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

Chenghui Xiong, Yongliang Xia, Peng Zheng, Shaohua Shi and Chengshu Wang*

Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, 300 Fenglin Road, Shanghai 200032, China

(Received 11 January 2010; final version received 3 February 2010)

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.
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 rotary 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 cm², 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 × 10⁶ 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 (Clontech, 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 Claverie (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™ 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 elements.
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, \( E = 2.0 \times 10^{-42}, 63 \text{ of } 860 \text{ ESTs} \)) 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

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.
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, 0.23, 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).
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 (Freimorsier 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

| Genes | Acc. No. | Description (E < 10^{-5}) | Transcript frequency (%) | Primers (F, forward; R, reverse) |
|-------|----------|-----------------------------|--------------------------|----------------------------------|
| Gene1 | GR227007 | RBP (RNA binding protein)   | 0.15 0.23 0.73 2.30       | F: ACTTCACCATGCAACAACCTTC R: GACCTGGCTTCGTCTGGCTT |
| Gene2 | GR225263 | 16 kDa allergen             | 0.08 0.12 0.55 0.64       | F: CACCGTACAGCCTGCGAGTA R: AGCCGCTTTGGCTGTAAGCA |
| Gene3 | GR225674 | Spermatogenesis associated CRA b | — 0.12 — —       | F: TTTATCCGGTCCTTATGACC R: AACCTGGTGGCTTCTTCTT |
| Gene4 | GR227833 | Unknown                     | 0.45 6.86 9.36 7.61       | F: TTGATGATGATAGCCGCGCTGAC R: GCTGAAACCAACCCAGAAC |
| Gene5 | GR227979 | Plasmin-sensitive surface protein (cell-wall protein) | 0.38 1.74 29.17 17.57 | F: GTTCCTTGGCAGCCTGACC |
| Gene6 | GR226824 | Cyanovirin-N family protein | 5.29 0.93 0.37 1.12       | F: AGCATCGGAGCGTTATAC R: AACGTCTTCAACACCGACG |
| Gene7 | GR225435 | Nuclear transport factor 2  | 0.68 0.12 0.37 0.37       | F: CTGACGCAGGCAATTTT |
| Gene8 | GR226742 | Lys M domain protein        | — — 0.18 —           | F: ACATCTCCACACCGCAAGT |
| Gene9 | GR226855 | Shwachman–Bodian–Diamond syndrome (SBDS) domain containing protein | 0.15 0.35 1.10 0.32 | F: ACCAGTGCCATACAGGG |
| Gene10| GR226225 | Calmodulin                  | 0.23 0.12 — 0.21        | F: CCAGAAGCTTTCGAGGTC |
| Gene11| GR225094 | Snodprot2                   | 0.08 — — —             | F: AAGACTCTTGCCAGCAAAGG |
| Gene12| GR224905 | GPI-anchored cell wall organization protein Ecm33 | 0.15 0.23 0.18 0.11 | F: CTGCCGTCGCAACCTTAC |
| Gene13| GR224296 | L-PSP endoribonuclease family protein | 0.15 0.58 0.18 0.64 | F: GCGTTGAGCCGCGATTA R: GCTGTACACCTTCGCTTC |
| 18S RNA| AB070375 | 18S RNA                     | NA NA NA NA            | F: GCCAGGAAGCACTAAGGA |

Note: (–) Means not detected in EST analysis of different libraries; NA, not available. 18S RNA gene was amplified as positive control in Figure 3.
The upregulation of ubiquitin (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, $E = 2 \times 10^{-89}$) (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*, *C. 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 et al., 2004; 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*, *C. 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 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 adenosine 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.

**Acknowledgements**

This work was supported by the programs from Science and Technology Commission of Shanghai Municipality (08DZ1970200) and the Ministry of Science and Technology of China (2007BA132B03). The authors also appreciate Professor Raymond J. St. Leger for critical reading this paper.

**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 Sceharomycyes cerevisiae gene encoding C-4 sterol methyl oxidase. Proc Natl Acad Sci USA 93: 186–190.

Bidoehka 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 zea-maydis identify novel genes expressed during vegetative, infectious, and reproductive growth. BMC Genomics 9: 523.

Bontemps F, van den Berge H, 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. Cordyssinocan, 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.

Coppen 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, Wraith SP. 2007. Mycoinsecticides and Mycoacaricicides: 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.

Haldén P, Savolainen K, Tyyrälä J, Vuento M, Kuusela P. 1996. Purification and characterisation of a plasmid-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 tatt and its teleomorph, Cordyceps tatt (Hypocreales, Clavicipitaceae). Mycologia 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.

Kanazuki 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 KKW. 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 itp 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 Beauveria bassiana teleomorphs. Mycologia 94: 376–383.

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.

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

| Acc. No. | Library | No. | Function | Best match accession | E value | Description | Organisms |
|----------|---------|-----|----------|----------------------|---------|-------------|-----------|
| GR224452 | LM      | 1.a| 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 tritic-repentis |
| GR225111 | LM      | 1  | 1.a      | XP_001276018         | 2.0E-43 | GNAT family acetyltransferase, putative lantionine synthetase C-like protein, expressed | Aspergillus clavatus |
| GR225444 | RM      | 1  | 1.a      | ABB47829             | 5.0E-08 | | Oryza sativa Japonica |
| GR225933 | RM      | 1  | 1.a      | XP_960754             | 1.0E-82 | N-acetyltransferase 5 tyrosinase central domain protein tyrosinase | Neurospora crassa |
| GR226607 | RF      | 2  | 1.a      | XP_001264010         | 7.0E-06 | | Neurospora fischeri |
| GR226647 | RF      | 1  | 1.a      | EDP56958             | 2.0E-16 | | 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 | Neurosartorya fischeri |
| GR228019 | RM/PF   | 3  | 1.a      | ABU48597             | 1.0E-51 | Xaa-Pro dipeptidase GLYC NECR Serine hydroxymethyltransferase, cytosolic | Trichophyton tonsurans |
| GR228241 | PF      | 1  | 1.a      | XP_386466             | 7.0E-59 | cysteine dioxygenase subfamily | Gibberella zeae |
| GR228378 | PF      | 1  | 1.a      | XP_750969             | 7.0E-45 | homogenisate 1,2-dioxynegase related to 3-phosphoserine aminotransferase | Aspergillus fumigatus |
| GR228619 | PF      | 1  | 1.a      | CAD70964             | 2.0E-53 | | 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 citrate synthase, mitochondrial precursor | Neurosartorya fischeri |
| GR224372 | LM      | 1  | 1.b      | XP_001228276         | 2.0E-14 | | Chaetomium globosum |
| GR224513 | LM/PF   | 4  | 1.b      | ABH10639             | 2.0E-11 | fructose bisphosphate 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 transaldolase | Neosartorya fischeri |
| GR224889 | LM      | 1  | 1.b      | XP_366548             | 3.0E-45 | pyruvate decarboxylase | Magnaporthe grisea |
| GR225165 | LM      | 3  | 1.b      | XP_001219658         | 1.0E-107| | Chaetomium globosum |
| GR225216 | LM      | 1  | 1.b      | YP_001173410         | 2.0E-33 | hydrolyse, alpha/beta fold family | Pseudomonas stutzeri |
| GR225327 | LM/RM   | 2  | 1.b      | BAF98892             | 1.0E-52 | formate oxidase 2 | Debaryomyces vanrijae |
| GR225333 | LM      | 1  | 1.b      | XP_001548578         | 1.0E-12 | fumarate hydratase | Botrytis 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 cyclopentanone | Aspergillus clavatus |
| GR225647 | RM      | 1  | 1.b      | XP_001938825         | 8.0E-69 | | Pyrenophora tritic-repentis |
| GR225777 | RM      | 1  | 1.b      | XP_962927             | 3.0E-129| malate dehydrogenase, mitochondrial precursor | Neurospora crassa |
| 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| phosho-dolichol synthase mannose                                           | Hypocrea jecorina    |
| GR226313    | RF      | 1   | 1.b      | XP_001246410         | 2.0E-08 | 1,3-beta-glucan synthase                                                     | Coccidioides immitis |
| GR226373    | RF      | 1   | 1.b      | XP_751328            | 2.0E-27 | endo-1,4-alpha-glucanase                                                     | Aspergillus fumigatus|
| GR226546    | RF      | 1   | 1.b      | XP_750969            | 8.0E-43 | homogentisate                                                               | Aspergillus fumigatus|
| GR226556    | RF      | 1   | 1.b      | XP_001939469         | 3.0E-83 | 1,2-dioxygenase                                                             | Pyrenophora tritici-repentis|
| GR226678    | RF      | 1   | 1.b      | XP_001939425         | 7.0E-71 | alpha-1,3-mannosyltransferase                                               | Pyrenophora tritici-repentis|
| GR227412    | RM/PF   | 2   | 1.b      | XP_961145            | 7.0E-57 | 1,4-alpha-glucan branching enzyme                                           | Neurospora crassa    |
| GR228571    | PF      | 1   | 1.c      | 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 | Fus16, 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      | AAXO7629             | 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 | cyclopanone-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                                                    | 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 | superfamily protein                                                         | 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                                                          | Botrytis fuckeliana  |
| GR227506    | PF      | 1   | 1.c      | XP_001547868         | 6.0E-24 | oleate-induced peroxisomal protein                                          | Botrytis 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   | d        | XP_001561243         | 6.0E-102| ATP phosphoribosyltransferase rRNA intron-encoded homing endonuclease       | Botryotinia fuckeliana                  |
| GR224306  | LM      | 1   | d        | AAK13589             | 1.0E-06 | GIY-YIG endonuclease adenine phosphoribosyltransferase ribonucleotide reductase small subunit RnRA inosine triphosphate pyrophosphatase (tipase) | Oryza sativa (rice)                    |
| GR224309  | LM/RM   | 7   | d        | YP_002213592         | 5.0E-12 | GIY-YIG endonuclease adenine phosphoribosyltransferase ribonucleotide reductase small subunit RnRA inosine triphosphate pyrophosphatase (tipase) | Cordyceps brongniartii                 |
| GR224460  | LM      | 1   | d        | XP_963727            | 6.0E-58 | ribonuclease (tipase)                                                      | Neurospora crassa                      |
| GR224515  | LM      | 1   | d        | XP_753417            | 1.0E-79 | DNA endonuclease I-Ceu (23S rRNA intron 1 protein)                         | Aspergillus fumigatus                 |
| GR224569  | PF/LM   | 3   | d        | XP_001273892         | 3.0E-27 | inosine triphosphate pyrophosphatase (tipase)                              | Aspergillus clavatus                  |
| GR224757  | LM      | 1   | d        | XP_754074            | 9.0E-65 | predicted nucleotide kinase                                                | Aspergillus fumigatus chloroplast      |
| GR224973  | LM/PF   | 3   | d        | P37621               | 3.0E-11 | DNA endonuclease I-Ceu (23S rRNA intron 1 protein)                         | Chlamydomonas eugametos               |
| GR225995  | RM      | 2   | d        | XP_001263831         | 3.0E-68 | phosphoribosyl-aminomimidazole-succinocarboxamide synthase                 | Neosartorya fischeri                  |
| GR226201  | RM      | 1   | d        | YP_810411            | 3.0E-11 | nucleotide/transferase                                                     | Oenococcus oeni                       |
| GR226685  | RF/PF   | 3   | d        | XP_570103            | 8.00E-60| UTP-glucose-1-phosphate uridylyltransferase                                | Cryptococcus neoformans               |
| GR226872  | PF      | 1   | d        | XP_964453            | 3.0E-133| uracil                                                                     | Verticillium albo-atum                 |
| GR228018  | RM/PF   | 2   | d        | XP_955968            | 8.0E-105| uracil                                                                     | Neurospora crassa                     |
| GR228442  | PF      | 1   | d        | XP_749865            | 9.0E-50 | s'-nucleotidase                                                            | Aspergillus fumigatus                 |
| GR224294  | LM/RM   | 2   | e        | CAD71132             | 6.0E-41 | related to DCG1 protein                                                     | Neurospora crassa                     |
| GR225213  | LM      | 1   | e        | XP_001262166         | 5.0E-43 | isoflavone reductase family protein                                        | Neosartorya fischeri                  |
| GR225487  | RM      | 1   | e        | AAL77224             | 4.0E-27 | thioredoxin II                                                            | Podospora anserina                    |
| GR225544  | RM      | 1   | e        | XP_001939670         | 4.0E-19 | glutation S-transferase                                                    | Pyrenophora tritici-repentis          |
| GR226897  | PF      | 1   | e        | P13998               | 4.0E-58 | Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase)                | Kluyveromyces lactis                  |
| GR225246  | LM      | 7   | f        | ACB56643             | 5.0E-73 | coproporphyrinogen III oxidase                                             | Trichoderma aureoviride               |
| GR226569  | RM/RF   | 4   | f        | XP_751220            | 2.0E-51 | choline sulfatase                                                           | Aspergillus fumigatus                 |
| GR227819  | PF      | 2   | f        | EDL80237             | 5.0E-07 | pantothenate kinase 2                                                      | Rattus norvegicus                     |
| GR227840  | PF      | 1   | f        | XP_001543015         | 4.0E-59 | riboflavin synthase alpha chain                                            | Ajellomyces capsulatus                |
| GR228219  | PF      | 1   | f        | XP_962504            | 3.0E-67 | ferrochelatase, mitochondrial precursor                                   | Neurospora crassa                     |
| GR224080  | LM      | 2   | d        | NP_775409            | 1.0E-32 | cytochrome oxidase subunit III                                             | Lecanicillium muscarium               |
| GR224113  | LM      | 1   | d        | EDP53376             | 2.0E-17 | FAD binding domain protein                                                 | Aspergillus fumigatus                 |
| GR224206  | LM/RM   | 2   | d        | XP_001225654         | 2.0E-106| adenylate kinase                                                           | Chaetomium globosum                   |
| GR224260  | LM      | 19  | d        | XP_386224            | 1.0E-36 | ATP9 NEUCR ATP synthase protein 9, mitochondrial precursor (Lipid-binding protein) | Gibberella zeae                     |
| GR224281  | LM      | 1   | d        | Q5K8S8              | 1.0E-14 | vacuolar ATP synthase subunit e (V-ATPase) subunit e) (Vacuolar proton pump subunit e) | Cryptococcus neoformans               |
| GR224301  | LM/RF   | 2   | d        | XP_362271            | 3.0E-28 | vacuolar ATPase                                                           | Magnaporthe grisea                    |
| GR224302  | LM      | 1   | d        | XP_001276002         | 4.0E-05 | AAA family ATPase, putative NADH-ubiquinone oxidoreductase chain 5 subunit 6 | Aspergillus clavatus                  |
| GR224359  | LM      | 1   | d        | YP_001876510         | 3.0E-77 | NADH dehydrogenase subunit 6                                              | Beauveria bassiana                    |
| GR224390  | LM      | 1   | d        | XP_965776            | 1.0E-70 | ATP synthase D chain, mitochondrial precursor                              | Neurospora crassa                     |
| GR224444  | LM      | 1   | d        | XP_965645            | 1.0E-92 | ATP synthase alpha chain, mitochondrial precursor                          | Neurospora crassa                     |
| 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 monoxygenase, putative 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 | Aspergillus fumigatus |
| GR224744 | LM/RM/RF| 3   | 2        | NP_010609            | 2.0E-06 | NADPH:adrenodoxin oxidoreductase, mitochondrial precursor | Saccharomyces cerevisiae |
| GR224745 | LM      | 1   | 2        | YP_001876504         | 2.0E-56 | NADPH:adrenodoxin oxidoreductase, mitochondrial precursor | 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 NADH dehydrogenase subunit 5 | Aspergillus clavatus |
| GR224927 | LM      | 1   | 2        | YP_001876502         | 2.0E-42 | FAD binding domain protein 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 cytochrome oxidase subunit III | Neurospora crassa |
| GR226010 | RM/LM   | 5   | 2        | YP_002213610         | 3.0E-89 | glutaredoxin 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)
| 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                                                      | Botrytis fuckeliana             |
| GR226184  | RM      | 1 2          | XP_747154            | 2.0E-61 | cytochrome P450                                                              | Aspergillus fumigatus           |
| GR226235  | RM      | 1 2          | NP_775409            | 7.0E-31 | cytochrome oxidase OrdA-like                                                | 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_001525446         | 2.0E-91 | H+ ATPase C subunit                                                        | Botrytis 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          | XP_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)                         | Gibberella zeae                 |
| 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 | 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 L4                                                    | Gibberella zeae                 |
| GR224813  | LM      | 1 3.a        | XP_001560156         | 8.0E-78 | 40S ribosomal protein S11                                                   | Botrytis fuckeliana             |
| GR224876  | LM/RF   | 4 3          | 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          | 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          | XP_387224            | 1.0E-73 | RIBOSOMAL PROTEIN S13                                                       | Gibberella zeae                 |

(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/RM| 6   | 3.a       | XP_001229209         | 2.0E-31     | 60S ribosomal protein L29                                                  | Chaetomium globosum         |
| GR225385    | LM      | 1   | 3.a       | XP_961514            | 2.0E-21     | 40S ribosomal protein S29                                                  | Neurospora crassa           |
| GR225736    | LM/RM   | 3   | 3.a       | XP_749081            | 5.0E-36     | ribonucleoprotein (LSM5)                                                   | Stachybotrys elegans        |
| 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 MR2                                     | 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/RF   | 5   | 3.a       | XP_001248452         | 2.0E-64     | 40S ribosomal protein S15                                                  | Coccidioides immitis        |
| GR226608    | LM/RM   | 4   | 3.a       | ACG48268             | 1.0E-88     | 60S ribosomal protein L9                                                   | Zea mays                    |
| GR226609    | RM/RF   | 2   | 3.a       | XP_001265242         | 2.0E-17     | 50S ribosomal protein YmL27                                                | Neosartorya fischeri        |
| GR226695    | LM/RF/RM| 4   | 3.a       | XP_0012292578        | 2.0E-58     | 60S ribosomal protein L32                                                  | Chaetomium globosum         |
| GR226126    | RM      | 1   | 3.a       | XP_963540            | 2.0E-68     | 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/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 sclerotorum     |
| GR227806    | PF      | 1   | 3.a       | NP_011731            | 9.0E-10     | mitochondrial ribosomal protein of the small subunit; Mrps17p              | 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/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/RF/PF| 20  | 3.b       | XP_746529            | 2.0E-27     | L-PSP endoribonuclease family protein                                      | Aspergillus fimigatus       |
| 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 translation initiation factor SU1                | Magnaporthe grisea          |
| GR224979    | LM/RM/PF| 7   | 3.b       | XP_754980            | 3.0E-42     | eukaryotic translation initiation factor 5                                  | Aspergillus fimigatus       |
| GR225030    | LM      | 1   | 3.b       | XP_957252            | 5.0E-37     | eukaryotic translation initiation factor                                    | Neurospora crassa           |
| GR225375    | LM/RM/PF| 6   | 3.b       | XP_001262870         | 2.0E-33     | L-PSP endoribonuclease family protein (Hmf1), putative                     | Neosartorya fischeri       |
| 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 3 subunit EifC3, 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 EifC3, 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            |
| GR224550  | LM/PF   | 4   | 3.c      | XP_001263333         | 2.0E-09 | proteasome subunit alpha type                                               | Neosartorya fischeri            |
| GR224553  | 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                                              | Aspergillus clavatus            |
| GR224415  | LM/RM/RF| 4   | 3.c      | XP_957331            | 2.0E-100| proteasome component PRE6 related to ubiquitin-conjugating enzyme           | Neurospora crassa               |
| GR224416  | LM      | 1   | 3.c      | CAE76523             | 2.0E-61 | ubiquitin-conjugating enzyme prob                                                                                             | Neurospora crassa               |
| GR224468  | LM      | 1   | 3.c      | CAD21393             | 1.0E-53 | 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-11 | 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 (Rpn), putative                      | Neurospora crassa               |
| 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 ubiquin homol                                  | Magnaporthe grisea              |
| GR225144  | LM      | 1   | 3.c      | NP_001007844         | 2.0E-19 | ubiquitin related modifier 1                                               | Gallus gallus (chicken)         |
| GR225243  | LM      | 1   | 3.c      | XP_001259989         | 4.0E-43 | dipeptidyl peptidase III                                                   | Neurospora 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                                                    | Neurospora crassa               |
| GR225783  | RM      | 1   | 3.c      | XP_001259989         | 5.0E-60 | dipeptidyl peptidase III                                                   | Neurospora fischeri             |
| GR225906  | RM      | 1   | 3.c      | XP_751155            | 1.0E-84 | proteasome regulatory particle subunit (Rpn)                                | 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      | AB30123              | 1.0E-19 | subtilisin-like protease                                                    | Epichloe festucae               |
| GR226027  | RM      | 1   | 3.c      | XP_001259989         | 2.0E-49 | dipeptidyl peptidase III                                                   | Neurospora fischeri             |
| GR226570  | RF      | 1   | 3.c      | XP_750213            | 2.0E-43 | ubiquitin-protein ligase (Hul4)                                             | Aspergillus fumigatus           |
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 ubiquitin-like activating enzyme (UlaA) | Botryotinia fuckeliana |
| GR227130 | RM/PF   | 3   | 3.c      | XP_750948            | 6.0E-64  | | 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 (Rpn1), putative | Neosartorya fischeri |
| GR228171 | PF      | 1   | 3.c      | NP_588156.1| 2.0E-53 | ubiquitin-conjugating enzyme protease inhibitor (predicted) | Coccidioides immitis |
| GR228195 | LM/RM/RF/PF | 7  | 3.c      | XP_001247866         | 2.0E-07  | ring-box 1 | Schizosaccharomyces pombe |
| GR228330 | PF/LM   | 4   | 3.c      | XP_001931304         | 1.0E-48  | proteasome regulatory particle subunit (Rpn1) | Pyrenophora tritici-repentis |
| GR228374 | PF      | 2   | 3.c      | XP_751155            | 9.0E-68  | | 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 | Neurospora crassa |
| GR224298 | LM/RM   | 2   | 3.d      | AAC49417             | 1.0E-179 | N-acetyltransferase kinase | Colletotrichum trifolii |
| GR224386 | LM      | 1   | 3.d      | XP_751767            | 3.0E-44  | geranylgeranyl transferase 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 dolichyl-phosphate mannosyltransferase polypeptide 2 | 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 dolichyl-phosphate mannosyltransferase polypeptide 3 | Aspergillus fumigatus |
| GR225078 | LM      | 1   | 3.d      | XP_001561084         | 5.0E-11  | dolichyl-phosphate mannosyltransferase polypeptide 3 | Botryotinia fuckeliana |
| 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 triiti-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 triiti-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      | 1   | 3.d      | XP_001938168         | 1.0E-48 | di-trans,poly-cis-decaprenylcistransferase ribosome biogenesis protein BRX1 | Pyrenophora triiti-repentis |
| GR226032 | RM/PF   | 4   | 3.d      | XP_956973            | 5.0E-60 | defective in culin neddylation protein 1 | Neurospora crassa |
| GR226272 | RF      | 1   | 3.d      | XP_001936409         | 1.0E-24 | mamnosylphosphate transferase (Mmm4) | Aspergillus fumigatus |
| GR226320 | RF      | 1   | 3.d      | XP_752633            | 9.0E-17 | T-complex protein 1, beta subunit | Sclerotinia sclerotiorum |
| GR226612 | RF      | 1   | 3.d      | XP_001595013         | 4.0E-79 | T-complex protein 1 subunit alpha | Neurospora crassa |
| GR226632 | RF      | 1   | 3.d      | XP_955906            | 6.0E-123| T-complex protein 1 subunit | 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 | Neurosartorya 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-RNA synthetase | Ajellomyces capsulatus |
| GR224557 | LM      | 1   | 4.a      | EDP56308             | 5.0E-58 | prolyl-RNA synthetase | Aspergillus fumigatus |
| GR224755 | LM/PF/RF| 3   | 4.a      | XP_956014            | 8.0E-48 | isoleucyl-RNA 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-RNA synthetase, mitochondrial precursor | Neurospora crassa |
| GR225058 | LM      | 1   | 4.a      | XP_956014            | 1.0E-121| isoleucyl-RNA synthetase, mitochondrial precursor | Neurospora crassa |
| GR225136 | LM/PF   | 2   | 4.a      | XP_001270015         | 1.0E-91 | tryptophanyl-RNA synthetase | Aspergillus clavatus |
| GR225703 | RM      | 1   | 4.a      | XP_001259727         | 3.0E-12 | cysteinyl-RNA synthetase | Neosartorya fischeri |
| GR225730 | RM      | 63  | 4.a      | XP_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)
| 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                                              | Pyrenophora tritici-repentis|
| 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 fumigatus       |
| 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/RP/F | 1   | 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                                                | Epichloë 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 protein required for cell viability Rrp17                | Cryptococcus neoformans     |
| GR228098  | PF      | 2   | 4.b      | XP_749086            | 6.0E-21 | small nuclear ribonucleoprotein LSM2                                      | 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 transcriptional activator hac1.                       | Cryptococcus neoformans     |
| GR224471  | LM      | 1   | 4.c      | Q8TTF3               | 1.0E-17 | retinoblastoma-binding protein                                             | Hypocreanectria jeocorina   |
| GR224483  | LM      | 1   | 4.c      | XP_001275208         | 4.0E-32 | transcription regulator NOT2 family protein                               | Aspergillus clavatus        |
| GR224484  | LM      | 1   | 4.c      | XP_001260584         | 8.0E-13 | cutinase G-box binding protein                                             | Neosartorya fischeri        |
| GR224750  | LM/PF/RF/ RM | 7 | 4.c   | AAB04132             | 1.0E-32 | CBF/NF-Y family transcription factor, putative bromodomain associated     | Nectria haematococca        |
| GR224759  | LM      | 3   | 4.c      | XP_001274352         | 3.0E-26 | CBF/NF-Y family transcription factor, putative bromodomain associated     | Aspergillus clavatus        |
| GR224803  | LM      | 1   | 4.c      | XP_001263017         | 4.0E-30 | C6 finger domain protein, putative                                         | 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     | Ajellomyces capsulatus        |
| GR225159     | LM/PF   | 2   | 4.c      | XP_001268279         | 9.0E-31 | IIA gamma chain 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      | QP98W3               | 3.0E-37 | Zinc finger transcription factor ace1 (ACEI) | Hypocrea jecorina             |
| GR225559     | RM      | 1   | 4.c      | XP_750680            | 9.0E-21 | telomere silencing protein         | 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(H)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 metallocregulatory protein | Neurospora crassa             |
| GR226374     | RF      | 1   | 4.c      | XP_754595            | 2.0E-06 | Cer4-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-17 | 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 | Cer4-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_001215000         | 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)
| Acc. No.   | Library | No. | Function       | Best match accession | E value | Description                                           | Organisms                        |
|-----------|---------|-----|----------------|-----------------------|---------|-----------------------------------------------------|----------------------------------|
| GR224419  | LM      | 6   |                | XP_653447             | 5.0E-08 | viral A-type inclusion protein repeat, putative       | Entamoeba histolytica           |
| GR224475  | LM/RF/RM| 9   |                | XP_961133             | 4.0E-157| actin                                                | Neurospora crassa               |
| GR224662  | LM      | 1   |                | XP_001262492          | 2.0E-106| nuclear envelope protein Brr6, putative              | Neosartorya fischer             |
| GR224742  | LM/RM   | 13  |                | CAC85551              | 2.0E-156| beta tubulin                                         | Cordyceps bassiana             |
| GR224838  | LM/RF/RF| 4   |                | X_P_749087            | 1.0E-37 | tropomyosin                                         | Aspergillus fumigatus           |
| GR224857  | LM      | 1   |                | CAC85618              | 2.0E-115| beta-tubulin                                        | Blumeria graminis              |
| GR225171  | LM      | 1   |                | XP_391032             | 3.0E-72 | ARP3_NEUCR actin-like protein 3                    | Gibberella zeae                |
| GR225220  | LM/RM/PF| 13  |                | XP_001931556          | 2.0E-44 | coflin                                               | Pyrenophora tritici-repentis     |
| GR225289  | LM      | 3   |                | XP_001247626          | 4.0E-67 | probable F-actin capping protein alpha subunit       | Coccidioides immitis            |
| GR225469  | RM/RF   | 7   |                | XP_001323413          | 2.0E-07 | ankyrin repeat protein                               | Trichomonas vaginalis          |
| GR225587  | RM      | 1   |                | XP_653447             | 2.0E-07 | viral A-type inclusion protein repeat, putative      | Entamoeba histolytica           |
| GR225612  | PF/RM/LM| 8   |                | P_655659              | 2.0E-71 | ARP (actin-related protein) 2/3 complex 20 kDa subunit | Neurospora crassa               |
| GR225743  | RM      | 1   |                | NP_001128241          | 1.0E-05 | actin, gamma 1                                       | Pan troglodytes                 |
| GR225921  | PF/RM   | 5   |                | P_753773              | 2.0E-28 | integral membrane protein                            | Aspergillus fumigatus           |
| GR225945  | RM      | 1   |                | XP_001075107          | 2.0E-07 | PREDICTED: similar to filaggrin 2                   | Rattus norvegicus               |
| GR225968  | RM      | 1   |                | XP_001247194          | 1.0E-120| finbrin                                              | Coccidioides immitis            |
| GR226192  | RM/RF   | 2   |                | XP_652359             | 3.0E-67 | myosin regulatory light chain cdc4                   | Neurospora crassa               |
| GR226362  | RF      | 1   |                | XP_001940723          | 2.0E-07 | integral membrane protein                            | Pyrenophora tritici-repentis     |
| GR226418  | RF      | 2   |                | CAC85551              | 1.0E-153| beta tubulin                                         | Cordyceps bassiana             |
| GR226499  | LM/RF/RM| 15  |                | ACB47222              | 2.0E-59 | microtubule-associated protein                      | Gibberella zeae                |
| GR227167  | PF      | 5   |                | CAL35988              | 2.0E-22 | myosin class II heavy chain (ISS)                    | Ostreococcus tauri              |
| GR227916  | PF      | 4   |                | XP_001323413          | 4.0E-06 | ankyrin repeat protein                               | Trichomonas vaginalis          |
| GR224502  | LM      | 1   |                | XP_754824             | 6.0E-103| cell surface spherulin 4-like protein                | Aspergillus fumigatus           |
| GR224929  | LM/PF   | 28  |                | P80544                | 5.0E-30 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR224936  | LM      | 1   |                | P80544                | 7.0E-16 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR224939  | LM      | 1   |                | P80544                | 1.0E-20 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR224948  | LM      | 1   |                | P80544                | 5.0E-15 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR224951  | LM      | 4   |                | P80544                | 2.0E-26 | surface protein SdrI                                  | Staphylococcus aureus           |
| GR224955  | LM      | 1   |                | P80544                | 1.0E-14 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR225083  | LM      | 2   |                | XP_001268510          | 4.0E-54 | extracellular proline-serine rich protein           | Aspergillus clavatus            |
| GR225184  | LM/PF   | 8   |                | CAL38822              | 7.0E-14 | surface protein 1                                    | Glomerella lindeemuthiana       |
| GR226047  | RM      | 1   |                | XP_001012930          | 1.0E-27 | von Willebrand factor type A domain containing protein | Tetrahymena theRMophila         |
| GR226110  | RM/PF/RF| 4   |                | XP_754260             | 2.0E-08 | extracellular serine-rich protein                    | Aspergillus fumigatus           |
| GR226267  | RF      | 2   |                | P80544                | 3.0E-19 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR226397  | RF      | 1   |                | P80544                | 2.0E-15 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR226680  | RF      | 1   |                | XP_001308251          | 9.0E-05 | flocculin, putative                                   | Trichomonas vaginalis          |
| GR226718  | LM/RF   | 5   |                | ABS59365              | 1.0E-14 | hydrophobin                                          | Trichoderma atrovireide         |
| GR226746  | RF      | 1   |                | P80544                | 1.0E-14 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR226864  | PF      | 1   |                | P80544                | 3.0E-23 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| GR226870  | PF      | 4   |                | P80544                | 2.0E-11 | plasmin-sensitive surface protein (cell-wall protein) | Staphylococcus aureus           |
| 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  |
| GR227535 | PF      | 1   | 5.c      | P80544               | 3.0E-21 | plasmin-sensitive surface protein (cell-wall protein)    | Staphylococcus aureus |
| GR227708 | PF      | 2   | 5.c      | P80544               | 3.0E-05 | 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| 17  | 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 translocale 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    |
| 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 | ABD17825 | 1.0E-13 | oligopeptide transporter 4 | Candida albicans |
| GR226264 | RF | 1 | 5.d | XP_001885161 | 5.0E-17 | MFS polypeptide transporter | Laccaria bicolor |
| GR226341 | RF | 1 | 5.d | AA590992 | 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-40 | small oligopeptide transporter, OPT family | Neosartorya fischeri |
| GR226482 | RF | 1 | 5.d | XP_001931051 | 2.0E-105 | mitochondrial 2-oxodicarboxylate carrier 2 | Pyrenophora triticica-repentis |
| GR226526 | RF | 1 | 5.d | XP_963201 | 1.0E-21 | amino acid permease 2 | Pyrenophora triticica-repentis |
| GR226665 | RF/LM | 3 | 5.d | XP_001540563 | 5.0E-91 | BET3 family protein | Aspergillus fumigatus |
| GR226821 | RF | 1 | 5.d | XP_001931051 | 2.0E-110 | SEC61 gamma subunit-like protein | Magnaporthe grisea |
| GR226987 | PF | 1 | 5.d | AAW69344 | 2.0E-20 | major facilitator superfamily transporter | Magnaporthe grisea |
| GR227146 | PF | 1 | 5.d | ACC64449 | 5.0E-49 | major facilitator superfamily transporter | Neosartorya fischeri |
| 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 fumigatus |
| GR227454 | RM/RF/PF | 5 | 5.d | XP_001264763 | 1.0E-72 | vesicle-mediated transport protein Vd24, 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 | Magnaporthe grisea |
| GR228329 | PF | 1 | 5.d | AAO49453 | 3.0E-79 | major facilitator superfamily transporter | Neosartorya fischeri |
| GR228514 | PF | 2 | 5.d | AAX98686 | 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 | Neosartorya fischeri |
| GR224704 | LM/RF | 2 | 5.e | XP_961277 | 3.0E-168 | AP-1 complex subunit gamma-1 | Neurospora crassa |
| GR224743 | LM/RF | 4 | 5.e | XP_001931051 | 3.0E-43 | SNARE complex subunit (Syn8) | Pyrenophora triticica-repentis |
| GR224986 | LM | 1 | 5.e | XP_001540563 | 1.0E-136 | coatomer alpha subunit | Neosartorya fischeri |
| GR225152 | LM/RF | 2 | 5.e | XP_001260516 | 3.0E-12 | AP-2 adaptor complex subunit beta, putative | Neosartorya fischeri |
| GR225156 | LM/RF | 5 | 5.e | XP_361669 | 1.0E-93 | RAS small monomeric GTPase Rab6 | Magnaporthe grisea |
| GR225162 | LM/RF | 3 | 5.e | XP_637974 | 8.0E-11 | Ran GTPase binding protein | Dictyostelium discoideum |
### Appendix Table 1. (Continued)

| Acc. No.     | Library | No. | Function | Best match accession | E value | Description | Organisms                      |
|--------------|---------|-----|----------|----------------------|---------|-------------|--------------------------------|
| GR225235     | LM      | 1   |          | O94111               | 6.0E-37 | dynein light chain, cytoplasmic (8 kDa cytoplasmic dynein light chain) | Emericella nidulans |
| GR225302     | LM      | 1   |          | BAF36375             | 2.0E-29 | v-SNARE      | Aspergillus oryzae             |
| GR225314     | LM      | 1   |          | XP_959517            | 7.0E-71 | exportin-1   | Neurospora crassa              |
| GR225338     | LM      | 1   |          | EDU42664             | 2.0E-43 | chloride channel protein 3 | Pyrenophora tritici-repentis   |
| GR225425     | RM      | 1   |          | XP_001208943         | 2.0E-142| coatomer alpha subunit | Aspergillus terreus            |
| GR225435     | RM/RM/RM/RF/PF | 19 |          | XP_001538550         | 7.0E-44 | nuclear transport factor 2 | Botryotinia fuckeliana         |
| GR225445     | RM      | 1   |          | XP_753522            | 4.0E-25 | COP1-coated vesicle protein | Aspergillus fumigatus          |
| GR225518     | RM      | 1   |          | AAC184188            | 2.0E-125| coatomer alpha subunit | Aspergillus nidulans           |
| GR225533     | RM      | 1   |          | XP_001933231         | 5.0E-56 | clathrin light chain | Pyrenophora tritici-repentis   |
| GR225542     | RM      | 1   |          | XP_001246273         | 2.0E-85 | trafficking protein particle complex subunit 2, putative rab GDP-dissociation inhibitor | Neurospora crassa |
| GR225640     | RM/PF   | 5   |          | XP_957338            | 3.0E-83 | Golgi membrane protein (Rer1) | Neurospora crassa |
| GR225808     | RM      | 1   |          | XP_001592488         | 4.0E-81 | endosomal P24B protein | Sclerotinia sclerotiorum       |
| GR225949     | RM      | 1   |          | XP_369779            | 2.0E-14 | ER membrane protein channel protein (Wsc4) | Aspergillus fumigatus |
| GR226104     | RM      | 1   |          | Q5YCW8               | 1.0E-54 | chitin synthase export chaperone | Fusarium oxysporum |
| GR226113     | RM      | 1   |          | XP_001494104         | 3.0E-75 | coatomer zeta subunit | Botryotinia fuckeliana |
| GR226165     | PF/RM/LM | 4  |          | XP_748017            | 4.0E-78 | endosomal cargo receptor (Erp3) | Aspergillus fumigatus |
| GR226171     | RM      | 1   |          | XP_754900            | 4.0E-06 | plasma membrane channel protein (Aqy1) | Aspergillus fumigatus |
| GR226251     | RM      | 1   |          | XP_756483            | 1.0E-52 | ER membrane protein (Wsc4) | Aspergillus fumigatus |
| GR226342     | RF      | 1   |          | XP_386822            | 2.0E-89 | SAR1_TRIRE GTP-binding protein SAR1 | Gibberella zeae |
| GR226713     | RF/PF   | 3   |          | XP_001260746         | 1.0E-98 | vesicular-fusion protein sec17 | Neosartorya fischeri |
| GR226937     | RM/PF   | 2   |          | XP_001440147         | 8.0E-71 | AP-2 complex subunit sigma | Pyrenophora tritici-repentis |
| GR227029     | PF      | 1   |          | XP_001545795         | 3.0E-07 | sorting nexin-like protein | Botryotinia fuckeliana |
| GR227141     | PF      | 2   |          | XP_961017            | 3.0E-61 | protein yop-1 (YIP1 partner precursor) | Neurospora crassa |
| GR227221     | PF      | 1   |          | XP_001541792         | 1.0E-15 | mitochondrial intermembrane space translocase subunit | Ajellomyces capsulatus |
| GR227407     | RM/PF   | 2   |          | CAD36979             | 1.0E-84 | related to the member of the syntaxin family of t-SNAREs TLG2 | Neurospora crassa |
| GR227481     | PF      | 1   |          | XP_001273433         | 4.0E-94 | mRNA transport regulator (Mtr10), putative | Aspergillus clavatus |
| GR227767     | PF      | 2   |          | XP_956972            | 5.0E-92 | GTP-binding protein ypt3 | Neurospora crassa |
| GR227949     | RF/PF   | 3   |          | XP_750622            | 2.0E-53 | endosomal cargo receptor (Erv1) | Aspergillus fumigatus |
| GR228326     | RM/PF   | 2   |          | CAC28785             | 3.0E-112| probable gamma-adaptin precursor | Neurospora crassa |
| GR228590     | PF      | 1   |          | XP_752998            | 2.0E-74 | vacuolar protein sorting-associated protein Vps28 | Aspergillus fumigatus |
| GR224089     | LM      | 1   |          | AAP92916             | 3.0E-25 | putative serine/threonine phosphatase 2C ptc2 | Hypocrea fectoria |

(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 (Gtr2) | Neosartorya fischeri |
| GR224368 | LM      | 1   | 5.f      | XP_753016            | 3.0E-61  | small monomeric GTPase | 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 | Hypocrea jecorina |
| GR224712 | LM/PM   | 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  | Rho small monomeric GTPase RhoA | Aspergillus clavatus |
| GR225229 | LM/RM   | 2   | 5.f      | XP_001932161         | 2.0E-41  | AhpC/TSA family protein related to dock180 protein | Pyrenophora tritici-repentis |
| GR225255 | LM      | 2   | 5.f      | CAE75725             | 4.0E-84  | 16 kDa allergen | Neurospora crassa |
| GR225263 | LM/RM/PF| 17  | 5.f      | ABP04053             | 7.0E-41  | phosphoinositide phosphatase (Sac1), putative | Penicillium chrysogenum |
| GR225308 | LM      | 1   | 5.f      | XP_001271698         | 3.0E-58  | related to dock180 protein | Aspergillus clavatus |
| GR225318 | LM      | 2   | 5.f      | YP_612174            | 3.0E-13  | metabolic phospholipid phosphodiesterase | 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 | 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      | AAR90465             | 1.0E-05  | serine/threonine kinase | Leptosphaeria maculans |
| GR225767 | RM      | 1   | 5.f      | XP_001549877         | 1.0E-16  | septum-promoting GTP-binding protein | Botrytis cinerea |
| 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 neofoRman |
| 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_001271026         | 2.0E-84  | GTPase activating protein | 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   | 8   | 5.f      | XP_001267009         | 8.0E-77  | calcineurin subunit B (protein phosphatase 2B regulatory subunit) (calcineurin regulatory subunit) | 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 guanylate 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)
| 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-09 | 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 subunit 2 | Trichomonas vaginalis |
| GR226948 | PF | 1 | 5.f | XP_965733 | 1.0E-05 | COP9 signalosome complex | 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 | Neurosartorya 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 | regulatory B subunit | Neurospora crassa |
| GR228196 | PF | 1 | 5.f | EDP51958 | 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 | Coniopteris acuta |
| 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 flocosum |
| GR224812 | LM | 1 | 6.d | XP_752563 | 4.0E-58 | mitochondrial dynamin GTPase (Msp1) | Aspergillus fumigatus |
| Acc. No.       | Library No. | Function No. | 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.d                  | 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 antispheae        |
| GR224629      | LM          | 1            | 7.e                  | AAL77224  | 3.0E-27 thioredoxin II                          | Podospora anserina            |
| GR224634      | LM          | 1            | 7.e                  | CAC28808  | 2.0E-117 related to tetracycline efflux protein  | 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      |
| GR22503      | LM          | 3            | 7.a                  | XP_001225918 | 2.0E-11 heat shock 70 kDa protein                | Chaetomium globosum           |
| GR225138      | LM/PF       | 4            | 7.a                  | CAK54362  | 2.0E-39 rapamycin binding protein FKB12          | 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/LM/RM    | 13           | 7.a                  | XP_001931291 | 3.0E-41 DnaJ domain protein Psi                  | Pyrenophora tritici-repensis  |
| 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 reinharditii    |
| 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                  | Trichoderma atroviride        |
| GR226504      | RF          | 1            | 7.a                  | XP_753264  | 4.0E-30 Hsp90 binding co-chaperone (Sba1)        | Aspergillus fumigatus         |
| GR226819      | PF          | 2            | 7.a                  | XP_203356  | 2.0E-07 orf261 (related to DNA repair)           | Mortierella verticillata      |
| GR227936      | RM/PF       | 2            | 7.a                  | XP_959180  | 9.0E-125 Amphilphys-like, reduced viability upon starvation protein rvs167p | Neurospora crassa             |
| GR227939      | PF          | 1            | 7.a                  | XP_001266719 | 3.0E-42 unfolded protein response                | Neosartorya fischeri          |
| GR228520      | PF/RM       | 2            | 7.a                  | XP_001481437 | 2.0E-34 Hsp70 family chaperone                   | Aspergillus fumigatus         |
| GR228692      | 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_00378594 | 6.0E-110 catalase/peroxidase HPI                 | Burkholderia abonensis Bu     |
| GR223094      | LM/PF       | 3            | 7.c                  | ABE97921  | 4.0E-05 snodprot2                                | Hypocrea virens               |
| GR228625      | PF          | 1            | 7.c                  | XP_001269050 | 3.0E-12 transposase                             | Aspergillus clavatus          |
| GR226603      | RF          | 1            | 8                    | CAB56797  | 5.0E-39 equisetin synthetase, putative           | Magnaporthe grisea            |
| GR242079      | LM          | 1            | 9                    | Unknown   | Unknown                                         |                                 |
| GR242083      | LM          | 1            | 9                    | Unknown   | Unknown                                         |                                 |
| GR242106      | LM          | 2            | 9                    | Unknown   | Unknown                                         |                                 |
| GR242110      | LM          | 1            | 9                    | Unknown   | Unknown                                         |                                 |
| GR242112      | LM          | 1            | 9                    | Unknown   | Unknown                                         |                                 |
| GR224117      | LM/RM       | 2            | 9                    | XP_381543  | 1.0E-38 hypothetical protein FG01367.1           | Gibberella zeae               |

(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 | *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 | *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 | 9        | XP_001799364         | 2.0E-11 | hypothetical protein | *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* |
| 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* |
| GR224312 | LM      | 24  | 9        | XP_001622255         | 6.6E-02 | predicted protein | *Nematostella vectensis* |
| GR224314 | LM/PF/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 | *Phaeosphaeria nodorum* |
| GR224340 | LM      | 1   | 9        | unknown              |         |             |           |
| GR224346 | LM      | 1   | 9        | unknown              |         |             |           |
| GR224357 | LM      | 1   | 9        | XP_001396793         | 3.0E-18 | hypothetical protein | *An15g02550* |
| 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* |
| 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* |
| 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)
| 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 | *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 | *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 | *Chaetomium globosum* |
| GR224603 | LM | 1 | 9 | XP_383837 | 6.0E-09 | hypothetical protein | *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 | *Chaetomium globosum* |
| GR224678 | LM | 1 | 9 | XP_389536 | 8.0E-05 | hypothetical protein | *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 | *Gibberella zeae* |
| GR224705 | LM | 1 | 9 | XP_390143 | 2.0E-26 | hypothetical protein | *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 | *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 | *Gibberella zeae* |
| Acc. No. | Library | No. | Function | Best match accession | E value | Description | Organisms |
|---------|---------|-----|----------|----------------------|---------|-------------|-----------|
| GR224765 | LM | 1 | 9 | XP_001393559 | 5.0E-35 | hypothetical protein | Aspergillus niger |
| GR224768 | LM | 1 | 9 | | | unknown | |
| GR224771 | LM | 1 | 9 | | | unknown | |
| GR224776 | LM | 1 | 9 | XP_001223919 | 6.0E-06 | hypothetical protein | 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 | 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 | 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 | 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 | Gibberella zeae |
| GR224854 | LM | 1 | 9 | XP_388916 | 5.0E-94 | hypothetical protein | 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 | 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 | Gibberella zeae |
| GR224922 | LM | 1 | 9 | XP_388050 | 7.0E-46 | hypothetical protein | Gibberella zeae |
| GR224926 | LM | 1 | 9 | | | unknown | Phaeosphaeria nodorum |
| GR224930 | LM | 2 | 9 | XP_001804800 | 1.0E-09 | hypothetical protein | SNOG_14618 |
| 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 | 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/RF/PF| 4   | 9        | XP_387218            | 2.0E-31     | hypothetical protein             | Gibberella zeae        |
| GR225088     | LM      | 1   | 9        |                      |             | XP_958054                       | Neurospora crassa      |
| GR225092     | LM      | 1   | 9        | XP_384167            | 1.0E-05     | hypothetical protein             | FG03991.1              |
| GR225108     | LM/RM   | 39  | 9        |                      |             | unknown                          |                         |
| GR225113     | LM      | 1   | 9        |                      |             | unknown                          |                         |
| GR225140     | LM/RM   | 2   | 9        | XP_389939            | 4.0E-11     | hypothetical protein             | FG09763.1              |
| GR225143     | LM/RM/PF| 6   | 9        | XP_387641            | 6.0E-13     | hypothetical protein             | FG07465.1              |
| GR225145     | LM/RM   | 2   | 9        |                      |             | unknown                          |                         |
| GR225166     | LM      | 1   | 9        |                      |             | unknown                          | Chaetomium globosum    |
| GR225170     | LM      | 1   | 9        |                      |             | unknown                          |                         |
| GR225175     | 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              |
| 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              |
| GR225284     | LM      | 1   | 9        |                      |             | unknown                          | Neurospora crassa      |
| GR225294     | LM      | 3   | 9        |                      |             | unknown                          |                         |
| GR225296     | LM      | 1   | 9        | XP_958921            | 2.0E-07     | hypothetical protein             | FG01945.1              |
| GR225317     | LM      | 1   | 9        | XP_001399016         | 2.0E-14     | hypothetical protein             | Aspergillus niger      |
| GR225322     | LM/RM   | 4   | 9        |                      |             | unknown                          |                         |
| GR225332     | LM      | 1   | 9        | XP_389764            | 8.0E-43     | hypothetical protein             | FG09588.1              |
| GR225335     | LM/RF/RM| 3   | 9        | XP_389727            | 2.0E-14     | hypothetical protein             | FG09551.1              |
| GR225347     | LM      | 2   | 9        | XP_387617            | 2.0E-36     | hypothetical protein             | FG07441.1              |
| GR225359     | LM      | 1   | 9        |                      |             | unknown                          | Laccaria bicolor       |
| GR225366     | LM      | 1   | 9        | XP_001876904         | 4.0E-14     | small secreted protein           |                         |

(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                      | Sclerotinia sclerotiorum     |
| GR225421| RM      | 1   | 9        | XP_001586820         | 2.0E-10 | predicted protein            |                              |
| 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         | Magnaporthe grisea           |
| GR225462| LM/RM/RF| 5  | 9        |                      |         | unknown                      |                              |
| GR225463| RM      | 1   | 9        | XP_001390130         | 1.0E-10 | hypothetical protein         | 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         | 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         | 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         | Gibberella zeae             |
| GR225564| RM      | 1   | 9        |                      |         | unknown                      |                              |
| GR225567| RM      | 1   | 9        | XP_001228381         | 9.0E-55 | hypothetical protein         | 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         | Gibberella zeae             |
| GR225595| RM/RF   | 2  | 9        | XP_389588            | 5.0E-27 | hypothetical protein         | Gibberella zeae             |
| GR225606| RM      | 1   | 9        |                      |         | unknown                      |                              |
| GR225611| RM      | 1   | 9        | XP_001522653         | 7.0E-65 | hypothetical protein         | 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            | *Gibberella zeae*        |
| GR225718    | RM      | 1   | 9        | XP_390946            | 6.0E-26     | hypothetical protein            | *Gibberella zeae*        |
| GR225722    | RM      | 1   | 9        | XP_385533            | 7.0E-49     | hypothetical protein            | *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            | *Chaetomium globosum*    |
| GR225755    | RM      | 1   | 9        | unknown              |             |                                 |                          |
| GR225757    | RM      | 1   | 9        | unknown              |             |                                 |                          |
| GR225764    | RM      | 1   | 9        | XP_386345            | 9.0E-14     | hypothetical protein            | *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            | *Botryotinia fuckeliana*  |
| GR225812    | RM      | 1   | 9        | XP_383092            | 2.0E-13     | hypothetical protein            | *Gibberella zeae*        |
| GR225815    | RM      | 1   | 9        | unknown              |             |                                 |                          |
| GR225822    | RM      | 1   | 9        | XP_001225652         | 2.0E-14     | hypothetical protein            | *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            | *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            | *Gibberella zeae*        |
| GR225900    | RM      | 1   | 9        | unknown              |             |                                 |                          |
| GR225905    | RM      | 2   | 9        | unknown              |             |                                 |                          |
| GR225911    | RM      | 1   | 9        | XP_387324            | 8.0E-35     | hypothetical protein            | *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            | *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            | *Gibberella zeae*        |
| GR225964    | RM      | 2   | 9        | unknown              |             |                                 |                          |
| GR225965    | RM      | 1   | 9        | unknown              |             |                                 |                          |
| GR225967    | RM      | 1   | 9        | unknown              |             |                                 |                          |
### Appendix Table 1. (Continued)

| Acc. No. | Library | No. | Function | Best match accession | E value | Description | Organisms               |
|----------|---------|-----|----------|----------------------|---------|-------------|-------------------------|
| GR225969 | RM      | 1   | 9        |                      |         |             |                         |
| GR225989 | RM      | 1   | 9        | XP_390839            | 1.0E-16 | hypothetical protein FG10663.1 | Gibberella zeae |
| GR225994 | RM      | 1   | 9        |                      |         |             |                         |
| GR225998 | RM      | 1   | 9        |                      |         |             |                         |
| GR226016 | RM      | 1   | 9        |                      |         |             |                         |
| GR226031 | RM      | 1   | 9        |                      |         |             |                         |
| GR226033 | RM      | 1   | 9        | XP_001226459         | 1.0E-12 | predicted protein Chaetomium globosum | Gibberella zeae |
| 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        |                      |         |             |                         |
| GR226049 | RM      | 1   | 9        |                      |         |             |                         |
| GR226065 | RM      | 1   | 9        |                      |         |             |                         |
| 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        |                      |         |             |                         |
| 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 | Gibberella zeae |
| 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        |                      |         |             |                         |
| GR226099 | RM      | 1   | 9        |                      |         |             |                         |
| GR226109 | LM/RM   | 3   | 9        |                      |         |             |                         |
| GR226118 | RM      | 1   | 9        | XP_001208562         | 8.0E-38 | predicted protein Aspergillus terreus | Gibberella zeae |
| GR226119 | RM      | 1   | 9        |                      |         |             |                         |
| GR226133 | RM      | 1   | 9        |                      |         |             |                         |
| GR226141 | RM      | 1   | 9        |                      |         |             |                         |
| GR226148 | RM      | 1   | 9        |                      |         |             |                         |
| GR226157 | RM      | 1   | 9        |                      |         |             |                         |
| GR226164 | RM      | 2   | 9        |                      |         |             |                         |
| GR226176 | LM/RM   | 3   | 9        |                      |         |             |                         |
| GR226191 | RM      | 1   | 9        |                      |         |             |                         |
| GR226193 | RM      | 1   | 9        |                      |         |             |                         |
| GR226196 | RM      | 1   | 9        |                      |         |             |                         |
| GR226206 | RM      | 1   | 9        |                      |         |             |                         |
| GR226207 | RM      | 1   | 9        | XP_388958            | 8.0E-02 | hypothetical protein FG08782.1 | Gibberella zeae |
| GR226211 | RM      | 4   | 9        |                      |         |             |                         |
| GR226222 | RM      | 1   | 9        |                      |         |             |                         |
| 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 | Gibberella zeae |
| 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        |                      |         |             |                         |
| GR226249 | RM      | 2   | 9        |                      |         |             |                         |
| GR226252 | RM/PF   | 3   | 9        |                      |         |             |                         |
| GR226257 | RF      | 3   | 9        |                      |         |             |                         |
| GR226261 | RF      | 1   | 9        | XP_381202            | 8.0E-12 | hypothetical protein FG01026.1 | Gibberella zeae |
| GR226274 | RF      | 1   | 9        |                      |         |             |                         |
| GR226286 | RF      | 2   | 9        |                      |         |             |                         |
| GR226288 | RF      | 1   | 9        | XP_001550658         | 7.0E-09 | hypothetical protein BC1G_11066 | Botryotinia fuckeliana |
| GR226296 | RF      | 1   | 9        |                      |         |             |                         |
| Acc. No.   | Library | No. | Function | Best match accession | $E$ value | Description                | Organisms                        |
|-----------|---------|-----|----------|----------------------|-----------|---------------------------|----------------------------------|
| GR226302  | RF      | 3   | 9        | XP_384459            | 3.0E-19   | hypothetical protein       | Gibberella zeae                 |
| GR226303  | PF/RF/RM| 9   | 9        | XP_001937997         | 3.0E-21   | hypothetical protein       | Pyrenophora tritici-repentis     |
| GR226309  | RF      | 1   | 9        | XP_001227232         | 7.0E-29   | hypothetical protein       | 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       | 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       | Aspergillus niger               |
| GR226359  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| GR226367  | RF      | 1   | 9        | XP_381530            | 3.0E-10   | hypothetical protein       | 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       | 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       | 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       | 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       | 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       | Aspergillus niger               |
| GR226489  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| GR226490  | RF      | 1   | 9        | XP_386314            | 9.0E-11   | hypothetical protein       | Gibberella zeae                 |
| GR226506  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| GR226508  | LM/RM/RF/PF | 9 | 9 | unknown |           |           |                           | Aspergillus fumigatus           |
| GR226521  | RF      | 1   | 9        | EDP55205             | 5.0E-05   | PT repeat family protein   |                                  |
| GR226522  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| GR226528  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| GR226537  | RF      | 1   | 9        | unknown              |           |                           |                                  |
| Acc. No.  | Library | No. | Function | Best match accession | E value | Description                  | Organisms               |
|-----------|---------|-----|----------|----------------------|---------|------------------------------|-------------------------|
| GR226539  | RF      | 1   | 9        | unknown              |         |                              |                         |
| GR226542  | RF      | 1   | 9        | unknown              |         |                              |                         |
| GR226543  | LM/RF   | 3   | 9        | XP_381480            | 1.0E-12 | hypothetical protein          | 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 | Candida albicans       |
| GR226572  | RF      | 1   | 9        | unknown              |         |                              |                         |
| GR226573  | RF      | 1   | 9        | XP_381349            | 3.0E-08 | hypothetical protein          | Gibberella zeae         |
| GR226575  | RF      | 1   | 9        | XP_001220992         | 1.0E-72 | hypothetical protein          | 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          | 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          | 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          | 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          | Coccidioides inimitis   |
| 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          | 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          | 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          | Gibberella zeae         |
| GR226809  | PF      | 4   | 9        | unknown              |         |                              |                         |

(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* |
| GR226844 | PF | 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 | 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 | *Gibberella zeae* |
| GR226968 | PF | 1 | 9 | XP_001246219 | 2.0E-07 | hypothetical protein | *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 | *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 | *Coccidioides immitis* |
| GR227042 | PF | 1 | 9 | unknown | | | |
| GR227052 | PF | 1 | 9 | XP_387928 | 1.0E-12 | hypothetical protein | *Gibberella zeae* |
| GR227053 | PF | 2 | 9 | unknown | | | |
| GR227055 | PF | 1 | 9 | unknown | | | |
| GR227066 | PF | 2 | 9 | XP_001398639 | 2.0E-28 | hypothetical protein | *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 | *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 | *Gibberella zeae* |
| GR227128 | PF | 1 | 9 | XP_958940 | 2.0E-05 | hypothetical protein | *Neurospora crassa* |
| GR227142 | PF/RF | 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 | *Gibberella zeae* |
| GR227265 | RF/PF | 3 | 9 | XP_384636 | 1.0E-29 | hypothetical protein | *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)
| 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       | Gibberella zeae            |
| GR227362   | PF/LM   | 5   | 9        | XP_382064            |         | hypothetical protein       | 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       | Phaeosphaeria nodorum      |
| GR227427   | PF      | 6   | 9        | XP_001802763         | 3.0E-17 | hypothetical protein       | 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   | Saccharomyces cerevisiae   |
|            |         |     |          |                      |         | unknown function, Tar1p   |                            |
| 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   | 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       | 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              |         |                           |                            |
### 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       | Neurospora crassa     |
| GR227826| PF      | 1   | 9        | XP_385092            | 4.0E-05 | hypothetical protein       | Gibberella zeae       |
| GR227833| LM/RM/RF/PF | 258 | 9        | XP_001540440         | 3.0E-07 | predicted protein          | Ajellomyces capsulatus|
| GR227850| PF      | 1   | 9        | XP_386443            | 5.0E-12 | hypothetical protein       | Gibberella zeae       |
| GR227921| PF      | 1   | 9        | XP_001405811         | 2.0E-33 | predicted protein          | Magnaporthe grisea    |
| GR227924| PF      | 1   | 9        | XP_390666            | 2.0E-26 | hypothetical protein       | Gibberella zeae       |
| GR227953| PF      | 130 | 9        | XP_001228381         | 2.0E-46 | hypothetical protein       | Chaetomium globosum   |
| GR227974| PF      | 2   | 9        | XP_385566            | 1.0E-06 | hypothetical protein       | Gibberella zeae       |
| GR227998| LM/RM/PF| 35  | 9        | XP_384575            | 3.0E-06 | hypothetical protein       | Gibberella zeae       |
| GR228021| PF      | 1   | 9        | XP_388280            | 1.0E-29 | hypothetical protein       | Gibberella zeae       |
| GR228048| PF      | 1   | 9        | XP_391772            | 7.0E-83 | hypothetical protein       | Gibberella zeae       |
| GR228055| PF      | 1   | 9        | XP_001911209         | 4.0E-53 | unnamed protein product    | Podospora anserina    |
| GR228072| PF      | 1   | 9        | XP_390382            | 1.0E-10 | hypothetical protein       | Gibberella zeae       |
| GR228105| PF      | 2   | 9        | XP_001405719         | 1.0E-07 | predicted protein          | Magnaporthe grisea    |
| GR228106| PF      | 1   | 9        | XP_385531            | 1.0E-44 | hypothetical protein       | Gibberella zeae       |
| GR228153| PF      | 1   | 9        | XP_001274870         | 3.0E-53 | conserved hypothetical protein | Aspergillus clavatus |
| Acc. No.   | Library | No. Function | accession | E value | Description | Organisms                  |
|-----------|---------|--------------|-----------|---------|-------------|----------------------------|
| GR228207  | PF      | 1 9          |           |         | access        |                            |
| 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* |
| GR228333  | PF      | 2 9          | XP_662849 | 8.0E-24 | hypothetical protein AN5245.2 | *Aspergillus nidulans* |
| GR228336  | PF      | 1 9          | XP_388966 | 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 | *Botrytina 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          | Q8J0N0    | 3.0E-15 | UPF0357 protein YCL012C precursor | *Saccharomyces paradoxus* |
| GR228449  | PF      | 1 9          |           |         | unknown      |                            |
| GR228478  | PF      | 1 9          |           |         | unknown      |                            |
| GR228483  | RM/PF   | 2 9          |           |         | unknown      |                            |
| GR228484  | PF      | 1 9          | XP_001547986 | 4.0E-32 | hypothetical protein BC1G_13677 | *Botrytina fuckeliana* |
| GR228491  | PF      | 5 9          | XP_387617 | 3.0E-48 | hypothetical protein FG0744.1 | *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* |

(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              |         | unknown      |           |
| GR228615 | PF      | 1   | 9        | unknown              |         | unknown      |           |
| GR228623 | PF      | 5   | 9        | XP_001804800         | 3.0E-16 | hypothetical protein SNOG_14618 | *Phaeosphaeria nodorum* |
| GR228628 | PF      | 1   | 9        | XP_001586480         | 2.0E-32 | hypothetical protein SS1G_12466 | *Sclerotinia sclerotiorum* |
| GR228644 | PF      | 2   | 9        | XP_001598271         | 9.0E-06 | hypothetical protein SS1G_00357 | *Sclerotinia sclerotiorum* |
| GR228654 | PF      | 2   | 9        | unknown              |         | unknown      |           |
| GR228666 | PF      | 1   | 9        | unknown              |         | unknown      |           |