GR227344	RM/RF/PF	3	3.d	EDP53478	4.0E-38	porphyromonas-type peptidyl-arginine deiminase superfamily	*Aspergillus fumigatus*
GR227356	PF	1	3.d	XP_001556929	5.0E-29	dolichyl-phosphate mannosyltransferase polypeptide 2	*Botryotinia fuckeliana*
GR227742	PF/LM	6	3.d	XP_001211750	5.0E-118	uroporphyrinogen decarboxylase	*Aspergillus terreus*
GR227892	PF	1	3.d	XP_748678	1.0E-16	transferase family protein	*Aspergillus fumigatus*
GR224462	LM	1	4.a	XP_001538108	8.0E-06	lysyl-tRNA synthetase	*Ajellomyces capsulatus*
GR224557	LM	1	4.a	EDP56308	5.0E-58	prolyl-tRNA synthetase	*Aspergillus fumigatus*
GR224755	LM/PF/RF	3	4.a	XP_956014	8.0E-48	isoleucyl-tRNA synthetase	*Neurospora crassa*
GR224943	LM	1	4.a	XP_755187	4.0E-13	DNA directed RNA polymerase II 15 kDa subunit	*Aspergillus fumigatus*
GR225043	LM	1	4.a	XP_964988	3.0E-84	threonyl-tRNA synthetase, mitochondrial precursor	*Neurospora crassa*
GR225058	LM	1	4.a	XP_956014	1.0E-121	isoleucyl-tRNA synthetase	*Neurospora crassa*
GR225136	LM/PF	2	4.a	XP_001270015	1.0E-91	tryptophanyl-tRNA synthetase	*Aspergillus clavatus*
GR225703	RM	1	4.a	XP_001259727	3.0E-12	cysteinyl-tRNA synthetase	*Neosartorya fischeri*
GR225730	RM	63	4.a	YP_223920	2.0E-42	RNA-dependent RNA polymerase	*Fusarium graminearum*
GR226545	RF	1	4.a	XP_746724	2.0E-16	RNA polymerase I subunit Rpa43	*Aspergillus fumigatus*
GR226787	RF	1	4.a	CAD70445	8.0E-137	DNA-dependent RNA polymerase II RPB140 (RPB2)	*Neurospora crassa*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR227862	PF	3	4.a	XP_965008	2.0E-29	DNA-directed RNA polymerases I/II/III subunit 10	*Neurospora crassa*
GR228439	RM/PF	2	4.a	XP_965434	5.0E-61	DNA-directed RNA polymerase II 19 kDa polypeptide	*Neurospora crassa*
GR228645	PF	1	4.a	CAC28816	8.0E-37	related to DNA-directed RNA polymerase 13.3K chain	*Neurospora crassa*
GR224094	LM	1	4.b	Q7SDM8	4.0E-101	tRNA (His) guanylyltransferase (tRNA-histidine guanylyltransferase	*Neurospora crassa*
GR224163	RM/LM	5	4.b	XP_001215514	6.0E-28	small nuclear ribonucleoprotein E	*Aspergillus terreus*
GR224280	LM	1	4.b	XP_750523	3.0E-40	adoMet-dependent tRNA methyltransferase (MTase) complex subunitTrm112	*Aspergillus fumigatus*
GR224534	LM/RM/PF	4	4.b	XP_753424	4.0E-32	rRNA processing protein Ebp2	*Aspergillus fumigatus*
GR225217	LM	1	4.b	EDU39847	5.0E-23	small nuclear ribonucleoprotein F	*Pyrenophora tritici-repentis*
GR225297	LM/PF/RM	9	4.b	NP_595747	2.0E-22	U6 snRNP-associated protein Lsm3	*Schizosaccharomyces pombe*
GR225731	RM	1	4.b	XP_001275883	5.0E-76	3′ exoribonuclease family protein	*Aspergillus clavatus*
GR225773	RM	1	4.b	XP_001939332	6.0E-59	coiled-coil domain-containing protein 25	*Pyrenophora tritici-repentis*
GR225791	RM	1	4.b	XP_001222580	3.0E-69	ATP-dependent RNA helicase	*Chaetomium globosum*
GR225918	RM	1	4.b	XP_001932517	9.0E-08	WD repeat domain phosphoinositide-interacting protein 4	*Pyrenophora tritici-repentis*
GR225962	RM	1	4.b	XP_001222580	2.0E-22	ATP-dependent RNA helicase	*Chaetomium globosum*
GR226088	RM/RF/PF	4	4.b	XP_752533	2.0E-24	small nuclear ribonucleoprotein Lsm8	*Aspergillus fumigatus*
GR226363	RM/RF	4	4.b	XP_001542609	3.0E-27	small nuclear ribonucleoprotein SmG	*Ajellomyces capsulatus*
GR226660	RF	1	4.b	ACB30143	8.0E-31	poly(A) RNA binding protein	*Epichloe festucae*
GR226813	PF	1	4.b	NP_499080	2.0E-15	SR Protein Kinase family member (spk-1)	*Caenorhabditis elegans*
GR226842	PF	1	4.b	NP_499080	5.0E-18	SR protein kinase family member (spk-1)	*Caenorhabditis elegans*
GR227687	PF	1	4.b	XP_368889	3.0E-37	small nuclear ribonucleoprotein LSM2	*Magnaporthe grisea*
GR227749	RM/PF	2	4.b	XP_755068	2.0E-10	R3H and G-patch domain protein	*Aspergillus fumigatus*
GR227931	PF	1	4.b	CAD21082	7.0E-18	RNA splicing factor Pad-1	*Neurospora crassa*
GR228046	PF	1	4.b	XP_570211	4.0E-34	WD-repeat protein	*Cryptococcus neoformans*
GR228098	PF	2	4.b	XP_749086	6.0E-21	protein required for cell viability Rrp17	*Aspergillus fumigatus*
GR224136	LM/RM/RF	4	4.c	XP_749463	2.0E-24	bZIP transcription factor	*Aspergillus fumigatus*
GR224213	PF/LM	4	4.c	XP_002147387	6.0E-17	C2H2 finger domain protein, putative	*Penicillium marneffei*
GR224394	LM/RM/PF	4	4.c	XP_568585	2.0E-33	zinc finger protein	*Cryptococcus neoformans*
GR224471	LM	1	4.c	Q8TFF3	1.0E-17	transcriptional activator hac1.	*Hypocrea jecorina*
GR224483	LM	1	4.c	XP_001275208	4.0E-32	retinoblastoma-binding protein	*Aspergillus clavatus*
GR224484	LM	1	4.c	XP_001260584	8.0E-13	transcription regulator NOT2 family protein	*Neosartorya fischeri*
GR224750	LM/PF/RF/RM	7	4.c	AAB04132	1.0E-32	cutinase G-box binding protein	*Nectria haematococca*
GR224759	LM	3	4.c	XP_001274352	3.0E-26	CBF/NF-Y family transcription factor, putative	*Aspergillus clavatus*
GR224803	LM	1	4.c	XP_001263017	4.0E-30	bromodomain associated protein	*Neosartorya fischeri*
GR225117	LM	1	4.c	EDP54660	1.0E-12	C6 finger domain protein, putative	*Aspergillus fumigatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225133	LM/PF	4	4.c	XP_001543976	9.0E-38	transcription initiation factor IIA gamma chain	*Ajellomyces capsulatus*
GR225159	LM/PF	2	4.c	XP_001268279	9.0E-31	phosphotransferase enzyme family protein	*Aspergillus clavatus*
GR225360	LM	2	4.c	XP_001262376	4.0E-75	AN1 zinc finger protein	*Neosartorya fischeri*
GR225433	RM/RF	2	4.c	Q9P8W3	3.0E-37	Zinc finger transcription factor ace1 (ACEI)	*Hypocrea jecorina*
GR225559	RM	1	4.c	XP_750680	9.0E-21	telomere silencing protein Zds1	*Aspergillus fumigatus*
GR225675	RM	1	4.c	XP_001268655	8.0E-10	C6 transcription factor, putative	*Aspergillus clavatus*
GR225819	RM	1	4.c	BAE98264	4.0E-96	Zn(II)2Cys6 transcription factor	*Fusarium oxysporum*
GR225860	RM	1	4.c	XP_752776	2.0E-14	C2H2 finger domain protein	*Aspergillus fumigatus*
GR225862	RM	2	4.c	XP_747329	4.0E-88	C6 transcription factor	*Aspergillus fumigatus*
GR226013	RM	1	4.c	XP_755959	4.0E-46	C2H2 finger domain protein	*Aspergillus fumigatus*
GR226082	RM	1	4.c	XP_752934	7.0E-17	C6 finger domain protein	*Aspergillus fumigatus*
GR226114	RM	1	4.c	XP_749434	2.0E-08	MYB DNA-binding domain protein	*Aspergillus fumigatus*
GR226145	RM	1	4.c	CAB10530	8.0E-22	EREBP-4 like protein	*Arabidopsis thaliana*
GR226212	RM	1	4.c	XP_001933607	2.0E-25	AN1-type zinc finger protein	*Pyrenophora tritici-repentis*
GR226221	RM/LM	3	4.c	ACG48240	1.0E-42	transcription factor BTF3	*Zea mays*
GR226371	RF	1	4.c	CAE76512	5.0E-38	related to metalloregulatory protein	*Neurospora crassa*
GR226374	RF	1	4.c	XP_754595	2.0E-06	Ccr4-Not transcription complex subunit (NOT1)	*Aspergillus fumigatus*
GR226408	RF	1	4.c	XP_001260614	9.0E-20	BAR domain protein	*Neosartorya fischeri*
GR226427	RF	1	4.c	XP_752988	2.0E-35	C6 transcription factor	*Aspergillus fumigatus*
GR226534	RF/RM/PF	6	4.c	A2QC41	2.0E-09	Mediator of RNA polymerase II transcription subunit 21	*Aspergillus niger*
GR226855	LM/RM/RF/PF	17	4.c	XP_751209	1.0E-19	RNA binding protein	*Aspergillus fumigatus*
GR227007	LM/RM/RF/PF	51	4.c	ABL74239	1.0E-60	RBP(RNA binding protein)	*Beauveria bassiana*
GR227202	PF	2	4.c	BAD93190	1.0E-21	transcription factor ATFA	*Aspergillus oryzae*
GR227306	RM/PF	3	4.c	XP_001258430	2.0E-179	SNF2 family N-terminal domain protein	*Neosartorya fischeri*
GR227562	RM/PF	2	4.c	XP_752200	5.0E-35	progesterone binding protein	*Aspergillus fumigatus*
GR227567	RM/PF	2	4.c	XP_001939724	9.0E-06	negative regulator of differentiation 1	*Pyrenophora tritici-repentis*
GR227828	PF	2	4.c	XP_665702	7.0E-05	G10 protein	*Cryptosporidium hominis*
GR227845	PF	2	4.c	XP_001272121	2.0E-09	GATA transcription factor LreB	*Aspergillus clavatus*
GR227973	PF	1	4.c	EDP52723	5.0E-25	Ccr4-Not transcription complex subunit (NOT1), putative	*Aspergillus fumigatus*
GR228139	PF	1	4.c	XP_001213918	8.0E-11	pH-response transcription factor pacC/RIM101	*Aspergillus terreus*
GR228498	PF	1	4.c	ABL74239	4.0E-56	RBP (RNA binding protein)	*Beauveria bassiana*
GR228607	PF	1	4.c	XP_001275933	1.0E-12	C2H2 finger domain protein, putative	*Aspergillus clavatus*
GR224828	LM	1	5.a	NP_014333	1.0E-30	Cell wall protein related to glucanases, possibly involved in cell wall septation; member of the SUN family; Sun4p	*Saccharomyces cerevisiae*
GR224905	LM/RM/RF/PF	19	5.a	XP_001934729	5.0E-29	GPI-anchored cell wall organization protein Ecm33	*Pyrenophora tritici-repentis*
GR225342	LM	1	5.a	AAL78814	5.0E-90	class V chitinase	*Hypocrea virens*
GR226256	RM	1	5.a	XP_001215003	7.0E-61	sphingolipid long chain base-responsive protein PIL1	*Aspergillus terreus*
GR226742	RF	1	5.a	XP_001266137	5.0E-27	LysM domain protein	*Neosartorya fischeri*
GR228648	RM/PF	2	5.a	XP_749757	2.0E-92	oligosaccharyl transferase subunit (gamma)	*Aspergillus fumigatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224419	LM	6	5.b	XP_653447	5.0E-08	viral A-type inclusion protein repeat, putative	*Entamoeba histolytica*
GR224475	LM/RF/PF/RM	9	5.b	XP_961133	4.0E-157	actin	*Neurospora crassa*
GR224662	LM	1	5.b	XP_001262492	2.0E-106	nuclear envelope protein Brr6, putative	*Neosartorya fischeri*
GR224742	PF/RM/LM	13	5.b	CAC85551	2.0E-156	beta tubulin	*Cordyceps bassiana*
GR224838	LM/RF/PF	4	5.b	XP_749087	1.0E-37	tropomyosin	*Aspergillus fumigatus*
GR224857	LM	1	5.b	CAC85618	2.0E-115	beta-tubulin	*Blumeria graminis*
GR225171	LM	1	5.b	XP_391032	3.0E-72	ARP3_NEUCR actin-like protein 3	*Gibberella zeae*
GR225220	LM/RM/PF	13	5.b	XP_001931556	2.0E-44	cofilin	*Pyrenophora tritici-repentis*
GR225289	LM	3	5.b	XP_001247626	4.0E-67	probable F-actin capping protein alpha subunit	*Coccidioides immitis*
GR225469	RM/RF	7	5.b	XP_001323413	2.0E-07	ankyrin repeat protein	Trichomonas vaginalis
GR225587	RM	1	5.b	XP_653447	2.0E-07	viral A-type inclusion protein repeat, putative	*Entamoeba histolytica*
GR225612	PF/RM/LM	8	5.b	XP_965549	2.0E-71	ARP (actin-related protein) 2/3 complex 20 kDa subunit	*Neurospora crassa*
GR225743	RM	1	5.b	NP_001128241	1.0E-05	actin, gamma 1	*Pan troglodytes*
GR225921	PF/RM	5	5.b	XP_753773	2.0E-28	integral membrane protein	*Aspergillus fumigatus*
GR225945	RM	1	5.b	XP_001075107	2.0E-07	PREDICTED: similar to filaggrin 2	*Rattus norvegicus*
GR225968	RM	1	5.b	XP_001247194	1.0E-120	fimbrin	*Coccidioides immitis*
GR226192	RM/RF	2	5.b	XP_962359	3.0E-67	myosin regulatory light chain cdc4	*Neurospora crassa*
GR226362	RF	1	5.b	XP_001940723	2.0E-07	integral membrane protein	*Pyrenophora tritici-repentis*
GR226418	RF	2	5.b	CAC85551	1.0E-153	beta tubulin	*Cordyceps bassiana*
GR226499	LM/PF/RF/RM	15	5.b	ACB47221	2.0E-59	microtubule-associated protein	*Gibberella zeae*
GR227167	PF	5	5.b	CAL53988	2.0E-22	myosin class II heavy chain (ISS)	*Ostreococcus tauri*
GR227916	PF	4	5.b	XP_001323413	4.0E-06	ankyrin repeat protein	*Trichomonas vaginalis*
GR224502	LM	1	5.c	XP_754824	6.0E-103	cell surface spherulin 4-like protein	*Aspergillus fumigatus*
GR224929	LM/PF	286	5.c	P80544	5.0E-30	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR224936	LM	1	5.c	P80544	7.0E-16	plasmin-sensitive surface protein (cell-wall protein) .	*Staphylococcus aureus*
GR224939	LM	1	5.c	P80544	1.0E-20	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR224948	LM	1	5.c	P80544	5.0E-15	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR224951	LM	4	5.c	AF402316	2.0E-26	surface protein SdrI	*Staphylococcus aureus*
GR224955	LM	1	5.c	P80544	1.0E-14	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR225083	LM	2	5.c	XP_001268510	4.0E-54	extracellular proline-serine rich protein	*Aspergillus clavatus*
GR225184	LM/RF/PF	8	5.c	CAL38822	7.0E-14	surface protein 1	*Glomerella lindemuthiana*
GR226047	RM	1	5.c	XP_001012930	1.0E-27	von Willebrand factor type A domain containing protein	*Tetrahymena theRMophila*
GR226110	RM/RF/PF	4	5.c	XP_754260	2.0E-08	extracellular serine-rich protein	*Aspergillus fumigatus*
GR226267	RF	2	5.c	P80544	3.0E-19	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR226397	RF	1	5.c	P80544	2.0E-15	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR226680	RF	1	5.c	XP_001308251	9.0E-05	flocculin, putative	*Trichomonas vaginalis*
GR226718	LM/RF	5	5.c	ABS59365	1.0E-14	hydrophobin	*Trichoderma atroviride*
GR226746	RF	1	5.c	P80544	1.0E-14	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR226864	PF	1	5.c	P80544	3.0E-23	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR226870	PF	4	5.c	P80544	2.0E-11	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226883	PF	1	5.c	P80544	2.0E-17	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227035	PF	1	5.c	P80544	6.0E-16	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227054	PF/RF	4	5.c	P80544	4.0E-24	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227057	PF	1	5.c	P80544	6.0E-17	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227112	PF	1	5.c	P80544	3.0E-21	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227134	PF	1	5.c	P80544	1.0E-20	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227227	PF	1	5.c	P80544	2.0E-18	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227443	PF	2	5.c	XP_001264121	1.0E-27	GPI anchored protein, putative	*Neosartorya fischeri*
GR227532	PF	1	5.c	P80544	3.0E-21	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227535	PF	2	5.c	P80544	3.0E-05	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227708	PF	1	5.c	P80544	3.0E-24	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227820	PF	3	5.c	P80544	1.0E-13	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227824	PF	2	5.c	P80544	4.0E-14	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227852	PF	1	5.c	P80544	3.0E-18	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227966	PF	1	5.c	P80544	8.0E-23	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227979	RM/RF/PF	175	5.c	P80544	8.0E-28	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR227994	PF	4	5.c	P80544	3.0E-26	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR228010	PF	1	5.c	P80544	6.0E-24	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR228490	PF	1	5.c	AAY66752	2.0E-05	ixodegrin-2A RGD containing protein	*Ixodes scapularis*
GR228602	PF	7	5.c	P80544	4.0E-22	plasmin-sensitive surface protein (cell-wall protein)	*Staphylococcus aureus*
GR224109	LM	1	5.d	XP_755859	3.0E-63	small oligopeptide transporter, OPT family	*Aspergillus fumigatus*
GR224116	LM/RM	2	5.d	XP_002171360	3.0E-66	pantothenate transporter	*Schizosaccharomyces japonicus*
GR224127	LM	1	5.d	XP_001598344	5.0E-56	GDP-mannose transporter	*Sclerotinia sclerotiorum*
GR224185	LM	1	5.d	XP_001260799	1.0E-73	MFS transporter, putative	*Neosartorya fischeri*
GR224250	LM	1	5.d	XP_001210923	7.0E-127	mitochondrial phosphate carrier protein	*Aspergillus terreus*
GR224686	LM	1	5.d	XP_369559	1.0E-69	plasma membrane zinc ion transporter, putative	*Magnaporthe grisea*
GR224783	LM	1	5.d	XP_381275	7.0E-55	RAN_BRUMA GTP-binding nuclear protein RAN/TC4	*Gibberella zeae*
GR224815	LM	1	5.d	XP_001265432	4.0E-95	Ras GTPase Rab11, putative	*Neosartorya fischeri*
GR224918	LM	1	5.d	ABG78607	2.0E-26	RING-5	*Gibberella zeae*
GR224972	LM	2	5.d	XP_001728212	4.0E-18	mitochondrial import inner membrane translocase subunit tim8	*Neurospora crassa*
GR225105	LM/PF	3	5.d	XP_002174319	1.0E-118	protein transport protein SEC23	*Neurospora crassa*
GR225223	LM/RM	2	5.d	XP_364530	1.0E-81	glycolipid transfer protein HET-C	*Magnaporthe grisea*
GR225330	LM	1	5.d	XP_957678	3.0E-100	protein transport protein SEC13	*Neurospora crassa*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225388	LM	1	5.d	XP_001274130	4.0E-33	phosphatidylinositol transporter, putative	*Aspergillus clavatus*
GR225445	RM	4	5.d	XP_001269052	6.0E-91	MFS transporter, putative	*Aspergillus clavatus*
GR225522	RM	1	5.d	XP_749930	1.0E-43	MFS transporter	*Aspergillus fumigatus*
GR225527	RM	1	5.d	ABD17825	1.0E-13	oligopeptide transporter 4	*Candida albicans*
GR225680	RM	1	5.d	NP_491412	7.0E-13	acyl-coenzyme A binding protein family member (acbp-1)	*Caenorhabditis elegans*
GR225758	RM	3	5.d	XP_001218345	8.0E-11	high-affinity nickel transport protein	*Aspergillus terreus*
GR225881	LM/RM	3	5.d	XP_963201	2.0E-110	ADP, ATP carrier protein	*Neurospora crassa*
GR225955	RM	1	5.d	XP_746960	1.0E-15	MFS transporter	*Aspergillus fumigatus*
GR225977	PF/RM/RF	8	5.d	XP_747772	4.0E-95	MFS (major facilitator superfamily) multidrug transporter	*Aspergillus fumigatus*
GR226264	RF	1	5.d	XP_001885161	5.0E-17	MFS polyamine transporter	*Laccaria bicolor*
GR226341	RF	1	5.d	AAS90092	2.0E-16	MFS aflatoxin efflux pump	*Aspergillus flavus*
GR226377	RF	1	5.d	AAF64435	5.0E-31	DHA14-like major facilitator	*Botryotinia fuckeliana*
GR226412	RF	1	5.d	XP_001260988	9.0E-46	small oligopeptide transporter, OPT family	*Neosartorya fischeri*
GR226482	RF	1	5.d	XP_001931051	2.0E-105	mitochondrial 2-oxodicarboxylate carrier 2	*Pyrenophora tritici-repentis*
GR226526	RF	1	5.d	XP_001939969	1.0E-21	amino acid permease 2	*Pyrenophora tritici-repentis*
GR226665	RF/LM	3	5.d	XP_001540563	5.0E-91	BET3 family protein	*Ajellomyces capsulatus*
GR226821	RM/PF	3	5.d	XP_001558322	2.0E-40	phosphatidylglycerol / phosphatidylinositol transfer protein	*Botryotinia fuckeliana*
GR226850	PF	1	5.d	XP_001246923	2.0E-16	siderophore iron transporter	*Coccidioides immitis*
GR226987	LM/PF/RM/RF	13	5.d	AAW69344	2.0E-20	protein transport protein SEC61 gamma subunit-like protein	*Magnaporthe grisea*
GR227146	PF	1	5.d	ACC64449	5.0E-49	major facilitator superfamily transporter	*Ajellomyces capsulatus*
GR227168	PF	1	5.d	XP_001258151	5.0E-42	maltose permease	*Neosartorya fischeri*
GR227174	PF	1	5.d	XP_754815	3.0E-74	GABA permease GabA	*Aspergillus fumigatus*
GR227251	PF	1	5.d	XP_001264732	9.0E-48	ABC multidrug transporter, putative	*Neosartorya fischeri*
GR227300	PF	1	5.d	XP_001270534	1.0E-08	MFS transporter, putative	*Aspergillus clavatus*
GR227454	RM/RF/PF	5	5.d	XP_001264673	1.0E-72	vesicle-mediated transport protein Vid24, putative	*Neosartorya fischeri*
GR227516	PF	1	5.d	XP_001258397	5.0E-41	mitochondrial carrier protein, putative	*Neosartorya fischeri*
GR227836	RM/PF	5	5.d	NP_595426	1.0E-51	NST UDP-N-acetylglucosamine transporter	*Schizosaccharomyces*
GR228170	PF	1	5.d	XP_001273915	1.0E-89	CorA family metal ion transporter, putative	*Aspergillus clavatus*
GR228329	PF	1	5.d	AAO49453	3.0E-79	major facilitator superfamily	*Leptosphaeria maculans*
GR228514	PF	2	5.d	AAX98668	3.0E-18	L-arabinose transporter	*Ambrosiozyma monospora*
GR224454	LM	1	5.e	XP_001549190	1.0E-48	mitochondrial import receptor subunit TOM40	*Botryotinia fuckeliana*
GR224540	LM	1	5.e	XP_957481	1.0E-94	coatomer beta subunit	*Neurospora crassa*
GR224608	LM	1	5.e	XP_001544767	6.0E-104	coatomer beta subunit	*Ajellomyces capsulatus*
GR224704	LM/RF	2	5.e	XP_961277	3.0E-168	AP-1 complex subunit gamma-1	*Neurospora crassa*
GR224743	LM/PF	4	5.e	XP_001931016	3.0E-43	SNARE complex subunit (Syn8)	*Pyrenophora tritici-repentis*
GR224986	LM	1	5.e	XP_001540526	1.0E-136	coatomer alpha subunit	*Ajellomyces capsulatus*
GR225152	LM/PF	2	5.e	XP_001260516	3.0E-12	AP-2 adaptor complex subunit beta, putative	*Neosartorya fischeri*
GR225156	LM/RM/PF	5	5.e	XP_361669	1.0E-93	RAS small monomeric GTPase Rab6	*Magnaporthe grisea*
GR225162	LM/PF	3	5.e	XP_637974	8.0E-11	Ran GTPase binding protein	*Dictyostelium discoideum*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225235	LM	1	5.e	O94111	6.0E-37	dynein light chain, cytoplasmic (8 kDa cytoplasmic dynein light chain)	*Emericella nidulans*
GR225302	LM	1	5.e	BAF36375	2.0E-29	v-SNARE	*Aspergillus oryzae*
GR225314	LM	1	5.e	XP_955917	7.0E-71	exportin-1	*Neurospora crassa*
GR225338	LM	1	5.e	EDU42664	2.0E-43	chloride channel protein 3	*Pyrenophora tritici-repentis*
GR225425	RM	1	5.e	XP_001208943	2.0E-142	coatomer alpha subunit	*Aspergillus terreus*
GR225435	LM/RM/RF/PF	19	5.e	XP_001558550	7.0E-44	nuclear transport factor 2	*Botryotinia fuckeliana*
GR225454	RM	1	5.e	XP_753522	4.0E-25	COPI-coated vesicle protein	*Aspergillus fumigatus*
GR225518	RM	1	5.e	AAC18088	2.0E-125	coatomer alpha subunit	*Aspergillus nidulans*
GR225666	RM	1	5.e	XP_001932321	5.0E-56	clathrin light chain	*Pyrenophora tritici-repentis*
GR225740	RM/RF	2	5.e	XP_001933724	1.0E-101	golgi transport complex component Cog5	*Pyrenophora tritici-repentis*
GR225769	RM	1	5.e	ABO38808	1.0E-44	CTR2 long splice variant	*Colletotrichum gloeosporioides*
GR225908	RM	1	5.e	XP_001246273	2.0E-85	ADP-ribosylation factor 6	*Coccidioides immitis*
GR225949	RM	1	5.e	XP_369779	2.0E-14	trafficking protein particle complex subunit 2, putative	*Magnaporthe grisea*
GR225966	RM/RF	3	5.e	XP_962059	7.0E-141	rab GDP-dissociation inhibitor	*Neurospora crassa*
GR225971	RM	1	5.e	XP_001940147	7.0E-71	AP-2 complex subunit sigma	*Pyrenophora tritici-repentis*
GR225978	RM	1	5.e	XP_751121	3.0E-08	Ran-interacting protein Mog1	*Aspergillus fumigatus*
GR225984	RM	1	5.e	XP_962059	6.0E-114	rab GDP-dissociation inhibitor	*Neurospora crassa*
GR226040	RM/PF	5	5.e	XP_957338	3.0E-83	Golgi membrane protein (Rer1)	*Neurospora crassa*
GR226048	RM	1	5.e	XP_001592488	4.0E-81	endosomal P24B protein	*Sclerotinia sclerotiorum*
GR226071	RM	1	5.e	EDL12637	1.0E-15	Der1-like domain family, member 2, isofoRM CRA_a	*Mus musculus*
GR226104	RM	1	5.e	Q5YCW8	1.0E-54	chitin synthase export chaperone	*Fusarium oxysporum*
GR226113	RM	1	5.e	XP_001549104	3.0E-75	coatomer zeta subunit	*Botryotinia fuckeliana*
GR226165	PF/RM/LM	4	5.e	XP_748017	4.0E-78	endosomal cargo receptor (Erp3)	*Aspergillus fumigatus*
GR226171	RM	1	5.e	XP_754900	4.0E-06	ER membrane protein (Wsc4)	*Aspergillus fumigatus*
GR226251	RM	1	5.e	XP_746483	1.0E-52	plasma membrane channel protein (Aqy1)	*Aspergillus fumigatus*
GR226342	RF	1	5.e	XP_386822	2.0E-89	SAR1_TRIRE GTP-binding protein SAR1	*Gibberella zeae*
GR226713	RF/PF	3	5.e	XP_001260746	1.0E-98	vesicular-fusion protein sec17	*Neosartorya fischeri*
GR226937	RM/PF	2	5.e	XP_001940147	8.0E-71	AP-2 complex subunit sigma	*Pyrenophora tritici-repentis*
GR227029	PF	1	5.e	XP_001545795	3.0E-07	sorting nexin-like protein	*Botryotinia fuckeliana*
GR227141	PF	2	5.e	XP_961017	3.0E-61	protein yop-1 (YIP1 partner protein 1) (YPT-interacting protein 2)	*Neurospora crassa*
GR227221	PF	1	5.e	XP_001541792	1.0E-15	mitochondrial intermembrane space translocase subunit Tim	*Ajellomyces capsulatus*
GR227407	RM/PF	2	5.e	CAD36979	1.0E-84	related to the member of the syntaxin family of t-SNAREs TLG2	*Neurospora crassa*
GR227481	PF	1	5.e	XP_001273433	4.0E-94	mRNA transport regulator (Mtr10), putative	*Aspergillus clavatus*
GR227767	PF	2	5.e	XP_956972	5.0E-92	GTP-binding protein ypt3	*Neurospora crassa*
GR227949	RF/PF	3	5.e	XP_750622	2.0E-53	endosomal cargo receptor (Erv14)	*Aspergillus fumigatus*
GR228326	RM/PF	2	5.e	CAC28785	3.0E-112	probable gamma-adaptin precursor	*Neurospora crassa*
GR228590	PF	1	5.e	XP_752998	2.0E-74	vacuolar protein sorting-associated protein Vps28	*Aspergillus fumigatus*
GR224089	LM	1	5.f	AAP92916	3.0E-25	putative serine/threonine phosphatase 2C ptc2	*Hypocrea jecorina*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224256	LM	7	5.f	XP_001266933	5.0E-89	Aha1 domain family, activator of Hsp90 ATPase	*Neosartorya fischeri*
GR224368	LM	1	5.f	XP_753016	3.0E-61	small monomeric GTPase (Gtr2)	*Aspergillus fumigatus*
GR224376	LM	1	5.f	XP_001262922	9.0E-20	protein kinase, putative	*Neosartorya fischeri*
GR224526	LM	1	5.f	XP_001271996	4.0E-76	Aha1 domain family	*Aspergillus clavatus*
GR224664	LM	1	5.f	XP_001262922	3.0E-24	protein kinase, putative	*Neosartorya fischeri*
GR224710	RM/LM	2	5.f	AAT40588	2.0E-28	cellulose signalling associated protein ENVOY	*Hypocrea jecorina*
GR224712	LM/RM/PF	11	5.f	XP_001932744	8.0E-111	Aha1 domain family	*Pyrenophora tritici-repentis*
GR224736	LM	1	5.f	XP_001266933	4.0E-73	Aha1 domain family	*Neosartorya fischeri*
GR224856	LM/RM	6	5.f	XP_002145004	4.0E-41	GMF family protein, Glia maturation factor	*Penicillium marneffei*
GR225013	LM	2	5.f	XP_001276085	6.0E-72	Rheb small monomeric GTPase RhbA	*Aspergillus clavatus*
GR225229	LM/RM	2	5.f	XP_001932161	2.0E-41	AhpC/TSA family protein	*Pyrenophora tritici-repentis*
GR225255	LM	2	5.f	CAE75725	4.0E-84	related to dock180 protein	*Neurospora crassa*
GR225263	LM/RM/RF/PF	17	5.f	ABP04053	7.0E-41	16 kDa allergen	*Penicillium chrysogenum*
GR225308	LM	1	5.f	XP_001271698	3.0E-58	phosphoinositide phosphatase (Sac1), putative	*Aspergillus clavatus*
GR225318	LM	2	5.f	YP_612174	3.0E-13	metal dependent phosphohydrolase	*Silicibacter sp*
GR225663	RM	1	5.f	XP_753908	9.0E-48	COP9 signalosome subunit 6 (CsnF)	*Aspergillus fumigatus*
GR225664	RM	3	5.f	AAT40588	6.0E-29	cellulose signalling associated protein ENVOY	*Hypocrea jecorina*
GR225715	RM	1	5.f	XP_001589707	1.0E-66	casein kinase I	*Sclerotinia sclerotiorum*
GR225744	RM	1	5.f	XP_750248	9.0E-71	SAM domain protein	*Aspergillus fumigatus*
GR225765	RM/PF	4	5.f	AAR99465	1.0E-05	serine/threonine kinase	*Leptosphaeria maculans*
GR225767	RM	1	5.f	XP_001549877	1.0E-16	septum-promoting GTP-binding protein 1	*Botryotinia fuckeliana*
GR225772	RM	2	5.f	Q875L0	1.0E-142	mitogen-activated protein kinase HOG1 (MAP kinase HOG1)	*Cryphonectria parasitica*
GR225781	RM	3	5.f	BAF63216	1.0E-108	Rho1, small GTPase-binding protein	*Cordyceps militaris*
GR225795	RM	1	5.f	XP_568762	3.0E-34	serine/threonine kinase receptor associated protein	*Cryptococcus neofoRMans*
GR225800	RM	1	5.f	XP_001932536	4.0E-23	phosphotransferase enzyme family protein	*Pyrenophora tritici-repentis*
GR225845	RM	1	5.f	CAD70304	1.0E-64	related to 3-phosphoinositide dependent protein kinase-1 (PDK1)	*Neurospora crassa*
GR226006	RM	1	5.f	XP_001270126	2.0E-84	GTPase activating protein (Tsc2), putative	*Aspergillus clavatus*
GR226039	RM	1	5.f	ABQ00173	8.0E-33	G-protein coupled receptor	*TrichodeRMa atroviride*
GR226075	RM	1	5.f	XP_001935440	3.0E-44	rho-type GTPase-activating protein 2	*Pyrenophora tritici-repentis*
GR226225	LM/PF/RM	8	5.f	XP_001267009	8.0E-77	calmodulin	*Neosartorya fischeri*
GR226230	LM/RM/PF	5	5.f	P87072	1.0E-89	calcineurin subunit B (protein phosphatase 2B regulatory subunit) (calcineurin regulatory subunit)	*Neurospora crassa*
GR226234	RM	1	5.f	BAA24436	3.0E-07	tenascin-X	*Mus musculus*
GR226297	RF	1	5.f	XP_001935066	2.0E-33	Rho guanyl nucleotide exchange factor	*Pyrenophora tritici-repentis*
GR226314	RF	1	5.f	Q86ZN7	3.0E-39	cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit)	*Trichoderma atroviride*
GR226326	RF	1	5.f	XP_001265166	2.0E-36	SAM (sterile alpha motif) domain protein	*Neosartorya fischeri*
GR226596	RF	1	5.f	XP_001221847	1.0E-24	guanine nucleotide-binding protein gamma subunit	*Chaetomium globosum*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226687	RF	1	5.f	AAK31624	2.0E-07	GTPase CDC42	*Colletotrichum trifolii*
GR226693	RF	1	5.f	ABD49713	7.0E-95	RAB/GTPase	*Metarhizium anisopliae*
GR226762	RF	1	5.f	XP_951695	8.0E-07	protein kinase	*Trypanosoma brucei*
GR226800	RF	1	5.f	XP_001940921	4.0E-83	ser/Thr protein phosphatase family protein	*Pyrenophora tritici-repentis*
GR226829	PF	2	5.f	XP_001305515	9.0E-09	CAMK family protein kinase	*Trichomonas vaginalis*
GR226948	PF	1	5.f	XP_965733	1.0E-05	COP9 signalosome complex subunit 2	*Neurospora crassa*
GR227119	PF	1	5.f	CAD21202	5.0E-18	related to transforming protein rho	*Neurospora crassa*
GR227339	PF	1	5.f	EDP50431	2.0E-62	GTPase activating protein (Gyp5), putative	*Aspergillus fumigatus*
GR227527	PF	1	5.f	AAG03077	4.0E-32	calcium-related spray protein	*Neurospora crassa*
GR227575	PF	2	5.f	XP_001265765	6.0E-18	signal recognition particle 14kD protein, putative	*Neosartorya fischeri*
GR227652	PF	1	5.f	AAA40934	3.0E-70	casein kinase I delta	*Rattus norvegicus*
GR227679	PF	2	5.f	BAF36499	6.0E-103	Rho-related protein RacA	*Epichloe festucae*
GR227789	PF	1	5.f	AAR19207	3.0E-99	MAP kinase kinase 1	*Podospora anserina*
GR227846	PF	1	5.f	XP_001211499	3.0E-42	COP9 signalosome complex subunit 5	*Aspergillus terreus*
GR227907	PF	1	5.f	XP_001270095	2.0E-60	camp independent regulatory protein	*Aspergillus clavatus*
GR228114	LM/PF/RF	8	5.f	XP_381190	8.0E-99	ARF_AJECA ADP-RIBOSYLATION FACTOR	*Gibberella zeae*
GR228119	RM/PF	2	5.f	AAD15987	1.0E-141	protein phosphatase 2A regulatory B subunit	*Neurospora crassa*
GR228196	PF	1	5.f	EDP51598	2.0E-95	Rho guanyl nucleotide exchange factor (Rom2), putative	*Aspergillus fumigatus*
GR228391	PF	1	5.f	CAD21199	5.0E-22	related to aimless RasGEF (aleA)	*Neurospora crassa*
GR228524	RM/PF	2	5.f	Q5BD89	8.0E-50	COP9 signalosome complex subunit 1 (CSN complex subunit 1)	*Emericella nidulans*
GR228547	PF	1	5.f	ABG66306	1.0E-39	regulatory subunit of protein kinase A	*Colletotrichum gloeosporioides*
GR225352	LM	3	6.a	AAW66450	4.0E-180	Septin 5	*Coccidioides posadasii*
GR225617	RM	1	6.a	XP_955871	6.0E-134	cell division control protein 10	*Neurospora crassa*
GR225787	LM/PF/RF/RM	9	6.a	XP_001226350	4.0E-171	guanine nucleotide-binding protein beta subunit-like protein	*Chaetomium globosum*
GR225997	RM	1	6.a	XP_001265820	2.0E-88	meiotic regulator-interacting protein, putative	*Neosartorya fischeri*
GR226111	RM	1	6.a	XP_755503	2.0E-05	Mob1 family protein	*Aspergillus fumigatus*
GR227117	PF	1	6.a	XP_001735693	3.0E-11	cell division control protein 15, CDC15, putative	*Entamoeba dispar*
GR224911	LM	1	6.b	AAQ02689	2.0E-44	meiosis-specific topoisomerase Spo11	*Sordaria macrospora*
GR225072	LM/RM	2	6.b	XP_959442	5.0E-46	histone H2A	*Neurospora crassa*
GR225545	RM/LM	3	6.b	XP_001243946	1.0E-37	histone H4	*Coccidioides immitis*
GR225711	LM/RM	4	6.b	CAD70303	9.0E-68	related to SWI/SNF complex 60 KDa subunit	*Neurospora crassa*
GR226448	RF	1	6.b	XP_750809	1.0E-32	SIR2 family histone deacetylase	*Aspergillus fumigatus*
GR228159	LM/RM/PF	9	6.b	BAD90802	3.0E-68	histone 3	*Conocephalum conicum*
GR226158	LM/RM	5	6.c	XP_751565	3.0E-10	DNA repair protein Rad1	*Aspergillus fumigatus*
GR224591	LM/RM/RF	9	6.d	AAW66612	3.0E-55	HEX1_EMENI Woronin body major protein	*Ophiostoma floccosum*
GR224812	LM	1	6.d	XP_752563	4.0E-58	mitochondrial dynamin GTPase (Msp1)	*Aspergillus fumigatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225271	LM/RF/PF	3	6.d	XP_956015	2.0E-108	conidiophore development protein hymA	*Neurospora crassa*
GR225589	RM	1	6.e	NP_001002887	7.0E-06	paternally expressed 3	*Bos taurus* (cattle)
GR225674	RM	1	6.e	EAW94604	1.0E-33	spermatogenesis associated 20, isofoRM CRA_b	*Homo sapiens*
GR227387	PF	2	6.e	XP_001264672	2.0E-71	Mago nashi domain protein	*Neosartorya fischeri*
GR224923	LM	1	6.f	XP_960686	2.0E-19	clock-controlled protein 6	*Neurospora crassa*
GR225357	PF/LM	4	6.f	XP_960686	2.0E-19	clock-controlled protein 6	*Neurospora crassa*
GR227238	RM/PF	2	6.f	XP_960686	3.0E-08	clock-controlled protein 6	*Neurospora crassa*
GR228131	PF	2	6.g	XP_753708	2.0E-63	Bax Inhibitor family protein	*Aspergillus fumigatus*
GR224197	LM	1	7.a	ABK56833	6.0E-05	elicitor protein	*Magnaporthe grisea*
GR224354	RF/LM	2	7.a	XP_001210911	2.0E-48	heat shock protein HSP98	*Aspergillus terreus*
GR224453	LM	1	7.a	ABD49719	3.0E-11	heat shock protein 30	*Metarhizium anisopliae*
GR224602	LM	3	7.a	AAL77224	1.0E-19	thioredoxin II	*Podospora anserina*
GR224629	LM	1	7.a	AAL77224	3.0E-27	thioredoxin II	*Podospora anserina*
GR224634	LM	1	7.a	CAC28808	2.0E-117	related to tetracycline efflux protein (otrb)	*Neurospora crassa*
GR224699	PF/LM/RM	8	7.a	ACB30155	1.0E-48	aminoglycoside phosphotransferase	*Epichloe festucae*
GR224751	LM/RM/PF	3	7.a	XP_001597950	1.0E-19	glucose repressible protein Grg1	*Sclerotinia sclerotiorum*
GR225003	LM	3	7.a	XP_001225918	2.0E-118	heat shock 70 kDa protein	*Chaetomium globosum*
GR225138	LM/PF	4	7.a	CAK54362	2.0E-39	rapamycin binding protein FKBP12	*Gibberella fujikuroi*
GR225211	LM	1	7.a	XP_961753	1.0E-89	heat shock 70 kDa protein, mitochondrial precursor	*Neurospora crassa*
GR225282	LM/RF	2	7.a	XP_001266956	4.0E-20	stress responsive A/B barrel domain protein	*Neosartorya fischeri*
GR225585	RM	2	7.a	XP_956748	1.0E-74	nuclear protein SNF4	*Neurospora crassa*
GR225925	PF/RM/LM	13	7.a	XP_001931291	3.0E-41	DnaJ domain protein Psi	*Pyrenophora tritici-repentis*
GR225956	RM	1	7.a	XP_001273319	2.0E-28	stress responsive A/B barrel domain protein	*Aspergillus clavatus*
GR226070	RM/RF	3	7.a	XP_001591945	4.0E-180	heat shock protein 90	*Sclerotinia sclerotiorum*
GR226127	RM	1	7.a	XP_001271053	3.0E-09	stress response protein (Ish1), putative	*Aspergillus clavatus*
GR226209	RM	1	7.a	XP_001692162	3.0E-12	DnaJ-like protein	*Chlamydomonas reinhardtii*
GR226328	LM/RM/RF/PF	7	7.a	XP_754386	3.0E-21	stress response RCI peptide	*Aspergillus fumigatus*
GR226388	RF	1	7.a	XP_001481437	2.0E-15	Hsp70 family chaperone	*Aspergillus fumigatus*
GR226401	RF	1	7.a	AAM73769	8.0E-50	stress response element binding protein	*Trichoderma atroviride*
GR226504	RF	1	7.a	XP_753264	4.0E-30	Hsp90 binding co-chaperone (Sba1)	*Aspergillus fumigatus*
GR226819	PF	2	7.a	YP_203356	2.0E-07	orf261 (related to DNA repair)	*Mortierella verticillata*
GR227936	RM/PF	2	7.a	XP_959180	9.0E-125	Amphiphysin-like, reduced viability upon starvation protein rvs167p	*Neurospora crassa*
GR227939	PF	1	7.a	XP_001266719	3.0E-42	unfolded protein response Orm1, putative	*Neosartorya fischeri*
GR228520	RM/PF	2	7.a	XP_001481437	2.0E-34	Hsp70 family chaperone	*Aspergillus fumigatus*
GR228629	PF	1	7.a	XP_753236	1.0E-21	glucose repressible protein Grg1	*Aspergillus fumigatus*
GR224680	LM	1	7.b	EDP50118	1.0E-61	epoxide hydrolase, putative	*Aspergillus fumigatus*
GR225234	LM	2	7.b	XP_001593991	5.0E-47	peroxiredoxin	*Sclerotinia sclerotiorum*
GR227203	PF	1	7.b	ZP_02378594	6.0E-110	catalase/peroxidase HPI	*Burkholderia ubonensis Bu*
GR225094	LM/PF	3	7.c	ABE97921	4.0E-05	snodprot2	*Hypocrea virens*
GR228625	PF	1	7.c	XP_001269050	3.0E-12	equisetin synthetase, putative	*Aspergillus clavatus*
GR226603	RF	1	8	CAB56797	5.0E-39	transposase	*Magnaporthe grisea*
GR224079	LM	1	9			Unknown	
GR224083	LM	1	9			Unknown	
GR224106	LM	2	9			Unknown	
GR224110	LM	1	9			Unknown	
GR224112	LM	1	9			Unknown	
GR224117	LM/RM	2	9	XP_381543	1.0E-38	hypothetical protein FG01367.1	*Gibberella zeae*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224138	LM	1	9			unknown	
GR224153	LM	1	9			unknown	
GR224160	LM	1	9			unknown	
GR224166	LM	1	9			unknown	
GR224169	LM	1	9	XP_001226082	4.0E-07	predicted protein	*Chaetomium globosum*
GR224181	LM/PF/RM	5	9	NP_594303	2.0E-18	DUF1761 family protein	*Schizosaccharomyces pombe*
GR224191	LM	1	9			unknown	
GR224194	LM/RF	2	9	XP_382684	2.0E-23	hypothetical protein FG02508.1	*Gibberella zeae*
GR224195	LM	1	9			unknown	
GR224203	LM	1	9			unknown	
GR224209	LM	1	9			unknown	
GR224214	LM	2	9	AAN75605	4.0E-12	NCP1 pseudogene	*Cryptococcus neoformans*
GR224215	LM	1	9	XP_385274	1.0E-50	hypothetical protein FG05098.1	*Gibberella zeae*
GR224216	LM	1	9	EDP49724	5.0E-28	DUF636 domain protein	*Aspergillus fumigatus*
GR224219	LM	1	9	XP_389602	4.0E-42	hypothetical protein FG09426.1	
GR224225	LM/RM	4	9	XP_001224184	6.0E-48	predicted protein	*Chaetomium globosum*
GR224231	LM/RF/RM/PF	19 2	9	XP_001799364		hypothetical protein SNOG_09061	*Phaeosphaeria nodorum*
GR224234	LM/RM	2	9	XP_001542902	4.0E-08	predicted protein	*Ajellomyces capsulatus*
GR224242	LM	1	9			unknown	
GR224244	LM	1	9			unknown	
GR224257	LM/PF	3	9	XP_386559	1.0E-18	hypothetical protein FG06383.1	*Gibberella zeae*
GR224279	LM	1	9			unknown	
GR224289	LM	1	9			unknown	
GR224297	LM	1	9			unknown	
GR224308	LM	1	9			unknown	
GR224310	LM/RM/PF	9	9	XP_388535	2.0E-62	hypothetical protein FG08359.1	*Gibberella zeae*
GR224312	LM	24	9	XP_001622255	6.6E-02	predicted protein	*Nematostella vectensis*
GR224314	LM/PF/RM/RF	46	9			unknown	
GR224317	LM	1	9			unknown	
GR224322	LM/PF	2	9			unknown	
GR224324	LM	1	9			unknown	
GR224326	LM	1	9			unknown	
GR224328	LM	1	9	XP_001826193	7.0E-42	hypothetical protein	*Aspergillus oryzae*
GR224332	LM	1	9	XP_001798865	4.0E-18	hypothetical protein SNOG_08555	*Phaeosphaeria nodorum*
GR224340	LM	1	9			unknown	
GR224346	LM	1	9			unknown	
GR224357	LM	1	9	XP_001396793	3.0E-18	hypothetical protein An15g02550	*Aspergillus niger*
GR224370	LM	1	9			unknown	
GR224389	LM	1	9			unknown	
GR224391	LM	2	9			unknown	
GR224393	LM	1	9	XP_384046	2.0E-05	hypothetical protein FG03870.1	*Gibberella zeae*
GR224396	LM	1	9			unknown	
GR224406	LM	1	9	XP_001215612	1.0E-41	predicted protein	*Aspergillus terreus*
GR224412	LM	1	9			unknown	
GR224414	LM/RM	4	9			unknown	
GR224418	LM	1	9	XP_390030	5.0E-10	hypothetical protein FG09854.1	*Gibberella zeae*
GR224426	LM	4	9			unknown	
GR224428	LM	1	9			unknown	
GR224436	LM	1	9			unknown	
GR224438	LM	1	9			unknown	
GR224440	LM	1	9			unknown	
GR224442	LM	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224459	LM	1	9			unknown	
GR224463	LM	1	9			unknown	
GR224469	LM	1	9			unknown	
GR224477	LM	1	9			unknown	
GR224479	LM	2	9			unknown	
GR224480	LM	1	9			unknown	
GR224487	LM	1	9			unknown	
GR224492	LM/PF	2	9	EDK86620	2.0E-05	hypothetical protein BMA721280_I0136	*Burkholderia mallei*
GR224498	LM/RM	3	9	XP_001910257	8.0E-13	unnamed protein product	*Podospora anserina*
GR224503	LM/PF	2	9			unknown	
GR224514	LM	1	9			unknown	
GR224517	LM/RM/PF	4	9			unknown	
GR224520	LM	3	9	XP_001394407	8.0E-33	hypothetical protein An11g04120	*Aspergillus niger*
GR224535	LM	2	9			unknown	
GR224556	LM	1	9			unknown	
GR224561	LM	1	9			unknown	
GR224579	LM	1	9			unknown	
GR224581	LM	1	9			unknown	
GR224587	LM	1	9	XP_001222855	4.0E-13	hypothetical protein CHGG_06760	*Chaetomium globosum*
GR224603	LM	1	9	XP_383837	6.0E-69	hypothetical protein FG03661.1	*Gibberella zeae*
GR224614	LM	1	9			unknown	
GR224620	LM	1	9			unknown	
GR224622	LM	1	9			unknown	
GR224625	LM	1	9			unknown	
GR224637	LM	2	9			unknown	
GR224642	LM/RM/PF	3	9			unknown	
GR224659	LM	1	9			unknown	
GR224663	LM	1	9			unknown	
GR224666	LM	1	9			unknown	
GR224667	LM/PF/RM	3	9			unknown	
GR224672	LM	1	9	XP_001220842	8.0E-15	hypothetical protein CHGG_01621	*Chaetomium globosum*
GR224678	LM	1	9	XP_389536	8.0E-05	hypothetical protein FG09360.1	*Gibberella zeae*
GR224684	LM	1	9	XP_001241796	5.0E-30	predicted protein	*Coccidioides immitis*
GR224687	LM/PF	2	9			unknown	
GR224693	LM	1	9			unknown	
GR224700	LM	1	9			unknown	
GR224701	LM	1	9	XP_387636	2.0E-30	hypothetical protein FG07460.1	*Gibberella zeae*
GR224705	LM	1	9	XP_390143	2.0E-26	hypothetical protein FG09967.1	*Gibberella zeae*
GR224707	LM	1	9			unknown	
GR224709	LM	1	9			unknown	
GR224715	LM	1	9			unknown	
GR224725	LM	1	9			unknown	
GR224730	LM	1	9	XP_001212602	7.0E-32	conserved hypothetical protein	*Aspergillus terreus*
GR224734	LM	1	9			unknown	
GR224738	LM/RF/PF	4	9			unknown	
GR224740	LM	1	9			unknown	
GR224741	LM	1	9			unknown	
GR224746	LM	1	9	XP_361363	2.0E-05	hypothetical protein MGG_03837	*Magnaporthe grisea*
GR224747	LM	1	9	XP_001909305	7.0E-15	unnamed protein product	*Podospora anserina*
GR224752	LM	2	9	XP_001481728	2.0E-14	DUF543 domain protein	*Aspergillus fumigatus*
GR224756	LM	1	9			unknown	
GR224762	LM	1	9			unknown	
GR224764	LM	1	9	XP_390997	3.0E-25	hypothetical protein FG10821.1	*Gibberella zeae*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR224765	LM	1	9	XP_001393559	5.0E-35	hypothetical protein An09g02450	*Aspergillus niger*
GR224768	LM	1	9			unknown	
GR224771	LM	1	9			unknown	
GR224776	LM	1	9	XP_001223919	6.0E-06	hypothetical protein CHGG_04705	*Chaetomium globosum*
GR224778	LM	1	9			unknown	
GR224781	LM	1	9			unknown	
GR224782	LM	1	9			unknown	
GR224786	LM	1	9			unknown	
GR224787	LM	1	9	XP_390997	3.0E-25	hypothetical protein FG10821.1	*Gibberella zeae*
GR224789	PF/RM/LM	4	9			unknown	
GR224794	LM	1	9			unknown	
GR224795	LM	2	9			unknown	
GR224797	LM	3	9	XP_748618	5.0E-05	hypothetical protein AFUA_3G02960	*Aspergillus fumigatus*
GR224802	LM	1	9			unknown	
GR224804	LM	1	9			unknown	
GR224818	LM/RM	2	9			unknown	
GR224822	LM	1	9			unknown	
GR224832	LM/RM	10	9	XP_387617	2.0E-43	hypothetical protein FG07441.1	*Gibberella zeae*
GR224834	LM	2	9			unknown	
GR224835	LM	1	9	XP_001876904	1.0E-17	small secreted protein	*Laccaria bicolor*
GR224844	LM	1	9			unknown	
GR224850	LM	1	9			unknown	
GR224853	LM	1	9	XP_387617	1.0E-19	hypothetical protein FG07441.1	*Gibberella zeae*
GR224854	LM	1	9	XP_388916	5.0E-94	hypothetical protein FG08740.1	*Gibberella zeae*
GR224859	LM	1	9			unknown	
GR224860	LM	1	9			unknown	
GR224861	LM	1	9			unknown	
GR224872	LM/RF	2	9			unknown	
GR224885	LM	1	9			unknown	
GR224896	LM	1	9			unknown	
GR224898	LM	2	9	XP_388740	8.0E-51	hypothetical protein FG08564.1	*Gibberella zeae*
GR224902	LM	1	9	XP_001727101	1.0E-43	hypothetical protein	*Aspergillus oryzae*
GR224912	LM/PF	3	9	XP_385060	8.0E-31	hypothetical protein FG04884.1	*Gibberella zeae*
GR224922	LM	1	9	XP_388050	7.0E-46	hypothetical protein FG07874.1	*Gibberella zeae*
GR224926	LM	1	9			unknown	
GR224930	LM	2	9	XP_001804800	1.0E-09	hypothetical protein SNOG_14618	*Phaeosphaeria nodorum*
GR224934	LM	1	9			unknown	
GR224935	LM/RM/RF/PF	6	9			unknown	
GR224938	LM	3	9	EDP51076	1.1E-01	conserved hypothetical protein	*Aspergillus fumigatus*
GR224940	LM/RM/PF	17	9			unknown	
GR224941	LM	1	9			unknown	
GR224952	LM/RF/RM	5	9			unknown	
GR224954	LM/PF	2	9			unknown	
GR224957	LM	1	9			unknown	
GR224959	LM/PF	5	9			unknown	
GR224961	LM/RM/PF	5	9	XP_390910	6.0E-62	hypothetical protein FG10734.1	*Gibberella zeae*
GR224962	LM	1	9			unknown	
GR224969	LM	1	9			unknown	
GR224971	LM	1	9			unknown	
GR224987	LM	1	9			unknown	
GR224999	LM	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225006	LM	2	9			unknown	
GR225027	LM	1	9			unknown	
GR225033	LM	1	9			unknown	
GR225034	LM	1	9			unknown	
GR225048	LM	1	9			unknown	
GR225049	LM	2	9			unknown	
GR225055	LM	6	9			unknown	
GR225059	LM/RF/PF	3	9	XP_001275834	1.0E-56	DUF866 domain protein	*Aspergillus clavatus*
GR225060	LM	1	9	XP_001825429	1.0E-50	hypothetical protein	*Aspergillus oryzae*
GR225082	LM	1	9	XP_368971	7.0E-24	predicted protein	*Magnaporthe grisea*
GR225084	LM	1	9			unknown	
GR225086	LM	2	9	XP_001911950	1.0E-07	unnamed protein product	*Podospora anserina*
GR225087	LM/RM/RF/PF	4	9			unknown	
GR225088	LM	1	9	XP_387218	2.0E-31	hypothetical protein FG07042.1	*Gibberella zeae*
GR225092	LM	1	9	XP_958054	3.0E-16	hypothetical protein NCU09529	*Neurospora crassa*
GR225093	LM	3	9			unknown	
GR225096	LM	1	9	XP_384167	1.0E-05	hypothetical protein FG03991.1	*Gibberella zeae*
GR225108	LM/RM	39	9			unknown	
GR225130	LM	1	9			unknown	
GR225140	LM/RM	2	9	XP_389939	4.0E-11	hypothetical protein FG09763.1	*Gibberella zeae*
GR225143	LM/RM/PF	6	9	XP_387641	6.0E-13	hypothetical protein FG07465.1	*Gibberella zeae*
GR225145	LM/RM	2	9			unknown	
GR225166	LM	1	9			unknown	
GR225170	LM	1	9	XP_001222914	4.0E-05	hypothetical protein CHGG_06819	*Chaetomium globosum*
GR225175	LM	1	9			unknown	
GR225176	LM	1	9			unknown	
GR225177	LM	1	9	XP_001910144	9.0E-13	unnamed protein product	*Podospora anserina*
GR225178	LM	1	9	XP_001910361	2.0E-05	unnamed protein product	*Podospora anserina*
GR225183	LM/PF	3	9			unknown	
GR225191	LM	37	9	CAG28683	3.0E-11	hypothetical protein	*Gibberella fujikuroi*
GR225201	LM	1	9			unknown	
GR225204	LM	1	9			unknown	
GR225218	LM	1	9			unknown	
GR225225	LM	2	9			unknown	
GR225233	LM/PF	2	9			unknown	
GR225237	LM/RM/PF	3	9			unknown	
GR225257	LM	1	9	XP_382121	3.0E-17	hypothetical protein FG01945.1	*Gibberella zeae*
GR225262	LM	1	9	XP_001267027	1.0E-36	conserved hypothetical protein	*Neosartorya fischeri*
GR225268	LM/RF/PF/RM	13	9	XP_001911900	8.0E-08	unnamed protein product	*Podospora anserina*
GR225275	LM	1	9	XP_388140	1.0E-16	hypothetical protein FG07964.1	*Gibberella zeae*
GR225284	LM	1	9			unknown	
GR225294	LM	3	9			unknown	
GR225296	LM	1	9	XP_958921	2.0E-07	hypothetical protein NCU09342	*Neurospora crassa*
GR225317	LM	1	9			unknown	
GR225322	LM/RM	4	9	XP_001399016	2.0E-14	hypothetical protein An18g05660	*Aspergillus niger*
GR225332	LM	1	9	XP_389764	8.0E-43	hypothetical protein FG09588.1	*Gibberella zeae*
GR225335	LM/RF/RM	3	9	XP_389727	2.0E-14	hypothetical protein FG09551.1	*Gibberella zeae*
GR225347	LM	2	9	XP_387617	2.0E-36	hypothetical protein FG07441.1	*Gibberella zeae*
GR225359	LM	1	9			unknown	
GR225366	LM	1	9	XP_001876904	4.0E-14	small secreted protein	*Laccaria bicolor*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225383	LM	1	9			unknown	
GR225389	LM	4	9			unknown	
GR225390	LM/PF	6	9			unknown	
GR225392	LM	1	9			unknown	
GR225395	LM	1	9			unknown	
GR225410	RM	1	9			unknown	
GR225415	RM	1	9			unknown	
GR225418	RM	1	9	XP_001228372	2.0E-20	predicted protein	*Chaetomium globosum*
GR225419	RM	1	9			unknown	
GR225421	RM	1	9	XP_001586820	2.0E-10	predicted protein	*Sclerotinia sclerotiorum*
GR225424	RM	1	9			unknown	
GR225439	RM	1	9	NP_596366	4.0E-12	DUF1741 family protein	*Schizosaccharomyces pombe*
GR225448	RM	1	9			unknown	
GR225457	RM	1	9			unknown	
GR225460	RM	3	9	XP_363212	2.0E-31	hypothetical protein MGG_08796	*Magnaporthe grisea*
GR225462	LM/RM/RF	5	9			unknown	
GR225463	RM	1	9	XP_001390130	1.0E-10	hypothetical protein An03g02320	*Aspergillus niger*
GR225464	RM	1	9			unknown	
GR225468	RM	1	9			unknown	
GR225476	RM	1	9	XP_001209487	8.0E-42	predicted protein	*Aspergillus terreus*
GR225486	RM	1	9			unknown	
GR225495	RM	1	9	XP_386205	5.0E-07	hypothetical protein FG06029.1	*Gibberella zeae*
GR225508	RM	1	9			unknown	
GR225511	RM	1	9			unknown	
GR225529	RM	1	9			unknown	
GR225533	RM	1	9			unknown	
GR225534	RM	3	9	XP_001903723	2.0E-09	unnamed protein product	*Podospora anserina*
GR225537	RM	1	9	XP_388280	4.0E-29	hypothetical protein FG08104.1	*Gibberella zeae*
GR225539	RM	1	9			unknown	
GR225547	RM	1	9			unknown	
GR225551	RM	1	9			unknown	
GR225554	RM/RF/PF	4	9			unknown	
GR225556	RM	1	9	XP_381732	2.0E-15	hypothetical protein FG01556.1	*Gibberella zeae*
GR225564	RM	1	9			unknown	
GR225567	RM	1	9	XP_001228381	9.0E-55	hypothetical protein CHGG_10454	*Chaetomium globosum*
GR225568	RM	1	9			unknown	
GR225570	RM	1	9			unknown	
GR225580	RM	1	9	XP_001938804	3.0E-16	conserved hypothetical protein	*Pyrenophora tritici-repentis*
GR225586	RM/RF	2	9	XP_384459	2.0E-11	hypothetical protein FG04283.1	*Gibberella zeae*
GR225595	RM/RF	2	9	XP_389588	5.0E-27	hypothetical protein FG09412.1	*Gibberella zeae*
GR225606	RM	1	9			unknown	
GR225611	RM	1	9	XP_001522653	7.0E-65	hypothetical protein MGCH7_ch7g753	*Magnaporthe grisea*
GR225618	RM	1	9			unknown	
GR225619	LM/RF/RM/PF	17	9	XP_001910376	7.0E-05	unnamed protein product	*Podospora anserina*
GR225627	RM	1	9			unknown	
GR225628	RM	1	9			unknown	
GR225634	RM	1	9			unknown	
GR225649	RM	1	9			unknown	
GR225653	RM	6	9			unknown	
GR225657	RM	1	9			unknown	
GR225673	RM	1	9			unknown	
GR225694	RM	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225697	RM	1	9	XP_387843	2.0E-25	hypothetical protein FG07667.1	*Gibberella zeae*
GR225718	RM	1	9	XP_390946	6.0E-26	hypothetical protein FG10770.1	*Gibberella zeae*
GR225722	RM	1	9	XP_385533	7.0E-49	hypothetical protein FG05357.1	*Gibberella zeae*
GR225728	RM	1	9			unknown	
GR225729	RM	1	9	XP_001226447	3.0E-07	predicted protein	*Chaetomium globosum*
GR225732	RM	1	9			unknown	
GR225753	RM	2	9	XP_001226805	3.0E-11	hypothetical protein CHGG_08878	*Chaetomium globosum*
GR225755	RM	1	9			unknown	
GR225757	RM	1	9			unknown	
GR225764	RM	1	9	XP_386345	9.0E-14	hypothetical protein FG06169.1	*Gibberella zeae*
GR225779	RM	1	9			unknown	
GR225792	LM/RM	4	9			unknown	
GR225798	RM	1	9			unknown	
GR225799	RM	1	9			unknown	
GR225801	RM	1	9			unknown	
GR225808	RM	1	9	XP_001910059	5.0E-23	unnamed protein product	*Podospora anserina*
GR225811	RM	1	9	XP_001545985	9.0E-16	hypothetical protein BC1G_15434	*Botryotinia fuckeliana*
GR225812	RM	1	9	XP_383092	2.0E-13	hypothetical protein FG02916.1	*Gibberella zeae*
GR225815	RM	1	9			unknown	
GR225822	RM	1	9	XP_001225652	2.0E-14	hypothetical protein CHGG_07996	*Chaetomium globosum*
GR225824	RM	1	9			unknown	
GR225825	PF/RM/LM	5	9	XP_001537941	5.0E-07	predicted protein	*Ajellomyces capsulatus*
GR225832	RM	1	9			unknown	
GR225833	RM	1	9			unknown	
GR225835	RM	1	9	XP_385442	7.0E-09	hypothetical protein FG05266.1	*Gibberella zeae*
GR225843	RM	1	9			unknown	
GR225854	RM	1	9			unknown	
GR225856	RM	1	9			unknown	
GR225874	RM	1	9	XP_001827600	5.0E-34	hypothetical protein	*Aspergillus oryzae*
GR225877	RM	1	9			unknown	
GR225880	RM	1	9	XP_361528	9.0E-08	predicted protein	*Magnaporthe grisea*
GR225882	RM	1	9	XP_001940571	1.0E-57	conserved hypothetical protein	*Pyrenophora tritici-repentis*
GR225889	RM	1	9	XP_387215	1.0E-43	hypothetical protein FG07039.1	*Gibberella zeae*
GR225900	RM	1	9	XP_001222440	7.0E-67	hypothetical protein CHGG_06345	*Chaetomium globosu*
GR225905	RM	2	9			unknown	
GR225911	RM	1	9	XP_387324	8.0E-35	hypothetical protein FG07148.1	*Gibberella zeae*
GR225920	RM	1	9			unknown	
GR225928	RM	1	9			unknown	
GR225932	RM	1	9			unknown	
GR225935	RM	1	9	XP_384282	3.0E-31	hypothetical protein FG04106.1	*Gibberella zeae*
GR225936	RM	1	9			unknown	
GR225937	RM	1	9			unknown	
GR225944	RM	1	9			unknown	
GR225948	RM	1	9			unknown	
GR225954	RM	1	9			unknown	
GR225959	RM	1	9	XP_389165	2.0E-05	hypothetical protein FG08989.1	*Gibberella zeae*
GR225964	RM	2	9			unknown	
GR225965	RM	1	9			unknown	
GR225967	RM	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR225969	RM	1	9			unknown	
GR225989	RM	1	9	XP_390839	1.0E-16	hypothetical protein FG10663.1	*Gibberella zeae*
GR225994	RM	1	9			unknown	
GR225998	RM	1	9			unknown	
GR226016	RM	1	9			unknown	
GR226031	RM	1	9			unknown	
GR226033	RM	1	9	XP_001226459	1.0E-12	predicted protein	*Chaetomium globosum*
GR226038	RM	1	9	XP_389703	7.0E-44	hypothetical protein FG09527.1	*Gibberella zeae*
GR226041	RM/PF	6	9	XP_001797642	3.0E-07	hypothetical protein SNOG_07301	*Phaeosphaeria nodorum*
GR226046	RM	1	9			unknown	
GR226049	RM	1	9			unknown	
GR226065	RM	1	9			unknown	
GR226068	RM/PF	10	9	XP_001802764	2.0E-77	hypothetical protein SNOG_12543	*Phaeosphaeria nodorum*
GR226072	RM	1	9	XP_388700	3.0E-107	hypothetical protein FG08524.1	*Gibberella zeae*
GR226077	RM	1	9			unknown	
GR226078	RM	1	9	EDP48741	4.0E-51	DUF567 domain protein	*Aspergillus fumigatus*
GR226080	RM	1	9	XP_001904347	1.0E-10	unnamed protein product	*Podospora anserina*
GR226090	RM	2	9	XP_388016	2.0E-27	hypothetical protein FG07840.1	*Gibberella zeae*
GR226093	RM	1	9	YP_001185952	5.0E-06	membrane protein-like protein	*Pseudomonas mendocina*
GR226098	RM	3	9			unknown	
GR226099	RM	1	9			unknown	
GR226109	LM/RM	3	9			unknown	
GR226118	RM	1	9	XP_001208562	8.0E-38	predicted protein	*Aspergillus terreus*
GR226119	RM	1	9			unknown	
GR226133	RM	1	9			unknown	
GR226141	RM	1	9			unknown	
GR226148	RM	1	9			unknown	
GR226157	RM	1	9			unknown	
GR226164	RM	2	9			unknown	
GR226176	LM/RM	3	9			unknown	
GR226191	RM	1	9			unknown	
GR226193	RM	1	9			unknown	
GR226196	RM	1	9			unknown	
GR226206	RM	1	9			unknown	
GR226207	RM	1	9	XP_388958	8.0E-02	hypothetical protein FG08782.1	*Gibberella zeae*
GR226211	RM	4	9			unknown	
GR226222	RM	1	9			unknown	
GR226226	RM	1	9	XP_390902	5.0E-56	hypothetical protein FG10726.1	*Gibberella zeae*
GR226231	RM	1	9	XP_001544384	1.0E-17	predicted protein	*Ajellomyces capsulatus*
GR226238	RM	1	9	XP_388858	3.0E-22	hypothetical protein FG08682.1	*Gibberella zeae*
GR226239	RM	1	9	XP_386702	3.0E-33	hypothetical protein FG06526.1	*Gibberella zeae*
GR226242	RM	1	9			unknown	
GR226249	RM	2	9			unknown	
GR226252	RM/PF	3	9			unknown	
GR226257	RF	3	9			unknown	
GR226261	RF	1	9	XP_381202	8.0E-12	hypothetical protein FG01026.1	*Gibberella zeae*
GR226274	RF	1	9			unknown	
GR226286	RF	2	9			unknown	
GR226288	RF	1	9	XP_001550658	7.0E-09	hypothetical protein BC1G_11066	*Botryotinia fuckeliana*
GR226296	RF	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226302	RF	3	9	XP_384459	3.0E-19	hypothetical protein FG04283.1	*Gibberella zeae*
GR226303	PF/RF/RM	9	9	XP_001937997	3.0E-21	hypothetical protein PTRG_07665	*Pyrenophora tritici-repentis*
GR226309	RF	1	9	XP_001227232	7.0E-29	hypothetical protein CHGG_09305	*Chaetomium globosum*
GR226312	RF	1	9			unknown	
GR226316	RF	1	9			unknown	
GR226317	RF	1	9			unknown	
GR226331	RF	1	9			unknown	
GR226333	RF	1	9			unknown	
GR226334	RF	1	9	XP_390228	2.0E-09	hypothetical protein FG10052.1	*Gibberella zeae*
GR226337	RF	1	9			unknown	
GR226343	RF	1	9			unknown	
GR226345	RF	2	9			unknown	
GR226346	RF	1	9			unknown	
GR226347	RF	1	9			unknown	
GR226349	RF	1	9			unknown	
GR226352	RF	1	9			unknown	
GR226356	RF	1	9			unknown	
GR226357	RF	1	9	XP_001399016	2.0E-16	hypothetical protein An18g05660	*Aspergillus niger*
GR226359	RF	1	9			unknown	
GR226367	RF	1	9	XP_381530	3.0E-10	hypothetical protein FG01354.1	*Gibberella zeae*
GR226369	RF	1	9			unknown	
GR226379	RF	1	9	XP_001217006	2.0E-64	predicted protein	*Aspergillus terreus*
GR226380	LM/RF	3	9	XP_956130	9.0E-09	hypothetical protein NCU03567	*Neurospora crassa*
GR226390	RF	1	9			unknown	
GR226393	RF	1	9			unknown	
GR226394	RF	1	9			unknown	
GR226396	RF	1	9			unknown	
GR226410	RF	1	9	XP_001390902	5.0E-05	hypothetical protein An06g00740	*Aspergillus niger*
GR226411	RF	1	9			unknown	
GR226413	RF	1	9			unknown	
GR226423	RF	1	9			unknown	
GR226424	RF	1	9	XP_381202	8.0E-44	hypothetical protein FG01026.1	*Gibberella zeae*
GR226426	RF	1	9			unknown	
GR226428	RF	2	9			unknown	
GR226430	RF	1	9			unknown	
GR226434	RF	1	9			unknown	
GR226443	RF	1	9	XP_001394584	3.0E-12	hypothetical protein An11g05990	*Aspergillus niger*
GR226446	RF	1	9			unknown	
GR226450	RF	1	9			unknown	
GR226471	RF	1	9			unknown	
GR226476	RF	1	9			unknown	
GR226485	RF	1	9			unknown	
GR226487	RF	1	9	XP_001399044	6.0E-23	hypothetical protein An18g05930	*Aspergillus niger*
GR226489	RF	1	9			unknown	
GR226490	RF	1	9	XP_386314	9.0E-11	hypothetical protein FG06138.1	*Gibberella zeae*
GR226506	RF	1	9			unknown	
GR226508	LM/RM/RF/PF	9	9			unknown	
GR226521	RF	1	9	EDP55205	5.0E-05	PT repeat family protein	*Aspergillus fumigatus*
GR226522	RF	1	9			unknown	
GR226528	RF	1	9			unknown	
GR226537	RF	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226539	RF	1	9			unknown	
GR226542	LM/RF	3	9			unknown	
GR226543	RF	1	9	XP_381480	1.0E-12	hypothetical protein FG01304.1	*Gibberella zeae*
GR226550	RF	1	9			unknown	
GR226551	RF/LM	3	9			unknown	
GR226552	RF	1	9	XP_717805	2.0E-13	potential mitochondrial protein Fmp16	*Candida albicans*
GR226572	RF	1	9			unknown	
GR226573	RF	1	9	XP_381349	3.0E-08	hypothetical protein FG01173.1	*Gibberella zeae*
GR226575	RF	1	9	XP_001220992	1.0E-72	hypothetical protein CHGG_01771	*Chaetomium globosum*
GR226576	RF	1	9			unknown	
GR226590	RF	1	9	XP_001543540	4.0E-18	predicted protein	*Ajellomyces capsulatus*
GR226604	RF	1	9			unknown	
GR226605	RF	1	9	XP_390037	1.0E-43	hypothetical protein FG09861.1	*Gibberella zeae*
GR226611	RF	3	9			unknown	
GR226618	RF/PF	17	9			unknown	
GR226621	RF/PF	5	9			unknown	
GR226637	RF	1	9			unknown	
GR226646	RF	1	9			unknown	
GR226649	RF	1	9			unknown	
GR226651	RF	1	9			unknown	
GR226655	RF	1	9			unknown	
GR226662	RF	1	9			unknown	
GR226666	RF	1	9			unknown	
GR226668	RF	1	9			unknown	
GR226672	RF	1	9	XP_001262176	2.0E-48	hypothetical protein NFIA_099130	*Neosartorya fischeri*
GR226695	RF	1	9			unknown	
GR226696	RF	1	9			unknown	
GR226700	RF	1	9			unknown	
GR226708	RF	1	9	XP_384459	3.0E-19	hypothetical protein FG04283.1	*Gibberella zeae*
GR226714	RF	1	9			unknown	
GR226715	RM/RF	3	9	XP_001585621	4.0E-14	predicted protein	*Sclerotinia sclerotiorum*
GR226717	RF	1	9			unknown	
GR226720	RF	1	9	XP_001243471	8.0E-05	hypothetical protein CIMG_07367	*Coccidioides immitis*
GR226724	RF	2	9			unknown	
GR226730	RF	2	9	XP_751886	1.0E-17	DUF563 domain protein	*Aspergillus fumigatus*
GR226741	RF	1	9	XP_001542717	1.0E-15	predicted protein	*Ajellomyces capsulatus*
GR226743	RF	2	9			unknown	
GR226751	RF	1	9	XP_001227847	2.0E-32	hypothetical protein CHGG_09920	*Chaetomium globosum*
GR226753	RF	1	9	EDP55176	4.0E-17	DUF1237 domain protein	*Aspergillus fumigatus*
GR226755	RF	1	9			unknown	
GR226770	RF	1	9	NP_594157	8.0E-10	DUF1748 family protein	*Schizosaccharomyces pombe*
GR226771	RF	1	9			unknown	
GR226774	RF	2	9	XP_001591439	7.0E-15	hypothetical protein SS1G_08066	*Sclerotinia sclerotiorum*
GR226780	RF	1	9	XP_364309	1.0E-36	predicted protein	*Magnaporthe grisea*
GR226781	RF	1	9			unknown	
GR226784	RF	1	9			unknown	
GR226786	RF	1	9			unknown	
GR226796	RF	1	9			unknown	
GR226802	PF	1	9			unknown	
GR226807	PF	3	9	XP_389721	6.0E-08	hypothetical protein FG09545.1	*Gibberella zeae*
GR226809	PF	4	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR226824	LM/RM/PF/RF	101	9	XP_001931533	5.0E-24	cyanovirin-N family protein	*Pyrenophora tritici-repentis*
GR226825	PF	1	9			unknown	
GR226844	PF/RM	5	9	XP_001590447	6.0E-18	predicted protein	*Sclerotinia sclerotiorum*
GR226860	PF	1	9			unknown	
GR226866	PF	1	9			unknown	
GR226874	PF	1	9			unknown	
GR226881	PF	1	9	XP_001538888	8.0E-18	predicted protein	*Ajellomyces capsulatus*
GR226886	PF	1	9			unknown	
GR226889	PF	2	9			unknown	
GR226894	PF	1	9			unknown	
GR226917	PF	1	9			unknown	
GR226934	PF	2	9			unknown	
GR226951	PF	1	9			unknown	
GR226963	PF	1	9			unknown	
GR226966	LM/PF/RM	5	9	XP_389843	8.0E-19	hypothetical protein FG09667.1	*Gibberella zeae*
GR226968	PF	1	9	XP_001246219	2.0E-07	hypothetical protein CIMG_05660	*Coccidioides immitis*
GR226970	PF	1	9			unknown	
GR226993	PF	1	9			unknown	
GR227004	PF	1	9			unknown	
GR227021	PF	1	9			unknown	
GR227022	PF	1	9			unknown	
GR227031	LM/PF/RM	14	9	XP_390055	4.0E-05	hypothetical protein FG09879.1	*Gibberella zeae*
GR227036	PF	1	9	XP_001825336	1.0E-34	hypothetical protein	*Aspergillus oryzae*
GR227039	PF	1	9	XP_001238918	7.0E-41	hypothetical protein CIMG_09940	*Coccidioides immitis*
GR227042	PF	1	9			unknown	
GR227052	PF	1	9	XP_387928	1.0E-12	hypothetical protein FG07752.1	*Gibberella zeae*
GR227053	PF	2	9			unknown	
GR227055	PF	1	9			unknown	
GR227066	PF	2	9	XP_001398639	2.0E-28	hypothetical protein An18g01800	*Aspergillus niger*
GR227073	PF	1	9			unknown	
GR227085	PF	1	9			unknown	
GR227091	PF	1	9			unknown	
GR227094	PF	1	9			unknown	
GR227095	RF/PF	2	9	XP_962543	6.0E-54	hypothetical protein NCU08330	*Neurospora crassa*
GR227096	PF	4	9			unknown	
GR227103	PF	1	9			unknown	
GR227110	PF	1	9			unknown	
GR227115	PF	1	9	XP_385409	1.0E-18	hypothetical protein FG05233.1	*Gibberella zeae*
GR227128	PF	1	9	XP_958940	2.0E-05	hypothetical protein NCU09701	*Neurospora crassa*
GR227142	PF/RM	6	9	XP_001824760	3.0E-52	hypothetical protein	*Aspergillus oryzae*
GR227172	PF	1	9			unknown	
GR227179	RM/PF	2	9	XP_001537960	9.0E-14	predicted protein	*Ajellomyces capsulatus*
GR227183	PF	1	9			unknown	
GR227197	PF	1	9			unknown	
GR227228	PF	1	9			unknown	
GR227231	PF	4	9			unknown	
GR227242	PF	1	9			unknown	
GR227247	PF	1	9	XP_380436	4.0E-10	hypothetical protein FG00260.1	*Gibberella zeae*
GR227265	RF/PF	3	9	XP_384636	1.0E-29	hypothetical protein FG04460.1	*Gibberella zeae*
GR227269	PF	1	9			unknown	
GR227279	PF	1	9			unknown	
GR227291	PF	1	9	XP_001540440	1.0E-13	predicted protein	*Ajellomyces capsulatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR227293	PF	1	9			unknown	
GR227304	PF	1	9	XP_001585581	2.0E-08	predicted protein	*Sclerotinia sclerotiorum*
GR227310	PF	1	9	XP_001540442	3.0E-49	predicted protein	*Ajellomyces capsulatus*
GR227319	PF	1	9			unknown	
GR227334	RF/PF	2	9			unknown	
GR227341	PF	1	9			unknown	
GR227360	PF	1	9	XP_388280	3.0E-24	hypothetical protein FG08104.1	*Gibberella zeae*
GR227362	PF/LM	5	9	XP_382064		hypothetical protein FG01888.1	*Gibberella zeae*
GR227366	PF	1	9			unknown	
GR227370	PF	1	9			unknown	
GR227371	PF	2	9			unknown	
GR227384	PF	1	9			unknown	
GR227392	PF	1	9			unknown	
GR227401	PF	1	9			unknown	
GR227408	PF	1	9			unknown	
GR227420	PF	1	9	XP_001796941	5.0E-25	hypothetical protein SNOG_06574	*Phaeosphaeria nodorum*
GR227427	PF	6	9	XP_001802763	3.0E-17	hypothetical protein SNOG_12542	*Phaeosphaeria nodorum*
GR227428	PF	1	9			unknown	
GR227429	PF	1	9			unknown	
GR227432	RM/RF/PF	4	9			unknown	
GR227435	PF	1	9			unknown	
GR227440	RM/PF	2	9			unknown	
GR227445	PF	1	9			unknown	
GR227451	PF	2	9			unknown	
GR227463	PF/RM	5	9			unknown	
GR227468	LM/RM/PF	4	9	NP_690845	2.0E-13	Mitochondrial protein of unknown function, Tar1p	*Saccharomyces cerevisiae*
GR227483	LM/PF	15	9	XP_364704	6.0E-12	conserved hypothetical protein	*Magnaporthe grisea*
GR227491	PF	2	9			unknown	
GR227508	PF	1	9			unknown	
GR227520	LM/RM/PF	124	9			unknown	
GR227536	PF	1	9			unknown	
GR227543	PF	1	9			unknown	
GR227570	PF	1	9			unknown	
GR227593	PF	1	9			unknown	
GR227614	PF	8	9			unknown	
GR227621	PF	1	9			unknown	
GR227627	RF/PF	2	9			unknown	
GR227633	PF	1	9			unknown	
GR227638	PF	2	9	XP_001215883	2.0E-51	predicted protein	*Aspergillus terreus*
GR227654	PF	2	9			unknown	
GR227669	PF	1	9			unknown	
GR227671	PF	1	9			unknown	
GR227674	PF	1	9			unknown	
GR227694	PF	1	9	XP_640303	2.0E-18	N2227-like domain-containing protein	*Dictyostelium discoideum*
GR227696	RM/PF	4	9			unknown	
GR227706	PF	1	9			unknown	
GR227712	PF	1	9	XP_384681	3.0E-05	hypothetical protein FG04505.1	*Gibberella zeae*
GR227724	PF	1	9			unknown	
GR227729	PF	1	9			unknown	
GR227759	PF	1	9			unknown	
GR227765	PF	2	9	XP_001540440	9.0E-28	predicted protein	*Ajellomyces capsulatus*
GR227777	PF	1	9			unknown	
GR227787	PF	1	9			unknown	
GR227793	PF	1	9			unknown	
GR227807	PF	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR227821	PF	1	9	XP_962814	8.0E-40	hypothetical protein NCU07881	*Neurospora crassa*
GR227826	PF	1	9	XP_385092	4.0E-05	hypothetical protein FG04916.1	*Gibberella zeae*
GR227833	LM/RM/RF/PF	258	9			unknown	
GR227847	PF	2	9	XP_001540440	3.0E-07	predicted protein	*Ajellomyces capsulatus*
GR227850	PF	1	9			unknown	
GR227896	LM/RM/PF	7	9	XP_386443	5.0E-12	hypothetical protein FG06267.1	*Gibberella zeae*
GR227897	PF	1	9			unknown	
GR227921	PF	1	9	XP_001405811	2.0E-33	predicted protein	*Magnaporthe grisea*
GR227924	PF	1	9			unknown	
GR227935	RM/PF	2	9	XP_390666	2.0E-26	hypothetical protein FG10490.1	*Gibberella zeae*
GR227953	PF	130	9			unknown	
GR227960	PF	1	9			unknown	
GR227974	PF	2	9	XP_001228381	2.0E-46	hypothetical protein CHGG_10454	*Chaetomium globosum*
GR227978	PF	2	9			unknown	
GR227982	LM/PF	12	9			unknown	
GR227996	PF	1	9	XP_385566	1.0E-06	hypothetical protein FG05390.1	*Gibberella zeae*
GR227998	LM/RM/PF	35	9			unknown	
GR228008	PF	1	9			unknown	
GR228012	LM/RM/RF/PF	13	9	XP_384575	3.0E-06	hypothetical protein FG04399.1	*Gibberella zeae*
GR228021	PF	1	9			unknown	
GR228022	PF	1	9			unknown	
GR228035	RF/PF/RM	38	9	XP_388280	1.0E-29	hypothetical protein FG08104.1	*Gibberella zeae*
GR228036	PF	1	9			unknown	
GR228048	PF	1	9	XP_391772	7.0E-83	hypothetical protein FG11596.1	*Gibberella zeae*
GR228055	PF	1	9			unknown	
GR228072	PF	1	9			unknown	
GR228075	PF	2	9	XP_001911209	4.0E-53	unnamed protein product	*Podospora anserina*
GR228081	PF	4	9			unknown	
GR228085	PF	1	9			unknown	
GR228087	PF	20	9			unknown	
GR228097	LM/PF	14	9			unknown	
GR228101	PF	2	9	XP_001405719	1.0E-07	predicted protein	*Magnaporthe grisea*
GR228106	PF	1	9			unknown	
GR228108	PF	1	9			unknown	
GR228112	PF	1	9			unknown	
GR228113	PF	1	9			unknown	
GR228142	PF	1	9	XP_390382	1.0E-10	hypothetical protein FG10206.1	*Gibberella zeae*
GR228153	PF	1	9			unknown	
GR228157	RM/PF	5	9	XP_385531	1.0E-44	hypothetical protein FG05355.1	*Gibberella zeae*
GR228158	PF	1	9			unknown	
GR228168	RF/PF	2	9			unknown	
GR228169	RM/PF	7	9			unknown	
GR228173	PF	2	9			unknown	
GR228176	PF	2	9			unknown	
GR228179	PF	1	9			unknown	
GR228183	PF	7	9			unknown	
GR228189	PF	1	9			unknown	
GR228193	PF	1	9			unknown	
GR228198	PF	2	9	XP_001224184	2.0E-32	predicted protein	*Chaetomium globosum*
GR228204	PF	1	9	NP_792422	4.0E-18	hypothetical protein PSPTO_2613	*Pseudomonas syringae*
GR228206	PF	1	9	XP_001274870	3.0E-53	conserved hypothetical protein	*Aspergillus clavatus*

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR228207	PF	1	9			unknown	
GR228210	PF	1	9			unknown	
GR228212	PF	1	9			unknown	
GR228214	RF/PF	2	9	XP_001912405	2.0E-40	unnamed protein product	*Podospora anserina*
GR228239	PF	1	9	XP_660186	2.0E-05	hypothetical protein AN2582.2	*Aspergillus nidulans*
GR228247	PF	1	9			unknown	
GR228283	RF/PF	2	9			unknown	
GR228288	PF	1	9			unknown	
GR228290	PF	2	9			unknown	
GR228296	PF	1	9			unknown	
GR228297	PF	4	9			unknown	
GR228299	PF	1	9			unknown	
GR228306	PF	2	9	XP_001262176	5.0E-29	conserved hypothetical protein	*Neosartorya fischeri*
GR228319	PF	1	9			unknown	
GR228333	PF	2	9	XP_662849	8.0E-24	hypothetical protein AN5245.2	*Aspergillus nidulans*
GR228336	PF	1	9	XP_388696	1.0E-14	hypothetical protein FG08520.1	*Gibberella zeae*
GR228339	PF	1	9			unknown	
GR228340	RF/PF	7	9	XP_001560184	8.0E-28	hypothetical protein BC1G_01016	*Botryotinia fuckeliana*
GR228343	PF	1	9			unknown	
GR228346	PF	1	9	XP_570260	2.0E-46	hypothetical protein	*Cryptococcus neoforman*
GR228352	PF	1	9			unknown	
GR228360	PF	1	9			unknown	
GR228365	PF	1	9			unknown	
GR228367	PF	2	9			unknown	
GR228368	PF	1	9			unknown	
GR228373	PF	1	9	EDP49866	6.0E-11	mitochondria protein Fmp29, putative	*Aspergillus fumigatus*
GR228379	PF	1	9	XP_001796249	6.0E-21	hypothetical protein SNOG_05853	*Phaeosphaeria nodorum*
GR228405	PF	2	9			unknown	
GR228411	PF	1	9			unknown	
GR228422	RM/PF	3	9			unknown	
GR228425	PF	1	9			unknown	
GR228437	PF	1	9	XP_646824	1.0E-05	hypothetical protein DDB_0233766	*Dictyostelium discoideum*
GR228446	PF	2	9			unknown	
GR228449	PF	1	9	Q8J0N0	3.0E-15	UPF0357 protein YCL012C precursor	*Saccharomyces paradoxus*
GR228478	PF	1	9			unknown	
GR228483	RM/PF	2	9			unknown	
GR228484	PF	1	9	XP_001547986	4.0E-32	hypothetical protein BC1G_13677	*Botryotinia fuckeliana*
GR228491	PF	5	9	XP_387617	3.0E-48	hypothetical protein FG07441.1	*Gibberella zeae*
GR228495	PF	1	9	XP_366184	8.0E-17	predicted protein	*Magnaporthe grisea*
GR228499	PF	1	9			unknown	
GR228505	PF	1	9			unknown	
GR228511	PF	1	9			unknown	
GR228517	RM/PF	18	9			unknown	
GR228519	PF	1	9			unknown	
GR228523	PF	1	9			unknown	
GR228531	PF	1	9			unknown	
GR228534	PF	1	9			unknown	
GR228536	PF	4	9			unknown	
GR228541	PF	1	9	XP_001540439	1.0E-42	predicted protein	*Ajellomyces capsulatus*
GR228570	PF	1	9	XP_658463	2.0E-05	hypothetical protein AN0859.2	*Aspergillus nidulans*
GR228594	PF	1	9	XP_001227781	2.0E-12	hypothetical protein CHGG_09854	*Chaetomium globosum*
GR228600	PF	1	9			unknown	
GR228601	PF	3	9			unknown	
GR228605	PF	1	9			unknown	

(*Continued*)

Appendix Table 1. (*Continued*).

Acc. No.	Library	No.	Function	Best match accession	*E* value	Description	Organisms
GR228608	PF	1	9	XP_751025	5.0E-05	DUF1446 domain protein	*Aspergillus fumigatus*
GR228612	PF	1	9			unknown	
GR228615	PF	1	9			unknown	
GR228623	PF	5	9	XP_001804800	3.0E-16	hypothetical protein SNOG_14618	*Phaeosphaeria nodorum*
GR228628	PF	1	9			unknown	
GR228644	PF	2	9	XP_001586480	2.0E-32	hypothetical protein SS1G_12466	*Sclerotinia sclerotiorum*
GR228654	PF	2	9			unknown	
GR228666	PF	1	9	XP_001598271	9.0E-06	hypothetical protein SS1G_00357	*Sclerotinia sclerotiorum*