An investigation of the role of CreB deubiquitinating enzyme in the regulation of carbon metabolism in Aspergillus nidulans

By

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Chapter 1: Introduction and Literature Review

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Thesis Abstract

In *A. nidulans*, carbon catabolite repression is regulated by the global repressor protein CreA which, in the presence of repressing carbon sources, represses those genes that are required to utilize less preferable carbon sources. Mutational analyses suggested that ubiquitination, mediated by CreD together with ubiquitin ligase HulA, and deubiquitination, mediated by the deubiquitinating enzyme CreB, are involved in the regulatory pathway in *A. nidulans*. However, the molecular mechanisms are still unknown.

Previously, partial loss-of-function alleles of *creA* and *creB* indicated genetic interaction, and this was extended to analysis of complete loss-of-function alleles. Both morphological and phenotypic analyses of the double null mutant confirmed genetic interactions between the genes. Moreover, RT-qPCR and enzyme assays also validated genetic interactions as the double null mutant showed synergistic effects for transcript levels and enzyme activity. Co-purifications of CreA and CreB expressed from their native promoters were used to determine whether CreA, or a protein in a complex with it, is a direct target of the CreB deubiquitinating enzyme, and no direct or indirect physical interactions were identified. The Phos-tag system was used to show that CreA is a phosphorylated protein, but no ubiquitination was detected using anti-ubiquitin antibodies and Western analysis. These findings were confirmed using mass spectrometry, which confirmed that CreA was differentially phosphorylated but not ubiquitinated. These results open up new questions regarding the molecular mechanism of CreA action, and how the ubiquitinating pathway involving CreB interacts with this regulatory network.

To identify any possible protein(s) that may form a bridge between CreA and CreB, independently purified lysates were analysed by mass spectrometry and, for both CreA and CreB, proteins were identified in repressing and derepressing conditions. Orthologues of the co-purified proteins were identified in *S. cerevisiae* and humans. Functional annotation analysis revealed that proteins that preferentially interact with CreA in repressing conditions include histones and the histone transcription regulator 3, Hir3. Proteins interacting with CreB were involved in cellular transportation and organization. Similar findings were obtained using yeast and human orthologues, although the yeast background generated a number of other biological processes involving Mig1p which were not present in the *A. nidulans* or human background analyses. Hir3 was present in repressing conditions for CreA, and in both growth conditions for CreB, suggesting that Hir3, or proteins interacting with Hir3, could be a possible target of CreB.

Earlier, genome-wide microarray analysis showed that CreA was involved in the transcriptional regulation of a significant number of genes in *A. nidulans*, however, this approach cannot show whether the targets are directly or indirectly regulated. To identify the direct targets, and whether CreA binds in derepressing conditions, ChIP-seq analyses were performed. CreA constitutively bound to the promoters of target genes in both growth conditions, indicating that the function of CreA may be controlled on the chromatin by post-translational modifications. A total of 1946 unique targets were identified for both strains in repressing and derepressing conditions including genes that are involved in carbohydrate metabolic/catabolic processes, alcohol biosynthetic processes, secondary metabolism, and sugar and amino acid transporters.

Declaration

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List of Publications

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Chapter 1

1. Introduction and Literature Review

1.1 Introduction

Eukaryote microorganisms have a complex physiology and metabolism similar to plants and animals and derive their energy from a variety of different substrates. Using this energy, they synthesize DNA, RNA, proteins, polysaccharides, vitamins and other metabolites which are essential for their survival. They show great metabolic diversity and adaptation to different environmental conditions by producing enzymes which are required for the utilization of preferred nutrient sources and by preventing the production of other enzymes which are needed to utilize less preferred nutrient sources. This kind of cellular management is beneficial for microorganisms. Firstly, the most favorable carbon sources have been used. Secondly, no wastage of energy has occurred. Microorganisms have achieved this metabolic optimization by exerting control at the level of transcription. The regulatory machinery activates and/or represses the target gene(s) depending on the stimuli or substrates. In the presence of a favorable carbon source, microorganisms express genes to utilize that preferred carbon source and simultaneously, repress genes that are needed to utilize less favorable carbon sources and save energy. This phenomenon is known as carbon catabolite repression (CCR).

Regulation of gene expression is a fundamental aspect of biology- it is what makes a nerve cell different from a white blood cell. CCR is used here as a model to understand the regulation of gene expression. CCR is present in both prokaryotic and eukaryotic organisms. In *E. coli*, transcriptional regulation of the ‘lac operon’ system has been extensively studied at the genetic, biochemical and molecular levels to understand induction and CCR in this prokaryotic organism. Many studies have been performed to elicit the CCR mechanism in eukaryotes, mainly in the unicellular yeast *Saccharomyces cerevisiae*, where a large number of genes have been found that are involved in the repression and derepression mechanisms (Gancedo 1998, Klein, et al. 1998). However, *S. cerevisiae* is strongly adapted for single-celled fermentation of sugar-rich media to ethanol, whereas many filamentous fungi can utilize a wide range of complex carbon sources in aerobic growth (Kelly 2004). Among the filamentous fungi, *Aspergillus nidulans* has been used as a model organism to understand CCR in multicellular eukaryotes. Industrial fungi including *Trichoderma reesei*, *Aspergillus oryzae* and *Sclerotinia sclerotiorum* have also been studied for a better understanding of CCR, as such studies are useful in an industrial context.

Studies of this global regulatory gene expression provide information which has a variety of applications in different fields including medicine, biotechnology, food industry and pharmaceuticals. A careful consideration of growth condition, use of favorable nutrients, strain selection, selected promoters for high gene expression, protein fusions and heterologous protein stabilization can lead to the optimized expression of many important enzymes (Agger, et al. 2002).

1.2 Carbon Catabolite Repression (CCR) Carbon catabolite repression (CCR), one of the global regulatory mechanisms where a very large number of genes can be regulated simultaneously with major changes in the environment, is a process ensuring energetically favorable carbon sources are utilized preferentially over the less readily metabolized carbon sources by reducing synthesis of enzymes that are required for the utilization of less favorable sources in the presence of the preferred sources. This is also known as “glucose repression”, however, xylose, sucrose and acetate are also strong repressing carbon sources whereas mannose, maltose, fructose, mannitol and galactose result in intermediate levels of repression and glycerol, melibiose, lactose, arabinose and ethanol result in weak or no CCR (Ruijter and Visser 1997). The degree of repression in particular carbon sources can vary in different species or even different strains of the same species (Kelly and Katz 2010). In yeast, genomic expression analysis revealed that many genes are differentially transcribed in response to varying glucose levels (DeRisi, et al. 1997). Glucose leads to the induction of some genes such as those encoding low-affinity glucose transporters, glycolytic enzymes and ribosomal proteins, while many genes are repressed in glucose media such as genes involved in the utilization of alternate carbon sources, gluconeogenesis, respiration and peroxisomal functions (Carlson 1999). Different elements of CCR in *S. cerevisiae* and *A. nidulans* as well as other filamentous fungi are discussed below.

1.3 Carbon Catabolite Repression in *Saccharomyces cerevisiae*

S. cerevisiae is a unicellular yeast and has been studied intensively as a eukaryotic model organism to investigate CCR using molecular and cell biology techniques. Like other microorganisms, *S. cerevisiae* can adapt its metabolism by optimizing the utilization of available carbon sources in the environment. Though glucose or fructose is the preferred carbon source, a range of other carbon sources can also be used. In *S. cerevisiae,* CCR acts at a transcriptional level, as in the presence of glucose, mRNA levels are reduced for the genes which are subject to repression (Carlson and Botstein

1982). Many proteins play vital roles in this regulatory pathway and are discussed below [Figure 1.1: CCR mechanisms and proteins involved in the CCR network of *S. cerevisiae* (Rolland, et al. 2002).

1.3.1 Mig1p & Other Repressors

The *MIG1* gene was first identified as a multi-copy inhibitor of the *GAL1* promoter in derepressing conditions (Nehlin and Ronne 1990). It was also isolated as an extragenic suppressor of *snf1* and *snf4* mutations (Schuller and Entian 1991). Mutations in the *MIG1* gene resulted in relief of repression in some systems which are normally subject to repression in the presence of wild-type copy of *MIG1*, indicating that *MIG1* is involved in the negative regulation of glucose repression (Hu, et al. 1995, Lundin, et al. 1994, Nehlin and Ronne 1990). Mig1p, encoded by *MIG1*, is a negatively acting DNA binding protein with two Cys$_2$-His$_2$ zinc fingers regions (Nehlin and Ronne 1990). DNaseI footprinting analysis showed that Mig1p can bind to the promoter of genes including *SUC2*, *GAL1*, *GAL4*, and *FBP1* (Mercado, et al. 1991, Nehlin, et al. 1991). Mig1p binds at the consensus sequence (G/C)(C/T)GGGG and an AT rich region 5' to the GC box. The AT rich regions are required for the stabilization of DNA-protein interaction by facilitating DNA bending (Lundin, et al. 1994). In the presence of high glucose concentration, LexA-Mig1 fusion protein can repress a reporter gene with several Lex operators in yeast, however, the repression is reduced when the glucose concentration is lowered and disappears in the presence of galactose (Treitel and Carlson 1995, Tzamarias and Struhl 1994). LexA, a bacterial repressor protein, can be used as an assay for repression when the operator sequence of LexA is inserted between the UAS and the TATA box protein (Smith, et al. 1988). This result suggested that derepression was a separate process from DNA binding. Deletion mapping analysis revealed that the C terminal 24 amino acids of Mig1p are sufficient for the repression activity of the protein when fused with the DNA binding domain. Two other internal functional domains (R1 & R2) have been identified which are required for the inhibition of Mig1p activity in the absence of glucose. Furthermore, a basic domain N-terminal to the zinc fingers could also be involved in targeting Mig1p to the nucleus (Ostling, et al. 1996). The function of Mig1p is regulated by glucose concentration through affecting its phosphorylation state catalyzed by the Snf1p kinase. Phosphorylation alters the subcellular localization of Mig1p which shuttles between the nucleus and cytoplasm (DeVit, et al. 1997, Treitel and Carlson 1995). Western analysis showed that Mig1p is readily phosphorylated by Snf1p and deletion of *SNF1* resulted in dephosphorylated

Mig1p with nuclear localization upon glucose depletion while transcription of glucose regulated promoters was constitutively repressed (Carlson 1999, Treitel, et al. 1998). Moreover, four phosphorylation sites were identified within the region of Mig1p required for glucose repression and *in vitro* analysis revealed that all four sites (Ser 222,278,311,381) were phosphorylated by Snf1p kinase, with sequences around the latter three sites having similarity with the consensus recognition motif for Snf1p (Smith, et al. 1999). Mig1p is located in the nucleus in the presence of glucose as the dephosphorylated form and in the cytoplasm as the phosphorylated form when glucose is absent. The subcellular localization of Mig1p is mediated by Snf1p protein kinase and the nuclear transport receptor Msn5p, a member of the β-importin family. Deletion of the *MSN5* gene allows normal phosphorylation of Mig1p but abolishes nuclear transport (DeVit and Johnston 1999, DeVit, et al. 1997). Mig1p recruits a general co-repressor complex as it alone cannot exert repression by binding to the target DNA. Analysis using a LexA-Mig1 fusion protein showed that repression of the target genes bearing LexA operators depends on Ssn6p-Tup1p which acts as a co-repressor complex (Treitel and Carlson 1995, Tzamarias and Struhl 1994). In addition, a yeast two hybrid screen showed a direct interaction between Mig1p and Ssn6p that indicated that Ssn6p provides the link between Mig1p and Tup1p (Treitel and Carlson 1995). ChIP assay revealed that Mig1p did not drive the Ssn6p-Tup1p complex to the *GAL1* promoter, rather physical interaction with HMG non histone proteins could be a reason for the Ssn6p-Tup1p complex to be tethered at the promoter site (Papamichos-Chronakis, et al. 2004).

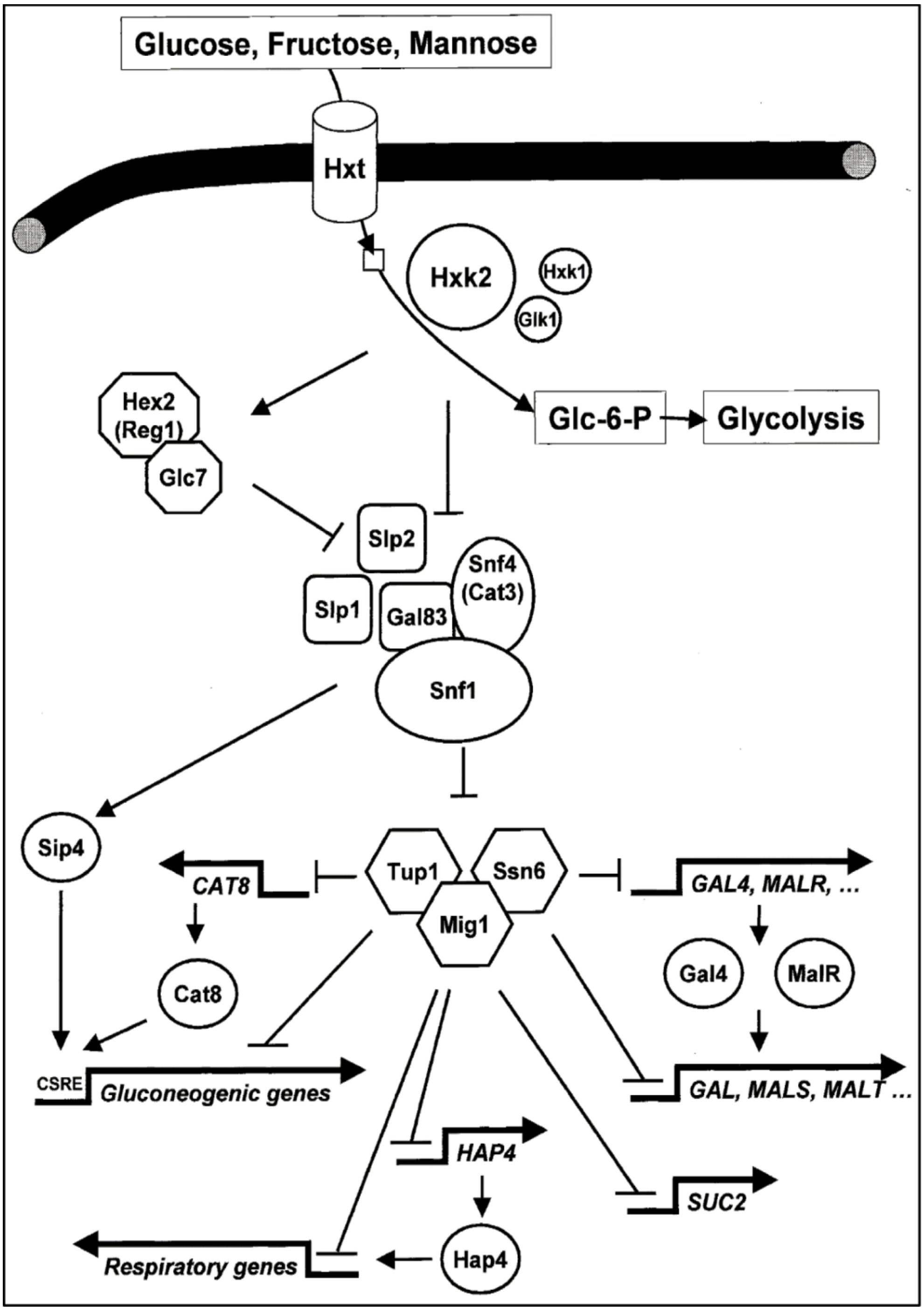

Figure 1.1 Carbon catabolite repression pathway of *S. cerevisiae*. In the presence of glucose, transported by Hxt transporters and phosphorylated by hexokinase Hxkt2/Hxk1 or glucokinase Glk1, Mig1 together with co-repressor complex Ssn6/Tup1 exerts repression on various genes including *GAL4* (galactose utilization), *MALR* (maltose utilization), *SUC2* (sucrose utilization), *HAP4* (respiratory genes) and *CAT8* (gluconeogenic genes). In glucose depleted conditions, the Snf1 complex including Snf4 and one of three regulatory subunits Gal83/Sip1/Sip2 inhibits the activity of the repression complex. Snf1 activity is regulated by the Reg1-Glc7 phosphatase complex. Snf1 kinase also activates Sip4 which together with Cat8 is required for gluconeogenic genes. Source : (Rolland, et al. 2002).

In addition to Mig1p, there are other Cys_2-His_2 zinc finger proteins in *S. cerevisiae*, including Mig2p, Mig3p, Nrg1p and Nrg2p. Like Mig1p, Mig2p also exerts glucose repression through Ssn6p-Tup1p. Double deletion of both *MIG1* and *MIG2* showed higher derepression than *MIG1* alone for *SUC2* expression but not for the *PCK1, FBP1, HXT2* and *GAL1* genes (Lutfiyya and Johnston 1996). Mig3p is very similar to Mig1p and Mig2p (Bohm, et al. 1997, Lutfiyya and Johnston 1996) and controlled by Snf1p (Kaniak, et al. 2004, Lutfiyya, et al. 1998). Mig3p binds to the Mig1p binding sites upstream from *SUC2* and when bound to upstream LexA operators, a LexA-Mig3 chimera functioned as a glucose dependent repressor of reporter gene expression. Mig3p is extensively phosphorylated and subjected to Snf1p dependent proteolysis when cells are shifted from glucose medium to galactose medium (Dubacq, et al. 2004). Nrg1p was identified in two different screens for factors mediating the repression of glucose regulated genes (Ahn, et al. 1995, Park, et al. 1999) and Nrg2p was discovered due to its interaction with Snf1p in two-hybrid system (Vyas, et al. 2001). Both proteins have shown glucose dependent repression of heterologous genes. Though Snf1p kinase has shown interaction with both proteins, none of them appeared to be phosphorylated by it (Berkey, et al. 2004, Vyas, et al. 2001).

A Mig1p like protein, involved in the CCR pathways, has also been identified in some yeasts including *Kluyveromyces lactis* (Cassart, et al. 1995), *K. marxianus* (Cassart, et al. 1997), *Schizosaccharomyces pombe* (Tanaka, et al. 1998), and *Candida albicans* (Gancedo et al, unpublished data). The zinc finger regions of Mig1 are conserved among these yeasts. Moreover, regions which are potential substrates for Snf1, are also conserved in *K. lactis* and *K. marxiamus* (Cassart, et al. 1997). Proteins showing similarity to Mig1p have also been identified in a number of ascomycete fungi including *A. nidulans* (Dowzer and Kelly 1991), *Aspergillus oryzae* (Kato, et al. 1996), *Aspergillus niger* (Drysdale, et al. 1993), *Sclerotinia sclerotiorum* (Vautard-Mey, et al. 1999), *Trichoderma reesei* (Strauss, et al. 1995), and *Neurospora crassa* (de la Serna, et al. 1999). Functional analysis showed that the N-terminal zinc finger region and the C-terminal Mig1 effector domain are required for repression and conserved in these fungi (Ostling, et al. 1996, Shroff, et al. 1997). Although the R1 and R2 regulatory domains of Mig1 are not conserved in the fungi, fungi do contain an acidic region containing a potential serine/threonine phosphorylation site and two ‘conserved regions’ (Kelly 2004).

1.3.2 Snf1p

The *SNF1* gene was first identified in screens for regulatory factors affecting the response to glucose (Ciriacy 1977, Entian and Zimmermann 1982). It was also identified in a screen for mutants that could ferment glucose but not sucrose (Carlson, et al. 1981). As *SNF1* inactivation impairs the utilization of other carbon sources including galactose and maltose, it is characterized as an important regulatory gene mediating glucose derepression. The *SNF1* gene encodes a protein which can be auto-phosphorylated mostly on serine but also on threonine residues. Substitution of Lys^{84} with Arg in the ATP binding site of Snf1p showed that the mutated protein was not functional as it failed to derepress invertase in glucose limited conditions, indicating that protein kinase activity is essential for its function (Celenza and Carlson 1989). Also, the conserved Thr^{210} in the activation loop is vital for the activation of Snf1p (Estruch, et al. 1992). There is evidence that Snf1p is functionally and physically linked with another protein, Snf4p. The *SNF4* gene was identified in a 'sucrose nonfermenting' screen (Neigeborn and Carlson 1984). The phenotypes of *SNF1* and *SNF4* mutations are similar including defective utilization of carbon sources such as sucrose, galactose, maltose, raffinose and lactate. It was shown that increased Snf1p dosage and *SNF1* mutations can partially restore glucose derepression in the absence of Snf4p (Celenza, et al. 1989, Estruch, et al. 1992, Leech, et al. 2003). Moreover, experiments showed that Snf4p was co-immunoprecipitated with Snf1p, and it was required for the maximal Snf1p protein kinase activity in vitro (Celenza and Carlson 1989).

The signaling of Snf1p controls the function of glucose repression as well as the balance the cellular energy levels. In the case of glucose repression, Snf1p plays a dual role as an activator and as a repressor depending on the concentration of glucose in the cell [reviewed by (Kayikci and Nielsen 2015)]. In high glucose concentrations, Snf1p remains inactive which results in Mig1p being non-phosphorylated and present in the nucleus to exert repression. Alternatively, in glucose-limited conditions, Snf1p activates and phosphorylates Mig1p to release glucose repression (Carlson 1999). Snf1p possesses two domains: an amino terminal catalytic domain (KD) and a carboxy terminal regulatory domain (RD) (Celenza and Carlson 1989). In the presence of glucose, Snf1p is auto-inhibited as the RD binds with the KD and restrains its protein kinase activity. However, in low glucose concentrations, the Snf4p subunit binds with the RD and counteracts the auto-inhibition process (Jiang and Carlson 1996). The deletion of the RD bypasses the requirement for Snf4p, suggesting that Snf4p is not the only target for glucose signaling (Celenza and Carlson 1989).

Three protein kinases Sak1, Eml1, and Tos3 phosphorylate Thr^{210} in the activation loop of Snf1p and have overlapping functions as deletion of all three kinases abolishes Snf1p activation. However, how glucose signal regulates these activating kinases is still unknown, although their contributions can vary with the availability of different carbon sources [reviewed by (Kayikci and Nielsen 2015)]. Snf1p associates with a heterotrimeric enzyme complex that contains catalytic α-subunit Snf1p, γ-subunit Snf4p and one of the three related β-subunits Gal83p, Sip1p or Sip2p. The β-subunit regulates the subcellular localization of the kinase complex [Figure 1.2; (Vincent, et al. 2001)]. Snf1p activity is also regulated by the catalytic subunit (Glc7p) of protein phosphatase 1 (PP1) together with Reg1p. The Glc7p-Reg1p complex interacts with the catalytic domain of Snf1p and changes the protein kinase conformation to its auto-inhibition state (Ludin, et al. 1998). Apart from its glucose repression role, Snf1p shows interaction with the transcriptional machinery and plays a role in chromatin modifications (Kuchin, et al. 2000). In addition to its role in CCR, Snf1p activity is also required for sporulation, glycogen storage, peroxisome biogenesis, temperature tolerance and at several meiosis steps (Carlson 1999, Rolland, et al. 2002).

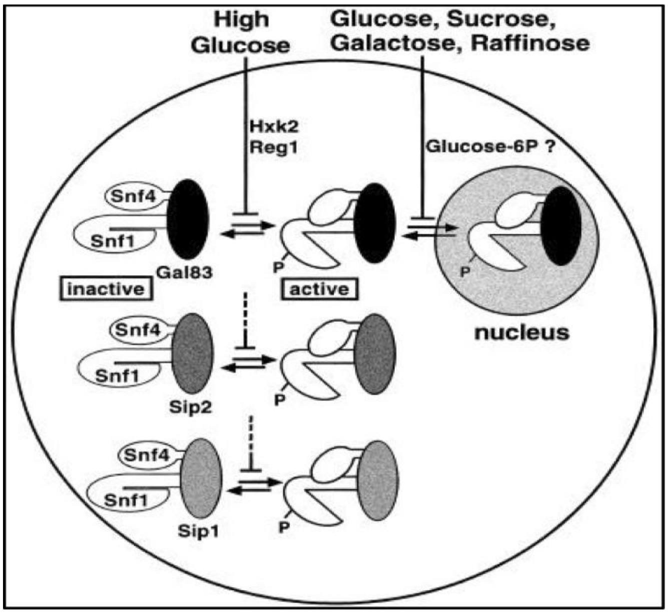

Figure 1.2 Regulation of Snf1 kinase activities. Snf1 forms a heterotrimeric complex with one of the three β subunits: Gal83 (black), Sip2 (dark gray), or Sip1 (light gray) and Snf4. Inactive Snf1 kinase complexes are in a closed conformation in which the Snf1 catalytic domain is auto-inhibited by the Snf1 regulatory domain. Active Snf1 complexes are shown in an open conformation and are phosphorylated (P). Source: (Vincent, et al. 2001).

The serine/threonine Snf1 kinase is widely conserved in eukaryotes and is required for cellular energy homeostasis [reviewed by (Kayikci and Nielsen 2015). The mammalian homolog of Snf1p kinase is AMP activated protein kinase (AMPK) which regulates metabolic enzymes in response to stresses that cause ATP depletion (Carlson 1999), and Snf1p is regulated by ADP which ensures a direct link with energy metabolism (Mayer, et al. 2011).

1.3.3 Snf4p

Like the *SNF1* gene, the *SNF4* gene is also required for the expression of glucose repressible genes in glucose deprived conditions (Celenza and Carlson 1989). The *SNF4* gene encodes Snf4p that is functionally related with Snf1p. Genetic evidence suggested that mutations cause similar phenotypes and show similar interactions with extragenic suppressors (Neigeborn and Carlson 1984, Neigeborn, et al. 1986). Celenza and Carlson (1989) reported that increased dosage of *SNF1* can compensate for a deletion in *SNF4,* indicating a functional relationship between these two genes. However, both the biochemical and genetic evidence suggested that the Snf1p has low residual activity in the absence of Snf4p. The interaction between Snf1p and Snf4p is regulated by glucose. In high glucose conditions, the interaction is inhibited while it is induced in glucose limited conditions. This was confirmed by using the yeast two-hybrid system (Jiang and Carlson 1997). However, in glucose starvation conditions, Snf1p activity increases in a Snf4p dependent manner (Woods, et al. 1994).

1.3.4 Reg1p & Glc7p

REG1 was identified via a 2-deoxy-D-glucose resistant mutant. In the presence of glucose these mutants can express invertase, maltase and malate dehydrogenase, indicating that *REG1* could play a role in CCR in *S. cerevisiae* (Entian and Zimmermann 1982, Zimmermann, et al. 1977). Tu and Carlson (1995) reported that Reg1p can interact with Glc7p in the yeast two-hybrid system and can be co-immunoprecipitated, suggesting these two proteins can work together. Glc7p, a protein phosphatase type I, regulates a variety of cellular processes including glycogen accumulation, normal progression through the G2/M phase of the cell cycle, actin organization and translation and sporulation [reviewed by (Gancedo 1998, Santangelo 2006)]. It has been hypothesized that, in the presence of glucose, the activity of Reg1p is increased and as a result the Reg1p-Glc7p phosphatase complex dephosphorylates Snf1p that leads to inactivation of this kinase protein [reviewed by (Kayikci and Nielsen

2015). Moreover, the Reg1p-Glc7p complex might also be involved in the dephosphorylation of the repressor protein, Mig1p (DeVit, et al. 1997)

1.3.5 Gal83p, Sip1p & Sip2p

One of these three β subunits is another component of the heterotrimeric enzyme complex of the Snf1p protein kinase. It was suggested that the β subunit acts as a bridging protein between Snf1p and Snf4p and strengthens the association of these proteins. Gal83p was identified for its effect on the glucose regulation of *GAL* gene expression (Erickson and Johnston 1993). Sip1p and Sip2p were identified in a two-hybrid screening for proteins that interact with Snf1p (Mylin, et al. 1994, Yang, et al. 1992). Experiments showed that these β subunits contain Snf4p binding C terminal domain independent of Snf1p, and an internal region that interacts with Snf1p (Jiang and Carlson 1997). Gal83p is thought to be the major contributor to glucose regulation by the Snf1p complex as it is the most abundant β subunit. Furthermore, when cells are grown in non-fermentable carbon sources, Gal83p is the only β subunit present in the nucleus, suggesting that the Snf1p/Gal83p form is responsible for most of the Snf1 kinase activity (Hedbacker, et al. 2004, Vincent, et al. 2001). Moreover, in glucose-limited conditions, Gal83p plays an important role in the regulation of estradiol biosynthetic genes (Zhang, et al. 2010). A strain containing a double mutation of *SIP2* and *GAL83* genes and expressing only the *SIP1* gene could utilize acetate but not ethanol or glycerol as alternative carbon sources. Moreover, Sip2p can compensate, to a lesser extent, when Gal83p is deleted but not Sip1p (Zhang, et al. 2010).

1.3.6 Ssn6p & Tup1p

The *SSN6* and *TUP1* genes were first identified in a screen of mutants with defects in CCR. Mutations in both the genes produce similar phenotypes including constitutive derepression of glucose-repressible genes, sporulation, mating defects, abnormal cell morphology and calcium-dependent flocculation (Trumbly 1992). Keleher, et al. (1992) first identified that these two proteins work as a co-repressor complex. In *S. cerevisiae*, this global co-repressor complex is responsible for the repression of over 180 genes that include genes regulated by glucose, DNA damage, mating type and oxygen availability. After recruitment by a DNA binding protein, the Ssn6p-Tup1p complex is thought to interact with RNA Polymerase II (Pol II) holoenzymes, histones and HDACs for repressing downstream genes (Malave and Dent 2006).

The *TUP1* gene encodes a protein with long stretches of glutamine and threonine whereas the *SSN6* gene encodes a protein with a high proportion of glutamine residues (Schultz and Carlson 1987, Williams and Trumbly 1990). The Ssn6 protein contains 10 tetratricopeptide repeats (TPR) near the N-terminal which form a superhelix with an internal cavity that accommodates the Tup1p amino terminal tetramer (Jabet, et al. 2000, Schultz, et al. 1990). The N-terminal domain of Tup1p folds into a helical structure and this structure is important for tetramerization and interaction with Ssn6p (Jabet, et al. 2000). Deletion analysis suggested that the N-terminal 72 residue stretch of Tup1p is necessary and sufficient for binding to Ssn6p (Tzamarias and Struhl 1994). Many experimental approaches revealed that Ssn6p and Tup1p can associate in a high molecular mass complex composed of 1 molecule of Ssn6p and 4 molecules of Tup1p (Varanasi, et al. 1996). Experiments suggested that the co-repressor complex was continuously bound to the *GAL1* promoter under both repressing and inducing conditions. This suggests that derepression does not depend on DNA binding. This result was also observed in the *MIG1Δ* strains (Papamichos-Chronakis, et al. 2002).

1.3.7 Glucose Transporters

Fermentation is the main mechanism by which yeast cells obtain their energy from glucose in spite of the presence of oxygen. However, a high glycolytic flux is necessary because fermentation is a relatively inefficient process for generating energy. By inducing a large number of glycolytic genes yeast cells can increase their glycolytic capacity. Furthermore, by induction of glucose transporter encoding *HXT* genes, yeast cells can increase glucose uptake capacity (Rolland, et al. 2002). There are 20 genes in the hexose transporter family, among them six genes (*HXT1–HXT4*, *HXT6*, *HXT7*) encode the major proteins responsible for glucose transport by facilitated diffusion (Kruckeberg 1996). Another two genes in this transport family, *SNF3* and *RGT2*, encode proteins that act as a glucose sensor and transmit signal for the induction of *HXT* gene expression (Ozcan, et al. 1996a). The expression of specific transporters largely depends on the amount of glucose present in the medium. High-affinity transporters like Hxt6p and Hxt7p are highly expressed during growth on non-fermentable carbon sources and are repressed by high levels of glucose. Low-affinity transporters such as Hxt1p and Hxt3p are induced by the presence of high concentration of glucose whereas intermediate affinity transporters, Hxt2p and Hxt4p are induced by low levels of glucose and repressed by high levels of glucose [Figure 1.3; (Rolland, et al. 2002)]. Experiments with mutants expressing different glucose transporters showed that the rate of glucose transport is determined by the strength of repression rather than the requirement of specific transporters (Reifenberger, et al. 1997). It was also reported that the constitutive expression of *GAL2*, encoding galactose permease, can activate glucose-induced cAMP signaling in a *HXT*- null strain, indicating that the transporters do not play any regulatory role in glucose-induced cAMP synthesis (Rolland, et al. 2000).

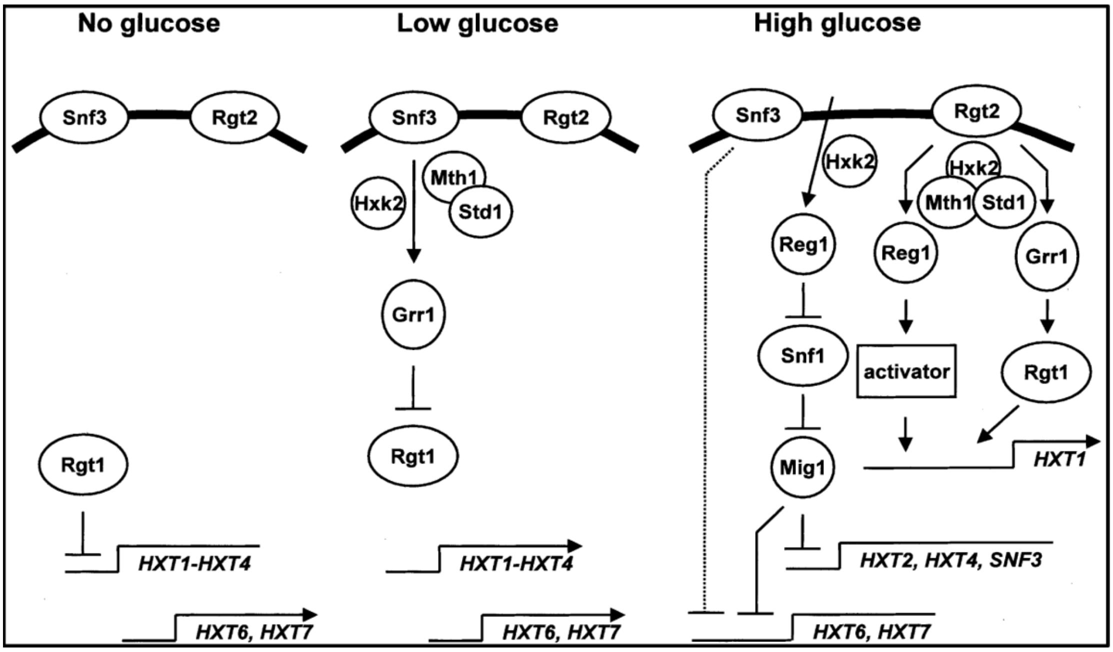

Figure 1.3 Regulation of glucose transporter genes expression in response to glucose. In the absence of glucose, Rgt1 represses the transcription of the *HXT1-4* genes. However, in low glucose conditions, the activity of Rgt1 is repressed via Grr1 mediated ubiquitination triggered by Snf3. When glucose is abundant, Rgt2 activates the low affinity transporter gene *HXT1* via Grr1-dependent conversion of Rgt1 into a transcriptional activator. Transcriptional regulators Mth1 and Std1 can bind to Rgt2 and repress HXT genes. In addition, a number of other transporters including *HXT2*, *HXT4, HXT6* and *SNF3* are repressed through Mig1 mediated repression pathways in high glucose conditions. Source : (Rolland, et al. 2002).

1.3.8 Snf3p & Rgt2p

Snf3p and Rgt2p are plasma membrane proteins which have high similarity with Hxt glucose transporters though they are unable to transport glucose (Ozcan, et al. 1998, Ozcan, et al. 1996a). The *SNF3* gene was identified in a screen for mutants deficient in the utilization of the trisaccharide raffinose. Moreover, the *SNF3* mutants are unable to grow fermentatively on low concentrations of glucose or fructose. Kinetic analysis showed that the *SNF3* gene is required for growth on low glucose concentrations by activating high affinity transporters (Figure 1.3) (Bisson, et al. 1987, Neigeborn, et al. 1986).

The *RGT2* gene is required for the maximal induction of *HXT1* expression in high levels of glucose (Ozcan, et al. 1996a). Both Snf3p and Rgt2p have long carboxy terminal cytoplasmic tails, which play an important role in glucose signaling. Deletion analysis showed that this carboxy terminal extension is required for Snf3p dependent expression of high-affinity transporter genes (Ozcan, et al. 1998, Vagnoli, et al. 1998). Replacing an arginine residue, conserved for glucose transporters, by lysine in a cytoplasmic loop of Snf3p or Rgt2p allows total induction of *HXT2* and partial induction of *HXT1* in the absence of glucose, suggesting that the mutated receptors adopt a conformation similar to that of the glucose bound Snf3p or Rgt2p and independent of carbon sources (Gancedo 2008, Ozcan, et al. 1996a).

In the absence of glucose, two transcriptional regulators Mth1p and Std1p bind to Rgt2p and enable it to repress the *HXT* genes. Both Mth1p and Std1p can substitute for one another, however, Mth1p is more abundant than Std1p in the absence of glucose (Figure 1.3) (Sabina and Johnston 2009).

1.3.9 Hxk2p

The *HXK2* gene was identified as one of the first genes involved in glucose repression (Entian and Zimmermann 1980, Zimmermann and Scheel 1977). Early experiments suggested that Hxk2p has a specific regulatory domain required for glucose repression (Entian and Frohlich 1984). However, *HXK2* mutants showed a correlation between glucose repression and glucose phosphorylation (Ma, et al. 1989, Rose, et al. 1991). Investigation of the intracellular location of Hxk2p revealed that a small proportion of Hxk2p is located within the nucleus, suggesting that Hxk2p requires nuclear localization for the non-metabolic role (Herrero, et al. 1998, Rodriguez, et al. 2001).

In high glucose concentration, Snf1p is inactivated and it was assumed that Hxk2p is involved in this inactivation (Treitel, et al. 1998). In the *HXK2* mutant, glucose repression of some genes that require Snf1p to be transcribed is weak. Overexpression of *REG1* can partially suppress the effects of *HXK2* mutation on glucose repression, which suggests that the presence of Hxk2p facilitates the dephosphorylation of Snf1p and subsequent inactivation by protein phosphatase complex Glc7p-Reg1p (Gancedo 2008, Sanz, et al. 2000). The interaction between Snf1p and Hxk2p was observed after growth in low or high glucose concentration (Ahuatzi, et al. 2007, Sanz, et al. 2000). It remains unclear whether Hxk2p controls the intrinsic activity of Snf1p or only its capacity to phosphorylate Mig1p (Gancedo 2008).

Experiments showed that Hxk2p interacts with Mig1p, and Lys^6 – Met^{15} of Hxk2p is needed for this interaction. This interaction is required for Hxk2p to remain in the nucleus and a correlation has been observed between Mig1p level in the cell and Hxk2p levels in the nucleus. As Mig1p localization to the nucleus is glucose dependent, it has been suggested that Hxk2p localization also depends on glucose levels. The binding between Mig1p and Hxk2p suggests that the main role of Hxk2p in glucose repression is to obstruct contact between Mig1p and Snf1p, which results in blocking of phosphorylation of Mig1p (Ahuatzi, et al. 2004, DeVit, et al. 1997) [Figure 1.4; (Gancedo 2008)].

In addition to its role in the CCR pathways, Hxk2p can be an important target to improve the production of biofuels. Bae, et al. (2014) reported that an *HXK2* deletion strain can utilize both glucose and galactose in the oxygen-limiting conditions as the transcription of *GAL* genes was increased in the absence of *HXK2* and galactose consumption rate was inversely proportional to the mRNA levels of *HXK2* genes.

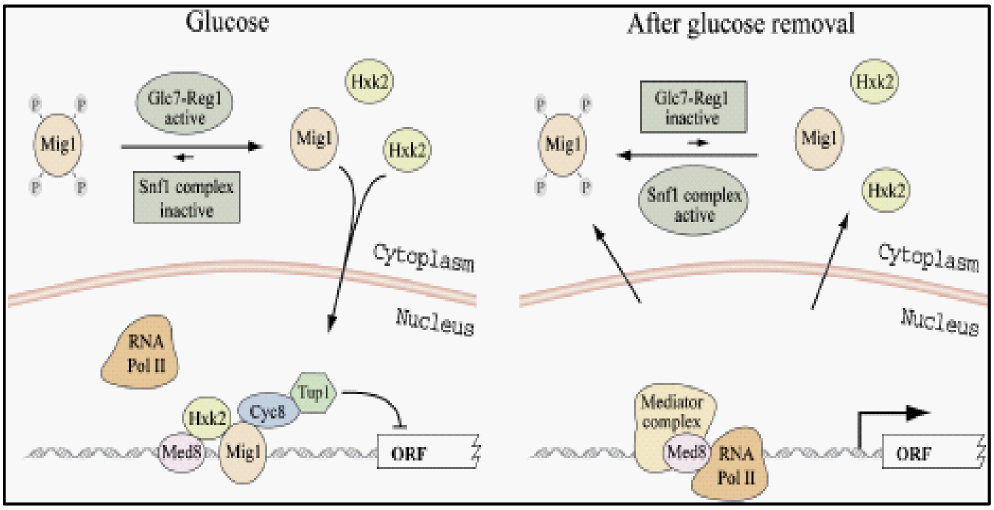

Figure 1.4 Model for the role of Hxk2 in the nucleus in glucose signaling. In the presence of glucose, Hxk2 binds with Mig1 and localizes into the nucleus which obstructs the interaction between Snf1 and Mig1. As a result, Mig1 together with the co-repressor complex exerts its repression activity. In addition, in the nucleus Hxk2 can also bind to Med8, a subunit of the mediator complex, which hinders RNA polymerase II activity at the promoter of the regulated gene. On the other hand, when glucose is depleted Mig1 is phosphorylated by Snf1. Both Mig1 and Hxk2 localize into the cytoplasm and Hxk2 dissociates from Med8, which then is able to recruit RNA polymerase II for transcription. Source : (Gancedo 2008).

1.3.10 Rgt1p

Rgt1p is a zinc finger-containing DNA binding protein that recruits the Ssn6p-Tup1p repressor to the promoters of specific genes. The Rgt1p repressor function is inhibited by low concentrations of glucose that result in derepression of *HXT* gene expression (Figure 1.3). Rgt1p is required for the full induction of the *HXT1* gene at high glucose concentration where it acts as an activator for gene expression. In addition, Grr1p is required for high glucose-induced activation and low glucose-induced inactivation of Rgt1p (Ozcan, et al. 1996b). Mutations in *GRR1*, another element of CCR pathways, lead to pleiotropic loss of glucose repression (Bailey and Woodword 1984).

1.4 Carbon catabolite repression in *Aspergillus nidulans*

A. nidulans (also known as *Emericella nidulans*) is a multicellular filamentous fungus which belongs to the *Aspergillus* form genus. CCR in *A. nidulans* is more complicated than in unicellular *S. cerevisiae* as yeast has restricted metabolic capacity whereas multicellular *A. nidulans* can metabolize a wide range of complex carbon sources. In addition, studies have revealed that the molecular mechanism of CCR as well as glucose sensing and signaling of *A. nidulans* is different from that seen in yeast (Kelly and Katz 2010).

There are two types of systems where genetic analysis has been used to understand CCR in *A. nidulans*. The first system involves genes regulated only by induction and carbon catabolite repression, such as the alcohol dehydrogenase I encoded by the *alcA* gene. The second system involves genes that are subject to both carbon catabolite and nitrogen metabolite repression such as acetamidase encoded by the *amdS* gene and the proline utilization cluster genes (Martinelli 1994). On the basis of metabolic functions, three groups of genes are regulated by CCR in filamentous fungi. Firstly, genes that encode enzymes that are required for utilization of less preferred carbon sources are in the first group. The second group includes genes that encode gluconeogenic and glyoxylate cycle enzymes. The final group consists of genes involved in secondary metabolism (Keller 2006). The proteins that play important roles in CCR of *A. nidulans* are discussed below.

1.4.1 CreA

The *creA* gene was identified as a suppressor of the *areA* loss of function phenotype. The *areA* gene encodes a positively acting DNA-binding protein that is required for expression of genes subject to ammonium repression (Arst and Cove 1973). Loss of function *areA* alleles cannot grow on most nitrogen sources in the presence of glucose due to the failure to express a range of genes subject to ammonium repression in the absence of ammonium. However, they can grow on certain compounds that provide both carbon and nitrogen sources such as acetamide and proline. Genes encoding enzymes require for the metabolism of proline and acetamide are regulated by both carbon catabolite repression and ammonium repression and the relief of either leads to expression of genes (Arst and Macdonald 1975, Hynes 1970). Other genes involved in the CCR regulatory network of *A. nidulans* were also identified by using this same genetic screening. The *creA* gene was also identified by other screening approaches such as selection of phenotypic suppressors of the *pycA* and *pdhA* loss of function mutants, as these strains require alternative sources of acetyl-CoA (Bailey and Arst 1975, Romano and Kornberg 1968, Romano and Kornberg 1969). In addition, phenotypic suppressors of the toxicity on fructose medium due to the *frA* mutation also included a *creA* mutation (Arst, et al. 1990, Ruijter, et al. 1996).

In *A. nidulans*, mutations in the *creA* gene lead to derepression, with no clear hierarchy, of a wide range of genes which are normally subject to repression in the presence of glucose (Arst and Cove 1973, Arst, et al. 1981, Scazzocchio, et al. 1995, Shroff, et al. 1996, Shroff, et al. 1997). However, some enzymes subject to CCR are not affected by the absence of *creA*, indicating that CreA independent mechanisms also exist (Penalva, et al. 1993). Experiments showed that mutations in *creA* lead to elevated levels of gene expression in both carbon catabolite repressing and derepressing conditions, indicating that CreA has roles in growth conditions that are generally regarded as repressing as well as derepressing (Kelly and Katz 2010). However, the role of CreA in totally non-repressing conditions is unknown as it is quite impossible to generate a completely non-repressing condition without causing starvation which triggers a cellular starvation response. The global transcriptional effects of *creA* were analyzed by performing a genome-wide microarray with WT and *creA* null mutant strains after growth in repressing and derepressing conditions (Mogensen, et al. 2006). Cluster analysis identified genes based on the expression profile, and revealed genes that were not regulated by CreA and genes that were either regulated or partially regulated by CreA, though, whether these genes were a direct target of CreA or an indirect target cannot be determined by these experiments (Mogensen, et al. 2006). The *creA* mutations affect colony morphology in complete medium with extreme alleles including *creA30* and *creA306* showing very small and compact colony morphology and sensitivity to toxic compounds such as acriflavine and molybdate (Arst, et al. 1990, Shroff, et al. 1997).

The *creA* gene contains a single open reading frame that encodes a protein containing two zinc finger structures of Cys_2 – His_2 type, an alanine-rich region and frequent S(T)PXX motifs (Dowzer and Kelly 1989, Dowzer and Kelly 1991). Mutations in the *creA* gene isolated *in vivo* are categorized as; first, missense mutations in the zinc finger region that are predicted to alter (*creA204*) or prevent (*creA306*) DNA binding and second, nonsense or frameshift mutations resulting in a truncated CreA protein. That is, mutations that either alter the DNA binding region, or lack the effector domain due to truncation lead to derepression (Kelly and Katz 2010, Shroff, et al. 1996). Analysis of

CreA truncated mutants has indicated that the region required for repression is located within 8 amino acids at the C-terminal end of CreA. Furthermore, there are 40 amino acids toward the C-terminus that are completely conserved in a number of filamentous fungi (Drysdale, et al. 1993, Shroff, et al. 1997).

CreA binds a DNA consensus recognition sequence, 5´SYGGRG3´ and this core recognition sequence is usually present in pairs (Cubero, et al. 2000, Kulmburg, et al. 1993, Panozzo, et al. 1998), however, the presence of the core sequence does not necessarily indicate *in vivo* functional binding as many promoters that are not regulated by CreA have this consensus sequence. Moreover, in a number of promoters, only subsets of consensus binding sites are functional, suggesting that residues other than the core consensus sequence or specific position on the promoter region could be vital for transcriptional repression (Garcia, et al. 2008, Panozzo, et al. 1998). In *A. nidulans*, alteration of nucleosome positioning was observed in the *alcA* and *alcR* promoters under different growth conditions. Nucleosome positioning of both these promoters was lost in induced conditions and partially restored with the addition of glucose. In a *creA* null mutant background, complete loss of nucleosome positioning was observed in both the *alcA* and *alcR* promoters in induced and induced-repressed conditions. However, in non-induced and repressed conditions, partial destabilization of nucleosome positioning was observed for the *alcA* promoter only (Mathieu, et al. 2005).

Analysis of the *creA* transcript revealed that its transcription is autoregulated and *creA* mRNA is present in relatively higher amounts in derepressing carbon sources than in repressing sources (Arst, et al. 1990, Shroff, et al. 1996). However, a strain containing a transgene expressing from a constitutive promoter is phenotypically similar to wild type, suggesting that this autoregulation is not a critical step in the regulatory mechanism (Roy, et al. 2008). Strauss, et al. (1999) reported that the addition of repressing or nonrepressing monosaccharides such as glucose, fructose or arabinose, to carbon-starved mycelia resulted in a rapid transient increase of the *creA* transcript but these were down regulated on repressing carbon sources.

Post-translational modifications of regulatory proteins play an important role in cell signaling pathways and phosphorylation is the most common form of post-translational modifications [reviewed by (Nguyen, et al. 2013)]. Phosphorylation plays an important role in the activity of CCR repressor proteins in yeast and other filamentous fungi (Cziferszky, et al. 2002, DeVit, et al. 1997, Vautard-Mey and Fevre 2000). However, alteration or deletion of equivalent amino acids or amino acid regions in CreA of *A. nidulans* has no effect on the repressor activity of the protein or phenotype (Roy, et al. 2008). In a strain expressing CreA:GFP from a constitutive promoter CreA was present in the nucleus at high levels under both repressing and derepressing conditions, but showed normal repression and derepression phenotypes (Roy, et al. 2008). Recent work on *snfA* (homolog of *S. cerevisiae SNF1*) suggested that the kinase protein is required for CreA mediated derepression of cellulase enzymes through alteration of CreA nuclear localization (Brown, et al. 2013), although the growth conditions of this experiment are more similar to starvation rather than derepression. Another recent study showed that cAMP-dependent protein kinase A (PKA) is involved in the CCR pathway of *A. nidulans* by mediating glucose dependent nuclear localization of CreA. Mutations in the *pkaA* gene showed decreased (25%), but not abolished, nuclear localization of CreA compare to WT (96%) in the glucose grown mycelia (de Assis, et al. 2015). A strain containing a *pkaAΔ* was measured for enzyme activity and it showed derepression for cellulases, while maintaining repression for β-glucosidase, xylanase and β-xylosidase in repressed-induced conditions (de Assis, et al. 2015), which is inconsistent with the fact that PKA is required for glucose-dependent nuclear localization of CreA.

In *A. nidulans*, regulation of CreA occurs both at post-transcriptional and transcriptional levels, and it is thought that the changes of CreA activity could be due to covalent modification/s of the protein and/or protein degradation which is supported by the presence of a sequence similar to a consensus sequence involved in ubiquitination (Strauss, et al. 1999). Roy, et al. (2008) also suggested that '*de novo*' protein synthesis is required to activate CreA as it was present in the nucleus in both repressing and derepressing conditions. Western analysis with a strain that expresses CreA from a constitutive promoter showed that at least a fraction of CreA is ubiquitinated (Kamlangdee 2008), however, overproduction of proteins can cause misfolding and degradation via the proteasome (Kraft, et al. 2010). In a recent article, Chu, et al. (2016) analyzed the ubiquitination sites in the proteome of *A. nidulans* and identified 1913 ubiquitinated proteins, though, CreA was not detected as a ubiquitinated protein. The total amount of CreA, in a western blot, was not significantly different in repressing and derepressing conditions, indicating that derepression does not require large-scale degradation of CreA (Kamlangdee 2008, Roy, et al. 2008).

The homologue of CreA has been identified in a number of fungi including *A. oryzae* (Kato, et al. 1996), *A. niger* (Drysdale, et al. 1993), *Aspergillus aculeatus*

(EMBLAB024314), *Gibberella fujikuroi* and *Botrytis cinerea* (Tudzynski, et al. 2000), *S. sclerotiorum* (Vautard-Mey, et al. 1999), *Acremonium chrysogenum* (Jekosch and Kuck 2000), *Humicola grisea* (Takashima, et al. 1998), *T. reesei* (Ilmen, et al. 1996), *Cochliobolus carbonum* (Tonukari, et al. 2003), *Trichoderma harzianum* (Ilmen, et al. 1996), *Metarhizium anisopliae* (Screen, et al. 1997), and *N. crassa* (de la Serna, et al. 1999). The N-terminal zinc finger regions and C-terminal Mig1p effector domain are conserved among these fungi. In addition, another region containing 42 amino acids shows conservation between all of the CreA proteins, and was initially referred to as the Rgr1-similar region due to some sequence similarity with a region of Rgr1p of *S. cerevisiae* (Dowzer and Kelly 1991, Sakai, et al. 1990). However, a hybrid *creA* gene construct containing the Rgr1p-similar region from *S. cerevisiae* failed to complement the *creA204* or *creA20* mutant alleles of *A. nidulans*, indicating that the sequence similarity might not be significant for fungi (Shroff, et al. 1997).

1.4.2 CreB & CreC

The *creB* and *creC* genes have been identified as suppressors of the *areA217* allele on glucose and acetamide medium using the same genetic screening that uncovered the mutations in the *creA* gene. In repressing conditions, mutations in the *creB* and *creC* genes result in a degree of derepression of enzymes that are normally subject to carbon catabolite repression, but only a subset of pathways is affected compared to the effect of mutation in the *creA* gene (Hynes and Kelly 1977, Kelly and Hynes 1977). In the absence of a repressing concentration of glucose, these same alleles fail to express enzymes that are required for the utilization of other carbon sources including quinate and proline (Hynes and Kelly 1977). Both mutants showed identical phenotypes and pleiotropic effects on carbon metabolism. However, the effects of both mutations are not additive in a strain that contains both mutations, indicating that the two proteins play a role in the same pathways (Hynes and Kelly 1977). Moreover, mutations in either gene can alter the sensitivity to toxic compounds giving, for example, increased sensitivity to acriflavine and decreased sensitivity to molybdate (Arst, et al. 1981) and showed little effects on colony morphology (Hynes and Kelly 1977). A strain containing *creB15* and *creC27* mutations also showed reduced uptake of proline and glutamate, but no effects could be measured on glucose uptake (Hynes and Kelly 1977, Kelly and Hynes 1977). Double mutants strains containing either *creB15* or *creC27* with *creA204* showed compact colony morphology like *creA204* and reduced utilization of proline like *creB15* or *creC27* (Hynes and Kelly 1977).

The *creB* gene encodes a protein containing 6 deubiquitinating homology (DUB) domains and a coiled-coil region that is involved in substrate recognition (Lockington and Kelly 2001). The activity of the DUB domain was confirmed by a standard bacterial assay for deubiquitination activity and bioinformatics analysis confirmed that CreB deubiquitinating enzyme falls into a ubiquitin processing protease (UBP/USP) family defined by the human homologue UBH1 (Lockington and Kelly 2001). Members of this novel subfamily of the ubiquitin processing proteases have also been identified in other eukaryotes like nematodes, Drosophila, Arabidopsis but no highly similar sequence was identified in *S. cerevisiae*. Thus, this subfamily could be involved in a conserved regulatory pathway (Kelly 2004). In addition, there are four highly significant PEST (proline, glutamic acid, serine and threonine) sequences found in CreB that, in other proteins, are known to serve as a proteolytic signal to target proteins for ubiquitination and rapid degradation (Rechsteiner and Rogers 1996).

The *creC* gene encodes a protein containing a proline-rich region near the N-terminus, a putative nuclear localization region and five WD40 motifs at the C terminus that form a propeller-like structure to facilitate protein-protein interaction (Neer, et al. 1994, Todd, et al. 2000). The analysis of different *creC* mutant alleles identified that the C-terminal WD40 motifs are required for the function of the protein (Todd, et al. 2000). The CreC protein is conserved across eukaryotes including humans, mice and *Drosophila*, however, it showed only weak sequence similarity in the WD40 repeat regions with the Tup1p protein of *S. cerevisiae* which is involved in the CCR regulatory network mediated by Mig1p (Kelly 2004). Another protein of *A. nidulans*, RcoA, is significantly more similar to Tup1p than CreC, though deletion of the *rcoA* gene showed no strong effects on the CCR pathway of the filamentous fungi (Hicks, et al. 2001, Todd, et al. 2000). Thus, it is very unlikely that RcoA is recruited by CreA for the repression mechanism.

Co-immunoprecipitation experiments with mycelia grown under repressing and derepressing conditions showed that the CreB and CreC proteins are present in a high molecular weight complex *in vivo* and neither protein is required for the presence of the other (Lockington and Kelly 2002). Western analysis with strains containing CreA:GFP in the *creB15* and *creC27* background indicated that CreC but not CreB is required for the stability of CreA (Ries, et al. 2016). However, other evidence is not consistent with that finding. Overexpression of CreB can override the lack of CreC but not vice versa (Lockington and Kelly 2002), and double mutant strains containing *creB15* and *creC27* showed phenotypes similar to the *creB15* strain (Hynes and Kelly 1977). Further, the genes encoding enzymes in pathways that are not derepressed in *creC* mutations are normally repressed, indicating active CreA is present.

In *A. nidulans*, some targets of the CreB deubiquitinating enzyme have been identified. The quinate permease, QutD, is a ubiquitinated protein which is co-immunoprecipitated with CreB, suggesting that QutD is a target of the CreB deubiquitinating enzyme (Kamlangdee 2008). In addition, the amount of QutD is lower in a *creB* mutant than WT, indicating that CreB plays a role in protein turnover (Kamlangdee 2008). Apart from QutD, some CreA was also co-immunoprecipitated with CreB using strains that constitutively express both CreA and CreB, suggesting a possible target for CreB deubiquitinating enzyme (Kamlangdee 2008), and this is further explored in this thesis.

1.4.3 CreD

The *creD34* mutation was identified as a suppressor of the *creC27* mutant phenotype of hypersensitivity on glucose medium containing fluoroacetamide. (Hynes and Kelly 1977, Kelly 1980). The *creD34* mutant also suppresses some other phenotypes of *creC27* related to CCR, such as derepression of alcohol dehydrogenase I (Hynes and Kelly 1977, Kelly 1980). In addition, this same mutant allele of *creD* gene suppresses some phenotypic effects of the *creB15* allele (Hynes and Kelly 1977, Kelly 1980). On the other hand, the *creD34* mutant strain showed more resistance than wild-type on glucose and fluoroacetamide medium, suggesting that the *creD34* mutation leads to tighter repression of enzymes subject to CCR (Boase and Kelly 2004). In a wild type background, the *creD34* mutation shows opposite phenotypes compared to *creA*, *creB* or *creC* mutations on toxic compounds, such as increased resistance to acriflavin and reduced sensitivity to molybdate (Boase and Kelly 2004). These phenotypic characteristics of *creD34* suggest that CreD plays an opposite role to the CreB-CreC complex in the CCR pathway of *A. nidulans* (Boase and Kelly 2004).

The *creD* gene encodes a protein containing an arrestin_N domain, an arrestin_C domain, a single proline rich PPXY motif and two basic sequence PXY motifs. Both the PPXY and PXY motifs are found in transcription factors and are implicated in protein-protein binding (Boase and Kelly 2004, Chen and Sudol 1995). The CreD protein shows high similarity with two proteins, Rod1p and Rog3p of *S. cerevisiae*. Both the Rod1p and Rog3p proteins interact with E3 ubiquitin protein ligase Rsp5p (Andoh, et al. 2002). In a bacterial two-hybrid system, CreD interacts with HECT ubiquitin protein ligase

HulA of *A. nidulans*, which is the homologue of Rsp5p, suggesting that CreD might be a component of the ubiquitination process involved in the regulatory network of CCR of *A. nidulans* (Boase and Kelly 2004).

1.4.4 AcrB

In *A. nidulans*, the *acrB2* mutation was isolated as a spontaneous resistant sector on acriflavin containing complete medium with the aims of understanding acriflavin toxicity and obtaining extra tools for genetic mapping (Roper and Kafer 1957). In addition, this same allele showed increased resistance to some dyes like crystal violet and malachite green when compared with the wild-type strain (Arst, et al. 1981). The *acrB2* mutant showed reduced utilization of a number of sugars as sole carbon sources such as fructose, cellobiose, raffinose and starch compared to both the wild type and the *creD34* mutant strain, indicating a failure to derepress the genes encoding enzymes required for their utilization (Boase, et al. 2003). Like the *creD34* mutant, *acrB* mutants showed resistance to acriflavin and sensitivity to molybdate and the effects of acriflavin resistance of *acrB2* and *creD34* are additive (Boase and Kelly 2004, Boase, et al. 2003). Both the *acrB2* and *creD34* mutations share similar phenotypes such as suppression of the *creB15* and *creC27* mutant phenotypes and deletion of *creD* and *acrB* can lead to tighter carbon catabolite repression, suggesting AcrB could be play a role in ubiquitination process of this regulatory network (Boase and Kelly 2004). The *acrB* gene encodes a protein that contains three transmembrane domains and a coiled coil region with no highly similar proteins present in higher eukaryotes or yeast (Boase, et al. 2003).

1.4.5 Hexose transporters & signaling pathways

Glucose is the primary source of carbon and energy for eukaryotic microorganisms including filamentous fungi such as *A. nidulans*. Thus, sensing of intra- and/or extra-cellular glucose levels and its transportation/uptake plays a vital role in the regulation of carbohydrate metabolism. There are two glucose transport systems that have been identified in *A. nidulans* (Kelly and Katz 2010). High-affinity transporters are expressed during carbon starvation (glucose concentration in micromolar range) and are repressed by glucose. On the other hand, low-affinity transporters are expressed when the concentration of glucose or other hexose is high (glucose concentration in millimolar range). To date, all the characterized fungal glucose transporters belong to the ‘Sugar Transporters’ clan of the major facilitator superfamily. In the *A. nidulans* genome, 109 genes have been identified that are predicted to encode proteins belonging to the sugar transporters clan of the major facilitator superfamily (Kelly and Katz 2010). Analysis of sugar uptake kinetics in *A. nidulans* revealed that glucose is transported through an energy consuming, carrier-mediated transport system (Forment, et al. 2006). Fungal glucose transporters can be regulated by the presence of both carbon sources and a global repressor protein. In the presence of glucose these transporters are either upregulated or repressed and glucose repression is mediated by the global repressor protein CreA (Forment, et al. 2006, Kelly and Katz 2010). In *A. nidulans*, the high-affinity glucose uptake system is repressed in the presence of glucose and derepressed in the absence of CreA. On the other hand, the low affinity uptake system is not induced by glucose in a complete loss of function allele of the *creA* gene (MacCabe, et al. 2003).

HxtA is a high affinity hexose transporter encoded by the *hxtA* gene. The expression of *hxtA* is induced during starvation and sexual development and repressed by the presence of glucose (Wei, et al. 2004). There is no obvious phenotype observed for the *hxtA* deleted strain in either various nutrient sources or different developmental stages. The Hxt protein shows high similarities with high-affinity transporters in other fungi species; however, in the presence of glucose, it does not functionally complement a *S. cerevisiae* strain containing no hexose transporters (Wei, et al. 2004).

Bioinformatic analysis in *A. nidulans* identified another four putative high affinity glucose transporter encoding genes *hxtB*, *hxtC*, *hxtD* and *hxtE*, which showed homology to other functionally characterized fungal glucose transporters (dos Reis, et al. 2013). Except *hxtD*, the other three transporters showed heterologous complementation in *S. cerevisiae* strain EBY.VW4000, which contains deletions of sugar transporter genes leading to an inability to grow on glucose, mannose, fructose or galactose as a sole carbon source, suggesting multiple substrates for these transporters. Genetic and biochemical evidence suggests that *hxtB* and *hxtD* correspond to the genes *mstC* and *mstA*, and that *mstC* and *sorA* are allelic genes (dos Reis, et al. 2013, Forment, et al. 2014, Wieczorke, et al. 1999). Unlike *hxtA*, *hxtB/mstC*, *hxtD/mstA and hxt E* showed increased transcript accumulation during vegetative growth and decreased accumulation in both sexual and asexual development (dos Reis, et al. 2013). Other than *hxtD/mstA*, null mutants of these high affinity transporters showed a reduction in both affinity and uptake for glucose compared to the WT strain, while, *hxtD/mstA* mutant strains showed increased affinity and uptake (dos Reis, et al. 2013). Like other high and low-affinity glucose transporters, deletion mutants of these four high-affinity transporters did not show any distinguishing phenotype in various carbon sources, indicating functional redundancy (dos Reis, et al. 2013).

Conversely, MstE is the only characterized low-affinity glucose transporter identified in *A. nidulans*. In repressing carbon sources, the *mstE* gene expression is at a higher level in germinating conidia while its expression is reduced during growth on nonrepressing carbon sources (Forment, et al. 2006, MacCabe, et al. 2003). However, the expression of *mstE* is dependent on the presence of a functional copy of *creA* as the *mstE* transcript was not detected in the *creA* deleted mutant even in the presence of repressible carbon sources (Forment, et al. 2006). Other than glucose, MstE showed affinity for mannose but not fructose or sorbitol (Forment, et al. 2006). A strain containing the *mstE* deletion showed no specific phenotype in a wide range of carbon sources and exhibited high-affinity kinetics (lower Km value), indicating that high-affinity transporters may be involved in these conditions (Forment, et al. 2006).

Oxidative phosphorylation is the primary method of glucose metabolism for aerobic filamentous fungi. Hexokinases catalyze the first step of glucose metabolism by phosphorylating glucose molecules. In *A. nidulans*, two genes, *frA* and *glkA*, encode catalytic hexokinases and a functional copy of only one of the two genes is required for utilization of glucose as a carbon source. Inactivation of both the genes is required to derepress genes that are subject to CreA mediated CCR, which differs from *S. cerevisiae* where disruption of one of the three hexokinase genes can cause derepression (Flipphi, et al. 2003, Ruijter, et al. 1996). Thus, glucose phosphorylation is essential to trigger repression in *A. nidulans* (Kelly and Katz 2010).

Besides the catalytic hexokinases, some atypical hexokinases such as HxkC and HxkD are present in *A. nidulans* which show only regulatory function and lack some of the highly conserved amino acids in the ATP- and sugar binding domain (Bernardo, et al. 2007). Experiments showed that both HxkC and HxkD modulate the activity of the p53 like transcriptional activator, XprG, and are involved in the response to carbon starvation (Katz, et al. 1996, Katz, et al. 2000). The HxkC protein is associated with mitochondria and may play a role in triggering programmed cell death in carbon starvation. On the other hand, the HxkD protein is localized in the nucleus which is consistent with its regulation role (Bernardo, et al. 2007, Kelly and Katz 2010).

1.5 Ubiquitination and Deubiquitination system

Regulation of gene expression is vitally important for normal cellular growth and development. Gene transcription is the first step of gene expression. Genes are transcribed when cells receive appropriate signals and involves the transcriptional machinery, general transcription factors and a specific chromatin structure. An appropriate level of gene expression is only possible when appropriate levels of active transcription proteins are present at the promoter region [reviewed by (Muratani and Tansey 2003)]. In recent years, ubiquitination and deubiquitination have been found to be involved in this regulation. The best known role of ubiquitination is to act as a signal for protein destruction via proteasome, however, ubiquitination is also involved in non-proteolytic tasks such as receptor internalization, ribosome function, nucleotide excision repair and protein function [reviewed by (Muratani and Tansey 2003)].

Ubiquitination is a highly dynamic process where ubiquitin, a small highly conserved protein of 76 amino acids, is covalently conjugated to a substrate protein. It is one of the important post-translational modification processes that regulate stability, function and localization of modified proteins. In the first step of ubiquitination, an ubiquitin activating enzyme (E1) is attached to the ubiquitin molecule by forming a thiol-ester bond in an ATP-dependent manner. The activating ubiquitin is then transferred to ubiquitin conjugating enzyme (E2) and subsequently to a lysine residue of target protein via ubiquitin ligase (E3) [review by (Reyes-Turcu, et al. 2009)]. Single or multiple ubiquitin molecules can be transferred to a target protein. Conjugation of single ubiquitin molecule (monoubiquitination) has been shown to be involved in membrane trafficking, histone function, transcription regulation, DNA repair and replication whereas attachment of multiple ubiquitin molecules (polyubiquitination) has been linked to protein degradation, protein localization, modification of protein activity, and interactions with macromolecules [Figure 1.5; (Kaiser and Huang 2005)]. Polyubiquitination of a target protein often leads to binding to the 26S proteasome which degrades the substrate into small peptides and recycles the ubiquitin tag (Kaiser and Huang 2005, Ventii and Wilkinson 2008). Mis-regulation of the ubiquitin system result in a number of diseases including cancers, mental retardation and neurodegenerative disorders including Parkinson’s disease, Huntington’s disease and Alzheimer’s disease [reviewed by (Hochstrasser 2009)].

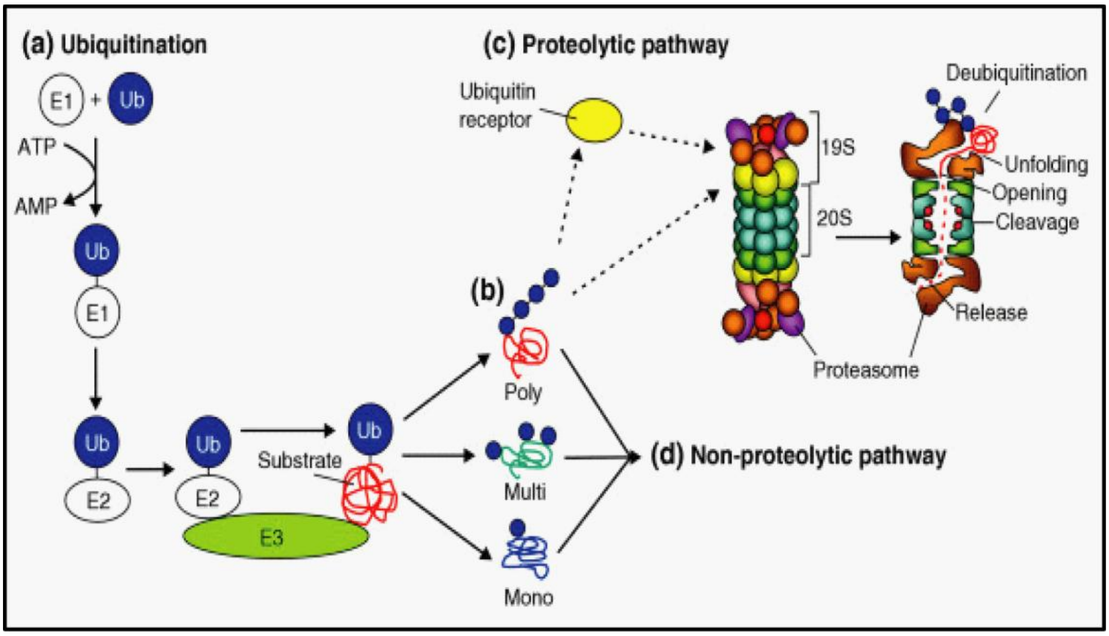

Figure 1.5 The Ubiquitin Proteasome System. At first, a ubiquitin activating enzyme (E1) activates ubiquitin which is then transferred to ubiquitin conjugating enzyme (E2). Ubiquitin is transferred to the lysine residues of substrates by E2 and/or ubiquitn ligase (E3). Ubiquitin can be attached to substrates as a single ubiquitin molecule (mono-ubiquitination), multiple ubiquitin molecules on the same protein (multi-ubiquitination) or by the formation of a ubiquitin chain (poly-ubiquitination). Ubiquitinated proteins are degraded either via the proteasome (poly-ubiquitinated) or by non-proteolytic pathways. Source: (Kaiser and Huang 2005).

In the ubiquitination process, substrate specificity is controlled by E3 ubiquitin ligases, thus, for any organism, a large number of E3 ubiquitin ligases is seen compared to only a few E1 ubiquitin activating enzymes and E2 ubiquitin conjugating enzymes [reviewed by (Rotin and Kumar 2009)]. There are two types of E3 ubiquitin ligases commonly detected depending on their ubiquitin transfer mechanisms to the substrate: HECT type and RING type. In the HECT ligases, a conserved cysteine residue of the E3 ligase forms a thioester bond with the C-terminal of ubiquitin and subsequently transfers ubiquitin to the substrate. On the other hand, RING type E3 ligases act as a scaffolding protein which facilitate the interaction between E2 conjugates and substrates; as a result, ubiquitin molecule/s transfers from E2 to the substrate [reviewed by (Rotin and Kumar 2009)].

The HECT domain was first identified in human papilloma virus (HPV) E-6 associated protein that contains around 350 amino acids at the C-terminus, and proteins containing this domain have been identified across many species ranging from yeast to human. The

HECT ligases also contain one or more protein-protein or protein-lipid interaction domains located at the amino terminus [reviewed by (Rotin and Kumar 2009)].

In S. cerevisiae, the HECT type E3 ubiquitin ligase Rsp5p is well characterized. This E3 ligase is involved in various cellular processes including mitochondrial inheritance, chromatin remodeling, regulation of transcription, regulation of endocytosis, sorting transmembrane proteins, transporters and receptors [reviewed by (Rotin and Kumar 2009)]. Rsp5p interacts with Rod1p and Rog3p proteins (Andoh, et al. 2002) and these two proteins showed high similarity with CreD and ApyA of *A. nidulans,* indicating that CreD might be involved in the ubiquitination process of the CCR regulatory network (Boase and Kelly 2004, Boase, et al. 2003). In a bacterial two-hybrid assay, CreD and ApyA interacted with the WW domain of HECT type ubiquitin ligase HulA of *A. nidulans* (Boase and Kelly 2004). As a strain containing an *apyA* gene disruption had no obvious CCR related phenotype (Denton, JA, personal communication), it is thought that the CreD-HulA complex might be responsible for ubiquitinating CreA or a protein in a complex with CreA and modifying the repressor activity.

The ubiquitination process is balanced by deconjugation of ubiquitin by deubiquitinating enzymes (DUBs). DUBs hydrolyze the ubiquitin-protein isopeptide bonds and remove ubiquitin signals. They are analogous to phosphatase and likely to be crucial regulatory proteins. Besides, DUBs can recycle ubiquitin molecules, activate ubiquitin pro-proteins and regenerate monoubiquitin from unused polyubiquitin molecules (Hicke and Dunn 2003, Kaiser and Huang 2005). DUBs are classified into five families: the ubiquitin C-terminal hydrolases (UCH), the ubiquitin specific proteases (USP/UBP), the ovarian tumor (OTU), the Josephin domain-papain-like cysteine proteases, and the JABI/MPN/Mov34 metalloenzyme (JAMM). Both UCH and USP/UBP were first recognized in the yeast ubiquitin system. Like ubiquitination, deubiquitination is also a highly regulated process and involved in a number of cellular functions including cell cycle regulation, proteasome and lysosome-dependent protein degradation, gene expression, DNA repair, microbial pathogenesis, and kinase activation. Moreover, mutations in genes encoding DUB enzymes have been connected to many diseases including cancers and neurological disorders (Reyes-Turcu, et al. 2009, Yan, et al. 2000).

In *S. cerevisiae*, Doa4p, a DUB, is required to recycle ubiquitin molecules from membrane proteins that are degraded in the lumen of the vacuole/lysosome. Prior to the degradation, these ubiquitinated membrane proteins are sorted, as ubiquitin serves as a sorting signal, into the multivesicular body (MVB) pathway and Doa4p catalyzes deubiquitination of these cargo proteins before sorting in the endosomal vesicle (Nikko and Andre 2007). In a *DOA4* mutant background, monomeric ubiquitin is reduced and MVB sorting of cargo proteins is also impaired (Nikko and Andre 2007). Experiments showed that the non-catalytic N-terminus of Doa4p associates with Bro1p, one of the highly conserved class E VPS protein, and mediates the recruitment of Doa4p to endosomes (Richter, et al. 2007). On the other hand, Bro1p interacts with a YPxL motif in the catalytic domain of Doa4p and activates its deubiquitinating activity (Richter, et al. 2007).

In *Drosophila*, the Fat facets DUB regulates endocytosis by deubiquitinating epsin, a component of clathrin based endocytosis machinery. The *fat facets* mutations were identified in a screening for a mutation that affects eye development and *liquid facets*, a dominant enhancer of *fat facets* was identified which encodes *Drosophila* epsin. Biochemical experiments showed that epsin interacts with Fat facets and ubiquitin modified epsin was detected when Fat facets activity is impaired (Chen, et al. 2002).

In *A. nidulans*, CreB protein has been identified as the first deubiquitinating enzyme that is involved in the CCR pathway. Experiments showed that CreB interacted with WD40 motifs in CreC and formed a high molecular weight complex. Some substrates for the CreB deubiquitinating enzyme have been identified in *A. nidulans*, and co-immunoprecipitation experiments showed that the quinate permease QutD is a target of the deubiquitinating enzyme CreB (Kamlangdee 2008, Lockington and Kelly 2001, Lockington, et al. 2002).

1.6 Carbon catabolite repression in Other filamentous fungi

Research has been undertaken on CreA homologues in other filamentous fungi including Cre1 in *T. reesei* and CRE1 in *S. sclerotiorum* (Ilmen, et al. 1996, Vautard-Mey, et al. 1999).

In *T. reesei*, mutations in the *cre1* gene lead to a higher expression of cellulases and xylanases. The transcriptional regulation of cellulases also depends on the transcriptional repressor Ace1 and the transcriptional activator Ace2 and Xyr1, and *xyr1* transcription is repressed by Cre1 (Aro, et al. 2003, Mach-Aigner, et al. 2008), although Portnoy, et al. (2011b) reported that Cre1 positively affect the induction of *xyr1* in lactose medium. Like CreA of A. *nidulans*, Cre1 transcription is autoregulated (Ilmen, et al. 1996). The *cre1* gene encodes the protein Cre1 which is similar to CreA of *A. nidulans*. Analysis of amino acid sequences showed that Cre1 has 50% sequence similarity with CreA of *A. nidulans*. Though the Cys_2-His_2 zinc finger region is conserved for both the fungi, the alanine-rich region of CreA has been substituted with eight glutamine and histidine in Cre1 which is thought to involve in protein-protein interaction (Ilmen, et al. 1996, Strauss, et al. 1995). Lichius, et al. (2014) reported that, in the presence of glucose, Cre1 rapidly shuttles from the cytoplasmic pool to the nucleus and again recycles into the cytoplasm upon depletion of glucose, suggesting sub-cellular localization of Cre1 is important for its transcriptional repression. Phosphorylation of Cre1 is important for its repression activity as experiments showed that phosphorylation at the Ser^{241} position of Cre1 is essential for DNA binding. Replacement of that serine residue with glutamic acid still conserves phosphorylation activity, however, replacement with alanine allows binding without phosphorylation and both these changes result in permanent carbon catabolite repression for cellobiohydrolase I expression. Unlike Mig1p of *S. cerevisiae*, Snf1 kinase is not involved in phosphorylation of Cre1, rather a casein kinase II like protein may be involved (Cziferszky, et al. 2002). In *A. nidulans,* there is no evidence of casein kinase II involvement in the phosphorylation of CreA, since the deletion of the potential casein kinase II phosphorylation site $SHED^{262\text{-}265}$ (equivalent to $SHDE^{241\text{-}244}$ of *T. reesei* and $SHEE^{266\text{-}269}$ of *S. sclerotinia*) in CreA showed repression and a phenotype identical to WT (Roy, et al. 2008). Genome-wide microarray analysis showed that Cre1 has some regulatory influence on around 250 genes including genes encoding plant cell wall degradation enzymes, enzymes required for nitrogen uptake, enzymes involved in chromatin remodeling, and components of the transcriptional mediator complex (Portnoy, et al. 2011a). Cre1 also plays an important role for proper positioning of nucleosomes in the *cbh1* coding region during repression (Ries, et al. 2014).

In *T. reesei*, Cre2, the homolog of CreB in *A. nidulans*, has also been identified. Mutations in the *cre2* gene showed phenotypes similar to the *creB* mutant phenotypes in both repressing and derepressing conditions. In addition, a strain containing the *cre2* mutation showed elevated expression of cellulase enzymes compared to the WT strain (Denton and Kelly 2011).

S. sclerotiorum is a phytopathogenic fungus that secretes a mixture of hydrolytic enzymes during infection that are active against the major components of the plant cell wall (Walton 1994). The *cre1* gene encodes the CRE1 protein, a homolog of CreA of *A.*

nidulans, and there is 59% sequence similarity between them (Vautard-Mey, et al. 1999). Besides the two zinc finger motifs, CRE1 has a stretch of basic amino acids and four RXXS motifs that are thought to act as a phosphorylation site. The carboxy-terminal end is rich in hydrophobic amino acids that together with zinc finger domains are required for repression activity (Cassart, et al. 1997). Experiments showed that CRE1 complemented the absence of CreA in *A. nidulans* but not Mig1p in *S. cerevisiae* (Vautard-Mey, et al. 1999). Western analysis showed that CRE1 was detected at higher levels in both glucose and glycerol-grown mycelia than in pectin grown mycelia, although no apparent difference in stability was identified (Vautard-Mey, et al. 1999). Sub-cellular localization of CRE1 was analyzed. In the presence of glucose, CRE1 was detected in the nucleus while it was in the cytoplasm when glucose was removed. In *A. nidulans*, CreAGFP expressing from a constitutive promoter was detected in the nucleus in both repressing and derepressing conditions (Roy, et al. 2008). Two recent studies showed that PKA, a cAMP-dependent protein kinase, and SnfA, a non-essential protein kinase, may also be important for glucose mediated repression and catabolite derepression respectively, by mediating CreA nuclear localization (Brown, et al. 2013, de Assis, et al. 2015). However, for both protein kinases, CreA nuclear localization was decreased but not fully abolished in derepressed conditions, and experimental conditions were more similar to starvation than derepression. The role of phosphorylation in the repressor activity of CRE1 was investigated, and here substitution of the Ser^{266} in CRE1 (equivalent to Ser^{241} in *T. reesei*) by alanine leads to derepression (Vautard-Mey, et al. 1999, Vautard-Mey and Fevre 2000), rather than the failure to derepress shown in *T. reesei* (Cziferszky, et al. 2002).

A. oryzae has been widely used for the production of Asian foods and beverages. This multicellular fungus can produce a variety of enzymes including cellulases, amylases, proteases, β-galactosidases and lipases. In the presence of glucose, the expression of these enzymes is repressed by CreA mediated CCR (Hunter, et al. 2013, Ichinose, et al. 2014). A null mutant of the *creA* gene showed similar morphological phenotypes as seen for *creA* deletion in *A. nidulans* (Ichinose, et al. 2014, Shroff, et al. 1997). Likewise, the *creB* mutations showed pleiotropic phenotypes and little effect on morphology as those seen in *A. nidulans* (Hunter, et al. 2013, Hynes and Kelly 1977, Ichinose, et al. 2014). However, a strain containing both the *creA* and *creB* deletions showed phenotypes similar to the *creA* deletion mutant (Ichinose, et al. 2014). As expected, mutations in either the *creA* or *creB* genes increase the expression of enzymes (α-amylase) which are normally repressed via CCR pathways (Hunter, et al. 2013, Ichinose, et al. 2014). Moreover, a strain with deletions of both these genes showed a greater increase in production of α-amylase than either of the single mutant strains (Ichinose, et al. 2014).

1.7 Carbon catabolite repression: *S. cerevisiae* vs *A. nidulans*

Carbon catabolite repression has been extensively studied in the unicellular yeast *S. cerevisiae*. Conversely, studies are still in an embryonic stage for multicellular filamentous fungi, however, existing evidence suggests that CCR is different in filamentous fungi than in the unicellular yeast, and also between filamentous fungi. In the case of metabolic processes, yeast shows restricted metabolic capacity, whereas filamentous fungi can metabolize a wide range of carbon and nitrogen sources in the presence of oxygen via the Krebs cycle. The repressor proteins of *S. cerevisiae* Mig1p and *A. nidulans* CreA show sequence similarity in the zinc finger regions and bind to the same consensus sequence in promoter regions. However, the glucose repression mechanisms are quite different between these two organisms. The shuttling of Mig1p between the cytoplasm and nucleus triggered by its phosphorylation by Snf1p kinase is one of the key regulatory steps in CCR of *S. cerevisiae*. In addition, the recruitment of the Ssn6p-Tup1p co-repressor complex is also essential for Mig1p to exert its repression activity. In *A. nidulans*, the upstream events of the repression mechanism are still not fully understood, however, evidence suggests that recruitment of the co-repressor complex or involvement of Snf1p kinase homolog is not critical for CreA mediated repression. CreA is detected in the nucleus in both repressing and derepressing conditions and mutational analysis confirms that the RcoA, the Tup1p homolog in *A. nidulans*, is not involved in the CCR pathways (Hicks, et al. 2001, Roy, et al. 2008). Recently, Brown, et al. (2013) reported that SnfA was involved in CreA mediated derepression of cellulase enzymes by altering CreA nuclear localization, though the growth conditions were more similar to starvation than derepression and CreA was present in the nucleus in glycerol which is considered a derepressing condition (Ruijter and Visser 1997). Conversely, no CreB like deubiquitinating enzyme has been identified in the CCR pathways of *S. cerevisiae*. Glucose phosphorylation by hexokinases is an important regulatory step to activate CCR in both organisms, however, the roles of the hexokinases differ between them. In *A. nidulans*, a functional copy of only one of the two hexokinases is enough to activate repression whereas, in *S.*

cerevisiae, mutations of one of the three hexokinases lead to derepression (Flipphi, et al. 2003).

1.8 Model of CCR mechanism in *A. nidulans*

Genetic and biochemical evidence confirmed that the DNA binding protein CreA is required for the repression of a wide range of genes subject to carbon catabolite repression. In addition, evidence also suggests that CreA plays a significant role or roles in carbon catabolite derepressing conditions, although the mechanism is still not clear as it is impossible to generate experimental conditions that are completely carbon catabolite derepressing without starvation and growth cessation. Early work using suppressor screening of either *areA* loss of function mutations or *pdhA* loss of function mutations allowed carbon sources to be ranked according to the degree of repression of genes (Arst and Cove 1973, Bailey and Arst 1975). Two independent experiments reported that post-translational modifications are likely to occur for the global repressor protein CreA to be active as a repressor which is another important element of the carbon catabolite repression mechanism (Kelly 2004, Roy, et al. 2008, Strauss, et al. 1999). Experimental evidence also indicates that the deubiquitinating enzyme CreB together with CreC play roles in both carbon catabolite repressing and derepressing conditions (Lockington, et al. 2002). As a deubiquitinating enzyme, some substrates of CreB have been identified and coimmunoprecipitation experiments show that at least a fraction of CreA is precipitated with CreB, suggesting that CreA is another possible target of this deubiquitinating enzyme (Kamlangdee 2008). In contrast, mutations in the *creD* gene lead to reverse phenotypes to the *creA*, *creB* and *creC* mutations, implying that CreD plays opposite roles in this regulatory pathway (Boase and Kelly 2004). Moreover, analysis implied that CreD interacts with E3 ubiquitin protein ligase, HulA, and might be involved in the ubiquitination process (Boase and Kelly 2004).

Considering the existing data, a model has been proposed to understand the carbon catabolite repression mechanism in *A. nidulans*. According to this model, in derepressing conditions, CreA or any protein bound to CreA is proposed to be ubiquitinated by the CreD-HulA ubiquitin ligase complex, resulting in conformational changes that modify CreA activity or target it to the proteasome for degradation. On the other hand, in repressing conditions, CreA or any protein bound to CreA might be directly recognized as a substrate of CreB via the coiled-coil region of CreB, to remove

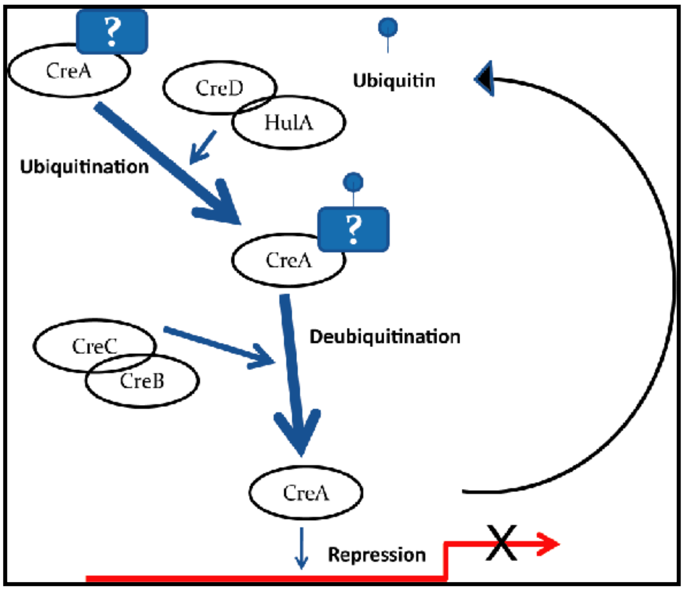

Figure 1.6 Model of CCR mechanism in *A. nidulans*. In derepressing conditions, CreA or a protein (?) bound to CreA is proposed to be ubiquitinated by the CreD-HulA ubiquitin ligase complex, leading to modification of CreA activity. Conversely, in repressing conditions, CreA or a protein (?) bound to CreA might be directly recognized as a substrate of CreB to remove the ubiquitin molecule(s) and activate CreA altering CreA binding to the consensus sequence in the promoter region of specific genes to exert its repression activity. Source: (Kelly 2004)

the ubiquitin molecule(s) and activate CreA or reduce the degradation of CreA via the proteasome. As a result, CreA binds to the consensus sequence in the promoter region of specific genes to exert its repression activity. In derepressing conditions, the deubiquitinating enzyme CreB might be subjected to a degree of proteolysis via a PEST mediated pathway allowing increased ubiquitination of CreA, resulting in increased degradation or modification of CreA activity (Boase and Kelly 2004, Kelly 2004) [Figure 1.6; (Kelly 2004)].

1.9 Unresolved questions in CCR

Although the zinc finger regions of transcription repressors are conserved among the species, the molecular mechanisms of carbon catabolite repression are different not only between *S. cerevisiae* and *A. nidulans* but also between other filamentous fungi. The cellular events involved in the CCR pathways of *S. cerevisiae* are well established. Recruitment of the co-repressor complex, Ssn6p-Tup1p, and involvement of Snf1p protein kinase are important regulatory steps in the CCR network of *S. cerevisiae*. However, both Tup1 and Snf1 kinase homologs in *A. nidulans* are not critically involved in the CCR regulatory pathways. Conversely, involvement of a ubiquitin ligase

(CreD) and a deubiquitination pathway (CreB) is not detected in the CCR pathway of *S. cerevisiae*. Although the proteins involved in the CCR processes of *A. nidulans* have been identified, the upstream molecular mechanisms are still unclear. How the transcriptional repressor CreA is activated or deactivated with the changes of nutritional conditions still remains unanswered. It is evident that the deubiquitinating enzyme CreB is involved in this regulatory process but how CreB plays its role is still not known. It has been suggested that sensing the nutritional status and transmitting the signal might involve both phosphorylation and ubiquitination signaling components. Previous studies speculated that CreA might require some modifications to become an active repressor. There is a great possibility that regulatory response to carbon starvation and components of this regulatory mechanism have an interaction with components of the carbon catabolite repression mechanism. The complete unraveling of these mechanisms can also provide an opportunity for better understanding of complex interactions between carbon and nitrogen repression.

1.10 *A. nidulans* as an experimental organism

Over the last 60 years, *A. nidulans* has been extensively used as a model organism to study cell biology. As in this project, *A. nidulans* is used as an 'experimental tool' to investigate research questions, it is important to understand the life cycle as well as various techniques successfully performed in this filamentous fungus. *A. nidulans* exhibits three different life cycles which can be manipulated for various laboratory experiments. In the asexual cycle, conidiophores grow from filamentous vegetative hyphae, and then elongate into the air to produce conidia which then disperse and start the cycle again. Generally, conidia can germinate within 3-8 hours and a fully mature colony is developed in 48 hours. Asexual spores are ideal for mutagenesis and generate pigments that can be used as markers to identify particular nuclei. Sexual development occurs by the production of presumed nurse cells and closed sexual fruiting bodies known as cleistothecia. The cleistothecia contain sexual spores or ascospores arranged in non-linear asci. The ascus is formed by the enlargement of a penultimate cell where a transient diploid zygote has formed by a fusion of its two nuclei. This diploid zygote then produces four nuclei by meiosis and then divides mitotically to generate eight nuclei. Under laboratory conditions, inter-crossing with any laboratory strains is possible through inducing its sexual cycle. The sexual cycle can be used for different mapping studies and cleistothecium analysis. The parasexual cycle consists of the formation of balanced heterokaryon. This cycle is useful for complementation, dominance, linkage analysis, recombination and centromere mapping (Davis, et al. 1993, Martinelli 1994, Todd, et al. 2007) [Figure 1.7; (Todd, et al. 2007)].

To date, research on *A. nidulans* has contributed to the understanding of various fundamental issues including gene action and recombination (Kafer 1958, Kafer 1961), cell cycle (Oakley and Morris 1981, Osmani, et al. 1988a, Osmani and Mirabito 2004, Osmani, et al. 1988b), spore development (Adams, et al. 1988, Clutterb.Aj 1969, Timberlake 1990), DNA repair (Goldman and Kafer 2004), metabolism and its control (Edited by Brambl 2004), secondary metabolism (Keller 2006), pH regulation (Espeso, et al. 1993, Penalva, et al. 2008) and signaling (Hicks, et al. 1997). The organism has several advantages including metabolic versatility, vegetative and rapid growth, compact colonial growth, availability of a collection of auxotrophic mutants, production of uninucleate conidia, asexual and sexual development, growth on wide range of carbon, nitrogen, sulfur, phosphorus sources as well as simple minimal medium - that make *A. nidulans* an excellent experimental model for classical genetic analysis (Todd, et al. 2007). Features including DNA-mediated transformation either as non-homologous or homologous integration, availability of selectable markers, tightly induced promoters for overexpression or conditional expression, RNA-mediated gene silencing, genome sequencing, ChIP-seq make *A. nidulans* an excellent tool for molecular genetic analysis (Suzuki, et al. 2012, Todd, et al. 2007).

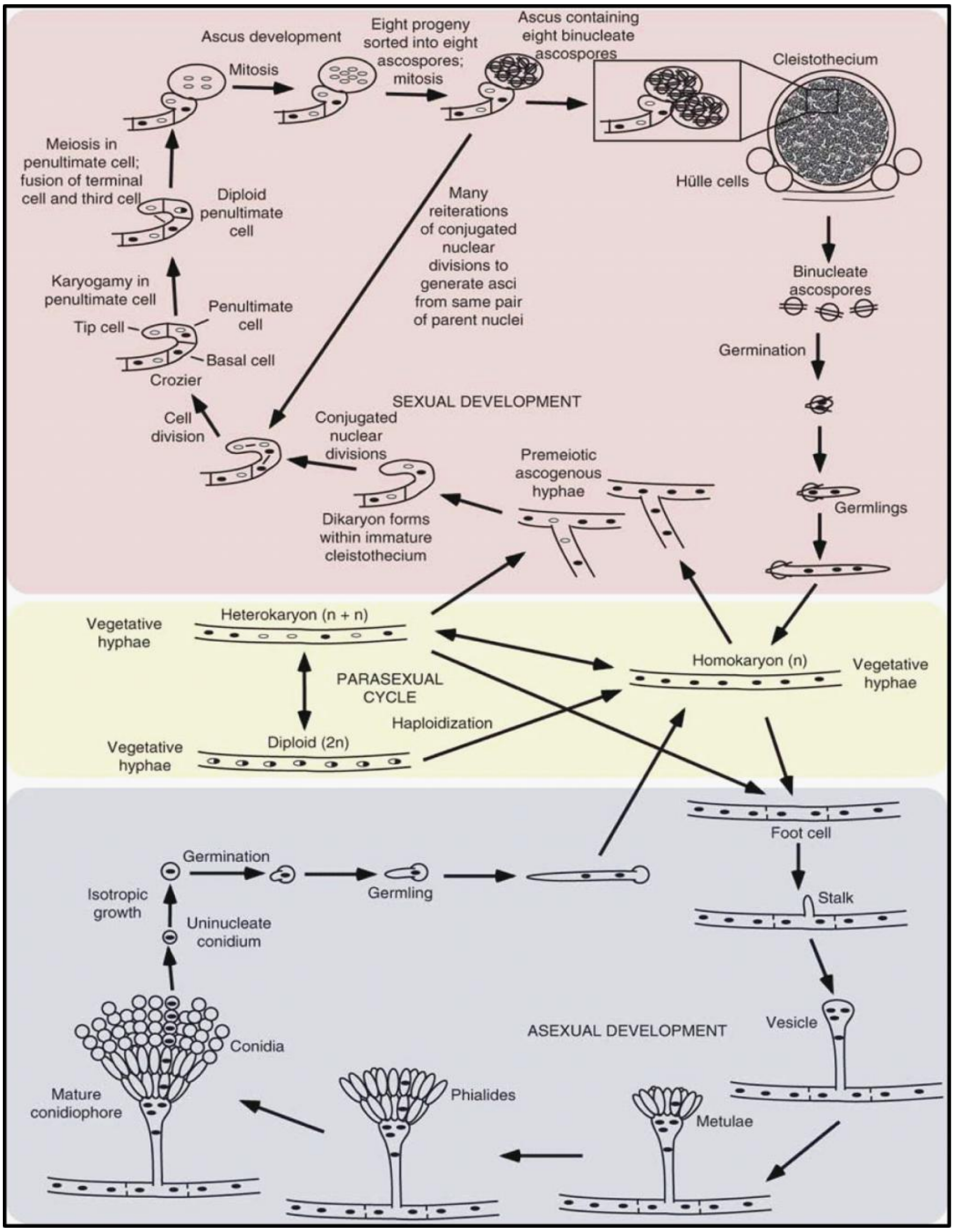

Figure 1.7 Life cycles of *A. nidulans*. *A. nidulans* shows three different life cycles. In the asexual cycle, conidiophores grow from filamentous vegetative hyphae, and then elongate into the air to produce conidia which then disperse and start the cycle again. In the parasexual cycle, vegetative hyphae from two individuals may fuse to form a heterokaryon and nuclei in a heterokaryon or a homokaryon may fuse to form a diploid. In the sexual cycle, presumed nurse cells and closed sexual fruiting bodies (cleistothecia) are produced. Cleistothecia contain sexual spores (ascospores) arranged in nonlinear asci. The ascus is formed by the enlargement of a penultimate cell where a transient diploid zygote has formed by a fusion of its two nuclei. This diploid zygote then produces four nuclei by meiosis and then divides mitotically to generate eight nuclei. Source: (Todd, et al. 2007).

1.11 Aims of the study

The carbon catabolite repression mechanism in *A. nidulans* has been extensively investigated. Mutational screening identified the *creA*, *creB*, *creC*, *creD* as major genes that are involved in this mechanism. Considering the genetic and biochemical evidence, a model of CCR has been proposed with the possible involvement of ubiquitination and deubiquitination pathways mediated by the CreD-HulA and CreB-CreC complexes respectively (Kelly 2004). Genetic screening showed that both the *creA* and *creB* positively affect the CCR pathways, though the molecular mechanism of interaction between *creA*/CreA and *creB*/CreB is unknown. A strain containing the *creA204* and *creB15* alleles was investigated to identify the genetic interaction between these genes (Hynes and Kelly 1977). As both the alleles were identified as partial loss of functions alleles, they exhibited relatively weak phenotypes compare to complete loss of functions alleles (Dowzer and Kelly 1991, Lockington and Kelly 2001). Coimmunoprecipitation experiments with strains expressing CreA and CreB from a constitutive promoter revealed that CreA might be a target for the deubiquitinating enzyme CreB, since a fraction of CreA was precipitated with CreB but not vice versa (Kamlangdee 2008). On the other hand, the *creD34* mutation indicates an opposite role for CreD which is thought to be involved in the ubiquitination of CreA (Boase and Kelly 2004). Both Strauss, et al. (1999) and Roy, et al. (2008) speculated that CreA requires post-translational modifications to become an active repressor. Western analysis with a CreA overexpressing strain showed that some fraction of CreA was present among the ubiquitinated proteins (Kamlangdee 2008). However, experiments using overexpressing strains can give a false positive indication especially when ubiquitination and deubiquitination pathways are involved as over-production of proteins can lead to misfolding and processing via the proteasome.

In *A. nidulans*, the global repressor protein CreA plays a role in both repressing and derepressing growth conditions. High-density microarray analysis of *creA* deleted and WT strains in grown in repressing and derepressing conditions was performed. Cluster analysis revealed the genes that are either regulated/partially regulated or not regulated by CreA, although this type of analysis does not reveal whether they are a direct or indirect target of CreA (Mogensen, et al. 2006). In *T. reesei*, similar approaches were taken to identify the genes that are regulated by the Cre1 (Portnoy, et al. 2011a).

In this work, experiments were carried out to investigate the genetic and biochemical interactions between the global repressor protein CreA and the deubiquitinating enzyme CreB. This included genetic analysis of strains containing null alleles of both genes, as well as biochemical analysis of strains that express proteins from their native promoters. In addition, post-translational modifications (phosphorylation and ubiquitination) of CreA were also investigated as phosphorylation of a protein can often be a marker to trigger subsequent ubiquitination [reviewed by (Nguyen, et al. 2013)]. As a global repressor protein, direct targets of CreA in both repressing and derepressing conditions were also determined.

The principle purpose of this project is to identify the molecular mechanisms of how the deubiquitinating enzyme CreB fits into the CCR regulatory pathways, and to reveal which genes are directly bound by CreA in repressing and derepressing conditions in *A. nidulans*.

The specific aims to be addressed in this work are:

Aim 1: Is CreA a direct target of CreB

In the proposed CCR model, CreA is suggested to be deubiquitinated by the CreB protein in the presence of glucose (Kelly 2004). Previously, a double mutant strain containing *creA204* and *creB15* alleles was analyzed, however, both the alleles are partial loss of functions alleles and showed relatively weak phenotypes compared to null mutants. On the other hand, CoIP studies using strains overexpressing CreA and CreB revealed that CreA might be a direct target for CreB (Kamlangdee 2008), though, overexpression of a protein can lead to a false positive indication especially when deubiquitination is involved. To investigate the genetic interactions between the *creA* and *creB* genes, a double null mutant strain will be generated by crossing the *creA* and *creB* null mutants and comparing this with single null mutant and/or WT in various systems that are subject to the CCR regulatory network. To identify whether CreA is a target of CreB, epitope-tagged CreA and CreB strains that express proteins from their native promoters will be generated and both proteins will be purified after growth in repressing and derepressing conditions. After Western transfers, proteins will be detected using antibodies directed against the epitope tag. Purified proteins will also be analyzed by LCMS to identify co-purified proteins.

Aim 2: Post-translational modifications of CreA: phosphorylated and/or ubiquitinated?

The epitope-tagged CreA strain that expresses proteins from a native promoter will be grown in repressing and derepressing conditions and proteins will be purified. For phosphorylation, a phosphate-affinity polyacrylamide gel electrophoresis system will be used to detect mobility shifts implying phosphorylation. The dinuclear metal complex acts as a selective phosphate binding tag molecule in an aqueous solution at a neutral pH. The degree of migration of phosphoproteins is altered compared to those of their nonphosphorylated counterpart because the tag molecules trap phosphoproteins reversibly during electrophoresis (Kinoshita, et al. 2009). Westerns will be performed in the presence of appropriate controls to detect any altered mobility for CreA. For ubiquitination, purified CreA and appropriate controls will be separated by SDS-PAGE and CreA will be detected using an antibody directed against the epitope tag. Anti-ubiquitin antibody will be used to determine the ubiquitination status. In addition to westerns, LSMS will be carried out with purified CreA to detect any phosphorylated and/or ubiquitinated peptides.

Aim 3: To determine the full range of genes directly regulated by CreA

High-density microarray of *A. nidulans* showed an overview of the global transcriptional response caused by deletion of *creA* (Mogensen, et al. 2006). However, no experiments have been performed to identify direct targets of CreA. For this, ChIP-seq will be performed using an epitope-tagged CreA strain that expresses protein from a native promoter in both repressed and derepressed conditions. DNA samples obtained in the ChIP experiments will be sequenced and the sequences will be mapped to the reference genome to identify the directly regulated genes. Wild-type and CreAΔ strains will be used as negative controls in this experiment.

Chapter 2

Statement of Authorship

Title of Paper	The CreB deubiquitinating enzyme does not directly target the CreA repressor protein in *Aspergillus nidulans*.
Publication Status	
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Principal Author

Name of Principal Author (Candidate)	Md Ashiqul Alam		
Contribution to the Paper	Generation of CreABΔ strain; phenotype analysis of CreABΔ strain in various plate growth tests; enzyme assay, RTqPCR and statistical analysis; generation of CreAcTAP, CreBFLAG, CreBcTAP strains; Co-purification analysis of CreAcTAP and CreBFLAG; western analysis for ubiquitination and phosphorylation status of CreA; purification of CreA and CreB for mass spectrometry analysis; MS data analysis; generation of various *nkuAΔ* strains; co-drafted the manuscript.		
Overall percentage (%)	70%		
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.		
Signature		Date	26/09/16

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

the candidate's stated contribution to the publication is accurate (as detailed above);

permission is granted for the candidate in include the publication in the thesis; and

the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Niyom Kamlangdee		
Contribution to the Paper	Generation of over-expressed strains T3.6, T3H2, diploid; CoIP analysis of T3.6, T3H2 and diploid strains; western analysis of T3H2 for ubiquitination status of CreA. (10%)		
Signature		Date	19.9.2016

Name of Co-Author	Joan M. Kelly		
Contribution to the Paper	Directed research; co-drafted the manuscript (20%).		
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ORIGINAL ARTICLE

The CreB deubiquitinating enzyme does not directly target the CreA repressor protein in *Aspergillus nidulans*

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Abstract Ubiquitination/deubiquitination pathways are now recognized as key components of gene regulatory mechanisms in eukaryotes. The major transcriptional repressor for carbon catabolite repression in *Aspergillus nidulans* is CreA, and mutational analysis led to the suggestion that a regulatory ubiquitination/deubiquitination pathway is involved. A key unanswered question is if and how this pathway, comprising CreB (deubiquitinating enzyme) and HulA (ubiquitin ligase) and other proteins, is involved in the regulatory mechanism. Previously, missense alleles of *creA* and *creB* were analysed for genetic interactions, and here we extended this to complete loss-of-function alleles of *creA* and *creB*, and compared morphological and biochemical phenotypes, which confirmed genetic interaction between the genes. We investigated whether CreA, or a protein in a complex with it, is a direct target of the CreB deubiquitination enzyme, using co-purifications of CreA and CreB, first using strains that overexpress the proteins and then using strains that express the proteins from their native promoters. The Phos-tag system was used to show that CreA is a phosphorylated protein, but no ubiquitination was detected using anti-ubiquitin antibodies and Western analysis. These findings were confirmed using mass spectrometry, which confirmed that CreA was differentially phosphorylated but not ubiquitinated. Thus, CreA is not a direct target of CreB, and nor are proteins that form part of a stable complex with CreA a target of CreB. These results open up new questions regarding the molecular mechanism of CreA repressing activity, and how the ubiquitination pathway involving CreB interacts with this regulatory network.

Keywords Regulatory deubiquitination · Transcriptional repression · CreA DNA-binding protein · CreB deubiquitinating enzyme · *Aspergillus nidulans* · Carbon catabolite repression

Introduction

In eukaryotic microorganisms, efficient growth is achieved through the interaction of regulatory networks including those governing carbon and nitrogen metabolism, sulphur, pH balance and salt tolerance (Kelly and Katz 2010; New et al. 2014; Penalva et al. 2008; Pisyk et al. 2015; Wong et al. 2008). These mechanisms allow the most efficient use of the available nutrients and rapid adaptation to changing environmental conditions. In the case of carbon, carbon catabolite repression (CCR) allows the microorganisms to use favourable carbon sources and simultaneously repress the expression of genes that are required to metabolize less favoured carbon sources. The regulatory networks are not independent, with close interactions between the networks

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for carbon and nitrogen repression, and starvation stress. Portney and colleagues reported that some of the transcriptional effect of CCR is via the regulation of transporters and the use of nitrogen substrates (Portnoy et al. 2011). We wish to use the model filamentous fungus, *Aspergillus nidulans,* to dissect and thus understand the molecular mechanism of CCR, which is an important pathway for potential manipulation in biotechnological applications in processes such as heterologous protein expression and ethanol fuel production.

In the filamentous fungus *Aspergillus nidulans*, CreA, a Cys_2-His_2 DNA-binding zinc finger transcriptional repressor protein, is involved in CCR (Dowzer and Kelly 1989, 1991). Missense and frameshift mutations in the *creA* gene result in partial derepression of a range of pathways subject to CCR, and in addition have significant effects on morphology. Complete loss-of-function mutations of the *creA* gene show strong morphological changes and high levels of derepression (Shroff et al. 1996, 1997). Homologues of CreA have been identified in a number of other filamentous fungi. In *Trichoderma reesei* and *Aspergillus oryzae*, strains with a deletion of the *creA* homologous gene also showed a more compact colony morphology than the WT strain (Ichinose et al. 2014; Ilmen et al. 1996). In *A. nidulans*, the activity of CreA is not critically regulated by sub-cellular localization as some CreA was present in the nucleus in both carbon catabolite repressing and derepressing conditions (Roy et al. 2008). Moreover, derepression does not require large scale degradation of CreA (Kamlangdee 2008). Strauss and colleagues reported that the regulation of CreA occurs at both transcriptional and post-transcriptional levels, and speculated that CreA activity could be changed due to modification of the protein which is supported by the presence of a sequence similar to a consensus sequence involved in ubiquitination (Strauss et al. 1999). Very recently, Ries and colleagues (2016) presented some preliminary evidence that CreA is ubiquitinated, based on a smear above the CreA band in a Western blot probed with an anti-ubiquitin antibody which was more intense in conditions that led to less repression.

Screens designed to select mutations that affect CCR also identified the *creB* and *creC* genes. In repressing conditions, mutations in the *creB* and *creC* genes result in expression of some enzymes including alcohol dehydrogenase, acetamidase, and acetyl co-enzyme A synthetase under conditions where they are usually absent due to CCR (Hynes and Kelly 1977; Kelly and Hynes 1977). In addition, these same mutant alleles show a pleiotropic range of phenotypes that are unrelated to CCR, such as poor growth on quinate and proline where these compounds provide the sole source of carbon (Hynes and Kelly 1977). Unlike *creA* mutations, complete and partial loss-of-function alleles of the *creB* gene show only small effects on colony morphology (Hynes and Kelly 1977; Lockington and Kelly 2001). The *creB* gene encodes a deubiquitinating enzyme of the ubiquitin processing protease family (Ubp/Usp) (Lockington and Kelly 2001) and the *creC* gene encodes a protein containing WD-40 repeats (Todd et al. 2000). Co-immunoprecipitation experiments have shown that both proteins are present in a complex and overexpression of CreB can compensate the lack of CreC but not vice versa, suggesting that CreB is the active partner of this complex (Lockington and Kelly 2002).

On the other hand, the *creD* gene was identified as a suppressor of the *creC27* mutant phenotype on medium containing fluoroacetamide in the presence of glucose. This mutation, *creD34*, can also suppress some phenotypic effects of *creB15* and, to a small extent, *creA204* (Hynes and Kelly 1977; Kelly 1980), suggesting that the *creD* gene plays an opposite role to the *creA*, *creB* and *creC* genes in the regulatory network of CCR. The *creD* gene encodes an arrestin motif protein that interacts with a ubiquitin protein ligase, HulA, indicating its involvement in the ubiquitination process in this regulatory network (Boase and Kelly 2004).

Based on the genetic screening results and identification of proteins that are potentially involved in the ubiquitination and deubiquitination pathways, a model was proposed that in derepressing conditions, the CreD/HulA complex might be involved in the ubiquitination of the repressor protein CreA, or a protein that acts in a complex with CreA, modifying its activity and preventing repression. Whereas in the presence of carbon sources that trigger repression, the deubiquitinating enzyme CreB, together with CreC, might remove the ubiquitin molecule or molecules and thus restore the repressing activity of CreA or a CreA complex (Kelly 2004).

CCR has also been studied in the unicellular yeast, *Saccharomyces cerevisiae*, and in a range of filamentous fungi. In *S. cerevisiae*, the repressor Mig1p has some sequence similarities with CreA, notably the DNA-binding domain, and the consensus sequence to which it binds, an acidic region and a small repression domain. The cellular events involved in repression and derepression are understood in *S. cerevisiae*, and important proteins are the Snf1 kinase, required for nuclear export of Mig1p in derepressing conditions, which is necessary for expression of genes required for catabolic pathways to provide glucose, and the Tup1p-Ssn6p corepressor complex which is involved in initiating a repressive chromatin structure in a number of separate repression pathways (Gancedo 1998; Kayikci and Nielsen 2015). In filamentous fungi, the upstream events that trigger repression and derepression, and the role of an Snf1-like kinase remain unclear, and there may be different mechanisms in different filamentous fungi. At least in *A. nidulans, Neurospora crassa and Penicillium marneffei,* the

Tup1p homologues are not critically involved (Hicks et al. 2001; Todd et al. 2003; Yamashiro et al. 1996). A SnfA-like kinase is not involved in CCR in *T. reesei* (Cziferszky et al. 2002, 2003) or *Fusarium graminearum* (Yu et al. 2014), and *snfA* mutants have little effect on many carbon catabolite repression phenotypes in *A. nidulans* (Hynes, MJ, Pers. Comm.). Recent work suggests that the nonessential protein kinases SnfA (homologue of Snf1p in *S. cerevisiae*) and SchA might be involved in nuclear export of CreA and hence mediate derepression of at least cellulases in *A. nidulans* (Brown et al. 2013), although the conditions used were more akin to starvation than derepression, which is supported by the elevation of the XprG starvation response transcription factor, and CreA is known to be degraded in starvation conditions (Alam et al., unpublished). *A. nidulans* genes encoding catalytic hexokinases, *frA*/*hxkA* and *glkA,* have been shown to be involved in CCR, and while mutations in these individual genes do not affect growth on glucose, nor lead to carbon catabolite derepression (Arst et al. 1990; Flipphi et al. 2003), inactivation of both *frA* and *glkA*, which results in neither fructose nor glucose being phosphorylated, results in derepression of genes subject to CCR. This suggests that phosphorylation is required to trigger repression in *A. nidulans*, but HxkA and GlkA must have overlapping function in CCR (Flipphi et al. 2003).

To unravel the regulatory steps in CCR in *A. nidulans*, it is important to investigate the possible interaction between CreA and CreB, as both positively affect repression. Previously, a double mutant strain containing the *creA204* and *creB15* alleles was used to probe the genetic interaction between them (Hynes and Kelly 1977); however, both alleles were subsequently found to be missense alleles (Dowzer and Kelly 1991; Lockington and Kelly 2001) with only relatively weak phenotypes compared to loss-of-function alleles. In this study, first we describe evidence for genetic interaction in the double null mutant strain containing *creAΔ99* and *creB1937.* In *A. oryzae*, a double null mutant strain for the *creA* and *creB* genes has shown improved production for α-amylase enzymes compared with the *creA* and *creB* single mutants and WT strains (Ichinose et al. 2014). Secondly, we used strains containing tagged versions of CreA and CreB and co-purification, both in strains where the constructs were overexpressed and in strains where the constructs were expressed from their own promoters, to resolve the question as to whether the proteins are directly interacting or in a complex.

Materials and methods

Strains and media

Aspergillus nidulans strains used and their genotypes are shown in Table 1. *Aspergillus* media are based on those described by Cove (1966). Carbon and nitrogen sources were added aseptically to the media to reach the final concentrations as shown. Transformation of *A. nidulans* was based on the procedure of Tilburn et al. (1983).

Table 1 List of strains

Strains	Genotype	References
WT	*biA1; niiA4*	Pateman et al. (1967)
CreB1937	*yA1 pabaA1; creB1937*	Lockington and Kelly (2001)
CreAΔ99	*yA1 pabaA1; creAΔ99*	Shroff et al. (1997)
CreBΔ16	*biA1; creB1937; niiA4;*	Cross WT × CreB1937
CreABΔ	*yA1 pabaA1 creAΔ99; creB1937*	This work
CreA$^{\mathrm{cTAP}}$14	*yA1 creAΔ99::pGEMTeasyCreA*^{cTAP}*; pyroA4; argB2*	This work
CreB$^{\mathrm{FLAG}}$14	*yA1pabaA1; creB1937::pGEMTeasyCreB*^{FLAG}	This work
CreA$^{\mathrm{cTAP}}$CreB$^{\mathrm{FLAG}}$15	*yA1creAΔ99::pGEMTeasyCreA*^{cTAP}*; creB1937::pGEMTeasyCreB*^{FLAG}*; pyroA4*	This work
CreAΔ99nkuAΔ	*yA1 creAΔ99; pyroA2; nkuAΔ*	This work
CreB1937nkuAΔ	*yA1 pabaA1; creB1937; nkuAΔ*	This work
H17A12	*yA1 adE20 suA1adE20; areA217; riboB2*	Hynes (1975)
JKABA3	*yA1 pabaA1; creAΔ99; creB1937; areA217; niiA4*	This work
TA3H2	*yA1 pabaA4 creAΔ::argB*$^{+}$*; argB2; niiAx riboB2*[pGPD::CreA$^{\mathrm{HA2His6}}$;pPL3]	Kamlangdee (2008)
T3.6	*yA1 pabaA1; creB1937; riboB2::[pPL3]pGPDCreBFLAG*	Lockington and Kelly (2002)
TA3H2/T3.6	Diploid from TA3H2/T3.6	Kamlangdee (2008)
T7	*yA1 pabaA1; riboB2::[pPL3]pGPDCreA*^{HAGFP}	Kamlangdee (2008)
S4	*yA1 pabaA1; riboB2::CreA*^{HAGFP}	(Lockington, Unpublished)
CreB$^{\mathrm{cTAP}}$15	*yA1 pabaA1;creB1937::pGEMTeasyCreB*^{cTAP}*; pyroA4*	This work
CreB1937 nkuAΔ_1	*yA1 pabaA1; creB1937; pyroA4; nkuAΔ*	This work

Table 2 List of oligonucleotides

Name	Sequence (5′–3′)	Purpose
349	TTGCTGGGAGGGGGCATC	Detection of CreAΔ99
350	GCAACCAGGATCGTCAGT	
2056	GCGGTCATTACGGCTCTAGG	Detection of CreB1937
2255	CCTACCAAGTGTTTCCGAACTG	
Tap_GA_2	AGTGCCACCTGACGCGCCCTCAAGCAGCAGGCGATC	5′CreA fragment (CreA$^{\mathrm{cTAP}}$ construct)
Tap_GA_3	TCTTTTCCATGAACCTCTCAGCCAAGTCAC	
Tap_GA_4	TGAGAGGTTCATGGAAAAGAGAAGATGGAAAAAG	cTAP fragment (CreA$^{\mathrm{cTAP}}$ construct)
Tap_GA_5	TTTGGCCGGATCAGGTTGACTTCCCCGC	
Tap_GA_6	GTCAACCTGATCCGGCCAAAAAACTTCG	3′CreA fragment (CreA$^{\mathrm{cTAP}}$ construct)
Tap_GA_7	CACCCGCCGCGCTTAATGCGCCGAATAGTAAACTGCTGAGGCGCTTG	
ArgB_F	TCAAGGGCCTGATGCAAT	Detection of single copy *argB* gene in CreA$^{\mathrm{cTAP}}$14
ArgB_R	TATATTTAGGGACGGAATGATCTC	
cTAP_Test_F	TGAATTTGTTGTCGACTTTCGG	Homologous integration
CreAcTAP Homo	TCGCTCCAGGCTATCACACGC	
CreB_Gene_F	ATGTTCCTGCGATTTGTCTG	CreB fragment (7 kb)
CreB_Gene_R	TCACTTTACTTCCTCACCTCCTC	
CreB_F	AGAGGTGCAGTCTCAAATCAGC	5′CreB with FLAG tag
FLAG_CreB_RC_R	GGAAGAAACGGCACAACTCACTTGTCGTCATCGTCTTTGTAGTCTGATGAGAGGATAA	
FLAG_CreB_F	GTTGTGCCGTTTCTTCCTGG	3′CreB fragment
CreB3′Rev_new	AACCCAGCATTCCACAAGC	
FLAG_test_R	CTTGTCGTCATCGTCTTTGTAGTC	Homologous integration
nkuA_F	GCGAGCGGTGTATGTCAGTA	*nkuAΔ* checking
nkuA_R	CGTTATTAGCGTCCGTCACA	
alcAf2	GAGGCTCTGGACTTCTTCGCT	*alcA* expression (RTqPCR)
alcAr2	GCGATTCTGCCTTGTTCCATA	
tubC3F	TAACCTGCTCAACCCTGTTCC	*tubC* expression (RTqPCR)
tubC3R	CATAGAGCACAGAGCAGTTTGGAC	
5′B5′TAP_RP	TCTTTTCCATTGATGAGAGGATATTAAAGGAC	5′ CreB fragment (CreB$^{\mathrm{cTAP}}$ construct)
TAP 5′ 3′B_FP	CCTCTCATCAATGGAAAAGAGAAGATGGAAAAAG	cTAP fragment (CreB$^{\mathrm{cTAP}}$ construct)
TAP5′3′B_RP	ACGGCACAACTCAGGTTGACTTCCCCGC	
3′B3′TAP_FP	GTCAACCTGAGTTGTGCCGTTTCTTCCTG	3′ CreB fragment (CreB$^{\mathrm{cTAP}}$ construct)

Genetic analysis techniques were based on Todd et al. (2007). The CreABΔ strain (containing both *creAΔ99* and *creB1937*) was derived by meiotic crossing of CreAΔ99 and CreBΔ16 (Supplementary Fig. 1). DNA was extracted using DNeasy Plant Mini Kit (Qiagen). PCR was performed with gene-specific primers (Table 2) using Phusion HF polymerase (NEB) in a Mastercycler gradient (Eppendorf) PCR cycler. Amplicons were separated by 1 % agarose gel electrophoresis, and purified using a MiniElute Gel Extraction kit (Qiagen). Sequencing was performed by the Australian Genomic Research Facility (AGRF) from purified DNA.

A diploid strain (TA3H2/T3.6) was developed by fusing two haploid strains TA3H2 and T3.6 (see Table 1 for genotype) that overexpress His/HA tagged CreA (CreA$^{\mathrm{2HAHis}}$) and FLAG tagged CreB (CreB$^{\mathrm{FLAG}}$) (Lockington and Kelly 2002), respectively. Diploids that express both the proteins were selected for CoIP. The strains were phenotypically wildtype. For Western analysis, strains were incubated in 1 % glucose at 37 °C with shaking. CreA was purified using a His-Trap HP column (GE Healthcare) and Anti-HA Matrix (Roche). Detection of proteins was carried out by probing with anti-FLAG peroxidase linked monoclonal antibody (Sigma) for CreB$^{\mathrm{FLAG}}$ and anti-HA monoclonal antibody conjugated with peroxidase (Roche) for CreA^{2HAHis}.

The construct used to generate the strain CreA^{cTAP}14, containing a TAP-tagged version of CreA, was generated by fusion PCR (Szewczyk et al. 2006) and contains sequences that are 5′ to *creA* including the native promoter, the *creA* coding sequence, a C-terminal TAP-tag and sequences 3′ to *creA* (Supplementary Fig. 3). The fusion product was then ligated into the pGEMTeasy vector (Promega), to produce pGEMTeasy CreA^{cTAP}. The plasmid was transformed into an *nkuA* deletion strain (CreAΔ99nkuAΔ) for homologous integration (Nayak et al. 2006), and colonies that were complemented for CreA were selected. The strains were phenotypically wildtype. Homologous integration was confirmed by genomic PCR using a primer internal to the TAP-tag and another ORF-specific primer, which generated a 3 kb DNA fragment for CreA^{cTAP}14. Plate testing was performed with synthetic media containing allyl alcohol to confirm expression of CreA. For Western analysis, CreA^{cTAP}14 was incubated in 1 % glucose (repressing) or 1 % arabinose (derepressing) with 0.1 % fructose at 37 °C for 20–24 h with shaking. Mycelia were harvested, press dried and lyophilized overnight. CreA^{cTAP} was purified as described by Bayram et al. (2012) and detected by probing with anti-TAP conjugated with peroxidase polyclonal antibody (GeneScript). In the Western analysis, the CreA^{cTAP}(~63 kDa) protein was detected, together with N-terminally processed CreA of lower molecular weight. The processing of the N-terminus of the CreA protein has been detected previously in a strain containing an N-terminal Myc tagged CreA, when CreA could not be detected by anti-Myc antibody in WB analysis (Lockington, unpublished), and smaller CreA variants were detected in previous published work (Roy et al. 2008).

The strains CreB^{FLAG}14 and CreB^{cTAP}15 were generated and tested in an analogous way to CreA^{cTAP}14, except using *creB* sequences and a FLAG-tag or cTAP-tag (Supplementary Figs. 4, 5). Transformants that were fully complemented for CreB were selected, and the expression of CreB in CreB^{FLAG}14 and CreB^{cTAP}15 was confirmed by growth testing on quinate plus ammonium tartrate medium. The growth conditions for Western analysis were the same as for CreA^{cTAP}14. CreB^{FLAG} (~85 kDa) was purified using Anti-FLAG M2 affinity gel matrix (Sigma), and detected by probing with anti-FLAG peroxidase linked monoclonal antibody (Sigma). CreB^{cTAP} (~106 kDa) was purified and detected as for the CreA^{cTAP}14 strain.

A strain was developed (CreA^{cTAP}CreB^{FLAG}15) that contains both CreA^{cTAP} and CreB^{FLAG} by a genetic cross between CreA^{cTAP}14 and CreB^{FLAG}14 (Supplementary Fig. 6). Phenotypically wildtype progeny from the cross were selected and confirmed using PCR and Western analysis.

Enzyme assays

Estimates of β-galactosidase and α-amylase activities were made using plate tests based on the procedures described in Shroff et al. (1997). Enzyme assays for alcohol dehydrogenase (ADH) were performed according the method described in Hynes and Kelly (1977). Strains were incubated in 50 mM ethyl methyl ketone (EMK) and 1 % glucose or only 50 mM EMK representing repressed-induced and induced conditions, respectively. 0.1 % fructose was added to all media to prevent starvation of strains. After 24 h of incubation at 37 °C with shaking, proteins were extracted and enzyme activity was determined by the ethanol dependent reduction of NAD at 340 nm at 25 °C. Absorbance was measured using a Spectramax M2 spectrophotometer (Molecular Device, USA).

Reverse-transcription quantitative real time PCR (RT-qPCR)

RNA was extracted from the same mycelia that were used for ADH enzyme assay using RNeasy Plant Mini Kit (Qiagen). First strand synthesis of cDNA was performed using the cDNA synthesis kit protocol (Promega). RT-qPCRs were performed with 50 ng cDNA, specific primers and Power SYBR green master mix PCR solution (Applied Biosystem) using an ABI Prism 7000 Sequence Detection System (Applied Biosystem). The PCR cycling conditions were as follows: 2 min at 50 °C, 10 min at 95 °C and 40 cycles of 15 s at 95 °C and 1 min at 60 °C. In all experiments appropriate negative controls containing no DNA template were used. A standard curve was prepared by serial dilution of cDNA for each experiment. RT-qPCR was performed in triplicate for each sample. Cycle thresholds for each triplicate were averaged and normalized against the expression of *tubC* (β-tubulin), which was used as an endogenous control, as described in Semighini et al. (2002). The relative standard curve method for quantification was used to determine the relative fold change in the expression of experimental samples compared to the endogenous control. Three biological replicates were used for calculation of the expression of gene of interest.

Detection of phosphorylation

An acryl amide pendant Mn^{2+} Phos-tag ligand system (Wako Pure Chemical Industry, Japan) and phosphate affinity SDS-PAGE was used for detection of phosphorylated proteins indicated by a mobility shift. The dinuclear metal complex acts as a selective phosphate binding-tag molecule in an aqueous solution at a neutral pH. The degree of migration of phosphoproteins is altered compared to those of their nonphosphorylated counterpart, because the tag molecules trap phosphoproteins reversibly during electrophoresis (Kinoshita et al. 2009a). CreA was immunoprecipitated from T7, expressing CreA^{HAGFP} from the *gpdA* promoter, in repressing and in derepressing conditions. Purified samples were treated with bovine alkaline phosphatase (Sigma) for 60 min according to the manufacturer's protocol, along with β-casein as a positive control. Alkaline phosphatase treated and untreated samples were separated using a 10 % SDS-acrylamide gel containing 100 µmol/L Phos-tag solution. Samples were transferred to PVDF membrane, and β-caseins were detected using Coomassie blue staining and CreA^{HAGFP} was detected by probing with anti-HA peroxidase high-affinity antibody (Roche).

Detection of ubiquitination

UbiQapture-Q matrix (Biomol) was used to purify ubiquitinated proteins. The TA3H2 (CreA^{HAHis}) strain that overexpresses *creA* from the *gpdA* promoter was grown overnight in 1 % glucose at 37 °C. Three fractions (total extract, unbound fraction, immunoprecipitate) of TA3H2 and WT strains were separated by SDS-PAGE and transferred to PVDF membrane. CreA^{HAHis} was detected by probing with anti-HA peroxidase high-affinity antibody (Roche). An anti-ubiquitin antibody was also used to detect whether purified proteins were ubiquitinated. Two strains, T7 and S4, that express CreA^{HAGFP} from the *gpdA* and native promoter, respectively, were grown in 1 % glucose (repressing) and 1 % arabinose (derepressing) overnight at 37 °C. CreA^{HAGFP} was purified from the total lysate using anti-HA matrix (Roche). IP samples were loaded in duplicate and probed with anti-HA peroxidase high-affinity antibody (Roche) and anti-ubiquitin conjugated with peroxidase antibody (Abcam). Free ubiquitin was added as a positive control.

Proteomics analysis

CreA and CreB were purified from CreA^{cTAP}14 and CreB^{cTAP}15 using the TAP purification protocol (Bayram et al. 2012) and separated by SDS-PAGE. Proteins were fixed using 10 % acetic acid and 40 % methanol solution for 2 h at room temperature. Coomassie staining of the gel was performed with CBB G-250 solution for overnight at room temperature.

For CreA, detection of proteins by LC–MS was performed as described in Meding et al. (2013) by The Adelaide Proteomics Center. Raw data files were subjected to the Proteome Discover software (Thermo Scientific) to set up the workflow.

For CreB, Nano-LC–ESI–MS/MS was performed using an Ultimate 3000 RSLC system (Thermo-Fisher Scientific, Waltham, USA) coupled to an Impact HD™ QTOF mass spectrometer (Bruker Daltonics, Bremen, Germany) via an Advance CaptiveSpray source (Bruker Daltonics). Peptide samples were pre-concentrated onto a C18 trapping column (Acclaim PepMap100 C18 75 µm × 20 mm, Thermo-Fisher Scientific) at a flow rate of 5 µL/min in 2 % (v/v) ACN 0.1 % (v/v) FA for 10 min. Peptide separation was performed using a 75 µm ID C18 column (Acclaim PepMap100 C18 75 µm × 50 cm, Thermo-Fisher Scientific) at a flow rate of 0.2 µL/min using a linear gradient from 5 to 45 % B (A: 5 % (v/v) ACN 0.1 % (v/v) FA, B: 80 % (v/v) ACN 0.1 % (v/v) FA) over 70 min, followed by a 20-min wash with 90 % B, and a 20 min equilibration with 5 % A. MS scans were acquired in the mass range of 300–2200 *m*/*z* in a data-dependent fashion using Bruker's Shotgun Instant Expertise™ method. This method uses IDAS (intensity-dependent acquisition speed) to adapt the speed of acquisition depending on the intensity of precursor ions (fixed cycle time), and RT^2 (RealTime Re-Think) to exclude previously selected precursor ions from undergoing re-fragmentation unless the chromatographic peak intensity of the ion has increased by a factor of 5. Singly charged precursor ions were excluded from acquisition. Collision energy ranged from 23 to 65 % as determined by the *m*/*z* of the precursor ion.

Nano-LC–ESI-MS/MS data analysis

All spectra were analysed using the MaxQuant software (version 1.5.2.8) with the Andromeda search engine against the UniProt *Emericella nidulans* database (downloaded on the 10th of January 2016). The standard Bruker QTOF settings in MaxQuant were used with a mass error tolerance of 40 ppm. The variable modifications of oxidation of methionine, phosphorylation of serine/threonine/tyrosine, ubiquitination of lysine, and the fixed modification of carbamidomethyl of cysteines were specified, with the digestion enzyme specified as trypsin. The false discovery rate (FDR) was set to 1 % for both proteins and peptides, with a minimum peptide length of 7 amino acids.

Results

The CreABΔ strain; a double null mutant for the *creA* and *creB* genes

Genetic analysis of a double mutant for the *creA* and *creB* genes using the *creA204* and *creB15* alleles has been previously published (Hynes and Kelly 1977). Subsequent molecular analysis revealed that both the alleles contain missense mutations and are only partial loss-of-function alleles showing only intermediate phenotypic effects (Lockington and Kelly 2001; Shroff et al. 1996).

Null alleles of the *creA* gene, such as *creA*Δ*99* in which the DNA-binding region of the *creA* gene is disrupted by inserting the $argB^{+}$ gene, were developed using gene replacement techniques. This allele is designed to truncate CreA after the first 45 amino acids, and results in similar phenotypes to the naturally occurring null allele, *creA303*, which theoretically encodes the first 68 amino acids but no zinc finger region or any other putative functional regions (Shroff et al. 1997). On the other hand, a null allele of the *creB* gene, *creB1937,* which was identified during molecular analysis of the gene, contains a G to A mutation which is predicted to result in a truncation of CreB after the first 12 amino acids (Lockington and Kelly 2001). This is the first reported analysis of a strain that is a null mutant for both the *creA* and *creB* genes in *A. nidulans*. To observe the genetic effects due to the functional loss of both the *creA* and *creB* genes, we developed a double null mutant strain, CreABΔ by crossing the CreAΔ99 and CreBΔ16 strains. The double null mutant strain CreABΔ was confirmed using molecular genetic techniques (see "Materials and methods"; Table 1; Supplementary Fig. 1).

Phenotypic analysis

Phenotypes of the CreABΔ strain were observed in a range of carbon and nitrogen sources (Fig. 1; Supplementary Fig. 2). CreAΔ99 grows as a very compact colony on both complete and synthetic complete media, whereas *creB1937* containing strains (CreB1937 and CreBΔ16) showed only slight effects on colony morphology on these media. However, the double null mutant CreABΔ strain showed an intermediate effect on colony morphology showing a less compact and dense colony, suggesting some suppression of the effects of *creA*Δ99 on morphology by *creB1937* (Fig. 1a, c).

Addition of allyl alcohol to synthetic complete medium serves as an indicator of repression or derepression of *alcA*, which encodes alcohol dehydrogenase I, which is subject to carbon catabolite repression in the wildtype strain.

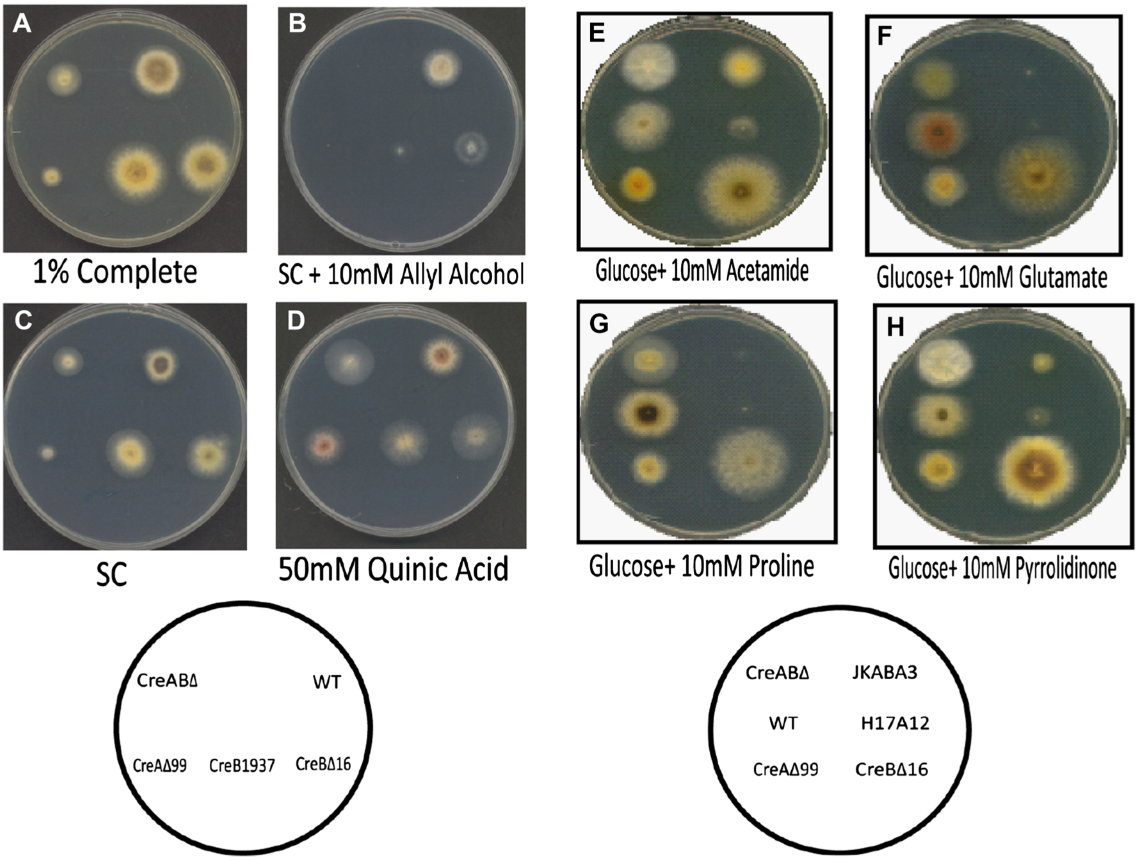


Fig. 1 Phenotypic analysis of strain CreABΔ. Strains were grown on range of media as indicated at the *bottom of each panel* at 37 °C for 2–3 days panel. In **e**, **f**, **g** and **h** the phenotype of CreABΔ was compared with a triple mutant strain which also contained the *areA217* allele (JKABA3), and scored for suppression of the effects of *areA217.* 10 mM ammonium tartrate was used as nitrogen source in **b**, **c** and **d**, and although tartrate provides a very weak carbon source, it is not a significant carbon source in these tests where carbon starvation is not being tested. Strains keys are at the *bottom of the figure*. H17A12 carries the *areA217* mutation (see Table 1)

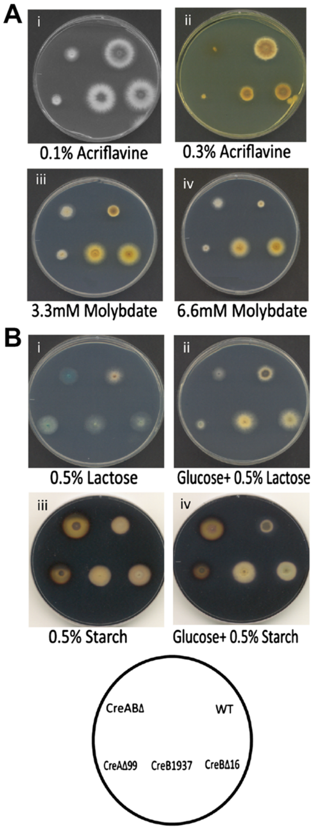
CreAΔ99, CreB1937 and CreBΔ16 were sensitive to allyl alcohol, with *creAΔ99* leading to a more extreme phenotype, indicating higher levels of derepression due to the *creAΔ99* mutation. The double null mutant CreABΔ strain was as sensitive as CreAΔ99 in this test (Fig. 1b).

Strains containing *creB1937* (CreB1937 and CreBΔ16) show reduced growth on some sole carbon sources, including quinate and proline, due to failure to express enzymes and permeases that are needed to metabolize those carbon sources, while strains containing *creAΔ* mutations (CreAΔ99) show very little effect in these conditions (Hynes and Kelly 1977). The double null mutant strain, CreABΔ, grew as weakly as CreB1937 and CreBΔ16 on quinate medium. In addition, the effects on colony morphology due to the *creAΔ99* allele are less apparent on this carbon source (Fig. 1d).

The CreABΔ strain was also tested for growth on acetamide, glutamate, proline and pyrrolidinone as a carbon and/or nitrogen source. When these compounds were used as carbon sources, the CreB1937 and CreBΔ16 strains grew more poorly than WT, while the CreAΔ99 strain had little effect on growth. The CreABΔ double mutant strain showed strong growth on acetamide, but showed weak growth like CreB1937 and CreBΔ16 on the other compounds (Supplementary Fig. 2). On the other hand, when these nutrients were used as the sole nitrogen source with glucose provided as a carbon source, CreB1937 and CreBΔ16 showed stronger growth on acetamide and pyrrolidinone and weaker growth on glutamate and proline, than the WT. However, CreAΔ99 showed strong utilization of acetamide, but had little effects on utilization of other nutrient sources. The double null mutant showed strong growth on acetamide like CreAΔ99, but was similar to the CreB1937 and CreBΔ16 phenotypes on other media (Supplementary Fig. 2).

The suppression of the *areA217* mutant phenotype was tested in a strain that was triple mutant for the *creA*, *creB* and *areA* genes. Strains carrying loss-of-function alleles of *areA* grow poorly, in the presence of glucose, on nitrogen sources that also provide carbon sources (Arst and Cove 1973). Mutations affecting carbon catabolite repression can suppress this phenotype. A strain that contained *creAΔ99*, *creB1937* and *areA217* (JKABA3) showed strong suppression of the *areA217* mutant phenotype on glucose plus acetamide medium, but failed to suppress *areA217* on the other nitrogen sources tested (Fig. 1e–h).

creA mutants cause sensitivity to acriflavine and molybdate, while *creB* mutants lead to increased sensitivity to acriflavine but resistance to molybdate (Arst 1981). Phenotypes of the CreABΔ strain were observed in the presence of the toxic compounds acriflavine and molybdate. The CreABΔ strain showed increased sensitivity to acriflavine (Fig. 2a i–ii), but resistance to molybdate like the CreB1937 and CreBΔ16 (Fig. 2a iii–iv).



C

	CreABΔ	CreAΔ99	CreBΔ16	WT
0.5% Starch	0.15**	0.29****	0.03*	0.01
Glucose + 0.5% Starch	0.13****	0.24***	0.00	0.00

Fig. 2 Resistance to toxic compounds; and β galactosidase and α amylase activities of CreABΔ strain. Strains were grown on media containing: for toxicity, the concentrations of acriflavine and molybdate shown (**a**, *i–iv*); for an estimation of β galactosidase activity, 0.5 % lactose + X-gal (100 μg/ml) (**b**, *i–ii*); for an estimation of α amylase activity, 0.5 % starch (**b**, *iii–iv*). β Galactosidase activity was estimated by the formation of blue precipitate due to break down of X-gal by β galactosidase enzyme. To estimate α amylase activity, the clear zone was measured after 2 days by adding iodine solution to the plates. Estimates were calculated using the distance between the edge of the clear zone and edge of the colony divided by the diameter of the colony. Part **c** shows the average clear zone of three biological replicates. Unpaired *t* test (two-tailed) compared with WT in respective conditions: ****< 0.00005; ***<0.0005; **<0.005; *< 0.05. All plates contain 10 mM ammonium tartrate, and were incubated at 37 °C for 2 days. A strains key is at the *bottom of the figure*

Plate testing as a measure of enzyme activity

β-Galactosidase is required to breakdown lactose into galactose and glucose and the expression is a subject to carbon catabolite repression (Shroff et al. 1997). β-Galactosidase activity can be estimated by growing a colony on a solid agar medium containing X-gal as an indicator, which is broken down by β-galactosidase to produce bright blue colour. Strains were grown in 0.5 % lactose alone and also in the presence of 1 % glucose. While the WT strain produced very little blue pigment, and only when glucose was absent, both CreAΔ99, CreB1937 and CreBΔ16 resulted in increased blue pigment whether glucose was present or absent. The CreABΔ strain produced higher blue pigment than either of the parents in both the presence and absence of glucose (Fig. 2b i–ii). This result indicates that higher levels of expression were achieved when both the *creA* and *creB* genes were mutated whether glucose was present in the media or not.

Aspergillus nidulans secrets α-amylases into the media surrounding a colony when starch is present. Total α-amylase activity can be estimated by adding iodine solution to the medium which interacts with starch to produce a deep blue colour. In contrast, the area where starch has been digested by α-amylases appears as a nonstained clear zone. The distance between the edge of the clear zone and edge of the colony divided by the diameter of the colony allows an estimate of the amount of α-amylase secreted by the colony (Shroff et al. 1997). In the presence of glucose, the WT strain does not express α-amylases as these enzymes are subject to carbon catabolite repression. To estimate the amount of α-amylases secretion, strains were incubated with 0.5 % starch and/or 1 % glucose, and after 2 days incubation, the clear zone was measured. CreAΔ99 produced the biggest clear zone in both the growing conditions, whereas CreBΔ1937 and CreBΔ16 produced little clear zone and only in the absence of glucose. In the presence of glucose, CreBΔ1937 and CreBΔ16 formed no clear zone like the WT strain. The double null mutant strain had less α-amylases activity than the CreAΔ99, but more than CreBΔ1937 and CreBΔ16 (Fig. 2b iii–iv). Figure 2c shows the average ratio of clear zone produced by the strains in three biological replicates.

Alcohol dehydrogenase activity (enzyme assay and RTqPCR)

The extent of derepression in the CreABΔ strain was also investigated by assaying alcohol dehydrogenase activity (ADH). Alcohol dehydrogenase I (ADHI) is encoded by the *alcA* gene and it is required to breakdown ethanol to acetaldehyde (Lockington et al. 1985; Pateman et al. 1983). Expression of *alcA* is regulated both by specific induction and carbon catabolite repression. A co-inducer, such as ethanol or ethyl methyl ketone (EMK), is required for expression, but when glucose is also present carbon catabolite repression mediated by CreA prevents the transcription of both the structural gene *alcA* and the regulatory gene required for induction *alcR* (Kulmburg et al. 1993; Kulmburg et al. 1992). Strains were incubated in 1 % glucose plus 50 mM EMK medium, or in 50 mM EMK medium alone, representing repressed-induced and induced conditions, respectively. 0.1 % fructose and 10 mM ammonium tartrate were added to all media. Enzyme activity was determined after 24 h incubation [see "Materials and methods"; (Hynes and Kelly 1977)].

In repressed-induced conditions there was undetectable enzyme activity in the WT, whereas CreAΔ99 showed activity in these conditions which was as expected, and CreB1937 showed marginal activity (which is less than previously published results with the *creB15* allele (Hynes and Kelly 1977)). The double null mutant showed higher levels of enzyme activity than either of the parent strains. In inducing conditions, CreAΔ99, CreB1937 and the double null strain showed similar activity to the WT strain (Fig. 3a).

The CreB deubiquitinating enzyme is thought to play an important role in carbon catabolite repression of *A. nidulans,* possibly by removing a ubiquitin molecule from CreA, or a protein complexed with CreA. Experimental evidence suggests that CreB also has other targets including QutD (Kamlangdee 2008). Poly-ubiquitination/deubiquitination plays a role in degradation by the proteasome, but ubiquitination/deubiquitination is also known to play a number of other regulatory roles in the cell [reviewed in (Kaiser and Huang 2005)]. Due to the possible involvement of an ubiquitination–deubiquitination system that causes protein degradation, RT-qPCR was performed to confirm whether the differences in alcohol dehydrogenase activity were reflected at the mRNA level.

RNA was extracted from the same mycelia that were used for ADH enzyme assay. In repressed-induced conditions, there was undetectable *alcA* mRNA in the WT, whereas CreAΔ99 showed *alcA* mRNA in these conditions which was as expected. However, *alcA* mRNA was not detectable in CreB1937, although previous experiments using the *creB1937* allele did show some *alcA* mRNA (Hunter et al. 2013). The double null mutant strain gave indication of higher *alcA* mRNA than either CreAΔ99 or CreB1937 in all replicates, but this was not statistically significant overall due to the variation between replicates (Fig. 3b).

Are CreB and CreA present in the cell in a complex?

Since the plate tests and enzyme assays confirmed a genetic interaction between *creA* and *creB*, co-immunoprecipitation experiments were performed to investigate whether the products of these two genes are present in a complex. Since there are no antibodies available to CreA, a diploid strain (TA3H2/T3.6) was constructed by fusing two haploid strains TA3H2 and T3.6, that express His/HA tagged CreA (CreA^{2HAHis}) and FLAG tagged CreB (CreB^{FLAG}), respectively, from the constitutively expressing *gpdA* promoter [(Lockington et al. 2002; Roy et al. 2008); Table 1]. The diploid strain and the haploid parent strains were grown in

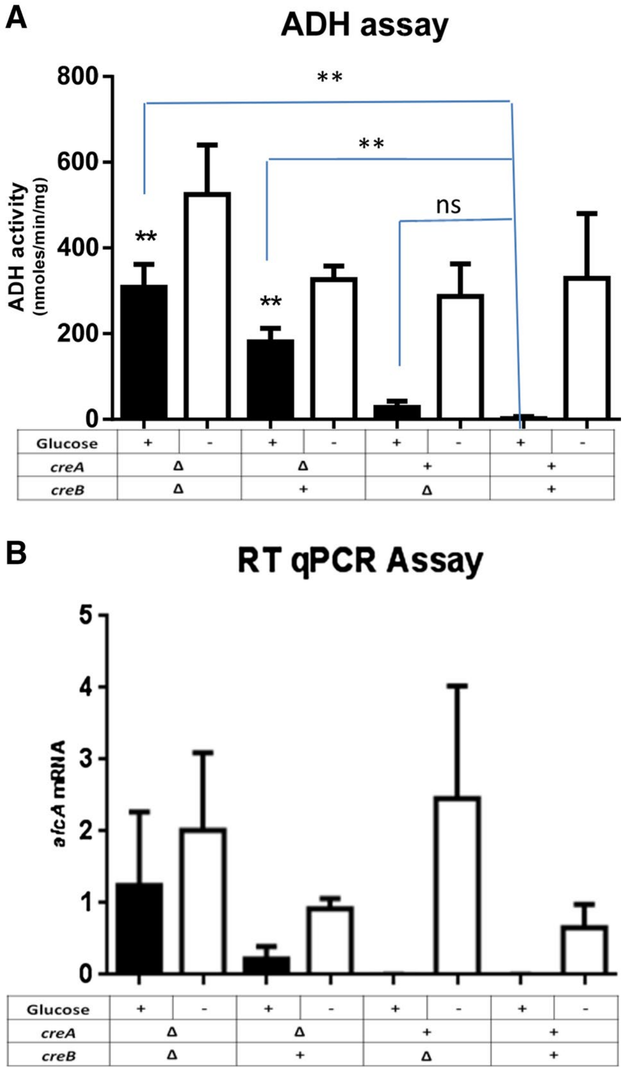


Fig. 3 Alcohol dehydrogenase activity and *alcA* expression in CreABΔ. Strains were grown in media containing 0.1 % fructose + 50 mM EMK + 10 mM ammonium tartrate with and without 1 % glucose for 24 h at 37 °C with continuous shaking. The alcohol dehydrogenase reaction was initiated by 2.8 ml of assay buffer with NAD, ethanol and 0.1 ml of crude extract. ADH activity was determined by ethanol dependent reduction of NAD at 340 nm at 25 °C. This graph represents the average ADH activity of three biological replicates. Unpaired *t* tests (two-tailed) compared with WT in respective conditions were calculated, and *p* values are shown for repressed-induced conditions (**<0.005); No significant *p* values were detected between relevant samples from induced mycelia (**a**). RNA extracted from the same mycelia were used to generate cDNA and qPCR was performed using SYBR green as detector. Cycle thresholds for each triplicate were averaged and normalized against the expression of *tubC.* This graph represents average *alcA* mRNA of three biological replicates. Unpaired *t* tests (two-tailed) compared with WT in respective conditions were calculated, and no significant *p values* were detected between the relevant samples. In the induced conditions, this probably indicates no significant difference, but the variation is large. In repressed conditions, although not statistically significant, the graph is included to indicate a possible trend in the double null strain (**b**). *Error bars* represent the standard errors of the means

glucose medium, and proteins were extracted and initial Westerns showed that CreA^{2HAHis} and CreB^{FLAG} could be detected as expected using anti-HA and anti-FLAG antibodies, respectively. CreA was purified from the lysate using a two-step procedure, firstly by using a His-trap column, and then the eluate was subjected to a further round of purification using anti-HA matrix. The purified proteins were analysed by Western transfer. When probed with anti-FLAG antibody, after two rounds of purification for CreA^{2HAHis}, CreB^{FLAG} was also co-purified in the diploid strain, but not in the haploid strain containing CreB^{FLAG} (Fig. 4). This indicates that in this strain, at least some CreB and CreA may exist in a complex in vivo in *A. nidulans*. However, when CreB^{FLAG} was purified from the lysate using anti-FLAG matrix, no CreA^{2HAHis} was detected in the diploid strain (results not shown), possibly indicating that CreB has a range of substrates, and any one interaction was below the range of detection.

These experiments were designed using overexpressed *creA* and *creB*, in order to allow detection. However, native *creA* transcription is autoregulated, and furthermore, overproduction of proteins can lead to misfolding and processing via the proteasome, a particularly important consideration since CreB is a deubiquitinating enzyme. In addition, strains that are both mutant for *creB* and overexpressing *creA* show normal levels of CCR, so overexpression of *creA* partially overrides the requirement for *creB* for repression (Lockington, RA, personal communication). Since indications of interaction were detected in the overexpressing strains, experiments using strains that express the proteins from their native promoters were undertaken. New strains containing CreA^{cTAP} (CreA^{cTAP}14) and CreB^{FLAG} (CreB^{FLAG}14) were constructed in which the fusion genes are expressed from their native promoters (Supplementary Fig. 4), and a strain containing both constructs (CreA^{cTAP}CreB^{FLAG}15) was derived from a meiotic cross. CreA^{cTAP}CreB^{FLAG}15 was incubated in both repressing and derepressing conditions, and proteins were purified using the TAP protocol for CreA^{cTAP} or the anti-FLAG matrix for CreB^{FLAG}. The WT strain was used as a negative control in these experiments. The purified samples were loaded in duplicate, and the membranes were probed with the antibody specific to the tag. CreA^{cTAP} purified by the TAP purification protocol was probed with anti-FLAG peroxidase linked (Sigma) that detected CreB^{FLAG} in the positive control CreB^{FLAG}14, but no CreB^{FLAG} was detected for CreA^{cTAP}CreB^{FLAG}15 in either repressing or derepressing conditions (Fig. 5a). CreA^{cTAP} purified by the TAP purification protocol was also probed with anti-TAP conjugated with peroxidase (GeneScript) and CreA^{cTAP} was detected in both repressing and derepressing conditions (Fig. 5b). Similarly, CreB^{FLAG} purified by FLAG purification was

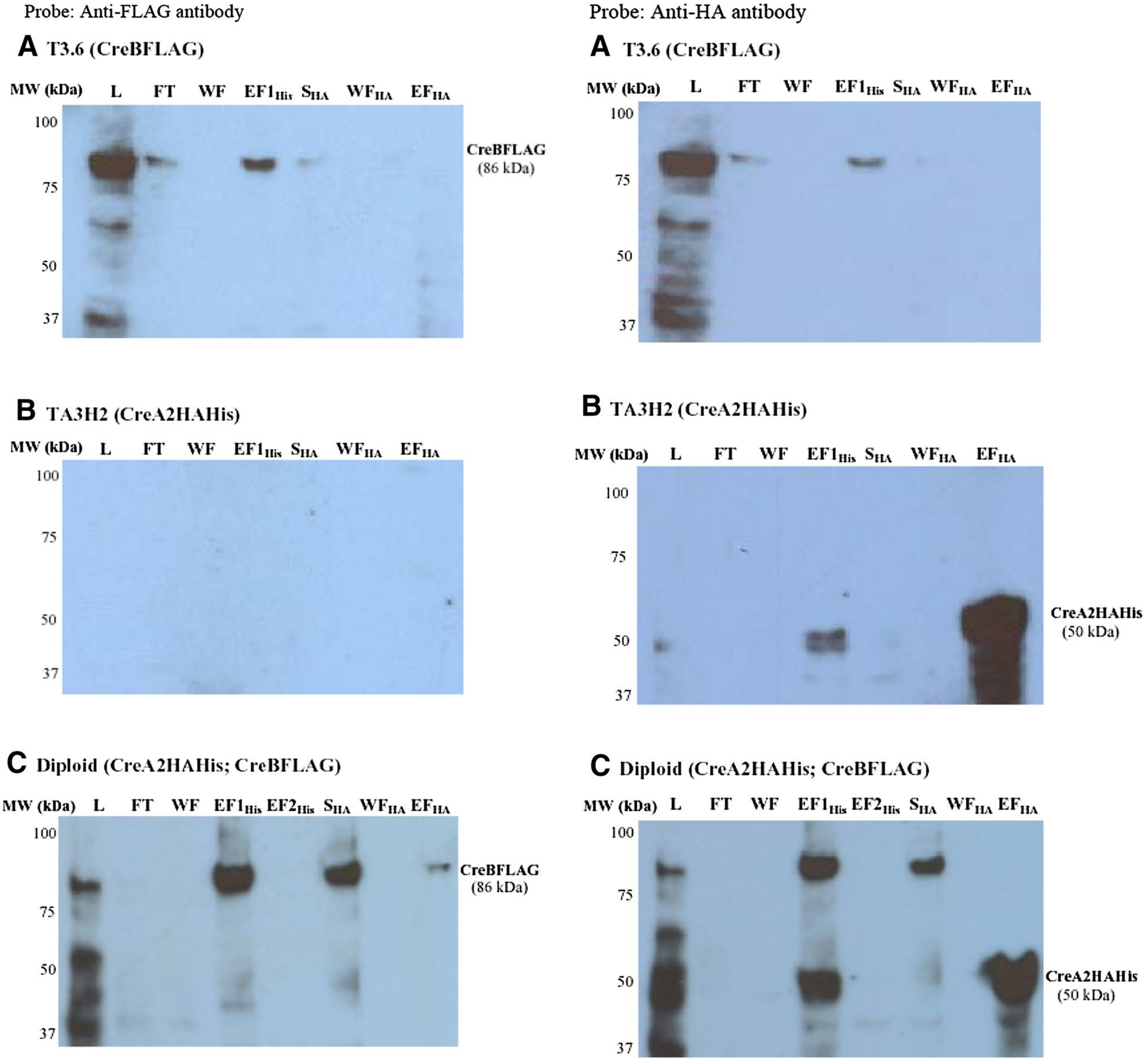
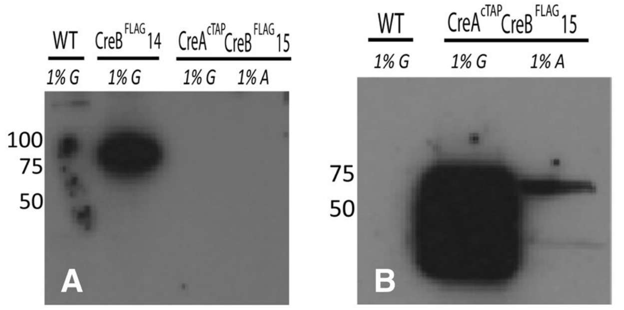


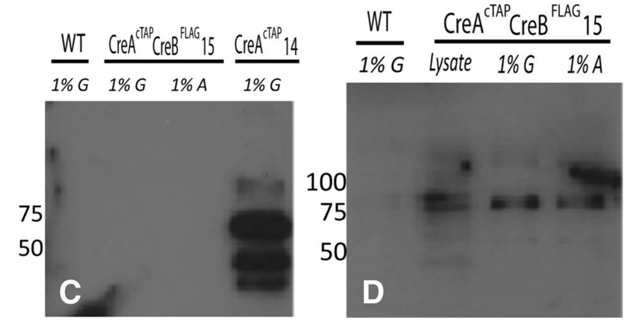
Fig. 4 CreB is present in a complex with CreA in overexpressing strains. Total proteins were extracted from three strains, T3.6 (Part **a**), TA3H2 (Part **b**), and TA3H2/T3.6 (Part **c**), that were grown in 1 % glucose for 18 h. CreA was purified from total protein using a His-Trap HP column (GE Healthcare) and further purified using anti-HA matrix (Roche). Total protein lysate (L); flow through from His-Trap column (FT); Wash fraction from His-Trap column (WF); eluted fractions from His-Trap column ($EF1_{His}$ and $EF2_{His}$); supernatant of HA-matrix (S_{HA}); wash fraction of HA-matrix (WF_{HA}); eluted fraction of HA-matrix (EF_{HA}). Samples were separated by SDS-PAGE, transferred to PVDF membrane and probed firstly with anti-FLAG monoclonal antibody conjugated with peroxidase (Sigma; LHS) and then further probed with anti-HA monoclonal antibody conjugated with peroxidase (Roche: RHS). In part A (LHS; probed with anti-FLAG) there is some $CreB^{FLAG}$ signal carried over in the T3.6 haploid after a single purification of CreA using a His-trap column, which is the reason that CreA needed to be purified in a two-step process, first using the His column, followed by anti-HA matrix, to ensure that there were no carry-over proteins. Note that the stripping of the Anti-FLAG probe from the membranes in the LHS of the figure was partial, and the signal is carried over to the Anti-HA probed analysis in the RHS of the figure. Because the proteins are different molecular weights, this does not affect the interpretation of the experiment

probed with anti-TAP conjugated with peroxidase (GeneScript) and anti-FLAG peroxidase linked (Sigma), respectively. Probing with anti-TAP antibody detected $CreA^{cTAP}$ in the positive control, $CreA^{cTAP}14$; however, CreA was not detected in $CreA^{cTAP}CreB^{FLAG}15$ in either of the two conditions (Fig. 5c), whereas $CreB^{FLAG}$ was detected for $CreA^{cTAP}CreB^{FLAG}15$ in both the lysate and purified fractions (Fig. 5d). These results indicate that CreA and CreB



Purification: TAP
Probe: Anti-FLAG

Purification: TAP
Probe: Anti-TAP



Purification: FLAG
Probe: Anti-TAP

Purification: FLAG
Probe : Anti-FLAG

Fig. 5 $\text{CreA}^{\text{cTAP}}$ and $\text{CreB}^{\text{FLAG}}$ are not co-purified when expressed from their native promoters. $\text{CreA}^{\text{cTAP}}\text{CreB}^{\text{FLAG}}$15 was incubated in 1 % glucose and 1 % arabinose representing repressing and derepressing conditions, respectively. Proteins were purified using TAP (**a**, **b**) or FLAG (**c**, **d**) protocols. IP samples were loaded in duplicate and separated by SDS-PAGE, transferred to PVDF membrane and probed with specific antibody. For TAP purified proteins, one half of the membrane was probed with anti-FLAG peroxidase linked (Sigma) that detected $\text{CreB}^{\text{FLAG}}$ in the positive control $\text{CreB}^{\text{FLAG}}$14 but not in $\text{CreA}^{\text{cTAP}}\text{CreB}^{\text{FLAG}}$15 (**a**); and the other half of the membrane was probed with anti-TAP conjugated with peroxidase (GeneScript) that detected CreAcTAP in $\text{CreA}^{\text{cTAP}}\text{CreB}^{\text{FLAG}}$15 in both conditions (**b**). For FLAG-purified proteins, one half of the membrane was probed with anti-TAP conjugated with peroxidase (GeneScript) that detected $\text{CreA}^{\text{cTAP}}$ in $\text{CreA}^{\text{cTAP}}$14, which acts as a positive control, but $\text{CreA}^{\text{cTAP}}$ was not detected in $\text{CreA}^{\text{cTAP}}\text{CreB}^{\text{FLAG}}$15 (**c**). The other half of the membrane was probed with anti-FLAG peroxidase linked (Sigma), and $\text{CreB}^{\text{FLAG}}$ was detected for $\text{CreA}^{\text{cTAP}}\text{CreB}^{\text{FLAG}}$15 in both IP samples and the lysate (**d**). The WT strain was used as negative control in these experiments

are not present in the same complex, at least at levels that are detectable using these procedures.

Post-translational modifications: is CreA a phosphorylated or ubiquitinated protein?

The absence of interaction between CreA and CreB in co-purification experiments led us to investigate the phosphorylation and ubiquitination status of the CreA protein directly. The interaction between phosphorylation and ubiquitination, two of the major post-translational modifications, can play an important role in eukaryotic regulation, and phosphorylation of protein can be a marker to trigger subsequent ubiquitination (reviewed in (Nguyen et al. 2013). The Phos-tag system (Wako Pure Chemical Industries, Japan; M&M) that binds with phosphorylated proteins and alters their mobility was used to study the phosphorylation status of CreA. CreA was immunoprecipitated from T7 grown in conditions that were either repressing or derepressing, and samples were treated with bovine alkaline phosphatase (AP), and separated using phosphate affinity SDS-PAGE, with treated and untreated β-casein as positive control. β-Casein was detected by staining with Coomassie blue and $\text{CreA}^{\text{HAGFP}}$ was detected by probing a Western blot with anti-HA antibody peroxidase high-affinity antibody (Roche). β-Casein was detected in both AP treated and untreated samples, with dephosphorylation detected as the AP-treated sample showed altered mobility (Fig. 6a). $\text{CreA}^{\text{HAGFP}}$ was detected in both repressing and derepressing conditions, with clear evidence of altered mobility in AP-treated protein from repressed conditions, but little change in protein from derepressed conditions (Fig. 6b). In the Phos-tag system, dephosphorylated proteins are detected by altered mobility compared to the phosphoprotein counterparts, usually increased mobility. However, dephosphorylation of some phosphoproteins can result in slower mobility, for example the loss of a phosphate group during dephosphorylation favours the self-association of β-casein (Yoshikawa et al. 1974), which is consistent with the lower mobility band in the control track. Lower mobility bands in Phos-tag SDS-PAGE have been detected during partial dephosphorylation of β-casein (Kinoshita et al. 2009b), and the decreased mobility of $\text{CreA}^{\text{HAGFP}}$ may be due to partial dephosphorylation. Altered mobility bands were clearly detected for CreA extracted from repressing conditions, and this indication that CreA is a phosphorylated protein was confirmed using mass spectrometry (see below).

To determine the ubiquitination status of CreA, proteins were extracted from TA3H2, which overexpressed HA- and His6- tagged CreA, and ubiquitinated proteins were purified using UbiCapture-Q matrix (Enzo life Sciences; M&M). In Western blots, CreA was strongly detected in both the total lysate and unbound fractions and weakly in the fraction purified for ubiquitinated proteins. As expected no band was detected for WT in all three sample fractions. This result suggests that at least a fraction of CreA is ubiquitinated in a strain that overexpressed CreA (Data not shown). In this experiment, *creA* was overexpressed in order to allow detection. However, since native *creA* transcription is autoregulated, and furthermore, overproduction of proteins can lead to misfolding and processing via the proteasome as ubiquitinated protein, these indications

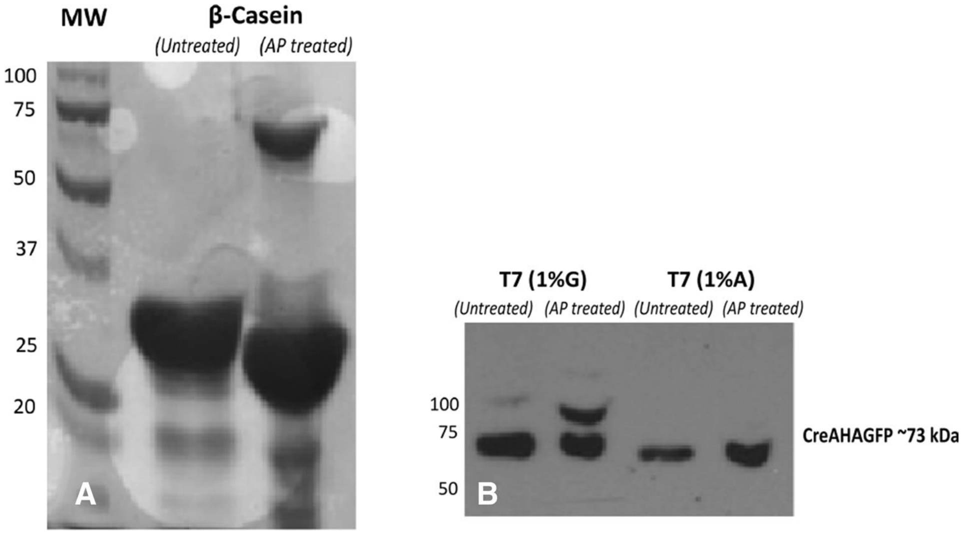
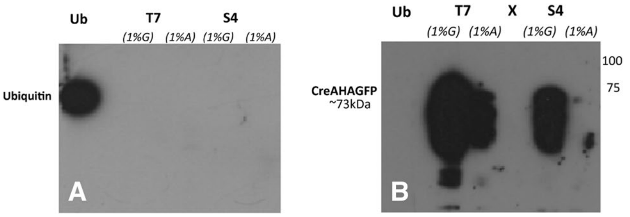


Fig. 6 Phosphorylation status of CreA. Strain T7 was grown in 1 % glucose for 18 h with shaking at 37 °C and then treated for 4 h at 37 °C with shaking in two different conditions 1 % glucose (G) and 1 % arabinose (A) that represent repressing and derepressing conditions, respectively. CreA was purified from total proteins by immunoprecipitation using anti-HA matrix (Roche). IP samples were treated with bovine alkaline phosphatase (Sigma) for 60 min and separated by SDS-PAGE using 'Phos tag' (Wako Pure Chemical Industries, Japan). β-Casein (1 µg/µl) was used as positive control and incubated in Coomassie blue stain overnight (**a**). The blot was probed using anti-HA peroxidase high-affinity antibody (Roche) (**b**)

of ubiquitination were followed up using a strain that expressed the protein from the native promoter.

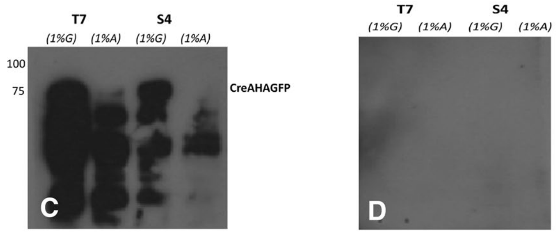
Proteins were extracted from T7 (*creA* overexpressed) and S4 (*creA* expressed from native promoter) after growth in glucose or arabinose, and CreA^{HAGFP} was immunoprecipitated (Fig. 7). When probed with an anti-ubiquitin antibody, no ubiquitinated CreA was detected for either T7 or S4 in either repressing or derepressing conditions (Fig. 7a, d). As expected, CreA^{HAGFP} was detected for both strains in both conditions when the membranes (Fig. 7b, c) were probed with an anti-HA antibody. These results indicate that CreA detected in these experiments is not ubiquitinated.

In Western blots, the sensitivity of the antibody is critical for detection of proteins of interest, and the sensitivity of the anti-ubiquitin antibody used is apparently low as a high concentration of free ubiquitin (positive control) was required for detection (results not shown). To obtain further confirmation regarding the post-translational modifications as well as physical interactions between CreA and CreB, mass spectrometry analysis of CreA and CreB proteins was undertaken. CreA^{cTAP}14 and CreB^{cTAP}15 were incubated in either repressing (1 % G) or derepressing (1 % A) conditions, along with the WT strain in the repressing (1 % G) condition. Both CreA^{cTAP} and CreB^{cTAP} were separately purified using the TAP purification protocol, separated by SDS-PAGE, and stained with Coomassie blue (M&M). Only a few very weak nonspecific bands were detected in the WT sample. For CreA^{cTAP}14, 6 bands were analysed from the sample grown in repressing conditions and 7 bands were analysed from the sample grown in derepressing conditions (Fig. 8a), while for CreB^{cTAP}15, 3 bands were analysed from the sample grown in repressing conditions and 4 bands were analysed from the sample grown in derepressing conditions (Fig. 8b). These bands were digested with trypsin (Promega) and peptide fragments were analysed using LC–MS (Adelaide Proteomic Centre). Using a MaxQuant search, CreA and CreB proteins were identified and analysed for post-translational modifications including ubiquitination, phosphorylation and oxidation. To identify phosphorylated peptide/s in CreA the data were searched with modified variables for phosphorylation (ST and/or Y). A SRPNSPNSTAPSSPTFSHDSLSPTPDHTPLATPAHSPR (aa 277–314) peptide with three phosphorylated STY sites (SRPNSPNSTAPS$^{(p)}$S$^{(p)}$PTFSHDSLSPTPDHTPLATPAHS$^{(p)}$PR) was present only in repressed conditions, whereas the peptide with two phosphorylated STY sites (S$^{(p)}$RPNSPNSTAPS$^{(p)}$SPTFSH DSLSPTPDHTPLATPAHSPR) was detected in both conditions. The LKPLS$^{(p)}$PSELHLPSIR (aa 315–329) peptide was identified as STY phosphorylated only in repressed conditions. The SHS$^{(p)}$HEDEDSYASHR (aa 260–273) STY phosphorylated peptide was detected in both conditions (Table 3). To identify ubiquitinated peptide/s in CreA, the data were searched again with modified variables for ubiquitination (CKST). However, no ubiquitinated peptide was detected for CreA in either repressed or derepressed conditions.



Purification: HA
Probe: Anti-Ubiquitin

Purification: HA
Probe: Anti-HA



Purification: HA
Probe: anti-HA

Purification: HA
Probe: Anti-Ubiquitin

Fig. 7 Ubiquitination status of CreA. Two strains T7 (*creA* expressed from the *gpdA* promoter) and S4 (*creA* expressed from the native promoter) were grown in 1 % glucose for 18 h with shaking at 37 °C and then treated for 4 h at 37 °C with shaking in two different conditions 1 % glucose (G) and 1 % arabinose (A) that represent repressing and derepressing states, respectively. CreA was purified from total proteins by immunoprecipitation using anti-HA affinity matrix (Roche). IP samples, loaded in duplicate, were separated by SDS-PAGE, transferred to PVDF membrane and divided into two for specific antibody probing. The first half was probed with anti-ubiquitin conjugated with peroxidase antibody (Abcam) that detected free ubiquitin as the positive control (due to the small MW of ubiquitin, Ub was loaded only for the final 20 min of the electrophoresis) (**a**), and this same membrane was stripped and probed with anti-HA peroxidase high-affinity antibody (Roche) for detection of CreA (**b**). The other half of the membrane was first probed with anti-HA peroxidase high-affinity antibody (Roche) for the detection of CreA (**c**), and then this same membrane was stripped and probed with anti-ubiquitin conjugated with peroxidase antibody (Abcam) (**d**)

Furthermore, no CreB was detected among the co-purified proteins with CreA, and CreA was not present among proteins that were co-purified with CreB in repressed and derepressed conditions (results not shown). However, CreC was detected with CreB in both experimental conditions which serves as an excellent internal positive control (Lockington and Kelly 2001). Taken together, both Western blots and MS analysis confirmed that CreA is differentially phosphorylated, but is not an ubiquitinated protein, and CreA and CreB are not present in a stable complex.

Discussion

In *A. nidulans*, it has been proposed that ubiquitination and deubiquitination systems, involving products of the *creD, hulA*, *creB* and *creC* genes, are involved in the carbon catabolite repression mechanism (Kelly 2004). Although mutations in the *creB* gene confirmed the association of CreB with the CCR regulatory network, the role of the CreB deubiquitinating enzyme is not fully understood at the molecular level. The effects of *creB* missense mutations in a *creA* missense mutant background have been studied (Hynes and Kelly 1977); however, the effects of a null *creB* mutant in a null *creA* background had not previously been investigated.

Mutations in *creA* and *creB* cause morphological effects on solid media. Mutations in the *creA* gene produce the same range of morphological characteristics across the alleles that include slower growth rate and smaller colony size than the wildtype strain (Shroff et al. 1996). Null alleles of *creA* are viable, but they show extreme effects on colony morphology in all growth conditions tested (Shroff et al. 1997). Conversely, both partial and complete loss-of-function alleles of the *creB* gene cause only a small effect on colony morphology (Hynes and Kelly 1977; Lockington and Kelly 2001). A strain that contains partial loss-of-function alleles *creA204* and *creB15* was morphologically similar to a strain containing *creA204* alone (Hynes and Kelly 1977). A strain that was a complete loss-of-function for both the *creA* and *creB* genes was developed. In this strain, the extreme colony morphology of *creA*Δ was suppressed to some extent in that it showed a less compact and less dense colony than a strain containing *creA*Δ alone, indicating that the total loss of both proteins leads to fewer effects on morphology than the loss of CreA alone. This is consistent with the finding of *creB* alleles among suppressors of the effects of *creA204* on morphology on complete medium (JMK and Lockington, RA, unpublished). Thus in *A. nidulans*, the effects of the mutations on morphology indicate a genetic interaction. How *creA* mutations result in morphological effects is not known at the molecular level, but the partial suppression of the morphological changes by *creB* mutations implies that the complete failure to deubiquitinate one or more unknown target proteins (not CreA) relieves this effect. In *A. oryzae*, a strain containing a deletion of both the *creA* and *creB* genes retained the phenotype of *creA*Δ in minimal media (Ichinose et al. 2014).

Mutations in *creA* and *creB* cause reduced CCR for some enzymes and permeases. It was reported previously that in the presence of carbon sources such as glucose and sucrose, mutations in the *creA* and *creB* gene can lead to derepression of alcohol dehydrogenase I, encoded by the *alcA* gene (Bailey and Arst 1975; Hynes and Kelly 1977; Shroff et al. 1996, 1997). Like the single *creA*Δ strain, the *creA*Δ *creB*Δ double null mutant also led to high levels of *alcA* expression in the presence of glucose as detected using a plate test monitoring toxicity of allyl alcohol, whereas strains containing the *creB*Δ mutant showed at least partial relief of CCR. Enzyme assays of alcohol dehydrogenase

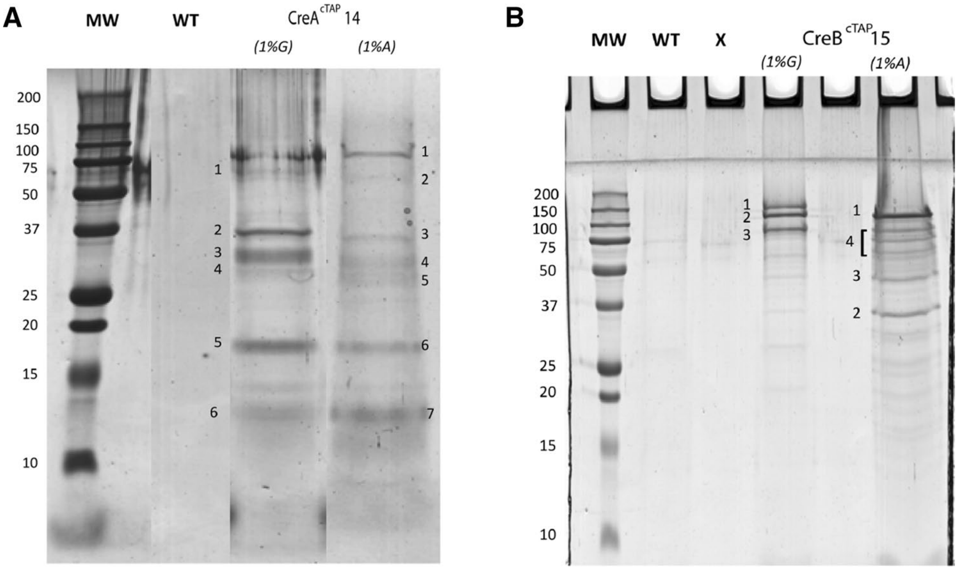


Fig. 8 Bands purified using the TAP purification protocol from CreA^{cTAP}14 and CreB^{cTAP}15. CreA^{cTAP}14 and CreB^{cTAP}15 were incubated in both repressing (1 % G) and derepressing (1 % A) conditions. Both CreA^{cTAP} and CreB^{cTAP} were purified by using TAP purification protocol. Purified samples, including WT as a negative control, were separated by two individual SDS-PAGE. Proteins were fixed for 2 h and Coomassie stained overnight at room temperature. In WT, no band was detected. For CreA^{cTAP}14 6 and 7 bands (**a**), and for CreB^{cTAP}15 (**b**) 3 and 4 bands were selected in repressing and derepressing conditions, respectively. All bands were processed for proteomic analysis at Adelaide Proteomic Center

Table 3 Peptides identified in repressed and derepressed conditions by LCMS with modified variables

Peptides	Modifications	PEP	Repressed	Derepressed
ASSGMDINLLATAASQVER	Unmodified	6.5595E−76	Detected	Not detected
ASSGMDINLLATAASQVER	Oxidation (M)	4.7078E−62	Detected	Not detected
SHSHEDEDSYASHR	Unmodified	8.9241E−32	Detected	Detected
VAVQDMLNPSGFTSVSSSTANSVAGGDLAER	Unmodified	1.9348E−27	Detected	Detected
VAVQDMLNPSGFTSVSSSTANSVAGGDLAER	Oxidation (M)	2.1195E−21	Detected	Detected
GLPSLSAYAISHSMSR	Unmodified	8.2313E−20	Detected	Not detected
KLPIPQVPK	Unmodified	2.5919E−19	Detected	Detected
GLPSLSAYAISHSMSR	Oxidation (M)	1.02E−13	Detected	Not detected
LKPLSPSELHLPSIR	Unmodified	1.75E−12	Detected	Detected
LKPLS(ph)PSELHLPSIR	Phospho (STY)	5.28E−12	Detected	Not detected
SHS(ph)HEDEDSYASHR	Phospho (STY)	7.61E−12	Detected	Detected
ASSGMDINLLATAASQVERDESFGFR	Oxidation (M)	4.16E−08	Detected	Not detected
DESFGFR	Unmodified	3.00E−07	Detected	Not detected
LPIPQVPK	Unmodified	8.97E−06	Detected	Detected
SNLSPYSR	Unmodified	1.37E−05	Detected	Not detected
S(ph)RPNSPNSTAPS(ph)SPTFSHDSLSPTPDHTPLATPAHSPR	2 Phospho (STY)	4.39E−05	Detected	Detected
SHHMYGPR	Unmodified	1.51E−04	Detected	Not detected
SRPNSPNSTAPS(ph)S(ph)PTFSHDSLSPTPDHTPLATPAHS(ph)PR	3 Phospho (STY)	9.87E−03	Detected	Not detected

PEP posterior error probability

I activity showed that the double null mutant strain had the highest level of derepression and elevation in both repressed-induced and induced conditions, indicating a synergistic effect. Using RTqPCR, synergy was confirmed at the transcript level. Higher *alcA* expression was detected for the double null mutant than either of the single null mutants in repressed-induced conditions, again indicating genetic interaction. Though some partial relief of CCR was observed for the *creB*Δ mutant in the plate tests and enzyme assays, no significant derepression was detected for *alcA* transcription, whereas Hunter et al. (2013) reported that the *creB1937* allele showed more *alcA* expression than a wildtype strain in these conditions, and the reason for this difference is unknown. The extent of derepression achieved by the double null mutant was also determined using plate assays for β-galactosidase and α-amylase that are required for the breakdown of lactose and starch, respectively. The expression of β-galactosidase was highest in the double null mutant in both the presence and absence of glucose, indicating elevation and a synergistic interaction. For α-amylase, the double null mutation led to less expression in either the presence or absence of glucose than the *creA*Δ null mutant alone, but more than the *creB*Δ and the wildtype strains. Thus in *A. nidulans*, the effects of the mutations on CCR indicate a genetic interaction.

In *A. nidulans*, mutations in the *creB* gene produce a pleiotropic range of phenotypes which are unrelated to CCR; for example, reduced growth on quinate as a sole carbon source (Hynes and Kelly 1977). These are likely to be due to effects on permeases, and the quinate permease QutD, required for the induction of quinate dehydrogenase, is one of the direct targets of deubiquitinating enzyme, CreB (Kamlangdee 2008). Mutations in the *creA* gene have little to no effect for quinate utilization. The double null mutant strain showed as poor growth on quinate as a sole carbon source as the single *creB*Δ mutant strain. These findings support the suggestion that the role of CreB in conditions that do not lead to CCR, such as the direct effects on permeases, is independent of its role in CCR.

The finding of a clear genetic interaction between *creA* and *creB* mutant alleles led us to investigate whether the CreA and CreB proteins directly interact or form part of a complex. In other systems, substrates of deubiquitinating proteins have been identified using protein co-purification methods. For example, liquid facets was shown to be a substrate of the fat facets deubiquitinating enzyme in *Drosophila* (Chen et al. 2002). In addition, FANCD2 and p53 were co-immunoprecipitated as a substrate with USP1 and USP7 in HEK293 and H460 cell lysate, respectively (Li et al. 2002; Nijman et al. 2005). Thus, we used co-purification methods to identify whether CreA was a substrate for CreB. In preliminary experiments, strains containing CreA tagged with HA and His6 and CreB tagged with FLAG were constructed, with the tagged constructs expressed from the constitutive *gpdA* promoter (Punt et al. 1990). When CreA was purified, some CreB was copurified, indicating that in this strain, at least some CreB and CreA may exist in a complex in vivo. However, when CreB was purified, no CreA was detected, which may suggest that CreB has a range of substrates, and any one interaction was below the range of detection. However, these preliminary experiments do not confirm that the interaction occurs physiologically when the proteins are expressed from their own promoters. Thus strains were constructed that express the proteins from their native promoters at their native loci. This was particularly important as in the native state transcription of *creA* is autoregulated (Shroff et al. 1996), and moreover, overexpression of CreA can partially override the requirement of CreB for repression (Lockington, RA, personal communication), and further, inappropriate expression of proteins can lead to misfolding and processing via the proteasome. The possibility of processing misfolded and mis-expressed proteins via the proteasome is of vital importance because of the involvement of ubiquitination and deubiquitination pathways in proteasomal degradation (Goldberg 2003; Kraft et al. 2010). Co-purifications were performed in a strain that expresses CreA and CreB from their native promoters, and when CreA was purified no CreB was co-purified, and when CreB was purified no CreA was co-purified, and thus CreA and CreB do not physically interact, and nor are they part of a single stable complex that can be purified via these means.

Previously, two separate experiments concluded that CreA requires post-translational modifications to become an active repressor (Roy et al. 2008; Strauss, et al. 1999). Post-translational modifications in terms of phosphorylation and ubiquitination and their interactions has played important roles in cell signalling pathways and phosphorylation of protein can often be a marker to trigger subsequent ubiquitination [reviewed in (Nguyen et al. 2013)]. Both Western blots and MS analysis showed that CreA is phosphorylated in both repressing and derepressing conditions, and the numbers of phosphopeptides and phosphorylation sites were varied between these two conditions. Mass spectrometry analysis showed that a tri-phosphorylated form of the aa 277–314 peptide was only detected in repressed conditions, whereas a di-phosphorylated form was present in both repressed and derepressed conditions. In addition, mono-phosphorylated peptide aa 315–329, LKPLS$^{(p)}$PSELHLPSIR, was only identified in repressed conditions. Whether either of these differential phosphorylations has regulatory significance requires further experimentation. The role of phosphorylation in the repressor activity of CreA and its homolog has been investigated previously. In *T. reesei*, phosphorylation of the Ser^{241} residue of Cre1 is required for DNA binding. Replacing of Ser^{241} by glutamic acid mimics phosphorylation, but replacing by alanine allows binding without phosphorylation, with the latter leading to permanent carbon catabolite repression for cellobiohydrolase I expression (Cziferszky et al. 2002). On the other hand, substitution of Glu^{244} by valine results in no phosphorylation, binding or repression (Cziferszky et al. 2002). In *S. sclerotiorum*, Ser^{266} (equivalent to Ser^{241} in *T. reesei*) substitution by alanine leads to derepression

(Vautard-Mey and Fevre 2000). In *A. nidulans*, deletion of amino acid region SHED$^{262–265}$ of CreA (equivalent to SNDE$^{241–244}$ of Cre1 in *T. reesei* and SHEE$^{266–269}$ of CRE1 in *S. sclerotiorum*) showed little effect on carbon catabolite repression (Roy et al. 2008). The amino acid region aa 277–314 of CreA is conserved in several ascomycetes and in *T. reesei*, although deletion of this amino acid region did not affect phosphorylation of the Cre1 protein (Cziferszky et al. 2002). In *S. cerevisiae*, phosphorylation of Mig1p by Snf1 kinase is essential to exert repression (DeVit and Johnston 1999; DeVit et al. 1997), although no Snf1 kinase-like target motif was identified in Cre1 of *T. reesei,* where casein kinase II is involved in the phosphorylation of Ser^{241} of Cre1 (Cziferszky et al. 2002). Recently, Brown et al. (2013) suggested that *A. nidulans* SnfA was required for CreA derepression of cellulase enzymes through alteration of CreA nuclear localization, however mycelia were incubated in conditions that are more similar to starvation than derepression and the elevation of the XprG starvation response transcription factor supports that starvation occurred, and CreA is known to be degraded in starvation conditions (Alam, et al. unpublished). CreA nuclear localization was reduced but not fully abolished in glycerol (31 %) which is considered as a condition in which derepression occurs (Ruijter and Visser 1997) compared to glucose (100 %) (Brown et al. 2013). Incubation in MM with 1 % Avicel for 3–5 days could lead to starvation as incubation in Avicel for 5 h showed similar CreA nuclear localization as incubation without a carbon source for the same length of time (Brown et al. 2013). Microarray analysis also indicated a starvation response. In *A. nidulans*, carbon starvation can induce complex changes in transcriptomes and involves regulation of biological processes including programmed cell death, secondary metabolite production, and the production of extracellular hydrolases and proteases (Szilagyi et al. 2013). Genes that are involved in glucose utilization and carbohydrate synthesis were down-regulated though genes that are involved in carbohydrate hydrolysis were up-regulated (Szilagyi et al. 2013). In addition, genes involved in protein synthesis, autophagy and nucleases and peptidases were up-regulated, indicating that CreA might be degraded in starvation conditions. This observation is in agreement with Western analysis that showed CreA was not detected in strains incubated in starvation conditions (Alam et al., unpublished). However, although there was clear evidence for phosphorylation of CreA, our Western blot and MS analyses provided no evidence that CreA is ubiquitinated. Recently, Ries et al. (2016) used an anti-ubiquitin antibody to probe purified CreA::GFP, and a smear was identified between 60 and 100 kDa, which led them to conclude that CreA may be ubiquitinated; however, there was no indication of a ladder of CreA due to differently ubiquitinated species, and our MS evidence makes that very unlikely. Moreover, CreA was not present in the ubiquitinated sites in the *A. nidulans* proteome analysis of Chu et al. (2016).

Our finding that the CreB deubiquitinating enzyme does not act directly on CreA or proteins in a complex with CreA raises a number of pressing questions, the first being how is CreB involved in CCR. Chu et al. (2016), analysed the ubiquitinated sites in the *A. nidulans* proteome, and identified 1913 ubiquitinated proteins. Proteins that were ubiquitinated were very different in *S. cerevisiae* compared to *A. nidulans*, and the *A. nidulans*–specific proteins are enriched for those that are involved in transcription and protein–protein interactions. CreB itself was present among the proteins identified, and it has a potential ubiquitination site, KEPQPLPMTPLEK. Also present were CreC (Todd et al. 2000), HulA (Boase and Kelly 2004) and AcrB (Boase et al. 2003), all implicated by mutational analysis to be involved in CCR. It has been suggested that all the phenotypes of *creB* mutant strains can be accounted for by effects on permeases and transporters, and it is clear that CreB does directly affect a range of permeases and transporters (Arst 1981; Hynes and Kelly 1977; Kamlangdee 2008), but even though extensive studies have been undertaken, only very mild effects on glucose uptake have been demonstrated (Espeso et al. 1995; Strauss et al. 1999). In addition, alcohol dehydrogenase activity is derepressed in *creB* mutant strains, but some other enzymes normally subjected to CCR are not, and if the effect was via effects on a glucose permease then a wider range of enzyme activities might be expected to be affected. The inducer, ethanol, does not require active transport into the cell, which argues against a role for CreB in the stability of permeases affecting inducer availability.

The second pressing question is how CreA is regulated to allow it to act as a repressor. CCR is well studied in the unicellular yeast, *S. cerevisiae*, and the main proteins involved in regulating the Mig1p repressor are the Snf1 kinase which is necessary for expression of genes required for catabolic pathways to provide glucose, and the Tup1p-Ssn6p co-repressor complex which is involved in initiating a repressive chromatin structure in a number of separate repression pathways (Gancedo 1998; Kayikci and Nielsen 2015). The Tup1p and Ssn6p homologues in *A. nidulans* are not centrally involved in the CCR mechanism, implying that the regulation of the repressor protein is quite different in the two species (Hicks et al. 2001), which is consistent with the ubiquitome study showing that yeast and *A. nidulans* have different ubiquitinated protein patterns in proteins involved in transcription (Chu et al. 2016). In *A. nidulans*, CreA was reported to be involved in the rearrangement of nucleosome positioning in carbon catabolite repressible promoters *alcA*, *alcR* and *prnD-prnB,* although the rearrangements did not correlate with derepression

(Garcia et al. 2004; Mathieu et al. 2005; Reyes-Dominguez et al. 2008). A similar result was observed with Cre1, a CreA homolog in *T. reesei*, in *cbh1* coding regions under repressing condition (Ries et al. 2014), though the molecular mechanism of nucleosome rearrangement remains unclear.

In eukaryotes, transcriptional activation and repression involves chromatin rearrangement and modifications of histone tails, including acetylation, phosphorylation, sumoylation, ubiquitination, and methylation (Brosch et al. 2008). In *S. cerevisiae*, the co-repressor complex Tup1p-Ssn6p mediates repression through the organization of chromatin and directly interacts with the amino terminal of H3 and H4 histones (Edmondson et al. 1996). In addition, repression of genes by Tup1p involves the utilization of H3/H2B specific histone deacetylase 1 (HDA1) in a number of promoters including *ENA1, GAL10, SUC2* (Wu et al. 2001). In *A. nidulans* the Tup1p homologue, RcoA, plays no crucial role in CCR (Hicks et al. 2001) although deletion of this gene showed rearrangement of nucleosome positioning in *alcR* and *prnD-prnB* promoters (Garcia et al. 2008).

Both ubiquitination and deubiquitination have been shown to be involved in transcriptional regulation. In yeast, histone H2B monoubiquitination by Rad6 precedes methylation and the recruitment of the SAGA complex, when Ubp8, a component of the SAGA histone acetyltransferase, deubiquitinates the monoubiquitinated histone H2B to allow transcriptional initiation (Reyes-Turcu et al. 2009, Shilatifard 2006). There are apparent differences between the DUB modules of the Yeast and *A. nidulans* SAGA complexes; in *S. cerevisiae* the DUB module consists of Sgf11p, Sus1p, and Ubp8p, whereas in *A. nidulans* there are no convincing homologues of Sgf11p and Sus1p in the genome, and the DUB module did not copurify with the complex (Georgakopoulos et al. 2012, 2013). Deletion of the *A. nidulans* SAGA components AcdX (Spt8p) and SptC (Spt3p) did not lead to carbon catabolite derepression, but there was some elevated expression (Georgakopoulos et al. 2012). Unlike Ubp8, deubiquitination of ubiquitinated H2B by Ubp10 results in gene silencing in the telomere region and at the rDNA locus (Emre et al. 2005).

Ubiquitination/deubiquitination pathways have multiple effects on gene transcription. We show here that the involvement of the CreB/HulA/CreD ubiquitinating/deubiquitinating pathway in CCR in *A. nidulans* does not involve direct interaction with the CreA protein, or proteins complexed with it. It is possible that the ubiquitination/deubiquitinating pathway affecting an aspect of nucleosome arrangement and chromatin structure interacts with the regulation by CreA. Further studies are required to reveal the role of the pathway in *A. nidulans*.

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References

Arst HNJ (1981) Aspects of the control of gene expression in fungi. In: Glover SW, Hopwood DA (eds) Symposium of the society for general microbiology, pp 131–160

Arst HN, Cove DJ (1973) Nitrogen metabolite repression in *Aspergillus nidulans*. Mol Gen Genet 126:111–141. doi:10.1007/bf00330988

Arst HN, Tollervey D, Dowzer CE, Kelly JM (1990) An inversion truncating the *creA* gene of *Aspergillus nidulans* results in carbon catabolite derepression. Mol Microbiol 4:851–854

Bailey C, Arst HN (1975) Carbon catabolite repressionin *Aspergillus nidulans*. Eur J Biochem 51:573–577. doi:10.1111/j.1432-1033.1975.tb03958.x

Bayram O, Bayram OS, Valerius O, Johnk B, Braus GH (2012) Identification of protein complexes from filamentous fungi with tandem affinity purification. Methods Mol Biol (Clifton, NJ) 944. doi:10.1007/978-1-62703-122-6_14

Boase NA, Kelly JM (2004) A role for *creD*, a carbon catabolite repression gene from *Aspergillus nidulans*, in ubiquitination. Mol Microbiol 53:929–940. doi:10.1111/j.1365-2958.2004.04172.x

Boase NA, Lockington RA, Adams JRJ, Rodbourn L, Kelly JM (2003) Molecular characterization and analysis of the *acrB* gene of *Aspergillus nidulans*: a gene identified by genetic interaction as a component of the regulatory network that includes the CreB deubiquitination enzyme. Genetics 164:95–104

Brosch G, Loidl P, Graessle S (2008) Histone modifications and chromatin dynamics: a focus on filamentous fungi. FEMS Microbiol Rev 32:409–439. doi:10.1111/j.1574-6976.2007.00100.x

Brown NA, de Gouvea PF, Krohn NG, Savoldi M, Goldman GH (2013) Functional characterisation of the non-essential protein kinases and phosphatases regulating *Aspergillus nidulans* hydrolytic enzyme production. Biotechnol Biofuels 6. doi:10.1186/1754-6834-6-91

Chen X, Zhang B, Fischer JA (2002) A specific protein substrate for a deubiquitinating enzyme: liquid facets is the substrate of fat facets. Genes Dev 16:289–294. doi:10.1101/gad.961502

Chu X-L, Feng M-G, Ying S-H (2016) Qualitative ubiquitome unveils the potential significances of protein lysine ubiquitination in hyphal growth of *Aspergillus nidulans*. Curr Genet 62:191–201. doi:10.1007/s00294-015-0517-7

Cove DJ (1966) Induction and repression of nitrate reductase in fungus *Aspergillus nidulans.* Biochim Biophys Acta, pp 51–56

Cziferszky A, Mach RL, Kubicek CP (2002) Phosphorylation positively regulates DNA binding of the carbon catabolite repressor Cre1 of *Hypocrea jecorina* (Trichoderma reesei). J Biol Chem 277:14688–14694. doi:10.1074/jbc.M200744200

Cziferszky A, Seiboth B, Kubicek CP (2003) The Snf1 kinase of the filamentous fungus *Hypocrea jecorina* phosphorylates regulation-relevant serine residues in the yeast carbon catabolite repressor Mig1 but not in the filamentous fungal counterpart Cre1. Fungal Genet Biol 40:166–175. doi:10.1016/s1087-1845(03)00082-3

DeVit MJ, Johnston M (1999) The nuclear exportin Msn5 is required for nuclear export of the Mig1 glucose repressor of *Saccharomyces cerevisiae*. Curr Biol 9:1231–1241. doi:10.1016/s0960-9822(99)80503-x

DeVit MJ, Waddle JA, Johnston M (1997) Regulated nuclear translocation of the Mig1 glucose repressor. Mol Biol Cell 8:1603–1618

Dowzer CEA, Kelly JM (1989) Cloning of the *creA* gene from *Aspergillus nidulans*—a gene involved in carbon catabolite repression. Curr Genet 15:457–459. doi:10.1007/bf00376804

Dowzer CEA, Kelly JM (1991) Analysis of the *creA* gene, a regulator of carbon catabolite repression in *Aspergillus nidulans*. Mol Cell Biol 11:5701–5709. doi:10.1128/MCB.11.11.5701

Edmondson DG, Smith MM, Roth SY (1996) Repression domain of the yeast global repressor Tup1 interacts directly with histones H3 and H4. Genes Dev 10:1247–1259. doi:10.1101/gad.10.10.1247

Emre NCT, Ingvarsdottir K, Wyce A, Wood A, Krogan NJ, Henry KW, Li KQ, Marmorstein R, Greenblatt JF, Shilatifard A, Berger SL (2005) Maintenance of low histone ubiquitylation by Ubp10 correlates with telomere-proximal Sir2 association and gene silencing. Mol Cell 17:585–594. doi:10.1016/j.molcel.2005.01.007

Espeso EA, Fernandezcanon JM, Penalva MA (1995) Carbon regulation of penicillin biosynthesis in *Aspergillus nidulans*—a minor effect of mutations in *creB* and *creC*. FEMS Microbiol Lett 126:63–67. doi:10.1111/j.1574-6968.1995.tb07391.x

Flipphi M, van de Vondervoort PJI, Ruijter GJG, Visser J, Arst HN, Felenbok A (2003) Onset of carbon catabolite repression in *Aspergillus nidulans*—parallel involvement of hexokinase and glucokinase in sugar signaling. J Biol Chem 278:11849–11857. doi:10.1074/jbc.M209443200

Gancedo JM (1998) Yeast carbon catabolite repression. Microbiol Mol Biol Rev 62:334–361

Garcia I, Gonzalez R, Gomez D, Scazzocchio C (2004) Chromatin Rearrangements in the *prnD-prnB* bidirectional promoter: dependence on transcription factors. Eukaryot Cell 3:144–156. doi:10.1128/ec.3.1.144-156.2004

Garcia I, Mathieu M, Nikolaev I, Felenbok B, Scazzocchio C (2008) Roles of the *Aspergillus nidulans* homologues of Tup1 and Ssn6 in chromatin structure and cell viability. FEMS Microbiol Lett 289:146–154. doi:10.1111/j.1574-6968.2008.01379.x

Georgakopoulos P, Lockington RA, Kelly JM (2012) SAGA complex components and acetate repression in *Aspergillus nidulans*. G3-genes genomes. Genetics 2:1357–1367. doi:10.1534/g3.112.003913

Georgakopoulos P, Lockington RA, Kelly JM (2013) The Spt-Ada-Gcn5 acetyltransferase (SAGA) complex in *Aspergillus nidulans*. Plos One 8. doi:10.1371/journal.pone.0065221

Goldberg AL (2003) Protein degradation and protection against misfolded or damaged proteins. Nature 426:895–899. doi:10.1038/nature02263

Hicks J, Lockington RA, Strauss J, Dieringer D, Kubicek CP, Kelly J, Keller N (2001) RcoA has pleiotropic effects on *Aspergillus nidulans* cellular development. Mol Microbiol 39:1482–1493. doi:10.1046/j.1365-2958.2001.02332.x

Hunter AJ, Morris TA, Jin B, Saint CP, Kelly JM (2013) Deletion of *creB* in *Aspergillus oryzae* increases secreted hydrolytic enzyme activity. Appl Environ Microbiol 79:5480–5487. doi:10.1128/aem.01406-13

Hynes MJ (1975) Studies on the role of areA gene in regulation of nitrogen catabolism in *Aspergillus nidulans*. Aust J Biol Sci 28:301–313

Hynes MJ, Kelly JM (1977) Pleiotropic mutants of *Aspergillus nidulans* altered in carbon metabolism. Mol Gen Genet 150:193–204. doi:10.1007/bf00695399

Ichinose S, Tanaka M, Shintani T, Gomi K (2014) Improved alpha-amylase production by *Aspergillus oryzae* after a double deletion of genes involved in carbon catabolite repression. Appl Microbiol Biotechnol 98:335–343. doi:10.1007/s00253-013-5353-4

Ilmen M, Thrane C, Penttila M (1996) The glucose repressor gene *cre1* of *Trichoderma*: isolation and expression of a full-length and a truncated mutant form. Mol Gen Genet 251:451–460. doi:10.1007/bf02172374

Kaiser P, Huang L (2005) Global approaches to understanding ubiquitination. Genome Biol 6. doi:10.1186/gb-2005-6-10-233

Kamlangdee N (2008) Indentifying target proteins of CreB deubiquitination enzyme in the fungus *Aspergillus nidulans*. PhD thesis, The University of Adelaide

Kayikci O, Nielsen J (2015) Glucose repression in *Saccharomyces cerevisiae*. Fems Yeast Res 15:OV68–OV68. doi:10.1093/femsyr/fov068

Kelly JM (1980) Pleiotropic mutants of *Aspergillus nidulans* affected in carbon metabolism. PhD Thesis, The University of Melbourne

Kelly JM (2004) The regulation of carbon metabolism in filamentous fungi. In: Esser K (ed) Biochemistry and molecular biology, pp 385–401

Kelly JM, Hynes MJ (1977) Increased and decreased sensitivity to carbon catabolite repression of enzymes of acetate metabolism in mutants of *Aspergillus nidulans*. Mol Gen Genet 156:87–92. doi:10.1007/bf00272256

Kelly JM, Katz ME (2010) Glucose. In: Borkovich KA, Ebbole DJ (eds) Cellular and molecular biology of filamentous fungi, pp 291–311

Kinoshita E, Kinoshita-Kikuta E, Koike T (2009a) Separation and detection of large phosphoproteins using Phos-tag SDS-PAGE. Nat Protoc 4:1513–1521. doi:10.1038/nprot.2009.154

Kinoshita E, Kinoshita-Kikutal E, Matsubara M, Aoki Y, Ohie S, Mouri Y, Koike T (2009b) Two-dimensional phosphate-affinity gel electrophoresis for the analysis of phosphoprotein isotypes. Electrophoresis 30:550–559. doi:10.1002/elps.200800386

Kraft C, Peter M, Hofmann K (2010) Selective autophagy: ubiquitin-mediated recognition and beyond. Nat Cell Biol 12:836–841

Kulmburg P, Sequeval D, Lenouvel F, Mathieu M, Felenbok B (1992) Identification of the promoter region involved in the autoregulation of the transcriptional activator ALCR in *Aspergillus nidulans*. Mol Cell Biol 12:1932–1939

Kulmburg P, Mathieu M, Dowzer C, Kelly J, Felenbok B (1993) Specific binding sites in the *alcR* and *alcA* promoters of the ethanol regulon for the CreA repressor mediating carbon catabolite repression in *Aspergillus nidulans*. Mol Microbiol 7:847–857. doi:10.1111/j.1365-2958.1993.tb01175.x

Li MY, Chen DL, Shiloh A, Luo JY, Nikolaev AY, Qin J, Gu W (2002) Deubiquitination of p53 by HAUSP is an important pathway for p53 stabilization. Nature 416:648–653. doi:10.1038/nature737

Lockington RA, Kelly JM (2001) Carbon catabolite repression in *Aspergillus nidulans* involves deubiquitination. Mol Microbiol 40:1311–1321. doi:10.1046/j.1365-2958.2001.02474.x

Lockington RA, Kelly JM (2002) The WD40-repeat protein CreC interacts with and stabilizes the deubiquitinating enzyme CreB in vivo in *Aspergillus nidulans*. Mol Microbiol 43:1173–1182. doi:10.1046/j.1365-2958.2002.02811.x

Lockington RA, Sealylewis HM, Scazzocchio C, Davies RW (1985) Cloning and characterization of the ethanol utilization regulon in *Aspergillus nidulans*. Gene 33:137–149. doi:10.1016/0378-1119(85)90088-5

Lockington RA, Rodbourn L, Barnett S, Carter CJ, Kelly JA (2002) Regulation by carbon and nitrogen sources of a family of cellulases in *Aspergillus nidulans*. Fungal Genet Biol 37:190–196. doi:10.1016/s1087-1845(02)00504-2

Mathieu M, Nikolaev I, Scazzocchio C, Felenbok B (2005) Patterns of nucleosomal organization in the *alc* regulon of *Aspergillus nidulans*: roles of the AlcR transcriptional activator and the CreA global repressor. Mol Microbiol 56:535–548. doi:10.1111/j.1365-2958.2005.04559.x

Meding S, Martin K, Gustafsson OJR, Eddes JS, Hack S, Oehler MK, Hoffmann P (2013) Tryptic peptide reference data sets for

MALDI imaging mass spectrometry on formalin-fixed ovarian cancer tissues. J Proteome Res 12. doi:10.1021/pr300996x

Nayak T, Szewczyk E, Oakley CE, Osmani A, Ukil L, Murray SL, Hynes MJ, Osmani SA, Oakley BR (2006) A versatile and efficient gene-targeting system for *Aspergillus nidulans*. Genetics 172:1557–1566. doi:10.1534/genetics.105.052563

New AM, Cerulus B, Govers SK, Perez-Samper G, Zhu B, Boogmans S, Xavier JB, Verstrepen KJ (2014) Different levels of catabolite repression optimize growth in stable and variable environments. Plos Biol 12. doi:10.1371/journal.pbio.1001764

Nguyen LK, Kolch W, Kholodenko BN (2013) When ubiquitination meets phosphorylation: a systems biology perspective of EGFR/MAPK signalling. Cell Commun Signal 11. doi:10.1186/1478-811x-11-52

Nijman SMB, Huang TT, Dirac AMG, Brummelkamp TR, Kerkhoven RM, D'Andrea AD, Bernards R (2005) The deubiquitinating enzyme USP1 regulates the Fanconi anemia pathway. Mol Cell 17:331–339. doi:10.1016/j.molcel.2005.01.008

Pateman JA, Rever BM, Cove DJ (1967) Genetic and biochemical studies of nitrate reduction in *Aspergillus nidulans*. Biochem J 104:103–111. doi:10.1042/bj1040103

Pateman JA, Doy CH, Olsen JE, Norris U, Creaser EH, Hynes M (1983) Regulation of alcohol dehydrogenase (ADH) and aldehyde dehydrogenase (ALDDH) in *Aspergillus nidulans*. Proc R Soc Ser B Biol Sci 217:243–264. doi:10.1098/rspb.1983.0009

Penalva MA, Tilburn J, Bignell E, Arst HN (2008) Ambient pH gene regulation in fungi: making connections. Trends Microbiol 16:291–300. doi:10.1016/j.tim.2008.03.006

Pisyk S, Natorff R, Sienko M, Skoneczny M, Paszewski A, Brzywczy J (2015) The *Aspergillus nidulans* metZ gene encodes a transcription factor involved in regulation of sulfur metabolism in this fungus and other Eurotiales. Curr Genet 61:115–125. doi:10.1007/s00294-014-0459-5

Portnoy T, Margeot A, Linke R, Atanasova L, Fekete E, Sandor E, Hartl L, Karaffa L, Druzhinina IS, Seiboth B, Le Crom S, Kubicek CP (2011) The CRE1 carbon catabolite repressor of the fungus *Trichoderma reesei*: a master regulator of carbon assimilation. Bmc Genomics 12. doi:10.1186/1471-2164-12-269

Punt PJ, Dingemanse MA, Kuyvenhoven A, Soede RDM, Pouwels PH, Vandenhondel C (1990) Functional elements in the promoter region of the *Aspergillus nidulans gpdA* gene encoding glyceraldehyde-3-phosphate dehydrogenase. Gene 93:101–109. doi:10.1016/0378-1119(90)90142-e

Reyes-Dominguez Y, Narendja F, Berger H, Gallmetzer A, Fernandez-Martin R, Garcia I, Scazzocchio C, Strauss J (2008) Nucleosome positioning and histone H3 acetylation are independent processes in the *Aspergillus nidulans prnD-prnB* bidirectional promoter. Eukaryot Cell 7:656–663. doi:10.1128/ec.00184-07

Reyes-Turcu FE, Ventii KH, Wilkinson KD (2009) Regulation and cellular roles of ubiquitin-specific deubiquitinating enzymes. Annu Rev Biochem 78:363–397. doi:10.1146/annurev.biochem.78.082307.091526

Ries L, Belshaw NJ, Ilmen M, Penttila ME, Alapuranen M, Archer DB (2014) The role of CRE1 in nucleosome positioning within the *cbh1* promoter and coding regions of *Trichoderma reesei*. Appl Microbiol Biotechnol 98:749–762. doi:10.1007/s00253-013-5354-3

Ries LNA, Beattie SR, Espeso EA, Cramer RA, Goldman GH (2016) Diverse regulation of the CreA carbon catabolite repressor in *Aspergillus nidulans*. Genetics. doi:10.1534/genetics.116.187872

Roy P, Lockington RA, Kelly JM (2008) CreA-mediated repression in *Aspergillus nidulans* does not require transcriptional auto-regulation, regulated intracellular localisation or degradation of CreA. Fungal Genet Biol 45:657–670. doi:10.1016/j.fgb.2007.10.016

Ruijter GJG, Visser J (1997) Carbon repression in *Aspergilli*. FEMS Microbiol Lett 151:103–114. doi:10.1111/j.1574-6968.1997.tb12557.x

Semighini CP, Marins M, Goldman MHS, Goldman GH (2002) Quantitative analysis of the relative transcript levels of ABC transporter *Atr* genes in *Aspergillus nidulans* by real-time reverse transcription-PCR assay. Appl Environ Microbiol 68:1351–1357. doi:10.1128/aem.68.3.1351-1357.2002

Shilatifard A (2006) Chromatin modifications by methylation and ubiquitination: Implications in theregulation of gene expression. Annu Rev Biochem 75:243–269. doi:10.1146/annurev.biochem.75.103004.142422

Shroff RA, Lockington RA, Kelly JM (1996) Analysis of mutations in the *creA* gene involved in carbon catabolite repression in *Aspergillus nidulans*. Can J Microbiol 42:950–959. doi:10.1139/m96-122

Shroff RA, Oconnor SM, Hynes MJ, Lockington RA, Kelly JM (1997) Null alleles of *creA*, the regulator of carbon catabolite repression in *Aspergillus nidulans*. Fungal Genet Biol 22:28–38. doi:10.1006/fgbi.1997.0989

Strauss J, Horvath HK, Abdallah BM, Kindermann J, Mach RL, Kubicek CP (1999) The function of CreA, the carbon catabolite repressor of *Aspergillus nidulans*, is regulated at the transcriptional and post-transcriptional level. Mol Microbiol 32:169–178. doi:10.1046/j.1365-2958.1999.01341.x

Szewczyk E, Nayak T, Oakley CE, Edgerton H, Xiong Y, Taheri-Talesh N, Osmani SA, Oakley BR (2006) Fusion PCR and gene targeting in *Aspergillus nidulans*. Nat Protoc 1:3111–3120. doi:10.1038/nprot.2006.405

Szilagyi M, Miskei M, Karanyi Z, Lenkey B, Pocsi I, Emri T (2013) Transcriptome changes initiated by carbon starvation in *Aspergillus nidulans*. Microbiology (Reading, England) 159:176–190. doi:10.1099/mic.0.062935-0

Tilburn J, Scazzocchio C, Taylor GG, Zabickyzissman JH, Lockington RA, Davies RW (1983) Transformation by integration in *Aspergillus nidulans*. Gene 26:205–221. doi:10.1016/0378-1119(83)90191-9

Todd RB, Lockington RA, Kelly JM (2000) The *Aspergillus nidulans creC* gene involved in carbon catabolite repression encodes a WD40 repeat protein. Mol Gen Genet 263:561–570. doi:10.1007/s004380051202

Todd RB, Greenhalgh JR, Hynes MJ, Andrianopoulos A (2003) TupA, the *Penicillium marneffei* Tup1p homologue, represses both yeast and spore development. Mol Microbiol 48:85–94. doi:10.1046/j.1365-2958.2003.03426.x

Todd RB, Davis MA, Hynes MJ (2007) Genetic manipulation of *Aspergillus nidulans*: meiotic progeny for genetic analysis and strain construction. Nat Protoc 2:811–821. doi:10.1038/nprot.2007.112

Vautard-Mey G, Fevre M (2000) Mutation of a putative AMPK phosphorylation site abolishes the repressor activity but not the nuclear targeting of the fungal glucose regulator CRE1. Curr Genet 37:328–332. doi:10.1007/s002940050535

Wong KH, Hynes MJ, Davis MA (2008) Recent advances in nitrogen regulation: a comparison between *Saccharomyces cerevisiae* and filamentous fungi. Eukaryot Cell 7:917–925. doi:10.1128/ec.00076-08

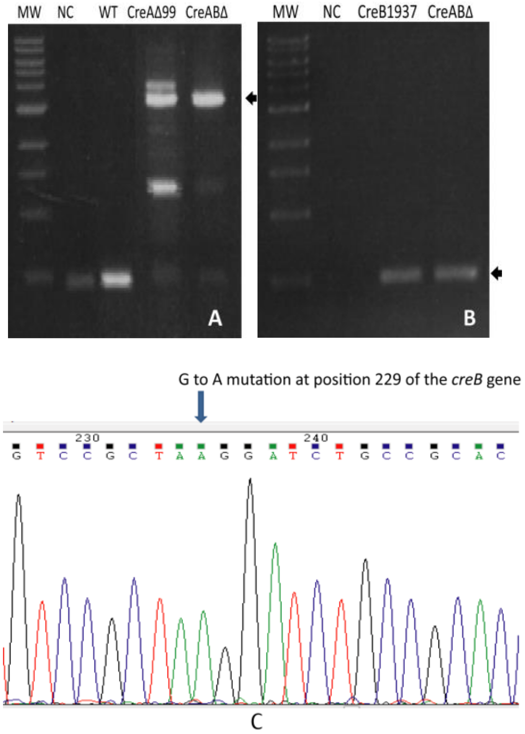
Wu JS, Suka N, Carlson M, Grunstein M (2001) TUP1 utilizes histone H3/H2B-specific HDA1 deacetylase to repress gene activity in yeast. Mol Cell 7:117–126. doi:10.1016/s1097-2765(01)00160-5

Yamashiro CT, Ebbole DJ, Lee BU, Brown RE, Bourland C, Madi L, Yanofsky C (1996) Characterization of *rco-1* of *Neurospora crassa*, a pleiotropic gene affecting growth and development that encodes a homolog of Tup1 of *Saccharomyces cerevisiae*. Mol Cell Biol 16:6218–6228

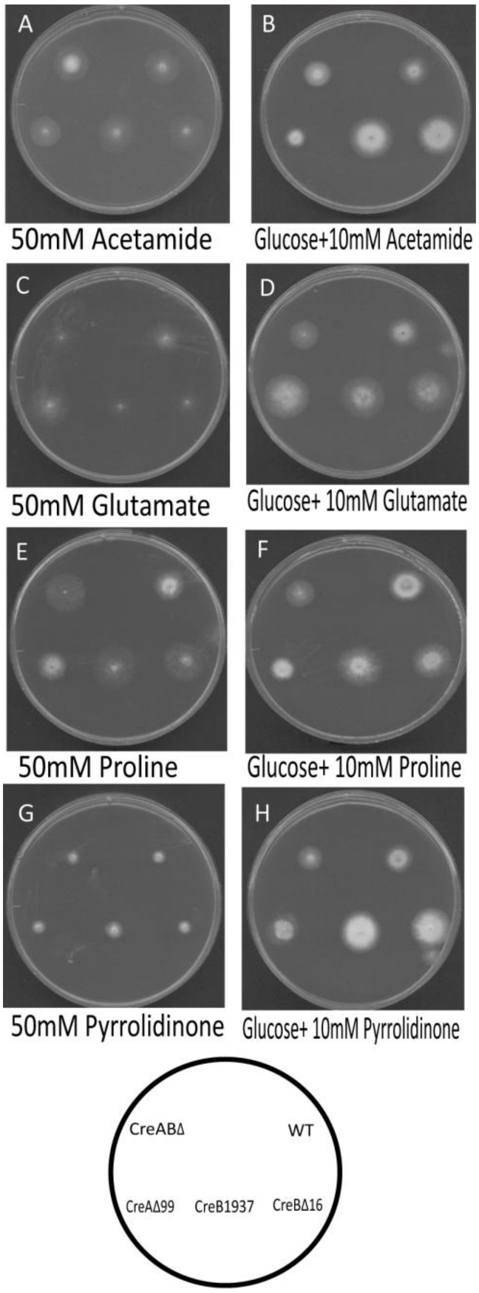
Yoshikawa M, Tamaki M, Sugimoto E, Chiba H (1974) Effect of dephosphorylation on self-association and precipitation of beta-casein. Agric Biol Chem 38:2051–2052. doi:10.1271/bbb1961.38.2051

Yu J, Son H, Park AR, Lee SH, Choi GJ, Kim JC, Lee YW (2014) Functional characterization of sucrose non-fermenting 1 protein kinase complex genes in the Ascomycete *Fusarium graminearum*. Curr Genet 60:35–47. doi:10.1007/s00294-013-0409-7

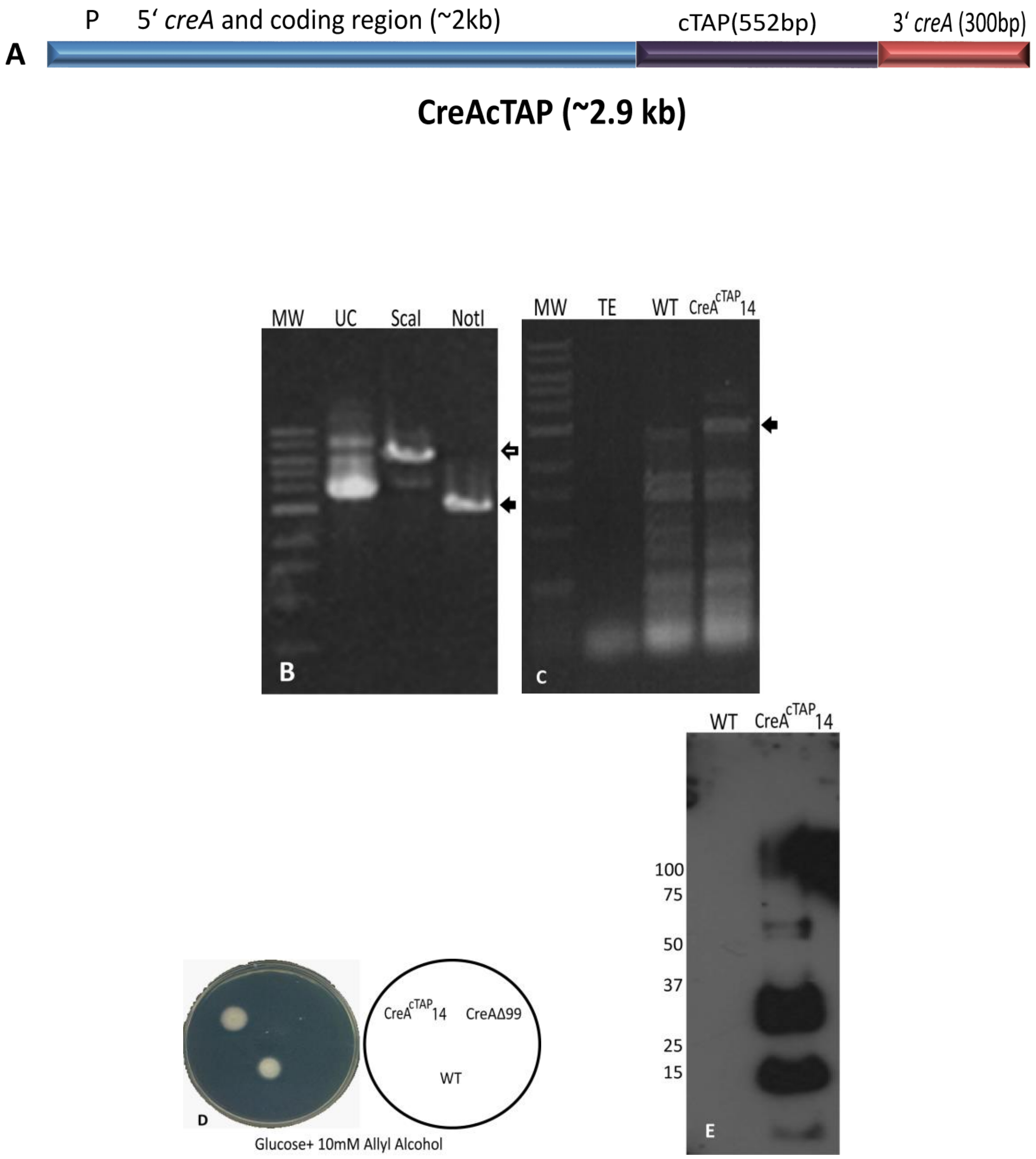
Chapter 2
Supplementary



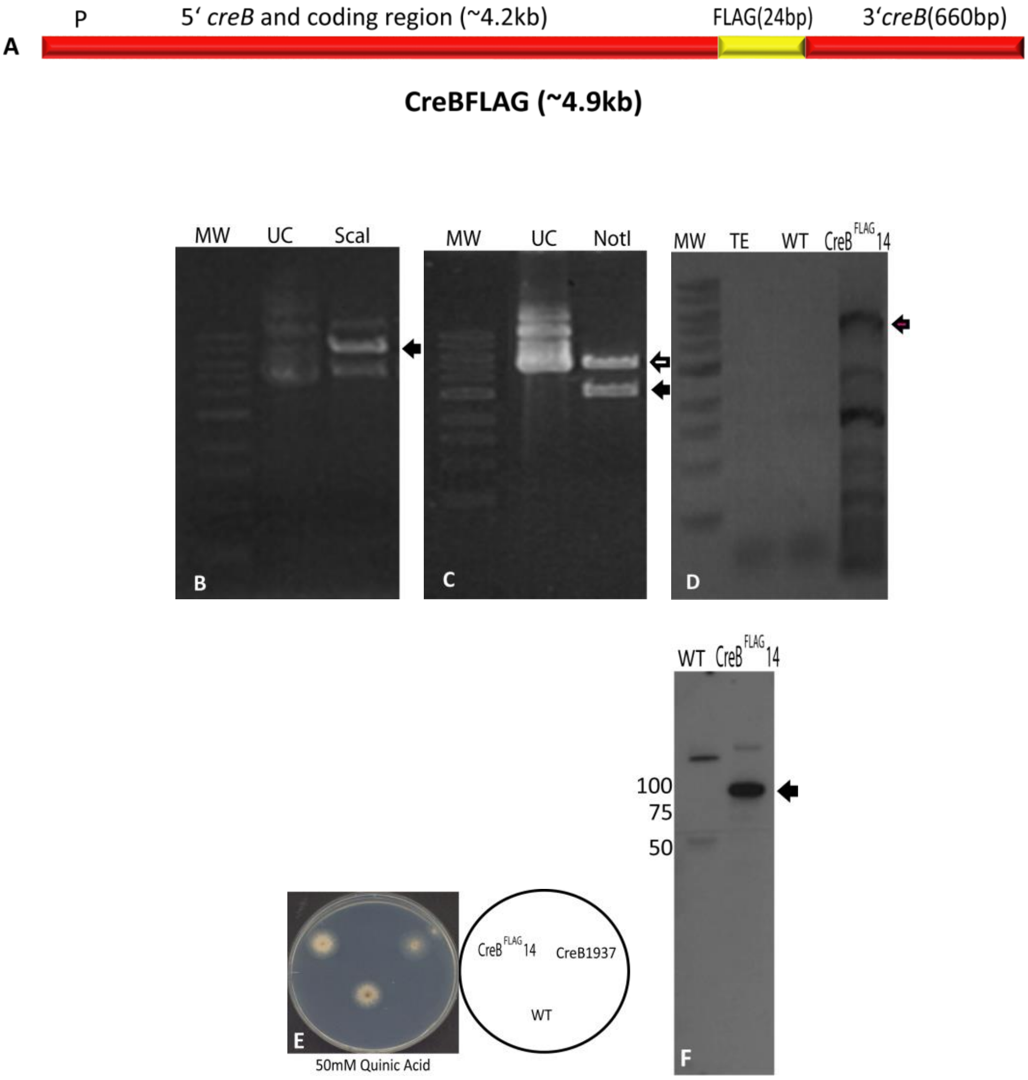
Supplementary Figure 1 **Confirmation of strain that is double null mutant for *creA* and *creB*.** The double null mutant strain (CreABΔ) was generated by genetic crossing of two null mutant strains, CreAΔ99 and CreBΔ16 and confirmed by PCR and sequencing. Using allele specific primers for *creAΔ99*, amplicons of ~3 kb band were detected for both CreAΔ99 and CreABΔ (A). For *creB1937*, 0.5 kb amplicons were detected for CreB1937 and CreABΔ (B). The amplicons in B were sequenced to confirm the G to A mutation at position 229 of the *creB* gene (C). MW = 1 kb DNA ladder.



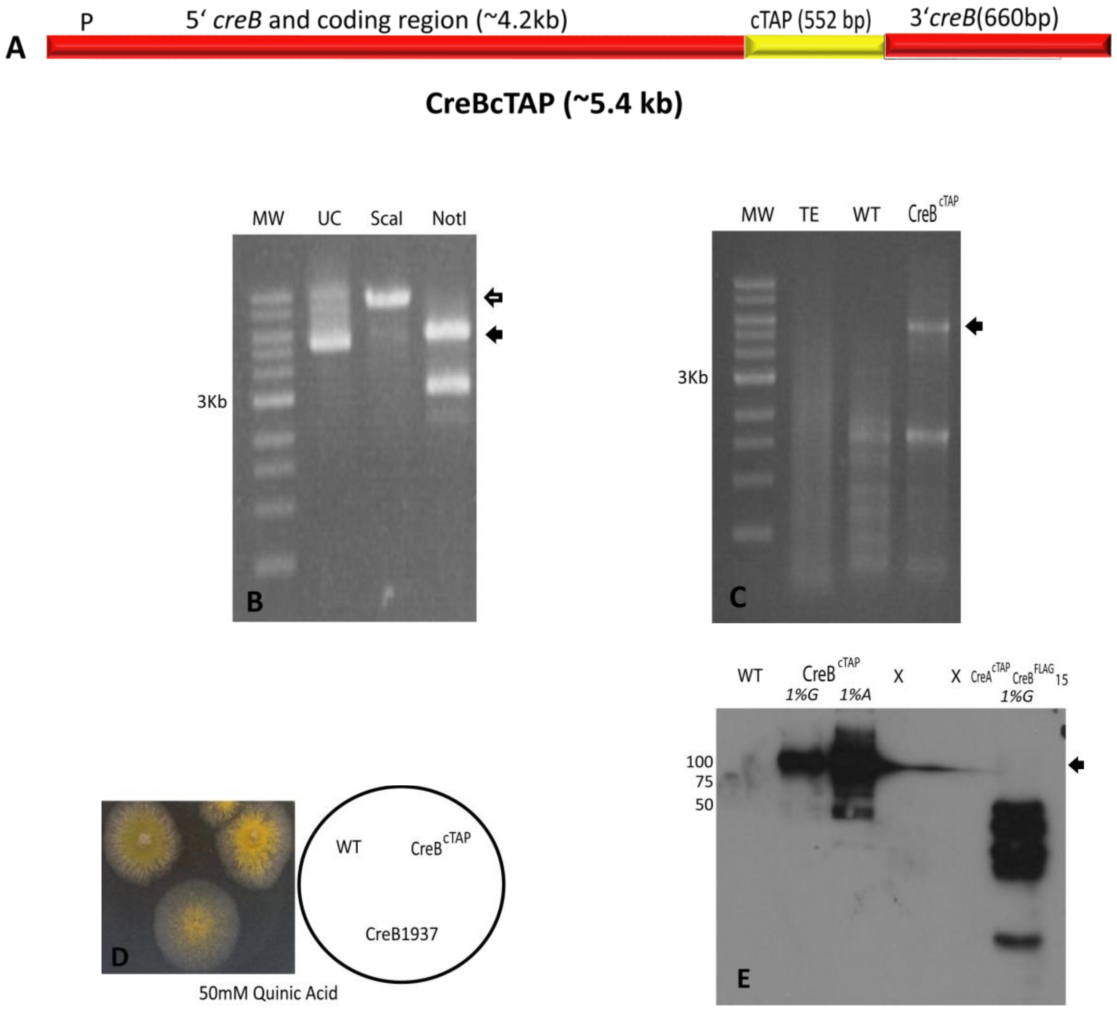
Supplementary Figure 2 **Additional Phenotypic analysis of strain CreABΔ.** Strains were grown on media as indicated at the bottom of each panel at 37°C for 2-3 days. In panels A, C, E and G compounds indicated were present as both carbon and nitrogen sources, whereas in panel B, D, F and H compounds indicated were present only as nitrogen sources, with 1% glucose as the carbon source. Strains keys are at the bottom of the figure.



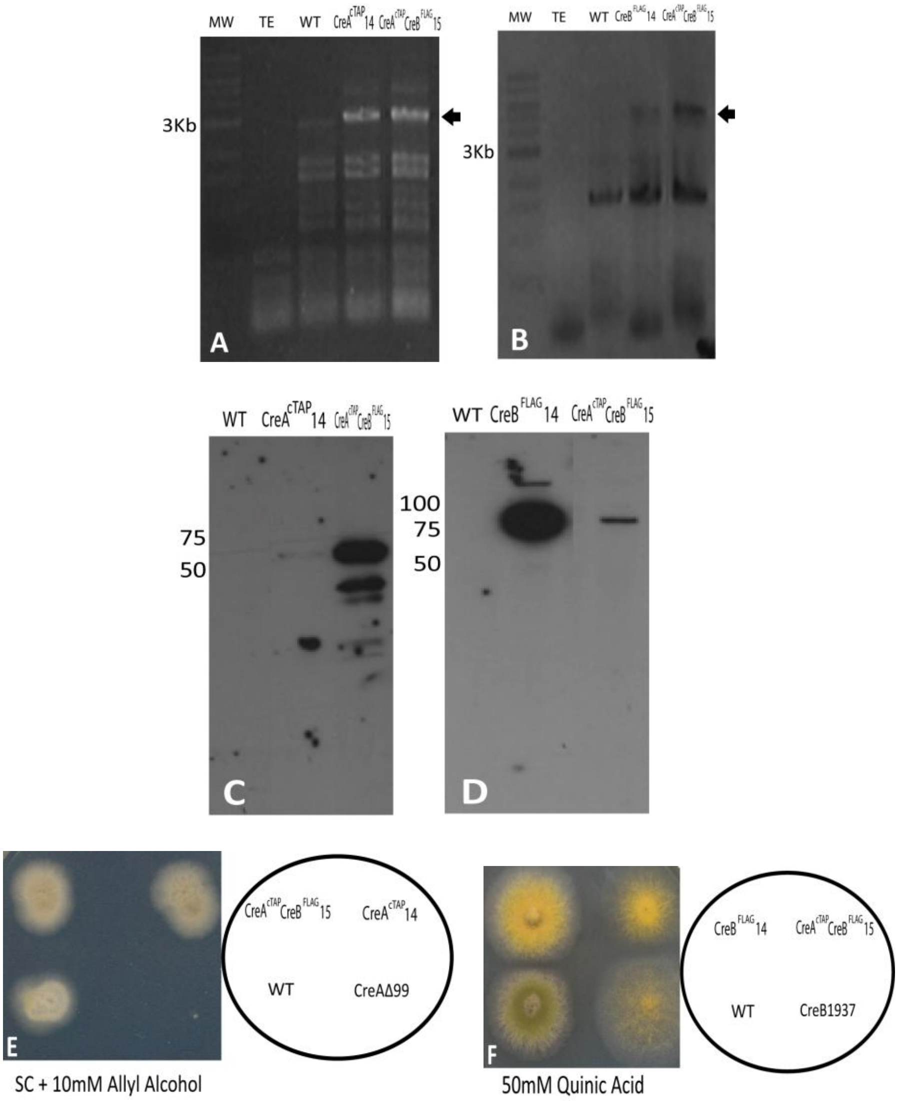
Supplementary Figure 3 **Construction of a strain containing CreA$^{\mathbf{cTAP}}$:** CreA^{cTAP} (~2.9 kb) was generated including the native promoter by fusion PCR (A) and ligated into the pGEMTeasy vector and transformed into DH5α. The pGEMTeasyCreA^{cTAP} plasmid was confirmed by ScaI (B, top arrow, 6 kb) and NotI (B, bottom arrow, 2.9 kb) digestions. The plasmid was transformed into CreAΔ99 *nkuA*Δ and CreA complementing colonies were selected. Homologous integration was confirmed by genomic PCR using a primer internal to the tag and another ORF specific primer which gave a 3 kb band for CreA^{cTAP}14 (C). Plate testing confirmed complementation of CreA^{cTAP} to WT on glucose + allyl alcohol (D). CreA^{cTAP} was purified using the TAP purification protocol, separated by SDS PAGE, transferred to PVDF membrane and probed with anti-TAP conjugated with peroxidase polyclonal antibody (GeneScript). CreA^{cTAP} (~63kDa) was detected together with N-terminal processed CreA^{cTAP} which showed smaller size bands (E). 1 kb DNA ladder was used in agarose GE.



Supplementary Figure 4 **Construction of a strain containing CreB^{FLAG}:** CreB^{FLAG} (~4.9 kb) was generated including the native promoter by fusion PCR (A) and ligated into the pGEMTeasy vector and transformed into DH5α. The pGEMTeasyCreB^{FLAG} plasmid was confirmed by ScaI (B,7.9 kb) and NotI (C top arrow, 4.9 kb and bottom arrow pGEMTeasy, 3 kb) digestions. The plasmid was transformed into a CreB1937 nkuAΔ strain and CreB complementing colonies were selected. Homologous integration was confirmed by genomic PCR using a primer internal to the FLAG- tag and another ORF specific primer which gave a 5.3 kb band for CreB^{FLAG} (D). Plate testing confirmed complementation of CreB^{FLAG}14 to WT on 50 mM quinic acid + 10 mM ammonium tartrate (E). CreB^{FLAG} was purified using AntiFLAGM2:: agarose (Sigma), separated by SDS PAGE, transferred to PVDF membrane and probed with anti-FLAG peroxidase linked monoclonal antibody Sigma). CreB^{FLAG} (~85kDa) was detected (F). 1 kb DNA ladder was used in agarose GE.



Supplementary Figure 5 **Construction of a strain containing CreB^{cTAP}:** CreB^{cTAP} (~5.4 kb) was generated including the native promoter by fusion PCR (A) and ligated into the pGEMTeasy vector and transformed into DH5α. The pGEMTeasyCreB^{cTAP} plasmid was confirmed by ScaI (B top arrow,~8.4 kb) and NotI (B bottom arrow, 5.4 kb) digestions. The plasmid was transformed into a CreB1937 nkuAΔ_1 strain and CreB complementing colonies were selected. Homologous integration was confirmed by genomic PCR using a primer internal to the TAP- tag and another ORF specific primer which gave a 5.5 kb band for CreB^{cTAP} (C). Plate testing confirmed complementation of CreB^{cTAP} to WT on 50 mM quinic acid + 10 mM ammonium tartrate (D). CreB^{cTAP} was purified using TAP purification protocol, separated by SDS PAGE, transferred to PVDF membrane and probed with anti-TAP conjugated with peroxidase polyclonal antibody (GeneScript). CreB^{cTAP} (~106 kDa) was detected (E). CreA^{cTAP}CreB^{FLAG}15 was used as positive control for TAP tag. 1 kb DNA ladder was used in agarose GE.



SC + 10mM Allyl Alcohol

50mM Quinic Acid

Supplementary Figure 6 **Generation of strain containing CreA^{cTAP} and CreB^{FLAG}:** CreA^{cTAP}CreB^{FLAG}15 was generated by crossing CreA^{cTAP}14 and CreB^{FLAG}14. Genomic DNA was extracted from progeny and PCR was performed using a primer internal to the tag (cTAP or BFLAG) and another ORF specific primer. For CreA^{cTAP}14, 3 kb **(A)** and for CreB^{FLAG}14, 5.3 kb **(B)** bands were detected. Proteins were purified using specific protocol (TAP or FLAG), separated by SDS PAGE, transferred to PVDF membrane and probed with anti-TAP conjugated with peroxidase (GeneScript) or anti-FLAG peroxidase linked (Sigma) that detected CreA^{cTAP} **(C)** and CreB^{FLAG} **(D)**. 1 kb DNA ladder was used in agarose GE. Plate testing confirmed complementation to wildtype in the CreA^{cTAP}CreB^{FLAG}15 strain on glucose + allyl alcohol (E) and 50 mM quinic acid + 10 mM ammonium tartrate (F).

Chapter 3

Statement of Authorship

Title of Paper	Proteins interacting with CreA and CreB in the carbon catabolite repression network in *Aspergillus nidulans*.
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Principal Author

Name of Principal Author (Candidate)	Md Ashiqul Alam
Contribution to the Paper	Generation of CreAcTAP and CreBcTAP strains; purification of CreA and CreB for mass spectrometry analysis; MS data analysis, Bioinformatics analysis, co-drafted the manuscript
Overall percentage (%)	80%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.

Signature		Date	13.12.16

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Joan M. Kelly
Contribution to the Paper	Directed research and co-drafted the manuscript (20%)

Signature		Date	13.12.16

Please cut and paste additional co-author panels here as required.

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ORIGINAL ARTICLE

Proteins interacting with CreA and CreB in the carbon catabolite repression network in *Aspergillus nidulans*

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Abstract In *Aspergillus nidulans*, carbon catabolite repression (CCR) is mediated by the global repressor protein CreA. The deubiquitinating enzyme CreB is a component of the CCR network. Genetic interaction was confirmed using a strain containing complete loss-of-function alleles of both *creA* and *creB*. No direct physical interaction was identified between tagged versions of CreA and CreB. To identify any possible protein(s) that may form a bridge between CreA and CreB, we purified both proteins from mycelia grown in media that result in repression or derepression. The purified proteins were analysed by LC/MS and identified using MaxQuant and Mascot databases. For both CreA and CreB, 47 proteins were identified in repressing and derepressing conditions. Orthologues of the co-purified proteins were identified in *S. cerevisiae* and humans. Gene ontology analyses of *A. nidulans* proteins and yeast and human orthologues were performed. Functional annotation analysis revealed that proteins that preferentially interact with CreA in repressing conditions include histones and histone transcription regulator 3 (Hir3). Proteins interacting with CreB tend to be involved in cellular transportation and organization. Similar findings were obtained using yeast and human orthologues, although the yeast background generated a number of other biological processes involving Mig1p which were not present in the *A. nidulans* or human background analyses. Hir3 was present in repressing conditions for CreA and in both growth conditions for CreB, suggesting that Hir3, or proteins interacting with Hir3, could be a possible target of CreB.

Keywords Histone transcription regulator 3 · Transcriptional repression · CreA DNA-binding protein · CreB deubiquitinating enzyme · *Aspergillus nidulans* · Carbon catabolite repression · Gene ontology

Introduction

Over the last 60 years, *Aspergillus nidulans*, a multicellular filamentous fungus, has been extensively used as a model organism to study eukaryotic cell biology. It can adjust its metabolism according to the availability of nutrients in the environment. Carbon source metabolism is regulated through induction, and via carbon catabolite repression (CCR) which is mediated by the global repressor protein, CreA (Arst and Cove 1973; Bailey and Arst 1975; Dowzer and Kelly 1991; Hynes and Kelly 1977). Apart from CreA, mutational analysis identified genes that encode a deubiquitinating enzyme CreB, a WD-40 repeat protein CreC (Hynes and Kelly 1977; Kelly and Hynes 1977; Lockington and Kelly 2001; Todd et al. 2000) and an arrestin motif protein CreD (Boase and Kelly 2004; Hynes and Kelly 1977; Kelly 1980) involved in CCR of *A. nidulans*. The CreD protein shows high similarity to the Rod1p and Rog3p proteins from *S. cerevisiae* which interact with ubiquitin ligase Rsp5p (Boase and Kelly 2004). In a bacterial 2-hybrid system, CreD was shown to interact with the

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ubiquitin ligase HulA which is a homolog of Rsp5p in *A. nidulans*, indicating the possible involvement of CreD in the ubiquitination pathway of glucose repression (Boase and Kelly 2004). These findings led to the prediction that ubiquitination/deubiquitination pathways could play an important role in CCR, and this is reinforced by the presence of an amino acid sequence that is similar to a consensus sequence involved in ubiquitination in CreA (Strauss et al. 1999). Moreover, Roy et al. (2008) reported that CreA requires post-translational modification(s) to become an active repressor. Recent studies regarding the regulation of CreA showed that CreA is partially dependent on 'de novo' protein synthesis and regulated by ubiquitination (Ries et al. 2016). In addition, the WD-40 repeat protein CreC, a component of CreB/CreC deubiquitinating complex, was suggested to be essential for CreA stability and functions, although this is not consistent with previous studies including phenotypic analysis of *creB* mutations and that overexpression of CreB can compensate the lack of CreC but not vice versa (Lockington and Kelly 2002; Ries et al. 2016). Both western and mass spectrometry (MS) analysis confirmed that CreA was differentially phosphorylated in repressing and derepressing conditions but not ubiquitinated (Alam et al. 2016). In addition, co-purifications and MS analysis both indicated no direct or indirect (through another protein/protein complex) physical interactions exist between CreA and CreB proteins (Alam et al. 2016). However, strains containing both partial and complete loss-of-function alleles of the *creA* and *creB* genes showed a higher extent of derepression than either of the single mutants, confirming genetic interaction between the repressor gene and the gene that encodes the deubiquitinating enzyme (Alam et al. 2016; Hynes and Kelly 1977). These results raise new questions as to how the deubiquitnating enzyme CreB modulates CreA function in CCR.

To investigate whether there were proteins that interacted with either CreA or CreB, the proteins were separately purified and the co-purified products were analysed by MS. Gene ontology (GO) analyses were performed with the co-purified proteins. In this way, we categorized the proteins in terms of biological process, cellular components and molecular functions that are significantly over or under-represented with respect to a given population background of the organism. Apart from functional annotation, GO can also be used to validate and interpret new system-wide data and evaluation of protein interactions considering that interacting proteins tend to classify in the same or similar GO terms (Chagoyen and Pazos 2010). Human and yeast orthologues of purified proteins were also determined, as the repressor proteins of *A. nidulans* and *S. cerevisiae* have similar zinc finger regions and DNA-binding specificities (despite differences in the CCR mechanisms between these organisms), and the CreB deubiquitination enzyme is conserved across eukaryotes including humans. GO analysis was also performed for these orthologous proteins.

Materials and methods

Strains and media

A. nidulans strains used and their genotypes are shown in Table 1a. *Aspergillus* media are based on those described by Cove (1966). Carbon and nitrogen sources were added aseptically to the media to reach the final concentration as shown.

Table 1 List of strains and oligonucleotides

Strains	Genotype	References
(a)		
WT	*biA1; niiA4*	Pateman et al. (1967)
CreA^{cTAP}14	*yA1 creAΔ99::pGEMTeasyCreA*^{cTAP}*; pyroA4; argB2*	Alam et al. (2016)
CreB^{cTAP}15	*yA1 pabaA1;creB1937::pGEMTeasyCreB*^{cTAP}*; pyroA4*	Alam et al. (2016)
MH11069	*pyroA4; riboB2 nkuAΔ*	(Hynes MJ, Unpublished)

Name	Sequence (5′–3′)	Purpose
(b)		
5′H2A.Z_F	GGTCTCATGACCCGCATTAG	5′H2A.Z fragment
5′H2A.Z_R	CCCATGTGATTTTGGAAAAGCGTTGAGATTC	
Afu_ribo_F_H2A.Z	CTTTTCCAAAATCACATGGGATTAAAATATGG	*Afu ribo* fragment
Afu_ribo_R_H2A.Z	TCCGCAGTGCTTACATGAGTGTGACGAGCATAC	
3′H2A.Z_F	ACTCATGTAAGCACTGCGGATACCCAACAC	3′ H2A.Z fragment
3′H2A.Z_R	TTTAGCTTAGTGAAAGAACTGCGC	

Construction of an H2A.ZΔ strain

Experiments to generate a complete loss-of-function strain for H2A.Z were undertaken using gene replacement techniques (Miller et al. 1985). A construct containing *Aspergillus fumigatus riboB*+ flanked by regions upstream and downstream of the coding regions of *A. nidulans htz1* was constructed using fusion PCR (Szewczyk et al. 2006). The fusion product was ligated to pGEMTeasy (Promega) and transformed into an *nkuA*Δ strain (MH11069) to replace the *htz1* coding region with the *A. fumigatus riboB*+ gene (Nayak et al. 2006), and riboflavine-independent colonies were selected.

Proteomic analysis

CreA and CreB were purified from CreA^{cTAP}14 and CreB^{cTAP}15 mycelia after growth in repressing (1% glucose) or derepressing (1% arabinose) conditions using the TAP purification protocol (Bayram et al. 2012) and separated by SDS-PAGE. Proteins were fixed using 10% acetic acid and 40% methanol solution for 2 h at RT. Coomassie staining of the gel was performed with CBB G-250 solution overnight at room temperature [Figure 8 of Alam et al. (2016)]. Proteins were detected and identified as described in Meding et al. (2013) and Alam et al. (2016). For CreA ^{cTAP}14, equivalent gel slices were examined from both repressing (1% glucose) and derepressing (1% arabinose) conditions, covering the range from approximately 12–100 kDa. For CreB^{cTAP}15, equivalent gel slices were examined from repressing (1% glucose) and derepressing (1% arabinose) conditions covering the range from approximately 50–150 kDa. For derepressing (1% arabinose) conditions the molecular weight range from approximately 35–50 kDa was also analysed. One of the purified proteins was Hir3, and as the theoretical molecular weights of the *A. nidulans*, human and yeast proteins are 233, 246, and 192 kDa, respectively (SGD, uniprot and genecards human gene database), it is larger than the estimated gel-slice ranges. This indicates some degree of degradation in the samples during co-purification. Whilst non-specific pull-down controls were included in all pull-down experiments, there were no bands evident, and thus we did not include the control samples in the MS experiments, rather we used the two independent pull-down experiments for CreA and CreB as internal controls for each other.

Raw data files were analysed by Mascot and MaxQuant databases. For Mascot analysis, files were submitted to Mascot (v 2.2; Matrix Science Inc: Boston, USA) by the Proteome Discoverer Daemon (Thermo Scientific). Peak lists in the range from 350 to 5000 *m*/*z* were searched against the Swiss-Prot database as 'All entries', 'Mammals and *A. nidulans*' and '*A. nidulans*', with a *p* value of 0.01. Proteins were identified on the basis of having at least two matching unique peptides. Data analysis by MaxQuant was described previously in Alam et al. (2016). Protein detection and data analysis was performed by the Adelaide Proteomics Centre.

Identifications of human and yeast orthologues

Human and yeast (*S. cerevisiae*) orthologues of *A. nidulans* proteins detected by Mascot and MaxQuant search were first identified using the KEGG database (Kanehisa et al. 2016). Protein blast for each protein was performed against the human protein reference database (http://www.hprd.org/index_html) and the *Saccharomyces* genome database (http://yeastgenome.org/) to detect the "top-hit" aligned human and yeast protein with respect to the *A. nidulans* protein. "Top-hit" orthologues were compared with KEGG identified orthologues. Human and yeast orthologues were confirmed using the HGNC (HUGO Gene Nomenclature Committee) comparison of orthology predictions (HCOP) tool (http://www.genenames.org/cgi-bin/hcop). Orthologues were identified according to amino acid sequence similarity, but it is not known whether they are functional homologues.

GO analysis

NCBI Gene IDs of *A. nidulans* proteins and their human and yeast orthologues were obtained from the Uniprot data base using Uniprot accession numbers.

Functional annotations of genes in terms of GO enrichment were performed using the DAVID (v6.7) web application (Huang et al. 2009). For GO enrichment analysis, *p*-value (modified Fisher's exact test) was set at 0.01 with minimum 2 query genes involved in a GO term. Due to the small number of query genes, this *p*-value was used as a statistical tool for selecting the significantly enriched GO terms. Population background was set as default which in this particular analysis selected *A. nidulans*, *H. sapiens* and *S. cerevisiae* all genome genes.

Results

Proteins detected in CreA and CreB purifications

To identify proteins that are in a complex with CreA or CreB, purifications of CreA and CreB in both repressing (1% glucose) and derepressing (1% arabinose) conditions were performed. Proteins were detected as described in "Materials and methods", and those either having *Q*-value and posterior error probabilities (PEP) <1% (MaxQuant) or positive emPAI values (Mascot) were selected for further analysis.

For CreA, a total of 47 proteins were detected either by Mascot or MaxQuant searches in both conditions (Table 2). Among these proteins only 14 were identified using MaxQuant which is considered to be more stringent than Mascot; however, strict filtering to avoid false-positive data can generate false-negative results (Jagtap et al. 2013). Conversely, Mascot allows user-specified search criteria at the risk of generating false-positive results. Among the 47 proteins identified by either the Mascot or MaxQuant searches, 16 proteins were detected only in repressing conditions including canonical and variant histones, histone transcription regulator protein, and proteins involved in transcriptional processes. Another 17 proteins including actin, tubulin, 60S ribosomal proteins, heat shock protein, serine/threonine kinase and phosphatase and proteins involved in cellular organization were identified only in derepressing conditions. The remaining 14 proteins were detected in both repressing and derepressing conditions, including CreA as expected, and canonical histones and proteins participating in transcriptional and translational processes. Importantly, as expected, neither CreB nor CreC were present among the proteins detected.

Similar analyses were performed to detect proteins co-purified with the CreB deubiquitinating enzyme, and 47 proteins were identified in total. The MaxQuant search identified 31 proteins, including 18 proteins that were also detected by the Mascot search engine. Among them, 7 proteins were detected only in repressing conditions including the TATA box-binding protein, autophagy-related protein, pre-mRNA splicing factor, heme-binding peroxidase and rRNA biogenesis protein, and 25 proteins were present only in derepressing conditions including proteins involved in cellular materials transportation and localization, the nitrogen assimilation transcription factor, and 40S ribosomal proteins. Another 15 proteins were identified in both repressing and derepressing conditions (Table 3). The CreB deubiquitinating enzyme was detected in both conditions as expected, together with CreC which serves as an internal control in this experiment, as the presence of CreB and CreC in one stable complex has been detected previously (Lockington and Kelly 2002). Importantly, again as expected, CreA was not present among the proteins detected.

Actin, tubulin, 60S ribosomal proteins, and heat shock proteins were present in both CreA and CreB co-purifications, and as these have been reported as false positive in previous studies (Gingras et al. 2007), these are most probably not significant.

Gene ontology analysis of proteins co-purified with CreA^{cTAP}

GO analysis of proteins that were co-purified with CreA was performed as described in "Materials and methods".

Proteins co-purifying with CreA in repressing conditions

Functional annotation analysis of *A. nidulans* proteins in repressing conditions identified six biological processes. Among them chromatin assembly and nucleosome organization showed significant enrichment with *p*-values less than 0.0001 and false discovery rate (FDR) less than 0.01. All six histone proteins, including the H2A variant H2A.Z that co-purified with CreA were involved in these processes, which may be expected of a transcription factor interacting with the transcriptional machinery. Other proteins interacting with CreA, albeit with higher FDR, are involved in chromosomal organization processes, including the chromosome segregation protein, SudA, and the DNA polymerase epsilon catalytic subunit A, Dpoe (Table 4a).

The mechanisms of CCR have been extensively studied in both yeast and filamentous fungi. Despite similarities in the zinc finger regions and repressor domain of the repressor proteins, there are differences in glucose signalling, repression mechanism, involvement of ubiquitination/deubiquitination proteins and glucose metabolism between these two eukaryotes. On the other hand, proteins including CreB and CreC that are involved in the ubiquitination/deubiquitination network in filamentous fungi, are also conserved in higher eukaryotes including humans. The GO term data base for *A. nidulans* proteins is likely to be less complete than the potentially equivalent proteins in the human and yeast databases due to the smaller number of proteins that have been comprehensively analysed. Further, analysis of the human and yeast proteins may provide some clues as to the function of *A. nidulans* genes of unknown function. Thus, both human and yeast orthologues of co-purified proteins were identified and analysed ("Materials and methods").

The human orthologues of the *A. nidulans* proteins were identified (Supplementary Table 1), and similar GO terms with significant fold enrichment and *p*-values less than 0.0001 were identified when analysed against the human protein database (Table 4b). As in the analysis of the *A. nidulans* proteins, histone orthologues were present in the chromatin assembly, nucleosome and chromosome organization biological terms. In addition, the histone transcription regulator 3 (Hir3) homologue, Cabin1, and chromosome segregation protein, Smc3, were also present.

Table 2 List of proteins identified in CreA^{cTAP} proteomic analysis in repressing and derepressing conditions

	Accession	Protein Description	Gene	NCBI ID
Repressed	APSB_EMENI	Anucleate primary sterigmata protein B	*apsB*	2874340
	BGLJ_EMENI	Probable beta-glucosidase J	*bglJ*	2869049
	FKBP4_EMENI	FK506-binding protein 4	*fpr4*	2873328
	GPA1_EMENI	Guanine nucleotide-binding protein subunit alpha	*fadA*	2876430
	H2AZ_EMENI	Histone H2A.Z	*htz1*	2869194
	H3_EMENI	Histone H3	*hhtA*	2876509
	H42_EMENI	Histone H4.2	*hhfB*	2875549
	HAS1_EMENI	ATP-dependent RNA helicase has1	*has1*	2875602
	HIR3_EMENI*	Histone transcription regulator 3 homolog	*hir3*	2874143
	MED8_EMENI	Mediator of RNA polymerase II transcription subunit 8	*med8*	2875539
	MIRC_EMENI	Siderophore iron transporter mirC	*mirC*	2869709
	PANB_EMENI	3-methyl-2-oxobutanoate hydroxymethyltransferase	*panB*	2874758
	RS19_EMENI	40S ribosomal protein S19	*rps19*	2873483
	RSE1_EMENI	Pre-mRNA-splicing factor rse1	*rse1*	2871744
	STCK_EMENI	Putative sterigmatocystin biosynthesis fatty acid synthase subunit beta	*stcK*	2869366
	SUDA_EMENI	Chromosome segregation protein sudA	*sudA*	2871258
Derepressed	ACSA_EMENI	Acetyl-coenzyme A synthetase	*facA*	2871910
	ACTG_EMENI*	Actin, gamma	*acnA*	2870269
	ATG1_EMENI*	Serine/threonine-protein kinase atg1	*atg1*	2874875
	CLU_EMENI	Clustered mitochondria protein homolog	*clu1*	2872707
	DYHC_EMENI	Dynein heavy chain, cytoplasmic	*nudA*	2875894
	GATB_EMENI	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	*nempA*	2873984
	HSP70_EMENI*	Heat shock 70 kDa protein	*hsp70*	2871415
	LOC1_EMENI	60S ribosomal subunit assembly/export protein loc1	*loc1*	2870323
	LONP2_EMENI	Lon protease homolog 2, peroxisomal	*AN0122*	2875898
	MASY_EMENI	Malate synthase, glyoxysomal	*acuE*	2870422
	MUS81_EMENI	Crossover junction endonuclease mus81	*mus81*	2874172
	MYO1_EMENI	Myosin-1	*myoA*	2875672
	PP2B_EMENI	Serine/threonine-protein phosphatase 2B catalytic subunit	*cnaA*	2868443
	PRP5_EMENI	Pre-mRNA-processing ATP-dependent RNA helicase prp5	*prp5*	2877043
	RL37_EMENI	60S ribosomal protein L37	*rpl37*	2872582
	SEPA_EMENI	Cytokinesis protein sepA	*sepA*	2870211
	TBB1_EMENI*	Tubulin beta-1 chain	*benA*	2876958
Repressed and Derepressed	CREA_EMENI	DNA-binding protein creA	*creA*	2870784
	CUTI2_EMENI	Cutinase 2	*AN7541*	2869670
	CWC27_EMENI	Peptidyl-prolyl isomerase cwc27	*cwc27*	2869127
	DPOE_EMENI	DNA polymerase epsilon catalytic subunit A	*pol2*	2874392
	EIF3A_EMENI	Eukaryotic translation initiation factor 3 subunit A	*tif32*	2874000
	EIF3H_EMENI	Eukaryotic translation initiation factor 3 subunit H	*AN1270*	2877041
	H2A_EMENI	Histone H2A	*htaA*	2873871
	H2B_EMENI	Histone H2B	*htbA*	2874197
	H41_EMENI	Histone H4.1	*hhfA*	2876510
	HSP7M_EMENI*	Heat shock 70 kDa protein	*AN6010*	2871135
	IRS4_EMENI	Increased rDNA silencing protein 4	*irs4*	2875869
	MED17_EMENI	Mediator of RNA polymerase II transcription subunit 17	*srb4*	2874164
	RS3A_EMENI*	40S ribosomal protein S1	*rps1*	2868357
	TMEDA_EMENI*	Endoplasmic reticulum vesicle protein 25	*erv25*	2873588

Shaded present in both Mascot and Max Quant databases; *unshaded* present in only Mascot

* Present in both CreA and CreB pull-down experiments

Table 3 List of proteins identified in CreB^{cTAP} proteomics analysis in repressing and derepressing conditions

	Accession	Protein Description	Gene	NCBI ID
Repressed	ACVS_EMENI	N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase	*acvA*	2874260
	ATG13_EMENI	Autophagy-related protein 13	*atg13*	2874917
	CCPR2_EMENI	Putative heme-binding peroxidase	*AN5440*	2871733
	PNG1_EMENI	**Protein PNG1**	***png1***	2871572
	RSE1_EMENI	**Pre-mRNA-splicing factor rse1**	***rse1***	2873208
	RRP36_EMENI	rRNA biogenesis protein rrp36	*rrp36*	2871744
	TBP_EMENI	**TATA-box-binding protein (TATA sequence-binding protein) (TBP)**	***tbpA tbp***	2872776
Derepressed	ATG1_EMENI*	Serine/threonine-protein kinase atg1	*atg1*	2874875
	BRO1_EMENI	Vacuolar protein-sorting protein bro1	*broA*	
	CISY_EMENI	Citrate synthase, mitochondrial	*citA*	2868998
	DHE4_EMENI	NADP-specific glutamate dehydrogenase	*gdhA*	2872176
	G3P_EMENI	Glyceraldehyde-3-phosphate dehydrogenase	*gpdA*	2868966
	IF4A_EMENI	ATP-dependent RNA helicase eIF4A	*tif1*	2874390
	KCC1_EMENI	Calcium/calmodulin-dependent protein kinase	*cmkA*	2874845
	MANBA_EMENI	**Beta-mannosidase A (EC 3.2.1.25) (Mannanase A) (Mannase A)**	***mndA***	2874889
	MCR1_EMENI	**NADH-cytochrome b5 reductase 2**	***mcr1***	2876210
	MDJ1_EMENI	DnaJ homolog 1, mitochondrial	*AN10778*	2870728
	NACA_EMENI	Nascent polypeptide-associated complex subunit alpha	*egd2*	2870379
	NCPR_EMENI	NADPH--cytochrome P450 reductase	*cprA*	2876366
	NIRA_EMENI	Nitrogen assimilation transcription factor nirA	*nirA*	2875872
	NMT_EMENI	Glycylpeptide N-tetradecanoyltransferase	*swoF*	2873262
	NSA2_EMENI	**Ribosome biogenesis protein nsa2**	***nsa2***	2874412
	NST1_EMENI	**Stress response protein nst1**	***nst1***	2872751
	PAM17_EMENI	Presequence translocated-associated motor subunit pam17, mitochondrial	*pam17*	
	PDX1_EMENI	Pyridoxal 5'-phosphate synthase subunit pyroA	*pyroA*	2869370
	RS3A_EMENI*	40S ribosomal protein S1	*rps1*	2868357
	RSSA_EMENI	**40S ribosomal protein S0**	***rps0***	2874532
	SEC16_EMENI	COPII coat assembly protein sec16	*sec16*	2870538
	TBA2_EMENI	**Tubulin alpha-2 chain**	***tubB***	2869740
	TMEDA_EMENI*	Endoplasmic reticulum vesicle protein 25	*erv25*	2873588
	TPS1_EMENI	Alpha,alpha-trehalose-phosphate synthase [UDP-forming]	*tpsA*	2871815
	XYL2_EMENI	Probable D-xylulose reductase A	*xdhA*	2868103
Repressed and Derepressed	ACTG_EMENI*	Actin, gamma	*acnA*	2870269
	AIM24_EMENI	**Altered inheritance of mitochondria protein 24, mitochondrial**	***aim24***	
	ATG2_EMENI	Autophagy-related protein 2	*atg2*	2871780
	APSA_EMENI	**Anucleate primary sterigmata protein A**	***apsA***	2869470
	BGALA_EMENI	**Probable beta-galactosidase A (EC 3.2.1.23) (Lactase A)**	***lacA***	2876531
	CREB_EMENI	Ubiquitin carboxyl-terminal hydrolase creB	*creB*	2873003
	CREC_EMENI	Catabolite repression protein creC	*creC*	2873591
	HIR3_EMENI*	Histone transcription regulator 3 homolog	*hir3*	2874143
	HSP70_EMENI*	Heat shock 70 kDa protein	*hsp70*	2871415
	HSP7M_EMENI*	Heat shock 70 kDa protein	*AN6010*	2871135
	P2OX_EMENI	**Pyranose 2-oxidase (P2Ox)**	***p2ox***	2870329
	STCL_EMENI	Versicolorin B desaturase	*stcL*	2869354
	TBA1_EMENI	Tubulin alpha-1 chain	*tubA*	2876093
	TBB1_EMENI*	Tubulin beta-1 chain	*benA*	2876958
	TBB2_EMENI	Tubulin beta-2 chain	*tubC*	2870526

Shaded present in both MaxQuant and Mascot database; *bold* present only in MaxQuant; *unshaded* present only in Mascot

* Present in both CreA and CreB pull-down experiments

Table 4 GO analysis—biological processes for proteins co-purified with CreA^{cTAP}

Category	Biological term	Count	*p*-value	Fold enrichment	FDR
(a) *A. nidulans*					
Repressed					
GOTERM_BP_3	GO:0031497~chromatin assembly	6	**2.31E−07**	38.95	**2.38E−04**
GOTERM_BP_3	GO:0034728~nucleosome organization	6	**1.83E−06**	26.38	**1.89E−03**
GOTERM_BP_3	GO:0051276~chromosome organization	8	**6.77E−05**	7.13	6.98E−02
GOTERM_BP_3	GO:0034622~cellular macromolecular complex assembly	6	2.25E−03	6.06	2.30E+00
GOTERM_BP_3	GO:0065003~macromolecular complex assembly	6	4.96E−03	5.05	5.01E+00
GOTERM_BP_3	GO:0034621~cellular macromolecular complex subunit organization	6	5.51E−03	4.93	5.54E+00
Derepressed					
GOTERM_BP_3	GO:0031497~chromatin assembly	3	8.09E−03	20.92	8.76E+00
(b) *H. sapiens*					
Repressed					
GOTERM_BP_3	GO:0031497~chromatin assembly	5	**7.28E−06**	36.84	**8.36E−03**
GOTERM_BP_3	GO:0034728~nucleosome organization	5	**9.50E−06**	34.47	1.09E−02
GOTERM_BP_3	GO:0065003~macromolecular complex assembly	8	**3.06E−05**	7.71	3.52E−02
GOTERM_BP_3	GO:0051276~chromosome organization	7	**5.34E−05**	9.25	6.13E−02
GOTERM_BP_3	GO:0034622~cellular macromolecular complex assembly	6	**8.25E−05**	12.10	9.47E−02
GOTERM_BP_3	GO:0034621~cellular macromolecular complex subunit organization	6	1.42E−04	10.77	1.63E−01
GOTERM_BP_3	GO:0044260~cellular macromolecule metabolic process	15	4.57E−03	1.84	5.12E+00
Derepressed					
GOTERM_BP_3	GO:0034622~cellular macromolecular complex assembly	5	2.61E−03	8.14	3.03E+00
GOTERM_BP_3	GO:0034621~cellular macromolecular complex subunit organization	5	3.96E−03	7.25	4.56E+00
GOTERM_BP_3	GO:0065003~macromolecular complex assembly	6	6.75E−03	4.67	7.66E+00
(c) *S. cerevisiae*					
Repressed					
GOTERM_BP_3	GO:0031497~chromatin assembly	7	**1.58E−08**	36.98	**1.84E−05**
GOTERM_BP_3	GO:0034728~nucleosome organization	7	**6.47E−07**	20.34	**7.52E−04**
GOTERM_BP_3	GO:0009889~regulation of biosynthetic process	15	**6.64E−05**	2.98	7.72E−02
GOTERM_BP_3	GO:0051172~negative regulation of nitrogen compound metabolic process	8	1.41E−04	6.34	1.63E−01
GOTERM_BP_3	GO:0034622~cellular macromolecular complex assembly	9	1.77E−04	5.09	2.05E−01
GOTERM_BP_3	GO:0065003~macromolecular complex assembly	10	1.88E−04	4.36	2.18E−01
GOTERM_BP_3	GO:0009890~negative regulation of biosynthetic process	8	2.01E−04	5.99	2.34E−01
GOTERM_BP_3	GO:0031323~regulation of cellular metabolic process	15	2.28E−04	2.67	2.65E−01
GOTERM_BP_3	GO:0080090~regulation of primary metabolic process	15	2.47E−04	2.65	2.86E−01
GOTERM_BP_3	GO:0031324~negative regulation of cellular metabolic process	8	3.04E−04	5.60	3.53E−01
GOTERM_BP_3	GO:0010605~negative regulation of macromolecule metabolic process	8	4.25E−04	5.30	4.94E−01
GOTERM_BP_3	GO:0019222~regulation of metabolic process	15	4.87E−04	2.49	5.65E−01
GOTERM_BP_3	GO:0009892~negative regulation of metabolic process	8	6.36E−04	4.96	7.37E−01
GOTERM_BP_3	GO:0051276~chromosome organization	9	8.39E−04	4.05	9.71E−01
GOTERM_BP_3	GO:0051171~regulation of nitrogen compound metabolic process	12	8.71E−04	2.92	1.01E+00
GOTERM_BP_3	GO:0060255~regulation of macromolecule metabolic process	14	8.78E−04	2.51	1.02E+00
GOTERM_BP_3	GO:0034621~cellular macromolecular complex subunit organization	9	1.70E−03	3.64	1.96E+00
GOTERM_BP_3	GO:0048523~negative regulation of cellular process	8	2.10E−03	4.05	2.42E+00

Table 4 continued

Category	Biological term	Count	*p*-value	Fold enrichment	FDR
GOTERM_BP_3	GO:0050794~regulation of cellular process	16	2.37E−03	2.04	2.73E+00
GOTERM_BP_3	GO:0048519~negative regulation of biological process	8	3.76E−03	3.66	4.29E+00
Derepressed					
GOTERM_BP_3	GO:0051293~establishment of spindle localization	3	1.81E−03	44.38	2.21E+00
GOTERM_BP_3	GO:0040001~establishment of mitotic spindle localization	3	1.81E−03	44.38	2.21E+00
GOTERM_BP_3	GO:0051276~chromosome organization	8	6.29E−03	3.36	7.46E+00

Bold: *p*-value <0.0001; FDR <0.01

Other proteins expected to interact with the gene expression machinery were present, including mediator of RNA polymerase II transcription subunit 17, Med17, a co-activator that is required for RNA polymerase II dependent gene transcription (Baek et al. 2006), eukaryotic translation initiation factor 3 subunit A, required for the initiation of protein synthesis (Zhou et al. 2008), and splicing factor 3B subunit 3, Sf3b3, essential for the formation of splicing complex assembly by binding of U2 snRNP to the branchpoint sequence in pre-mRNA (Das et al. 1999).

The *S. cerevisiae* orthologues of the *A. nidulans* proteins were also identified (Supplementary Table 2). GO terms were analysed and 16 biological processes with a *p*-value lower than 0.001 were identified including those that were observed in *A. nidulans* and humans (Table 4c). Two biological processes, chromatin assembly and nucleosome organization, showed high fold enrichment ≥20 with FDR value less than ≤0.001. Histone orthologous proteins including histone transcription regulator 3, Hir3, were present in the chromatin assembly and nucleosome organization biological processes. An orthologue of Fkbp4 in yeast, a member of the FK506-binding protein family that catalyses cis–trans isomerization of proline and interacts with histones to facilitate nucleosome assembly, was also present (Nelson et al. 2006; Park et al. 2014). Besides these histone orthologous proteins, ATP-dependent RNA helicase, Has1, and pre-mRNA splicing factor, Rse1, were present. In addition, a number of metabolic and biosynthetic biological processes, some negatively regulated, were generated with yeast orthologues. Regulatory protein Mig1p, the homologue of CreA, was identified to be involved in all negatively regulated biological processes together with histone proteins and FK506-binding protein Fkbp4. However, histone transcription regulator 3, Hir3, was not present in either of these negatively regulated processes.

Thus, in repressing conditions, the chromosomal assembly and nucleosome and chromosomal organization biological processes were present in all three analyses and histone proteins were the major contributors of these processes. In *S. cerevisiae*, repressor protein Mig1p was involved in the regulation, negatively in some cases, of various metabolic pathways which was not observed for CreA in *A. nidulans* or its orthologue in humans, reinforcing that the repressor proteins in these two organisms may have different modes of action despite sequence similarities, although this may be an artefact as the GO description for CreA is likely to be less comprehensive than that for Mig1. One apparent difference is the histone transcription regulator 3, Hir3, which was present in transcription related biological processes in humans and yeast, but not in *A. nidulans*, but this may be an artefact due to the absence of any studies on the Hir3 homologue in *A. nidulans* resulting in its absence in the GO term database. In *S. cerevisiae*, Hir3 is one of the subunits of the Hir complex, which also consists of Hir1 and Hir2, and histone promoter control, Hpc2, that acts as a co-repressor of transcription of histone gene pairs and is also involved in nucleosome assembly to facilitate various cellular processes including transcription, and gene silencing (Amin et al. 2012).

Proteins co-purifying with CreA in derepressing conditions

In derepressing conditions, when analysed against *A. nidulans* there were no biological processes with *p*-values less than 0.0001 and false discovery rate (FDR) less than 0.01, with the most significant biological process, chromatin assembly, identified with higher *p*-value (≤0.01) and a FDR of <8.7 (Table 4a). This was also true in the analysis with human orthologous proteins, where again there were no biological processes with *p*-values less than 0.0001 and FDR less than 0.01, with the most significant biological process, cellular molecular complex organization and assembly with higher *p*-value (≤0.01) and a FDR of >3 (Table 4b). This trend was also apparent in the case of *S. cerevisiae* orthologues, where functional annotation with proteins from derepressing conditions generated no biological processes with *p*-values less than 0.0001 and FDR less than 0.01. The most significant biological processes involved spindle localization, but although the fold enrichment was high (40), the *p*-value (≤0.01) and a FDR of 2.2 did not support significance (Table 4c).

Thus, the biological processes identified for proteins co-purified in repressing conditions were not present for proteins co-purified in derepressing conditions, validating their significance in the repressing condition analysis. Further, the failure to identify any significant biological process for the proteins co-purified in derepressing conditions suggests that CreA may not play a role in these conditions.

Construction of H2A.Z deletion strain

H2A variant H2A.Z was present among the proteins co-purified with CreA. H2A.Z is evolutionarily conserved from budding yeast to mammals (Thatcher and Gorovsky 1994; Wu et al. 1982) and it comprises around 15% of total H2A but possesses a distinct function (Sarcinella et al. 2007). This histone variant is essential for the viability of *Tetrahymena*, *Drosophila* and mice (Faast et al. 2001; Liu et al. 1996; Ridgway et al. 2004). In yeast, deletion of *HTZ1* encoding H2A.Z resulted in slow growth but did not affect viability (Adam et al. 2001). Like canonical histones, H2A.Z can be modified post-translationally (acetylation, ubiquitination, methylation) and plays a role in nucleosome organization and transcriptional regulation [review by (Sevilla and Binda 2014; Weber and Henikoff 2014)]. Interestingly, H2A variant H2A.Z was co-purified with CreA only in repressing conditions, suggesting that H2A.Z may play a role in the transcription process involving CreA.

Thus, to investigate the role of histone variant H2A.Z in the transcription process involving CreA, experiments were undertaken to construct a strain that was a complete null mutant for *htz1,* by replacing the coding region of *htz1* with the *A. fumigatus ribo* gene (Fig. 1). However, after transforming into an *A. nidulans nkuAΔ* strain, riboflavin independent colonies appeared slowly, but they were all apparently heterokaryons, as they could not be streaked to single colonies on selective medium from conidial spores. Conidia were diluted and plated on selective and nonselective media, and smooth single colonies were present on nonselective medium, but no colonies were present on selective medium. Determined attempts were made to force a heterozygous diploid strain; however, no diploid colony could be isolated. Genomic DNA was extracted from the parent strain, heterokaryotic transformants, and the single colonies that were present on the nonselective medium, and PCR detected both wild type and deleted alleles in the heterokaryon, with only the wild-type allele in the other samples (Fig. 1). This confirms the formation of a heterokaryon, indicating that *htz1* is essential for the growth of haploid *A. nidulans*, and that a single copy is insufficient in a diploid.

Gene ontology analysis of proteins co-purified with CreB^{cTAP}

In *A. nidulans*, the CreB deubiquitinating enzyme is involved in the regulatory pathway of carbon catabolite repression (Lockington and Kelly 2001). A strain containing complete loss-of-function alleles of the *creA* and *creB* genes confirmed the genetic interactions of these two genes in some systems that are subject to CCR. However, at the protein level, no direct physical interaction was detected for CreA and CreB (Alam et al. 2016), suggesting the presence of a protein and/or protein complex that is modulated by CreB which ultimately modifies the regulation of CreA. Therefore, proteins that co-purified with CreB were detected and GO analysis was performed. Like CreA, functional annotation analyses of proteins co-purified with CreB were performed against '*A. nidulans*', '*H. sapiens*' and '*S. cerevisiae*' databases ("Materials and methods").

Proteins co-purifying with CreB in repressing conditions

In repressing conditions, analysis against *A. nidulans* generated two biological processes, microtubule-based movement and protein complex assembly with *p*-values ≤ 0.01 and high FDR ≥ 3 (Table 5a). With human orthologues, protein complex assembly, macromolecular complex assembly and microtubule-based movement biological processes were identified, but with *p*-value ≤ 0.01 and fold enrichment ≥ 6, and FDR was ≥ 2 (Table 5b). In *A. nidulans* and human (Supplementary Table 3) backgrounds, although some of the biological processes showed significant *p*-values, due to the high FDR these processes are unlikely to be biologically significant. Proteins involved in these processes were mainly tubulins which are highly expressed in eukaryotic cells, and TATA box-binding proteins. Analysis against the yeast database (Supplementary Table 4) identified six biological processes involved in cellular material localization, but again with high FDR value (≥ 3) (Table 5c). Proteins involved in these processes were autophagy-related proteins, Atg13 and Atg2, nuclear migration protein, Num1, heat shock protein, Hsp77, Actin, and tubulin. Num1p, the orthologue of Aim24 in *A. nidulans*, controls cytoplasmic microtubule functions and nuclear migration through the bud neck in anaphase cells (Farkasovsky and Kuntzel 1995). Autophagy-related protein 2 is a peripheral membrane protein required for vesicle formation during autophagy, pexophagy and the cytoplasm-to-vacuole transport pathway (Wang et al. 2001), while autophagy-related protein 13 is a regulatory subunit of the Atg1p signalling complex. Atg13p is required for autophosphorylation of Atg1p at

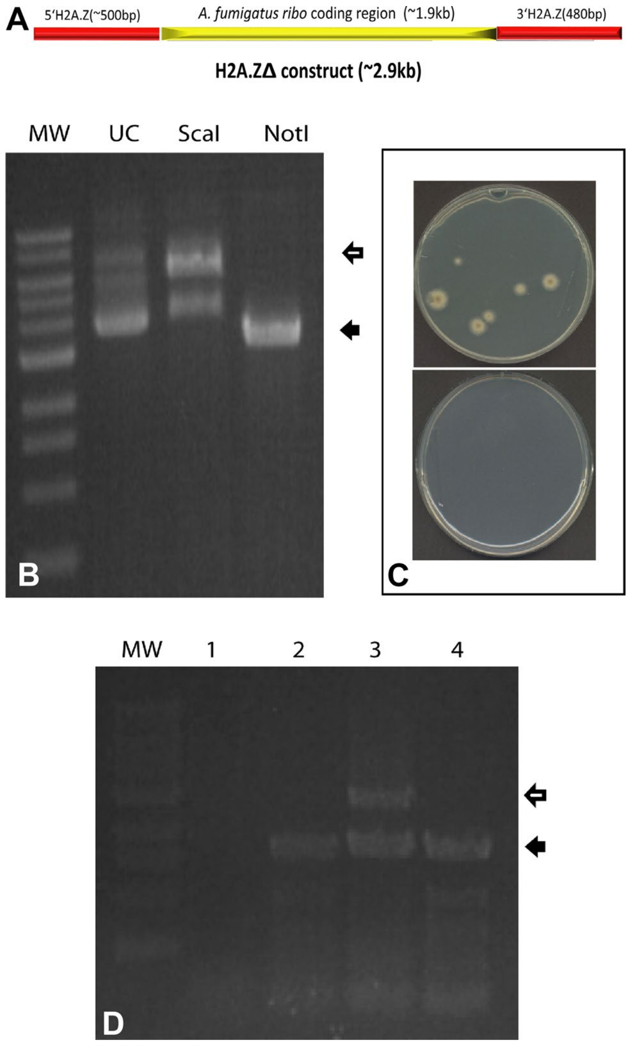

Fig. 1 Construction of a H2A.Z complete loss-of-function strain: construction of an H2A.ZΔ strain was attempted by inserting the *A. fumigatus ribo* gene into the coding region of *htz1* in *A. nidulans*. For this, a construct was generated by fusion PCR (**a**) with *A. fumigatus ribo* gene flanking with sequences 5′ and 3′ to the *htz1* gene (~2.9 kb). The construct was ligated into the pGEMTeasy vector and transformed into *E. coli* DH5α. The pGEMTeasy*Af*uribohtz1Δ plasmid was confirmed by ScaI (**b** *top arrow*, ~6 kb) and NotI (**b** *bottom arrow*, 2.9 kb) digestions. The plasmid was transformed into a MH11069 strain and riboflavin independent colonies were selected as well-balanced heterokaryons. Spores from the heterokaryon were diluted and plated with and without selection, and single colonies were only present on the unselective media (**c**). PCR was performed with gDNA of MH11069 (*lane 2*), an H2A.ZΔ heterokaryon (*lane 3*), and a colony from c (*lane 4*). *Lane 1* contains no DNA template. The *arrows* indicate bands of ~3 kb (**d** *top arrow*) and ~1.7 kb (**d** *bottom arrow*), consistent with the sizes predicted for the deleted and wild-type alleles, respectively

Thr^{226} position and involved in vesicle formation during autophagy and cytoplasm-to-vacuole transport pathway (Yeh et al. 2010, 2011).

Proteins co-purifying with CreB in derepressing conditions

In derepressing conditions, *A. nidulans* proteins generated four biological processes involving microtubule-based movement, protein transport and localization (Table 5a). Among these, microtubule-based movement showed significant fold enrichment (≥24) with lower *p*-value (≤0.001) and FDR (≤0.5), and as expected tubulin proteins were involved in this GO term. The protein transport biological process also showed significant fold change (≥4) and lower *p*-value (≤0.01). Proteins present in this biological process were involved in vacuole transport, autophagy, protein folding, 'de novo' co-translational protein folding, ER to Golgi vesicle-mediated transport, and protein localization. Endoplasmic reticulum vesicles protein, Erv25 is a constituent of COPII-coated endoplasmic reticulum-derived transport vesicles which are required for efficient transport of secretory proteins to Golgi. Sec16, a COPII coat assembly protein is involved in proper COPII coat assembly which is in turn required for the formation of transport vesicles from the ER and the selection of cargo molecules. Analysis against human database generated microtubule-based movement biological process with a *p*-value ≤0.001 and FDR of ≥1.8 involving tubulin proteins (Table 5b). Like *A. nidulans*, similar biological processes, including intracellular transport, protein transport and localization processes, were identified in the yeast analysis (Table 5c) in derepressing conditions involving yeast orthologues Sec16p, Erv25p, Apg2p, Ssc1p proteins. In addition, vacuolar sorting proteins, Bro1p, Pam17p, 40S ribosomal protein S0-A, nuclear migration protein, Num1p, and heat shock proteins were also present in these biological processes. In *S. cerevisiae*, Bro1p is involved in protein localization and transport as well as protein deubiquitination and ubiquitin dependent protein catabolic process (Luhtala and Odorizzi 2004; Springael et al. 2002) and Pam17p is a component of PAM complex and involved in protein import into mitochondrial matrix (van der Laan et al. 2005). These results suggest that proteins co-purified with CreB were mainly involved in cellular materials transport and organization in both repressing and derepressing conditions.

Discussion

Although the function of CreA is known in the sense that it acts as a DNA-binding protein and represses transcription, little is known about the signalling and mechanisms of repression and derepression. Unlike in *S. cerevisiae*, repression does not involve the recruitment of a Tup1p/Ssn6-like repressor complex (Hicks et al. 2001), and Snf1 and nuclear location are apparently not crucially involved in the derepression

Table 5 GO analysis—biological processes for proteins co-purified with CreB^{cTAP}

Category	Term	Count	p value	Fold enrichment	FDR
(a) *A. nidulans*					
Repressed					
GOTERM_BP_3	GO:0007018~microtubule-based movement	3	2.80E−03	34.88	2.96E+00
GOTERM_BP_3	GO:0006461~protein complex assembly	4	5.16E−03	10.33	5.39E+00
Derepressed					
GOTERM_BP_3	GO:0007018~microtubule-based movement	4	4.55E−04	24.71	5.13E−01
GOTERM_BP_3	GO:0015031~protein transport	7	3.67E−03	4.39	4.07E+00
GOTERM_BP_3	GO:0045184~establishment of protein localization	7	3.86E−03	4.35	4.28E+00
GOTERM_BP_3	GO:0008104~protein localization	7	7.05E−03	3.84	7.68E+00
(b) *H. sapiens*					
Repressed					
GOTERM_BP_3	GO:0006461~protein complex assembly	5	1.45E−03	8.89	1.52E+00
GOTERM_BP_3	GO:0065003~macromolecular complex assembly	5	3.97E−03	6.75	4.11E+00
GOTERM_BP_3	GO:0007018~microtubule-based movement	3	5.95E−03	23.83	6.10E+00
Derepressed					
GOTERM_BP_3	GO:0007018~microtubule-based movement	4	1.62E−03	16.43	1.89E+00
GOTERM_BP_3	GO:0019538~protein metabolic process	13	7.08E−03	2.15	8.04E+00
(c) *S. cerevisiae*					
Repressed					
GOTERM_BP_3	GO:0007018~microtubule-based movement	3	2.53E−03	36.98	2.90E+00
GOTERM_BP_3	GO:0046907~intracellular transport	8	2.83E−03	3.57	3.24E+00
GOTERM_BP_3	GO:0051656~establishment of organelle localization	4	2.90E−03	12.76	3.33E+00
GOTERM_BP_3	GO:0040023~establishment of nucleus localization	3	3.01E−03	33.90	3.45E+00
GOTERM_BP_3	GO:0051649~establishment of localization in cell	8	4.35E−03	3.31	4.94E+00
GOTERM_BP_3	GO:0051640~organelle localization	4	6.80E−03	9.43	7.63E+00
Derepressed					
GOTERM_BP_3	GO:0046907~intracellular transport	12	1.49E−03	2.83	1.78E+00
GOTERM_BP_3	GO:0051649~establishment of localization in cell	12	2.74E−03	2.63	3.26E+00
GOTERM_BP_3	GO:0015031~protein transport	10	4.82E−03	2.86	5.68E+00
GOTERM_BP_3	GO:0045184~establishment of protein localization	10	7.81E−03	2.66	9.04E+00
GOTERM_BP_3	GO:0007018~microtubule-based movement	3	9.41E−03	19.58	1.08E+01

process (Roy et al. 2008). Brown et al. (2013) showed that the nonessential protein kinases SnfA (homologue of Snf1p in *S. cerevisiae*) and SchA might be involved in nuclear localization of CreA and hence mediate derepression of at least cellulases in *A. nidulans*, although the growth conditions used were more similar to starvation than derepression, and CreA is known to be degraded in starvation conditions (Alam et al., unpublished). Thus, we aimed to identify proteins that are co-purified with CreA in a step towards understanding its mode of action. Similarly, we know that CreB is an active deubiquitinating protein, and some targets involved in transport are known. However, there is evidence that CreB is also involved in CCR for some systems, but the mechanism has not been elucidated. Thus, we purified CreA and CreB from mycelia grown in repressing and derepressing conditions, and identified proteins that were co-purified.

Here, we have analysed gene ontology (GO) in terms of biological process with the proteins detected by MS that were co-purified with either CreA or CreB proteins. Human and yeast orthologues of the purified proteins were also identified and analysed to generate GO terms, and they were compared with GO terms generated against the *A. nidulans* background, since differences in CCR mechanisms exist between yeast and filamentous fungi and ubiquitination/deubiquitination networks are conserved in higher eukaryotes including humans. Proteins co-purified with CreA and CreB showed clear distinctions between them. As a transcription factor, CreA interacted with the proteins that are involved in the transcriptional and translational machinery; whereas proteins co-purified with the CreB deubiquitinating enzyme were involved in cellular component transportation, localization and organization.

For CreA, in repressing conditions, canonical histones, histone variant H2A.Z, and histone transcription regulator, Hir3, were the major proteins co-purified and involved in biological processes like chromatin assembly, nucleosome and chromatin organizations. Histone variant H2A.Z is evolutionary conserved from budding yeast to humans (Thatcher and Gorovsky 1994; Wu et al. 1982) and is essential for the viability of *Tetrahymena*, *Drosophila* and mice (Faast et al. 2001; Liu et al. 1996; Ridgway et al. 2004). In *S. cerevisiae*, H2A.Z is required for normal proliferation as deletion of *HTZ1* encoding H2A.Z, resulted in slow growth (Adam et al. 2001), and our failure to generate a haploid deletion strain indicates that this is also true for *A. nidulans*. H2A.Z plays both positive and negative roles in transcriptional regulation and nucleosome organization (Sevilla and Binda 2014; Weber and Henikoff 2014). Whole genome microarray analysis identified that 214 genes showed decreased expression in a *HTZ1* mutant strain, and 107 genes showed increased expression (Meneghini et al. 2003). The activated genes were chiefly located near the telomeres and H2A.Z was required for the normal expression of these genes by antagonizing Sir2-dependent silencing (Meneghini et al. 2003). On the other hand, in a *HTZ1*-deleted strain, transcriptional activation of the *GAL1* and *GAL10* genes were impaired due to reduced recruitment of RNA polymerase II and TATA-binding protein (Adam et al. 2001). Similar roles of H2A.Z were also evident in higher eukaryotes including humans where differential localization of H2A.Z was responsible for transcriptional regulation of the p21 cell cycle inhibitor protein (Gevry et al. 2007). Transcription regulation can also be modulated by nucleosome positioning and assembly due to altered accessibility of transcription factor-binding sites (Wyrick et al. 1999). Both H2A.Z and the Hir complex have been reported to modify nucleosome positioning and assembly and hence regulate gene transcription (Amin et al. 2012; Fan et al. 2002; Fillingham et al. 2009; Sevilla and Binda 2014). Genome-wide analysis showed that H2A.Z is enriched within the few nucleosomes adjacent to transcriptional start site (TSS) and can alter nucleosome positioning (Fan et al. 2002; Sevilla and Binda 2014) and in *A. nidulans*, altered nucleosome positioning at the *alcA* and *alcR* promoters were observed in different growth conditions although there was no correlation with repression and derepression (Mathieu et al. 2005). It has been reported that post-translational modifications including ubiquitination of H2A.Z can alter transcriptional regulation of many genes (Sevilla and Binda 2014). All histone proteins including histone variant H2A.Z that co-purified with CreA were present among the ubiquitome proteins identified by Chu et al. (2016), and none of them were co-purified with the CreB deubiquitinating enzyme. Histone transcription regulator 3 homolog Hir3 was co-purified with both CreA and CreB, though it was not detected among the ubiquitome proteins in *A. nidulans* (Chu et al. 2016). Network analysis using GeneMANIA (Warde-Farley et al. 2010) with *S. cerevisiae* orthologues showed that Hir3 has genetic interaction with Htz1, Med8, Hta1, Mig1, Panb, and Hsp77 proteins. GO analysis against the yeast background showed that Hir3 was involved in the regulation of various cellular and biosynthetic processes together with Mig1p, but not in the negatively regulated biological processes where only Mig1p was involved. On the other hand, Htz1 showed strong genetic interaction with Med8 and Erv25 and rather weakly with Mig1, Hir3, Smc3, and Hta1 in a similar network analysis. As components of the Mediator complex, Med8 transmits activation or repression signals from DNA bound transcription factors to the core transcription machinery, RNA Pol II and general initiation factors (Zhu et al. 2011). It has been reported that Mediator can interact with a co-repressor complexes such as Ssn6/Tup1 that may play a role in targeting Mediator to specific regions of chromatin (Gromoller and Lehming 2000; Han et al. 2001) and Mediator occupancy in transcriptionally silent regions, with de-acetylation of H4K16 could explain the role of Mediator in the repression of genes (Zhu et al. 2011). Med8 also specifically binds to the UASs of the *SUC2* promoter, DRSs of the *HXK2* gene and interacts with the carboxy terminal of the RNA Pol II, indicating that Med8 might be involved in linking the activating and repressing transcription complexes with the transcription machinery (Chaves et al. 1999). Moreover, mammalian MED8 plays a role in recruiting ubiquitin ligase activity directly to the RNA pol II transcription machinery (Brower et al. 2002). Interestingly, Med8 was detected among the ubiquitome proteins (Chu et al. 2016) and co-purified with CreA in repressing conditions.

Like Hir3, another histone chaperon Fkbp4, which is a member of the FK506-binding protein family, co-purified with CreA only in repressing conditions. The protein family contains a highly conserved protein domain that binds with the immunosuppressant FK506 and rapamycin, and also catalyses peptidylprolyl cis–trans isomerization in protein substrates (PPIase) (Arevalo-Rodriguez et al. 2004). Fkbp4 facilitates nucleosome assembly in vitro and a *FPR4* mutant which lacks Fkbp4p showed differential gene expression in *S. cerevisiae* (Park et al. 2014). Like Hir3, Fkbp4 was also not detected by GO analysis as being involved in any biological processes in *A. nidulans*; however, for both Hir3 and Fkbp-4, this is possibly an artefact due to their not having been studied in this organism.

In derepressing conditions, no biological processes regarding transcription or translation were identified, clearly indicating that CreA does not interact in the same way with the components of transcription machinery during derepressing conditions.

Gene ontologies between *S. cerevisiae* and *A. nidulans* showed differences in repressing conditions. Apart from chromatin and nucleosome assembly/organization due to conserved histone proteins, a number of biological processes related to biosynthetic and metabolic processes were identified for Mig1p in *S. cerevisiae*, whereas these biological processes were not observed for CreA in *A. nidulans*.

The GO analysis of proteins co-purified with CreB revealed no significant biological processes in repressing conditions, suggesting that CreB is not involved in characterized networks in *A. nidulans* in these conditions. In derepressing conditions, transport of protein and cellular materials is the key biological process observed, consistent with the general finding that deubiquitinating enzymes can target a variety of substrates including transporters/permeases, scaffolds, adapters and ubiquitin receptors. In *A. nidulans*, quinate permease QutD, involved in the transportation of quinic acid, has been confirmed as a substrate of CreB (Kamlangdee 2008). Sec16, which localizes to the ER exit sites and is required for correct COPII coat assembly functioning, can play a role in integrating nutrient signalling by modifying functional organization according to the signal induced by exogenous stimuli (Sprangers and Rabouille 2015). Monoubiquitination of COPII component Sec31 can alter the size and function of COPII vesicles, and it is speculated that this kind of post-translational modifications could play a role in cargo loading and GTP hydrolysis involving Sec16 (Jin et al. 2012; Lord et al. 2011). In *A. nidulans*, Sec16 was present among the ubiquitome proteins with a potential ubiquitination site of TQTKPIYFPSEESR (Chu et al. 2016).

Alam et al. (2016) showed that CreA and CreB are not present in a single stable complex, and here we aimed to identify proteins or protein complexes that may reveal the link between CreA and CreB involvement in CCR. In *T. reesei*, it has been shown, at least for *cbh1*, nucleosome positioning in the promoter and coding regions are different in repressing compared to induced conditions, and the positioning of nucleosomes in the promoter region in derepressing conditions prevents CreA binding. Further, the positioning of nucleosomes in the coding region in repressing conditions depends on the presence of Cre1 (Ries et al. 2014). The proteins that co-purify with CreA are consistent with these findings in *T. reesei*, as nucleosome and chromatin organization biological processes were present in repressing but not derepressing conditions. Histone transcription regulator 3 homolog Hir3 was co-purified with both CreA and CreB, which opens up the suggestion that the involvement of CreB in CCR is via its involvement in the modification of Hir3 or a protein in the Hir3 regulatory process.

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References

Adam M, Robert F, Larochelle M, Gaudreau L (2001) H2A.Z is required for global chromatin integrity and for recruitment of RNA polymerase II under specific conditions. Mol Cell Biol 21:6270–6279. doi:10.1128/mcb.21.18.6270-6279.2001

Alam MA, Kamlangdee N, Kelly JM (2016) The CreB deubiquitinating enzyme does not directly target the CreA repressor protein in Aspergillus nidulans. Curr Genet. doi:10.1007/s00294-016-0666-3

Amin AD, Vishnoi N, Prochasson P (2012) A global requirement for the HIR complex in the assembly of chromatin. Biochim Et Biophys Acta Gene Regul Mech 1819:264–276. doi:10.1016/j.bbagrm.2011.07.008

Arevalo-Rodriguez M, Wu XY, Hanes SD, Heitman J (2004) Prolyl isomerases in yeast. Front Biosci 9:2420–2446. doi:10.2741/1405

Arst HN, Cove DJ (1973) Nitrogen metabolite repression in *Aspergillus nidulans*. Mol Gen Genet 126:111–141. doi:10.1007/bf00330988

Baek HJ, Kang YK, Roeder RG (2006) Human mediator enhances basal transcription by facilitating recruitment of transcription factor IIB during preinitiation complex assembly. J Biol Chem 281:15172–15181. doi:10.1074/jbc.M601983200

Bailey C, Arst HN (1975) Carbon catabolite repression in *Aspergillus nidulans*. Eur J Biochem 51:573–577. doi:10.1111/j.1432-1033.1975.tb03958.x

Bayram O, Bayram OS, Valerius O, Johnk B, Braus GH (2012) Identification of protein complexes from filamentous fungi with tandem affinity purification. Methods Mol Biol 944:191–205. doi:10.1007/978-1-62703-122-6_14

Boase NA, Kelly JM (2004) A role for *creD*, a carbon catabolite repression gene from *Aspergillus nidulans*, in ubiquitination. Mol Microbiol 53:929–940. doi:10.1111/j.1365-2958.2004.04172.x

Brower CS, Sato S, Tomomori-Sato C, Kamura T, Pause A, Stearman R, Klausner RD, Malik S, Lane WS, Sorokina I, Roeder RG, Conaway JW, Conaway RC (2002) Mammalian mediator subunit mMED8 is an Elongin BC-interacting protein that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin ligase. Proc Natl Acad Sci USA 99:10353–10358. doi:10.1073/pnas.162424199

Brown NA, de Gouvea PF, Krohn NG, Savoldi M, Goldman GH (2013) Functional characterisation of the non-essential protein kinases and phosphatases regulating *Aspergillus nidulans* hydrolytic enzyme production. Biotechnol Biofuels 6:91. doi:10.1186/1754-6834-6-91

Chagoyen M, Pazos F (2010) Quantifying the biological significance of gene ontology biological processes-implications for the analysis of systems-wide data. Bioinformatics 26:378–384. doi:10.1093/bioinformatics/btp663

Chaves RS, Herrero P, Moreno F (1999) Med8, a subunit of the mediator CTD complex of RNA polymerase II, directly binds to regulatory elements of SUC2 and HXK2 genes. Biochem Biophys Res Commun 254:345–350. doi:10.1006/bbrc.1998.9954

Chu XL, Feng MG, Ying SH (2016) Qualitative ubiquitome unveils the potential significances of protein lysine ubiquitination in hyphal growth of *Aspergillus nidulans*. Curr Genet 62:191–201. doi:10.1007/s00294-015-0517-7

Cove DJ (1966) The induction and repression of nitrate reductase in the fungus *Aspergillus nidulans*. Biochim Et Biophys Acta 113:51–56

Das BK, Xia L, Palandjian L, Gozani O, Chyung Y, Reed R (1999) Characterization of a protein complex containing spliceosomal proteins SAPS 49, 130, 145, and 155. Mol Cell Biol 19:6796–6802. doi:10.1128/MCB.19.10.6796

Dowzer CEA, Kelly JM (1991) Analysis of the *creA* gene, a regulator of carbon catabolite repression in *Aspergillus nidulans*. Mol Cell Biol 11:5701–5709. doi:10.1128/MCB.11.11.5701

Faast R, Thonglairoam V, Schulz TC, Beall J, Wells JRE, Taylor H, Matthaei K, Rathjen PD, Tremethick DJ, Lyons I (2001) Histone variant H2A.Z is required for early mammalian development. Curr Biol 11:1183–1187. doi:10.1016/s0960-9822(01)00329-3

Fan JY, Gordon F, Luger K, Hansen JC, Tremethick DJ (2002) The essential histone variant H2A.Z regulates the equilibrium between different chromatin conformational states. Nat Struct Biol 9:172–176. doi:10.1038/nsb767

Farkasovsky M, Kuntzel H (1995) Yeast Num1p associates with the mother cell cortex during S/G2 phase and affects microtubular functions. J Cell Biol 131:1003–1014. doi:10.1083/jcb.131.4.1003

Fillingham J, Kainth P, Lambert JP, van Bakel H, Tsui K, Pena-Castillo L, Nislow C, Figeys D, Hughes TR, Greenblatt J, Andrews BJ (2009) Two-color cell array screen reveals interdependent roles for histone chaperones and a chromatin boundary regulator in histone gene repression. Mol Cell 35:340–351. doi:10.1016/j.molcel.2009.06.023

Gevry N, Chan HM, Laflamme L, Livingston DM, Gaudreau L (2007) p21 transcription is regulated by differential localization of histone H2A.Z. Genes Dev 21:1869–1881. doi:10.1101/gad.1545707

Gingras A-C, Gstaiger M, Raught B, Aebersold R (2007) Analysis of protein complexes using mass spectrometry. Nat Rev Mol Cell Biol 8:645–654. doi:10.1038/nrm2208

Gromoller A, Lehming N (2000) Srb7p is a physical and physiological target of Tup1p. EMBO J 19:6845–6852. doi:10.1093/emboj/19.24.6845

Han SJ, Lee JS, Kang JS, Kim YJ (2001) Med9/Cse2 and Gal11 modules are required for transcriptional repression of distinct group of genes. J Biol Chem 276:37020–37026. doi:10.1074/jbc.M105596200

Hicks J, Lockington RA, Strauss J, Dieringer D, Kubicek CP, Kelly J, Keller N (2001) RcoA has pleiotropic effects on *Aspergillus nidulans* cellular development. Mol Microbiol 39:1482–1493. doi:10.1046/j.1365-2958.2001.02332.x

Huang DW, Sherman BT, Lempicki RA (2009) Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nat Protoc 4:44–57. doi:10.1038/nprot.2008.211

Hynes MJ, Kelly JM (1977) Pleiotropic mutants of *Aspergillus nidulans* altered in carbon metabolism. Mol Gen Genet 150:193–204. doi:10.1007/bf00695399

Jagtap P, Goslinga J, Kooren JA, McGowan T, Wroblewski MS, Seymour SL, Griffin TJ (2013) A two-step database search method improves sensitivity in peptide sequence matches for metaproteomics and proteogenomics studies. Proteomics 13:1352–1357. doi:10.1002/pmic.201200352

Jin LY, Pahuja KB, Wickliffe KE, Gorur A, Baumgartel C, Schekman R, Rape M (2012) Ubiquitin-dependent regulation of COPII coat size and function. Nature 482:495–500. doi:10.1038/nature10822

Kamlangdee N (2008) Indentifying target proteins of CreB deubiquitination enzyme in the fungus *Aspergillus nidulans*. *PhD thesis*, The University of Adelaide

Kanehisa M, Sato Y, Kawashima M, Furumichi M, Tanabe M (2016) KEGG as a reference resource for gene and protein annotation. Nucleic Acids Res 44(D1):D457–462. doi:10.1093/nar/gkv1070

Kelly JM (1980) Pleiotropic mutants of *Aspergillus nidulans* affected in carbon metabolism. *PhD Thesis*, La Trobe University

Kelly JM, Hynes MJ (1977) Increased and decreased sensitivity to carbon catabolite repression of enzymes of acetate metabolism in mutants of *Aspergillus nidulans*. Mol Gen Genet 156:87–92. doi:10.1007/bf00272256

Liu XW, Li B, Gorovsky MA (1996) Essential and nonessential histone H2A variants in *Tetrahymena thermophila*. Mol Cell Biol 16:4305–4311. doi:10.1128/MCB.16.8.4305

Lockington RA, Kelly JM (2001) Carbon catabolite repression in *Aspergillus nidulans* involves deubiquitination. Mol Microbiol 40:1311–1321. doi:10.1046/j.1365-2958.2001.02474.x

Lockington RA, Kelly JM (2002) The WD40-repeat protein CreC interacts with and stabilizes the deubiquitinating enzyme CreB in vivo in *Aspergillus nidulans*. Mol Microbiol 43:1173–1182. doi:10.1046/j.1365-2958.2002.02811.x

Lord C, Bhandari D, Menon S, Ghassemian M, Nycz D, Hay J, Ghosh P, Ferro-Novick S (2011) Sequential interactions with Sec23 control the direction of vesicle traffic. Nature 473:181–186. doi:10.1038/nature09969

Luhtala N, Odorizzi G (2004) Bro1 coordinates deubiquitination in the multivesicular body pathway by recruiting Doa4 to endosomes. J Cell Biol 166:717–729. doi:10.1083/jch.200403139

Mathieu M, Nikolaev I, Scazzocchio C, Felenbok B (2005) Patterns of nucleosomal organization in the *alc* regulon of *Aspergillus nidulans*: roles of the AlcR transcriptional activator and the CreA global repressor. Mol Microbiol 56:535–548. doi:10.1111/j.1365-2958.2005.04559.x

Meding S, Martin K, Gustafsson OJR, Eddes JS, Hack S, Oehler MK, Hoffmann P (2013) Tryptic peptide reference data sets for MALDI imaging mass spectrometry on formalin-fixed ovarian cancer tissues. J Proteome Res 12(308–315):12. doi:10.1021/pr300996x

Meneghini MD, Wu M, Madhani HD (2003) Conserved histone variant H2A.Z protects euchromatin from the ectopic spread of silent heterochromatin. Cell 112:725–736. doi:10.1016/s0092-8674(03)00123-5

Miller BL, Miller KY, Timberlake WE (1985) Direct and indirect gene replacements in *Aspergillus nidulans*. Mol Cell Biol 5:1714–1721. doi:10.1128/MCB.5.7.1714

Nayak T, Szewczyk E, Oakley CE, Osmani A, Ukil L, Murray SL, Hynes MJ, Osmani SA, Oakley BR (2006) A versatile and efficient gene-targeting system for *Aspergillus nidulans*. Genetics 172:1557–1566. doi:10.1534/genetics.105.052563

Nelson CJ, Santos-Rosa H, Kouzarides T (2006) Proline isomerization of histone H3 regulates lysine methylation and gene expression. Cell 126:905–916. doi:10.1016/j.cell.2006.07.026

Park SK, Xiao HJ, Lei M (2014) Nuclear FKBPs, Fpr3 and Fpr4 affect genome-wide genes transcription. Mol Genet Genom 289:125–136. doi:10.1007/s00438-013-0794-0

Pateman JA, Rever BM, Cove DJ (1967) Genetic and biochemical studies of nitrate reduction in *Aspergillus nidulans*. Biochem J 104:103–111. doi:10.1042/bj1040103

Ridgway P, Brown KD, Rangasamy D, Svensson U, Tremethick DJ (2004) Unique residues on the H2A.Z containing nucleosome surface are important for *Xenopus laevis* development. J Biol Chem 279:43815–43820. doi:10.1074/jbc.M408409200

Ries L, Belshaw NJ, Ilmen M, Penttila ME, Alapuranen M, Archer DB (2014) The role of CRE1 in nucleosome positioning within the *cbh1* promoter and coding regions of *Trichoderma reesei*. Appl Microbiol Biotechnol 98:749–762. doi:10.1007/s00253-013-5354-3

Ries LNA, Beattie SR, Espeso EA, Cramer RA, Goldman GH (2016) Diverse Regulation of the CreA Carbon Catabolite Repressor in *Aspergillus nidulans*. Genetics 203:335–352. doi:10.1534/genetics.116.187872

Roy P, Lockington RA, Kelly JM (2008) CreA-mediated repression in *Aspergillus nidulans* does not require transcriptional auto-regulation, regulated intracellular localisation or degradation of CreA. Fungal Genet Biol 45:657–670. doi:10.1016/j.fgb.2007.10.016

Sarcinella E, Zuzarte PC, Lau PNI, Draker R, Cheung P (2007) Monoubiquitylation of H2A.Z distinguishes its association with euchromatin or facultative heterochromatin. Mol Cell Biol 27:6457–6468. doi:10.1128/mcb.00241-07

Sevilla A, Binda O (2014) Post-translational modifications of the histone variant h2az. Stem Cell Res 12:289–295. doi:10.1016/j.scr.2013.11.004

Sprangers J, Rabouille C (2015) SEC16 in COPII coat dynamics at ER exit sites. Biochem Soc Trans 43:97–103. doi:10.1042/bst20140283

Springael JY, Nikko E, Andre B, Marini AM (2002) Yeast Npi3/Bro1 is involved in ubiquitin-dependent control of permease trafficking. FEBS Lett 517:103–109. doi:10.1016/s0014-5793(02)02586-3

Strauss J, Horvath HK, Abdallah BM, Kindermann J, Mach RL, Kubicek CP (1999) The function of CreA, the carbon catabolite repressor of *Aspergillus nidulans*, is regulated at the transcriptional and post-transcriptional level. Mol Microbiol 32:169–178. doi:10.1046/j.1365-2958.1999.01341.x

Szewczyk E, Nayak T, Oakley CE, Edgerton H, Xiong Y, Taheri-Talesh N, Osmani SA, Oakley BR (2006) Fusion PCR and gene targeting in *Aspergillus nidulans*. Nat Protoc 1:3111–3120. doi:10.1038/nprot.2006.405

Thatcher TH, Gorovsky MA (1994) Phylogenetic analysis of the core histones H2A, H2B, H3, and H4. Nucleic Acids Res 22:174–179. doi:10.1093/nar/22.2.174

Todd RB, Lockington RA, Kelly JM (2000) The *Aspergillus nidulans creC* gene involved in carbon catabolite repression encodes a WD40 repeat protein. Mol Gen Genet 263:561–570. doi:10.1007/s004380051202

van der Laan M, Chacinska A, Lind M, Perschil I, Sickmann A, Meyer HE, Guiard B, Meisinger C, Pfanner N, Rehling P (2005) Pam17 is required for architecture and translocation activity of the mitochondrial protein import motor. Mol Cell Biol 25:7449–7458. doi:10.1128/mcb.25.17.7449-7458.2005

Wang CW, Kim J, Huang WP, Abeliovich H, Stromhaug PE, Dunn WA Jr, Klionsky DJ (2001) Apg2 is a novel protein required for the cytoplasm to vacuole targeting, autophagy, and pexophagy pathways. J Biol Chem 276:30442–30451. doi:10.1074/jbc.M102342200

Warde-Farley D, Donaldson SL, Comes O, Zuberi K, Badrawi R, Chao P, Franz M, Grouios C, Kazi F, Lopes CT, Maitland A, Mostafavi S, Montojo J, Shao Q, Wright G, Bader GD, Morris Q (2010) The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. Nucleic Acids Res 38:W214–W220. doi:10.1093/nar/gkq537

Weber CM, Henikoff S (2014) Histone variants: dynamic punctuation in transcription. Genes Dev 28:672–682. doi:10.1101/gad.238873.114

Wu RS, Tsai S, Bonner WM (1982) Patterns of histone variant synthesis can distinguish G0 from G1 cells. Cell 31:367–374. doi:10.1016/0092-8674(82)90130-1

Wyrick JJ, Holstege FCP, Jennings EG, Causton HC, Shore D, Grunstein M, Lander ES, Young RA (1999) Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast. Nature 402:418–421. doi:10.1038/46567

Yeh YY, Wrasman K, Herman PK (2010) Autophosphorylation within the Atg1 activation loop is required for both kinase activity and the induction of autophagy in *Saccharomyces cerevisiae*. Genetics 185:871–882. doi:10.1534/genetics.110.116566

Yeh YY, Shah KH, Herman PK (2011) An Atg13 Protein-mediated Self-association of the Atg1 Protein Kinase Is Important for the Induction of Autophagy. J Biol Chem 286:28931–28939. doi:10.1074/jbc.M111.250324

Zhou M, Sandercock AM, Fraser CS, Ridlova G, Stephens E, Schenauer MR, Yokoi-Fong T, Barsky D, Leary JA, Hershey JW, Doudna JA, Robinson CV (2008) Mass spectrometry reveals modularity and a complete subunit interaction map of the eukaryotic translation factor eIF3. Proc Natl Acad Sci USA 105:18139–18144. doi:10.1073/pnas.0801313105

Zhu XF, Zhang YQ, Bjornsdottir G, Liu ZL, Quan A, Costanzo M, Lopez MD, Westholm JO, Ronne H, Boone C, Gustafsson CM, Myers LC (2011) Histone modifications influence mediator interactions with chromatin. Nucleic Acids Res 39:8342–8354. doi:10.1093/nar/gkr551

Chapter 3
Supplementary

Supplementary Table 1: Human orthologues of CreA co-purified proteins

	Protein Accession	Protein Description	Gene	NCBI ID	Identities/ Positives (%)	Fungal Proteins
Repressed						APSB_EMENI
						BGLJ_EMENI
	FKBP2_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP2 (PPIase FKBP2)	*FKBP2 FKBP13*	2286	50/71	FKBP4_EMENI
	GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2	*GNAI2 GNAI2B*	2771	53/68	GPA1_EMENI
	H2AZ_HUMAN	Histone H2A.Z (H2A/z)	*H2AFZ H2AZ*	3015	71/84	H2AZ_EMENI
	H33_HUMAN	Histone H3.3	*H3F3A H3.3A*	3021	91/97	H3_EMENI
	H4_HUMAN	Histone H4	*HIST1H4A H4/A H4FA*	121504	91/97	H42_EMENI
	DDX18_HUMAN	ATP-dependent RNA helicase DDX18	*DDX18*	8886	61/79	HAS1_EMENI
	CABIN_HUMAN	Calcineurin-binding protein cabin-1 (Calcineurin inhibitor) (CAIN)	*CABIN1 KIAA0330*	23523	24/35	HIR3_EMENI
	MED8_HUMAN	Mediator of RNA polymerase II transcription subunit 8	*MED8*	112950	27/43	MED8_EMENI
						MIRC_EMENI
						PANB_EMENI
	RS19_HUMAN	40S ribosomal protein S19	*RPS19*	6223	52/72	RS19_EMENI
	SF3B3_HUMAN	Splicing factor 3B subunit 3	*SF3B3*	23450	50/67	RSE1_EMENI
						STCK_EMENI
	SMC3_HUMAN	Structural maintenance of chromosomes protein 3	*SMC3*	9126	40/61	SUDA_EMENI
Derepressed	ACSA_HUMAN	Acetyl-coenzyme A synthetase, cytoplasmic (EC 6.2.1.1)	*ACSS2 ACAS2*	55902	45/64	ACSA_EMENI
	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin)	*ACTG1 ACTG*	71	90/96	ACTG_EMENI
	ULK3_HUMAN	Serine/threonine-protein kinase ULK3 (EC 2.7.11.1)	*ULK3*	25989	39/55	ATG1_EMENI
	CLU_HUMAN	Clustered mitochondria protein homolog	*CLUH KIAA0664*	23277	32/51	CLU_EMENI
	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	*DYNC1H1*	1778	50/68	DYHC_EMENI
	GATB_HUMAN	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	*GATB*	5188	35/52	GATB_EMENI
	HSP7C_HUMAN	Heat shock cognate 71 kDa protein	*HSPA8 HSC70*	3312	71/82	HSP70_EMENI
						LOC1_EMENI
	LONP2_HUMAN	Lon protease homolog 2, peroxisomal (EC 3.4.21.-)	*LONP2 LONP*	83752	35/53	LONP2_EMENI
						MASY_EMENI
	MUS81_HUMAN	Crossover junction endonuclease MUS81 (EC 3.1.22.-)	*MUS81*	80198	28/45	MUS81_EMENI
	MYO1F_HUMAN	Unconventional myosin-If (Myosin-Ie)	*MYO1F*	4542	43/61	MYO1_EMENI
	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	*PPP3CA*	5530	62/76	PP2B_EMENI
	DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46	*DDX46 KIAA0801*	9879	55/67	PRP5_EMENI
	RL37_HUMAN	60S ribosomal protein L37 (G1.16)	*RPL37*	6167	71/82	RL37_EMENI
	DIAP2_HUMAN	Protein diaphanous homolog 2 (Diaphanous-related formin-2) (DRF2)	*DIAPH2 DIA*	1730	26/44	SEPA_EMENI
	TBB4B_HUMAN	Tubulin beta-4B chain (Tubulin beta-2 chain) (Tubulin beta-2C chain)	*TUBB4B TUBB2C*	10383	81/91	TBB1_EMENI
Repressed and Derepressed	EGR3_HUMAN	Early growth response protein 3 (EGR-3) (Zinc finger protein pilot)	*EGR3 PILOT*	1960	48/69	CREA_EMENI
						CUTI2_EMENI
	CWC27_HUMAN	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	*CWC27*	10283	39/50	CWC27_EMENI
	DPOE1_HUMAN	DNA polymerase epsilon catalytic subunit A (EC 2.7.7.7)	*POLE POLE1*	5426	42/59	DPOE_EMENI
	EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A (eIF3a)	*EIF3A*	8661	35/54	EIF3A_EMENI
	EIF3H_HUMAN	Eukaryotic translation initiation factor 3 subunit H (eIF3h)	*EIF3H EIF3S3*	8667	33/54	EIF3H_EMENI
	H2AX_HUMAN	Histone H2AX (H2a/x) (Histone H2A.X)	*H2AFX H2AX*	3014	75/78	H2A_EMENI
	H2B1L_HUMAN	Histone H2B type 1-L (Histone H2B.c) (H2B/c)	*HIST1H2BL H2BFC*	8340	82/96	H2B_EMENI
	H4_HUMAN	Histone H4	*HIST1H4A H4/A H4FA*	121504	91/96	H41_EMENI
	GRP75_HUMAN	Stress-70 protein, mitochondrial (PBP74)	*HSPA9*	3313	64/79	HSP7M_EMENI
						IRS4_EMENI
	MED17_HUMAN	Mediator of RNA polymerase II transcription subunit 17	*MED17*	9440		MED17_EMENI
	RS3A_HUMAN	40S ribosomal protein S3a (v-fos transformation effector protein)	*RPS3A FTE1 MFTL*	6189	60/75	RS3A_EMENI
	TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10	*TMED10 TMP21*	10972	36/58	TMEDA_EMENI

MED17_HUMAN was not identified as orthologue of MED17_EMENI in both KEGG and HPRD databases.

Shaded - no clear orthologue

Supplementary Table 2: *S. cerevisiae* orthologues of CreA co-purified proteins

	Protein Accession	**Protein Description**	**Gene**	**NCBI Gene ID**	**Identities/ Positives (%)**	**Fungal Proteins**
Repressed	USO1_YEAST	Intracellular protein transport protein USO1 (Int-1)	*USO1*	851501	20/44	APSB_EMENI
	RT23_YEAST	37S ribosomal protein S23, mitochondrial (DAP-3)	*RSM23*	852748	24/47	BGLJ_EMENI
	FKBP4_YEAST	FK506-binding protein 4 (EC 5.2.1.8)	*FPR4*	851170	53/73	FKBP4_EMENI
	GPA2_YEAST	Guanine nucleotide-binding protein alpha-2 subunit (GP2-alpha)	*GPA2*	856741	44/62	GPA1_EMENI
	H2AZ_YEAST	Histone H2A.Z	*HTZ1*	854150	79/90	H2AZ_EMENI
	H3_YEAST	Histone H3	*HHT1*	852295	95/98	H3_EMENI
	H4_YEAST	Histone H4	*HHF1*	852294	93/96	H42_EMENI
	HAS1_YEAST	ATP-dependent RNA helicase HAS1 (EC 3.6.4.13)	*HAS1*	855335	73/85	HAS1_EMENI
	HIR3_YEAST	Histone transcription regulator 3	*HIR3*	853605	22/40	HIR3_EMENI
	MED8_YEAST	Mediator of RNA polymerase II transcription subunit 8	*MED8*	852492	35/58	MED8_EMENI
	ARN1_YEAST	Siderophore iron transporter ARN1 (Ferrichrome permease)	*ARN1*	856345	24/45	MIRC_EMENI
	PANB_YEAST	3-methyl-2-oxobutanoate hydroxymethyltransferase	*ECM31*	852474	42/61	PANB_EMENI
	RS19B_YEAST	40S ribosomal protein S19-B (RP55B) (S16a) (YS16B)	*RPS19B*	855414	65/84	RS19_EMENI
	RSE1_YEAST	Pre-mRNA-splicing factor RSE1	*RSE1*	854956	27/50	RSE1_EMENI
	FAS1_YEAST	Fatty acid synthase subunit beta (EC 2.3.1.86)	*FAS1*	853653	34/52	STCK_EMENI
	SMC3_YEAST	Structural maintenance of chromosomes protein 3	*SMC3*	853371	35/56	SUDA_EMENI
Derepressed	ACS2_YEAST	Acetyl-coenzyme A synthetase 2 (EC 6.2.1.1)	*ACS2*	850846	62/77	ACSA_EMENI
	ACT_YEAST	Actin	*ACT1*	850504	92/97	ACTG_EMENI
	ATG1_YEAST	Serine/threonine-protein kinase ATG1	*ATG1*	852695	52/65	ATG1_EMENI
	CLU_YEAST	Clustered mitochondria protein 1	*CLU1*	855025	30/48	CLU_EMENI
	DYHC_YEAST	Dynein heavy chain, cytoplasmic	*DYN1*	853928	37/59	DYHC_EMENI
	GATB_YEAST	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	*PET112*	852198	31/54	GATB_EMENI
	HSP71_YEAST	Heat shock protein SSA1 (Heat shock protein YG100)	*SSA1*	851259	72/82	HSP70_EMENI
	LOC1_YEAST	60S ribosomal subunit assembly/export protein LOC1	*LOC1*	850551	26/43	LOC1_EMENI
	LONM_YEAST	Lon protease homolog, mitochondrial (EC 3.4.21.-)	*PIM1*	852259	41/59	LONP2_EMENI
	MASZ_YEAST	Malate synthase 2, glyoxysomal (EC 2.3.3.9)	*DAL7*	854849	64/78	MASY_EMENI
	MUS81_YEAST	Crossover junction endonuclease MUS81 (EC 3.1.22.-)	*MUS81*	851994	36/55	MUS81_EMENI
	MYO5_YEAST	Myosin-5 (Actin-dependent myosin-I MYO5)	*MYO5*	855136	61/74	MYO1_EMENI
	PP2B2_YEAST	Serine/threonine-protein phosphatase 2B catalytic subunit A2	*CMP2*	854946	56/76	PP2B_EMENI
	PRP5_YEAST	Pre-mRNA-processing ATP-dependent RNA helicase PRP5	*PRP5*	852539	38/58	PRP5_EMENI
	RL37A_YEAST	60S ribosomal protein L37-A (L43) (YL35) (YP55)	*RPL37A*	850882	70/81	RL37_EMENI
	BNI1_YEAST	Protein BNI1 (Pointed projection formation protein 3)	*BNI1*	855450	39/62	SEPA_EMENI
	TBB_YEAST	Tubulin beta chain (Beta-tubulin)	*TUB2*	850506	78/88	TBB1_EMENI
Repressed and Derepressed	MIG1_YEAST	Regulatory protein MIG1	*MIG1*	852848	50/62	CREA_EMENI
						CUTI2_EMENI
	CWC27_YEAST	Peptidyl-prolyl isomerase CWC27 (PPIase CWC27)	*CWC27*	856041	29/48	CWC27_EMENI
	DPOE_YEAST	DNA polymerase epsilon catalytic subunit A (EC 2.7.7.7)	*POL2*	855459	50/66	DPOE_EMENI
	EIF3A_YEAST	Eukaryotic translation initiation factor 3 subunit A (eIF3a)	*RPG1*	852371	43/62	EIF3A_EMENI
	RPN11_YEAST	Ubiquitin carboxyl-terminal hydrolase RPN11 (EC 3.4.19.12)	*RPN11*	850554	36/60	EIF3H_EMENI
	H2A1_YEAST	Histone H2A.1	*HTA1*	851811	74/81	H2A_EMENI
	H2B2_YEAST	Histone H2B.2	*HTB2*	852284	88/96	H2B_EMENI
	H4_YEAST	Histone H4	*HHF1*	852294	91/95	H41_EMENI
	HSP77_YEAST	Heat shock protein SSC1, mitochondrial	*SSC1*	853503	73/84	HSP7M_EMENI
	TAX4_YEAST	Protein TAX4	*TAX4*	853362	40/57	IRS4_EMENI
	MED17_YEAST	Mediator of RNA polymerase II transcription subunit 17	*MED17*	856743	32/56	MED17_EMENI
	RS3A2_YEAST	40S ribosomal protein S1-B (RP10B)	*RPS1B*	854939	69/89	RS3A_EMENI
	TMEDA_YEAST	Endoplasmic reticulum vesicle protein 25	*ERV25*	854997	50/68	TMEDA_EMENI

Shaded - no clear orthologue

Supplementary Table 3: Human orthologues of CreB co-purified proteins

	Protein Accession	**Protein Description**	**Gene**	**NCBI ID**	**Identities/ Positives (%)**	**Fungal Protein**
Repressed	ACSF4_HUMAN	Acyl-CoA synthetase family member 4	*ACSF4*	132949	24/40	ACVS_EMENI
	ATG13_HUMAN	Autophagy-related protein 13	*ATG13*	9776		ATG13_EMENI
						CCPR2_EMENI
	NGLY1_HUMAN	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	*NGLY1 PNG1*	55768	44/60	PNG1_EMENI
	SF3B3_HUMAN	Splicing factor 3B subunit 3 (SF3b130)	*SF3B3*	23450	50/67	RSE1_EMENI
	RRP36_HUMAN	Ribosomal RNA processing protein 36 homolog	*RRP36*	88745	30/49	RRP36_EMENI
	TBP_HUMAN	TATA-box-binding protein (TATA sequence-binding protein)	*TBP*	6908	81/90	TBP_EMENI
Derepressed	ULK3_HUMAN	Serine/threonine-protein kinase ULK3	*ULK3*	25989	39/55	ATG1_EMENI
	PDC6I_HUMAN	Programmed cell death 6-interacting protein (PDCD6-interacting protein)	*PDCD6IP*	10015	27/43	BRO1_EMENI
	CISY_HUMAN	Citrate synthase, mitochondrial (EC 2.3.3.1)	*CS*	1431	60/75	CISY_EMENI
	DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3)	*GLUD1*	2746	25/42	DHE4_EMENI
	G3PT_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific (EC 1.2.1.12)	*GAPDHS*	26330	63/76	G3P_EMENI
	IF4A2_HUMAN	Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) (EC 3.6.4.13))	*EIF4A2*	1974	73/84	IF4A_EMENI
	KCC1D_HUMAN	Calcium/calmodulin-dependent protein kinase type 1D (EC 2.7.11.17)	*CAMK1D*	57118	43/65	KCC1_EMENI
	MANBA_HUMAN	Beta-mannosidase (EC 3.2.1.25)	*MANBA*	4126	27/47	MANBA_EMENI
	NB5R1_HUMAN	NADH-cytochrome b5 reductase 1 (b5R.1) (EC 1.6.2.2)	*CYB5R1*	51706	36/54	MCR1_EMENI
	DNJA3_HUMAN	DnaJ homolog subfamily A member 3, mitochondrial	*DNAJA3*	9093	31/46	MDJ1_EMENI
	NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha (NAC-alpha)	*NACA*	4666	70/90	NACA_EMENI
	NCPR_HUMAN	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	*POR CYPOR*	5447	38/56	NCPR_EMENI
						NIRA_EMENI
	NMT2_HUMAN	Glycylpeptide N-tetradecanoyltransferase 2 (EC 2.3.1.97)	*NMT2*	9397	48/62	NMT_EMENI
	NSA2_HUMAN	Ribosome biogenesis protein NSA2 homolog	*NSA2*	10412	63/78	NSA2_EMENI
						NST1_EMENI
						PAM17_EMENI
						PDX1_EMENI
	RS3A_HUMAN	40S ribosomal protein S3a	*RPS3A*	6189	60/75	RS3A_EMENI
	RSSA_HUMAN	40S ribosomal protein SA (37 kDa laminin receptor precursor) (NEM/1CHD4)	*RPSA*	3921	58/73	RSSA_EMENI
	SC16A_HUMAN	Protein transport protein Sec16A (SEC16 homolog A)	*SEC16A*	9919	24/39	SEC16_EMENI
	TBA1B_HUMAN	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous)	*TUBA1B*	10376	67/81	TBA2_EMENI
	TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10	*TMED10*	10972	36/58	TMEDA_EMENI
						TPS1_EMENI
	DHSO_HUMAN	Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase)	*SORD*	6652	42/61	XYL2_EMENI
Repressed and Derepressed	ACTG_HUMAN	Actin, cytoplasmic 2 (Gamma-actin)	*ACTG1*	71	90/96	ACTG_EMENI
	RT24_HUMAN	28S ribosomal protein S24, mitochondrial (MRP-S24)	*MRPS24*	64951	32/53	AIM24_EMENI
	ATG2B_HUMAN	Autophagy-related protein 2 homolog B	*ATG2B*	55102	29/47	ATG2_EMENI
						APSA_EMENI
	GLBL3_HUMAN	Beta-galactosidase-1-like protein 3 (EC 3.2.1.-)	*GLB1L3*	112937	31/47	BGALA_EMENI
	UBP12_HUMAN	Ubiquitin carboxyl-terminal hydrolase 12 (EC 3.4.19.12)	*USP12 UBH1*	219333	46/61	CREB_EMENI
						CREC_EMENI
	CABIN_HUMAN	Calcineurin-binding protein cabin-1 (Calcineurin inhibitor) (CAIN)	*CABIN1*	23523	24/35	HIR3_EMENI
	HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	*HSPA8*	3312	71/82	HSP70_EMENI
	GRP75_HUMAN	Stress-70 protein, mitochondrial	*HSPA9*	3313	64/79	HSP7M_EMENI
						P2OX_EMENI
	CP3A7_HUMAN	Cytochrome P450 3A7 (EC 1.14.14.1) (CYPIIIA7)	*CYP3A7*	1551	28/46	STCL_EMENI
	TBA1A_HUMAN	Tubulin alpha-1A chain (Alpha-tubulin 3) (Tubulin B-alpha-1)	*TUBA1A*	7846	77/87	TBA1_EMENI
	TBB4A_HUMAN	Tubulin beta-4A chain	*TUBB4A*	10382	81/91	TBB1_EMENI
	TBB2B_HUMAN	Tubulin beta-2B chain	*TUBB2B*	347733	73/86	TBB2_EMENI

Shaded - no clear orthologue

Supplementary Table 4: *S. cerevisiae* orthologues of CreB co-purified proteins

	Protein Accession	**Protein Description**	**Gene**	**NCBI ID**	**Identities/ Positives (%)**	**Fungal Protein**
Repressed	LYS2_YEAST	L-2-aminoadipate reductase (EC 1.2.1.31) (EC 1.2.1.95)	*LYS2*	852412	37/56	ACVS_EMENI
	ATG13_YEAST	Autophagy-related protein 13	*ATG13*	856315	27/44	ATG13_EMENI
	CCPR_YEAST	Cytochrome c peroxidase, mitochondrial (CCP) (EC 1.11.1.5)	*CCP1*	853940	46/63	CCPR2_EMENI
	PNG1_YEAST	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	*PNG1*	856009	39/57	PNG1_EMENI
	RSE1_YEAST	Pre-mRNA-splicing factor RSE1	*RSE1*	854956	27/50	RSE1_EMENI
	RRP36_YEAST	rRNA biogenesis protein RRP36	*RRP36*	854461	29/45	RRP36_EMENI
	TBP_YEAST	TATA-box-binding protein	*SPT15*	856891	91/94	TBP_EMENI
Derepressed	ATG1_YEAST	Serine/threonine-protein kinase ATG1 (EC 2.7.11.1)	*ATG1*	852695	52/65	ATG1_EMENI
	BRO1_YEAST	Vacuolar-sorting protein BRO1	*BRO1*	856021	28/48	BRO1_EMENI
	CISY1_YEAST	Citrate synthase, mitochondrial (EC 2.3.3.1)	*CIT1*	855732	66/79	CISY_EMENI
	DHE4_YEAST	NADP-specific glutamate dehydrogenase 1 (NADP-GDH 1)	*GDH1*	854557	65/77	DHE4_EMENI
	G3P1_YEAST	Glyceraldehyde-3-phosphate dehydrogenase 1 (GAPDH 1)	*TDH1*	853395	66/80	G3P_EMENI
	IF4A_YEAST	ATP-dependent RNA helicase eIF4A (EC 3.6.4.13)1/2) (p37)	*TIF1*	853303	68/82	IF4A_EMENI
	KCC2_YEAST	Calcium/calmodulin-dependent protein kinase II (EC 2.7.11.17)	*CMK2*	854144	55/73	KCC1_EMENI
						MANBA_EMENI
	MCR1_YEAST	NADH-cytochrome b5 reductase 2 (EC 1.6.2.2)	*MCR1*	853707	47/65	MCR1_EMENI
	MDJ1_YEAST	DnaJ homolog 1, mitochondrial	*MDJ1*	850530	35/50	MDJ1_EMENI
	NACA_YEAST	Nascent polypeptide-associated complex subunit alpha (NAC-alpha)	*EGD2*	856600	52/76	NACA_EMENI
	NCPR_YEAST	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	*NCP1*	856438	42/63	NCPR_EMENI
	CHA4_YEAST	Activatory protein CHA4	*CHA4*	850787	22/41	NIRA_EMENI
	NMT_YEAST	Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97)	*NMT1*	850892	50/65	NMT_EMENI
	NSA2_YEAST	Ribosome biogenesis protein NSA2 (NOP7-associated protein 2)	*NSA2*	856863	70/81	NSA2_EMENI
	NST1_YEAST	Stress response protein NST1	*NST1*	855633	36/67	NST1_EMENI
	PAM17_YEAST	Presequence translocated-associated motor subunit PAM17, mitochondrial	*PAM17*	853939	33/51	PAM17_EMENI
	SNZ3_YEAST	Probable pyridoxal 5'-phosphate synthase subunit SNZ3	*SNZ3*	850485	56/68	PDX1_EMENI
	RS3A2_YEAST	40S ribosomal protein S1-B (RP10B)	*RPS1B*	854939	69/89	RS3A_EMENI
	RSSA1_YEAST	40S ribosomal protein S0-A (Nucleic acid-binding protein NAB1A)	*RPS0A*	853128	69/82	RSSA_EMENI
	SEC16_YEAST	COPII coat assembly protein SEC16 (Protein transport protein SEC16)	*SEC16*	856020	27/49	SEC16_EMENI
	TBA1_YEAST	Tubulin alpha-1 chain	*TUB1*	854889	65/78	TBA2_EMENI
	TMEDA_YEAST	Endoplasmic reticulum vesicle protein 25	*ERV25*	854997	50/68	TMEDA_EMENI
	TPS1_YEAST	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit	*TPS1*	852423	63/79	TPS1_EMENI
	DHSO1_YEAST	Sorbitol dehydrogenase 1 (EC 1.1.1.14) (L-iditol 2-dehydrogenase 1)	*SOR1*	853624	49/62	XYL2_EMENI
Repressed and Derepressed	ACT_YEAST	Actin	*ACT1*	850504	92/97	ACTG_EMENI
	AIM24_YEAST	Altered inheritance of mitochondria protein 24, mitochondrial	*AIM24*	853543	21/44	AIM24_EMENI
	ATG2_YEAST	Autophagy-related protein 2 (Sporulation-specific protein 72)	*ATG2*	855479	40/58	ATG2_EMENI
	NUM1_YEAST	Nuclear Migration Protein	*NUM1*	851727	41/56	APSA_EMENI
						BGALA_EMENI
	UBP9_YEAST	Ubiquitin carboxyl-terminal hydrolase 9 (EC 3.4.19.12)	*UBP9*	856835	36/55	CREB_EMENI
	TUP1_YEAST	General transcriptional corepressor TUP1	*TUP1*	850445	35/56	CREC_EMENI
	HIR3_YEAST	Histone transcription regulator 3	*HIR3*	853605	22/40	HIR3_EMENI
	HSP71_YEAST	Heat shock protein SSA1 (Heat shock protein YG100)	*SSA1*	851259	72/82	HSP70_EMENI
	HSP77_YEAST	Heat shock protein SSC1, mitochondrial	*SSC1*	853503	73/84	HSP7M_EMENI
						P2OX_EMENI
	CP56_YEAST	Cytochrome P450-DIT2 (EC 1.14.14.-)	*DIT2*	852011	23/42	STCL_EMENI
	TBA1_YEAST	Tubulin alpha-1 chain	*TUB1*	854889	73/84	TBA1_EMENI
	TBB_YEAST	Tubulin beta chain (Beta-tubulin)	*TUB2*	850506	78/88	TBB1_EMENI
	TBB_YEAST	Tubulin beta chain (Beta-tubulin)	*TUB2*	850506	78/88	TBB2_EMENI

Shaded - no clear orthologue

Chapter 4

4.1 Introduction

Filamentous fungi can utilize a wide variety of carbon sources and survive in a changing nutritional environmental. In *A. nidulans*, carbon metabolism is controlled by the carbon catabolite repression (CCR) regulatory network, which allows preferred carbon sources to be used while simultaneously repressing genes that are required to metabolize less favoured carbon sources. This CCR regulatory network is mediated by the Cys$_2$-His$_2$ type DNA-binding transcription factor CreA, encoded by the *creA* gene (Dowzer and Kelly 1989, Dowzer and Kelly 1991). CreA has been shown to bind the consensus motif 5'-SYGGRG-3', usually present in pairs, of promoter regions of target genes, though promoters not regulated by CreA also exist with this core consensus sequence (Cubero, et al. 2000, Kulmburg, et al. 1993, Panozzo, et al. 1998), suggesting that the specific position of promoters and/or residues other than the consensus sequence are important (Garcia, et al. 2008, Panozzo, et al. 1998). Similar core binding sites for CreA homologues in other filamentous fungi, such as *A. oryzae* (Kato, et al. 1996) and *T. reesei* (Takashima, et al. 1998), have also been identified. Mutational analyses have revealed a number of targets of CreA, which are normally repressed in the presence of repressing carbon sources (Arst and Cove 1973, Arst, et al. 1981, Shroff, et al. 1996, Shroff, et al. 1997). Mutations in genes encoding the deubiquitinating enzyme CreB and the arrestin motif protein CreD, interacting with ubiquitin ligase HulA, gave rise to speculation that ubiquitination and deubiquitination might be involved in mechanisms for repression and derepression in the CCR network of *A. nidulans* (Boase and Kelly 2004, Hynes and Kelly 1977, Kelly 2004, Lockington and Kelly 2001). However, the precise molecular mechanism/s of CreA mediated repression, including whether there is binding to the consensus sequence in derepressing conditions, are still unknown.

The global transcriptional effect of CreA has been analysed using a genome-wide microarray, where WT and *creA* null mutant strains grown in either repressing or derepressing conditions were compared (Mogensen, et al. 2006). Microarray analysis identified 200 genes that showed significant transcript level differences, and cluster analysis based on the expression profiles revealed genes that were either regulated or partially regulated by CreA and genes that were not affected (Mogensen, et al. 2006). In *T. reesei,* genome-wide microarray revealed that 47.3% of genes showed higher transcript levels in a *CRE1* mutant strain, and 29.0% showed lower transcript levels in a *CRE1* mutant strain (Portnoy, et al. 2011), possibly indicating repression and induction respectively. However, microarray analysis indicates transcript levels, and cannot show whether the genes are direct or indirect targets of the global repressor protein.

Chromatin immunoprecipitation (ChIP) assays combined with DNA-sequencing (ChIP-seq) is a widely used approach to identify DNA binding sites for transcription factors such as CreA on a genome-wide scale. This approach provides high-resolution and accurate mapping of the protein-DNA binding loci (Ma and Wong 2011). ChIP-seq has been used in a number of filamentous fungi including White Collar Complex (WCC) in *Neurospora crassa* (Smith, et al. 2010), Tri6 in *Fusarium graminearum* (Nasmith, et al. 2011), SrbA in *Aspergillus fumigatus* (Chung, et al. 2014), LAE1 in *T. reesei* (Seiboth, et al. 2012), and MAT1-1-1 and PcVelA in *Penicillium chrysogenum* (Becker, et al. 2015, Becker, et al. 2016), to identify genome-wide direct targets and binding motifs of TFs. In *S. cerevisiae*, silenced chromatin structure was investigated by analysing ChIP-seq data of Sir proteins, histones and histone modification, H4K16-acetyl (Thurtle and Rine 2014). This chapter presents ChIP-seq experiments using the global repressor protein CreA, using strains containing tagged versions of CreA, and strains containing either a deletion of *creA* or a non-tagged version of CreA as controls, with strains grown in both repressing and derepressing conditions. Sequencing data were analysed to identify the direct targets and binding pattern of CreA in both repressing and derepressing conditions.

4.2 Materials and Methods

Strains and media *A. nidulans* strains used and their genotypes are shown in Table 1. *Aspergillus* media are based on those described by Cove (1966). Carbon and nitrogen sources were added aseptically to the media to reach the final concentrations as shown.

Table 1: List of strains

Strains	Genotype	Reference
WT	*biA1; niiA4*	(Pateman, et al. 1967)
CreAΔ99	*yA1 pabaA1; creAΔ99*	(Shroff, et al. 1997)
T7	*yA1 pabaA1; riboB2::[pPL3]pGPDCreA*^{HAGFP}	(Kamlangdee 2008)
S4	*yA1 pabaA1; riboB2::CreA*^{HAGFP}	(Lockington, Unpublished)

Chromatin immunoprecipitation and library preparation Strains were incubated in 1% glucose (repressing) or 1% arabinose (derepressing) medium for 20-24 hrs at 37°C with shaking. 0.1% fructose was added to all media to prevent starvation of strains. Mycelia were treated and the lysate prepared as described in Suzuki, et al. (2012). The supernatant containing chromatin fragments with an average size of ~ 200-500 bp was recovered and chromatin immuno-precipitation was performed, as described in Fan, et al. (2008), using 100 µl of the respective chromatin supernatant, 2 µg of anti-GFP (Abcam) and 10 µl bead volume of Protein A Sepharose (GE Healthcare). ChIP-seq library preparation was performed as described in Wong, et al. (2013).

Sequencing Sequencing was performed using the Illumina Hiseq2500 platform. The read length was 100 bp, and the reads were paired end.

Data analysis Reads were mapped to the *A. nidulans FGSC A4* genome (http://www.aspergillusgenome.org/) using Bowtie2 (Langmead, et al. 2009). Reads that aligned concordantly as pair ends were retained and used for peak calling. The resulting Binary Alignment/Map (BAM) files were used as input for peak calling and for plotting. Peaks were called using Model-based Analysis for ChIP-Sequencing (MACS) (Zhang, et al. 2008) with default settings except for 'mfold' set as 3,500 due to high signal to noise ratio. Both WT and CreAΔ99 were used as negative controls. The MACS identified peaks were ranked by p-values and the top 70% peaks [the p-value at the 70% cut-off value was 6.95429×10^{-18} (T7, repressing), 8.97429×10^{-18} (T7, derepressing), 7.58578×10^{-15} (S4, repressing), and 1.07895×10^{-15} (S4, derepressing)], which were determined manually on Genome-browser to include the majority of confident peaks, were selected for downstream analysis. The peaks gained from MACS were ranked and the top 70% peaks were used. Peaks were visually inspected on genome-browser above and below 70% cut-off and found that 70% removes most false negative peaks. All the peaks were mapped to genome features without cut-off and thresholds, just according to the peaks positions. The differences between peak numbers and target gene number are due to the genes with multiple peaks. HOMER (Hypergeometric Optimization of Motif EnRichment; http://homer.salk.edu/homer/) was used to identify genes whose ATG is within 1000 bp of peaks summit and the closest gene of each peak is referred to as a CreA target. Heatmap plots were generated by R scripts, alignment genome reads were mapped to the genome region tiles (with 50bp bin size for each tile) and then each tile was normalized to total read numbers, and then the matrix for corresponding binding signals was generated and displayed by heatmap.2 for the graph. Venn diagrams were generated with the R package 'vennerable' [R Core Team (2016)].

4.3 Results

4.3.1 ChIP-seq assay of CreA

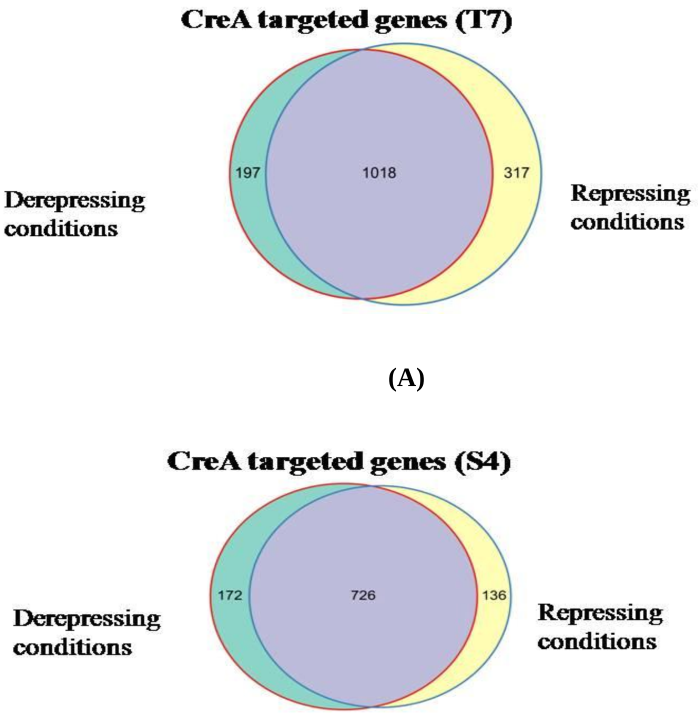
To identify the direct targets as well as binding patterns of CreA in repressing and derepressing conditions, ChIP-seq experiments were performed with strains that express epitope-tagged CreA from its native promoter (S4, CreAHAGFP) and from the constitutive *gpdA* promoter (T7, CreAHAGFP) in both repressing (1% glucose) and derepressing (1% arabinose) conditions (M&M). For the negative control, WT that expresses CreA without any epitope tag and CreAΔ99 that lacks any functional CreA were included. In ChIP-seq assays, the use of negative controls can significantly increase the sensitivity and specificity of the peak detection. The ChIP-seq experimental design and results for the T7 and S4 strains in repressing (1% glucose) and derepressing (1% arabinose) conditions are shown in Table 2. Although, both CreAΔ99 and WT generated a very large number of reads, most of the reads are for non-specific regions instead of peak regions.

Table 2: ChIP-seq for CreA in repressing and derepressing conditions.

Sample	No of raw reads	No of mapped reads	% mapped	No of MACS peaks	No of target genes
S4 (repressing)	7,644,471	7,225,266	94.52	1,405	862
S4 (derepressing)	11,171,241	9,780,903	87.55	1,453	1,034
T7 (repressing)	18,953,038	18,029,856	95.13	1,879	1,335
T7 (derepressing)	4,539,040	4,006,280	88.26	1,997	1,215
WT (repressing)	1,799,711	1,561,319	86.75	18	
WT (derepressing)	4,394,046	3,987,285	90.74	32	
CreΔ99 (repressing)	2,858,575	2,576,355	90.13	54	
CreΔ99 (derepressing)	3,821,522	3,609,915	94.46	21	

4.3.2 Genome-wide CreA binding patterns in repressing and derepressing conditions

Peaks called using the MACS program (see M&M) identified a total of 1532 unique targets in T7 and 1034 unique targets in S4 (see M&M). Venn diagram plots show that around 67% (T7) and 70% (S4) of the targets were detected in both conditions (Figure 1A & 1B), suggesting that CreA binds most of the promoters irrespective of growth conditions.

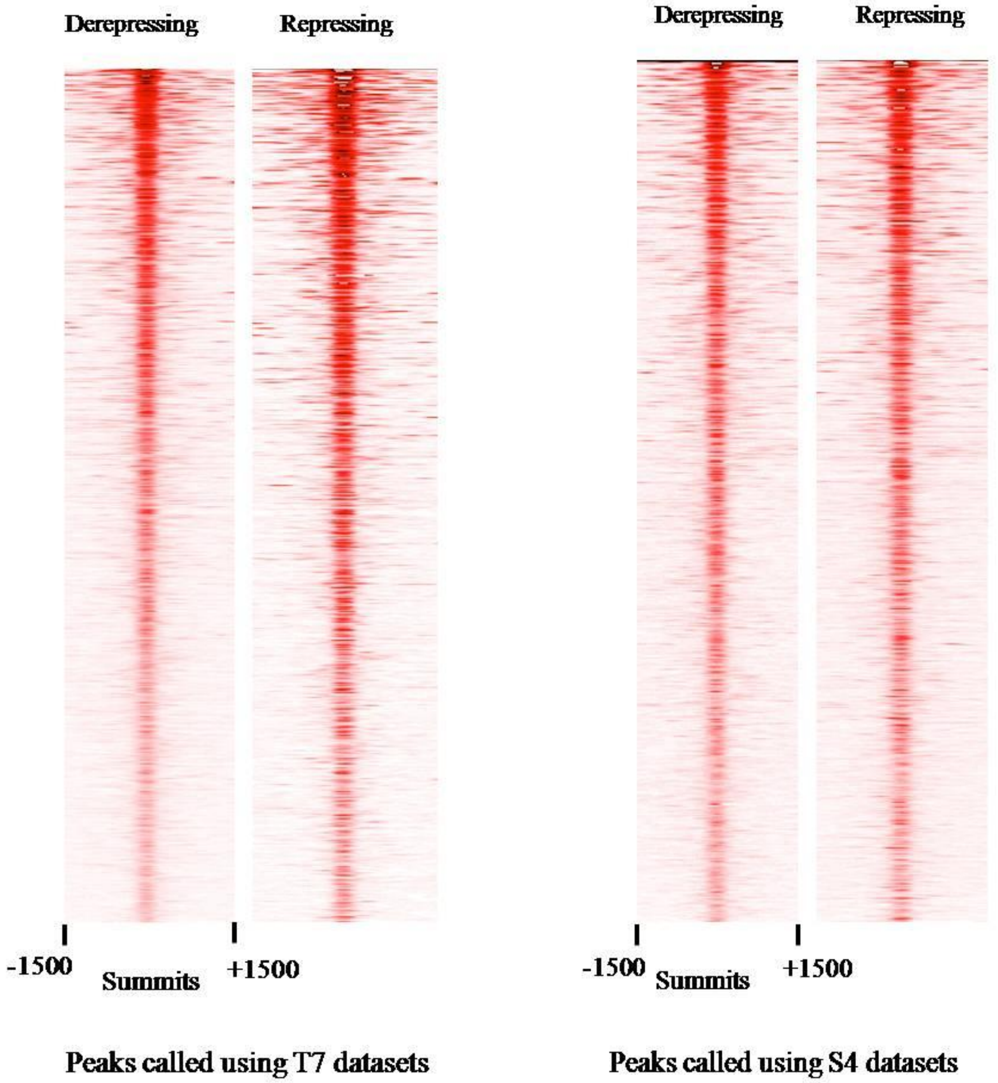


(A)

(B)

Figure 1: Venn diagram of CreA targeted genes for T7 (A) and S4 (B) in repressing and derepressing conditions.

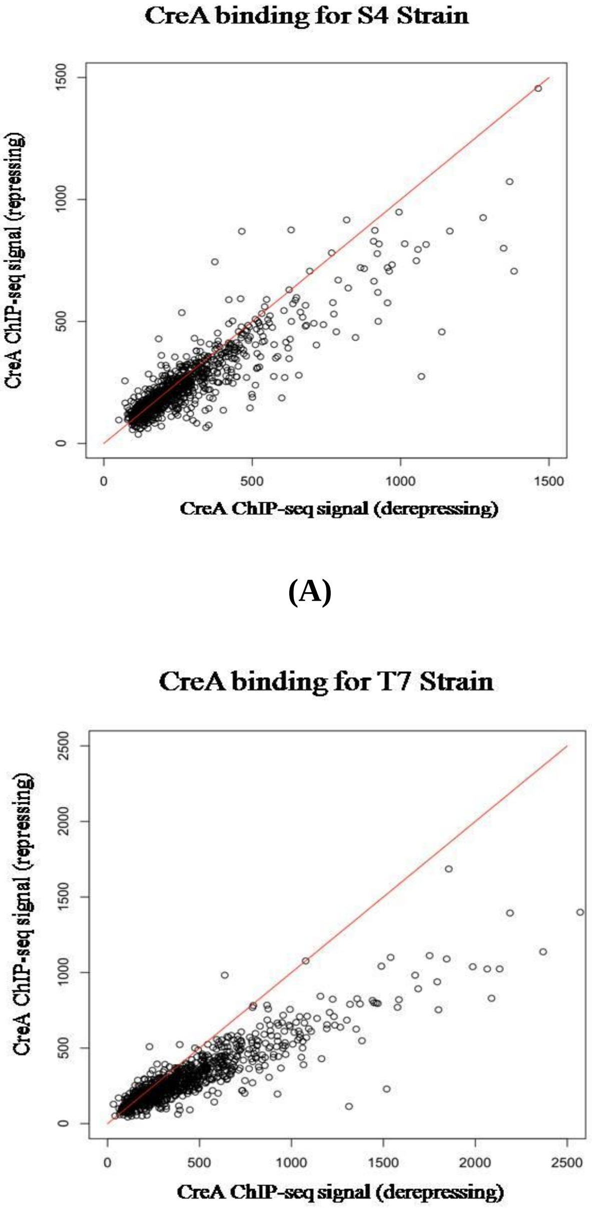
Although, a significant number of targets were detected either only in repressing or derepressing conditions for both strains, a signal density at the promoter regions of the unique targets showed similar binding patterns for both T7 and S4 (Figure 2A & 2B) in both growth conditions.



(A) (B)

Figure 2: Signal density at the promoters of the target genes for T7 (A) and S4 (B) in repressing and derepressing conditions.

The global repressor protein CreA binds to the consensus sequence of the promoter regions of target genes and regulates the transcriptional processes. GO analysis with proteins co-purified with CreA in repressing conditions revealed chromatin assembly and nucleosome organization as the main biological processes, implying that CreA interacts with the transcriptional machinery in these conditions. However, no such biological process was identified with the proteins co-purified with CreA in derepressing conditions (Alam and Kelly, unpublished). As the signal density at the promoters of targets showed similar CreA binding in both conditions, we performed additional analyses to verify this fact. The ChIP-seq signal count of all unique targets in both conditions were acquired and plotted against each other. If the targets are identical with similar binding levels, then all the signals will be highly correlated, whereas if there are any unique targets only for repressing or derepressing conditions, then high binding for one but not the other one will be observed. Based on this, a signal count plot of the S4 stain (Figure 3A) showed that there were very few targets that are unique to either repressing or derepressing conditions, and the binding levels were well correlated between the growth conditions. Similar analysis with the T7 strain also showed that CreA bound to the promoters of target genes in both growth conditions (Figure 3B). These results reinforce that CreA binds these promoters in both repressing and derepressing conditions.

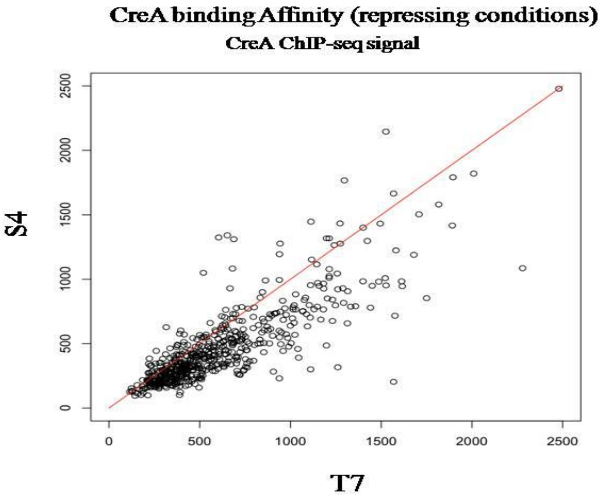


(A)

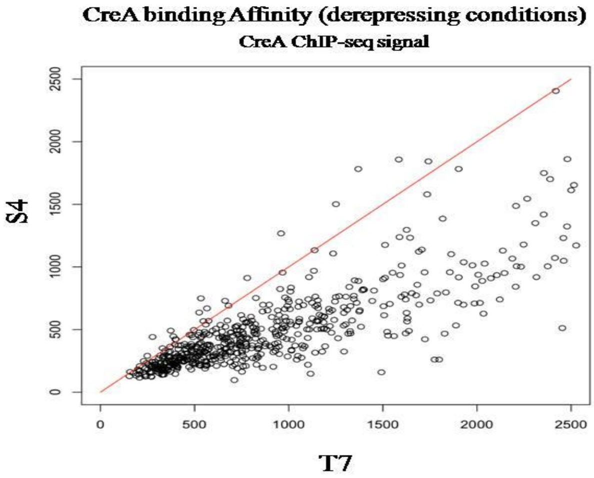
(B)

Figure 3: CreA ChIP-seq signal count plot for S4 (A) and T7 (B) in repressing and derepressing conditions.

Interestingly, the ChIP-seq signal count plot of T7 showed that the CreA ChIP-seq signal was higher in derepressing conditions compared to repressing conditions (plot skewed to derepressing conditions (Figure 3B). To investigate this, firstly, signal plot datasets of both T7 and S4 were compared in a single graph, either for repressing or derepressing conditions, to determine whether this skewed binding pattern is due to stronger binding signal due to overexpression of CreA in the T7 strain compared with the S4 strain that expresses CreA from the native promoter. As expected, in both growth conditions, a skewed plot was observed towards T7 due to overexpression of CreA (Figure 4A & 4B).



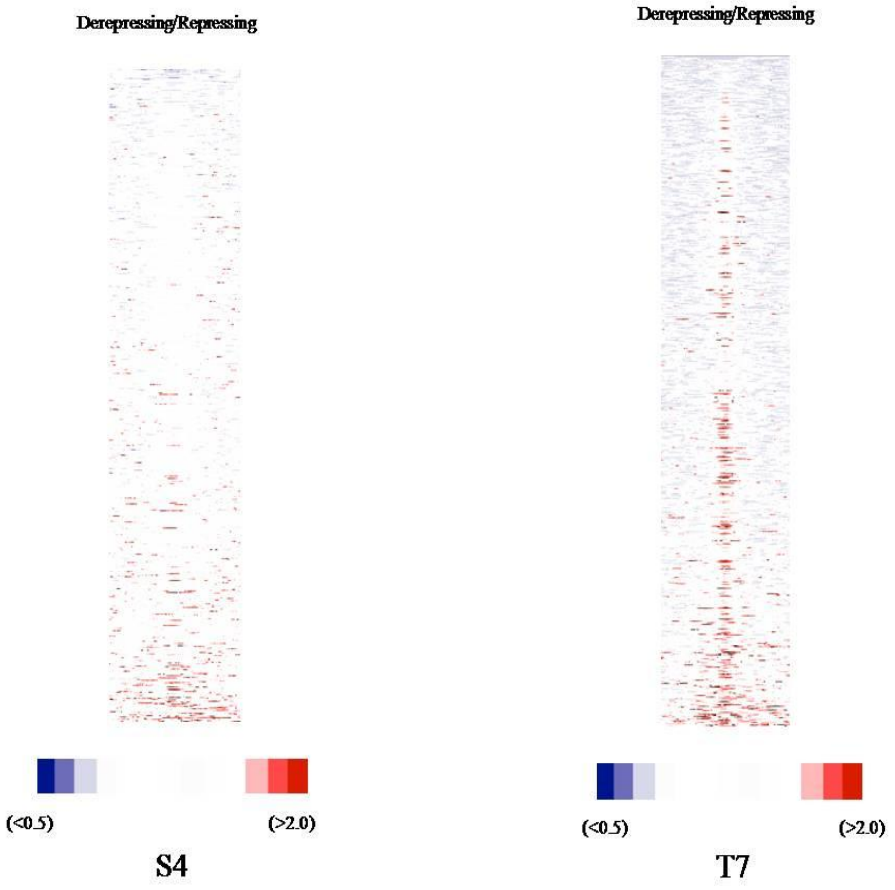
(A)



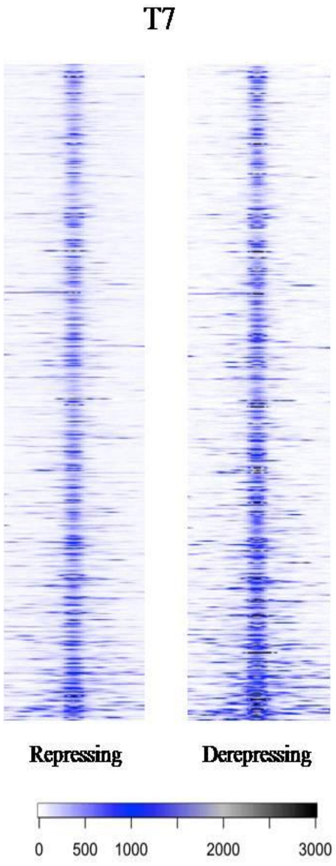
(B)

Figure 4: Comparison of CreA binding affinity for S4 and T7 either repressing (A) or derepressing (B) conditions.

Secondly, promoters with stronger signals were identified and compared in repressing and derepressing conditions for S4 and T7 (Figure 5A & 5B). For both the strains, a number of promoters showed stronger signal in derepressing conditions than in repressing conditions. When analysed for CreA binding, these promoters have CreA binding under both growth conditions (Figure 5C), suggesting that these signals were not specific for derepressing conditions. However, these plots indicate a slightly higher CreA binding in derepressing conditions.



(A) (B)



(C)

Figure 5: Comparison of promoters with strong signals in repressing and derepressing conditions for S4 (A) and T7 (B). (Red indicates higher than 2 fold signal in derepressing conditions). CreA binding on the promoters with strong signal for T7 in repressing and derepressing conditions (C).

4.3.3 Genome-wide direct targets of CreA

Although ChIP-seq analysis of the strains in repressing and derepressing conditions have identified 1532 (T7) and 1034 (S4) enriched binding sites for CreA, the targets of these strains overlap very well with almost 90% of targets in the S4 strain also identified in the T7 strain (M&M, Supplementary Table 1). A single unique target list (1946 genes after considering overlap, Supplementary Table 1) from both strains was cross-referenced using the Uniprot database which allowed the identification of 1320 targets, 50% of which are denoted as ‘uncharacterized’ (Supplementary Table 2; The remaining 626 targets were not present in the Uniprot database). A number of targets such as *alcA*, *alcR*, *amdS*, and *facA* that were detected in the ChIP-seq assay, were also identified previously using mutational analysis which showed that transcriptional regulation of these genes was controlled by CreA mediated CCR (Arst and Cove 1973, Kulmburg, et al. 1993, Scazzocchio, et al. 1995, Shroff, et al. 1996, Shroff, et al. 1997). In addition, genes involved in secondary metabolism and components of the velvet complex, nitrogen metabolic processes, pH response regulator, iron transporters, serine/threonine protein kinase, cell wall synthesis/biogenesis, autophagy related proteins, and ribosomal proteins were identified. Moreover, a number of sugar transporters of the Major Facilitator Superfamily (MFS), low affinity glucose transporter MstE, putative monosaccharide sugar transporter MstF, amino acid transporters, and permeases were also detected as direct targets of CreA. As expected, CreA itself is present in the target list as the transcription of *creA* is autoregulated (Arst, et al. 1990, Shroff, et al. 1996). Interestingly, both *creB* (encoding the CreB deubiquitinating enzyme) and *creD* (encoding the CreD arrestin motif protein) involved in the CCR network of *A. nidulans* were also detected as a direct target of CreA (Table 3 shows some well annotated targets of CreA).

Table 3: Selected Targets of CreA

Entry name	Protein names	Gene names	Length
PANB_EMENI	3-methyl-2-oxobutanoate hydroxymethyltransferase	*panB*	349
RSSA_EMENI	40S ribosomal protein S0	*rps0*	293
AMDS_EMENI	Acetamidase	*amdS*	548
ACPA_EMENI	Acetate permease A (Monocarboxylate transporter acpA)	*acpA*	298
ACSA_EMENI	Acetyl-coenzyme A synthetase (Acetate--CoA ligase) (Acyl-activating enzyme)	*facA acuA*	670
TREA_EMENI	Acid trehalase (Alpha,alpha-trehalase) (Alpha,alpha-trehalose glucohydrolase)	*treA*	1054
ADH1_EMENI	Alcohol dehydrogenase 1 (Alcohol dehydrogenase I) (ADH I)	*alcA*	350
ADH3_EMENI	Alcohol dehydrogenase 3 (Alcohol dehydrogenase III) (ADH III)	*alcC adh3*	352
ALDH_EMENI	Aldehyde dehydrogenase (ALDH)	*aldA aspA*	497
ATG13_EMENI	Autophagy-related protein 13	*atg13*	974
AT222_EMENI	Autophagy-related protein 22-2	*atg22-2*	593
ATG8_EMENI	Autophagy-related protein 8 (Autophagy-related ubiquitin-like modifier atg8)	*atg8*	118
PUT2_EMENI	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	*prnC*	572
VEA_EMENI	Developmental and secondary metabolism regulator veA (Velvet complex subunit A)	*veA*	573
CREA_EMENI	DNA-binding protein creA (Carbon catabolite repressor A)	*creA*	416
EGLD_EMENI	Endo-beta-1,4-glucanase D (Endoglucanase D)	*eglD*	357
ENO_EMENI	Enolase (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	*enoA*	438
EIF3H_EMENI	Eukaryotic translation initiation factor 3 subunit H (eIF3h)	*AN1270*	366
FDH_EMENI	Formate dehydrogenase (FDH)	*aciA*	365
G3P_EMENI	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	*gpdA*	336
CRED_EMENI	HECT-type ubiquitin ligase-interacting protein creD	*creD*	597
H2B_EMENI	Histone H2B	*htbA htb1*	140
H41_EMENI	Histone H4.1	*hhfA*	103
ACEA_EMENI	Isocitrate lyase (ICL)	*acuD*	538
M2DH_EMENI	Mannitol 2-dehydrogenase (M2DH) (MDH)	*AN2815*	502
MTLD_EMENI	Mannitol-1-phosphate 5-dehydrogenase (M1PDH) (MPD) (MPDH)	*mpdA*	386
MNS1B_EMENI	Mannosyl-oligosaccharide alpha-1,2-mannosidase 1B	*mns1B msdS*	505
NIR_EMENI	Nitrite reductase [NAD(P)H]	*niiA*	1104
NMRA_EMENI	Nitrogen metabolite repression protein nmrA	*nmrA*	352
NPR3_EMENI	Nitrogen permease regulator 3 (Required for meiotic nuclear division protein 11)	*npr3 rmd11*	816
AREA_EMENI	Nitrogen regulatory protein areA	*areA*	876
PCKA_EMENI	Phosphoenolpyruvate carboxykinase [ATP]	*acuF*	600
PALF_EMENI	pH-response regulator protein palF/RIM8	*palF*	775
PALI_EMENI	pH-response regulator protein palI/RIM9	*palI*	549
CWC25_EMENI	Pre-mRNA-splicing factor cwc25	*cwc25*	415
BTGE_EMENI	Probable beta-glucosidase btgE	*btgE*	555
BGLG_EMENI	Probable beta-glucosidase G (Beta-D-glucoside glucohydrolase G)	*bglG*	819
XYL2_EMENI	Probable D-xylulose reductase A (Xylitol dehydrogenase A)	*xdhA*	359
SCONB_EMENI	Probable E3 ubiquitin ligase complex SCF subunit sconB (Sulfur controller B)	*sconB mapB1*	678
EGLC_EMENI	Probable glucan endo-1,3-beta-glucosidase eglC	*eglC*	465
UAPC_EMENI	Purine permease	*uapC*	580
KAPC_EMENI	Putative transcription factor kapC	*kapC*	278
PDC_EMENI	Pyruvate decarboxylase	*pdcA*	568
DHQA_EMENI	Quinate dehydrogenase	*qutB*	329
ALCR_EMENI	Regulatory protein alcR	*alcR*	821
LAEA_EMENI	Secondary metabolism regulator laeA (Velvet complex subunit laeA)	*laeA*	374
ATG1_EMENI	Serine/threonine-protein kinase atg1 (Autophagy-related protein 1)	*atg1*	935
STE20_EMENI	Serine/threonine-protein kinase ste20	*ste20*	848
PP1_EMENI	Serine/threonine-protein phosphatase PP1	*bimG*	323
MIRB_EMENI	Siderophore iron transporter mirB	*mirB*	604
MIRC_EMENI	Siderophore iron transporter mirC	*mirC*	607
MET3_EMENI	Sulfate adenylyltransferase (ATP-sulfurylase)	*met3*	574
SODC_EMENI	Superoxide dismutase [Cu-Zn]	*sodA*	154
TBP_EMENI	TATA-box-binding protein (TATA sequence-binding protein) (TBP)	*tbpA*	268
TBB1_EMENI	Tubulin beta-1 chain (Beta-1-tubulin)	*benA rhiA*	447
TBB2_EMENI	Tubulin beta-2 chain (Beta-2-tubulin)	*tubC*	449
UBP16_EMENI	Ubiquitin carboxyl-terminal hydrolase 16	*ubp16*	624
CREB_EMENI	Ubiquitin carboxyl-terminal hydrolase creB	*creB*	766
ATG12_EMENI	Ubiquitin-like protein ATG12 (Autophagy-related protein 12)	*atg12*	166
VELB_EMENI	Velvet complex subunit B	*velB*	369

4.4 Discussion

Although the function of CreA as a global repressor protein is evident, little is known about the specific targets of this DNA binding transcription factor. Genome-wide microarray demonstrated the involvement of CreA in transcriptional regulation of a number of genes; however, whether these genes are directly or indirectly regulated by CreA is not known (Mogensen, et al. 2006). In addition, the binding patterns to the consensus sequence in the promoter region of a target gene in various growth conditions also need to be identified to understand the molecular mechanism/s of global repressor protein CreA.

This chapter reported the results of ChIP-seq analysis of strains that express CreA either from the constitutive *gpdA* promoter (T7 strain) or from its native promoter (S4 strain) in both repressing and derepressing conditions. The overexpressing strain provides an opportunity to identify as many direct targets as possible; whereas analysis using the native promoter strain represents accurate biological events inside the cell. Peak calling using the MACS program (Zhang, et al. 2008) showed that there were more unique targets in T7 than in S4, which is expected as the amount of *creA* expression is more in T7 due to presence of the constitutive promoter. Western analysis with T7 and S4 also showed more CreA detection for T7 in both repressing and derepressing conditions (Alam et al, unpublished). Moreover, the CreA binding affinity was skewed towards T7 in both repressing and derepressing conditions (Figure 4A &4B). Almost 90% of the unique targets identified for S4 overlapped with those in T7. Similar results have been observed using another two strains that express differently tagged CreA from its native promoter (Wong, C, personal communication).

For both T7 and S4, a significant number of unique targets were identified in both repressing and derepressing conditions using MACS. However, signal density and ChIP-seq signal plots for both strains in both growth conditions showed that CreA binds most of the unique targets in both repressing and derepressing conditions. Furthermore, analysing the unique targets that were initially identified either only in repressing or derepressing conditions confirmed that CreA bound to most of the promoters irrespective of growth conditions. These results indicated that for regulated transcription mediated by CreA DNA binding, sub-cellular localization and/or protein levels alone are insufficient, rather it might be controlled at the chromatin, possibly through post-translational modifications of histones and/or histone transcription regulator 3 (Hir3) or a protein interacting with Hir3 (Chapter 4), and/or nucleosome rearrangement at the promoter or coding regions.. CreA has been reported to be involved in the rearrangement of nucleosome positioning at the carbon catabolite repressible promoters *alcA*, *alcR* and *prnD-prnB,* although the rearrangements did not correlate with derepression (Garcia, et al. 2004, Mathieu, et al. 2005, Reyes-Dominguez, et al. 2008). In *T. reesei*, a similar result was observed with Cre1, a CreA homolog, in *cbh1* coding regions under repressing condition (Ries, et al. 2014), though the molecular mechanism of nucleosome rearrangement remains unclear.

Although CreA binds to the promoter regions under both growth conditions, a slightly higher CreA binding was observed in derepressing conditions. This finding is consistent as *creA* was detected in higher amounts at the transcript level in derepressing conditions (Shroff, et al. 1996), emphasizing the role of CreA in carbon catabolite derepressing conditions.

CreA itself is present in the unique target list which is expected as its transcription is autoregulated (Arst, et al. 1990, Shroff, et al. 1996). Identification of genes such as *alcA*, *alcR*, and *amdS* as a direct target of CreA provide an excellent internal control for the ChIP-seq experiment as binding to the consensus sequence for CreA has been detected in the promoter regions of these genes (Arst and Cove 1973, Kulmburg, et al. 1993, Panozzo, et al. 1998). The ChIP-seq analysis clearly showed that CreA is a wide domain transcription factor directly acting on different genes involved in various cellular processes, although a large number of unique targets identified in the ChIP-seq assay are ‘uncharacterized’ and provide opportunity for future investigations. Mutational analysis confirmed the involvement of the *creB* and *creD* genes in the CCR pathway (Boase and Kelly 2004, Hynes and Kelly 1977, Lockington and Kelly 2001) and it has been speculated that ubiquitination/deubiquitination networks mediated by CreD and CreB might play a role on the transcriptional repression by CreA in the presence of derepressing and repressing carbon sources respectively (Kelly 2004). However, a recent study showed that CreA is not an ubiquitinated protein, and nor does it interact either directly or indirectly to form a stable complex with the CreB deubiquitinating enzyme (Alam, et al. 2016). Identification of the CreB deubiquitinating enzyme and the CreD arrestin motif protein as a direct target of CreA provides new aspect to the CCR regulatory network of *A. nidulans* and needs further investigation.

Acknowledgement & Statement of contribution

We would like to thank Dr. Chris (Koon Ho) Wong and his lab members Dr. Yingying and Liguo for ChIP-seq experiments and bioinformatics analysis. Md. Ashiqul Alam contributed in research design, construction of strain (not included in analysis due to poor quality data), prepared and sent all strains to Dr. Chris Wong, interpretation of data and writing this chapter.

Chapter 4
Supplementary

(Attached as soft copy in CD at the back)

Supplementary Table 1: List of unique targets of S4 and T7

Supplementary Table 2: List of targets cross referenced by Uniprot

Chapter 5

General Discussion

Carbon regulation of *A. nidulans* is controlled by the CCR regulatory network which allows utilizing most favourable carbon sources while repressing genes that are required to utilize less favourable carbon nutrients. This CCR regulation is mediated by the DNA binding global repressor protein CreA encoded by the *creA* gene (Arst and Cove 1973, Dowzer and Kelly 1991). Mutational screening and biochemical analyses confirmed that a deubiquitinating enzyme and a protein interacting with ubiquitin ligase are involved in CCR (Hynes and Kelly 1977, Lockington and Kelly 2001). Although the absence of the deubiquitinating enzyme CreB affects CCR for some pathways, its role is still unknown at the molecular level. Previous work showed evidence of genetic interaction between *creA* and *creB* missense alleles, and hinted at protein-protein interaction between the proteins. This project had three aims; to investigate the genetic interaction between *creA* and *creB* null alleles; to determine whether CreA is a direct target for the deubiquitinating enzyme CreB; and to identify direct targets of the global repressor protein CreA.

Genetic interaction between *creA* and *creB* alleles was previously identified using a double mutant strain containing the *creA204* and *creB15* alleles (Hynes and Kelly 1977). As both the alleles were reported to be missense alleles and showed relatively weak phenotype compared to null alleles (Dowzer and Kelly 1991, Lockington and Kelly 2001), hence a *creA* and *creB* double null mutant strain was developed to investigate the genetic interaction between these two genes (Alam, et al. 2016). Morphological analysis showed that the extreme compact colony morphology on complete medium due to the *creA* null mutation was partially suppressed by the *creB* null mutation, whereas this morphological suppression was not observed in the double mutant strain of *creA204* and *creB15* alleles (Alam, et al. 2016, Hynes and Kelly 1977), suggesting that the complete loss of both proteins might have less effects on colony morphology than the complete loss of CreA alone, however, the molecular mechanism/s of morphological suppression is not known (Alam, et al. 2016). In *A. oryzae*, a double null mutant strain of *creA* and *creB* genes retained the morphology of a *creA* null mutant in minimal media (Ichinose, et al. 2014).

Generally, *creA* mutations can suppress the effects of *areA217* for the utilization of proline in the presence of repressing carbon sources (Bailey and Arst 1975). On the other hand, *creB* mutations showed weak growth phenotype due to probable effects of *creB* mutations on permeases (Hynes and Kelly 1977). The *creA204creB15* double mutant strain showed reduced utilization of proline in the presence of glucose compared to *creB15* alone (Hynes and Kelly 1977), and this was also the case for the double null mutant strain compared to the single *creAΔ* mutant , implying that effect of *creB* mutations on proline permease is epistatic to the effects of *creA* mutations on derepression. In *A. nidulans*, the quinate permease, QutD was identified as a ubiquitinated protein and a target of CreB deubiquitinating enzyme (Kamlangdee 2008). The double null mutant also showed reduced growth on quinic acid as a sole carbon source, like the *creB* mutations, whereas strains with *creA* mutations show very little effects (Hynes and Kelly 1977).

It is evident that in the presence of glucose, mutations in the *creA* and *creB* genes can lead to derepression of alcohol dehydrogenase I. The double null mutant showed highest ADHI activity in enzyme assays in repressed-induced conditions, more than the addition of single *creAΔ* and *creBΔ* mutant strains,. This synergistic effect in the double null mutant confirmed the interaction at least for ADHI expression (Alam, et al. 2016). In *A. oryzae*, similar synergistic expression of α-amylase was observed for the double null mutant of the *creA* and *creB* genes in submerged culture (Ichinose, et al. 2014).

Although the role of CreB deubiquitinating enzyme in CCR is not identified, it is thought that CreB might be involved in CCR by removing ubiquitin molecule/s from CreA. Ubiquitination/deubiquitination pathways are known to play regulatory roles in the cell in addition to protein degradation (Kaiser and Huang 2005). The possible involvement of a ubiquitination/deubiquitination network in CCR pathways led to the investigation of *alcA* mRNA levels. Like the enzyme assay, synergy was also observed for the *alcA* expression for the double null mutant in repressed-induced conditions, again confirming the genetic interaction between the *creA* and *creB* genes (Alam, et al. 2016).

The indication of a clear genetic interaction led us to investigate whether CreA or any protein complexed with CreA is a direct target of the CreB deubiquitinating enzyme. Previously, CoIP analyses with strains overexpressing CreA and CreB hinted at a possible direct interaction as CreB was co-purified with CreA, although, CreA was not detected when CreB was purified (Kamlangdee 2008). However, over-expression can lead to mis-folding of proteins (Goldberg 2003), and this is particularly important when proteins involved in ubiquitination and deubiquitination pathways are in question, as mis-folded and mis-expressed proteins can be targeted and processed via the proteasome (Kraft, et al. 2010). In addition, experiments with over-expressing proteins do not confirm that the interaction occurs at physiological levels where proteins are expressed from their native promoters. Moreover, native *creA* transcription is autoregulated and over-expression of CreA can override the requirement of CreB for repression (Lockington, RA, personal communication). Hence, co-purification experiments were performed with strains that express both CreA and CreB from their native promoters. Western analysis performed in both directions showed CreA was not detected when CreB was purified and no CreB was detected when CreA was purified, suggesting that CreA and CreB do not physically interact and nor are they part of a single stable complex that can be purified via this means (Alam, et al. 2016).

It has been speculated previously that CreA requires post-translational modifications or '*de novo*' protein synthesis to become an active repressor (Ries, et al. 2016, Roy, et al. 2008, Strauss, et al. 1999). Post-translational modifications such as phosphorylation and ubiquitination have important roles in cell signalling, and phosphorylation of a protein can be a marker to trigger subsequent ubiquitination [reviewed by (Nguyen, et al. 2013)]. As no direct physical interaction between CreA and CreB was detected, it raised a new question as to whether CreA, or any protein complexed with CreA, is ubiquitinated. In addition, a weak CreA signal was detected when ubiquitinated proteins were purified using an over-expressing strain of CreA (Kamlangdee 2008), indicating that CreA might be aubiquitinated proteins, although over production of protein can cause inappropriate folding and degradation via the proteasome as discussed above. Similarly, western analysis with a CreA over-expressing strain provided an indication that CreA might also be a phosphoprotein (Alam, et al. 2016). Mass spectrometry analysis with purified CreA expressing from its native promoter, showed that two phosphopeptides, SHS$_{(p)}$HEDEDSYASHR (aa 260-273) andS$_{(p)}$RPNSPNSTAPS$_{(p)}$SPTFSHDSLSPTPDHTPLATPAHSPR (aa 277- 314)were detected in both repressing and derepressing conditions. A differentially phosphorylated form of the latter peptide, SRPNSPNSTAPS$_{(p)}$S$_{(p)}$PTFSHDSLSPTPDHTPLATPAHS$_{(p)}$PR (aa 277- 314),was only present in repressed conditions. In addition, another phosphorylated peptide, LKPLS$_{(p)}$PSELHLPSIR (aa 315-329), was also identified in only repressed conditions (Alam, et al. 2016). Phosphorylation of repressor proteins plays an important role in the CCR pathways of yeast and other filamentous fungi. In *T. reesei*, phosphorylation of the Ser^{241} residue of Cre1 is required for DNA binding and replacing of Ser^{241} by glutamic acid mimics phosphorylation, however, replacing by alanine allows binding without phosphorylation, with the latter leading to permanent carbon catabolite repression for cellobiohydrolase I expression (Cziferszky, et al. 2002). Substitution of Glu^{244} by valine results in no phosphorylation, binding or repression (Cziferszky, et al. 2002). In *S. sclerotiorum*, Ser^{266} (equivalent to Ser^{241} in *T. reesei*) substitution by alanine leads to derepression (Vautard-Mey and Fevre 2000). Deletion of the amino acid region SHED$^{262\text{-}265}$ of CreA (equivalent to SNDE$^{241\text{-}244}$ of Cre1 in *T. reesei* and SHEE$^{266\text{-}269}$ of CRE1 in *S. sclerotiorum*) showed little effect on carbon catabolite repression in *A. nidulans* (Roy, et al. 2008). In *S. cerevisiae*, phosphorylation of Mig1p by Snf1p is essential for derepression in non-repressing carbon sources (Carlson 1999, DeVit and Johnston 1999, DeVit, et al. 1997). However, the potential region of Mig1p for Snf1p phosphorylation is not conserved in CreA or its homologues in filamentous fungi (Kelly 2004). Whether these differences in the number of phosphopeptides and phosphorylation sites of one of these peptides between repressed and derepressed conditions of CreA has potential regulatory significance requires further investigations. In *S. cerevisiae*, Snf1 kinase mediated phosphorylation of Mig1p is important for derepression activity since phosphorylation regulates the sub-cellular localization of the repressor protein (DeVit, et al. 1997). In *A. nidulans*, CreA expressed from a constitutive promoter was detected in the nucleus at high levels in both repressing and derepressing conditions (Roy, et al. 2008). Although, recent studies claimed that the SnfA kinase (homolog of *S. cerevisiae* Snf1 kinase) was required for derepression of cellulase enzymes through alteration of CreA nuclear localization (Brown, et al. 2013), the experimental conditions used in that study were more similar to starvation rather than derepression, and microarray analysis showed that XprG, starvation response transcription factor was elevated in the experimental conditions (Brown, et al. 2013). In *A. nidulans*, carbon starvation can result in changes in transcriptomes as well as regulation of biological processes including programmed cell death, secondary metabolite production, and production of hydrolases and proteases (Szilagyi, et al. 2013). Genes that are involved in glucose utilization and carbohydrate synthesis were down-regulated, although genes that are involved in carbohydrate hydrolysis, protein synthesis, autophagy and nucleases and peptidases were up-regulated (Szilagyi, et al. 2013).Western analysis also showed that CreA was not detected in strains incubated in starvation conditions (Alam et al., unpublished), which may explain the apparent changed location of CreA.

On the other hand, both western and MS analysis showed that CreA is not a ubiquitinated protein in either repressing or derepressing conditions (Alam, et al. 2016). Recently, Ries, et al. (2016) suggested that CreA may a ubiquitinated protein based on a smear, detected between 60 kDa to 100 kDa, which was present when purified CreA:GFP was probed with an anti-ubiquitin antibody. However, when CreA was probed with anti-GFP antibody, no ladder of differentially ubiquitinated CreA species was detected in that same molecular weight range. The MS evidence makes it very unlikely that CreA is a ubiquitinated protein. Moreover, CreA was not present among the proteins identified with ubiquitin target sites in the *A. nidulans* proteome analysis of Chu, et al. (2015).

The key findings of the preceding chapter led us to investigate whether there were any protein/s that interact with both CreA and CreB and regulate the activity of CreA. For this, proteins co-purified with both CreA and CreB in repressing and derepressing conditions were identified. Yeast and human orthologues of the purified proteins were also determined. Although, the CCR mechanisms of *S. cerevisiae* and *A. nidulans* are different, repressor proteins of both these organisms share some similarities including zinc finger regions and DNA binding specificities. On the other hand, ubiquitination/deubiquitination pathways are conserved in higher eukaryotes including human. Gene ontology (GO) analyses in terms of biological process were performed. GO analysis was used for categorization of proteins that were significantly over or under represented in respect to a given population background of a respective organism. In addition, GO analysis can also be used to validate and interpret new system-wide data and evaluation of protein interactions considering that interacting proteins tend to classify in the same or similar GO terms (Chagoyen and Pazos 2010).

It is evident that, in the presence of repressing carbon sources such as glucose or sucrose, the global repressor protein CreA represses the transcription of a number of genes that are required for the utilization of less favoured carbon sources. Although, the precise molecular mechanism/s of CreA mediated transcriptional regulation is not known, however, it is understandable that as a DNA-binding transcription factor (TF), CreA interacts with the transcriptional machinery for repressing activity. Our findings showed that proteins including histones, histone variants, and a histone transcription regulator, co-purified with CreA in repressing conditions, and are implicated to be involved in the transcriptional processes. GO analysis also validated these findings as chromatin assembly and nucleosome organization were the highly enriched biological processes identified with significantly less *p-values* and FDR. Although, some histone proteins were purified in derepressing conditions, no biological process was identified that is related to the transcriptional regulation. These results provide an indication that chromatin structure and nucleosomal positioning may be involved in CreA mediated transcriptional regulation.

In *A. nidulans*, previous studies showed that CreA was reported to be involved in the rearrangement of nucleosome positioning in carbon catabolite repressible promoters *alcA*, *alcR* and *prnD-prnB*, although the rearrangements did not correlate with derepression (Garcia, et al. 2004, Mathieu, et al. 2005, Reyes-Dominguez, et al. 2008). In *T. reesei*, Cre1, the homologue of CreA, is involved in nucleosome positioning in the coding region of the *cbh1* gene in repressing conditions. Moreover, nucleosome positioning in the promoter and coding regions are different in repressing compared to induced conditions, and the positioning of nucleosomes in the promoter region in inducing conditions may prevent CreA binding (Ries, et al. 2014).

Histone proteins are the primary components of chromatin and nucleosomes and play important roles in gene regulation. Although, canonical histones such as H2A and H2B were co-purified with CreA in both repressing and derepressing conditions, histone variant H2A.Z was only identified in repressing conditions. H2A.Z has been reported to be modified post-translationally including acetylation, methylation and ubiquitination, and plays roles in both transcriptional regulation (positive and negative) and nucleosome positioning [review by (Sevilla and Binda 2014)]. In addition, H2A.Z was identified in the ubiquitome proteins separated from *A. nidulans* (Chu, et al. 2015), suggesting that it could be a probable target for CreB deubiquitinating enzyme. However, experiments undertaken to generate a H2A.Z knockout strain showed that H2A.Z is essential for growth of haploid, and a single copy is insufficient for growth of a diploid of *A. nidulans*. H2A.Z is evolutionary conserved across species (Thatcher and Gorovsky 1994, Wu, et al. 1982) and essential for the viability of a number of organisms including *Tetrahymena*, *Drosophila* and mice (Faast, et al. 2001, Liu, et al. 1996, Ridgway, et al. 2004). In *S. cerevisiae*, deletion of H2A.Z results in slow growth but it is not essential for viability (Adam, et al. 2001).

Regulation of gene transcription follows the same basic principle across eukaryotes. As expected, analysis of human and yeast orthologues also showed chromatin assembly and nucleosome organization as the highly enriched biological processes involving histone orthologues in repressing conditions. Apart from that, Mig1p of *S. cerevisiae* was involved in the regulation, negatively in some cases, of various metabolic pathways which was not observed for CreA in *A. nidulans* or its orthologue in humans, reinforcing that the repressor proteins in these two organisms have different modes of action despite sequence similarities. Another apparent difference is the histone transcription regulator 3, Hir3, co-purified in repressing conditions, which was present in transcription related biological processes in humans and yeast, but not in *A. nidulans*, although this could be an artefact due to the absence of any studies on the Hir3 homologue in *A. nidulans* resulting in its absence in the GO term database. In *S. cerevisiae*, Hir3 is one of the subunits of the Hir complex, which also consists of Hir1 and Hir2, and histone promoter control, Hpc2, that acts as a co-repressor of transcription of histone gene pairs and is also involved in nucleosome assembly to facilitate various cellular processes including transcription and gene silencing (Amin, et al. 2012). Our network analysis with yeast orthologues also indicated the involvement of Hir3 in transcriptional process as it showed genetic interaction with H2A, H2A.Z, and Med8, all co-purified with CreA in repressing conditions. As a component of the Mediator complex, Med8 transmits activation or repression signals from DNA bound transcription factors to the core transcription machinery, RNA Pol II and general initiation factors (Zhu, et al. 2011). In addition, a number of studies showed that Mediator can interact with the co-repressor complex Ssn6p-Tup1p or bind to the upstream activating sequences (UASs) of the *SUC2* promoter, downstream repressing sequences (DRSs) of the *HXK2* gene and may play roles in the regulation of gene transcription (Chaves, et al. 1999, Gromoller and Lehming 2000, Han, et al. 2001). Furthermore, mammalian MED8 plays a role in recruiting ubiquitin ligase activity directly to the RNA pol II transcription machinery (Brower, et al. 2002). Interestingly, Med8 was present among the ubiquitome proteins separated in *A. nidulans* (Chu, et al. 2015). It would not be surprising that Med8 could be another probable target for the CreB deubiquitinating enzyme that may play role/s in transcriptional regulation of CreA and require further investigation.

Conversely, no significant biological process was identified with proteins, or their human and yeast orthologues purified with CreB, in repressing conditions. In derepressing conditions, protein transport and cellular material localization were the key biological processes identified, which is consistent with the general findings that deubiquitinating enzymes can target a variety of substrates including transporters/permeases, scaffolds, adapters and ubiquitin receptors (Reyes-Turcu, et al. 2009). In *S. cerevisiae*, the deubiquitinating enzyme Ubp1 plays a role in protein trafficking in the early endocytic pathway (Schmitz, et al. 2005). In *A. nidulans*, quinate permease QutD, involved in the transportation of quinic acid, has been confirmed as a substrate of CreB (Kamlangdee 2008). It has been suggested that *creB* mutant phenotypes could be due to its effects on the permeases and transporters, and some evidence showed that CreB does directly affect a range of permeases and transporters (Arst 1981, Hynes and Kelly 1977, Kamlangdee 2008). However, in the case of glucose uptake, *creB* mutations showed only very mild effects (Espeso, et al. 1995, Strauss, et al. 1999). In addition, ADH activity is derepressed in *creB* mutant strains, but some other enzymes normally subjected to CCR are not. If *creB* mutations have effects on glucose permease then a wider range of enzyme activities might be expected to be affected. The inducer, ethanol, does not require active transport into the cell, which argues against a role for CreB in the stability of permeases affecting inducer availability.

Both ubiquitination and deubiquitination have been reported to be involved in transcriptional regulation. In yeast, histone H2B monoubiquitination by Rad6 precedes methylation and the recruitment of the SAGA complex, when Ubp8, a component of the SAGA histone acetyltransferase, deubiquitinates the monoubiquitinated histone H2B to allow transcriptional initiation (Reyes-Turcu, et al. 2009, Shilatifard 2006). However, there are apparent differences between the DUB module of yeast and *A. nidulans* SAGA complex (Georgakopoulos, et al. 2012, Georgakopoulos, et al. 2013). On the other hand, deubiquitination of ubiquitinated H2B by Ubp10 results in gene silencing in the telomere region and at the rDNA locus (Emre, et al. 2005).

Histone proteins, specifically, histone transcription regulator 3, Hir3 was co-purified with both CreA and CreB, although, at least in *A. nidulans*, it was not involved in any biological processes, possibly an artefact due to lack of studies in this organism. It could be possible that CreB might interact with Hir3 or any components of the Hir3 regulatory processes which leads to nucleosome rearrangement and alteration of chromatin structure that facilitate transcriptional regulation by CreA.

To elucidate the molecular mechanism/s of CreA mediated repression, it is important to understand the binding patterns of CreA in both repressing and derepressing conditions. As the core consensus sequence that CreA binds has been identified in promoters which are not regulated by CreA, it is speculated that specific position of promoters and/or residues other than the core consensus sequence might play a role in CreA mediated repression (Garcia, et al. 2008, Panozzo, et al. 1998).

ChIP-seq assay, performed with strains that express CreA either from the constitutive promoter or from its native promoter in both growth conditions, showed that most of the promoters bound by CreA were bound in both repressing and derepressing conditions. Further analysis focussing on a subset of unique targets, which were identified either in repressing or derepressing conditions, confirmed that CreA was bound to these promoters regardless of growth conditions. These results suggest that CreA activity might be regulated at the level of the chromatin, possibly by post-translational modifications and/or nucleosome rearrangement. The involvement of CreA in the nucleosome rearrangement at CCR repressible promoters were reported previously in *A. nidulans*. In *T. reesei*, Cre1 is required for correct nucleosome positioning at least for the *cbh1* coding region in repressing conditions. Nucleosome positioning in the promoter and coding regions are different between repressing and inducing conditions and nucleosome positioning of the promoter region in inducing conditions reportedly prevents Cre1 binding. Conversely, no apparent differences were detected in the nucleosome positioning between the WT and *cre1* mutant in glycerol-sophorose media, suggesting no role for Cre1 in nucleosome positioning in this condition (Ries, et al. 2014). The findings of Chapter 3 showed that histone proteins were co-purified with CreA in both growth conditions; however biological processes related to transcription were only identified for repressing conditions. This is consistent with the ChIP-seq results in Chapter 4.

As a basic component of chromatin, nucleosomes can offer platforms for various regulatory factors and chromatin remodelling enzymes. Transcriptional regulation can be altered due to changes in the chromatin structure triggered by different cellular activity as well as environmental conditions such as the presence of various carbon sources (Brosch, et al. 2008). In addition, nucleosome positioning can alter the binding of transcription factor and RNA polymerase assembly and this positioning can depend on various factors such as DNA sequence, physical force, and actions of different transcription factors (Arya, et al. 2010). It would be interesting to identify whether CreA plays any role in alteration of nucleosome rearrangement and/or chromatin structure in different growth conditions.

ChIP-seq analysis identifies direct targets of CreA at a genome-wide scale, and the analysis identified a large number of genes as directly bound by CreA. However, a large number of these unique targets are not functionally characterized. It would be of great interest to identify the potential role/s of these uncharacterized targets of CreA. Surprisingly, both CreB and CreD were identified among the direct targets of CreA. It has been evident from mutational analysis that *creB* and *creD* affect the CCR pathway of *A. nidulans*, although the molecular nature of the effect is unknown (Boase and Kelly 2004, Hynes and Kelly 1977). The CreB deubiquitinating enzyme targets permeases and transporters, but there are no convincing results to show it targets glucose permeases. Further, overexpression of CreA can compensate the requirement of CreB (Lockington RA, personal communication). The finding that CreA binds the *creB* promoter may provide a further avenue to investigate the role of CreB in CCR.

In conclusion, the findings outlined in this thesis will be of great interest to a broad range of researchers. This thesis provides some key answers to the understanding of the molecular mechanisms involved in CCR control, and opens up a number of new aspects which require further investigation. Any findings in this key model organism can be directly applied to a number of industrial and pathogenic fungi which have great economic impact on various sectors including health and medicine, food, biofuel, biotechnology and pharmaceuticals.

References

Adam M, Robert F, Larochelle M, Gaudreau L (2001) H2A.Z is required for global chromatin integrity and for recruitment of RNA polymerase II under specific conditions. Molecular and Cellular Biology 21: 6270-6279 doi: 10.1128/mcb.21.18.6270-6279.2001

Adams TH, Boylan MT, Timberlake WE (1988) *brlA* is necessary and sufficient to direct conidiophore development in *Aspergillus nidulans*. Cell 54: 353-362 doi: 10.1016/0092-8674(88)90198-5

Agger T, Petersen JB, O'Connor SM, Murphy RL, Kelly JM, Nielsen J (2002) Physiological characterisation of recombinant Aspergillus nidulans strains with different creA genotypes expressing A-oryzae alpha-amylase. Journal of Biotechnology 92: 279-285 doi: 10.1016/s0168-1656(01)00366-2

Ahn JH, Park SH, Kang HS (1995) Inactivation of the UAS1 of STA1 by glucose and STA10 and identification of 2 loci, SNS1 and MSS1, involved in STA10 dependent repression in Saccharomyces cerevisiae. Molecular & General Genetics 246: 529-537 doi: 10.1007/bf00298959

Ahuatzi D, Herrero P, de la Cera T, Moreno F (2004) The glucose-regulated nuclear localization of hexokinase 2 in Saccharomyces cerevisiae is Mig1-dependent. Journal of Biological Chemistry 279: 14440-14446 doi: 10.1074/jbc.M313431200

Ahuatzi D, Riera A, Pelaez R, Herrero P, Moreno F (2007) Hxk2 regulates the phosphorylation state of Mig1 and therefore its nucleocytoplasmic distribution. Journal of Biological Chemistry 282: 4485-4493 doi: 10.1074/jbc.M606854200

Alam MA, Kamlangdee N, Kelly JM (2016) The CreB deubiquitinating enzyme does not directly target the CreA repressor protein in Aspergillus nidulans. Current Genetics: 1-21 doi: 10.1007/s00294-016-0643-x

Amin AD, Vishnoi N, Prochasson P (2012) A global requirement for the HIR complex in the assembly of chromatin. Biochimica Et Biophysica Acta-Gene Regulatory Mechanisms 1819: 264-276 doi: 10.1016/j.bbagrm.2011.07.008

Andoh T, Hirata Y, Kikuchi A (2002) PY motifs of Rod1 are required for binding to Rsp5 and for drug resistance. Febs Letters 525: 131-134 doi: 10.1016/s0014-5793(02)03104-6

Aro N, Ilmen M, Saloheimo A, Penttila M (2003) ACEI of Trichoderma reesei is a repressor of cellulase and xylanase expression. Applied and Environmental Microbiology 69: 56-65 doi: 10.1128/aem.69.1.56-65.2003

Arst HN, Cove DJ (1973) Nitrogen metabolite repression in *Aspergillus nidulans*. Molecular & General Genetics 126: 111-141 doi: 10.1007/bf00330988

Arst HN, Jones SA, Bailey CR (1981) A method for the selection of deletion mutations in the L-proline catabolism genen cluster of *Aspergillus nidulans*. Genetical Research 38: 171-195 doi:

Arst HN, Macdonald DW (1975) Gene cluster in *Aspergillus nidulans* with an internally located cis-acting regulatory region. Nature 254: 26-31 doi: 10.1038/254026a0

Arst HN, Tollervey D, Dowzer CEA, Kelly JM (1990) An inversion truncating the *creA* gene of *Aspergillus nidulans* results in carbon catabolite derepression. Molecular Microbiology 4: 851-854 doi: 10.1111/j.1365-2958.1990.tb00656.x

Arst HNJ (1981) Aspects of the control of gene expression in fungi Glover, S W And D A Hopwood (Symposium of the Society for General Microbiology), pp. P131-160.

Arya G, Maitra A, Grigoryev SA (2010) A structural perspective on the where, how, why, and what of nucleosome positioning. Journal of biomolecular structure & dynamics 27: 803-820 doi: 10.1080/07391102.2010.10508585

Bae YH, Kweon DH, Park YC, Seo JH (2014) Deletion of the HXK2 gene in Saccharomyces cerevisiae enables mixed sugar fermentation of glucose and galactose in oxygen-limited conditions. Process Biochemistry 49: 547-553 doi: 10.1016/j.procbio.2014.01.030

Bailey C, Arst HN (1975) Carbon catabolite repressionin *Aspergillus nidulans*. European Journal of Biochemistry 51: 573-577 doi: 10.1111/j.1432-1033.1975.tb03958.x

Bailey RB, Woodword A (1984) Isolation and characterization of a pleiotropic glucose repression resistant mutant of Saccharomyces cerevisiae. Molecular & general genetics : MGG 193: 507-512 doi:

Becker K, Beer C, Freitag M, Kuck U (2015) Genome-wide identification of target genes of a mating-type -domain transcription factor reveals functions beyond sexual development. Molecular Microbiology 96: 1002-1022 doi: 10.1111/mmi.12987

Becker K, Ziemons S, Lentz K, Freitag M, Kuck U (2016) Genome-Wide Chromatin Immunoprecipitation Sequencing Analysis of the Penicillium chrysogenum Velvet Protein PcVelA Identifies Methyltransferase PcLlmA as a Novel Downstream Regulator of Fungal Development. mSphere 110.1128/mSphere.00149-16

Berkey CD, Vyas VK, Carlson M (2004) Nrg1 and Nrg2 transcriptional repressors are differently regulated in response to carbon source. Eukaryotic Cell 3: 311-317 doi: 10.1128/ec.3.2.311-317.2004

Bernardo SMH, Gray K-A, Todd RB, Cheetham BF, Katz ME (2007) Characterization of regulatory non-catalytic hexokinases in Aspergillus nidulans. Molecular Genetics and Genomics 277: 519-532 doi: 10.1007/s00438-006-0203-z

Bisson LF, Neigeborn L, Carlson M, Fraenkel DG (1987) The *snf3* gene is required for high affinity glucose transport in *Saccharomyces cerevisiae*. Journal of Bacteriology 169: 1656-1662 doi:

Boase NA, Kelly JM (2004) A role for *creD*, a carbon catabolite repression gene from *Aspergillus nidulans*, in ubiquitination. Molecular Microbiology 53: 929-940 doi: 10.1111/j.1365-2958.2004.04172.x

Boase NA, Lockington RA, Adams JRJ, Rodbourn L, Kelly JM (2003) Molecular characterization and analysis of the *acrB* gene of *Aspergillus nidulans*: A gene identified by genetic interaction as a component of the regulatory network that includes the CreB deubiquitination enzyme. Genetics 164: 95-104 doi:

Bohm S, Frishman D, Mewes HW (1997) Variations of the C2H2 zinc finger motif in the yeast genome and classification of yeast zinc finger proteins. Nucleic Acids Research 25: 2464-2469 doi: 10.1093/nar/25.12.2464

Brosch G, Loidl P, Graessle S (2008) Histone modifications and chromatin dynamics: a focus on filamentous fungi. Fems Microbiology Reviews 32: 409-439 doi: 10.1111/j.1574-6976.2007.00100.x

Brower CS, Sato S, Tomomori-Sato C, Kamura T, Pause A, Stearman R, Klausner RD, Malik S, Lane WS, Sorokina I, Roeder RG, Conaway JW, Conaway RC (2002) Mammalian mediator subunit mMED8 is an Elongin BC-interacting protein that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin ligase. Proceedings of the National Academy of Sciences of the United States of America 99: 10353-10358 doi: 10.1073/pnas.162424199

Brown NA, de Gouvea PF, Krohn NG, Savoldi M, Goldman GH (2013) Functional characterisation of the non-essential protein kinases and phosphatases regulating Aspergillus nidulans hydrolytic enzyme production. Biotechnology for Biofuels 610.1186/1754-6834-6-91

Carlson M (1999) Glucose repression in yeast. Current Opinion in Microbiology 2: 202-207 doi: 10.1016/s1369-5274(99)80035-6

Carlson M, Botstein D (1982) 2 differentially regulated messenger RNAs with different 5' ends encode secreted and intracellular forms of yeast invertase. Cell 28: 145-154 doi: 10.1016/0092-8674(82)90384-1

Carlson M, Osmond BC, Botstein D (1981) Mutants of yeast defective in sucrose utilization. Genetics 98: 25-40 doi:

Cassart JP, Georis I, Ostling J, Ronne H, Vandenhaute J (1995) The Mig1 repressor from *Kluyveromyces lactis* - cloning, sequencing and functional analysis in *Saccharomyces cerevisiae* Febs Letters 371: 191-194 doi: 10.1016/0014-5793(95)00909-s

Cassart JP, Ostling J, Ronne H, Vandenhaute J (1997) Comparative analysis in three fungi reveals structurally and functionally conserved regions in the Mig1 repressor. Molecular & General Genetics 255: 9-18 doi:

Celenza JL, Carlson M (1989) Mutational analysis of the *Saccharomyces cerevisiae* Snf1 protein kinase and evidence for functional interaction with Snf4 protein. Molecular and Cellular Biology 9: 5034-5044 doi:

Celenza JL, Carlson M (1989) Mutational analysis of the *Saccharomyces cerevisiae* Snf1 protein kinase and evidence for functional interaction with Snf4 protein. Molecular and Cellular Biology 9: 5034-5044 doi:

Celenza JL, Eng FJ, Carlson M (1989) Molecular analysis of the snf4 gene of Saccharomyces cerevisiae- evidence for physical association of the Snf4 protein with the Snf1 protein kinase. Molecular and Cellular Biology 9: 5045-5054 doi:

Chagoyen M, Pazos F (2010) Quantifying the biological significance of gene ontology biological processes-implications for the analysis of systems-wide data. Bioinformatics 26: 378-384 doi: 10.1093/bioinformatics/btp663

Chaves RS, Herrero P, Moreno F (1999) Med8, a subunit of the mediator CTD complex of RNA polymerase II, directly binds to regulatory elements of SUC2 and HXK2 genes. Biochemical and Biophysical Research Communications 254: 345-350 doi: 10.1006/bbrc.1998.9954

Chen HI, Sudol M (1995) The WW domain of YES-associated protein binds a proline rich ligand that differs from the consensus established for SRC homology 3- binding modules. Proceedings of the National Academy of Sciences of the United States of America 92: 7819-7823 doi: 10.1073/pnas.92.17.7819

Chen X, Zhang B, Fischer JA (2002) A specific protein substrate for a deubiquitinating enzyme: Liquid facets is the substrate of fat facets. Genes & Development 16: 289-294 doi: 10.1101/gad.961502

Chu X-L, Feng M-G, Ying S-H (2015) Qualitative ubiquitome unveils the potential significances of protein lysine ubiquitination in hyphal growth of *Aspergillus nidulans*. Current Genetics: 1-11 doi: 10.1007/s00294-015-0517-7

Chung D, Barker BM, Carey CC, Merriman B, Werner ER, Lechner BE, Dhingra S, Cheng C, Xu W, Blosser SJ, Morohashi K, Mazurie A, Mitchell TK, Haas H, Mitchell AP, Cramer RA (2014) ChIP-seq and in vivo transcriptome analyses of the Aspergillus fumigatus SREBP SrbA reveals a new regulator of the fungal hypoxia response and virulence. PLoS pathogens 10: e1004487 doi: 10.1371/journal.ppat.1004487

Ciriacy M (1977) Isolation and characterization of yeast mutants defective in intermediary carbon metabolism and in carbon catabolite repression. Molecular & General Genetics 154: 213-220 doi: 10.1007/bf00330840

Clutterb.Aj (1969) A mutational analysis of conidial development in *Aspergillus nidulans*. Genetics 63: 317-& doi:

Cove DJ (1966) Induction and repression of nitrate reductase in fungus *Aspergillus nidulans* Biochimica Et Biophysica Acta, pp. 51-56.

Cubero B, Gomez D, Scazzocchio C (2000) Metabolite repression and inducer exclusion in the proline utilization gene cluster of Aspergillus nidulans. Journal of Bacteriology 182: 233-235 doi:

Cziferszky A, Mach RL, Kubicek CP (2002) Phosphorylation positively regulates DNA binding of the carbon catabolite repressor Cre1 of Hypocrea jecorina (Trichoderma reesei). Journal of Biological Chemistry 277: 14688-14694 doi: 10.1074/jbc.M200744200

Davis MA, Kelly JM, Hynes MJ (1993) Fungal catabolic gene regulation: molecular genetic analysis of the *amdS* gene of *Aspergillus nidulans*. Genetica 90: 133-145 doi: 10.1007/bf01435035

de Assis LJ, Ries LNA, Savoldi M, dos Reis TF, Brown NA, Goldman GH (2015) Aspergillus nidulans protein kinase A plays an important role in cellulase production. Biotechnology for Biofuels 810.1186/s13068-015-0401-1

de la Serna I, Ng D, Tyler BM (1999) Carbon regulation of ribosomal genes in Neurospora crassa occurs by a mechanism which does not require Cre-1, the homologue of the Aspergillus carbon catabolite repressor, CreA. Fungal Genetics and Biology 26: 253-269 doi: 10.1006/fgbi.1999.1121

Denton JA, Kelly JM (2011) Disruption of Trichoderma reesei cre2, encoding an ubiquitin C-terminal hydrolase, results in increased cellulase activity. Bmc Biotechnology 1110.1186/1472-6750-11-103

DeRisi JL, Iyer VR, Brown PO (1997) Exploring the metabolic and genetic control of gene expression on a genomic scale. Science 278: 680-686 doi: 10.1126/science.278.5338.680

DeVit MJ, Johnston M (1999) The nuclear exportin Msn5 is required for nuclear export of the Mig1 glucose repressor of Saccharomyces cerevisiae. Current Biology 9: 1231-1241 doi: 10.1016/s0960-9822(99)80503-x

DeVit MJ, Waddle JA, Johnston M (1997) Regulated nuclear translocation of the Mig1 glucose repressor. Molecular Biology of the Cell 8: 1603-1618 doi:

dos Reis TF, Menino JF, Bom VLP, Brown NA, Colabardini AC, Savoldi M, Goldman MHS, Rodrigues F, Goldman GH (2013) Identification of Glucose Transporters in Aspergillus nidulans. Plos One 810.1371/journal.pone.0081412

Dowzer CEA, Kelly JM (1989) Cloning of the *creA* gene from *Aspergillus nidulans*- a gene involved in carbon catabolite repression. Current Genetics 15: 457-459 doi: 10.1007/bf00376804

Dowzer CEA, Kelly JM (1991) Analysis of the *creA* gene, a regulator of carbon catabolite repression in *Aspergillus nidulans*. Molecular and Cellular Biology 11: 5701-5709 doi: 10.1128/MCB.11.11.5701

Drysdale MR, Kolze SE, Kelly JM (1993) The *Aspergillus niger* carbon catabolite repressor encoding gene, *creA*. Gene 130: 241-245 doi: 10.1016/0378-1119(93)90425-3

Dubacq C, Chevalier A, Mann C (2004) The protein kinase snf1 is required for tolerance to the ribonucleotide reductase inhibitor hydroxyurea. Molecular and Cellular Biology 24: 2560-2572 doi: 10.1128/mcb.24.6.2560-2572.2004

Edited by Brambl RM, G.A (2004) The Mycota: A comprehensive treatise on fungi as experimental systems for basic and applied research. III

Emre NCT, Ingvarsdottir K, Wyce A, Wood A, Krogan NJ, Henry KW, Li KQ, Marmorstein R, Greenblatt JF, Shilatifard A, Berger SL (2005) Maintenance of low histone ubiquitylation by Ubp10 correlates with telomere-proximal Sir2 association and gene silencing. Molecular Cell 17: 585-594 doi: 10.1016/j.molcel.2005.01.007

Entian KD, Frohlich KU (1984) Saccharomyces cerevisiae mutants provide evidence of hexokinase PII as a bifunctional enzyme with catalytic and regulatory doimains for triggering carbon catabolite repression. Journal of Bacteriology 158: 29-35 doi:

Entian KD, Zimmermann FK (1980) Glycolytic enzymes and intermediates in carbon catabolite repression mutants of *Saccharamyces cerevisiae*. Molecular & General Genetics 177: 345-350 doi: 10.1007/bf00267449

Entian KD, Zimmermann FK (1982) New genes involved in carbon catabolite repression and derepression in the yeast *Saccharomyces cerevisiae*. Journal of Bacteriology 151: 1123-1128 doi:

Erickson JR, Johnston M (1993) Genetic and molecular characterization of Gal83 - its interaction and similarities with other genes involved in glucose repression in *Saccharomyces cerevisiae*. Genetics 135: 655-664 doi:

Espeso EA, Fernandezcanon JM, Penalva MA (1995) Carbon regulation of penicillin biosynthesis in *Aspergillus nidulans*- a minor effect of mutations in *creB* and *creC*. Fems Microbiology Letters 126: 63-67 doi: 10.1111/j.1574-6968.1995.tb07391.x

Espeso EA, Tilburn J, Arst HN, Penalva MA (1993) pH regulation is a major determinanat in expression of a fungal penicillin biosynthetic gene. Embo Journal 12: 3947-3956 doi:

Estruch F, Treitel MA, Yang XL, Carlson M (1992) N-terminal mutations modulate yeast Snf1 protein kinase function. Genetics 132: 639-650 doi:

Faast R, Thonglairoam V, Schulz TC, Beall J, Wells JRE, Taylor H, Matthaei K, Rathjen PD, Tremethick DJ, Lyons I (2001) Histone variant H2A.Z is required for early mammalian development. Current Biology 11: 1183-1187 doi: 10.1016/s0960-9822(01)00329-3

Fan X, Lamarre-Vincent N, Wang Q, Struhl K (2008) Extensive chromatin fragmentation improves enrichment of protein binding sites in chromatin immunoprecipitation experiments. Nucleic Acids Res 36: e125 doi: 10.1093/nar/gkn535

Flipphi M, van de Vondervoort PJI, Ruijter GJG, Visser J, Arst HN, Felenbok A (2003) Onset of carbon catabolite repression in *Aspergillus nidulans* - Parallel involvement of hexokinase and glucokinase in sugar signaling. Journal of Biological Chemistry 278: 11849-11857 doi: 10.1074/jbc.M209443200

Forment JV, Flipphi M, Ramon D, Ventura L, MacCabe AP (2006) Identification of the mstE gene encoding a glucose-inducible, low affinity glucose transporter in Aspergillus nidulans. Journal of Biological Chemistry 281: 8339-8346 doi: 10.1074/jbc.M508198200

Forment JV, Flipphi M, Ventura L, Gonzalez R, Ramon D, MacCabe AP (2014) High-Affinity Glucose Transport in *Aspergillus nidulans* Is Mediated by the Products of Two Related but Differentially Expressed Genes. Plos One 910.1371/journal.pone.0094662

Gancedo JM (1998) Yeast carbon catabolite repression. Microbiology and Molecular Biology Reviews 62: 334-361 doi:

Gancedo JM (2008) The early steps of glucose signalling in yeast. Fems Microbiology Reviews 32: 673-704 doi: 10.1111/j.1574-6976.2008.00117.x

Garcia I, Gonzalez R, Gomez D, Scazzocchio C (2004) Chromatin Rearrangements in the *prnD-prnB* bidirectional promoter: Dependence on transcription factors. Eukaryotic Cell 3: 144-156 doi: 10.1128/ec.3.1.144-156.2004

Garcia I, Mathieu M, Nikolaev I, Felenbok B, Scazzocchio C (2008) Roles of the *Aspergillus nidulans* homologues of Tup1 and Ssn6 in chromatin structure and cell viability. Fems Microbiology Letters 289: 146-154 doi: 10.1111/j.1574-6968.2008.01379.x

Georgakopoulos P, Lockington RA, Kelly JM (2012) SAGA Complex Components and Acetate Repression in *Aspergillus nidulans*. G3-Genes Genomes Genetics 2: 1357-1367 doi: 10.1534/g3.112.003913

Georgakopoulos P, Lockington RA, Kelly JM (2013) The Spt-Ada-Gcn5 Acetyltransferase (SAGA) Complex in *Aspergillus nidulans*. Plos One 810.1371/journal.pone.0065221

Goldberg AL (2003) Protein degradation and protection against misfolded or damaged proteins. Nature 426: 895-899 doi: 10.1038/nature02263

Goldman GH, Kafer E (2004) *Aspergillus nidulans* as a model system to characterize the DNA damage response in eukaryotes. Fungal Genetics and Biology 41: 428-442 doi: 10.1016/j.fgb.2003.12.001

Gromoller A, Lehming N (2000) Srb7p is a physical and physiological target of Tup1p. Embo Journal 19: 6845-6852 doi: 10.1093/emboj/19.24.6845

Han SJ, Lee JS, Kang JS, Kim YJ (2001) Med9/Cse2 and Gal11 modules are required for transcriptional repression of distinct group of genes. Journal of Biological Chemistry 276: 37020-37026 doi: 10.1074/jbc.M105596200

Hedbacker K, Hong SP, Carlson M (2004) Pak1 protein kinase regulates activation and nuclear localization of Snf1-Gal83 protein kinase. Molecular and Cellular Biology 24: 8255-8263 doi: 10.1128/mcb.24.18.8255-8263.2004

Herrero P, Martinez-Campa C, Moreno F (1998) The hexokinase 2 protein participates in regulatory DNA-protein complexes necessary for glucose repression of the SUC2 gene in Saccharomyces cerevisiae. Febs Letters 434: 71-76 doi: 10.1016/s0014-5793(98)00872-2

Hicke L, Dunn R (2003) Regulation of membrane protein transport by ubiquitin and ubiquitin-binding proteins. Annual Review of Cell and Developmental Biology 19: 141-172 doi: 10.1146/annurev.cellbio.19.110701.154617

Hicks J, Lockington RA, Strauss J, Dieringer D, Kubicek CP, Kelly J, Keller N (2001) RcoA has pleiotropic effects on *Aspergillus nidulans* cellular development. Molecular Microbiology 39: 1482-1493 doi: 10.1046/j.1365-2958.2001.02332.x

Hicks JK, Yu JH, Keller NP, Adams TH (1997) *Aspergillus* sporulation and mycotoxin production both require inactivation of the FadA G alpha protein-dependent signaling pathway. Embo Journal 16: 4916-4923 doi: 10.1093/emboj/16.16.4916

Hochstrasser M (2009) Origin and function of ubiquitin-like proteins. Nature 458: 422-429 doi: 10.1038/nature07958

Hu Z, Nehlin JO, Ronne H, Michels CA (1995) Mig1 dependent and Mig1 independent glucose regulation of *mal* gene expression in *Saccharomyces cerevisiae*. Current Genetics 28: 258-266 doi: 10.1007/bf00309785

Hunter AJ, Morris TA, Jin B, Saint CP, Kelly JM (2013) Deletion of *creB* in *Aspergillus oryzae* Increases Secreted Hydrolytic Enzyme Activity. Applied and Environmental Microbiology 79: 5480-5487 doi: 10.1128/aem.01406-13

Hynes MJ (1970) Induction and repression of amidase enzymes in *Aspergillus nidulans*. Journal of Bacteriology 103: 482-& doi:

Hynes MJ, Kelly JM (1977) Pleiotropic mutants of *Aspergillus nidulans* altered in carbon metabolism. Molecular & General Genetics 150: 193-204 doi: 10.1007/bf00695399

Ichinose S, Tanaka M, Shintani T, Gomi K (2014) Improved alpha-amylase production by *Aspergillus oryzae* after a double deletion of genes involved in carbon catabolite repression. Applied Microbiology and Biotechnology 98: 335-343 doi: 10.1007/s00253-013-5353-4

Ilmen M, Thrane C, Penttila M (1996) The glucose repressor gene *cre1* of *Trichoderma*: Isolation and expression of a full-length and a truncated mutant form. Molecular & General Genetics 251: 451-460 doi: 10.1007/bf02172374

Jabet C, Sprague ER, VanDemark AP, Wolberger C (2000) Characterization of the N-terminal domain of the yeast transcriptional repressor Tup1 - Proposal for an association model of the repressor complex Tup1 center dot Ssn6. Journal of Biological Chemistry 275: 9011-9018 doi: 10.1074/jbc.275.12.9011

Jekosch K, Kuck U (2000) Loss of glucose repression in an Acremonium chrysogenum beta-lactam producer strain and its restoration by multiple copies of the cre1 gene. Applied Microbiology and Biotechnology 54: 556-563 doi:

Jiang R, Carlson M (1996) Glucose regulates protein interactions within the yeast SNF1 protein kinase complex. Genes & Development 10: 3105-3115 doi: 10.1101/gad.10.24.3105

Jiang R, Carlson M (1997) The Snf1 protein kinase and its activating subunit, Snf4, interact with distinct domains of the Sip1/Sip2/Ga183 component in the kinase complex. Molecular and Cellular Biology 17: 2099-2106 doi:

Kafer E (1958) An 8-chromosome map of *Aspergillus nidulans*. Advances in Genetics Incorporating Molecular Genetic Medicine 9: 105-145 doi: 10.1016/s0065-2660(08)60161-3

Kafer E (1961) The processes of spontaneous recombination in vegetative nuclei of *Aspergillus nidulans*. Genetics 46

Kaiser P, Huang L (2005) Global approaches to understanding ubiquitination. Genome Biology 610.1186/gb-2005-6-10-233

Kamlangdee N (2008) Indentifying target proteins of CreB deubiquitination enzyme in the fungus *Aspergillus nidulans*. *PhD thesis*, The University of Adelaide.

Kaniak A, Xue ZX, Macool D, Kim JH, Johnston M (2004) Regulatory network connecting two glucose signal transduction pathways in *Saccharomyces cerevisiae*. Eukaryotic Cell 3: 221-231 doi: 10.1128/ec.3.1.221-231.2004

Kato M, Sekine K, Tsukagoshi N (1996) Sequence-specific binding sites in the Taka-amylase A G2 promoter for the CreA repressor mediating carbon catabolite repression. Bioscience Biotechnology and Biochemistry 60: 1776-1779 doi:

Katz ME, Flynn PK, vanKuyk PA, Cheetham BF (1996) Mutations affecting extracellular protease production in the filamentous fungus Aspergillus nidulans. Molecular & General Genetics 250: 715-724 doi: 10.1007/bf02172983

Katz ME, Masoumi A, Burrows SR, Shirtliff CG, Cheetham BF (2000) The Aspergillus midulans xprF gene encodes a hexokinase-like protein involved in the regulation of extracellular proteases. Genetics 156: 1559-1571 doi:

Kayikci O, Nielsen J (2015) Glucose repression in *Saccharomyces cerevisiae*. Fems Yeast Research 15: OV68-OV68 doi: doi: 10.1093/femsyr/fov068

Keleher CA, Redd MJ, Schultz J, Carlson M, Johnson AD (1992) Ssn6-Tup1 is a general repressor of transcription in yeast. Cell 68: 709-719 doi: 10.1016/0092-8674(92)90146-4

Keller N (2006) Aspergillus nidulans: a model for elucidation of Aspergillus fumigatus secondary metabolism. Molecular Principles of Fungal Pathogenesis-Print: 235-243 doi:

Kelly JM (1980) Pleiotropic mutants of *Aspergillus nidulans* affected in carbon metabolism. *PhD Thesis*, The University of Melbourne.

Kelly JM (2004) The regulation of carbon metabolism in filamentous fungi. In: Esser K (ed) Biochemistry and Molecular Biology, , pp. 385-401.

Kelly JM, Hynes MJ (1977) Increased and decreased sensitivity to carbon catabolite repression of enzymes of acetate metabolism in mutants of *Aspergillus nidulans*. Molecular & General Genetics 156: 87-92 doi: 10.1007/bf00272256

Kelly JM, Katz ME (2010) Glucose. In: Borkovich KA, Ebbole DJ (eds) Cellular and molecular biology of Filamentous Fungi

pp. 291-311.

Kinoshita E, Kinoshita-Kikuta E, Koike T (2009) Separation and detection of large phosphoproteins using Phos-tag SDS-PAGE. Nature Protocols 4: 1513-1521 doi: 10.1038/nprot.2009.154

Klein CJL, Olsson L, Nielsen J (1998) Glucose control in *Saccharomyces cerevisiae*: The role of MIG1 in metabolic functions. Microbiology-Uk 144: 13-24 doi:

Kraft C, Peter M, Hofmann K (2010) Selective autophagy: ubiquitin-mediated recognition and beyond. Nature Cell Biology 12: 836-841 doi:

Kruckeberg AL (1996) The hexose transporter family of Saccharomyces cerevisiae. Archives of Microbiology 166: 283-292 doi: 10.1007/s002030050385

Kuchin S, Treich I, Carlson M (2000) A regulatory shortcut between the Snf1 protein kinase and RNA polymerase II holoenzyme. Proceedings of the National Academy of Sciences of the United States of America 97: 7916-7920 doi: 10.1073/pnas.140109897

Kulmburg P, Mathieu M, Dowzer C, Kelly J, Felenbok B (1993) Specific binding sites in the *alcR* and *alcA* promoters of the ethanol regulon for the CreA repressor mediating carbon catabolite repression in *Aspergillus nidulans* Molecular Microbiology 7: 847-857 doi: 10.1111/j.1365-2958.1993.tb01175.x

Langmead B, Trapnell C, Pop M, Salzberg SL (2009) Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10: R25 doi: 10.1186/gb-2009-10-3-r25

Leech A, Nath N, McCartney RR, Schmidt MC (2003) Isolation of mutations in the catalytic domain of the Snf1 kinase that render its activity independent of the Snf4 subunit. Eukaryotic Cell 2: 265-273 doi: 10.1128/ec.2.2.265-273.2003

Lichius A, Seidl-Seiboth V, Seiboth B, Kubicek CP (2014) Nucleo-cytoplasmic shuttling dynamics of the transcriptional regulators XYR1 and CRE1 under conditions of cellulase and xylanase gene expression in Trichoderma reesei. Molecular Microbiology 94: 1162-1178 doi: 10.1111/mmi.12824

Liu XW, Li B, Gorovsky MA (1996) Essential and nonessential histone H2A variants in *Tetrahymena thermophila*. Molecular and Cellular Biology 16: 4305-4311 doi: 10.1128/MCB.16.8.4305

Lockington RA, Kelly JM (2001) Carbon catabolite repression in *Aspergillus nidulans* involves deubiquitination. Molecular Microbiology 40: 1311-1321 doi: 10.1046/j.1365-2958.2001.02474.x

Lockington RA, Kelly JM (2002) The WD40-repeat protein CreC interacts with and stabilizes the deubiquitinating enzyme CreB in vivo in *Aspergillus nidulans*. Molecular Microbiology 43: 1173-1182 doi: 10.1046/j.1365-2958.2002.02811.x

Lockington RA, Rodbourn L, Barnett S, Carter CJ, Kelly JA (2002) Regulation by carbon and nitrogen sources of a family of cellulases in *Aspergillus nidulans*. Fungal Genetics and Biology 37: 190-196 doi: 10.1016/s1087-1845(02)00504-2

Ludin K, Jiang R, Carlson M (1998) Glucose-regulated interaction of a regulatory subunit of protein phosphatase 1 with the Snf1 protein kinase in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America 95: 6245-6250 doi: 10.1073/pnas.95.11.6245

Lundin M, Nehlin JO, Ronne H (1994) Importance of a flanking AT-rich region in target site recognition by the GC box binding zinc finger protein Mig1. Molecular and Cellular Biology 14: 1979-1985 doi:

Lutfiyya LL, Iyer VR, DeRisi J, DeVit MJ, Brown PO, Johnston M (1998) Characterization of three related glucose repressors and genes they regulate in Saccharomyces cerevisiae. Genetics 150: 1377-1391 doi:

Lutfiyya LL, Johnston M (1996) Two zinc-finger-containing repressors are responsible for glucose repression of SUC2 expression. Molecular and Cellular Biology 16: 4790-4797 doi:

Ma H, Bloom LM, Walsh CT, Botstein D (1989) The residual enzymatic phosphorylation activity of hexokinase II mutants is correlated with glucose repression in *Saccharomyces cerevisiae*. Molecular and Cellular Biology 9: 5643-5649 doi:

Ma W, Wong WH (2011) The analysis of ChIP-Seq data. Methods in enzymology 497: 51-73 doi: 10.1016/b978-0-12-385075-1.00003-2

MacCabe AP, Miro P, Ventura L, Ramon D (2003) Glucose uptake in germinating Aspergillus nidulans conidia: involvement of the creA and sorA genes. Microbiology-Sgm 149: 2129-2136 doi: 10.1099/mic.0.26349-0

Mach-Aigner AR, Pucher ME, Steiger MG, Bauer GE, Preis SJ, Mach RL (2008) Transcriptional Regulation of xyr1, Encoding the Main Regulator of the Xylanolytic and Cellulolytic Enzyme System in Hypocrea jecorina. Applied and Environmental Microbiology 74: 6554-6562 doi: 10.1128/aem.01143-08

Malave TM, Dent SYR (2006) Transcriptional repression by Tup1-Ssn6. Biochemistry and Cell Biology-Biochimie Et Biologie Cellulaire 84: 437-443 doi: 10.1139/o06-73

Martinelli JRK (1994) *Aspergillus* : 50 years on. 29: 33-58 doi:

Mathieu M, Nikolaev I, Scazzocchio C, Felenbok B (2005) Patterns of nucleosomal organization in the *alc* regulon of *Aspergillus nidulans*: roles of the AlcR transcriptional activator and the CreA global repressor. Molecular Microbiology 56: 535-548 doi: 10.1111/j.1365-2958.2005.04559.x

Mayer FV, Heath R, Underwood E, Sanders MJ, Carmena D, McCartney RR, Leiper FC, Xiao B, Jing C, Walker PA, Haire LF, Ogrodowicz R, Martin SR, Schmidt MC, Gamblin SJ, Carling D (2011) ADP Regulates SNF1, the Saccharomyces cerevisiae Homolog of AMP-Activated Protein Kinase. Cell Metabolism 14: 707-714 doi: 10.1016/j.cmet.2011.09.009

Mercado JJ, Vincent O, Gancedo JM (1991) Regions in the promoter of the yeast fbp1 gene implicated in catabolite repression may bind the product of the regulatory gene mig1. Febs Letters 291: 97-100 doi: 10.1016/0014-5793(91)81112-l

Mogensen J, Nielsen HB, Hofmann G, Nielsen J (2006) Transcription analysis using high-density micro-arrays of Aspergillus nidulans wild-type and creA mutant during growth on glucose or ethanol. Fungal Genetics and Biology 43: 593-603 doi: 10.1016/j.fgb.2006.03.003

Muratani M, Tansey WR (2003) How the ubiquitin-proteasome system controls transcription. Nature Reviews Molecular Cell Biology 4: 192-201 doi: 10.1038/nrm1049

Mylin LM, Bushman VL, Long RM, Yu X, Lebo CM, Blank TE, Hopper JE (1994) Sip1 is a catabolite repression specific negative regulator of *gal* gene expression. Genetics 137: 689-700 doi:

Nasmith CG, Walkowiak S, Wang L, Leung WW, Gong Y, Johnston A, Harris LJ, Guttman DS, Subramaniam R (2011) Tri6 is a global transcription regulator in the phytopathogen Fusarium graminearum. PLoS pathogens 7: e1002266 doi: 10.1371/journal.ppat.1002266

Neer EJ, Schmidt CJ, Nambudripad R, Smith TF (1994) The ancient regulatory protein family of WD- repeat proteins. Nature 371: 297-300 doi: 10.1038/371297a0

Nehlin JO, Carlberg M, Ronne H (1991) Control of yeast *gal* genes by Mig1 repressor- a transcriptional cascade in the glucose response. Embo Journal 10: 3373-3377 doi:

Nehlin JO, Ronne H (1990) Yeast Mig1 repressor is related to the mammalian early growth response and wilms tumor finger proteins. Embo Journal 9: 2891-2898 doi:

Neigeborn L, Carlson M (1984) Genes affecting the regulation of *suc2* gene expression by glucose repression in *Saccharomyces cerevisiae*. Genetics 108: 845-858 doi:

Neigeborn L, Rubin K, Carlson M (1986) Suppressors of *snf2* mutations restore invertase derepression and cause temperature sensitive lethality in yeast. Genetics 112: 741-753 doi:

Nguyen LK, Kolch W, Kholodenko BN (2013) When ubiquitination meets phosphorylation: a systems biology perspective of EGFR/MAPK signalling. Cell Communication and Signaling 1110.1186/1478-811x-11-52

Nikko E, Andre B (2007) Evidence for a direct role of the Doa4 deubiquitinating enzyme in protein sorting into the MVB pathway. Traffic 8: 566-581 doi: 10.1111/j.1600-0854.2007.00553.x

Oakley BR, Morris NR (1981) A beta-tubulin mutation in *Aspergillus nidulans* that blocks microtubule function without blocking assembly. Cell 24: 837-845 doi: 10.1016/0092-8674(81)90109-4

Osmani SA, Engle DB, Doonan JH, Morris NR (1988a) Spindle formation and chromatin condensation in cells blocled at interphase by mutation of a negative cell-cycle control gene. Cell 52: 241-251 doi: 10.1016/0092-8674(88)90513-2

Osmani SA, Mirabito PM (2004) The early impact of genetics on our understanding of cell cycle regulation in *Aspergillus nidulans*. Fungal Genetics and Biology 41: 401-410 doi: 10.1016/j.fgb.2003.11.009

Osmani SA, Pu RT, Morris NR (1988b) Mitotic induction and maintenance by overexpression of a G2-specific gene that encodes a potential protein kinase. Cell 53: 237-244 doi: 10.1016/0092-8674(88)90385-6

Ostling J, Carlberg M, Ronne H (1996) Functional domains in the Mig1 repressor. Molecular and Cellular Biology 16: 753-761 doi:

Ozcan S, Dover J, Johnston M (1998) Glucose sensing and signaling by two glucose receptors in the yeast Saccharomyces cerevisiae. Embo Journal 17: 2566-2573 doi: 10.1093/emboj/17.9.2566

Ozcan S, Dover J, Rosenwald AG, Wolfl S, Johnston M (1996a) Two glucose transporters in Saccharomyces cerevisiae are glucose sensors that generate a signal for induction of gene expression. Proceedings of the National Academy of Sciences of the United States of America 93: 12428-12432 doi: 10.1073/pnas.93.22.12428

Ozcan S, Leong T, Johnston M (1996b) Rgt1p of Saccharomyces cerevisiae, a key regulator of glucose-induced genes, is both an activator and a repressor of transcription. Molecular and Cellular Biology 16: 6419-6426 doi:

Panozzo C, Cornillot E, Felenbok B (1998) The CreA repressor is the sole DNA-binding protein responsible for carbon catabolite repression of the alcA gene in Aspergillus nidulans via its binding to a couple of specific sites. Journal of Biological Chemistry 273: 6367-6372 doi: 10.1074/jbc.273.11.6367

Papamichos-Chronakis M, Gligoris T, Tzamarias D (2004) The Snf1 kinase controls glucose repression in yeast by modulating interactions between the Mig1 repressor and the Cyc8-Tupl co-repressor. Embo Reports 5: 368-372 doi: 10.1038/sj.embor.7400120

Papamichos-Chronakis M, Petrakis T, Ktistaki E, Topalidou I, Tzamarias D (2002) Cti6, a PHD domain protein, bridges the Cyc8-Tup1 corepressor and the SAGA coactivator to overcome repression at GAL1. Molecular Cell 9: 1297-1305 doi: 10.1016/s1097-2765(02)00545-2

Park SH, Koh SS, Chun JH, Hwang HJ, Kang HS (1999) Nrg1 is a transcriptional repressor for glucose repression of STA1 gene expression in Saccharomyces cerevisiae. Molecular and Cellular Biology 19: 2044-2050 doi:

Pateman JA, Rever BM, Cove DJ (1967) Genetic and biochemical studies of nitrate reduction in *Aspergillus nidulans*. Biochemical Journal 104: 103-& doi: 10.1042/bj1040103

Penalva MA, Espeso E, Perezesteban B, Orejas M, Fernandezcanon JM, Martinezblanco H (1993) Expression of fungal genes involved in penicillin biosynthesis. World Journal of Microbiology & Biotechnology 9: 461-467 doi: 10.1007/bf00328034

Penalva MA, Tilburn J, Bignell E, Arst HN (2008) Ambient pH gene regulation in fungi: making connections. Trends in Microbiology 16: 291-300 doi: 10.1016/j.tim.2008.03.006

Portnoy T, Margeot A, Linke R, Atanasova L, Fekete E, Sandor E, Hartl L, Karaffa L, Druzhinina IS, Seiboth B, Le Crom S, Kubicek CP (2011a) The CRE1 carbon catabolite repressor of the fungus *Trichoderma reesei*: a master regulator of carbon assimilation. Bmc Genomics 1210.1186/1471-2164-12-269

Portnoy T, Margeot A, Seidl-Seiboth V, Le Crom S, Ben Chaabane F, Linke R, Seiboth B, Kubicek CP (2011b) Differential Regulation of the Cellulase Transcription Factors XYR1, ACE2, and ACE1 in Trichoderma reesei Strains Producing High and Low Levels of Cellulase. Eukaryotic Cell 10: 262-271 doi: 10.1128/ec.00208-10

Rechsteiner M, Rogers SW (1996) PEST sequences and regulation by proteolysis. Trends in Biochemical Sciences 21: 267-271 doi: 10.1016/s0968-0004(96)10031-1

Reifenberger E, Boles E, Ciriacy M (1997) Kinetic characterization of individual hexose transporters of Saccharomyces cerevisiae and their relation to the triggering mechanisms of glucose repression. European Journal of Biochemistry 245: 324-333 doi: 10.1111/j.1432-1033.1997.00324.x

Reyes-Dominguez Y, Narendja F, Berger H, Gallmetzer A, Fernandez-Martin R, Garcia I, Scazzocchio C, Strauss J (2008) Nucleosome positioning and histone H3 acetylation are independent processes in the *Aspergillus nidulans prnD-prnB* bidirectional promoter. Eukaryotic Cell 7: 656-663 doi: 10.1128/ec.00184-07

Reyes-Turcu FE, Ventii KH, Wilkinson KD (2009) Regulation and Cellular Roles of Ubiquitin-Specific Deubiquitinating Enzymes. Annual Review of Biochemistry 78: 363-397 doi: 10.1146/annurev.biochem.78.082307.091526

Richter C, West M, Odorizzi G (2007) Dual mechanisms specify Doa4-mediated deubiquitination at multivesicular bodies. Embo Journal 26: 2454-2464 doi: 10.1038/sj.emboj.7601692

Ridgway P, Brown KD, Rangasamy D, Svensson U, Tremethick DJ (2004) Unique residues on the H2A.Z containing nucleosome surface are important for *Xenopus laevis* development. Journal of Biological Chemistry 279: 43815-43820 doi: 10.1074/jbc.M408409200

Ries L, Belshaw NJ, Ilmen M, Penttila ME, Alapuranen M, Archer DB (2014) The role of CRE1 in nucleosome positioning within the *cbh1* promoter and coding regions of *Trichoderma reesei*. Applied Microbiology and Biotechnology 98: 749-762 doi: 10.1007/s00253-013-5354-3

Ries LNA, Beattie SR, Espeso EA, Cramer RA, Goldman GH (2016) Diverse Regulation of the CreA Carbon Catabolite Repressor in Aspergillus nidulans. Genetics 10.1534/genetics.116.187872

Rodriguez A, de la Cera T, Herrero P, Moreno F (2001) The hexokinase 2 protein regulates the expression of the GLK1, HXK1 and HXK2 genes of Saccharomyces cerevisiae. Biochemical Journal 355: 625-631 doi:

Rolland F, de Winde JH, Lemaire K, Boles E, Thevelein JM, Winderickx J (2000) Glucose-induced cAMP signalling in yeast requires both a G-protein coupled receptor system for extracellular glucose detection and a separable hexose kinase-dependent sensing process. Molecular Microbiology 38: 348-358 doi: 10.1046/j.1365-2958.2000.02125.x

Rolland F, Winderickx J, Thevelein JM (2002) Glucose-sensing and -signalling mechanisms in yeast. Fems Yeast Research 2: 183-201 doi: 10.1111/j.1567-1364.2002.tb00084.x

Romano AH, Kornberg HL (1968) Regulation of sugar utilization by *Aspergillus nidulans*. Biochimica Et Biophysica Acta 158: 491-& doi: 10.1016/0304-4165(68)90312-7

Romano AH, Kornberg HL (1969) Regulation of sugar uptake by *Aspergillus nidulans*. Proceedings of the Royal Society of London Series B-Biological Sciences 173: 475-& doi: 10.1098/rspb.1969.0072

Roper JA, Kafer E (1957) Acriflavin resistant mutants of *Aspergillus nidulans*. Journal of General Microbiology 16: 660-& doi:

Rose M, Albig W, Entian KD (1991) Glucose repression in Saccharomyces cerevisiae is directly associated with hexose phosphorylation by hexokinase-PI and hexokinase-PII. European Journal of Biochemistry 199: 511-518 doi: 10.1111/j.1432-1033.1991.tb16149.x

Rotin D, Kumar S (2009) Physiological functions of the HECT family of ubiquitin ligases. Nature Reviews Molecular Cell Biology 10: 398-409 doi: 10.1038/nrm2690

Roy P, Lockington RA, Kelly JM (2008) CreA-mediated repression in *Aspergillus nidulans* does not require transcriptional auto-regulation, regulated intracellular localisation or degradation of CreA. Fungal Genetics and Biology 45: 657-670 doi: 10.1016/j.fgb.2007.10.016

Ruijter GJG, Panneman H, vandenBroeck HC, Bennett JM, Visser J (1996) Characterisation of the Aspergillus nidulans frA1 mutant: Hexose phosphorylation and apparent lack of involvement of hexokinase in glucose repression. Fems Microbiology Letters 139: 223-228 doi: 10.1111/j.1574-6968.1996.tb08206.x

Ruijter GJG, Visser J (1997) Carbon repression in Aspergilli. Fems Microbiology Letters 151: 103-114 doi: 10.1111/j.1574-6968.1997.tb12557.x

Sabina J, Johnston M (2009) Asymmetric Signal Transduction through Paralogs That Comprise a Genetic Switch for Sugar Sensing in Saccharomyces cerevisiae. Journal of Biological Chemistry 284: 29635-29643 doi: 10.1074/jbc.M109.032102

Sakai A, Shimizu Y, Kondou S, Chibazakura T, Hishinuma F (1990) Structure and molecular analysis of *RGR1*, a gene required for glucose repression of *Saccharomyces cerevisiae*. Molecular and Cellular Biology 10: 4130-4138 doi:

Santangelo GM (2006) Glucose signaling in Saccharomyces cerevisiae. Microbiology and Molecular Biology Reviews 70: 253-+ doi: 10.1128/mmbr.70.1.253-282.2006

Sanz P, Alms GR, Haystead TAJ, Carlson M (2000) Regulatory interactions between the Reg1-Glc7 protein phosphatase and the Snf1 protein kinase. Molecular and Cellular Biology 20: 1321-1328 doi: 10.1128/mcb.20.4.1321-1328.2000

Scazzocchio C, Gavrias V, Cubero B, Panozzo C, Mathieu M, Felenbok B (1995) Carbon catabolite repression in *Aspergillus nidulans* - a review. Canadian Journal of Botany-Revue Canadienne De Botanique 73: S160-S166 doi:

Schmitz C, Kinner A, Kolling R (2005) The deubiquitinating enzyme Ubp1 affects sorting of the ATP-binding cassette-transporter Ste6 in the endocytic pathway. Mol Biol Cell 16: 1319-1329 doi: 10.1091/mbc.E04-05-0425

Schuller HJ, Entian KD (1991) Extragenic suppressor of yeast glucose derepression mutants leading to constitutive synthesis of several glucose repressible enzymes. Journal of Bacteriology 173: 2045-2052 doi:

Schultz J, Carlson M (1987) Molecular analysis of *ssn6*, a gene functionally related to the Snf1 protein kinase of *Saccharomyces cerevisiae*. Molecular and Cellular Biology 7: 3637-3645 doi:

Schultz J, Marshallcarlson L, Carlson M (1990) The N-terminal TPR region is the functional domain of Ssn6, a nuclear phosphoprotein of Saccharomyces cerevisiae. Molecular and Cellular Biology 10: 4744-4756 doi:

Screen S, Bailey A, Charnley K, Cooper R, Clarkson J (1997) Carbon regulation of the cuticle-degrading enzyme PR1 from Metarhizium anisopliae may involve a trans-acting DNA binding protein CRR1, a functional equivalent of the Aspergillus nidulans CREA protein. Current Genetics 31: 511-518 doi: 10.1007/s002940050238

Seiboth B, Karimi RA, Phatale PA, Linke R, Hartl L, Sauer DG, Smith KM, Baker SE, Freitag M, Kubicek CP (2012) The putative protein methyltransferase LAE1 controls cellulase gene expression in Trichoderma reesei. Mol Microbiol 84: 1150-1164 doi: 10.1111/j.1365-2958.2012.08083.x

Sevilla A, Binda O (2014) Post-translational modifications of the histone variant h2az. Stem Cell Research 12: 289-295 doi: 10.1016/j.scr.2013.11.004

Shilatifard A (2006) Chromatin modifications by methylation and ubiquitination: Implications in the regulation of gene expression. Annual Review of Biochemistry 75: 243-269 doi: 10.1146/annurev.biochem.75.103004.142422

Shroff RA, Lockington RA, Kelly JM (1996) Analysis of mutations in the *creA* gene involved in carbon catabolite repression in *Aspergillus nidulans*. Canadian Journal of Microbiology 42: 950-959 doi: 10.1139/m96-122

Shroff RA, Oconnor SM, Hynes MJ, Lockington RA, Kelly JM (1997) Null alleles of *creA*, the regulator of carbon catabolite repression in *Aspergillus nidulans*. Fungal Genetics and Biology 22: 28-38 doi: 10.1006/fgbi.1997.0989

Smith FC, Davies SP, Wilson WA, Carling D, Hardie DG (1999) The Snf1 kinase complex from Saccharomyces cerevisiae phosphorylates the transcriptional repressor protein Mig1p in vitro at four sites within or near regulatory domain 1. Febs Letters 453: 219-223 doi: 10.1016/s0014-5793(99)00725-5

Smith GM, Mileham KA, Cooke SE, Woolston SJ, George HK, Charles AD, Brammar WJ (1988) The *Escherichia coli* LexA repressor operator system works in Mammalian cells. Embo Journal 7: 3975-3982 doi:

Smith KM, Sancar G, Dekhang R, Sullivan CM, Li S, Tag AG, Sancar C, Bredeweg EL, Priest HD, McCormick RF, Thomas TL, Carrington JC, Stajich JE, Bell-Pedersen D, Brunner M, Freitag M (2010) Transcription factors in light and circadian clock signaling networks revealed by genomewide mapping of direct targets for neurospora white collar complex. Eukaryot Cell 9: 1549-1556 doi: 10.1128/ec.00154-10

Strauss J, Horvath HK, Abdallah BM, Kindermann J, Mach RL, Kubicek CP (1999) The function of CreA, the carbon catabolite repressor of *Aspergillus nidulans*, is regulated at the transcriptional and post-transcriptional level. Molecular Microbiology 32: 169-178 doi: 10.1046/j.1365-2958.1999.01341.x

Strauss J, Mach RL, Zeilinger S, Hartler G, Stoffler G, Wolschek M, Kubicek CP (1995) Cre1, the carbon catabolite repressor protein from *Trichoderma reesei*. Febs Letters 376: 103-107 doi: 10.1016/0014-5793(95)01255-5

Suzuki Y, Murray SL, Wong KH, Davis MA, Hynes MJ (2012) Reprogramming of carbon metabolism by the transcriptional activators AcuK and AcuM in Aspergillus nidulans. Molecular Microbiology 84: 942-964 doi: 10.1111/j.1365-2958.2012.08067.x

Szilagyi M, Miskei M, Karanyi Z, Lenkey B, Pocsi I, Emri T (2013) Transcriptome changes initiated by carbon starvation in Aspergillus nidulans. Microbiology-Sgm 159: 176-190 doi: 10.1099/mic.0.062935-0

Takashima S, Nakamura A, Hidaka M, Masaki H, Uozumi T (1998) Isolation of the creA gene from the cellulolytic fungus Humicola grisea and analysis of CreA binding sites upstream from the cellulase genes. Bioscience Biotechnology and Biochemistry 62: 2364-2370 doi: 10.1271/bbb.62.2364

Tanaka N, Ohuchi N, Mukai Y, Osaka Y, Ohtani Y, Tabuchi M, Bhuiyan MSA, Fukui H, Harashima S, Takegawa K (1998) Isolation and characterization of an invertase and its repressor genes from Schizosaccharomyces pombe. Biochemical and Biophysical Research Communications 245: 246-253 doi: 10.1006/bbrc.1998.8406

Thatcher TH, Gorovsky MA (1994) Phylogenetic analysis of the core histones H2A, H2B, H3, and H4. Nucleic Acids Research 22: 174-179 doi: 10.1093/nar/22.2.174

Thurtle DM, Rine J (2014) The molecular topography of silenced chromatin in Saccharomyces cerevisiae. Genes Dev 28: 245-258 doi: 10.1101/gad.230532.113

Timberlake WE (1990) Molecular genetics of *Aspergillus nidulans*. Annual Review of Genetics 24: 5-36 doi:

Todd RB, Davis MA, Hynes MJ (2007) Genetic manipulation of *Aspergillus nidulans*: meiotic progeny for genetic analysis and strain construction. Nature Protocols 2: 811-821 doi: 10.1038/nprot.2007.112

Todd RB, Lockington RA, Kelly JM (2000) The *Aspergillus nidulans creC* gene involved in carbon catabolite repression encodes a WD40 repeat protein. Molecular and General Genetics 263: 561-570 doi: 10.1007/s004380051202

Tonukari NJ, Scott-Craig JS, Walton JD (2003) Isolation of the carbon catabolite repressor (CREA) gene from the plant-pathogenic fungus Cochliobolus carbonum. DNA Sequence 14: 103-107 doi: 10.1080/1042517031000073727

Treitel MA, Carlson M (1995) Repression by Ssn6-Tup1 is directed by Mig1, a repressor activator protein. Proceedings of the National Academy of Sciences of the United States of America 92: 3132-3136 doi: 10.1073/pnas.92.8.3132

Treitel MA, Kuchin S, Carlson M (1998) Snf1 protein kinase regulates phosphorylation of the mig1 repressor in Saccharomyces cerevisiae. Molecular and Cellular Biology 18: 6273-6280 doi:

Trumbly RJ (1992) Glucose repression in the yeast Saccharomyces cerevisiae. Molecular Microbiology 6: 15-21 doi: 10.1111/j.1365-2958.1992.tb00832.x

Tu JL, Carlson M (1995) *REG1* binds to protein phosphatase type-1 and regulates glucose repression in *Saccharomyces cerevisiae*. Embo Journal 14: 5939-5946 doi:

Tudzynski B, Liu SJ, Kelly JM (2000) Carbon catabolite repression in plant pathogenic fungi: isolation and characterization of the Gibberella fujikuroi and Botrytis cinerea creA genes. Fems Microbiology Letters 184: 9-15 doi: 10.1111/j.1574-6968.2000.tb08982.x

Tzamarias D, Struhl K (1994) Functional dissection of the yeast Cyc8-Tup1 transcriptional co-repressor complex. Nature 369: 758-761 doi: 10.1038/369758a0

Vagnoli P, Coons DM, Bisson LF (1998) The C-terminal domain of Snf3p mediates glucose-responsive signal transduction in Saccharomyces cerevisiae. Fems Microbiology Letters 160: 31-36 doi: 10.1111/j.1574-6968.1998.tb12886.x

Varanasi US, Klis M, Mikesell PB, Trumbly RJ (1996) The Cyc8 (Ssn6)-Tup1 corepressor complex is composed of one Cyc8 and four Tup1 subunits. Molecular and Cellular Biology 16: 6707-6714 doi:

Vautard-Mey G, Cotton P, Fevre M (1999) Expression and compartmentation of the glucose repressor CRE1 from the phytopathogenic fungus Sclerotinia sclerotiorum. European Journal of Biochemistry 266: 252-259 doi: 10.1046/j.1432-1327.1999.00857.x

Vautard-Mey G, Fevre M (2000) Mutation of a putative AMPK phosphorylation site abolishes the repressor activity but not the nuclear targeting of the fungal glucose regulator CRE1. Current Genetics 37: 328-332 doi: 10.1007/s002940050535

Ventii KH, Wilkinson KD (2008) Protein partners of deubiquitinating enzymes. Biochemical Journal 414: 161-175 doi: 10.1042/bj20080798

Vincent O, Townley R, Kuchin S, Carlson M (2001) Subcellular localization of the Snf1 kinase is regulated by specific beta subunits and a novel glucose signaling mechanism. Genes & Development 15: 1104-1114 doi: 10.1101/gad.879301

Vyas VK, Kuchin S, Carlson M (2001) Interaction of the repressors Nrg1 and Nrg2 with the Snf1 protein kinase in Saccharomyces cerevisiae. Genetics 158: 563-572 doi:

Walton JD (1994) Deconstructing the Cell Wall. Plant Physiol 104: 1113-1118 doi:

Wei HJ, Vienken K, Weber R, Bunting S, Requena N, Fischer R (2004) A putative high affinity hexose transporter, hxtA, of Aspergillus nidulans is induced in vegetative hyphae upon starvation and in ascogenous hyphae during cleistothecium formation. Fungal Genetics and Biology 41: 148-156 doi: 10.1016/j.fgb.2003.10.006

Wieczorke R, Krampe S, Weierstall T, Freidel K, Hollenberg CP, Boles E (1999) Concurrent knock-out of at least 20 transporter genes is required to block uptake of hexoses in Saccharomyces cerevisiae. Febs Letters 464: 123-128 doi: 10.1016/s0014-5793(99)01698-1

Williams FE, Trumbly RJ (1990) Characterization of *tup1*, a mediator of glucose repression in *Saccharomyces cerevisiae*. Molecular and Cellular Biology 10: 6500-6511 doi:

Wong KH, Jin Y, Moqtaderi Z (2013) Multiplex Illumina sequencing using DNA barcoding. Current protocols in molecular biology / edited by Frederick M Ausubel [et al] Chapter 7: Unit 7 11 doi: 10.1002/0471142727.mb0711s101

Woods A, Munday MR, Scott J, Yang XL, Carlson M, Carling D (1994) Yeasst Snf1 is functionally related to mammalian AMP activated protein kinase and regulates acetyl coA carboxyase in vivo. Journal of Biological Chemistry 269: 19509-19515 doi:

Wu RS, Tsai S, Bonner WM (1982) Patterns of histone variant synthesis can distinguish G0 from G1 cells. Cell 31: 367-374 doi: 10.1016/0092-8674(82)90130-1

Yan N, Doelling JH, Falbel TG, Durski AM, Vierstra RD (2000) The ubiquitin-specific protease family from arabidopsis. AtUBP1 and 2 are required for the resistance to the amino acid analog canavanine. Plant Physiology 124: 1828-1843 doi: 10.1104/pp.124.4.1828

Yang XO, Hubbard EJA, Carlson M (1992) A protein kinase substrate identified by the 2 hybrid system. Science 257: 680-682 doi: 10.1126/science.1496382

Zhang J, Olsson L, Nielsen J (2010) The beta-subunits of the Snf1 kinase in Saccharomyces cerevisiae, Gal83 and Sip2, but not Sip1, are redundant in glucose derepression and regulation of sterol biosynthesis. Molecular Microbiology 77: 371-383 doi: 10.1111/j.1365-2958.2010.07209.x

Zhang Y, Liu T, Meyer CA, Eeckhoute J, Johnson DS, Bernstein BE, Nusbaum C, Myers RM, Brown M, Li W, Liu XS (2008) Model-based analysis of ChIP-Seq (MACS). Genome Biol 9: R137 doi: 10.1186/gb-2008-9-9-r137

Zhu XF, Zhang YQ, Bjornsdottir G, Liu ZL, Quan A, Costanzo M, Lopez MD, Westholm JO, Ronne H, Boone C, Gustafsson CM, Myers LC (2011) Histone modifications influence mediator interactions with chromatin. Nucleic Acids Research 39: 8342-8354 doi: 10.1093/nar/gkr551

Zimmermann FK, Kaufmann I, Rasenberger H, Haussmann P (1977) Genetics of carbon catabolite repression in Saccharomyces cerevisiae- genes involved in derepression process. Molecular & General Genetics 151: 95-103 doi: 10.1007/bf00446918

Zimmermann FK, Scheel I (1977) Mutants of *Saccharomyces cerevisiae* resistant to carbon catabolite repression. Molecular & General Genetics 154: 75-82 doi: 10.1007/bf00265579

Chapter 4

Supplementary Table 1

Unique Targets of S4 and T7

ANIA_5975	Putative-mannitol-1-phosphate-5-dehydrogenase-with-a-predicted-role-in-mannose/mannitol,-fructose,-and-sorbose/sorbitol-metabolism;-expression-upregulated-after-exposure-to-farnesol
ANIA_6808	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity,-transferase-activity,-transferring-acyl-groups-other-than-amino-acyl-groups,-zinc-ion-binding-activity-and-role-in-oxidation-reduction-process
ANIA_6169	Has-domain(s)-with-predicted-Rho-guanyl-nucleotide-exchange-factor-activity,-lipid-binding-activity,-role-in-regulation-of-Rho-protein-signal-transduction-and-intracellular-localization
ANIA_9451	Protein-of-unknown-function;-overexpression-confers-the-"fluffy"-phenotype;-transcript-is-induced-by-nitrate
ANIA_6278	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12540,-Aspergillus-versicolor-:-Aspve1_0041153,-Aspergillus-sydowii-:-Aspsy1_0058158-and-Aspergillus-terreus-NIH2624-:-ATET_01222
ANIA_6413	Ortholog-of-A.-nidulans-FGSC-A4-:-AN8328,-AN3395,-AN3241,-AN10369,-AN1930,-AN2386,-AN1738,-AN9266,-AN10886,-AN7232,-AN7406,-AN7774,-AN12202
ANIA_6749	Has-domain(s)-with-predicted-methyltransferase-activity-and-role-in-metabolic-process
ANIA_6499	Putative-malate-dehydrogenase-with-a-predicted-role-in-the-methylglyoxal-bypass-or-the-TCA-cycle;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_6390	Has-domain(s)-with-predicted-homogentisate-1,2-dioxygenase-activity-and-role-in-L-phenylalanine-catabolic-process,-oxidation-reduction-process,-tyrosine-metabolic-process
ANIA_6249	Putative-calcineurin-binding-protein,-calcipressin
ANIA_6062	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_5918	Putative-catalase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism
ANIA_6644	Putative-bifunctional-dethiobiotin-synthetase/adenosylmethionine-8-amino-7-oxononanoate-aminotransferase,-enzyme-of-the-biotin-biosynthesis-pathway;-common-mutation-in-laboratory-strains
ANIA_6845	Has-domain(s)-with-predicted-iron-ion-transmembrane-transporter-activity,-role-in-iron-ion-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6730	Low-to-moderate-capacity,-broad-specificity-purine-permease;-putative-paralog-of-UapA;-localized-to-the-cell-periphery,-relocalizes-to-vacuoles-in-the-presence-of-ammonium
ANIA_5937	Has-domain(s)-with-predicted-manganese-ion-binding,-nutrient-reservoir-activity-and-apoplast-localization
ANIA_5929	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_6386	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_6167	Has-domain(s)-with-predicted-FMN-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_10767	Purine-cytosine-transporter;-localized-to-the-plasma-membrane;-abundantly-expressed-in-ascogenous-hyphae,-hulle-cells-and-young-asci
ANIA_6060	Has-domain(s)-with-predicted-DNA-binding,-RNA-binding-activity-and-role-in-RNA-metabolic-process
ANIA_6130	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_5859	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_6114	Ortholog(s)-have-5'-deoxyribose-5-phosphate-lyase-activity,-DNA-directed-DNA-polymerase-activity,-DNA-directed-RNA-polymerase-activity,-role-in-transcription,-DNA-dependent-and-cytosol,-nucleus-localization
ANIA_5939	Putative-5'-nucleotidase-with-a-predicted-role-in-nucleotide-salvage-pathways;-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_6597	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04070,-A.-niger-CBS-513.88-:-An15g01310,-A.-oryzae-RIB40-:-AO090701000131,-A.-niger-ATCC-1015-:-210062-mRNA-and-Aspergillus-versicolor-:-Aspve1_0044247
ANIA_6740	
ANIA_6239	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6793,-A.-fumigatus-Af293-:-Afu3g03390,-Afu7g00330,-A.-niger-CBS-513.88-:-An03g03530-and-A.-oryzae-RIB40-:-AO090103000170,-AO090701000114
ANIA_5877	Putative-fatty-acyl-CoA-synthetase
ANIA_5832	Putative-Ras-GTPase
ANIA_6412	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_10740	Ortholog(s)-have-cytosol-localization
ANIA_6116	Ortholog-of-A.-fumigatus-Af293-:-Afu2g08820,-A.-niger-CBS-513.88-:-An12g04450,-A.-oryzae-RIB40-:-AO090011000818,-A.-niger-ATCC-1015-:-56711-mRNA-and-Aspergillus-versicolor-:-Aspve1_0040989
ANIA_10866	Has-domain(s)-with-predicted-ATP-binding-activity
ANIA_10751	
ANIA_7946	Has-domain(s)-with-predicted-ferric-iron-binding,-oxidoreductase-activity,-acting-on-single-donors-with-incorporation-of-molecular-oxygen,-incorporation-of-two-atoms-of-oxygen-activity
ANIA_6772	Ortholog-of-A.-nidulans-FGSC-A4-:-AN11002,-A.-fumigatus-Af293-:-Afu8g07350,-A.-niger-CBS-513.88-:-An01g01560,-A.-oryzae-RIB40-:-AO090120000069-and-A.-niger-ATCC-1015-:-191468-mRNA,-36394-mRNA
ANIA_6089	Putative-60-kilodalton-heat-shock-protein
ANIA_5857	Ortholog-of-A.-fumigatus-Af293-:-Afu2g08080,-A.-niger-CBS-513.88-:-An05g00670,-A.-oryzae-RIB40-:-AO090011000893,-A.-niger-ATCC-1015-:-211680-mRNA-and-Aspergillus-versicolor-:-Aspve1_0130457
ANIA_6104	Ortholog-of-A.-fumigatus-Af293-:-Afu2g09510,-A.-niger-CBS-513.88-:-An16g06890,-A.-oryzae-RIB40-:-AO090011000722,-A.-niger-ATCC-1015-:-205026-mRNA-and-Aspergillus-versicolor-:-Aspve1_0082923
ANIA_6290	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12370,-A.-niger-CBS-513.88-:-An02g04480,-A.-oryzae-RIB40-:-AO090026000369,-A.-niger-ATCC-1015-:-36891-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041143
ANIA_6941	Ortholog-of-A.-fumigatus-Af293-:-Afu3g03520,-A.-oryzae-RIB40-:-AO090011000166,-A.-niger-ATCC-1015-:-210994-mRNA,-Aspergillus-versicolor-:-Aspve1_0035126-and-Aspergillus-sydowii-:-Aspsy1_0142977
ANIA_6875	Kinesin-family-protein
ANIA_6625	Ortholog-of-A.-fumigatus-Af293-:-Afu6g03900,-A.-niger-CBS-513.88-:-An15g01620,-A.-oryzae-RIB40-:-AO090701000157,-A.-niger-ATCC-1015-:-182538-mRNA-and-Aspergillus-versicolor-:-Aspve1_0031206
ANIA_6753	Putative-NADH-dependent-flavin-oxidoreductase;-menadione-stress-induced-protein
ANIA_6451	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6859	Ortholog-of-A.-fumigatus-Af293-:-Afu5g13070,-A.-niger-CBS-513.88-:-An14g06090,-A.-oryzae-RIB40-:-AO090120000432,-A.-niger-ATCC-1015-:-211265-mRNA-and-Aspergillus-versicolor-:-Aspve1_0077735
ANIA_5830	Has-domain(s)-with-predicted-hydrolase-activity,-acting-on-acid-halide-bonds,-in-C-halide-compounds,-phosphoglycolate-phosphatase-activity-and-role-in-metabolic-process
ANIA_5822	Serine/threonine-protein-kinase-involved-in-DNA-damage-checkpoint-and-G2/M-transition;-ortholog-of-S.-pombe-wee1
ANIA_10853	Protein-involved-in-hyphal-growth-and-polarity
ANIA_6245	Ortholog-of-A.-fumigatus-Af293-:-Afu2g13120,-A.-oryzae-RIB40-:-AO090026000269,-A.-niger-ATCC-1015-:-206515-mRNA,-Aspergillus-versicolor-:-Aspve1_0130327-and-Aspergillus-sydowii-:-Aspsy1_0150794
ANIA_6755	Putative-acyl-coA-dehydrogenase
ANIA_6747	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_6327	
ANIA_5973	Protein-with-sequence-similarity-to-protein-kinase-C
ANIA_6538	Has-domain(s)-with-predicted-phospholipid-binding-activity
ANIA_6296	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12300,-A.-niger-CBS-513.88-:-An02g04340,-A.-oryzae-RIB40-:-AO090026000420,-A.-niger-ATCC-1015-:-173727-mRNA-and-Aspergillus-versicolor-:-Aspve1_0129544
ANIA_6423	Ortholog-of-A.-fumigatus-Af293-:-Afu3g00960,-A.-niger-CBS-513.88-:-An16g08680,-A.-oryzae-RIB40-:-AO090009000250-and-A.-niger-ATCC-1015-:-194055-mRNA
ANIA_6220	Ortholog-of-S.-cerevisiae-:-YMR155W,-A.-fumigatus-Af293-:-Afu2g13390,-A.-niger-CBS-513.88-:-An02g02260,-A.-oryzae-RIB40-:-AO090026000316-and-A.-niger-ATCC-1015-:-122575-mRNA
ANIA_5949	Ortholog-of-A.-fumigatus-Af293-:-Afu2g10330,-A.-niger-CBS-513.88-:-An16g04660,-A.-oryzae-RIB40-:-AO090011000605,-A.-niger-ATCC-1015-:-48964-mRNA-and-Aspergillus-versicolor-:-Aspve1_0052189
ANIA_6317	Class-VI-chitin-synthase-with-a-role-in-chitin-biosynthesis;-involved-in-hyphal-tip-growth;-contains-a-myosin-like-domain;-mutation-is-synthetically-lethal-with-csmA-mutation;-localized-at-hyphal-tips-and-septa
ANIA_6560	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04600,-A.-niger-CBS-513.88-:-An15g00728,-A.-oryzae-RIB40-:-AO090701000086,-A.-niger-ATCC-1015-:-141194-mRNA-and-Aspergillus-versicolor-:-Aspve1_0806496
ANIA_6255	Putative-cytochrome-c-oxidase-subunit-with-a-predicted-role-in-energy-metabolism
ANIA_6247	Ortholog-of-A.-fumigatus-Af293-:-Afu2g13100,-A.-niger-CBS-513.88-:-An02g01810,-A.-oryzae-RIB40-:-AO090026000266,-A.-niger-ATCC-1015-:-206509-mRNA-and-Aspergillus-versicolor-:-Aspve1_0083125
ANIA_10847	
ANIA_5908	Putative-triose-phosphate-isomerase-with-a-predicted-role-in-glycolysis
ANIA_5955	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_6075	Has-domain(s)-with-predicted-ammonia-lyase-activity,-role-in-L-phenylalanine-catabolic-process,-biosynthetic-process-and-cytoplasm-localization
ANIA_6693	Protein-of-unknown-function;-transcript-repressed-by-nitrate
ANIA_6685	Ortholog(s)-have-role-in-cellular-bud-site-selection,-cellular-protein-localization,-positive-regulation-of-establishment-of-bipolar-cell-polarity-regulating-cell-shape
ANIA_6669	Putative-sugar-transporter
ANIA_6613	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04265,-A.-niger-CBS-513.88-:-An15g01490,-A.-oryzae-RIB40-:-AO090701000146,-Aspergillus-versicolor-:-Aspve1_0137113-and-Aspergillus-sydowii-:-Aspsy1_0164382
ANIA_6371	Ortholog-of-A.-fumigatus-Af293-:-Afu2g14000,-A.-niger-CBS-513.88-:-An02g04960,-A.-oryzae-RIB40-:-AO090026000160,-A.-niger-ATCC-1015-:-206767-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041308
ANIA_6347	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_5860	Low-affinity-glucose-transporter-of-the-major-facilitator-superfamily-(MFS);-transcriptionally-repressed-by-growth-on-xylose
ANIA_6865	Ortholog(s)-have-endoplasmic-reticulum,-nuclear-envelope-localization
ANIA_6857	Ortholog(s)-have-alpha-1,2-mannosyltransferase-activity,-role-in-protein-glycosylation-and-Golgi-apparatus-localization
ANIA_6849	Ortholog(s)-have-role-in-cellular-response-to-heat,-cellular-response-to-hydrogen-peroxide
ANIA_6366	Ortholog(s)-have-endoplasmic-reticulum-localization

ANIA_5988	Ortholog-of-A.-fumigatus-Af293-:-Afu2g10190,-A.-niger-CBS-513.88-:-An16g04790,-A.-oryzae-RIB40-:-AO090011000617,-A.-niger-ATCC-1015-:-56409-mRNA-and-Aspergillus-versicolor-:-Aspve1_0052229
ANIA_10843	
ANIA_10742	
ANIA_6126	Putative-acetyl-CoA-carboxylase-with-a-predicted-role-in-cytosolic-fatty-acid-formation
ANIA_6118	Dicarboxylic-amino-acid-permease,-mediates-high-affinity-transport-of-L-glutamate-and-L-aspartate;-regulated-by-nitrogen-metabolite-repression;-mutants-fail-to-utilize-aspartate-as-a-sole-nitrogen-source
ANIA_5828	Has-domain(s)-with-predicted-heme-binding-activity
ANIA_6785	Ortholog-of-A.-fumigatus-Af293-:-Afu7g06760,-N.-fischeri-NRRL-181-:-NFIA_028050,-Aspergillus-versicolor-:-Aspve1_0046596,-Aspergillus-sydowii-:-Aspsy1_0034771-and-Aspergillus-terreus-NIH2624-:-ATET_09165
ANIA_6920	Subunit-of-the-endosomal-sorting-complex-required-for-transport-III-(ESCRT-III);-mediates-recruitment-of-calpain-like-cysteine-protease-PalB-to-the-ESCRT-III-complex;-mutant-inefficiently-processes-the-pacC-transcript
ANIA_6697	Putative-Sun-family-protein
ANIA_6840	Putative-hydroxyacylglutathione-hydrolase-with-a-predicted-role-in-the-methylglyoxal-bypass
ANIA_10819	Has-domain(s)-with-predicted-ATP-binding,-protein-kinase-activity-and-role-in-protein-phosphorylation
ANIA_6963	Ortholog(s)-have-flavin-linked-sulfhydryl-oxidase-activity-and-role-in-oxidation-reduction-process
ANIA_6280	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12520,-A.-niger-CBS-513.88-:-An02g04750,-A.-oryzae-RIB40-:-AO090026000847,-A.-niger-ATCC-1015-:-36909-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041151
ANIA_6264	Has-domain(s)-with-predicted-transcription-cofactor-activity,-role-in-multicellular-organismal-development-and-nucleus-localization
ANIA_6342	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_5980	Ortholog-of-A.-fumigatus-Af293-:-Afu2g10310,-A.-niger-CBS-513.88-:-An16g04680,-A.-oryzae-RIB40-:-AO090011000607,-A.-niger-ATCC-1015-:-183811-mRNA-and-Aspergillus-versicolor-:-Aspve1_0623740
ANIA_3880	Putative-acyl-coA-dehydrogenase
ANIA_10518	Protein-of-unknown-function;-protein-induced-by-farnesol
ANIA_4218	Ortholog(s)-have-GDP-binding,-GTP-binding,-translation-elongation-factor-activity,-role-in-tRNA-export-from-nucleus,-translational-elongation-and-cytosol,-mitochondrion,-nucleus-localization
ANIA_6727	Ortholog-of-A.-nidulans-FGSC-A4-:-AN8146,-A.-fumigatus-Af293-:-Afu6g03180,-Afu7g05880,-A.-niger-CBS-513.88-:-An07g02000,-An01g14710-and-Aspergillus-versicolor-:-Aspve1_0079826
ANIA_6639	Putative-2-methylcitrate-dehydratase-with-a-predicted-role-in-lysine-metabolism
ANIA_6074	Ortholog(s)-have-mRNA-binding,-protein-heterodimerization-activity,-role-in-mRNA-cleavage,-mRNA-polyadenylation-and-mRNA-cleavage-factor-complex-localization
ANIA_6066	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_6201	Ortholog-of-A.-fumigatus-Af293-:-Afu2g11830,-A.-oryzae-RIB40-:-AO090026000461,-Aspergillus-versicolor-:-Aspve1_0052426,-Aspergillus-sydowii-:-Aspsy1_0151758-and-Aspergillus-terreus-NIH2624-:-ATET_01122
ANIA_6058	DUF833-domain-containing-protein;-intracellular,-menadione-stress-induced-protein
ANIA_5823	L-ornithine-N5-monooxygenase;-involved-in-siderophore-biosynthesis;-null-mutant-inviable-unless-medium-is-supplemented-with-siderophores
ANIA_5943	Ortholog-of-A.-nidulans-FGSC-A4-:-AN8548,-AN8661,-AN4642,-A.-fumigatus-Af293-:-Afu3g00850,-Afu4g08850-and-A.-niger-CBS-513.88-:-An02g13470,-An11g00090,-An03g01430,-An12g09260
ANIA_5935	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_5848	Ortholog-of-A.-fumigatus-Af293-:-Afu2g08010,-A.-niger-CBS-513.88-:-An05g00570,-A.-oryzae-RIB40-:-AO090011000900,-A.-niger-ATCC-1015-:-42514-mRNA-and-Aspergillus-versicolor-:-Aspve1_0052083
ANIA_3709	Ortholog-of-A.-niger-CBS-513.88-:-An06g01900,-A.-oryzae-RIB40-:-AO090003001584,-Aspergillus-acidus-:-Aspfo1_0052254-and-Aspergillus-versicolor-:-Aspve1_0683286
ANIA_3602	Putative-deadenylase-with-a-predicted-role-in-RNA-processing;-disruption-leads-to-a-stabilization-of-transcripts
ANIA_8074	Has-domain(s)-with-predicted-ubiquitin-thiolesterase-activity,-zinc-ion-binding-activity-and-role-in-ubiquitin-dependent-protein-catabolic-process
ANIA_6275	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12570,-A.-niger-CBS-513.88-:-An02g01500,-A.-oryzae-RIB40-:-AO090026000362,-A.-niger-ATCC-1015-:-206469-mRNA-and-Aspergillus-versicolor-:-Aspve1_0028223
ANIA_6712	Putative-phospholipase-D;-expression-upregulated-after-exposure-to-farnesol
ANIA_8138	Alpha-galactosidase,-involved-in-degradation-of-mannans;-predicted-role-in-galactose-and-galactitol-metabolism;-glycoside-hydrolase-family-36-(GH36);-transcriptionally-induced-by-growth-on-xylose
ANIA_8031	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02250,-A.-niger-CBS-513.88-:-An02g10580,-A.-oryzae-RIB40-:-AO090102000288,-A.-niger-ATCC-1015-:-37331-mRNA-and-Aspergillus-versicolor-:-Aspve1_0311838
ANIA_6463	Has-domain(s)-with-predicted-transferase-activity,-transferring-phosphorus-containing-groups-activity
ANIA_6559	Predicted-DDE1-transposon-related-ORF
ANIA_6702	Ortholog(s)-have-Golgi-apparatus,-endoplasmic-reticulum-localization
ANIA_6651	Ortholog(s)-have-ATP-binding,-ATPase-activity,-role-in-poly(A)+-mRNA-export-from-nucleus,-ribosomal-small-subunit-biogenesis-and-cytosol,-mitochondrion,-polysome-localization
ANIA_6643	Putative-biotin-synthase-with-a-predicted-role-in-Coenzyme-A-and-pantothenate-biosynthesis
ANIA_6805	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6664	Has-domain(s)-with-predicted-role-in-cell-wall-macromolecule-catabolic-process
ANIA_7892	Small-heat-shock-protein;-molecular-chaperone;-expression-upregulated-after-exposure-to-farnesol
ANIA_8034	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02210,-A.-niger-CBS-513.88-:-An02g10730,-A.-oryzae-RIB40-:-AO090102000294,-Aspergillus-versicolor-:-Aspve1_0139469-and-Aspergillus-sydowii-:-Aspsy1_0033693
ANIA_11046	Protein-of-unknown-function;-transcript-is-induced-by-nitrate
ANIA_3998	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_6525	Putative-formate-dehydrogenase-with-a-predicted-role-in-oxalic-acid-metabolism;-intracellular;-protein-abundance-decreased-by-menadione-stress;-inducible-by-acetate;-expression-reduced-after-exposure-to-farnesol
ANIA_3636	Has-domain(s)-with-predicted-phospholipase-C-activity-and-role-in-intracellular-signal-transduction,-lipid-metabolic-process
ANIA_8251	bZIP-transcription-factor;-physically-interacts-with-CCAAT-complex-protein-HapB-and-HapE-by-two-hybrid;-synthetically-lethal-with-sreA;-expression-repressed-by-iron;-mutants-have-increased-ferricrocin-and-decreased-triacetyl-fusarinine-C
ANIA_3891	
ANIA_10507	Ortholog(s)-have-mRNA-binding,-unfolded-protein-binding-activity,-role-in-cellular-response-to-unfolded-protein,-mRNA-export-from-nucleus-in-response-to-heat-stress,-protein-folding-and-cytosol,-nucleus-localization
ANIA_4207	Ortholog(s)-have-role-in-endosomal-transport-and-AP-1-adaptor-complex,-endosome-localization
ANIA_3845	
ANIA_3837	Putative-invertase;-sucrose-hydrolyzing-enzyme
ANIA_10805	Has-domain(s)-with-predicted-hydrolase-activity-and-role-in-metabolic-process
ANIA_6354	Putative-ubiquitin-C-terminal-hydrolase;-ortholog-of-S.-cerevisiae-Ubp12p;-expression-reduced-after-exposure-to-farnesol;-transcript-upregulated-in-response-to-camptothecin
ANIA_5992	Ortholog(s)-have-role-in-DNA-replication-initiation-and-MCM-complex-localization
ANIA_3729	Putative-1,3-beta-glucan-synthase-with-a-predicted-role-in-glucan-biosynthesis
ANIA_11044	Predicted-DDE1-transposon-related-ORF
ANIA_3996	Has-domain(s)-with-predicted-methyltransferase-activity-and-role-in-metabolic-process
ANIA_3730	Putative-1,3-beta-transglycosidase-with-a-predicted-role-in-glucan-processing
ANIA_3587	Ubiquitin-processing-protease-involved-in-carbon-catabolite-repression
ANIA_3581	Thioredoxin-reductase-with-a-predicted-role-in-pyrimidine-metabolism;-putative-flavoprotein;-intracellular,-menadione-stress-induced-protein;-transcripts-of-two-different-sizes-have-been-detected
ANIA_3573	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-oxidation-reduction-process
ANIA_8279	Ortholog-of-S.-cerevisiae-Can1p-which-has-arginine-transmembrane-transporter-activity;-basic-amino-acid-transporter;-expression-reduced-after-exposure-to-farnesol
ANIA_5976	Putative-beta-glucosidase
ANIA_4243	Has-domain(s)-with-predicted-3-beta-hydroxy-delta5-steroid-dehydrogenase-activity,-nucleotide-binding-activity-and-role-in-oxidation-reduction-process,-steroid-biosynthetic-process
ANIA_3881	Has-domain(s)-with-predicted-ADP-binding,-ATP-binding,-nucleoside-triphosphatase-activity-and-role-in-apoptotic-process,-nucleoside-metabolic-process
ANIA_3640	Ortholog-of-N.-fischeri-NRRL-181-:-NFIA_060750
ANIA_3497	Putative-cytochrome-P450
ANIA_3632	Ortholog(s)-have-iron-sulfur-cluster-binding-activity,-role-in-iron-sulfur-cluster-assembly-and-cytosol,-membrane,-nucleus-localization
ANIA_7868	Ortholog-of-A.-fumigatus-Af293-:-Afu2g04540,-A.-niger-CBS-513.88-:-An04g07800,-A.-oryzae-RIB40-:-AO090003000256,-A.-niger-ATCC-1015-:-195339-mRNA-and-Aspergillus-versicolor-:-Aspve1_0037800
ANIA_6487	Putative-aspartyl-protease;-ortholog-of-S.-cerevisiae-BAR1;-expression-reduced-after-exposure-to-farnesol
ANIA_6630	Putative-nascent-polypeptide-associated-complex-subunit-alpha;-induced-by-rapamycin-induced-autophagy
ANIA_3995	Putative-delta-aminolevulinic-acid-dehydratase
ANIA_6754	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_6084	Ortholog-of-A.-fumigatus-Af293-:-Afu2g09220,-A.-niger-CBS-513.88-:-An12g04880,-A.-oryzae-RIB40-:-AO090011000773,-A.-niger-ATCC-1015-:-211565-mRNA-and-Aspergillus-versicolor-:-Aspve1_0082910
ANIA_5956	Has-domain(s)-with-predicted-DNA-binding,-transposase-activity-and-role-in-DNA-integration,-transposition,-DNA-mediated
ANIA_6831	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6182	Putative-hexose-1-phosphate-uridylyltransferase-with-a-predicted-role-in-galactose-and-galactitol-metabolism;-expression-upregulated-after-exposure-to-farnesol
ANIA_10752	Ortholog-of-A.-fumigatus-Af293-:-Afu2g11470,-A.-niger-CBS-513.88-:-An02g03450,-N.-fischeri-NRRL-181-:-NFIA_086710,-A.-clavatus-NRRL-1-:-ACLA_070420-and-Aspergillus-versicolor-:-Aspve1_0040617

ANIA_6172	Ortholog-of-A.-fumigatus-Af293-:-Afu2g08340,-A.-niger-CBS-513.88-:-An05g00970,-A.-oryzae-RIB40-:-AO090011000871,-Aspergillus-versicolor-:-Aspve1_0028126-and-Aspergillus-sydowii-:-Aspsy1_0151670
ANIA_6581	Has-domain(s)-with-predicted-ATP-binding,-ATPase-activity,-coupled-to-transmembrane-movement-of-substances-activity,-role-in-transport-and-integral-to-membrane-localization
ANIA_6565	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04550,-A.-niger-CBS-513.88-:-An15g00790,-A.-niger-ATCC-1015-:-183143-mRNA,-Aspergillus-versicolor-:-Aspve1_0136558-and-Aspergillus-sydowii-:-Aspsy1_0164397
ANIA_6128	Has-domain(s)-with-predicted-transferase-activity,-transferring-hexosyl-groups-activity,-role-in-carbohydrate-metabolic-process-and-membrane-localization
ANIA_6834	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6014	Putative-long-chain-fatty-acid-CoA-ligase-with-a-predicted-role-in-fatty-acid-metabolism
ANIA_4170	Arrestin-domains-and-PY-motif-containing-protein-with-homology-to-Saccharomyces-cerevisiae-Rod1p-and-Rog3p-proteins;-expression-reduced-after-exposure-to-farnesol
ANIA_6880	Has-domain(s)-with-predicted-inositol-1,4,5-trisphosphate-3-kinase-activity
ANIA_6733	Ortholog(s)-have-sequence-specific-DNA-binding-activity-and-cytoplasm,-nucleus,-spindle-localization
ANIA_5894	Ortholog(s)-have-RNA-polymerase-II-core-binding,-TFIIF-class-binding-transcription-factor-activity,-chromatin-binding-activity
ANIA_5886	Alpha-isopropylmalate-isomerase-with-a-predicted-role-in-valine,-leucine,-and-isoleucine-metabolism;-protein-expressed-at-increased-levels-in-a-hapX-mutant-versus-wild-type;-transcript-is-induced-by-nitrate;-protein-induced-by-farnesol
ANIA_6426	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5101,-A.-fumigatus-Af293-:-Afu1g07730/mep1,-A.-niger-CBS-513.88-:-An07g10410,-A.-oryzae-RIB40-:-AO090012001025-and-A.-niger-ATCC-1015-:-48208-mRNA
ANIA_6418	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6168	Putative-malate-dehydrogenase-with-a-predicted-role-in-oxidation-of-malate-to-pyruvate
ANIA_6835	Putative-cytochrome-P450;-expression-upregulated-after-exposure-to-farnesol
ANIA_6703	Putative-major-facilitator-superfamily-(MFS)-permease
ANIA_6445	Putative-aryl-alcohol-oxidase-related-protein
ANIA_6010	Hsp70-family-protein;-required-for-conidial-germination;-protein-expressed-at-increased-levels-during-osmoadaptation
ANIA_6061	Has-domain(s)-with-predicted-role-in-response-to-stress
ANIA_6534	Putative-mannosylinositol-phosphorylceramide-(MIP2C)-synthase-with-a-predicted-role-in-sphingoglycolipid-metabolism
ANIA_6518	Has-domain(s)-with-predicted-hydrolase-activity,-acting-on-carbon-nitrogen-(but-not-peptide)-bonds-activity-and-role-in-carbohydrate-metabolic-process
ANIA_6284	Ortholog-of-A.-fumigatus-Af293-:-Afu2g12430,-A.-niger-CBS-513.88-:-An02g04620,-A.-oryzae-RIB40-:-AO090026000390,-A.-niger-ATCC-1015-:-46977-mRNA-and-Aspergillus-versicolor-:-Aspve1_0641422
ANIA_6031	Has-domain(s)-with-predicted-nitronate-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_6023	Has-domain(s)-with-predicted-FMN-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5900	Ortholog-of-A.-fumigatus-Af293-:-Afu2g11100,-A.-niger-CBS-513.88-:-An02g03000,-A.-oryzae-RIB40-:-AO090026000554,-A.-niger-ATCC-1015-:-52169-mRNA-and-Aspergillus-versicolor-:-Aspve1_0027804
ANIA_6437	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0052718-and-Aspergillus-sydowii-:-Aspsy1_0031878
ANIA_6195	Transcriptional-regulator-that-mediates-carbon-catabolite-repression;-mutants-display-increased-extracellular-protease-activity
ANIA_6504	
ANIA_5999	Carbamoyl-phosphate-synthase,-large-subunit;-predicted-role-in-arginine-or-pyrimidine-metabolism;-protein-induced-by-farnesol
ANIA_6262	Ortholog-of-A.-oryzae-RIB40-:-AO090026000341,-A.-niger-ATCC-1015-:-52129-mRNA,-Aspergillus-versicolor-:-Aspve1_0130107,-Aspergillus-sydowii-:-Aspsy1_0058174-and-Aspergillus-terreus-NIH2624-:-ATET_01256
ANIA_10854	Ortholog(s)-have-AMP-activated-protein-kinase-activity,-protein-serine/threonine-kinase-activator-activity
ANIA_6657	Ortholog-of-A.-fumigatus-Af293-:-Afu6g03400,-A.-niger-CBS-513.88-:-An15g02040,-Aspergillus-versicolor-:-Aspve1_0086179-and-Aspergillus-sydowii-:-Aspsy1_0157063
ANIA_10761	Predicted-PIN-domain-containing-RNA-binding-protein;-expression-upregulated-after-exposure-to-farnesol
ANIA_10745	Ortholog(s)-have-mitochondrion-localization
ANIA_6037	Putative-glucose-6-phosphate-isomerase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-mutant-defective-in-hyphal-polarity-and-conidiation
ANIA_6004	Protein-with-an-RNA-recognition-motif;-protein-expressed-at-increased-levels-in-a-hapX-mutant-versus-wild-type;-expression-upregulated-after-exposure-to-farnesol
ANIA_6972	
ANIA_6964	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0093575
ANIA_6948	Putative-transglycosidase-with-a-predicted-role-in-glucan-processing
ANIA_6359	Protein-involved-in-sulfur-metabolite-repression;-contains-an-F-box-and-seven-WD-repeats
ANIA_5989	Putative-NAD-dependent-epimerase/dehydratase;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_6692	
ANIA_6684	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_6048	Putative-aspartate-transaminase-with-a-predicted-role-in-amino-acid-metabolism;-palA-dependent-expression-independent-of-pH;-induced-by-carbon-starvation-induced-autophagy
ANIA_6885	Ortholog-of-A.-fumigatus-Af293-:-Afu5g13250,-A.-niger-CBS-513.88-:-An14g04640,-A.-oryzae-RIB40-:-AO090120000468,-A.-niger-ATCC-1015-:-53850-mRNA-and-Aspergillus-versicolor-:-Aspve1_0048220
ANIA_6877	
ANIA_6869	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_6207	Ortholog(s)-have-mitochondrion-localization
ANIA_10807	Has-domain(s)-with-predicted-RNA-binding-activity
ANIA_6794	
ANIA_10844	Putative-fructose-2,6-bisphosphate-2-phosphatase
ANIA_6768	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_6365	Ortholog(s)-have-cytoplasm-localization
ANIA_6778	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10789	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_6758	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_6238	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6107	Putative-voltage-gated-anion-channel-protein-with-a-role-in-copper-homeostasis
ANIA_6330	Putative-elongation-factor-2;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_10834	Protein-with-an-acyl-CoA-dehydrogenase-domain
ANIA_5864	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6460	Ortholog-of-A.-nidulans-FGSC-A4-:-AN12398,-A.-oryzae-RIB40-:-AO090023000067,-AO090010000683,-Aspergillus-flavus-NRRL-3357-:-AFL2T_03967,-AFL2T_11823-and-Aspergillus-versicolor-:-Aspve1_0086685
ANIA_6436	Has-domain(s)-with-predicted-ATP-binding,-ATPase-activity,-coupled-to-transmembrane-movement-of-substances-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_6960	Has-domain(s)-with-predicted-metal-ion-transmembrane-transporter-activity,-role-in-metal-ion-transport,-transmembrane-transport-and-membrane-localization
ANIA_5846	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_6787	Putative-cytochrome-P450
ANIA_10779	Putative-transglycosidase-required-for-1,6-beta-glucan-biosynthesis
ANIA_6846	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_6838	Beta-tubulin,-highly-conserved-component-of-microtubules;-A.-nidulans-has-two-beta-tubulin-genes,-tubC-and-benA;-expression-of-tubC-increases-during-conidiation
ANIA_6588	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04300,-A.-niger-CBS-513.88-:-An15g01200,-A.-oryzae-RIB40-:-AO090701000121,-A.-niger-ATCC-1015-:-137591-mRNA-and-Aspergillus-versicolor-:-Aspve1_0137171
ANIA_6723	Putative-2,3-dihydroxybenzoate-carboxylyase
ANIA_6473	Ortholog-of-A.-fumigatus-Af293-:-Afu1g16430,-N.-fischeri-NRRL-181-:-NFIA_009010,-Aspergillus-versicolor-:-Aspve1_0315435,-Aspergillus-sydowii-:-Aspsy1_0091751-and-Aspergillus-terreus-NIH2624-:-ATET_06548
ANIA_6690	Ortholog-of-S.-cerevisiae-:-YMR166C,-A.-fumigatus-Af293-:-Afu7g05390,-A.-niger-CBS-513.88-:-An07g02810,-A.-oryzae-RIB40-:-AO090005000379-and-A.-niger-ATCC-1015-:-215077-mRNA
ANIA_6908	Ortholog-of-A.-fumigatus-Af293-:-Afu5g13560,-A.-niger-CBS-513.88-:-An14g05050,-A.-oryzae-RIB40-:-AO090113000013,-Aspergillus-versicolor-:-Aspve1_0077681-and-Aspergillus-sydowii-:-Aspsy1_0589528
ANIA_6666	
ANIA_6293	Protein-with-role-in-utilization-of-gluconeogenic-carbon-sources;-contains-a-Zn(2)-Cys(6)-DNA-binding-motif;-ortholog-of-S.-cerevisiae-Rds2p
ANIA_6680	Putative-G-protein-coupled-receptor
ANIA_6352	Protein-with-arabinan-endo-1,5-alpha-L-arabinosidase-activity,-involved-in-degradation-of-pectin
ANIA_6529	Ortholog-of-A.-fumigatus-Af293-:-Afu6g04880,-A.-niger-CBS-513.88-:-An15g00440,-A.-oryzae-RIB40-:-AO090701000051,-A.-niger-ATCC-1015-:-53386-mRNA-and-Aspergillus-versicolor-:-Aspve1_0805161
ANIA_6406	
ANIA_6379	
ANIA_11053	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03110,-A.-niger-CBS-513.88-:-An09g05280,-An01g14890,-A.-oryzae-RIB40-:-AO090701000457,-AO090102000514-and-A.-niger-ATCC-1015-:-188240-mRNA,-35383-mRNA

ANIA_3670	Ortholog-of-A.-fumigatus-Af293-:-Afu4g12380,-A.-niger-CBS-513.88-:-An01g07790,-A.-oryzae-RIB40-:-AO090009000446,-A.-niger-ATCC-1015-:-171996-mRNA-and-Aspergillus-versicolor-:-Aspve1_0087047
ANIA_4008	Has-domain(s)-with-predicted-O-methyltransferase-activity
ANIA_10496	Putative-regulator-of-mannosylphosphorylation
ANIA_3606	Ortholog-of-A.-fumigatus-Af293-:-Afu4g12700,-A.-niger-CBS-513.88-:-An03g02800,-A.-oryzae-RIB40-:-AO090009000298,-A.-niger-ATCC-1015-:-205058-mRNA-and-Aspergillus-versicolor-:-Aspve1_0055483
ANIA_8078	Phenylacetate-2-hydroxylase;-cytochrome-P450-monooxygenase-involved-in-phenylacetate-utilization;-transcript-is-induced-by-phenylacetate
ANIA_7914	Putative-alcohol-dehydrogenase;-member-of-the-F9775-secondary-metabolite-gene-cluster;-induced-by-rapamycin-induced-autophagy
ANIA_8135	Has-domain(s)-with-predicted-transferase-activity,-transferring-hexosyl-groups-activity-and-role-in-metabolic-process
ANIA_11040	Ortholog(s)-have-role-in-coenzyme-A-biosynthetic-process-and-endoplasmic-reticulum,-mitochondrion,-nuclear-envelope-localization
ANIA_8121	Putative-5'-phosphoribosylformyl-glycinamidine-synthetase-with-a-predicted-role-in-purine-metabolism
ANIA_4197	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_3970	Kinesin-family-protein
ANIA_3954	Putative-phosphogluconate-dehydrogenase-(decarboxylating)-with-a-predicted-role-in-the-pentose-phosphate-shunt
ANIA_3591	Protein-with-similarity-to-bacterial-propionyl-CoA-yielding-methylmalonate-semialdehyde-dehydrogenase;-may-be-involved-in-isoleucine-and-valine-catabolism
ANIA_8289	Ortholog-of-A.-fumigatus-Af293-:-Afu7g03670,-A.-niger-CBS-513.88-:-An13g00010,-A.-niger-ATCC-1015-:-54766-mRNA,-Aspergillus-versicolor-:-Aspve1_0137821-and-Aspergillus-sydowii-:-Aspsy1_1173898
ANIA_4196	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_3961	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0054191
ANIA_3953	Has-domain(s)-with-predicted-nucleic-acid-binding,-nucleotide-binding-activity
ANIA_3945	Ortholog-of-A.-fumigatus-Af293-:-Afu6g08130,-A.-niger-CBS-513.88-:-An11g01990,-A.-oryzae-RIB40-:-AO090003000113,-A.-niger-ATCC-1015-:-52888-mRNA-and-Aspergillus-versicolor-:-Aspve1_0052972
ANIA_4190	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein;-palA-dependent-expression-independent-of-pH
ANIA_10458	
ANIA_3763	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3755	Has-domain(s)-with-predicted-protein-kinase-binding-activity-and-role-in-regulation-of-cyclin-dependent-protein-kinase-activity
ANIA_3747	Ortholog(s)-have-Rab-geranylgeranyltransferase-activity-and-role-in-ER-to-Golgi-vesicle-mediated-transport,-negative-regulation-of-G0-to-G1-transition,-protein-geranylgeranylation,-protein-targeting-to-membrane
ANIA_3739	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_3925	Has-domain(s)-with-predicted-catalytic-activity,-cation-binding-activity-and-role-in-carbohydrate-metabolic-process
ANIA_3675	Transcription-factor-of-the-Gcn4p-c-Jun-like-transcriptional-activator-family;-involved-in-cross-pathway-control-of-amino-acid-biosynthesis-in-response-to-amino-acid-starvation;-role-in-sexual-development;-contains-two-5'-uORFs
ANIA_7874	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_7858	Has-domain(s)-with-predicted-aspartic-type-endopeptidase-activity-and-role-in-proteolysis
ANIA_7943	Has-domain(s)-with-predicted-hydrolase-activity-and-role-in-metabolic-process
ANIA_3482	
ANIA_8188	Putative-GTP-cyclohydrolase-I-with-a-predicted-role-in-folate-biosynthesis
ANIA_7975	
ANIA_8095	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3607	Putative-zinc-finger-transcription-factor-involved-in-blue-light-responsive-differentiation;-interacts-with-VeA,-FphA,-and-LreA;-similar-to-N.-crassa-blue-light-sensing-component-WC-2
ANIA_4654	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01720,-A.-niger-CBS-513.88-:-An07g05260,-A.-niger-ATCC-1015-:-53266-mRNA,-Aspergillus-versicolor-:-Aspve1_0042815-and-Aspergillus-sydowii-:-Aspsy1_0155851
ANIA_10581	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08640,-A.-niger-CBS-513.88-:-An07g04900,-A.-niger-ATCC-1015-:-129373-mRNA,-Aspergillus-versicolor-:-Aspve1_0042746-and-Aspergillus-sydowii-:-Aspsy1_0091352
ANIA_4515	Putative-transglycosidase-with-a-predicted-role-in-glucan-processing;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_10602	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-oxidation-reduction-process
ANIA_4695	Putative-Woronin-body-protein;-HapX-regulated-gene;-protein-induced-by-farnesol
ANIA_4687	Beta-subunit-of-3-methylcrotonyl-CoA-carboxylase,-involved-in-leucine-degradation
ANIA_11099	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_4814	Ortholog(s)-have-Golgi-apparatus,-endoplasmic-reticulum,-fungal-type-vacuole-localization
ANIA_8785	Ortholog(s)-have-L-aspartate-transmembrane-transporter-activity,-L-glutamate-transmembrane-transporter-activity,-antiporter-activity,-uniporter-activity
ANIA_8777	Acetamidase,-produces-ammonium-and-acetate-from-acetamide,-allowing-utilization-of-acetamide-as-sole-carbon-or-nitrogen-source;-transcript-induced-under-low-nitrogen-conditions
ANIA_4409	Ornithine-carbamoyltransferase-of-the-arginine-biosynthesis-pathway;-catalyzes-a-step-in-the-biosynthesis-of-arginine-precursor-ornithine;-mutants-show-reduced-rate-of-DNA-damage-repair;-protein-abundance-decreased-by-menadione
ANIA_10610	Ortholog(s)-have-protein-binding,-bridging-activity,-role-in-protein-import-into-peroxisome-matrix,-docking-and-peroxisomal-membrane-localization
ANIA_4310	Ortholog(s)-have-role-in-phosphate-containing-compound-metabolic-process-and-cytoplasm,-nucleus-localization
ANIA_4482	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3664	Ortholog(s)-have-cell-surface-localization
ANIA_8271	Predicted-basic-helix-loop-helix-transcription-factor,-involved-in-regulation-of-phosphate-acquisition
ANIA_3517	Ortholog-of-Aspergillus-sydowii-:-Aspsy1_0162744
ANIA_8652	
ANIA_8644	Ortholog-of-A.-fumigatus-Af293-:-Afu1g01940,-A.-niger-CBS-513.88-:-An04g08240,-A.-oryzae-RIB40-:-AO090026000236,-AO090010000588,-AO090011000050,-AO090009000101-and-A.-niger-ATCC-1015-:-51452-mRNA
ANIA_8636	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_8628	Has-domain(s)-with-predicted-cofactor-binding,-nucleotide-binding,-oxidoreductase-activity,-acting-on-the-CH-OH-group-of-donors,-NAD-or-NADP-as-acceptor-and-transferase-activity,-more
ANIA_4224	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_3713	
ANIA_7950	Putative-glucan-endo-1,3-beta-D-glucosidase-with-predicted-role-in-degradation-of-glucans;-glycosyl-phosphatidylinositol-(GPI)-linked-protein
ANIA_4273	Ortholog-of-A.-fumigatus-Af293-:-Afu7g03800,-A.-niger-CBS-513.88-:-An13g00220,-A.-oryzae-RIB40-:-AO090026000834,-A.-niger-ATCC-1015-:-213656-mRNA-and-Aspergillus-versicolor-:-Aspve1_0055273
ANIA_3895	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_10442	Predicted-guanine-nucleotide-exchange-factor
ANIA_8269	90-kilodalton-heat-shock-protein;-physically-associates-with-importin-alpha,-KapA;-palA-dependent-expression-independent-of-pH
ANIA_4935	Ortholog(s)-have-protein-serine/threonine-kinase-activity,-role-in-negative-regulation-of-meiosis,-protein-phosphorylation-and-cytosol,-nucleus-localization
ANIA_5055	Has-domain(s)-with-predicted-aminopeptidase-activity,-metalloexopeptidase-activity-and-role-in-cellular-process,-proteolysis
ANIA_3928	Putative-thiazole-synthase,-enzyme-of-the-thiamine-biosynthesis-pathway
ANIA_8277	Putative-bifunctional-enzyme-with-a-predicted-role-in-methionine-metabolism;-O-acetlylhomoserine-(homocysteine-synthase)
ANIA_8146	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6727,-A.-fumigatus-Af293-:-Afu6g03180,-Afu7g05880,-A.-niger-CBS-513.88-:-An07g02000,-An01g14710-and-Aspergillus-versicolor-:-Aspve1_0079826
ANIA_4291	Predicted-mariner-transposon-related-ORF
ANIA_3520	Ortholog-of-A.-niger-CBS-513.88-:-An04g10140,-Aspergillus-brasiliensis-:-Aspbr1_0153268,-A.-niger-ATCC-1015-:-55208-mRNA-and-Aspergillus-acidus-:-Aspfo1_0032523
ANIA_7880	Putative-fatty-acyl-CoA-synthase-with-a-predicted-role-in-cytosolic-fatty-acid-formation
ANIA_4042	Putative-C-22-sterol-desaturase-with-a-predicted-role-in-sterol-metabolism;-putative-cytochrome-P450
ANIA_4034	Component-of-AnCP/AnCF-CCAAT-binding-complex;-can-act-as-both-a-positive-and-negative-regulator-of-transcription
ANIA_3914	Putative-transglycosidase-with-a-predicted-role-in-glucan-processing
ANIA_8231	Putative-S-adenosylmethionine-decarboxylase-with-a-predicted-role-in-arginine-metabolism
ANIA_3796	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0083942,-Aspergillus-sydowii-:-Aspsy1_0148764,-Aspergillus-terreus-NIH2624-:-ATET_03647-and-Aspergillus-carbonarius-ITEM-5010-:-Acar5010_005404
ANIA_4051	Has-domain(s)-with-predicted-heme-binding,-iron-ion-binding,-oxygen-binding-activity-and-role-in-oxygen-transport
ANIA_4035	Positively-acting-regulatory-gene;-putative-Zn(II)2Cys6-transcription-factor;-inducer-of-acetamide-and-enzymes-of-omega-amino-acid-and-lactam-catabolism
ANIA_3681	Ortholog-of-A.-fumigatus-Af293-:-Afu4g12530/cccA,-A.-niger-CBS-513.88-:-An01g08010,-A.-oryzae-RIB40-:-AO090009000468,-A.-niger-ATCC-1015-:-35907-mRNA-and-Aspergillus-versicolor-:-Aspve1_0087058
ANIA_3907	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity
ANIA_8009	Ortholog-of-A.-fumigatus-nmt1-and-S.-cerevisiae-THI13;-repressed-by-starvation-induced-autophagy;-this-locus-is-reported-to-contain-an-upstream-open-reading-frame-(uORF)
ANIA_4252	Ortholog-of-A.-nidulans-FGSC-A4-:-AN10165,-A.-fumigatus-Af293-:-Afu1g06580/hel10,-Afu1g11910,-A.-niger-CBS-513.88-:-An18g05640,-An08g04120-and-A.-oryzae-RIB40-:-AO090001000456,-AO090001000373
ANIA_10528	

ANIA_3974	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0135108,-Aspergillus-sydowii-:-Aspsy1_0057545-and-Aspergillus-terreus-NIH2624-:-ATET_08256
ANIA_7953	Has-domain(s)-with-predicted-iron-ion-binding,-oxidoreductase-activity,-acting-on-paired-donors,-with-incorporation-or-reduction-of-molecular-oxygen-and-2-oxoglutarate-as-one-donor,-more
ANIA_7937	Protein-responsive-to-Concanamycin-A
ANIA_4276	
ANIA_10461	
ANIA_8029	Putative-plasma-membrane-high-affinity-K+-transporter
ANIA_4264	Ortholog-of-A.-fumigatus-Af293-:-Afu7g03900,-A.-niger-CBS-513.88-:-An13g00320,-A.-oryzae-RIB40-:-AO090026000826,-A.-niger-ATCC-1015-:-213674-mRNA-and-Aspergillus-versicolor-:-Aspve1_0031762
ANIA_4256	Ortholog-of-A.-fumigatus-Af293-:-Afu7g04030,-A.-oryzae-RIB40-:-AO090012000139,-Aspergillus-brasiliensis-:-Aspbr1_0048631,-N.-fischeri-NRRL-181-:-NFIA_099750-and-A.-clavatus-NRRL-1-:-ACLA_005720
ANIA_3649	Ortholog(s)-have-role-in-fatty-acid-metabolic-process
ANIA_8256	Has-domain(s)-with-predicted-structural-constituent-of-ribosome-activity,-role-in-translation-and-ribosome-localization
ANIA_7878	Putative-branched-chain-amino-acid-aminotransferase-with-a-predicted-role-in-valine,-leucine,-and-isoleucine-metabolism
ANIA_8076	Predicted-DNA-binding-protein;-locus-contains-the-conserved-upstream-open-reading-frame-(uORF)-AN8076-uORF
ANIA_8211	Ortholog(s)-have-histone-demethylase-activity-(H3-trimethyl-K4-specific)-activity
ANIA_8051	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02120,-A.-niger-CBS-513.88-:-An02g11160,-A.-oryzae-RIB40-:-AO090003001306,-A.-niger-ATCC-1015-:-197766-mRNA-and-Aspergillus-versicolor-:-Aspve1_0138990
ANIA_7923	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7907	Putative-glyoxylate-bleomycin-resistance-protein;-member-of-the-F9775-secondary-metabolite-gene-cluster
ANIA_3941	Protein-tyrosine-phosphatase-involved-in-cell-cycle-control;-required-for-progression-through-G2;-homolog-of-S.-pombe-cdc25
ANIA_10453	Ortholog(s)-have-protein-channel-activity,-role-in-protein-import-into-mitochondrial-inner-membrane-and-mitochondrial-inner-membrane-protein-insertion-complex-localization
ANIA_4154	Has-domain(s)-with-predicted-1-alkyl-2-acetylglycerophosphocholine-esterase-activity-and-role-in-lipid-catabolic-process
ANIA_4135	Putative-delta-9-stearic-acid-desaturase;-converts-palmitic-acid-and-stearic-acid-to-palmitoleic-acid-and-oleic-acid;-null-mutant-has-decreased-fatty-acid-content;-synthetically-lethal-with-sdeA-mutation
ANIA_3781	Has-domain(s)-with-predicted-inorganic-phosphate-transmembrane-transporter-activity,-role-in-phosphate-ion-transport-and-membrane-localization
ANIA_3773	Ortholog-of-A.-oryzae-RIB40-:-AO090003001452,-Aspergillus-flavus-NRRL-3357-:-AFL2T_01630,-Aspergillus-versicolor-:-Aspve1_0083991,-Aspve1_0118939-and-Aspergillus-sydowii-:-Aspsy1_0040240,-Aspsy1_0088693
ANIA_3765	Putative-G-protein-coupled-receptor
ANIA_4180	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3548	
ANIA_4025	Has-domain(s)-with-predicted-hydrolase-activity,-tubulin-tyrosine-ligase-activity-and-role-in-cellular-protein-modification-process
ANIA_3776	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10420	Putative-alpha-glucosidase-with-a-predicted-role-in-starch-metabolism;-transcriptionally-induced-by-isomaltose-in-an-amyR-dependent-manner
ANIA_4120	Has-domain(s)-with-predicted-nitronate-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_4078	
ANIA_10513	Has-domain(s)-with-predicted-calcium-dependent-cysteine-type-endopeptidase-activity,-role-in-proteolysis-and-intracellular-localization
ANIA_3835	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_8270	Has-domain(s)-with-predicted-GTP-binding-activity-and-role-in-cell-cycle
ANIA_3639	Putative-dihydrolipoamide-transacylase;-alpha-keto-acid-dehydrogenase-E2-subunit
ANIA_8262	Secretin-like-G-protein-coupled-receptor
ANIA_11582	
ANIA_3706	S.-cerevisiae-ortholog-RPS10A-has-role-in-rRNA-export-from-nucleus;-palA-dependent-expression-independent-of-pH
ANIA_8148	
ANIA_8041	Glyceraldehyde-3-phosphate-dehydrogenase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-the-gpdA-promoter-is-a-commonly-used-regulatory-sequence-for-driving-constitutive-heterologous-gene-expression
ANIA_11061	Has-domain(s)-with-predicted-transferase-activity,-transferring-acyl-groups-other-than-amino-acyl-groups-activity
ANIA_8176	Has-domain(s)-with-predicted-structural-constituent-of-ribosome-activity,-role-in-translation-and-ribosome-localization
ANIA_8168	Regulatory-protein-involved-in-nitrogen-metabolite-repression
ANIA_7933	Has-domain(s)-with-predicted-methyltransferase-activity-and-role-in-metabolic-process
ANIA_3566	Putative-alpha-mannosidase-with-a-predicted-role-in-mannose-polymer-metabolism
ANIA_8266	Ortholog-of-A.-oryzae-RIB40-:-AO090138000120,-N.-fischeri-NRRL-181-:-NFIA_062350,-Aspergillus-flavus-NRRL-3357-:-AFL2T_08795-and-Aspergillus-versicolor-:-Aspve1_0047270
ANIA_3552	
ANIA_10509	
ANIA_11597	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03300,-A.-niger-CBS-513.88-:-An09g05625,-A.-niger-ATCC-1015-:-188256-mRNA,-Aspergillus-versicolor-:-Aspve1_0203178-and-Aspergillus-sydowii-:-Aspsy1_0050662
ANIA_4102	Putative-beta-glucosidase;-induced-by-carbon-starvation-induced-autophagy
ANIA_3499	Has-domain(s)-with-predicted-ATP-binding,-phosphotransferase-activity,-alcohol-group-as-acceptor-activity-and-role-in-amino-sugar-metabolic-process,-peptidoglycan-turnover
ANIA_3642	Ortholog(s)-have-role-in-ascospore-formation,-intracellular-protein-transport,-retrograde-transport,-endosome-to-Golgi-and-cytosol,-endosome,-nucleus,-retromer-complex-localization
ANIA_8102	Putative-pepsin-like-aspartic-protease;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_8235	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03710,-A.-niger-CBS-513.88-:-An09g06450,-A.-oryzae-RIB40-:-AO090102000581,-A.-niger-ATCC-1015-:-56877-mRNA-and-Aspergillus-versicolor-:-Aspve1_0047225
ANIA_4058	Putative-dihydroxy-acid-dehydratase-with-a-predicted-role-in-branched-chain-amino-acid-biosynthesis
ANIA_4201	Putative-acyl-CoA-synthetase/AMP-binding-domain-protein
ANIA_3791	Ortholog-of-A.-fumigatus-Af293-:-Afu2g03990,-A.-niger-CBS-513.88-:-An07g08650,-A.-oryzae-RIB40-:-AO090005001527,-A.-niger-ATCC-1015-:-180777-mRNA-and-Aspergillus-versicolor-:-Aspve1_0053136
ANIA_7971	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_3603	Has-domain(s)-with-predicted-tRNA-(adenine-N1-)-methyltransferase-activity,-role-in-tRNA-methylation-and-tRNA-(m1A)-methyltransferase-complex-localization
ANIA_8083	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4121	
ANIA_4113	Putative-histidine-containing-phosphotransfer-protein;-expression-upregulated-after-exposure-to-farnesol;-palA-dependent-expression-independent-of-pH
ANIA_4105	Putative-erythromycin-esterase-family-protein
ANIA_3735	Predicted-Ras-GTPase-activating-protein-(Ras-GAP)
ANIA_3493	Has-domain(s)-with-predicted-threonine-type-endopeptidase-activity,-role-in-proteolysis-involved-in-cellular-protein-catabolic-process-and-proteasome-core-complex-localization
ANIA_3719	MAP-kinase,-component-of-a-signaling-module-SteD-SteC-MkkB-MpkB-that-controls-coordination-of-development-and-secondary-metabolism;-phosphorylates-VeA-in-vitro
ANIA_4071	Ortholog(s)-have-role-in-dolichol-biosynthetic-process,-dolichol-linked-oligosaccharide-biosynthetic-process,-polyprenol-catabolic-process,-pseudohyphal-growth
ANIA_3935	Ortholog-of-A.-niger-CBS-513.88-:-An11g01810,-A.-oryzae-RIB40-:-AO090003000098,-Aspergillus-versicolor-:-Aspve1_0664899,-Aspergillus-sydowii-:-Aspsy1_0057505-and-Aspergillus-terreus-NIH2624-:-ATET_05830
ANIA_3804	Ortholog(s)-have-IgE-binding-activity
ANIA_3688	Response-regulator,-part-of-a-two-component-signal-transduction-system-involved-in-control-of-stress-response-and-conidiation;-transcript-induced-by-hydrogen-peroxide
ANIA_11581	
ANIA_7891	Putative-beta-1,4-endoglucanase
ANIA_7883	Ortholog-of-A.-nidulans-FGSC-A4-:-AN4396,-A.-niger-CBS-513.88-:-An11g03830,-Aspergillus-brasiliensis-:-Aspbr1_0113618,-A.-niger-ATCC-1015-:-38981-mRNA-and-Aspergillus-acidus-:-Aspfo1_0215105
ANIA_8237	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03730,-A.-niger-CBS-513.88-:-An09g06430,-A.-oryzae-RIB40-:-AO090102000583,-A.-niger-ATCC-1015-:-50026-mRNA-and-Aspergillus-versicolor-:-Aspve1_0143307
ANIA_3876	Ortholog(s)-have-carnitine-transmembrane-transporter-activity,-polyamine-transmembrane-transporter-activity
ANIA_11431	
ANIA_8129	Gal4-type-Zn(II)2Cys6-binuclear-cluster-DNA-binding-protein;-negative-regulator-of-asexual-development;-mutant-produces-increased-amounts-of-extracellular-proteinase-during-carbon-starvation
ANIA_3956	Ortholog-of-A.-fumigatus-Af293-:-Afu6g08010,-A.-niger-CBS-513.88-:-An11g02120,-A.-oryzae-RIB40-:-AO090003001561,-A.-niger-ATCC-1015-:-179443-mRNA-and-Aspergillus-versicolor-:-Aspve1_0131913
ANIA_3948	Ortholog(s)-have-Golgi-apparatus-localization
ANIA_7920	Has-domain(s)-with-predicted-hydrolase-activity,-acting-on-carbon-nitrogen-(but-not-peptide)-bonds-activity-and-role-in-nitrogen-compound-metabolic-process
ANIA_4172	Ortholog-of-A.-fumigatus-Af293-:-Afu6g07930,-A.-niger-CBS-513.88-:-An11g02850,-A.-oryzae-RIB40-:-AO090003000141,-A.-niger-ATCC-1015-:-208713-mRNA-and-Aspergillus-versicolor-:-Aspve1_0086847
ANIA_3794	Ortholog(s)-have-nucleus,-spindle-localization
ANIA_4148	Sugar-transporter;-transcriptionally-induced-by-growth-on-xylose

ANIA_8098	
ANIA_8241	Endochitinase-with-a-predicted-role-in-chitin-hydrolysis;-glycosylphosphatidylinositol-(GPI)-anchored-protein;-modiﬁed-by-O-linked-glycosylation;-localized-to-germination-sites,-hyphal-branch-points-and-regions-of-polarized-growth
ANIA_3503	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3793	Catalytic-subunit-of-protein-phosphatase-Z-(PPZ);-role-in-resistance-to-oxidative-stress
ANIA_4147	
ANIA_3785	Ortholog(s)-have-role-in-ascospore-formation,-heterochromatin-maintenance,-negative-regulation-of-histone-acetylation,-nucleosome-assembly-and-positive-regulation-of-chromatin-silencing-at-centromere,-more
ANIA_4041	Ortholog-of-A.-fumigatus-Af293-:-Afu4g00280,-A.-oryzae-RIB40-:-AO090701000844,-N.-fischeri-NRRL-181-:-NFIA_045350,-Aspergillus-flavus-NRRL-3357-:-AFL2T_06411-and-A.-clavatus-NRRL-1-:-ACLA_078580
ANIA_8181	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03060,-A.-niger-CBS-513.88-:-An09g05240,-A.-oryzae-RIB40-:-AO090102000509,-A.-niger-ATCC-1015-:-188502-mRNA-and-Aspergillus-versicolor-:-Aspve1_0143297
ANIA_8165	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02890,-A.-niger-CBS-513.88-:-An09g04870,-A.-oryzae-RIB40-:-AO090102000485,-A.-niger-ATCC-1015-:-43232-mRNA-and-Aspergillus-versicolor-:-Aspve1_0047117
ANIA_7939	Ortholog(s)-have-intracellular-localization
ANIA_3799	Ortholog(s)-have-low-affinity-zinc-ion-transmembrane-transporter-activity,-role-in-low-affinity-zinc-ion-transport,-response-to-zinc-ion-and-plasma-membrane-localization
ANIA_4062	Ortholog-of-A.-fumigatus-Af293-:-Afu1g05370,-A.-niger-CBS-513.88-:-An18g04210,-A.-oryzae-RIB40-:-AO090009000407,-A.-niger-ATCC-1015-:-42867-mRNA-and-Aspergillus-versicolor-:-Aspve1_0770039
ANIA_3684	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_3889	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_10557	Putative-ATP-dependent-RNA-helicase;-protein-levels-decrease-in-response-to-farnesol
ANIA_8605	Putative-peptidyl-prolyl-cis-trans-isomerase-(PPIase);-cyclophilin
ANIA_3551	
ANIA_4064	Putative-ADP/ATP-carrier-protein-with-a-predicted-role-in-energy-metabolism;-palA-dependent-expression-independent-of-pH
ANIA_4590	Sugar-transporter;-transcriptionally-induced-by-growth-on-xylose
ANIA_4566	Class-I-chitin-synthase-with-a-role-in-chitin-biosynthesis;-involved-with-ChsA-in-septum-formation-and-conidiation;-protein-expressed-at-high-levels-in-young-cleistothecia-and-in-mature-ascospores
ANIA_4701	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08790,-A.-niger-CBS-513.88-:-An07g04640,-A.-oryzae-RIB40-:-AO090020000437,-A.-niger-ATCC-1015-:-209665-mRNA-and-Aspergillus-versicolor-:-Aspve1_0133751
ANIA_4569	Ortholog(s)-have-role-in-ubiquinone-biosynthetic-process-and-mitochondrial-inner-membrane-localization
ANIA_4704	
ANIA_11108	Has-domain(s)-with-predicted-hydrolase-activity-and-role-in-metabolic-process
ANIA_4462	Putative-pyruvate-carboxylase-or-glutathione-synthase
ANIA_4295	Ortholog(s)-have-role-in-cardiolipin-metabolic-process,-cristae-formation,-negative-regulation-of-phosphatidylcholine-biosynthetic-process,-phosphatidylethanolamine-metabolic-process
ANIA_4422	Putative-aspartic-type-endopeptidase;-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_8774	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_4414	Putative-diphosphomevalonate-decarboxylase-with-a-predicted-role-in-sterol-metabolism
ANIA_8643	Ortholog(s)-have-role-in-cellular-response-to-heat,-cellular-response-to-hydrogen-peroxide
ANIA_5069	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02860,-A.-niger-CBS-513.88-:-An09g04830,-A.-oryzae-RIB40-:-AO090102000482,-A.-niger-ATCC-1015-:-212509-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041515
ANIA_5051	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_4487	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_4479	Putative-histidine-specific-protein-kinase,-part-of-a-two-component-signal-transduction-phosphorelay-system-involved-in-response-to-fungicides
ANIA_4622	Ortholog-of-A.-fumigatus-Af293-:-Afu2g02380,-A.-niger-CBS-513.88-:-An07g06420,-A.-oryzae-RIB40-:-AO090011000518,-A.-niger-ATCC-1015-:-53243-mRNA-and-Aspergillus-versicolor-:-Aspve1_0084793
ANIA_4614	Ortholog(s)-have-role-in-cellular-response-to-calcium-ion,-response-to-drug-and-RAVE-complex,-cytosol,-nucleus-localization
ANIA_5003	Ortholog(s)-have-role-in-negative-regulation-by-symbiont-of-host-inflammatory-response
ANIA_4391	Predicted-DDE1-transposon-related-ORF
ANIA_4746	Ortholog-of-A.-fumigatus-Af293-:-Afu3g06270,-A.-niger-CBS-513.88-:-An11g10070,-A.-niger-ATCC-1015-:-209093-mRNA,-Aspergillus-versicolor-:-Aspve1_0070854-and-Aspergillus-sydowii-:-Aspsy1_0087871
ANIA_4834	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07270,-A.-niger-CBS-513.88-:-An02g13430,-A.-oryzae-RIB40-:-AO090020000197,-A.-niger-ATCC-1015-:-37531-mRNA-and-Aspergillus-versicolor-:-Aspve1_0126541
ANIA_4818	Putative-histidine-containing-phosphotransfer-protein
ANIA_10548	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4853	Putative-membrane-protein-involved-in-a-signaling-pathway-that-activates-PacC-transcription-factor-in-response-to-alkaline-ambient-pH
ANIA_8639	Putative-alpha,alpha-trehalose-phosphate-synthase-(UDP-forming)-with-a-predicted-role-in-trehalose-biosynthesis
ANIA_4591	Ortholog(s)-have-phosphoglucomutase-activity-and-cytosol,-nucleus-localization
ANIA_4817	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4575	Ortholog-of-A.-oryzae-RIB40-:-AO090011000461,-Aspergillus-flavus-NRRL-3357-:-AFL2T_05228,-Aspergillus-versicolor-:-Aspve1_0042983-and-Aspergillus-sydowii-:-Aspsy1_0091136
ANIA_4336	Putative-L-arabinitol-4-dehydrogenase-with-a-predicted-role-in-L-arabinose/arabitol-and-D-xylose/D,L-xylulose/xylitol-metabolism
ANIA_5068	Ortholog-of-A.-nidulans-FGSC-A4-:-AN10146,-A.-fumigatus-Af293-:-Afu1g12190,-Afu5g02850,-A.-niger-CBS-513.88-:-An08g04540,-An09g04820-and-A.-oryzae-RIB40-:-AO090102000480,-AO090001000325
ANIA_4698	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08750,-A.-niger-CBS-513.88-:-An07g04700,-A.-niger-ATCC-1015-:-180062-mRNA,-Aspergillus-versicolor-:-Aspve1_0084699-and-Aspergillus-sydowii-:-Aspsy1_0155406
ANIA_4483	Ortholog(s)-have-protein-serine/threonine-kinase-activity,-role-in-protein-phosphorylation,-regulation-of-meiosis,-regulation-of-mitosis,-stress-activated-protein-kinase-signaling-cascade-and-cytoplasm,-nucleus-localization
ANIA_4848	Ortholog-of-A.-niger-CBS-513.88-:-An18g00170,-A.-oryzae-RIB40-:-AO090003001413,-Aspergillus-brasiliensis-:-Aspbr1_0048317,-Aspbr1_0201726-and-A.-niger-ATCC-1015-:-54071-mRNA
ANIA_4598	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_4741	Has-domain(s)-with-predicted-RNA-polymerase-II-transcription-cofactor-activity,-role-in-regulation-of-transcription-from-RNA-polymerase-II-promoter-and-mediator-complex-localization
ANIA_4328	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_8815	Putative-isoflavone-reductase-family-protein;-intracellular,-menadione-stress-induced-protein
ANIA_4733	Ortholog(s)-have-role-in-signal-transduction-and-Golgi-apparatus,-endoplasmic-reticulum,-mitochondrion,-plasma-membrane-localization
ANIA_4439	Ortholog(s)-have-ATPase-activity,-role-in-ER-associated-protein-catabolic-process,-invasive-growth-in-response-to-glucose-limitation,-pseudohyphal-growth-and-cytosol,-nucleus-localization
ANIA_4332	Acyl-CoA-dependent-ceramide-synthase;-mutants-show-hyphal-morphology-defects-and-an-increase-in-transition-from-asexual-to-sexual-development-however,-cleistothecia-maturation-and-ascospore-production-is-delayed
ANIA_10616	
ANIA_8661	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5943,-AN8548,-AN4642,-A.-fumigatus-Af293-:-Afu3g00850,-Afu4g08850-and-A.-niger-CBS-513.88-:-An02g13470,-An11g00090,-An03g01430,-An12g09260
ANIA_4586	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_4991	Predicted-inositol-phosphorylceramide-(IPC)-synthase-with-a-role-in-sphingolipid-metabolism;-mutation-confers-resistance-to-aureobasidin-A
ANIA_11442	
ANIA_4730	Ortholog(s)-have-mitochondrion,-ribosome-localization
ANIA_4722	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_8781	Ortholog-of-A.-niger-CBS-513.88-:-An07g03030,-Aspergillus-brasiliensis-:-Aspbr1_0150399,-N.-fischeri-NRRL-181-:-NFIA_026420,-A.-clavatus-NRRL-1-:-ACLA_006900-and-Aspergillus-acidus-:-Aspfo1_0056713
ANIA_4421	Has-domain(s)-with-predicted-FMN-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_4294	Ortholog(s)-have-mitochondrion-localization
ANIA_4691	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_4666	Ortholog(s)-have-phosphatidylinositol-binding-activity,-role-in-cellular-response-to-nitrogen-starvation,-piecemeal-microautophagy-of-nucleus-and-Golgi-apparatus,-endosome,-extrinsic-to-membrane,-fungal-type-vacuole-localization
ANIA_4535	Putative-F-box-protein
ANIA_4680	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08990,-A.-niger-CBS-513.88-:-An07g04160,-A.-oryzae-RIB40-:-AO090020000471,-A.-niger-ATCC-1015-:-200174-mRNA-and-Aspergillus-versicolor-:-Aspve1_0727063
ANIA_4906	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_4541	Ortholog-of-A.-fumigatus-Af293-:-Afu1g17750,-A.-niger-CBS-513.88-:-An07g07090,-A.-oryzae-RIB40-:-AO090026000620,-A.-niger-ATCC-1015-:-180112-mRNA-and-Aspergillus-versicolor-:-Aspve1_0134055
ANIA_5050	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4371	Ortholog-of-A.-nidulans-FGSC-A4-:-AN1972,-A.-fumigatus-Af293-:-Afu4g06510,-A.-niger-CBS-513.88-:-An04g05970,-An08g04550-and-A.-oryzae-RIB40-:-AO090003001143,-AO090023000935
ANIA_7895	Putative-oxidoreductase;-contains-Zn-dependent-alcohol-dehydrogenase-domain;-protein-expressed-at-increased-levels-during-osmoadaptation
ANIA_4988	Ortholog(s)-have-intracellular-localization
ANIA_4881	Ortholog-of-A.-niger-CBS-513.88-:-An02g06900,-A.-oryzae-RIB40-:-AO090003000669,-Aspergillus-versicolor-:-Aspve1_0061175,-Aspergillus-sydowii-:-Aspsy1_0796400-and-Aspergillus-terreus-NIH2624-:-ATET_04649
ANIA_8611	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-nucleoside-metabolic-process
ANIA_4744	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent

ANIA_8830	Predicted-protein-kinase-involved-in-halotolerance;-suppressor-of-molybdate-sensitivity-of-pacC-mutant
ANIA_8079	Has-domain(s)-with-predicted-DNA-binding,-protein-kinase-regulator-activity,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity
ANIA_4750	
ANIA_4255	Non-catalytic-atypical-hexokinase-involved-in-regulation-of-extracellular-proteases-in-response-to-carbon-starvation;-associates-with-mitochondria
ANIA_10520	Putative-alpha/beta-hydrolase
ANIA_4077	Has-domain(s)-with-predicted-DNA-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-chromosome,-centromeric-region-localization
ANIA_4126	Putative-dehydrogenase-with-a-predicted-role-in-metabolism-or-penicillin-biosynthesis
ANIA_4118	Ortholog(s)-have-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity
ANIA_4419	Ortholog(s)-have-protein-tyrosine-phosphatase-activity-and-role-in-ascospore-wall-assembly,-cAMP-mediated-signaling,-meiosis,-protein-dephosphorylation,-ribosomal-large-subunit-assembly
ANIA_8726	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4759	Predicted-Rab-guanine-nucleotide-exchange-factor-(Rab-GEF)
ANIA_5014	Ortholog(s)-have-cytosol,-nucleolus-localization
ANIA_10491	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_10483	Ortholog-of-A.-nidulans-FGSC-A4-:-AN2809,-A.-fumigatus-Af293-:-Afu2g16560,-Afu7g06360,-A.-niger-CBS-513.88-:-An16g00830-and-A.-oryzae-RIB40-:-AO090005000473,-AO090003001374,-AO090138000115
ANIA_4920	Putative-calcium-transporting-mitochondrial-ATPase-involved-in-calcium-homeostasis
ANIA_4769	ATP-sulfurylase-involved-in-sulfate-assimilation;-mutants-are-resistant-to-selenate
ANIA_4247	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_4239	Ortholog(s)-have-RSC-complex-localization
ANIA_8660	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_11097	Ortholog(s)-have-dioxygenase-activity,-role-in-secondary-metabolite-biosynthetic-process-and-cytoplasm-localization
ANIA_4820	Putative-succinate-semialdehyde-dehydrogenase-[NAD(P)+]-with-a-predicted-role-in-4-aminobutyrate-(GABA)-shunt
ANIA_4929	Ortholog-of-A.-fumigatus-Af293-:-Afu3g10610,-A.-niger-CBS-513.88-:-An02g06220,-A.-oryzae-RIB40-:-AO090003000605,-A.-niger-ATCC-1015-:-52257-mRNA-and-Aspergillus-versicolor-:-Aspve1_0128517
ANIA_10604	Ortholog-of-A.-fumigatus-Af293-:-Afu2g17760,-A.-niger-CBS-513.88-:-An03g02870,-Aspergillus-versicolor-:-Aspve1_0070749-and-Aspergillus-sydowii-:-Aspsy1_0148182
ANIA_8648	Has-domain(s)-with-predicted-RNA-binding,-RNA-directed-DNA-polymerase-activity,-ribonuclease-H-activity-and-role-in-RNA-dependent-DNA-replication
ANIA_4912	Ortholog(s)-have-Golgi-apparatus,-cell-division-site,-cell-tip-localization
ANIA_8118	Putative-cytochrome-c-oxidase-subunit-with-a-predicted-role-in-energy-metabolism
ANIA_8003	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02600,-A.-niger-CBS-513.88-:-An02g10100,-A.-niger-ATCC-1015-:-174284-mRNA,-Aspergillus-versicolor-:-Aspve1_0045487-and-Aspergillus-sydowii-:-Aspsy1_0033725
ANIA_4812	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_10475	Ortholog(s)-have-cytosol-localization
ANIA_3774	
ANIA_3901	Putative-lactic-acid-dehydrogenase-with-a-predicted-role-in-energy-metabolism
ANIA_4021	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_4013	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity,-role-in-transcription,-DNA-dependent-and-nucleus-localization
ANIA_4378	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4558	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_5067	Putative-transporter-of-the-major-facilitator-superfamily-(MFS);-expression-reduced-after-exposure-to-farnesol
ANIA_10530	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01690,-A.-niger-CBS-513.88-:-An14g03330,-A.-oryzae-RIB40-:-AO090701000773,-A.-niger-ATCC-1015-:-41738-mRNA-and-Aspergillus-carbonarius-ITEM-5010-:-Acar5010_173605
ANIA_7872	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_8275	Mitochondrial-citrate-synthase-with-a-predicted-role-in-the-TCA-cycle
ANIA_8204	Ortholog(s)-have-NAD+-diphosphatase-activity,-role-in-NADH-metabolic-process-and-cytosol,-nucleus,-peroxisome-localization
ANIA_8116	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02770,-A.-niger-CBS-513.88-:-An02g09830,-A.-oryzae-RIB40-:-AO090102000396,-A.-niger-ATCC-1015-:-52376-mRNA-and-Aspergillus-versicolor-:-Aspve1_0047008
ANIA_3690	Ortholog(s)-have-iron-ion-transmembrane-transporter-activity,-role-in-RNA-splicing,-mitochondrial-iron-ion-transport-and-mitochondrion-localization
ANIA_3916	Putative-glycerol-kinase-with-a-predicted-role-in-glycerol-metabolism
ANIA_3658	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_4589	Putative-translocon,-beta-subunit;-ortholog-of-S.-cerevisiae-Sss1p
ANIA_3818	Ortholog-of-A.-fumigatus-Af293-:-Afu2g03690,-A.-niger-CBS-513.88-:-An07g08250,-A.-oryzae-RIB40-:-AO090120000218,-A.-niger-ATCC-1015-:-126433-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041909
ANIA_4603	Putative-allantoinase-with-a-predicted-role-in-purine-metabolism
ANIA_4361	Putative-basic-region-and-leucine-zipper-(bZIP)-transcriptional-activator-with-a-role-in-regulating-sulfur-metabolism;-upregulated-in-A.-oryzae-and-A.-nidulans-under-hypoxic-growth-conditions
AN**IA_**4353	Has-domain(s)-with-predicted-3-oxoacyl-[acyl-carrier-protein]-synthase-activity-and-role-in-fatty-acid-biosynthetic-process
ANIA_4237	Ortholog-of-A.-fumigatus-Af293-:-Afu1g06160,-A.-niger-CBS-513.88-:-An18g05340,-A.-oryzae-RIB40-:-AO090001000437,-A.-niger-ATCC-1015-:-42949-mRNA-and-Aspergillus-versicolor-:-Aspve1_0064481
ANIA_10422	
ANIA_4122	Ortholog-of-A.-nidulans-FGSC-A4-:-AN2881,-AN10123,-AN0867,-A.-fumigatus-Af293-:-Afu1g13860,-Afu1g15180,-Afu3g11650-and-A.-niger-CBS-513.88-:-An08g07010,-An02g07440,-An01g13480
ANIA_4114	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_10459	Ortholog(s)-have-cytosol-localization
ANIA_4159	Putative-glutamate-ammonia-ligase-with-a-predicted-role-in-glutamate-and-glutamine-metabolism;-intracellular;-transcript-upregulated-by-nitrate-limitation;-protein-abundance-decreased-by-menadione-stress-and-induced-by-farnesol
ANIA_8175	Has-domain(s)-with-predicted-viral-capsid-localization
ANIA_8167	Ortholog-of-A.-fumigatus-Af293-:-Afu5g02950,-A.-niger-CBS-513.88-:-An09g05040,-A.-oryzae-RIB40-:-AO090102000494,-A.-niger-ATCC-1015-:-43220-mRNA-and-Aspergillus-versicolor-:-Aspve1_0143405
ANIA_8226	Has-domain(s)-with-predicted-role-in-Golgi-organization,-protein-transport-and-membrane-localization
ANIA_3504	Putative-alpha-1,4-glucosidase;-transcript-is-induced-by-nitrate
ANIA_7864	Putative-beta-1,4-xylosidase
ANIA_8218	Putative-thioredoxin-reductase
ANIA_10495	Has-domain(s)-with-predicted-CoA-transferase-activity-and-role-in-ketone-body-catabolic-process
ANIA_4195	Has-domain(s)-with-predicted-carbon-nitrogen-ligase-activity,-with-glutamine-as-amido-N-donor,-hydrolase-activity,-acting-on-carbon-nitrogen-(but-not-peptide)-bonds,-in-linear-amides-activity
ANIA_4329	Has-domain(s)-with-predicted-heme-binding-activity
ANIA_8590	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4785	Ortholog(s)-have-RNA-polymerase-II-core-promoter-proximal-region-sequence-specific-DNA-binding,-more
ANIA_4169	Ortholog(s)-have-role-in-ascospore-formation,-cellular-response-to-calcium-ion,-fungal-type-cell-wall-organization-and-cell-cortex,-cell-division-site,-cell-septum,-cytosol-localization
ANIA_3641	Ortholog(s)-have-gluconokinase-activity,-role-in-D-gluconate-metabolic-process-and-cytosol,-nucleus-localization
ANIA_4855	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07550,-A.-niger-CBS-513.88-:-An02g13140,-A.-oryzae-RIB40-:-AO090020000137,-A.-niger-ATCC-1015-:-173803-mRNA-and-Aspergillus-versicolor-:-Aspve1_0126888
ANIA_8791	Ortholog(s)-have-role-in-cellular-iron-ion-homeostasis-and-mitochondrion-localization
ANIA_4423	Has-domain(s)-with-predicted-nucleic-acid-binding-activity
ANIA_4275	
ANIA_4451	
ANIA_4443	Putative-methionine-synthase-with-a-predicted-role-in-methionine-metabolism;-protein-expressed-at-increased-levels-in-a-hapX-mutant-versus-wild-type
ANIA_8779	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_8814	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_8859	Putative-aspartate-kinase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_4214	Cell-end-marker-protein-kinase;-related-to-Schizosaccharomyces-pombe-Mod5;-null-mutant-exhibits-meandering-hyphal-phenotype;-interacts-with-TeaA;-predicted-prenylation;-wild-type-localization-requires-TeaA,-KipA
ANIA_4206	Has-domain(s)-with-predicted-heat-shock-protein-binding,-unfolded-protein-binding-activity-and-role-in-protein-folding
ANIA_8813	Has-domain(s)-with-predicted-ATP-binding,-ATPase-activity,-coupled-to-transmembrane-movement-of-substances-activity,-role-in-transport-and-integral-to-membrane-localization
ANIA_4888	Putative-pyruvate-decarboxylase-with-a-predicted-role-in-pyruvate-metabolism-or-penicillin-biosynthesis;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_5169	Has-domain(s)-with-predicted-phospholipid-binding-activity

ANIA_5517	Putative-F-box-protein
ANIA_5283	Ortholog-of-A.-nidulans-FGSC-A4-:-AN1572,-A.-fumigatus-Af293-:-Afu6g14000,-Afu8g05970,-A.-niger-CBS-513.88-:-An07g02380,-An08g07270-and-A.-oryzae-RIB40-:-AO090026000716,-AO090005000543
ANIA_5753	Ortholog-of-A.-fumigatus-Af293-:-Afu6g06840,-A.-niger-CBS-513.88-:-An18g06130,-A.-oryzae-RIB40-:-AO090020000272,-A.-niger-ATCC-1015-:-202682-mRNA-and-Aspergillus-versicolor-:-Aspve1_0131965
ANIA_5649	Ortholog-of-A.-nidulans-FGSC-A4-:-AN7262,-A.-fumigatus-Af293-:-Afu2g17000,-Afu4g13630,-A.-niger-CBS-513.88-:-An01g09380,-An04g09080-and-A.-oryzae-RIB40-:-AO090102000117,-AO090009000212
ANIA_8467	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_5429	Ortholog-of-A.-nidulans-FGSC-A4-:-AN8498,-AN8310,-AN11121,-A.-fumigatus-Af293-:-Afu3g01350-and-A.-niger-CBS-513.88-:-An12g08560,-An09g02370,-An13g02790,-An13g02620
ANIA_11622	
ANIA_5322	
ANIA_5731	Putative-chorismate-synthase-with-a-predicted-role-in-aromatic-amino-acid-biosynthesis
ANIA_8495	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_5465	Ortholog-of-A.-nidulans-FGSC-A4-:-AN2186,-AN10116,-A.-fumigatus-Af293-:-Afu1g13980,-Afu5g02460-and-A.-niger-CBS-513.88-:-An08g07120,-An02g10330,-An12g09760,-An07g05030,-An05g02480,-An12g10180
ANIA_11670	
ANIA_5604	Putative-fructose-bisphosphatase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-intracellular;-protein-abundance-decreased-by-menadione-stress;-expression-upregulated-after-exposure-to-farnesol
ANIA_5726	C2H2-type-zinc-finger-transcription-factor-involved-in-cation-homeostasis;-localized-to-nucleus-in-the-presence-of-calcium-chloride;-up-regulated-under-osmotic-stress-conditions
ANIA_5492	Has-domain(s)-with-predicted-deaminase-activity-and-role-in-purine-ribonucleoside-monophosphate-biosynthetic-process
ANIA_8498	Has-domain(s)-with-predicted-peptidase-activity
ANIA_5603	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3743,-A.-fumigatus-Af293-:-Afu4g11320,-Afu7g04400,-A.-niger-CBS-513.88-:-An13g00980,-An04g05280-and-A.-oryzae-RIB40-:-AO090005000127
ANIA_5361	Putative-beta-glucuronidase-with-a-predicted-role-in-carbohydrate-catabolism
ANIA_5314	Has-domain(s)-with-predicted-catalytic-activity,-pyridoxal-phosphate-binding-activity-and-role-in-metabolic-process
ANIA_5746	Putative-phosphopyruvate-hydratase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-intracellular;-protein-abundance-decreased-by-menadione-stress;-protein-induced-by-farnesol
ANIA_5449	Has-domain(s)-with-predicted-sulfuric-ester-hydrolase-activity-and-role-in-metabolic-process
ANIA_5350	Has-domain(s)-with-predicted-role-in-response-to-stress-and-integral-to-membrane-localization
ANIA_5342	Protein-expressed-at-increased-levels-during-osmoadaptation
ANIA_5318	Putative-non-ribosomal-peptide-synthetase;-expression-upregulated-after-exposure-to-farnesol
ANIA_5211	Ortholog(s)-have-1-phosphatidylinositol-3-phosphate-5-kinase-activity,-phosphatidylinositol-3-phosphate-binding-activity
ANIA_5257	Ortholog(s)-have-mitochondrion-localization
ANIA_5354	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity,-transferase-activity,-transferring-acyl-groups-other-than-amino-acyl-groups,-zinc-ion-binding-activity-and-role-in-oxidation-reduction-process
ANIA_8503	Ortholog-of-A.-niger-CBS-513.88-:-An13g03080,-Aspergillus-brasiliensis-:-Aspbr1_0044529,-Aspergillus-flavus-NRRL-3357-:-AFL2T_10601-and-Aspergillus-acidus-:-Aspfo1_0328979
ANIA_5231	Putative-exo-arabinanase
ANIA_5663	Ortholog-of-A.-fumigatus-Af293-:-Afu4g13710,-A.-niger-CBS-513.88-:-An01g09510,-A.-oryzae-RIB40-:-AO090010000145,-AO090009000200-and-A.-niger-ATCC-1015-:-171254-mRNA
ANIA_5540	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_5274	Ortholog(s)-have-sequence-specific-DNA-binding-activity
ANIA_8406	Putative-alcohol-dehydrogenase;-intracellular,-menadione-stress-induced-protein;-protein-expressed-at-decreased-levels-in-a-hapX-mutant-versus-wild-type
ANIA_5357	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_5349	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_8506	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_8415	Putative-acyl-coA-dehydrogenase;-member-of-the-aspyridone-(apd)-gene-cluster
ANIA_8367	Ortholog-of-A.-fumigatus-Af293-:-Afu4g14085,-A.-niger-CBS-513.88-:-An12g10420,-N.-fischeri-NRRL-181-:-NFIA_102230,-Aspergillus-flavus-NRRL-3357-:-AFL2T_11447-and-A.-fumigatus-A1163-:-AFUB_071240
ANIA_5099	Ortholog(s)-have-role-in-chromatin-remodeling-and-Rpd3L-Expanded-complex,-Rpd3S-complex-localization
ANIA_5234	Has-domain(s)-with-predicted-metal-ion-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5226	Acetate-permease,-involved-in-acetate-uptake;-has-similarity-to-GPR1/FUN34/YaaH-family-members;-transcript-induced-by-ethanol
ANIA_5218	Has-domain(s)-with-predicted-protein-dimerization-activity,-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_5373	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5782	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_8502	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_8553	Putative-catalase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism
ANIA_8537	Has-domain(s)-with-predicted-N,N-dimethylaniline-monooxygenase-activity,-NADP-binding,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_8573	
ANIA_8565	Putative-serine-O-acetyltransferase-with-a-predicted-role-in-cysteine-metabolism
ANIA_8549	
ANIA_5651	Ortholog(s)-have-RNA-polymerase-II-core-promoter-proximal-region-sequence-specific-DNA-binding,-more
ANIA_5671	Has-domain(s)-with-predicted-phospholipid-binding-activity
ANIA_4984	Putative-cyclin-dependent-protein-kinase;-locus-contains-the-conserved-upstream-open-reading-frame-(uORF)-AN4984-uORF
ANIA_4976	Putative-TATA-binding-protein;-contains-a-uORF-in-the-upstream-leader-sequence
ANIA_4544	Has-domain(s)-with-predicted-protein-tyrosine-phosphatase-activity,-protein-tyrosine/serine/threonine-phosphatase-activity-and-role-in-protein-dephosphorylation
ANIA_8755	Methylisocitrate-lyase;-predicted-role-in-the-glyoxylate-shunt;-mitochondrial-localization-signal-predicted
ANIA_4923	Putative-3-hydroxy-3-methylglutaryl-coenzyme-A-synthase-with-a-predicted-role-in-sterol-metabolism;-protein-expressed-at-decreased-levels-in-a-hapX-mutant-versus-wild-type;-expression-reduced-after-exposure-to-farnesol
ANIA_11093	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4866	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07720,-A.-oryzae-RIB40-:-AO090020000412,-A.-niger-ATCC-1015-:-173855-mRNA,-Aspergillus-versicolor-:-Aspve1_0051675-and-Aspergillus-sydowii-:-Aspsy1_0056549
ANIA_4349	Has-domain(s)-with-predicted-zinc-ion-binding-activity-and-role-in-intracellular-signal-transduction
ANIA_10550	Putative-transcriptional-regulator-with-homology-to-XlnR-and-AraR
ANIA_8837	Putative-ATP-dependent-NADH-kinase
ANIA_8707	Putative-fumarate-dehydratase-with-a-predicted-role-in-the-TCA-cycle
ANIA_4376	Putative-NADP-linked-glutamate-dehydrogenase;-predicted-role-in-glutamate/glutamine-metabolism;-involved-in-nitrogen-catabolite-repression;-induced-by-low-nitrate;-intracellular,-menadione-stress-induced-protein;-protein-induced-by-farnesol
ANIA_8839	Ortholog-of-A.-fumigatus-Af293-:-Afu5g05860,-A.-niger-CBS-513.88-:-An17g02060,-A.-niger-ATCC-1015-:-120073-mRNA,-Aspergillus-versicolor-:-Aspve1_0088196-and-Aspergillus-sydowii-:-Aspsy1_0159021
ANIA_4501	Putative-14-3-3-protein;-induced-by-carbon-starvation-induced-autophagy
ANIA_4518	Ortholog-of-A.-fumigatus-Af293-:-Afu2g03080,-A.-niger-CBS-513.88-:-An07g07480,-A.-oryzae-RIB40-:-AO090026000660,-Aspergillus-versicolor-:-Aspve1_0134145-and-Aspergillus-sydowii-:-Aspsy1_0163245
ANIA_4390	Putative-GPI-anchored-protein-with-similarity-to-Saccharomyces-cerevisiae-Ecm33p;-predicted-role-in-cell-wall-biosynthesis
ANIA_4608	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_4655	Ortholog(s)-have-2-iron,-2-sulfur-cluster-binding,-ferrous-iron-binding-activity,-role-in-cellular-iron-ion-homeostasis,-iron-sulfur-cluster-assembly,-tRNA-wobble-uridine-modification-and-mitochondrial-matrix-localization
ANIA_4956	Large-subunit-of-acetolactate-synthase-involved-in-branched-chain-amino-acid-biosynthesis-under-hypoxic-conditions
ANIA_4315	Ortholog(s)-have-role-in-regulation-of-translational-elongation-and-cytosolic-ribosome-localization
ANIA_8667	Wide-domain-GATA-type-transcription-factor;-mediates-nitrogen-metabolite-repression;-transcript-induced-by-nitrogen-starvation-and-degraded-in-response-to-ammonium-or-glutamine;-AreA-accumulates-in-the-nucleus-during-nitrogen-starvation
ANIA_10575	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_8770	Putative-bifunctional-enzyme-with-a-predicted-role-in-arginine-metabolism;-putative-acetylglutamate-kinase
ANIA_4410	
ANIA_4379	Ortholog-of-A.-fumigatus-Af293-:-Afu4g06670/aspf7,-A.-oryzae-RIB40-:-AO090023000918,-A.-niger-ATCC-1015-:-128537-mRNA,-Aspergillus-sydowii-:-Aspsy1_0036673-and-Aspergillus-terreus-NIH2624-:-ATET_05561
ANIA_8866	Putative-phosphoglycerate-dehydrogenase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_4692	
ANIA_4676	Ortholog-of-A.-fumigatus-Af293-:-Afu5g09010,-A.-niger-CBS-513.88-:-An07g04120,-A.-oryzae-RIB40-:-AO090020000473,-A.-niger-ATCC-1015-:-53289-mRNA-and-Aspergillus-versicolor-:-Aspve1_0084723
ANIA_4532	Putative-catechol-oxygenase
ANIA_4524	Has-domain(s)-with-predicted-DNA-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent

ANIA_4508	Bax-Inhibitor-family-protein;-accumulates-in-germinating-conidia-in-either-low-or-high-Pi-media-at-both-acidic-and-alkaline-pH
ANIA_8738	
ANIA_4565	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01860,-A.-niger-CBS-513.88-:-An07g05550,-A.-oryzae-RIB40-:-AO090120000188,-Aspergillus-versicolor-:-Aspve1_0084971-and-Aspergillus-sydowii-:-Aspsy1_0091128
ANIA_11120	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_4700	Protein-with-endo-beta-(1,3)-glucanase-activity,-involved-in-degradation-of-glucans
ANIA_11112	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4897	Ortholog(s)-have-role-in-asexual-sporulation-resulting-in-formation-of-a-cellular-spore,-cellular-response-to-heat-and-cell-septum,-cell-surface-localization
ANIA_5089	Ortholog-of-A.-oryzae-RIB40-:-AO090103000089,-Aspergillus-flavus-NRRL-3357-:-AFL2T_12280,-Aspergillus-terreus-NIH2624-:-ATET_03032-and-Aspergillus-aculeatus-ATCC16872-:-Aacu16872_034601
ANIA_4870	Ortholog-of-A.-fumigatus-Af293-:-Afu3g11290,-A.-niger-CBS-513.88-:-An02g07030,-A.-niger-ATCC-1015-:-47023-mRNA,-Aspergillus-versicolor-:-Aspve1_0571799-and-Aspergillus-sydowii-:-Aspsy1_0087725
ANIA_4745	Predicted-Rho-GTPase-activating-protein
ANIA_4397	Ortholog-of-S.-cerevisiae-Pcs60p
ANIA_10599	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-cellular-amino-acid-catabolic-process
ANIA_4900	Putative-bZIP-DNA-binding-protein-involved-in-regulating-nitrogen-metabolite-repression
ANIA_10595	Putative-septin;-present-only-in-filamentous-fungi
ANIA_5019	Has-domain(s)-with-predicted-5-methyltetrahydropteroyltriglutamate-homocysteine-S-methyltransferase-activity-and-role-in-methionine-biosynthetic-process
ANIA_8817	Ortholog-of-A.-fumigatus-Af293-:-Afu5g09420,-A.-niger-CBS-513.88-:-An15g02370,-A.-oryzae-RIB40-:-AO090020000561,-A.-niger-ATCC-1015-:-40493-mRNA-and-Aspergillus-versicolor-:-Aspve1_0141369
ANIA_4727	UDP-glucose-4-epimerase,-involved-in-galactose-metabolism;-converts-UDP-galactose-to-UDP-glucose;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_4786	Ortholog-of-A.-fumigatus-Af293-:-Afu3g06750,-A.-niger-CBS-513.88-:-An11g09580,-A.-oryzae-RIB40-:-AO090020000322,-A.-niger-ATCC-1015-:-39417-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051753
ANIA_10625	Has-domain(s)-with-predicted-nucleic-acid-binding,-ribonuclease-H-activity
ANIA_4325	
ANIA_4372	Protein-with-polygalacturonase-activity,-involved-in-degradation-of-pectin
ANIA_4940	Ortholog(s)-have-identical-protein-binding-activity,-role-in-cellular-response-to-stress,-reciprocal-meiotic-recombination-and-endoplasmic-reticulum,-mitochondrion,-plasma-membrane-localization
ANIA_5060	Ortholog-of-Aspergillus-flavus-NRRL-3357-:-AFL2T_03090,-Aspergillus-versicolor-:-Aspve1_0144439,-Aspergillus-sydowii-:-Aspsy1_0061440-and-Aspergillus-terreus-NIH2624-:-ATET_06090
ANIA_4367	Putative-chitin-synthase-III-with-a-predicted-role-in-chitin-biosynthesis;-transcript-is-induced-by-nitrate
ANIA_10603	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07510,-A.-niger-CBS-513.88-:-An02g13190,-A.-oryzae-RIB40-:-AO090020000145-and-Aspergillus-terreus-NIH2624-:-ATET_01722
ANIA_8655	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4563	Casein-kinase-I;-required-for-delivery-of-amino-acid-transporters-to-the-plasma-membrane
ANIA_5002	
ANIA_4323	Putative-branched-chain-amino-acid-aminotransferase-with-a-predicted-role-in-valine,-leucine,-and-isoleucine-metabolism
ANIA_8739	
ANIA_4990	Ortholog(s)-have-ferrous-iron-transmembrane-transporter-activity,-manganese-ion-transmembrane-transporter-activity
ANIA_4650	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01790,-A.-niger-CBS-513.88-:-An07g05410,-A.-oryzae-RIB40-:-AO090011000436,-Aspergillus-versicolor-:-Aspve1_0053771-and-Aspergillus-sydowii-:-Aspsy1_0059416
ANIA_4642	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5943,-AN8548,-AN8661,-A.-fumigatus-Af293-:-Afu3g00850,-Afu4g08850-and-A.-niger-CBS-513.88-:-An02g13470,-An11g00090,-An03g01430,-An12g09260
ANIA_11438	
ANIA_4792	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_4784	Ortholog-of-A.-fumigatus-Af293-:-Afu3g06710,-A.-oryzae-RIB40-:-AO090020000326,-A.-niger-ATCC-1015-:-39420-mRNA,-Aspergillus-versicolor-:-Aspve1_0127186-and-Aspergillus-sydowii-:-Aspsy1_0056625
ANIA_4768	Ortholog-of-A.-fumigatus-Af293-:-Afu3g06520,-A.-niger-CBS-513.88-:-An11g09800,-A.-oryzae-RIB40-:-AO090020000350,-A.-niger-ATCC-1015-:-209060-mRNA-and-Aspergillus-versicolor-:-Aspve1_0040163
ANIA_8741	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_4952	Ortholog-of-A.-fumigatus-Af293-:-Afu3g10350,-A.-niger-CBS-513.88-:-An16g04260,-A.-oryzae-RIB40-:-AO090003000585,-A.-niger-ATCC-1015-:-210546-mRNA-and-Aspergillus-versicolor-:-Aspve1_0027131
ANIA_8833	Ortholog-of-A.-niger-CBS-513.88-:-An17g01965,-A.-niger-ATCC-1015-:-134837-mRNA,-Aspergillus-versicolor-:-Aspve1_0046299,-Aspergillus-sydowii-:-Aspsy1_0093290-and-Aspergillus-terreus-NIH2624-:-ATET_09440
ANIA_8615	Putative-cytochrome-P450
ANIA_4360	Ortholog(s)-have-structural-molecule-activity
ANIA_4352	Ortholog(s)-have-mitochondrion-localization
ANIA_8756	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_4364	Ortholog-of-A.-fumigatus-Af293-:-Afu4g06520,-A.-niger-CBS-513.88-:-An04g00860,-A.-oryzae-RIB40-:-AO090023000934,-A.-niger-ATCC-1015-:-44301-mRNA-and-Aspergillus-versicolor-:-Aspve1_0133499
ANIA_10541	Has-domain(s)-with-predicted-DNA-binding,-protein-kinase-regulator-activity,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity
ANIA_4999	
ANIA_4758	Ortholog(s)-have-role-in-apoptotic-process-and-cytoplasm,-nucleus-localization
ANIA_11119	Has-domain(s)-with-predicted-cell-outer-membrane,-integral-to-membrane-localization
ANIA_5167	Has-domain(s)-with-predicted-phospholipid-binding,-zinc-ion-binding-activity
ANIA_5159	Ortholog(s)-have-1-alkyl-2-acetylglycerophosphocholine-esterase-activity,-role-in-cellular-response-to-oxidative-stress,-phospholipid-catabolic-process-and-cytosol,-nucleus-localization
ANIA_5672	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_5398	Has-domain(s)-with-predicted-iron-ion-binding,-oxidoreductase-activity,-acting-on-single-donors-with-incorporation-of-molecular-oxygen,-incorporation-of-two-atoms-of-oxygen-activity-and-role-in-oxidation-reduction-process
ANIA_5426	Putative-threonine-aldolase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_5324	Dehydrin-like-protein;-protein-induced-by-farnesol
ANIA_8346	Ortholog(s)-have-role-in-cellular-cadmium-ion-homeostasis,-cellular-response-to-cadmium-ion,-regulation-of-sulfur-metabolic-process-and-mitochondrion-localization
ANIA_5780	Ortholog-of-A.-niger-CBS-513.88-:-An18g06640,-A.-niger-ATCC-1015-:-43042-mRNA,-Aspergillus-versicolor-:-Aspve1_0053552,-Aspergillus-sydowii-:-Aspsy1_0852158-and-Aspergillus-terreus-NIH2624-:-ATET_07421
ANIA_5764	Transcript-induced-by-light-in-in-developmentally-competent-mycelia
ANIA_5756	
ANIA_9199	Putative-G-protein-coupled-receptor
ANIA_2912	Ortholog-of-A.-niger-CBS-513.88-:-An02g12880,-A.-niger-ATCC-1015-:-37485-mRNA,-Aspergillus-versicolor-:-Aspve1_0081767,-Aspergillus-sydowii-:-Aspsy1_0087435-and-Aspergillus-terreus-NIH2624-:-ATET_01690
ANIA_3032	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_3125	Has-domain(s)-with-predicted-role-in-response-to-stress-and-integral-to-membrane-localization
ANIA_2763	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_2739	Putative-DNA-polymerase-theta;-transcript-upregulated-in-response-to-camptothecin
ANIA_8551	Putative-transferase-with-a-predicted-role-in-the-pentose-phosphate-shunt-or-xylulose-metabolism
ANIA_5378	Ortholog(s)-have-siderophore-uptake-transmembrane-transporter-activity,-role-in-siderophore-transport,-transmembrane-transport-and-cytoplasmic-membrane-bounded-vesicle,-endosome-localization
ANIA_2749	Has-domain(s)-with-predicted-phospholipid-binding-activity
ANIA_9064	Xylitol-dehydrogenase-with-a-predicted-role-in-amino-acid-or-carbohydrate-metabolism;-putative-D-xylulose-reductase;-transcriptionally-induced-by-growth-on-xylose
ANIA_3004	Ortholog(s)-have-role-in-cellular-response-to-oxidative-stress-and-cytosol,-mitochondrion,-nucleus-localization
ANIA_9076	Transcript-repressed-by-light-in-developmentally-competent-mycelia
ANIA_9068	Ortholog-of-A.-niger-CBS-513.88-:-An12g00010,-A.-niger-ATCC-1015-:-50257-mRNA,-Aspergillus-versicolor-:-Aspve1_0047905,-Aspergillus-sydowii-:-Aspsy1_0104061-and-Aspergillus-terreus-NIH2624-:-ATET_01885
ANIA_5489	Ortholog-of-A.-fumigatus-Af293-:-Afu6g13220,-A.-niger-CBS-513.88-:-An08g10180,-A.-oryzae-RIB40-:-AO090003000447,-A.-niger-ATCC-1015-:-207748-mRNA-and-Aspergillus-versicolor-:-Aspve1_0084122
ANIA_5263	
ANIA_3182	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13220,-A.-niger-CBS-513.88-:-An02g09070,-A.-oryzae-RIB40-:-AO090012000811-and-Aspergillus-terreus-NIH2624-:-ATET_04087
ANIA_3408	Ortholog(s)-have-dipeptide-transporter-activity,-tripeptide-transporter-activity,-role-in-dipeptide-transport,-tripeptide-transport-and-fungal-type-vacuole,-plasma-membrane-localization
ANIA_2796	Predicted-LINE-transposon-related-ORF
ANIA_2626	Ortholog-of-A.-nidulans-FGSC-A4-:-AN1620,-A.-fumigatus-Af293-:-Afu8g02040/och3,-A.-niger-CBS-513.88-:-An03g01090/hocA,-An05g02320,-A.-oryzae-RIB40-:-AO090010000615-and-A.-niger-ATCC-1015-:-55132-mRNA
ANIA_3321	Has-domain(s)-with-predicted-aspartic-type-endopeptidase-activity-and-role-in-proteolysis
ANIA_10388	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_3456	Putative-cystathionine-gamma-synthase-with-a-predicted-role-in-methionine-metabolism
ANIA_5683	Ortholog-of-A.-fumigatus-Af293-:-Afu7g04240,-A.-oryzae-RIB40-:-AO090005000109,-A.-niger-ATCC-1015-:-44715-mRNA,-Aspergillus-versicolor-:-Aspve1_0699953-and-Aspergillus-sydowii-:-Aspsy1_0043760

ANIA_5659	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_2943	Putative-regulator-of-secondary-metabolism
ANIA_2685	Ortholog-of-A.-niger-ATCC-1015-:-184563-mRNA,-Aspergillus-versicolor-:-Aspve1_0134218,-Aspergillus-sydowii-:-Aspsy1_0155644-and-Aspergillus-terreus-NIH2624-:-ATET_06110
ANIA_2669	Has-domain(s)-with-predicted-role-in-response-to-stress-and-integral-to-membrane-localization
ANIA_3075	Zinc-finger-protein-of-unknown-function;-overexpression-confers-the-"fluffy"-phenotype
ANIA_2701	Ortholog-of-A.-fumigatus-Af293-:-Afu5g13970,-A.-niger-CBS-513.88-:-An14g05410,-A.-oryzae-RIB40-:-AO090113000103,-A.-niger-ATCC-1015-:-201720-mRNA-and-Aspergillus-versicolor-:-Aspve1_0134178
ANIA_3261	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_8523	Ortholog-of-A.-fumigatus-Af293-:-Afu5g09810,-A.-niger-CBS-513.88-:-An13g02380,-A.-niger-ATCC-1015-:-191783-mRNA,-Aspergillus-versicolor-:-Aspve1_0046869-and-Aspergillus-sydowii-:-Aspsy1_0049687
ANIA_2855	C2H2-finger-domain-transcription-factor;-undergoes-proteolytic-activation-in-response-to-alkaline-ambient-pH;-physically-interacts-with-PalA-by-two-hybrid-analysis
ANIA_3110	Ortholog(s)-have-role-in-ascospore-formation,-fungal-type-cell-wall-organization,-regulation-of-conjugation-with-cellular-fusion-and-cytoplasm-localization
ANIA_3102	Putative-histidine-containing-phosphotransfer-protein
ANIA_5235	Ortholog(s)-have-role-in-transcription-coupled-nucleotide-excision-repair-and-Ddb1-Ckn1-complex,-cytosol-localization
ANIA_5104	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_5278	Has-domain(s)-with-predicted-ATP-binding,-helicase-activity-and-role-in-viral-genome-replication
ANIA_5421	Has-domain(s)-with-predicted-N,N-dimethylaniline-monooxygenase-activity,-NADP-binding,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_8443	Ortholog-of-A.-fumigatus-Af293-:-Afu7g00720,-A.-niger-CBS-513.88-:-An12g10400,-A.-oryzae-RIB40-:-AO090701000239,-A.-niger-ATCC-1015-:-55184-mRNA-and-Aspergillus-sydowii-:-Aspsy1_0049797
ANIA_3348	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3303,-AN2044,-AN8727,-A.-fumigatus-Af293-:-Afu4g10080,-Afu7g00420,-Afu4g01242-and-A.-niger-CBS-513.88-:-An02g09530,-An03g00420,-An16g01900,-An16g06080,-An04g06980,-An03g00215
ANIA_3344	Putative-GNAT-type-acetyltransferase
ANIA_2974	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2939	Ortholog(s)-have-mitochondrion-localization
ANIA_2697	
ANIA_9131	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_8427	
ANIA_5171	
ANIA_5163	Ortholog-of-A.-fumigatus-Af293-:-Afu1g06970,-A.-niger-CBS-513.88-:-An07g09540,-A.-oryzae-RIB40-:-AO090012000949,-A.-niger-ATCC-1015-:-39631-mRNA-and-Aspergillus-versicolor-:-Aspve1_0320319
ANIA_3078	
ANIA_3221	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10407	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_11356	
ANIA_10335	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_10378	Has-domain(s)-with-predicted-protein-dimerization-activity,-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_3438	Has-domain(s)-with-predicted-ARF-guanyl-nucleotide-exchange-factor-activity,-phospholipid-binding-activity,-role-in-regulation-of-ARF-protein-signal-transduction-and-intracellular-localization
ANIA_10399	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_8534	Purine-transporter-with-high-affinity-for-hypoxanthine-and-adenine;-takes-up-purines-for-nucleotide-salvage-and-as-nitrogen-sources;-induced-by-uric-acid;-regulated-by-UaY-and-AreA
ANIA_5262	Has-domain(s)-with-predicted-cis-stilbene-oxide-hydrolase-activity,-epoxide-hydrolase-activity,-role-in-response-to-toxin-and-membrane-localization
ANIA_5254	Has-domain(s)-with-predicted-RNA-binding,-RNA-directed-DNA-polymerase-activity-and-role-in-RNA-dependent-DNA-replication
ANIA_10676	Ortholog(s)-have-UDP-galactose-transmembrane-transporter-activity,-role-in-UDP-galactose-transmembrane-transport,-conjugation-with-cellular-fusion,-galactomannan-biosynthetic-process,-protein-galactosylation-and-Golgi-membrane-localization
ANIA_5575	Ortholog-of-A.-fumigatus-Af293-:-Afu4g11602,-A.-oryzae-RIB40-:-AO090003001575,-A.-niger-ATCC-1015-:-193197-mRNA,-Aspergillus-versicolor-:-Aspve1_0029291-and-Aspergillus-sydowii-:-Aspsy1_0870778
ANIA_11476	Ortholog-of-A.-fumigatus-Af293-:-Afu2g03190,-Aspergillus-versicolor-:-Aspve1_0086542,-Aspve1_0089117,-Aspergillus-sydowii-:-Aspsy1_0093985-and-Aspergillus-brasiliensis-:-Aspbr1_0045764,-Aspbr1_0201559
ANIA_5168	Has-domain(s)-with-predicted-nucleoside-triphosphatase-activity,-nucleotide-binding-activity
ANIA_5580	Ortholog-of-A.-fumigatus-Af293-:-Afu4g11550,-A.-niger-CBS-513.88-:-An04g04940,-A.-niger-ATCC-1015-:-55036-mRNA,-Aspergillus-versicolor-:-Aspve1_0169641-and-Aspergillus-sydowii-:-Aspsy1_0057110
ANIA_8455	Ortholog-of-A.-fumigatus-Af293-:-Afu5g10940,-N.-fischeri-NRRL-181-:-NFIA_076300,-Aspergillus-flavus-NRRL-3357-:-AFL2T_12537,-A.-clavatus-NRRL-1-:-ACLA_014000-and-Aspergillus-versicolor-:-Aspve1_0042580
ANIA_5131	Ortholog(s)-have-role-in-CVT-pathway,-ER-to-Golgi-vesicle-mediated-transport,-autophagic-vacuole-assembly,-cellular-membrane-fusion-and-cellular-response-to-nitrogen-starvation,-more
ANIA_5582	
ANIA_5558	Broad-specificity-thermostable-alkaline-protease;-extracellular;-regulated-by-nitrogen,-carbon-and-sulfur-metabolite-repression;-transcript-repressed-by-light-in-developmentally-competent-mycelia
ANIA_5098	Ortholog(s)-have-spliceosomal-complex-localization
ANIA_5156	Pho80-like-cyclin-involved-in-regulation-of-development-and-phosphate-homeostasis,-interacts-with-the-cyclin-dependent-kinase-PhoA
ANIA_8321	
ANIA_5303	Ortholog-of-A.-fumigatus-Af293-:-Afu2g15100,-N.-fischeri-NRRL-181-:-NFIA_090360,-A.-clavatus-NRRL-1-:-ACLA_072370,-Aspergillus-versicolor-:-Aspve1_0086623-and-Aspergillus-sydowii-:-Aspsy1_0050370
ANIA_5440	Putative-cytochrome-c-peroxidase;-expression-upregulated-after-exposure-to-farnesol
ANIA_8462	Protein-of-unknown-function;-NeddH-associated-protein
ANIA_5524	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_5248	Has-domain(s)-with-predicted-ATP-dependent-helicase-activity-and-role-in-DNA-recombination
ANIA_8413	Putative-exporter;-member-of-the-aspyridone-(apd)-gene-cluster
ANIA_5225	Ortholog-of-A.-fumigatus-Af293-:-Afu7g01680,-Afu4g04605,-A.-niger-CBS-513.88-:-An13g04060,-An07g08820,-An12g01030,-A.-oryzae-RIB40-:-AO090206000029-and-A.-niger-ATCC-1015-:-44948-mRNA,-53175-mRNA
ANIA_5217	Protein-with-similarity-to-sphingolipid-long-chain-base-responsive-protein-Pil1;-putative-conserved-eiosome-component;-expression-upregulated-after-farnesol-exposure;-present-at-the-conidial-periphery-and-in-punctate-structures-in-mycelia
ANIA_5252	Has-domain(s)-with-predicted-zinc-ion-binding-activity-and-intracellular-localization
ANIA_5236	Ortholog(s)-have-Golgi-apparatus-localization
ANIA_5634	Isocitrate-lyase,-required-for-utilization-of-acetate-and-fatty-acids-as-carbon-sources;-transcriptional-induction-in-response-to-acetate-is-mediated-by-FacB;-transcriptional-induction-in-response-to-long-chain-fatty-acids-mediated-by-FarA
ANIA_5626	Acetyl-CoA-synthase,-required-for-utilization-of-acetate-as-a-carbon-source;-transcriptional-induction-by-acetate-is-mediated-by-FacB;-carbon-catabolite-repression-is-mediated-by-CreA
ANIA_8538	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_5144	Putative-6-phosphofructo-2-kinase-with-a-predicted-role-in-mannose/mannitol,-fructose,-and-sorbose/sorbitol-metabolism
ANIA_8401	Protein-with-alpha-N-arabinofuranosidase-activity,-involved-in-degradation-of-xylans;-putative-beta-1,4-xylosidase
ANIA_5228	Putative-NADH:flavin-oxidoreductase/NADH-oxidase;-intracellular,-menadione-stress-induced-protein
ANIA_9473	Ortholog-of-A.-fumigatus-Af293-:-Afu4g11270,-A.-niger-CBS-513.88-:-An04g05360,-A.-oryzae-RIB40-:-AO090003001094,-A.-niger-ATCC-1015-:-55020-mRNA-and-Aspergillus-versicolor-:-Aspve1_0694359
ANIA_5425	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5191	Ortholog(s)-have-3-hydroxyacyl-[acyl-carrier-protein]-dehydratase-activity,-role-in-fatty-acid-biosynthetic-process-and-mitochondrion-localization
ANIA_2937	Ortholog-of-A.-fumigatus-Af293-:-Afu3g08210,-A.-niger-CBS-513.88-:-An02g11760,-A.-niger-ATCC-1015-:-174968-mRNA,-Aspergillus-versicolor-:-Aspve1_0081742-and-Aspergillus-sydowii-:-Aspsy1_0042633
ANIA_3049	Putative-endo-mannanase-GH76-family-protein;-predicted-type-I-transmembrane-protein
ANIA_8485	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_5447	Putative-glutamate-decarboxylase-with-a-predicted-role-in-4-aminobutyrate-(GABA)-shunt
ANIA_8439	Protein-of-unknown-function;-transcript-is-induced-by-nitrate;-predicted-NirA-binding-site
ANIA_11475	
ANIA_8340	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2822	Has-domain(s)-with-predicted-transporter-activity,-role-in-transmembrane-transport,-water-transport-and-integral-to-membrane-localization
ANIA_2814	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_9121	Protein-with-a-glycogen-binding-domain-involved-in-sexual-development;-regulated-by-VeA-and-FlbA
ANIA_5129	70-kilodalton-heat-shock-protein;-protein-abundance-decreased-by-menadione-stress;-physically-associates-with-importin-alpha,-KapA;-palA-dependent-expression-independent-of-pH;-protein-induced-by-farnesol
ANIA_9501	Ortholog-of-A.-fumigatus-Af293-:-Afu8g06340,-A.-niger-CBS-513.88-:-An16g02390,-A.-niger-ATCC-1015-:-38061-mRNA,-38988-mRNA-and-Aspergillus-sydowii-:-Aspsy1_0093362
ANIA_5213	Ortholog(s)-have-Golgi-apparatus,-cell-division-site,-cell-tip-localization
ANIA_8512	Protein-of-unknown-function;-adjacent-to-tdi-(terrequinone-biosynthesis)-gene-cluster.-Not-required-for-terrequinone-biosynthesis
ANIA_11489	Protein-of-unknown-function;-transcript-is-induced-by-nitrate

ANIA_11115	Ortholog-of-A.-fumigatus-Af293-:-Afu6g02740,-A.-niger-CBS-513.88-:-An12g08340,-A.-oryzae-RIB40-:-AO090120000168,-Aspergillus-brasiliensis-:-Aspbr1_0129816-and-N.-fischeri-NRRL-181-:-NFIA_049060
ANIA_9476	Ortholog-of-Aspergillus-acidus-:-Aspfo1_0097096,-Aspfo1_0097585,-Aspfo1_0098396,-Aspfo1_0099194,-Aspfo1_0099992
ANIA_8351	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5728	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_10694	Ortholog-of-A.-fumigatus-Af293-:-Afu4g11740,-A.-niger-CBS-513.88-:-An01g06990,-A.-niger-ATCC-1015-:-51896-mRNA,-Aspergillus-versicolor-:-Aspve1_0042220-and-Aspergillus-sydowii-:-Aspsy1_0149194
ANIA_5593	Putative-F-box-protein;-NeddH-associated-protein;-required-for-control-of-sexual-development-in-response-to-light;-required-for-ascospore-maturation-development-of-fully-grown-sexual-fruit-bodies
ANIA_2896	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_9195	Ortholog-of-A.-fumigatus-Af293-:-Afu3g11890,-A.-niger-CBS-513.88-:-An01g14950,-A.-oryzae-RIB40-:-AO090010000214,-A.-niger-ATCC-1015-:-35377-mRNA-and-Aspergillus-versicolor-:-Aspve1_0141515
ANIA_3143	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13940,-A.-niger-CBS-513.88-:-An09g04780,-A.-oryzae-RIB40-:-AO090012000757,-A.-niger-ATCC-1015-:-50103-mRNA-and-Aspergillus-versicolor-:-Aspve1_0129064
ANIA_9187	Putative-F-box-protein
ANIA_5549	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10657	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_5430	
ANIA_8444	Protein-with-similarity-to-cellulose-synthase;-predicted-role-in-beta-glucan-synthesis
ANIA_5117	
ANIA_3050	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_8473	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_5568	Putative-F-box-protein
ANIA_9086	Ortholog(s)-have-Rab-guanyl-nucleotide-exchange-factor-activity,-role-in-ER-to-Golgi-vesicle-mediated-transport,-intra-Golgi-vesicle-mediated-transport-and-TRAPP-complex,-cis-Golgi-network-membrane,-cytosol,-nucleus-localization
ANIA_5200	Putative-kynurenine-3-monooxygenase-with-a-predicted-role-in-aromatic-amino-acid-biosynthesis
ANIA_5771	Protein-of-unknown-function;-transcript-is-induced-by-nitrate
ANIA_10717	Ortholog(s)-have-role-in-mitochondrial-respiratory-chain-complex-II-assembly-and-mitochondrion-localization
ANIA_10709	Putative-glutamine-fructose-6-phosphate-transaminase
ANIA_5372	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_5356	Putative-carnitine-transporter;-transcriptional-induction-in-response-to-acetate-is-mediated-by-FacB;-transcriptional-induction-in-response-to-long-chain-fatty-acids-is-mediated-by-FarA
ANIA_5776	Ortholog(s)-have-role-in-hypotonic-response-and-barrier-septum-localization
ANIA_5629	Putative-NADH-dehydrogenase-(ubiquinone)-with-a-predicted-role-in-energy-metabolism
ANIA_8544	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0033877-and-Aspergillus-sydowii-:-Aspsy1_0466900
ANIA_5445	Ortholog-of-A.-fumigatus-Af293-:-Afu6g13510,-A.-niger-CBS-513.88-:-An08g08780,-A.-oryzae-RIB40-:-AO090103000339,-A.-niger-ATCC-1015-:-55723-mRNA-and-Aspergillus-versicolor-:-Aspve1_0684657
ANIA_5170	Putative-Zn(II)2Cys6-transcription-factor;-negative-regulator-of-sexual-development
ANIA_8426	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_5146	Has-domain(s)-with-predicted-FMN-binding,-heme-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_5490	Ortholog-of-A.-niger-CBS-513.88-:-An08g10190,-A.-oryzae-RIB40-:-AO090003000446,-Aspergillus-brasiliensis-:-Aspbr1_0122785,-A.-niger-ATCC-1015-:-37923-mRNA-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_02543
ANIA_5716	Putative-inosine-5'-monophosphate-dehydrogenase-with-a-predicted-role-in-purine-metabolism
ANIA_5375	Has-domain(s)-with-predicted-RNA-polymerase-II-transcription-cofactor-activity,-role-in-regulation-of-transcription-from-RNA-polymerase-II-promoter-and-mediator-complex-localization
ANIA_8540	Siderophore-iron-transporter
ANIA_5367	Ortholog-of-A.-fumigatus-Af293-:-Afu2g17475,-A.-oryzae-RIB40-:-AO090138000095,-N.-fischeri-NRRL-181-:-NFIA_092880,-Aspergillus-flavus-NRRL-3357-:-AFL2T_08774-and-A.-clavatus-NRRL-1-:-ACLA_076380
ANIA_3442	Ortholog-of-A.-fumigatus-Af293-:-Afu3g05640,-A.-niger-CBS-513.88-:-An11g11000,-A.-niger-ATCC-1015-:-39526-mRNA,-Aspergillus-versicolor-:-Aspve1_0128704-and-Aspergillus-sydowii-:-Aspsy1_0030125
ANIA_3184	Putative-aldose-1-epimerase-with-a-predicted-role-in-glucose-metabolism;-transcriptionally-induced-by-growth-on-xylose
ANIA_9105	Ortholog-of-A.-fumigatus-Af293-:-Afu7g02050,-A.-niger-CBS-513.88-:-An12g00620,-A.-oryzae-RIB40-:-AO090038000582,-A.-niger-ATCC-1015-:-212814-mRNA-and-Aspergillus-versicolor-:-Aspve1_0409473
ANIA_3407	Has-domain(s)-with-predicted-serine-type-endopeptidase-activity-and-role-in-proteolysis
ANIA_8568	
ANIA_5296	Two-component-signaling-protein-with-histidine-kinase-and-response-regulator-domains;-involved-in-control-of-conidiation
ANIA_8461	Ortholog-of-A.-fumigatus-Af293-:-Afu3g00710,-A.-niger-CBS-513.88-:-An03g00770,-A.-oryzae-RIB40-:-AO090009000146,-A.-niger-ATCC-1015-:-214715-mRNA-and-Aspergillus-versicolor-:-Aspve1_0033697
ANIA_10196	Ortholog-of-A.-fumigatus-Af293-:-Afu8g04830,-A.-niger-CBS-513.88-:-An16g07980,-A.-oryzae-RIB40-:-AO090005000663,-Aspergillus-versicolor-:-Aspve1_0125148-and-Aspergillus-sydowii-:-Aspsy1_0692116
ANIA_2331	Protein-with-pectin-lyase-activity,-involved-in-degradation-of-pectin
ANIA_10307	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_9073	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_9149	Ortholog(s)-have-Golgi-apparatus,-cell-tip,-cytoplasmic-vesicle,-endoplasmic-reticulum-localization
ANIA_10370	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07980,-A.-niger-CBS-513.88-:-An16g01990,-A.-oryzae-RIB40-:-AO090005001498,-A.-niger-ATCC-1015-:-41302-mRNA-and-Aspergillus-versicolor-:-Aspve1_0164633
ANIA_1687	
ANIA_9100	Ortholog-of-A.-fumigatus-Af293-:-Afu7g02100,-A.-niger-CBS-513.88-:-An12g00570,-A.-oryzae-RIB40-:-AO090038000587,-A.-niger-ATCC-1015-:-50281-mRNA-and-Aspergillus-versicolor-:-Aspve1_0144629
ANIA_3361	Bacterial-rhodopsin-family-G-protein-coupled-receptor-like-protein
ANIA_3345	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_2643	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3287	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_1425	Putative-transcription-factor-containing-a-Zn2-Cys6-binuclear-cluster-domain;-required-for-transcriptional-activation-of-genes-involved-in-utilization-of-short-chain-fatty-acids;-highly-conserved-in-filamentous-ascomycetes
ANIA_1417	
ANIA_8918	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_2227	Putative-beta-glucosidase-with-a-predicted-role-in-degradation-of-glucans
ANIA_3206	Putative-aryl-alcohol-oxidase-related-protein;-protein-expressed-at-decreased-levels-in-a-hapX-mutant-versus-wild-type;-transcript-is-induced-by-nitrate
ANIA_2682	Has-domain(s)-with-predicted-FMN-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_2666	Putative-oxidoreductase-with-a-predicted-role-in-carbohydrate-or-amino-acid-metabolism;-putative-D-xylulose-reductase
ANIA_2658	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3530,-A.-fumigatus-Af293-:-Afu1g13760,-Afu4g00490,-Afu4g14350,-A.-niger-CBS-513.88-:-An09g01580,-A.-oryzae-RIB40-:-AO090166000071-and-A.-niger-ATCC-1015-:-188861-mRNA
ANIA_3087	Ortholog-of-A.-fumigatus-Af293-:-Afu3g12360,-A.-niger-CBS-513.88-:-An03g02910,-A.-oryzae-RIB40-:-AO090005000731,-A.-niger-ATCC-1015-:-45645-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051266
ANIA_3179	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13160,-A.-niger-CBS-513.88-:-An02g09030,-A.-oryzae-RIB40-:-AO090012000817,-A.-niger-ATCC-1015-:-207131-mRNA-and-Aspergillus-versicolor-:-Aspve1_0039289
ANIA_2852	Ortholog(s)-have-sequence-specific-DNA-binding-activity-and-cytosol,-nucleus-localization
ANIA_2836	Ortholog-of-A.-niger-CBS-513.88-:-An03g01740,-An16g00290,-Aspergillus-brasiliensis-:-Aspbr1_0043644,-Aspbr1_0049046,-Aspbr1_0132878-and-A.-niger-ATCC-1015-:-141246-mRNA,-45726-mRNA
ANIA_3072	Has-domain(s)-with-predicted-nucleic-acid-binding,-nucleotide-binding-activity
ANIA_2944	Transcriptional-co-activator-of-the-major-nitrogen-regulatory-protein-AreA;-transcript-is-induced-by-nitrate
ANIA_2928	Ortholog-of-A.-fumigatus-Af293-:-Afu3g08110,-A.-niger-CBS-513.88-:-An02g11620,-A.-oryzae-RIB40-:-AO090005001467,-Aspergillus-versicolor-:-Aspve1_0550880-and-Aspergillus-terreus-NIH2624-:-ATET_01658
ANIA_2686	Ortholog-of-A.-fumigatus-Af293-:-Afu5g14070,-A.-oryzae-RIB40-:-AO090113000122,-A.-niger-ATCC-1015-:-41891-mRNA,-Aspergillus-versicolor-:-Aspve1_0042658-and-Aspergillus-sydowii-:-Aspsy1_0047466
ANIA_3172	Ortholog-of-S.-cerevisiae-RPS0A-and-RPS0B;-expression-reduced-after-exposure-to-farnesol
ANIA_2794	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_9085	Ortholog(s)-have-spliceosomal-complex-localization
ANIA_3142	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13100,-A.-niger-CBS-513.88-:-An02g09000,-A.-oryzae-RIB40-:-AO090012000819,-A.-niger-ATCC-1015-:-52354-mRNA-and-Aspergillus-versicolor-:-Aspve1_0128413
ANIA_1670	Ortholog(s)-have-role-in-fungal-type-cell-wall-organization-and-hyphal-cell-wall-localization
ANIA_1646	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0064838-and-Aspergillus-sydowii-:-Aspsy1_0059989
ANIA_2913	Ortholog-of-A.-nidulans-FGSC-A4-:-AN4375,-A.-fumigatus-Af293-:-Afu3g07740,-Afu4g06610,-A.-niger-CBS-513.88-:-An04g00930-and-A.-oryzae-RIB40-:-AO090023000927,-AO090020000420
ANIA_3017	Has-domain(s)-with-predicted-cis-stilbene-oxide-hydrolase-activity,-epoxide-hydrolase-activity,-role-in-response-to-toxin-and-membrane-localization
ANIA_2243	Putative-carbamoyl-phosphate-synthase-or-aspartate-carbamoyltransferase-with-a-predicted-role-in-arginine-or-pyrimidine-metabolism
ANIA_2729	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization

ANIA_2630	
ANIA_2692	Phosphoprotein-regulated-by-proline-directed-phosphorylation;-multi-copy-suppressor-of-nimA1
ANIA_1523	Putative-F1F0-ATPase-complex-subunit-with-a-predicted-role-in-energy-metabolism
ANIA_2653	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_3447	Ortholog(s)-have-cytosol-localization
ANIA_3449	Ortholog(s)-have-ubiquitin-specific-protease-activity,-role-in-protein-deubiquitination,-regulation-of-transcription,-DNA-dependent-and-cytosol,-nucleus-localization
ANIA_3199	MFS-sugar-transporter;-induced-by-lactose-and-galactose
ANIA_2980	Ortholog(s)-have-structural-constituent-of-ribosome-activity,-role-in-cytoplasmic-translation-and-cytosolic-large-ribosomal-subunit,-nucleolus-localization
ANIA_9010	Ortholog(s)-have-nicotinamide-mononucleotide-transmembrane-transporter-activity,-role-in-nicotinamide-mononucleotide-transport-and-mitochondrion-localization
ANIA_1902	Ortholog-of-A.-fumigatus-Af293-:-Afu2g04170,-A.-niger-CBS-513.88-:-An11g02270,-A.-oryzae-RIB40-:-AO090003000203,-A.-niger-ATCC-1015-:-199159-mRNA-and-Aspergillus-versicolor-:-Aspve1_0050135
ANIA_2014	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_8967	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_9184	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_9168	Ortholog(s)-have-solute:hydrogen-symporter-activity,-role-in-glycerol-transport,-transmembrane-transport-and-plasma-membrane-localization
ANIA_2390	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-paired-donors,-with-incorporation-or-reduction-of-molecular-oxygen,-2-oxoglutarate-as-one-donor,-and-incorporation-of-one-atom-each-of-oxygen-into-both-donors-activity
ANIA_2366	Putative-trypsin-like-protease-with-a-role-in-the-proteolytic-cleavage-of-NmrA
ANIA_1996	Ortholog(s)-have-cytoplasm,-nucleus-localization
ANIA_10243	Ortholog(s)-have-role-in-fungal-type-cell-wall-organization-and-cytoplasm,-nucleus-localization
ANIA_2251	Putative-bestrophin-like-protein;-anion-channel-capable-of-transporting-a-wide-range-of-organic-anions-across-the-plasma-membrane;-currents-activated-by-elevated-cytosolic-Ca(2+)
ANIA_2956	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0081721-and-Aspergillus-sydowii-:-Aspsy1_0087389
ANIA_9515	Has-domain(s)-with-predicted-phosphatidylinositol-binding-activity-and-role-in-cell-communication
ANIA_3239	Has-domain(s)-with-predicted-acyl-CoA-dehydrogenase-activity-and-role-in-oxidation-reduction-process
ANIA_3150	Putative-gamma-glutamylcysteine-synthetase-with-a-predicted-role-in-glutathione-biosynthesis
ANIA_8985	Has-domain(s)-with-predicted-aldehyde-dehydrogenase-[NAD(P)+]-activity-and-role-in-cellular-aldehyde-metabolic-process,-oxidation-reduction-process
ANIA_8977	Putative-gluconolactonase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism;-transcript-upregulated-by-exposure-to-ethanol
ANIA_3076	
ANIA_3203	Putative-F-box-protein
ANIA_2698	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_9140	Putative-MFS-type-amino-acid-transporter;-transcript-repressed-by-nitrogen-limitation
ANIA_2809	Ortholog-of-A.-nidulans-FGSC-A4-:-AN10483,-A.-fumigatus-Af293-:-Afu2g16560,-Afu7g06360,-A.-niger-CBS-513.88-:-An16g00830-and-A.-oryzae-RIB40-:-AO090005000473,-AO090003001374,-AO090138000115
ANIA_3327	
ANIA_3085	Ortholog(s)-have-mitochondrion-localization
ANIA_2957	Ortholog-of-A.-fumigatus-Af293-:-Afu4g14680,-A.-niger-CBS-513.88-:-An02g11270,-A.-oryzae-RIB40-:-AO090038000089,-A.-niger-ATCC-1015-:-173463-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051391
ANIA_3223	Putative-6-phosphofructokinase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-upregulated-under-hypoxic-growth-conditions
ANIA_3366	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0051963-and-Aspergillus-sydowii-:-Aspsy1_0088131
ANIA_5351	Putative-ubiquitin-conjugating-enzyme
ANIA_8365	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_8453	Protein-with-pectate-lyase-activity,-involved-in-degradation-of-pectin
ANIA_8445	Putative-aminopeptidase-Y;-transcript-is-induced-by-nitrate
ANIA_5415	Has-domain(s)-with-predicted-O-methyltransferase-activity
ANIA_3469	Histone-H2B;-core-histone-protein
ANIA_11609	Ortholog-of-A.-nidulans-FGSC-A4-:-AN11757,-A.-oryzae-RIB40-:-AO090012000297,-Aspergillus-flavus-NRRL-3357-:-AFL2T_12268,-Aspergillus-versicolor-:-Aspve1_0088687-and-Aspergillus-sydowii-:-Aspsy1_0049837
ANIA_5210	Putative-pyruvate-kinase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-intracellular,-menadione-stress-induced-protein
ANIA_5202	
ANIA_5335	Putative-cytochrome-P450
ANIA_3145	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13930,-A.-niger-CBS-513.88-:-An09g04790,-A.-oryzae-RIB40-:-AO090012000761,-A.-niger-ATCC-1015-:-121829-mRNA-and-Aspergillus-versicolor-:-Aspve1_0081475
ANIA_2996	Putative-transcription-factor;-ortholog-of-S.-cerevisiae-Mbf1p;-expression-upregulated-after-exposure-to-farnesol
ANIA_5712	Putative-metacaspase
ANIA_5757	Putative-protein-kinase;-ortholog-of-S.-cerevisiae-Yck2p;-expression-reduced-after-exposure-to-farnesol
ANIA_5749	Has-domain(s)-with-predicted-metallopeptidase-activity-and-role-in-proteolysis
ANIA_5650	Ortholog(s)-have-Golgi-apparatus,-cell-division-site,-cell-tip,-endoplasmic-reticulum-localization
ANIA_9221	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_3129	Poly(ADP-ribose)-polymerase-(PARP);-predicted-to-function-during-the-DNA-damage-response;-transcript-induced-during-asexual-development-and-in-response-to-the-DNA-damaging-agents-MMS,-BLEO,-4-NQO-and-camptothecin
ANIA_3307	Putative-catalytic-subunit-of-the-alpha-1,3-glucan-synthase-complex
ANIA_11387	
ANIA_3387	Putative-G-protein-coupled-receptor
ANIA_3379	Ortholog-of-A.-fumigatus-Af293-:-Afu7g01170,-A.-niger-CBS-513.88-:-An12g01970,-An01g00420,-A.-oryzae-RIB40-:-AO090010000104,-AO090038000140-and-A.-niger-ATCC-1015-:-50335-mRNA
ANIA_3280	Ortholog(s)-have-role-in-positive-regulation-of-secondary-metabolite-biosynthetic-process
ANIA_3264	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3308	Putative-alpha-amylase-with-a-predicted-role-in-starch-metabolism;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_2954	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07870,-A.-niger-CBS-513.88-:-An02g11390,-A.-oryzae-RIB40-:-AO090005001484,-A.-niger-ATCC-1015-:-197780-mRNA-and-Aspergillus-versicolor-:-Aspve1_0164665
ANIA_3074	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6578,-A.-fumigatus-Af293-:-Afu3g09640,-Afu6g04490,-A.-niger-CBS-513.88-:-An15g01110,-A.-oryzae-RIB40-:-AO090701000110-and-A.-niger-ATCC-1015-:-183331-mRNA,-53405-mRNA
ANIA_3058	Putative-glycine-hydroxymethyltransferase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_3201	Putative-beta-galactosidase-with-a-predicted-role-in-lactose-metabolism
ANIA_1767	Has-domain(s)-with-predicted-catalytic-activity
ANIA_2664	Putative-beta-1,4-xylosidase
ANIA_5407	Has-domain(s)-with-predicted-Rab-GTPase-activator-activity,-role-in-regulation-of-Rab-GTPase-activity-and-intracellular-localization
ANIA_2953	Ortholog-of-A.-fumigatus-Af293-:-Afu3g07890,-A.-niger-CBS-513.88-:-An02g11360,-A.-oryzae-RIB40-:-AO090005001486,-A.-niger-ATCC-1015-:-207278-mRNA-and-Aspergillus-versicolor-:-Aspve1_0127196
ANIA_5526	Ortholog(s)-have-nucleolus-localization
ANIA_8548	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5943,-AN8661,-AN4642,-A.-fumigatus-Af293-:-Afu3g00850,-Afu4g08850-and-A.-niger-CBS-513.88-:-An02g13470,-An11g00090,-An03g01430,-An12g09260
ANIA_5276	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_2933	Ortholog-of-A.-fumigatus-Af293-:-Afu3g08170,-A.-niger-CBS-513.88-:-An02g11690,-A.-oryzae-RIB40-:-AO090005001460,-A.-niger-ATCC-1015-:-37407-mRNA-and-Aspergillus-versicolor-:-Aspve1_0127997
ANIA_3053	Putative-transglycosidase-with-a-predicted-role-in-glucan-processing
ANIA_2925	Putative-peroxisomal-import-protein-(peroxin)-with-a-role-in-fatty-acid-utilization;-required-for-growth-on-long-chain-fatty-acids
ANIA_3433	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_11167	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_3409	Protein-of-unknown-function;-transcript-repressed-by-nitrate
ANIA_2797	
ANIA_5157	Ortholog-of-A.-fumigatus-Af293-:-Afu1g07050,-A.-niger-CBS-513.88-:-An07g09610,-A.-oryzae-RIB40-:-AO090012000957,-A.-niger-ATCC-1015-:-39623-mRNA-and-Aspergillus-versicolor-:-Aspve1_0087662
ANIA_9156	Ortholog-of-A.-fumigatus-Af293-:-Afu3g09210,-A.-niger-CBS-513.88-:-An03g01290,-Aspergillus-versicolor-:-Aspve1_0034749,-Aspergillus-sydowii-:-Aspsy1_0160897-and-Aspergillus-terreus-NIH2624-:-ATET_08622
ANIA_3104	Putative-allantoicase-with-a-predicted-role-in-purine-metabolism
ANIA_9148	Putative-UTP-glucose-1-phosphate-uridylyltransferase-with-a-predicted-role-in-galactose-and-galactitol-metabolism;-protein-expressed-at-decreased-levels-in-a-hapX-mutant-versus-wild-type

ANIA_2726	
ANIA_2730	Putative-transporter-with-a-predicted-role-in-small-molecule-transport;-transcript-negatively-regulated-by-sulfate-and-methionine
ANIA_3397	Ortholog-of-A.-niger-CBS-513.88-:-An03g00310,-A.-niger-ATCC-1015-:-51389-mRNA,-Aspergillus-sydowii-:-Aspsy1_1179377-and-Aspergillus-terreus-NIH2624-:-ATET_09008
ANIA_3290	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent-and-nucleus-localization
ANIA_3251	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0180870-and-Aspergillus-sydowii-:-Aspsy1_0040252
ANIA_3227	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_3120	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_5220	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_3285	Ortholog-of-A.-fumigatus-Af293-:-Afu4g01270,-N.-fischeri-NRRL-181-:-NFIA_044020,-Aspergillus-versicolor-:-Aspve1_0066429,-Aspergillus-sydowii-:-Aspsy1_0157041-and-A.-fumigatus-A1163-:-AFUB_101760
ANIA_9167	Ortholog-of-A.-fumigatus-Af293-:-Afu3g01090,-N.-fischeri-NRRL-181-:-NFIA_001950,-A.-clavatus-NRRL-1-:-ACLA_063670,-Aspergillus-sydowii-:-Aspsy1_0097798-and-A.-fumigatus-A1163-:-AFUB_047320
ANIA_2891	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3975,-AN9193-and-A.-fumigatus-Af293-:-Afu1g10150,-Afu2g04380,-Afu3g15150,-Afu3g15280,-Afu6g03300
ANIA_2875	Putative-fructose-bisphosphate-aldolase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-intracellular,-menadione-stress-induced-protein;-palA-dependent-expression-independent-of-pH
ANIA_2760	Ortholog-of-A.-fumigatus-Af293-:-Afu3g06020,-A.-niger-CBS-513.88-:-An11g10520,-A.-oryzae-RIB40-:-AO090020000072,-A.-niger-ATCC-1015-:-178371-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051812
ANIA_5341	Ortholog(s)-have-calcium-ion-binding-activity,-role-in-cellular-response-to-drug,-regulation-of-conjugation-with-cellular-fusion-and-cytosol,-nucleus,-plasma-membrane-localization
ANIA_8347	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_9205	Ortholog-of-A.-fumigatus-Af293-:-Afu5g00100,-Afu7g06523,-A.-niger-CBS-513.88-:-An05g01030,-An16g01380,-A.-oryzae-RIB40-:-AO090011000069-and-A.-niger-ATCC-1015-:-41357-mRNA
ANIA_5775	Predicted-sequence-specific-DNA-binding-transcription-factor;-upregulated-in-A.-oryzae-and-A.-nidulans-under-hypoxic-growth-conditions
ANIA_5660	Putative-plasma-membrane-sensor-transducer;-N--and-O--glycosylated-and-localized-in-the-cell-wall-and-membrane;-mutants-display-a-high-frequency-of-swollen-hyphae-under-hypo-osmotic-conditions;-required-for-conidiation
ANIA_3259	Ortholog-of-A.-oryzae-RIB40-:-AO090011000035,-Aspergillus-flavus-NRRL-3357-:-AFL2T_04841,-Aspergillus-versicolor-:-Aspve1_0040331-and-Aspergillus-sydowii-:-Aspsy1_0029969
ANIA_3160	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_5245	
ANIA_2648	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_10402	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_3351	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_5669	Putative-succinyl-CoA:3-ketoacid-coenzyme-A-transferase
ANIA_2902	RNA-polymerase-II-C-terminal-domain-protein-phosphatase;-required-for-completion-of-mitosis;-locus-contains-the-conserved-upstream-open-reading-frame-(uORF)-AN2902-uORF
ANIA_2660	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6764,-AN7798,-A.-fumigatus-Af293-:-Afu8g01960-and-A.-niger-CBS-513.88-:-An15g04120,-An11g05430,-An01g12050,-An11g03480,-An01g01140
ANIA_9173	Sugar-transporter;-transcriptionally-induced-by-growth-on-xylose
ANIA_3113	UDP-galactofuranose-transporter;-11-membrane-predicted-spanning-regions;-required-for-wild-type-conidiophore-development,-conidiation,-cell-wall-architecture,-hyphal-morphology-and-drug-sensitivity;-required-for-cell-wall-galactofuranose
ANIA_2683	Ortholog-of-A.-fumigatus-Af293-:-Afu5g14320,-A.-niger-CBS-513.88-:-An14g05730,-A.-oryzae-RIB40-:-AO090001000197,-A.-niger-ATCC-1015-:-184760-mRNA-and-Aspergillus-versicolor-:-Aspve1_0042646
ANIA_2675	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_9216	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_2810	Ortholog(s)-have-metallopeptidase-activity
ANIA_2659	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_5589	Putative-glycerol-kinase-with-a-predicted-role-in-glycerol-metabolism;-required-for-growth-on-glycerol;-transcript-upregulated-by-growth-in-glycerol
ANIA_10329	Predicted-mariner-transposon-related-ORF
ANIA_3294	Protein-with-acetylxylan-esterase-activity,-involved-in-degradation-of-xylans
ANIA_3286	Ortholog-of-A.-nidulans-FGSC-A4-:-AN10390,-A.-fumigatus-Af293-:-Afu4g01280,-Afu5g00830,-A.-niger-CBS-513.88-:-An12g00980,-An11g04090,-An06g00150-and-A.-oryzae-RIB40-:-AO090138000050,-AO090010000179
ANIA_3278	Ortholog(s)-have-role-in-alkaloid-biosynthetic-process,-secondary-metabolic-process
ANIA_1716	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0037607,-Aspergillus-sydowii-:-Aspsy1_0084105-and-Aspergillus-terreus-NIH2624-:-ATET_05357
ANIA_11301	
ANIA_2200	Ortholog(s)-have-sulfonate-dioxygenase-activity-and-role-in-sulfur-compound-catabolic-process
ANIA_2924	Putative-nonribosomal-peptide-synthetase-(NRPS)-like-enzyme
ANIA_5196	Ortholog(s)-have-nucleus-localization
ANIA_8361	Ortholog-of-A.-fumigatus-Af293-:-Afu2g00370,-A.-niger-CBS-513.88-:-An12g10280,-A.-oryzae-RIB40-:-AO090701000625,-A.-niger-ATCC-1015-:-214831-mRNA-and-Aspergillus-versicolor-:-Aspve1_0155244
ANIA_5331	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_11623	
ANIA_5458	Ortholog-of-A.-fumigatus-Af293-:-Afu6g13346,-A.-oryzae-RIB40-:-AO090003000459,-Aspergillus-brasiliensis-:-Aspbr1_0122536,-N.-fischeri-NRRL-181-:-NFIA_059270-and-Aspergillus-versicolor-:-Aspve1_0042123
ANIA_3213	Protein-with-proline-rich-region-and-C-terminal-coiled-coil-domain;-physically-interacts-with-NudF;-GFP-fusion-localizes-to-spindle-pole-bodies-in-a-NudF-dependent-manner
ANIA_2843	
ANIA_3413	Protein-with-homology-to-ribosomal-protein-S2-and-S5;-ortholog-of-S.-cerevisiae-Rps2p;-expression-reduced-after-exposure-to-farnesol
ANIA_9457	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_3405	Ortholog-of-A.-niger-CBS-513.88-:-An12g02110,-A.-oryzae-RIB40-:-AO090010000118,-A.-niger-ATCC-1015-:-43750-mRNA,-Aspergillus-versicolor-:-Aspve1_0592672-and-Aspergillus-sydowii-:-Aspsy1_0830408
ANIA_3163	Putative-stomatin-ortholog,-predicted-to-have-scaffolding-functions-in-maintenance-of-lipid-microdomains-in-membranes;-mutation-affects-hyphal-morphology
ANIA_11181	Ortholog-of-A.-fumigatus-Af293-:-Afu7g01600,-A.-niger-CBS-513.88-:-An12g01100,-A.-oryzae-RIB40-:-AO090038000529,-Aspergillus-brasiliensis-:-Aspbr1_0418906-and-A.-niger-ATCC-1015-:-128744-mRNA
ANIA_3347	Putative-amino-acid-transporter;-expression-reduced-after-exposure-to-farnesol
ANIA_3044	Putative-arabinan-endo-1,5-alpha-L-arabinosidase-with-a-predicted-role-in-degradation-of-pectin;-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_3144	Protein-with-predicted-role-in-Golgi-to-endosome-transport,-Golgi-to-vacuole-transport,-vacuole-inheritance,-vesicle-docking-involved-in-exocytosis-and-vesicle-fusion;-locus-contains-conserved-upstream-open-reading-frame-(uORF)-AN3144-uORF
ANIA_10332	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3396	Putative-non-ribosomal-peptide-synthase-(NRPS)-responsible-for-microperfuranone-biosynthesis;-transcript-repressed-by-nitrogen-limitation
ANIA_3265	Arrestin-domains-and-PY-motif-containing-protein-with-homology-to-Saccharomyces-cerevisiae-Rod1p-and-Rog3p-proteins
ANIA_8889	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3359	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_2989	Ortholog(s)-have-intracellular-localization
ANIA_2036	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_2502	Ortholog-of-A.-fumigatus-Af293-:-Afu3g14130,-A.-oryzae-RIB40-:-AO090012000651,-A.-niger-ATCC-1015-:-43257-mRNA,-Aspergillus-versicolor-:-Aspve1_0026613-and-Aspergillus-sydowii-:-Aspsy1_0056074
ANIA_10252	Ortholog-of-A.-fumigatus-Af293-:-Afu4g10320,-A.-oryzae-RIB40-:-AO090003001189,-A.-niger-ATCC-1015-:-193449-mRNA,-Aspergillus-versicolor-:-Aspve1_0124793-and-Aspergillus-sydowii-:-Aspsy1_0084447
ANIA_1605	Ortholog-of-Aspergillus-sydowii-:-Aspsy1_0679421
ANIA_8979	Alcohol-dehydrogenase-with-a-role-in-two-carbon-compound-metabolism;-expression-is-negatively-regulated-by-glucose;-transcript-upregulated-by-exposure-to-ethanol;-protein-levels-decrease-in-response-to-farnesol
ANIA_2554	Ortholog-of-A.-fumigatus-Af293-:-Afu1g06730,-A.-niger-CBS-513.88-:-An18g05780,-A.-oryzae-RIB40-:-AO090001000761,-A.-niger-ATCC-1015-:-42981-mRNA-and-Aspergillus-versicolor-:-Aspve1_0026511
ANIA_10296	Ortholog(s)-have-fumarate-reductase-(NADH)-activity,-role-in-cellular-response-to-anoxia-and-cytosol,-mitochondrion,-plasma-membrane,-ribosome-localization
ANIA_2300	Putative-ATP-binding-cassette-(ABC)-transporter-of-the-P-glycoprotein-cluster;-has-a-role-in-protection-against-cytotoxic-agents,-in-antibiotic-secretion-and-in-the-efflux-of-the-azole-related-fungicide-fenarimol;-upregulated-by-farnesol
ANIA_2042	Ortholog(s)-have-cytosol-localization
ANIA_1664	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_1578	Ortholog-of-Aspergillus-brasiliensis-:-Aspbr1_0045436,-A.-niger-ATCC-1015-:-42227-mRNA,-Aspergillus-acidus-:-Aspfo1_0219711-and-Aspergillus-sydowii-:-Aspsy1_0046412
ANIA_11867	
ANIA_1844	Arrestin-related-protein-involved-in-a-signaling-pathway-that-activates-PacC-transcription-factor-in-response-to-alkaline-ambient-pH;-becomes-ubiquitylated-in-alkaline-pH
ANIA_1713	Ortholog(s)-have-calcium-independent-phospholipase-A2-activity,-lysophosphatidic-acid-acyltransferase-activity,-sterol-esterase-activity,-triglyceride-lipase-activity
ANIA_1471	
ANIA_2517	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity
ANIA_2509	Putative-tryptophan-2,3-dioxygenase-with-a-predicted-role-in-aromatic-amino-acid-biosynthesis
ANIA_2410	Has-domain(s)-with-predicted-hydrolase-activity-and-role-in-cellular-metabolic-process

ANIA_2136	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2005	Histidine-containing-phosphotransfer-protein,-part-of-a-two-component-signal-transducer-involved-in-the-HOG-signaling-pathway-that-regulates-osmotic-stress-response
ANIA_1520	Ortholog-of-A.-niger-CBS-513.88-:-An16g07440,-A.-oryzae-RIB40-:-AO090005000620,-A.-niger-ATCC-1015-:-214549-mRNA,-Aspergillus-versicolor-:-Aspve1_0126265-and-Aspergillus-sydowii-:-Aspsy1_0145694
ANIA_8886	Putative-pentafunctional-aroM-polypeptide-with-3-dehydroquinate-synthase,-3-dehydroquinate-dehydratase,-shikimate-5-dehydrogenase,-shikimate-kinase,-and-EPSP-synthase-activities;-has-a-predicted-role-in-aromatic-amino-acid-biosynthesis
ANIA_8943	Ortholog-of-A.-fumigatus-Af293-:-Afu2g00900,-Afu6g11560,-A.-niger-CBS-513.88-:-An01g11690,-An05g02420,-An03g01300-and-A.-oryzae-RIB40-:-AO090113000175,-AO090023000422
ANIA_8935	Putative-transferase-with-a-predicted-role-in-the-pentose-phosphate-shunt-or-xylulose-metabolism
ANIA_8927	Ortholog-of-A.-fumigatus-Af293-:-Afu5g01120,-A.-oryzae-RIB40-:-AO090003001298,-N.-fischeri-NRRL-181-:-NFIA_041050,-Aspergillus-flavus-NRRL-3357-:-AFL2T_01773-and-Aspergillus-sydowii-:-Aspsy1_0036301
ANIA_9047	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_2391	Ortholog-of-A.-fumigatus-Af293-:-Afu2g14510,-A.-niger-CBS-513.88-:-An02g00660,-An07g03040,-A.-oryzae-RIB40-:-AO090023000055,-AO090026000077,-AO090020000644-and-A.-niger-ATCC-1015-:-119171-mRNA
ANIA_2383	
ANIA_2609	Has-domain(s)-with-predicted-O-methyltransferase-activity,-RNA-binding-activity
ANIA_2375	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2165	Ortholog-of-A.-fumigatus-Af293-:-Afu2g15860,-A.-niger-CBS-513.88-:-An15g06160,-A.-oryzae-RIB40-:-AO090012000226,-A.-niger-ATCC-1015-:-48828-mRNA-and-Aspergillus-versicolor-:-Aspve1_0080752
ANIA_2134	Protein-of-unknown-function;-transcript-is-induced-by-nitrate
ANIA_1772	Type-B-feruloyl-esterase
ANIA_1432	Ortholog(s)-have-cytoplasm,-nucleus-localization
ANIA_2596	Putative-cytochrome-P450
ANIA_2588	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0047339-and-Aspergillus-sydowii-:-Aspsy1_0049555
ANIA_1439	Ortholog-of-A.-niger-CBS-513.88-:-An16g08810,-Aspergillus-brasiliensis-:-Aspbr1_0177001,-A.-clavatus-NRRL-1-:-ACLA_057630,-Aspergillus-acidus-:-Aspfo1_0060299-and-Aspergillus-versicolor-:-Aspve1_0068476
ANIA_8956	Has-domain(s)-with-predicted-inorganic-phosphate-transmembrane-transporter-activity,-role-in-phosphate-ion-transport-and-membrane-localization
ANIA_1430	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-oxidation-reduction-process
ANIA_1414	p53-like-transcription-factor-that-contains-a-Ndt80-like-DNA-binding-domain;-transcriptional-regulator-of-extracellular-proteases;-putative-acid-phosphatase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism
ANIA_2466	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2601	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10327	Ortholog-of-A.-niger-CBS-513.88-:-An05g01350,-A.-oryzae-RIB40-:-AO090010000120,-Aspergillus-brasiliensis-:-Aspbr1_0033982,-A.-niger-ATCC-1015-:-39005-mRNA-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_11379
ANIA_2343	Putative-nitroreductase;-intracellular,-menadione-stress-induced-protein
ANIA_1866	
ANIA_2113	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_2523	Class-III-chitin-synthase-with-a-role-in-chitin-biosynthesis;-required-for-normal-growth-and-conidiation;-constitutively-expressed-during-vegetative-growth,-sexual-and-asexual-development
ANIA_2335	Has-domain(s)-with-predicted-3-hydroxyisobutyrate-dehydrogenase-activity,-coenzyme-binding,-nucleotide-binding,-phosphogluconate-dehydrogenase-(decarboxylating)-activity-and-role-in-pentose-phosphate-shunt,-valine-metabolic-process
ANIA_8972	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1416	Has-domain(s)-with-predicted-N-acetyltransferase-activity,-hydrolase-activity,-hydrolyzing-O-glycosyl-compounds-activity-and-role-in-carbohydrate-metabolic-process
ANIA_2164	Ortholog(s)-have-cytosol,-nuclear-envelope-localization
ANIA_1794	Putative-cytochrome-P450;-expression-reduced-after-exposure-to-farnesol
ANIA_1778	Putative-ketopentoate-hydroxymethyl-transferase-with-a-predicted-role-in-Coenzyme-A-and-pantothenate-biosynthesis
ANIA_11347	Ortholog(s)-have-cytochrome-c-oxidase-activity,-role-in-mitochondrial-electron-transport,-cytochrome-c-to-oxygen-and-mitochondrial-respiratory-chain-complex-IV-localization
ANIA_1584	Ortholog(s)-have-transcription-cofactor-activity,-role-in-negative-regulation-of-calcium-ion-dependent-exocytosis-and-nucleus-localization
ANIA_1717	
ANIA_8917	Has-domain(s)-with-predicted-carbon-sulfur-lyase-activity-and-role-in-metabolic-process
ANIA_2488	Ortholog-of-A.-fumigatus-Af293-:-Afu3g00500,-A.-niger-CBS-513.88-:-An14g03080,-A.-niger-ATCC-1015-:-201546-mRNA,-Aspergillus-versicolor-:-Aspve1_0140182-and-Aspergillus-sydowii-:-Aspsy1_0048807
ANIA_2378	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_2505	Putative-F-box-protein;-NeddH-associated-protein;-required-for-asexual-and-for-sexual-development
ANIA_2435	Putative-ATP-citrate-synthase-with-a-predicted-role-in-TCA-intermediate-metabolism;-transcript-downregulated-upon-shift-from-glucose-to-ethanol-and-after-exposure-to-farnesol;-protein-induced-by-farnesol
ANIA_2427	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_2177	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_8928	Putative-plasma-membrane-ATP-binding-cassette-(ABC)-transporter-with-a-predicted-role-in-multidrug-resistance;-transcript-induced-by-the-fungicide-imazalil
ANIA_1602	Putative-beta-1,4-endoglucanase;-protein-with-cellulase-activity,-involved-in-degradation-of-glucans
ANIA_9000	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3193	Ortholog-of-A.-fumigatus-Af293-:-Afu4g02880,-A.-oryzae-RIB40-:-AO090001000177,-A.-niger-ATCC-1015-:-49321-mRNA,-Aspergillus-versicolor-:-Aspve1_0140454-and-Aspergillus-sydowii-:-Aspsy1_0414254
ANIA_11169	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_3177	Ortholog(s)-have-diacylglycerol-kinase-activity,-role-in-phosphatidic-acid-biosynthetic-process-and-integral-to-endoplasmic-reticulum-membrane-localization
ANIA_2884	Ortholog-of-A.-fumigatus-Af293-:-Afu3g11620,-A.-niger-CBS-513.88-:-An02g07410,-A.-niger-ATCC-1015-:-47034-mRNA,-Aspergillus-versicolor-:-Aspve1_0081798-and-Aspergillus-sydowii-:-Aspsy1_0776302
ANIA_2319	Ortholog-of-A.-niger-CBS-513.88-:-An14g04210,-A.-oryzae-RIB40-:-AO090010000485,-A.-niger-ATCC-1015-:-49373-mRNA,-Aspergillus-versicolor-:-Aspve1_0038405-and-Aspergillus-sydowii-:-Aspsy1_0039595
ANIA_10216	Ortholog-of-A.-fumigatus-Af293-:-Afu8g05640,-A.-niger-CBS-513.88-:-An15g04470,-A.-oryzae-RIB40-:-AO090005000578,-A.-niger-ATCC-1015-:-200704-mRNA-and-Aspergillus-versicolor-:-Aspve1_0123502
ANIA_1870	Putative-beta-1,4-xylosidase
ANIA_2542	Putative-pectate-lyase-with-a-predicted-role-in-the-degradation-of-pectin
ANIA_2526	Putative-ketol-acid-reductoisomerase-with-a-predicted-role-in-Coenzyme-A-and-pantothenate-biosynthesis-or-amino-acid-metabolism
ANIA_10268	
ANIA_2284	Putative-5-aminolevulinic-acid-synthase;-catalyzes-the-first-committed-step-in-the-synthesis-of-heme;-protein-expressed-at-increased-levels-in-a-hapX-mutant-compared-to-wild-type
ANIA_3090	Putative-heterotrimeric-G-protein-alpha-subunit
ANIA_2962	Putative-gamma-amino-n-butyrate-(GABA)-permease
ANIA_2746	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3001	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_2623	Isopenicillin-N-N-acyltransferase;-null-produces-reduced-levels-of-penicillin;-partially-redundant-with-aatB
ANIA_2316	Putative-cytochrome-c-oxidase-subunit-with-a-predicted-role-in-energy-metabolism
ANIA_1962	Has-domain(s)-with-predicted-DNA-binding-activity
ANIA_2130	Ortholog(s)-have-Ras-guanyl-nucleotide-exchange-factor-activity-and-role-in-Ras-protein-signal-transduction,-conjugation-with-cellular-fusion,-replicative-cell-aging,-traversing-start-control-point-of-mitotic-cell-cycle
ANIA_2870	Putative-GNAT-type-acetyltransferase
ANIA_3216	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_3208	Has-domain(s)-with-predicted-electron-carrier-activity,-flavin-adenine-dinucleotide-binding,-iron-ion-binding,-oxidoreductase-activity,-role-in-oxidation-reduction-process-and-integral-to-membrane-localization
ANIA_2846	Putative-glutathione-peroxidase-with-a-predicted-role-in-glutathione-biosynthesis;-protein-induced-by-farnesol
ANIA_2544	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2286	Alcohol-dehydrogenase-III-with-a-predicted-role-in-two-carbon-compound-metabolism;-required-for-long-term-survival-under-anaerobic-conditions;-regulated-at-both-the-transcriptional-and-translational-levels
ANIA_2582	Has-domain(s)-with-predicted-role-in-cell-wall-macromolecule-catabolic-process
ANIA_2574	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_2099	Putative-alternative-oxidase
ANIA_1697	Ortholog(s)-have-role-in-cellular-response-to-drug
ANIA_2114	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_1760	Ortholog(s)-have-role-in-ascospore-formation,-autophagy,-cellular-response-to-nitrogen-starvation-and-cytosol,-nucleus-localization
ANIA_11321	
ANIA_1551	Putative-beta-glucosidase-with-predicted-role-in-degradation-of-glucans;-covalently-bound-cell-wall-protein
ANIA_1543	Putative-succinate-dehydrogenase

ANIA_3357	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_3349	Putative-cytochrome-P450
ANIA_3250	Putative-transcriptional-regulator
ANIA_2405	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_2171	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_9041	Putative-3-hydroxyacyl-CoA-dehydrogenase-with-a-predicted-role-in-fatty-acid-metabolism
ANIA_2101	Ortholog-of-A.-fumigatus-Af293-:-Afu2g05080,-A.-niger-CBS-513.88-:-An11g04830,-A.-oryzae-RIB40-:-AO090003000311,-Aspergillus-versicolor-:-Aspve1_0477168-and-Aspergillus-sydowii-:-Aspsy1_0120628
ANIA_1596	Putative-short-chain-dehydrogenase;-member-of-the-PbcR-activated-diterpene-cluster
ANIA_1731	Putative-proline-dehydrogenase-with-a-predicted-role-in-proline-metabolism;-expression-is-regulated-by-carbon-and-nitrogen-repression;-negatively-regulated-by-CreA
ANIA_1588	Has-domain(s)-with-predicted-ATP-binding-activity
ANIA_2899	Ortholog-of-A.-fumigatus-Af293-:-Afu3g11450,-A.-niger-CBS-513.88-:-An02g07290,-A.-oryzae-RIB40-:-AO090003000699,-A.-niger-ATCC-1015-:-174539-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051442
ANIA_9141	Ortholog-of-A.-nidulans-FGSC-A4-:-AN7190,-AN11809,-A.-fumigatus-Af293-:-Afu7g01650,-Afu4g01322-and-A.-niger-CBS-513.88-:-An11g01200,-An16g08050,-An07g01700,-An04g08420
ANIA_2268	Ortholog(s)-have-structural-constituent-of-ribosome-activity-and-mitochondrial-large-ribosomal-subunit-localization
ANIA_2137	Has-domain(s)-with-predicted-protein-kinase-binding-activity,-role-in-regulation-of-G2/M-transition-of-mitotic-cell-cycle,-regulation-of-cyclin-dependent-protein-kinase-activity-and-nucleus-localization
ANIA_1993	Putative-aspartate-transaminase-with-a-predicted-role-in-alanine,-aspartate,-and-aromatic-amino-acid-metabolism
ANIA_1465	Ortholog-of-A.-fumigatus-Af293-:-Afu8g04560,-A.-niger-ATCC-1015-:-204925-mRNA,-Aspergillus-versicolor-:-Aspve1_0037223,-Aspergillus-sydowii-:-Aspsy1_0694197-and-Aspergillus-terreus-NIH2624-:-ATET_00080
ANIA_2201	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_2818	Ortholog-of-A.-niger-CBS-513.88-:-An12g03370,-An18g00460,-An07g00580,-A.-oryzae-RIB40-:-AO090103000478,-A.-niger-ATCC-1015-:-180130-mRNA-and-Aspergillus-versicolor-:-Aspve1_0051884
ANIA_9117	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity,-role-in-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2703	Ortholog-of-A.-fumigatus-Af293-:-Afu5g13990,-A.-niger-CBS-513.88-:-An14g05420,-A.-oryzae-RIB40-:-AO090113000104,-A.-niger-ATCC-1015-:-41882-mRNA-and-Aspergillus-versicolor-:-Aspve1_0042669
ANIA_9130	Has-domain(s)-with-predicted-cholinesterase-activity
ANIA_2815	Putative-mannitol-2-dehydrogenase-with-a-predicted-role-in-mannose/mannitol,-fructose,-and-sorbose/sorbitol-metabolism
ANIA_1910	Ortholog-of-A.-fumigatus-Af293-:-Afu6g07610,-A.-oryzae-RIB40-:-AO090003000190,-A.-niger-ATCC-1015-:-47870-mRNA,-Aspergillus-versicolor-:-Aspve1_0037877-and-Aspergillus-sydowii-:-Aspsy1_0039036
ANIA_2731	Ortholog(s)-have-ATPase-activator-activity,-unfolded-protein-binding-activity
ANIA_10350	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_1880	Ortholog-of-A.-fumigatus-Af293-:-Afu2g04350,-A.-niger-CBS-513.88-:-An11g03040,-A.-oryzae-RIB40-:-AO090003000221,-A.-niger-ATCC-1015-:-199211-mRNA-and-Aspergillus-versicolor-:-Aspve1_0124468
ANIA_1848	Zinc(II)2Cys6-putative-transcription-factor-involved-in-the-regulation-of-sexual-development;-mutant-produces-immature-cleistothecia-and-reduced-numbers-of-ascospores
ANIA_1733	Putative-delta-1-pyrroline-5-carboxylate-dehydrogenase-with-a-predicted-role-in-glutamate-and-glutamine-metabolism;-expression-is-negatively-regulated-by-CreA
ANIA_1573	Putative-aspartic-type-protease;-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_10300	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2702	
ANIA_3393	Protein-with-similarity-to-neutral-metalloprotease-II
ANIA_3385	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_3369	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_2880	Ortholog(s)-have-cell-division-site,-cell-tip-localization
ANIA_3226	HAS-domain-protein;-protein-levels-decrease-in-response-to-farnesol
ANIA_2001	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2484	Ortholog(s)-have-actin-monomer-binding,-guanyl-nucleotide-exchange-factor-activity-and-role-in-actin-filament-polymerization,-cytokinesis,-actomyosin-contractile-ring-assembly,-plasma-membrane-fusion-involved-in-cytogamy
ANIA_9025	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_8990	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2999	Putative-isocitrate-dehydrogenase-(NADP+)-with-a-predicted-role-in-the-TCA-cycle;-regulated-by-carbon-source;-alternative-transcription-start-sites-specify-mitochondrial-or-cytoplasmic-and-peroxisomal-protein-localization
ANIA_10372	
ANIA_2911	Basic-region-leucine-zipper-transcription-factor;-plays-a-role-in-the-response-of-conidia-to-stress;-expression-upregulated-after-exposure-to-farnesol
ANIA_9083	Putative-adenine-phosphoribosyltransferase-with-a-predicted-role-in-nucleotide-salvage-pathways;-intracellular;-protein-abundance-decreased-by-menadione-stress
ANIA_2578	Has-domain(s)-with-predicted-peroxidase-activity
ANIA_9012	Has-domain(s)-with-predicted-lyase-activity-and-role-in-metabolic-process
ANIA_9004	Has-domain(s)-with-predicted-monooxygenase-activity,-oxidoreductase-activity,-acting-on-paired-donors,-with-incorporation-or-reduction-of-molecular-oxygen-activity-and-role-in-oxidation-reduction-process
ANIA_2447	Ortholog-of-A.-fumigatus-Af293-:-Afu6g10550,-A.-niger-CBS-513.88-:-An11g00740,-A.-oryzae-RIB40-:-AO090023000218,-A.-niger-ATCC-1015-:-38750-mRNA-and-Aspergillus-versicolor-:-Aspve1_0124942
ANIA_2197	Has-domain(s)-with-predicted-N,N-dimethylaniline-monooxygenase-activity,-NADP-binding,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_8982	Predicted-protein-of-unknown-function;-member-of-the-alc-gene-cluster
ANIA_1449	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_8966	Has-domain(s)-with-predicted-neurotransmitter:sodium-symporter-activity,-role-in-neurotransmitter-transport-and-integral-to-membrane-localization
ANIA_3363	Kinesin-family-protein-required-for-the-normal-completion-of-mitosis;-required-for-separation-of-mitotic-spindle-pole-bodies
ANIA_2893	Putative-forkhead-associated-domain-protein;-transcript-upregulated-in-response-to-camptothecin
ANIA_2885	Ortholog(s)-have-DNA-binding,-bending,-sequence-specific-DNA-binding-activity-and-role-in-RNA-polymerase-III-transcriptional-preinitiation-complex-assembly,-chromatin-remodeling,-transcription-from-RNA-polymerase-II-promoter
ANIA_10261	Ortholog-of-A.-fumigatus-Af293-:-Afu2g05200,-A.-niger-CBS-513.88-:-An11g05260,-A.-oryzae-RIB40-:-AO090003000324,-Aspergillus-versicolor-:-Aspve1_0069204-and-Aspergillus-sydowii-:-Aspsy1_0141450
ANIA_10237	Has-domain(s)-with-predicted-iron-sulfur-cluster-binding,-structural-molecule-activity-and-role-in-iron-sulfur-cluster-assembly
ANIA_1450	Ortholog-of-A.-fumigatus-Af293-:-Afu8g04380,-A.-niger-CBS-513.88-:-An16g08670,-A.-oryzae-RIB40-:-AO090103000513,-A.-niger-ATCC-1015-:-57394-mRNA-and-Aspergillus-versicolor-:-Aspve1_0427988
ANIA_2367	Putative-Zn(II)2Cys6-transcription-factor;-PalA-dependent-expression-independent-of-pH
ANIA_1505	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3207,-A.-fumigatus-Af293-:-Afu2g15470,-Afu8g00720,-Afu8g05070-and-A.-niger-CBS-513.88-:-An07g04980,-An16g07680,-An14g02720,-An14g07130,-An15g05540
ANIA_2585	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2577	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-metabolic-process
ANIA_1918	Putative-phosphoenolpyruvate-carboxykinase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-transcriptionally-induced-by-acetate-and-after-exposure-to-farnesol
ANIA_1443	Ortholog-of-A.-fumigatus-Af293-:-Afu8g04310,-A.-niger-CBS-513.88-:-An16g08760,-A.-oryzae-RIB40-:-AO090103000048,-A.-niger-ATCC-1015-:-193764-mRNA-and-Aspergillus-versicolor-:-Aspve1_0049714
ANIA_1427	Ortholog(s)-have-cytoplasm-localization
ANIA_1958	
ANIA_0416	Ortholog(s)-have-Golgi-apparatus-localization
ANIA_0158	Ortholog(s)-have-2-alkenal-reductase-[NAD(P)]-activity,-AU-rich-element-binding,-NADPH:quinone-reductase-activity,-role-in-cellular-response-to-oxidative-stress-and-cytosol,-nucleus-localization
ANIA_0301	Ortholog-of-A.-fumigatus-Af293-:-Afu1g02770,-A.-niger-CBS-513.88-:-An01g05370,-A.-oryzae-RIB40-:-AO090005000817,-A.-niger-ATCC-1015-:-206033-mRNA-and-Aspergillus-versicolor-:-Aspve1_0078093
ANIA_0979	Ortholog-of-A.-fumigatus-Af293-:-Afu1g16680,-A.-niger-CBS-513.88-:-An01g10380,-A.-oryzae-RIB40-:-AO090005001032,-A.-niger-ATCC-1015-:-35723-mRNA-and-Aspergillus-versicolor-:-Aspve1_0049231
ANIA_1099	SH3-domain-protein-that-localizes-to-hyphal-tips-and-septa;-related-to-Schizosaccharomyces-pombe-Tea4;-required-for-selection-of-initial-polarity-of-germ-tube-emergence;-interacts-with-TeaA-at-hyphal-tips-and-SepA-at-hyphal-tips-and-septa
ANIA_8973	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_0746	Has-domain(s)-with-predicted-catalytic-activity,-coenzyme-binding,-nucleotide-binding-activity-and-role-in-cellular-metabolic-process
ANIA_0111	Ortholog(s)-have-cytosol,-spindle-pole-body,-spliceosomal-complex-localization
ANIA_0789	Ortholog-of-Aspergillus-sydowii-:-Aspsy1_0053160
ANIA_1052	Protein-involved-in-light-sensitive-control-of-differentiation-and-secondary-metabolism;-localizes-to-the-nucleus-in-dark-and-to-both-nucleus-and-cytoplasm-in-the-light;-induced-by-light;-AspGD-sequence-represents-the-veA1-mutant-allele
ANIA_0285	Putative-6-phosphogluconolactonase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism;-expression-upregulated-after-exposure-to-farnesol
ANIA_0412	Protein-of-unknown-function;-this-locus-is-reported-to-contain-an-upstream-open-reading-frame-(uORF)
ANIA_9295	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0213	Ortholog-of-A.-fumigatus-Af293-:-Afu5g10950,-A.-niger-CBS-513.88-:-An14g02320,-A.-oryzae-RIB40-:-AO090010000435,-A.-niger-ATCC-1015-:-201495-mRNA-and-Aspergillus-versicolor-:-Aspve1_0048464
ANIA_0991	Ortholog(s)-have-cytosol-localization
ANIA_1222	Putative-S-adenosylmethionine-synthetase;-predicted-role-in-methionine-metabolism;-expression-reduced-after-exposure-to-farnesol;-strongly-expressed-during-vegetative-growth,-downregulated-during-development-in-asexual-or-sexual-cultures

ANIA_0828	Putative-amidase;-expression-upregulated-after-exposure-to-farnesol
ANIA_0887	Putative-urea-amidolyase-with-a-predicted-role-in-nitrogen-metabolism;-required-for-the-utilization-of-lactams-such-as-2-pyrrolidinone
ANIA_0498	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10256	Has-domain(s)-with-predicted-DNA-binding,-RNA-binding,-RNA-directed-DNA-polymerase-activity,-role-in-DNA-integration,-RNA-dependent-DNA-replication-and-nucleus-localization
ANIA_2248	Putative-4-aminobutyrate-transaminase,-required-for-utilization-of-gamma-aminobutyric-acid-(GABA);-transcriptionally-regulated-by-AmdR
ANIA_1894	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_0350	Ortholog-of-A.-niger-CBS-513.88-:-An01g06100,-A.-niger-ATCC-1015-:-127223-mRNA,-Aspergillus-versicolor-:-Aspve1_0067306,-Aspergillus-sydowii-:-Aspsy1_0040909-and-Aspergillus-terreus-NIH2624-:-ATET_04877
ANIA_0334	Ortholog-of-A.-fumigatus-Af293-:-Afu1g02340,-A.-oryzae-RIB40-:-AO090005000866,-A.-niger-ATCC-1015-:-36079-mRNA,-Aspergillus-versicolor-:-Aspve1_0234299-and-Aspergillus-sydowii-:-Aspsy1_0145773
ANIA_9285	Ortholog-of-A.-fumigatus-grg1;-homologous-to-ccg-1-from-N.-crassa;-transcript-induced-by-light-in-developmentally-competent-mycelia
ANIA_2360	Has-domain(s)-with-predicted-acid-phosphatase-activity,-metal-ion-binding-activity
ANIA_2344	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1990	Putative-homocitrate-synthase-with-a-predicted-role-in-pyruvate-metabolism
ANIA_2336	Putative-phospholipase-C
ANIA_8949	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_0485	Ortholog-of-A.-fumigatus-Af293-:-Afu4g13930,-Afu6g12690,-A.-niger-CBS-513.88-:-An01g14510,-A.-oryzae-RIB40-:-AO090023000254-and-A.-niger-ATCC-1015-:-205368-mRNA,-207694-mRNA
ANIA_0612	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0158439-and-Aspergillus-sydowii-:-Aspsy1_0041325
ANIA_1569	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2055	Ortholog-of-A.-fumigatus-Af293-:-Afu4g09960,-A.-niger-CBS-513.88-:-An04g07090,-A.-oryzae-RIB40-:-AO090003001238,-A.-niger-ATCC-1015-:-214200-mRNA-and-Aspergillus-versicolor-:-Aspve1_0124972
ANIA_1460	Ortholog-of-A.-fumigatus-Af293-:-Afu8g04510,-A.-niger-CBS-513.88-:-An16g08480,-A.-oryzae-RIB40-:-AO090023000335,-A.-niger-ATCC-1015-:-45506-mRNA-and-Aspergillus-versicolor-:-Aspve1_0037216
ANIA_8953	Putative-alpha-glucosidase-with-a-predicted-role-in-maltose-metabolism;-transcriptionally-induced-by-isomaltose;-induced-by-rapamycin-induced-autophagy
ANIA_1428	Has-domain(s)-with-predicted-N-acetylglucosamine-6-phosphate-deacetylase-activity-and-role-in-N-acetylglucosamine-metabolic-process
ANIA_8945	TAM-domain-methyltransferase;-ortholog-of-A.-fumigatus-Afu8g01930
ANIA_2385	Protein-with-licheninase-activity,-involved-in-degradation-of-glucans:-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_2581	Putative-histidine-containing-phosphotransfer-protein
ANIA_0324	Ortholog-of-A.-oryzae-RIB40-:-AO090701000442,-A.-niger-ATCC-1015-:-52903-mRNA,-Aspergillus-versicolor-:-Aspve1_0048578,-Aspve1_0052669-and-Aspergillus-sydowii-:-Aspsy1_0045615,-Aspsy1_0143759
ANIA_0609	Ortholog(s)-have-role-in-N',N",N'"-triacetylfusarinine-C-biosynthetic-process,-cellular-response-to-hydrogen-peroxide,-cellular-response-to-iron-ion-starvation-and-ergosterol-biosynthetic-process,-more
ANIA_0367	Putative-integral-membrane-protein;-transcript-repressed-by-light-in-developmentally-competent-mycelia
ANIA_0121	porphobilinogen-deaminase;-heme-biosynthesis-enzyme-that-facilitates-growth-in-reactive-nitrogen-species-conditions;-transcriptionally-induced-by-reactive-nitrogen-species
ANIA_9008	Phytochrome-photoreceptor,-a-red-light-sensor-that-represses-sexual-development-under-red-light;-binds-chromophore-biliverdin;-interacts-with-VeA-and-LreB
ANIA_8971	Putative-integral-membrane-protein
ANIA_8885	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_2465	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1193	Putative-succinate-CoA-ligase-(GDP-forming),-alpha-chain
ANIA_1747	Ortholog(s)-have-mitochondrion-localization
ANIA_1089	Ortholog(s)-have-ubiquitin-protein-ligase-binding-activity-and-role-in-positive-regulation-of-ubiquitin-dependent-endocytosis,-regulation-of-intracellular-transport
ANIA_2350	L-amino-acid-oxidase-enzyme-with-broad-substrate-specificity
ANIA_10318	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_9028	Has-domain(s)-with-predicted-catalytic-activity,-coenzyme-binding,-nucleotide-binding-activity-and-role-in-cellular-metabolic-process
ANIA_2614	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1402	Has-domain(s)-with-predicted-acetyltransferase-activity,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_1160	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein;-S.-cerevisiae-ortholog-Srl1p-has-role-in-cell-wall-organization
ANIA_1013	Putative-60S-ribosomal-protein-L5;-ortholog-of-S.-cerevisiae-Rpl5p-which-is-an-RNA-binding-protein-with-a-role-in-ribosomal-large-subunit-assembly
ANIA_0651	Alpha-subunit-of-a-heterotrimeric-G-protein-composed-of-FadA,-SfaD,-GpgA-and-involved-in-regulation-of-proliferation-and-conidiophore-development;-mutant-produces-increased-amounts-of-extracellular-proteinase-during-carbon-starvation
ANIA_10077	Has-domain(s)-with-predicted-phosphatase-activity
ANIA_2549	Putative-acyl-CoA-ligase;-required-for-emericellamide-biosynthesis
ANIA_2192	Has-domain(s)-with-predicted-flavin-adenine-dinucleotide-binding,-oxidoreductase-activity,-acting-on-CH-OH-group-of-donors-activity-and-role-in-oxidation-reduction-process
ANIA_1986	Ortholog(s)-have-ferrous-iron-binding,-ferroxidase-activity,-iron-chaperone-activity,-role-in-cellular-iron-ion-homeostasis,-glutathione-metabolic-process,-iron-sulfur-cluster-assembly-and-mitochondrial-matrix-localization
ANIA_1275	Ortholog-of-A.-fumigatus-Af293-:-Afu1g09920,-A.-niger-CBS-513.88-:-An08g01730,-A.-oryzae-RIB40-:-AO090038000461,-A.-niger-ATCC-1015-:-47683-mRNA-and-Aspergillus-versicolor-:-Aspve1_0184397
ANIA_10171	Ortholog(s)-have-role-in-cellular-response-to-amino-acid-starvation,-meiosis,-regulation-of-TOR-signaling-cascade-and-Seh1-associated-complex,-cytosol,-extrinsic-to-fungal-type-vacuolar-membrane-localization
ANIA_0713	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0471	Putative-vacuolar-H+/Ca2+-exchanger
ANIA_8912	Ortholog(s)-have-role-in-ascospore-formation,-conjugation-with-cellular-fusion-and-Golgi-apparatus,-fungal-type-vacuole-membrane-localization
ANIA_9024	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_2475	Putative-sugar-transporter
ANIA_2282	Putative-MFS-transporter;-PalA-dependent-expression-independent-of-pH
ANIA_2532	Ortholog(s)-have-copper-ion-binding,-primary-amine-oxidase-activity,-quinone-binding-activity,-role-in-oxidation-reduction-process-and-external-side-of-fungal-type-cell-wall-localization
ANIA_2290	STE-like-transcription-factor-with-homeobox-and-zinc-finger-domains;-null-mutation-blocks-sexual-cycle-but-not-asexual-development,-forms-Hulle-cells-but-no-ascogenous-tissue-nor-cleistothecia
ANIA_10274	Putative-rhamnogalacturonan-hydrolase
ANIA_2556	Ortholog-of-A.-nidulans-FGSC-A4-:-AN0032,-A.-niger-CBS-513.88-:-An11g09050,-A.-oryzae-RIB40-:-AO090010000754-and-Aspergillus-versicolor-:-Aspve1_0039108,-Aspve1_0193129
ANIA_2400	
ANIA_0397	
ANIA_0266	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_0135	Ortholog(s)-have-mRNA-binding-activity-and-role-in-'de-novo'-cotranslational-protein-folding,-cellular-protein-localization,-cytokinesis,-actomyosin-contractile-ring-assembly
ANIA_1415	
ANIA_2190	Has-domain(s)-with-predicted-methyltransferase-activity
ANIA_9050	Zn(2)-Cys(6)-binuclear-domain-containing-protein;-predicted-sequence-specific-DNA-binding-transcription-factor-activity,-zinc-ion-binding-activity-and-a-role-in-regulation-of-transcription;-NeddH-associated-protein
ANIA_1952	Ortholog-of-A.-fumigatus-Af293-:-Afu4g13380,-A.-niger-CBS-513.88-:-An01g09090,-A.-niger-ATCC-1015-:-172439-mRNA,-Aspergillus-versicolor-:-Aspve1_0050177-and-Aspergillus-sydowii-:-Aspsy1_0142528
ANIA_2011	Ortholog(s)-have-phospholipid-translocating-ATPase-activity,-role-in-intracellular-protein-transport,-phospholipid-translocation-and-trans-Golgi-network-transport-vesicle-localization
ANIA_1407	Ortholog(s)-have-role-in-establishment-of-mitotic-sister-chromatid-cohesion-and-cytosol,-nucleus-localization
ANIA_8924	Ortholog-of-A.-fumigatus-Af293-:-Afu3g01860,-Aspergillus-versicolor-:-Aspve1_0047531,-Aspergillus-sydowii-:-Aspsy1_0050857-and-Aspergillus-terreus-NIH2624-:-ATET_06697
ANIA_2270	C2H2-zinc-finger-transcription-factor-involved-in-regulation-of-structural-genes-for-acetamidase-(amdS),-formate-dehydrogenase-(aciA),-and-alcohol-dehydrogenase-II-(alcB)
ANIA_9018	
ANIA_10030	Putative-alkaline-serine-protease;-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_10014	
ANIA_2386	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6413,-AN8328,-AN3395,-AN3241,-AN10369,-AN1930,-AN1738,-AN9266,-AN10886,-AN7232,-AN7406,-AN7774,-AN12202
ANIA_2543	Putative-rhamnogalacturonan-lyase;-transcript-repressed-by-nitrate
ANIA_10285	Ortholog-of-A.-fumigatus-Af293-:-Afu5g10660,-A.-niger-CBS-513.88-:-An14g04040,-A.-oryzae-RIB40-:-AO090010000472,-A.-niger-ATCC-1015-:-201613-mRNA-and-Aspergillus-terreus-NIH2624-:-ATET_07619
ANIA_2527	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-paired-donors,-with-incorporation-or-reduction-of-molecular-oxygen,-2-oxoglutarate-as-one-donor,-and-incorporation-of-one-atom-each-of-oxygen-into-both-donors-activity
ANIA_2277	Ortholog(s)-have-cell-division-site,-cytosol,-nucleus-localization
ANIA_2119	Ortholog(s)-have-sphingolipid-transporter-activity,-role-in-sphingolipid-metabolic-process-and-fungal-type-vacuole-membrane-localization
ANIA_1765	Ortholog-of-A.-fumigatus-Af293-:-Afu6g09120,-A.-oryzae-RIB40-:-AO090001000589,-N.-fischeri-NRRL-181-:-NFIA_054800,-Aspergillus-flavus-NRRL-3357-:-AFL2T_09236-and-A.-clavatus-NRRL-1-:-ACLA_083280
ANIA_9523	Ortholog-of-A.-fumigatus-Af293-:-Afu5g12040,-A.-niger-CBS-513.88-:-An18g02305,-A.-oryzae-RIB40-:-AO090120000321,-A.-niger-ATCC-1015-:-211856-mRNA-and-Aspergillus-versicolor-:-Aspve1_0216583

ANIA_0893	Putative-adenylosuccinate-synthase-with-a-predicted-role-in-purine-metabolism;-induced-by-ammonium-and-adenosine
ANIA_1947	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_2067	Predicted-PAK-(p21-activated-kinase)-family-protein;-similar-to-Saccharomyces-cerevisiae-Ste20p
ANIA_8923	Ortholog-of-A.-fumigatus-Af293-:-Afu3g01872,-N.-fischeri-NRRL-181-:-NFIA_002950-and-A.-fumigatus-A1163-:-AFUB_046550
ANIA_9043	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_8915	Has-domain(s)-with-predicted-transporter-activity,-role-in-oligopeptide-transport-and-membrane-localization
ANIA_8907	Putative-C-4-sterol-methyl-oxidase-with-a-predicted-role-in-sterol-metabolism
ANIA_2412	Calcium/calmodulin-dependent-protein-kinase-A;-essential-for-growth-and-nuclear-division;-expression-reduced-after-exposure-to-farnesol;-transcript-upregulated-in-response-to-camptothecin
ANIA_10191	Ortholog(s)-have-chromatin-binding,-histone-binding-activity
ANIA_2425	Ortholog-of-A.-fumigatus-Af293-:-Afu2g13850,-A.-niger-CBS-513.88-:-An02g05260,-A.-oryzae-RIB40-:-AO090026000188,-A.-niger-ATCC-1015-:-206783-mRNA-and-Aspergillus-versicolor-:-Aspve1_0025606
ANIA_2183	Ortholog-of-A.-fumigatus-Af293-:-Afu6g03800,-A.-niger-CBS-513.88-:-An15g01720,-A.-oryzae-RIB40-:-AO090701000169,-A.-niger-ATCC-1015-:-40438-mRNA-and-Aspergillus-versicolor-:-Aspve1_0038570
ANIA_2012	Ortholog-of-A.-fumigatus-Af293-:-Afu4g10200/rfeF,-A.-niger-CBS-513.88-:-An04g06870,-A.-oryzae-RIB40-:-AO090003001201,-A.-niger-ATCC-1015-:-214244-mRNA-and-Aspergillus-versicolor-:-Aspve1_0470876
ANIA_1917	Putative-mitochondrial-dicarboxylate-tricarboxylate-carrier
ANIA_2037	Has-domain(s)-with-predicted-NAD-binding,-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-cellular-amino-acid-metabolic-process,-oxidation-reduction-process
ANIA_1675	Putative-lysophospholipase-(phoshopholipase-B);-predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_0864	Ortholog-of-A.-fumigatus-Af293-:-Afu1g15220,-A.-niger-ATCC-1015-:-171583-mRNA,-Aspergillus-versicolor-:-Aspve1_0024039,-Aspergillus-sydowii-:-Aspsy1_0083917-and-Aspergillus-terreus-NIH2624-:-ATET_00831
ANIA_11337	Ortholog-of-A.-niger-CBS-513.88-:-An18g01250,-Aspergillus-brasiliensis-:-Aspbr1_0322983,-Aspergillus-acidus-:-Aspfo1_0209416-and-Aspergillus-versicolor-:-Aspve1_0038289
ANIA_1509	Ortholog-of-A.-fumigatus-Af293-:-Afu8g05120,-A.-niger-CBS-513.88-:-An16g07630,-A.-oryzae-RIB40-:-AO090005000631,-A.-niger-ATCC-1015-:-126898-mRNA-and-Aspergillus-versicolor-:-Aspve1_0433235
ANIA_8903	Putative-peptide-transporter;-transcript-upregulated-by-nitrate-limitation
ANIA_2474	Has-domain(s)-with-predicted-GTP-binding,-GTPase-activity,-role-in-GTP-catabolic-process,-intracellular-protein-transport,-nucleocytoplasmic-transport,-small-GTPase-mediated-signal-transduction-and-intracellular,-membrane-localization
ANIA_1940	Ortholog-of-A.-fumigatus-Af293-:-Afu4g13200,-A.-niger-CBS-513.88-:-An01g08880,-A.-oryzae-RIB40-:-AO090009000261,-A.-niger-ATCC-1015-:-51839-mRNA-and-Aspergillus-versicolor-:-Aspve1_0025339
ANIA_1797	Ortholog(s)-have-role-in-detection-of-glucose,-fructose-transport,-glucose-transport,-mannose-transport,-negative-regulation-of-meiosis-and-plasma-membrane-localization
ANIA_1686	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_1805	Putative-carbonic-anhydrase;-required-for-growth-in-ambient-CO2-conditions;-protein-expressed-at-increased-levels-during-osmoadaptation
ANIA_1571	Protein-with-alpha-arabinofuranosidase-activity,-involved-in-degradation-of-pectin
ANIA_1555	Class-IV-chitin-synthase-involved-in-chitin-biosynthesis
ANIA_9426	Has-domain(s)-with-predicted-ADP-binding,-ATP-binding,-identical-protein-binding,-microtubule-motor-activity,-role-in-apoptotic-process,-nucleoside-metabolic-process-and-kinesin-complex-localization
ANIA_0402	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0048646-and-Aspergillus-sydowii-:-Aspsy1_0055229
ANIA_1007	Putative-nitrite-reductase-with-a-predicted-role-in-nitrogen-metabolism;-transcript-stabilized-by-intracellular-nitrate
ANIA_11306	
ANIA_1622	
ANIA_2615	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_2500	Putative-nicotinamide-N-methyltransferase
ANIA_1995	Ortholog-of-A.-fumigatus-Af293-:-Afu4g10400,-A.-niger-CBS-513.88-:-An04g06400,-A.-oryzae-RIB40-:-AO090003001177,-A.-niger-ATCC-1015-:-51156-mRNA-and-Aspergillus-versicolor-:-Aspve1_0050215
ANIA_10295	Has-domain(s)-with-predicted-protein-dimerization-activity,-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_1835	Ortholog-of-A.-fumigatus-Af293-:-Afu6g11880,-A.-oryzae-RIB40-:-AO090701000551,-A.-niger-ATCC-1015-:-179808-mRNA,-Aspergillus-versicolor-:-Aspve1_0122785-and-Aspergillus-sydowii-:-Aspsy1_0055242
ANIA_1593	Putative-3-hydroxy-3-methylglutaryl-coenzyme-A-(HMG-CoA)-reductase-isozyme-with-a-predicted-role-in-sterol-metabolism;-member-of-the-PbcR-activated-diterpene-cluster
ANIA_1577	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0981	Has-domain(s)-with-predicted-integral-to-membrane-localization
ANIA_1085	Ortholog(s)-have-GTPase-activity,-role-in-endoplasmic-reticulum-inheritance,-endoplasmic-reticulum-membrane-fusion-and-cortical-endoplasmic-reticulum,-cytosol-localization
ANIA_1330	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_0821	Ortholog(s)-have-role-in-mitochondrial-genome-maintenance,-mitochondrion-inheritance,-phospholipid-transport,-protein-import-into-mitochondrial-outer-membrane-and-ERMES-complex,-cytosol,-nucleus-localization
ANIA_10116	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5465,-AN2186,-A.-fumigatus-Af293-:-Afu1g13980,-Afu5g02460-and-A.-niger-CBS-513.88-:-An08g07120,-An02g10330,-An12g09760,-An07g05030,-An05g02480,-An12g10180
ANIA_1614	Has-domain(s)-with-predicted-methyltransferase-activity-and-role-in-metabolic-process
ANIA_8881	Predicted-siderophore-transporter;-member-of-the-mitochondrial-carrier-family
ANIA_2555	Ortholog(s)-have-role-in-conjugation-with-cellular-fusion-and-cytosol,-nucleus-localization
ANIA_10297	Protein-with-similarity-to-nonribosomal-peptide-synthases-(NRPS-like);-putative-acyl-CoA-synthetase-with-an-NAD-binding-domain
ANIA_1923	Putative-alanine-transaminase-with-a-predicted-role-in-alanine-and-aspartate-metabolism;-intracellular,-menadione-stress-induced-protein
ANIA_2116	Has-domain(s)-with-predicted-catalytic-activity,-coenzyme-binding,-nucleotide-binding-activity-and-role-in-cellular-metabolic-process
ANIA_2015	Has-domain(s)-with-predicted-transferase-activity,-transferring-glycosyl-groups-activity-and-membrane-localization
ANIA_11329	
ANIA_1320	Has-domain(s)-with-predicted-serine-type-peptidase-activity-and-role-in-proteolysis
ANIA_1304	
ANIA_0942	Putative-L-arabinitol-4-dehydrogenase-with-a-predicted-role-in-L-arabinose/arabitol-and-D-xylose/D,L-xylulose/xylitol-metabolism;-transcriptionally-induced-by-growth-on-xylose
ANIA_0926	Non-essential-nuclear-transport-receptor-importin-beta2-subunit;-karyopherin-superfamily;-expression-reduced-after-exposure-to-farnesol
ANIA_10122	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_1761	Ortholog(s)-have-ubiquitin-protein-ligase-activity
ANIA_1753	Ortholog(s)-have-endoplasmic-reticulum,-mitochondrial-outer-membrane-localization
ANIA_1737	Putative-cytochrome-P450;-transcript-is-induced-by-nitrate
ANIA_2000	Polyubiquitin,-contains-four-head-to-tail-repeats-of-ubiqiutin;-transcript-upregulated-in-response-to-camptothecin
ANIA_1800	Transmembrane-histidine-kinase,-part-of-a-two-component-signal-transducer-involved-in-the-HOG-signaling-pathway-that-regulates-osmotic-stress-response'-transcript-upregulated-by-growth-in-glycerol
ANIA_1637	Putative-molybdenum-cofactor-sulfurase;-mutants-fail-to-accumulate-uric-acid;-necessary-for-post-translational-modification-of-xanthine-dehydrogenase-and-purine-hydroxylase-II;-nitrogen-metabolite-repression-mediated-by-AreA
ANIA_8896	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_1514	Has-domain(s)-with-predicted-DNA-binding-activity-and-nucleus-localization
ANIA_11304	Ortholog-of-A.-niger-CBS-513.88-:-An16g08580,-Aspergillus-brasiliensis-:-Aspbr1_0042925,-N.-fischeri-NRRL-181-:-NFIA_097160,-Aspergillus-flavus-NRRL-3357-:-AFL2T_12295-and-A.-clavatus-NRRL-1-:-ACLA_057790
ANIA_1719	Ortholog-of-A.-fumigatus-Af293-:-Afu4g08370,-A.-niger-CBS-513.88-:-An04g03180,-A.-oryzae-RIB40-:-AO090701000366,-A.-niger-ATCC-1015-:-124388-mRNA-and-Aspergillus-versicolor-:-Aspve1_0079829
ANIA_1620	Ortholog-of-A.-nidulans-FGSC-A4-:-AN2626,-A.-fumigatus-Af293-:-Afu8g02040/och3,-A.-niger-CBS-513.88-:-An03g01090/hocA,-An05g02320,-A.-oryzae-RIB40-:-AO090010000615-and-A.-niger-ATCC-1015-:-55132-mRNA
ANIA_1632	Ortholog(s)-have-protein-serine/threonine-kinase-activity
ANIA_1624	Subunit-9-of-the-mitochondrial-inner-membrane-F1F0-ATPase-complex;-mutation-confers-oligomycin-resistance;-palA-dependent-expression-independent-of-pH
ANIA_1608	Ortholog-of-A.-fumigatus-Af293-:-Afu4g09250,-A.-niger-CBS-513.88-:-An04g04280,-A.-oryzae-RIB40-:-AO090023000611-and-A.-niger-ATCC-1015-:-213011-mRNA
ANIA_1659	Putative-amino-acid-transporter;-transcript-is-induced-by-nitrate
ANIA_1536	Has-domain(s)-with-predicted-protein-dimerization-activity,-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_1518	Ortholog(s)-have-cytosol-localization
ANIA_2338	Ortholog-of-A.-fumigatus-Af293-:-Afu5g10240,-A.-oryzae-RIB40-:-AO090020000142,-AO090010000531,-Aspergillus-versicolor-:-Aspve1_0086387-and-Aspergillus-sydowii-:-Aspsy1_0034083
ANIA_1984	Ortholog(s)-have-TFIID-class-transcription-factor-binding,-chromatin-binding,-core-promoter-binding,-histone-acetyl-lysine-binding-activity
ANIA_1612	Ortholog(s)-have-inorganic-phosphate-transmembrane-transporter-activity,-manganese-ion-transmembrane-transporter-activity-and-role-in-manganese-ion-transport,-phosphate-ion-transport,-polyphosphate-metabolic-process
ANIA_8986	Ortholog-of-A.-oryzae-RIB40-:-AO090005001017,-Aspergillus-flavus-NRRL-3357-:-AFL2T_00983,-A.-clavatus-NRRL-1-:-ACLA_018770,-Aspergillus-versicolor-:-Aspve1_0047420-and-Aspergillus-sydowii-:-Aspsy1_0051004
ANIA_8978	Transcription-factor-involved-in-positive-regulation-of-the-ethanol-regulon;-contains-Zn(II)2Cys6-DNA-binding-domain
ANIA_11276	
ANIA_9340	Alpha,alpha-trehalase-with-a-role-in-trehalose-hydrolysis;-localized-to-the-conidial-cell-wall;-expression-upregulated-after-exposure-to-farnesol
ANIA_9308	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_0311	Ortholog-of-A.-fumigatus-Af293-:-Afu1g02600,-A.-niger-CBS-513.88-:-An01g05600,-A.-oryzae-RIB40-:-AO090005000834,-A.-niger-ATCC-1015-:-206019-mRNA-and-Aspergillus-versicolor-:-Aspve1_0232718

ANIA_10223	Putative-1-Cys-peroxiredoxin;-intracellular;-protein-abundance-decreased-by-menadione-stress;-expression-reduced-after-exposure-to-farnesol
ANIA_2017	Putative-alpha-glucosidase-with-a-predicted-role-in-maltose-metabolism;-transcriptionally-induced-by-isomaltose
ANIA_2009	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_1639	Ortholog(s)-have-role-in-cellular-response-to-alkyl-hydroperoxide-and-cytosol,-nucleus-localization
ANIA_1540	Ortholog-of-A.-niger-CBS-513.88-:-An16g07200
ANIA_2070	Ortholog-of-A.-fumigatus-Af293-:-Afu2g04750,-A.-niger-CBS-513.88-:-An11g04410,-A.-oryzae-RIB40-:-AO090003000278,-A.-niger-ATCC-1015-:-39038-mRNA-and-Aspergillus-versicolor-:-Aspve1_0038093
ANIA_1799	Has-domain(s)-with-predicted-triglyceride-lipase-activity-and-role-in-lipid-catabolic-process
ANIA_1396	Putative-FAD-dependent-glycerol-3-phosphate-dehydrogenase-with-a-predicted-role-in-glycerol-metabolism;-transcript-upregulated-by-growth-in-glycerol-and-after-exposure-to-farnesol;-protein-induced-by-farnesol
ANIA_1265	Putative-transcription-factor,-similar-to-S.cerevisiae-ZAP1-and-A.-fumigatus-zafA,-which-are-regulators-of-zinc-homeostasis
ANIA_0410	Essential-protein-phosphatase-required-for-the-completion-of-anaphase;-uORF-encoded-in-the-upstream-leader-sequence
ANIA_0136	
ANIA_0030	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_1213	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10650,-A.-niger-CBS-513.88-:-An08g02730,-A.-oryzae-RIB40-:-AO090038000354,-A.-niger-ATCC-1015-:-175686-mRNA-and-Aspergillus-versicolor-:-Aspve1_0119055
ANIA_0593	Putative-dehydrogenase;-expression-reduced-after-exposure-to-farnesol
ANIA_0535	
ANIA_10120	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_0332	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1151	Ortholog-of-A.-fumigatus-Af293-:-Afu6g11580,-A.-niger-CBS-513.88-:-An01g11680,-A.-oryzae-RIB40-:-AO090023000419,-A.-niger-ATCC-1015-:-172633-mRNA-and-Aspergillus-versicolor-:-Aspve1_0079114
ANIA_1184	Ortholog(s)-have-ribosome-localization
ANIA_0933	Putative-transglycosidase-with-a-predicted-role-in-glucan-processing;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_0581	Ortholog(s)-have-role-in-S-adenosylmethionine-biosynthetic-process-and-fungal-type-vacuole-membrane-localization
ANIA_0807	Methyltransferase-domain-protein;-velvet-complex-component-composed-of-VelB,-VeA-and-LaeA;-coordinates-asexual-development-in-response-to-light;-regulates-secondary-metabolism-and-is-required-for-Hulle-cell-formation
ANIA_0565	Multifunctional-enzyme-with-carbamoyl-phosphate-synthase-(CPSase)-and-aspartate-carbamoyltransferase-(ATCase)-activities-that-catalyze-the-first-two-steps-in-pyrimidine-biosynthesis
ANIA_0418	Putative-high-affinity-urea/H+-symporter;-regulated-by-nitrogen-catabolite-repression;-transcript-upregulated-by-nitrate-limitation
ANIA_0443	Putative-zinc-containing-alcohol-dehydrogenase;-protein-expressed-at-decreased-levels-in-a-hapX-mutant-versus-wild-type
ANIA_0169	
ANIA_1277	Protein-with-alpha-arabinofuranosidase-activity,-involved-in-degradation-of-pectin
ANIA_0992	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_1096	Has-domain(s)-with-predicted-protein-kinase-binding-activity-and-role-in-regulation-of-cyclin-dependent-protein-kinase-activity
ANIA_1246	Putative-phosphoglycerate-kinase-with-a-predicted-role-in-gluconeogenesis-and-glycolysis;-intracellular,-menadione-stress-induced-protein;-promoter-activity-is-greater-on-gluconeogenic-than-on-glycolytic-carbon-sources
ANIA_0495	Has-domain(s)-with-predicted-amino-acid-binding,-formyltetrahydrofolate-deformylase-activity,-hydroxymethyl-,-formyl--and-related-transferase-activity-and-role-in-'de-novo'-IMP-biosynthetic-process
ANIA_1112	Ortholog-of-A.-niger-CBS-513.88-:-An08g04015,-A.-niger-ATCC-1015-:-177236-mRNA,-Aspergillus-versicolor-:-Aspve1_0121244,-Aspergillus-sydowii-:-Aspsy1_0141456-and-Aspergillus-terreus-NIH2624-:-ATET_00372
ANIA_10104	Has-domain(s)-with-predicted-role-in-cell-wall-macromolecule-catabolic-process
ANIA_1334	Ortholog(s)-have-mRNA-binding,-small-GTPase-regulator-activity
ANIA_0859	
ANIA_0715	Has-domain(s)-with-predicted-intracellular-localization
ANIA_1047	Putative-heat-shock-protein
ANIA_0554	Aldehyde-dehydrogenase;-possible-roles-in-beta-alanine,-acetate,-acetaldehyde-and-ethanol-metabolism,-methylglyoxal-bypass,-penicillin-biosynthesis;-menadione-stress-decreased;-carbon-starvation-autophagy-induced;-hypoxia-upregulated
ANIA_0224	Ortholog(s)-have-Golgi-apparatus,-cytosol,-nucleus-localization
ANIA_0787	Putative-mannosyl-oligosaccharide-1,2-alpha-mannosidase-with-a-predicted-role-in-mannose-polymer-metabolism
ANIA_1050	Putative-3-ketoacyl-CoA-thiolase-with-a-predicted-role-in-fatty-acid-metabolism;-protein-is-mislocalized-in-a-pexG-mutant
ANIA_0390	Ortholog-of-A.-fumigatus-Af293-:-Afu2g15450,-A.-niger-CBS-513.88-:-An07g02450,-A.-niger-ATCC-1015-:-125764-mRNA,-Aspergillus-versicolor-:-Aspve1_0122514-and-Aspergillus-sydowii-:-Aspsy1_0165045
ANIA_0473	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0600	Ortholog-of-A.-fumigatus-Af293-:-Afu6g10940,-A.-niger-CBS-513.88-:-An06g01260,-A.-oryzae-RIB40-:-AO090023000524,-A.-niger-ATCC-1015-:-52539-mRNA-and-Aspergillus-versicolor-:-Aspve1_0058576
ANIA_1015	Putative-phosphorylase-with-a-predicted-role-in-glycogen-degradation
ANIA_9371	Ortholog-of-Aspergillus-brasiliensis-:-Aspbr1_0072586,-Aspergillus-acidus-:-Aspfo1_0149057,-Aspergillus-terreus-NIH2624-:-ATET_09282-and-Aspergillus-carbonarius-ITEM-5010-:-Acar5010_206420
ANIA_9339	Hyphal-catalase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism
ANIA_9240	Putative-C2H2-transcription-factor;-transcript-repressed-by-light-in-developmentally-competent-mycelia
ANIA_0227	Ortholog-of-A.-niger-CBS-513.88-:-An14g03700,-A.-oryzae-RIB40-:-AO090010000440,-Aspergillus-brasiliensis-:-Aspbr1_0190452-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_11608
ANIA_0176	Predicted-GATA-transcription-factor-involved-in-iron-uptake,-acts-as-a-repressor-of-siderophore-biosynthesis-under-high-iron-conditions;-mutants-accumulate-increased-amounts-of-iron
ANIA_0379	Ortholog-of-A.-fumigatus-Af293-:-Afu1g01760,-A.-niger-CBS-513.88-:-An01g06460,-A.-oryzae-RIB40-:-AO090005000918,-A.-niger-ATCC-1015-:-126217-mRNA-and-Aspergillus-versicolor-:-Aspve1_0048629
ANIA_10156	Has-domain(s)-with-predicted-phosphotransferase-activity,-alcohol-group-as-acceptor-activity
ANIA_1400	Ortholog-of-Aspergillus-sydowii-:-Aspsy1_0139843
ANIA_0780	Ortholog(s)-have-2-aminoadipate-transaminase-activity-and-cytoplasm,-nucleus-localization
ANIA_1126	Putative-ADP-ribosylation-factor-involved-in-hyphal-growth-and-secretion;-essential-gene;-ArfA-GFP-localizes-to-presumed-Golgi-compartments
ANIA_0764	Has-domain(s)-with-predicted-catechol-1,2-dioxygenase-activity,-ferric-iron-binding-activity-and-role-in-catechol-containing-compound-metabolic-process,-oxidation-reduction-process
ANIA_10172	Ortholog(s)-have-dicarboxylic-acid-transmembrane-transporter-activity,-role-in-mitochondrial-transport-and-mitochondrial-inner-membrane-localization
ANIA_1325	Ortholog(s)-have-cell-division-site,-cytosol-localization
ANIA_0287	Ortholog(s)-have-cytosol-localization
ANIA_0172	Ortholog-of-A.-fumigatus-Af293-:-Afu5g11310,-A.-niger-CBS-513.88-:-An01g02460,-A.-oryzae-RIB40-:-AO090026000711,-A.-niger-ATCC-1015-:-36316-mRNA-and-Aspergillus-versicolor-:-Aspve1_0118926
ANIA_0773	Has-domain(s)-with-predicted-electron-carrier-activity,-flavin-adenine-dinucleotide-binding,-iron-ion-binding,-oxidoreductase-activity,-role-in-oxidation-reduction-process-and-integral-to-membrane-localization
ANIA_0757	Ortholog(s)-have-tRNA-(cytosine-5-)-methyltransferase-activity,-role-in-tRNA-methylation-and-nucleus-localization
ANIA_0368	Has-domain(s)-with-predicted-RNA-binding,-RNA-directed-DNA-polymerase-activity,-ribonuclease-H-activity-and-role-in-RNA-dependent-DNA-replication
ANIA_0096	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity
ANIA_8947	Putative-exo-1,3-beta-glucanase-with-a-predicted-role-in-glucan-processing
ANIA_1693	Putative-F-box-protein
ANIA_0413	
ANIA_9380	Putative-chitin-deacetylase;-catalyzes-the-conversion-of-chitin-to-chitosan-by-the-deacetylation-of-N-acetyl-D-glucosamine-residues
ANIA_0627	Putative-FYVE-domain-containing-protein;-transcript-is-induced-by-nitrate;-predicted-NirA-binding-site
ANIA_0369	Has-domain(s)-with-predicted-aminopeptidase-activity,-metalloexopeptidase-activity-and-role-in-cellular-process,-proteolysis
ANIA_0331	Ortholog-of-A.-fumigatus-Af293-:-Afu1g02380,-A.-niger-CBS-513.88-:-An01g05810,-A.-niger-ATCC-1015-:-46629-mRNA,-Aspergillus-versicolor-:-Aspve1_0234209-and-Aspergillus-sydowii-:-Aspsy1_0040882
ANIA_9397	Putative-basic-leucine-zipper-(bZIP)-transcription-factor-that-regulates-the-unfolded-protein-response;-hacA-mRNA-expression-increased-in-the-presence-of-farnesol
ANIA_0200	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_1677	Short-chain-dehydrogenase;-transcriptionally-induced-by-growth-on-xylose
ANIA_1812	bZIP-transcription-factor;-induced-in-response-to-amino-acid-starvation
ANIA_1562	Ortholog-of-A.-fumigatus-Af293-:-Afu8g05700,-A.-niger-CBS-513.88-:-An15g04650,-A.-oryzae-RIB40-:-AO090005000573,-A.-niger-ATCC-1015-:-182901-mRNA-and-Aspergillus-versicolor-:-Aspve1_0049818
ANIA_9425	Has-domain(s)-with-predicted-carbon-carbon-lyase-activity-and-role-in-cellular-aromatic-compound-metabolic-process
ANIA_0633	Ortholog-of-A.-fumigatus-Af293-:-Afu1g16980,-A.-niger-CBS-513.88-:-An01g09880,-A.-oryzae-RIB40-:-AO090005000977,-A.-niger-ATCC-1015-:-121995-mRNA-and-Aspergillus-versicolor-:-Aspve1_0048883
ANIA_1027	Ortholog-of-A.-fumigatus-Af293-:-Afu1g12660,-A.-niger-CBS-513.88-:-An08g05410,-A.-oryzae-RIB40-:-AO090012000716,-A.-niger-ATCC-1015-:-38274-mRNA-and-Aspergillus-versicolor-:-Aspve1_0183745
ANIA_1109	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1817	Ortholog-of-A.-niger-CBS-513.88-:-An04g08430,-Aspergillus-brasiliensis-:-Aspbr1_0136562,-Aspergillus-flavus-NRRL-3357-:-AFL2T_00941-and-A.-clavatus-NRRL-1-:-ACLA_048750
ANIA_1583	Has-domain(s)-with-predicted-metal-ion-binding,-metallopeptidase-activity,-succinyl-diaminopimelate-desuccinylase-activity-and-role-in-lysine-biosynthetic-process,-proteolysis

ANIA_1066	Ortholog(s)-have-role-in-mitochondrial-respiratory-chain-complex-IV-assembly-and-integral-to-mitochondrial-inner-membrane,-mitochondrial-respiratory-chain-complex-IV,-mitochondrial-respiratory-chain-supercomplex-localization
ANIA_0688	Putative-transketolase-with-a-predicted-role-in-the-pentose-phosphate-shunt-or-xylulose-metabolism
ANIA_0122	Has-domain(s)-with-predicted-ATP-binding,-ATP-dependent-peptidase-activity,-serine-type-endopeptidase-activity-and-role-in-proteolysis
ANIA_0518	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6482,-A.-fumigatus-Af293-:-Afu1g15540,-A.-niger-CBS-513.88-:-An12g09790,-A.-oryzae-RIB40-:-AO090011000265-and-A.-niger-ATCC-1015-:-135685-mRNA
ANIA_0403	Has-domain(s)-with-predicted-flavin-adenine-dinucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_9370	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_0129	Putative-protein-tyrosine-phosphatase
ANIA_10090	Ortholog-of-A.-fumigatus-Af293-:-Afu1g04430,-A.-oryzae-RIB40-:-AO090003000908,-Aspergillus-brasiliensis-:-Aspbr1_0120638,-A.-niger-ATCC-1015-:-55463-mRNA-and-N.-fischeri-NRRL-181-:-NFIA_020340
ANIA_0263	Predicted-mariner-transposon-related-ORF
ANIA_0299	Putative-chitinase;-glycoside-hydrolase-family-18-(GH18)-protein-with-a-predicted-role-in-chitin-hydrolysis
ANIA_2395	Putative-beta-glucuronidase-with-a-predicted-role-in-polysaccharide-degradation
ANIA_2530	Heat-shock-protein-30;-expression-and-protein-levels-upregulated-after-exposure-to-farnesol
ANIA_0220	
ANIA_1276	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_2522	Ortholog-of-A.-fumigatus-Af293-:-Afu3g14410,-A.-niger-CBS-513.88-:-An09g04050,-A.-oryzae-RIB40-:-AO090701000592,-A.-niger-ATCC-1015-:-212570-mRNA-and-Aspergillus-versicolor-:-Aspve1_0039153
ANIA_0870	Putative-transporter-with-a-predicted-role-in-small-molecule-transport
ANIA_10181	Ortholog-of-A.-fumigatus-Af293-:-Afu1g09530,-A.-niger-CBS-513.88-:-An08g01090,-A.-oryzae-RIB40-:-AO090012000919,-Aspergillus-carbonarius-ITEM-5010-:-Acar5010_203013-and-N.-fischeri-NRRL-181-:-NFIA_016080
ANIA_0723	Ortholog-of-A.-fumigatus-Af293-:-Afu1g13990,-Afu6g13740,-A.-niger-CBS-513.88-:-An08g07150,-An05g01960,-A.-oryzae-RIB40-:-AO090103000371-and-A.-niger-ATCC-1015-:-38152-mRNA
ANIA_1189	Putative-calcium-transporting-vacuolar-ATPase-involved-in-calcium-homeostasis;-transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_1058	Has-domain(s)-with-predicted-extracellular-region-localization
ANIA_1113	
ANIA_10177	
ANIA_1220	Ortholog-of-A.-fumigatus-Af293-:-Afu2g02390,-Afu8g06040,-A.-niger-CBS-513.88-:-An08g02670,-A.-oryzae-RIB40-:-AO090011000529,-AO090005000537-and-A.-niger-ATCC-1015-:-180953-mRNA,-40652-mRNA,-52767-mRNA
ANIA_0826	Predicted-DDE1-transposon-related-ORF
ANIA_0254	Has-domain(s)-with-predicted-catalytic-activity,-coenzyme-binding,-nucleotide-binding-activity-and-role-in-cellular-metabolic-process
ANIA_10311	Putative-hyphal-cell-wall-mannoprotein;-expression-is-transcriptionally-upregulated-during-sexual-development;-expression-is-flbA-,-fadA--and-veA-dependent;-present-in-the-hyphal-cell-wall,-absent-from-the-conidial-cell-wall
ANIA_2303	Ortholog(s)-have-dolichyl-phosphate-mannose-glycolipid-alpha-mannosyltransferase-activity,-role-in-GPI-anchor-biosynthetic-process,-plasmid-maintenance-and-endoplasmic-reticulum-localization
ANIA_0493	PalA-dependent-expression-independent-of-pH
ANIA_0620	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0023747-and-Aspergillus-sydowii-:-Aspsy1_0086329
ANIA_0346	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_11261	
ANIA_1102	Putative-serine-C-palmitoyltransferase-with-a-predicted-role-in-sphingoglycolipid-metabolism
ANIA_0740	Has-domain(s)-with-predicted-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-oxidation-reduction-process
ANIA_1129	Has-domain(s)-with-predicted-N,N-dimethylaniline-monooxygenase-activity,-NADP-binding,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_0767	Ortholog(s)-have-RNA-binding-activity-and-role-in-mRNA-splicing,-via-spliceosome,-maturation-of-SSU-rRNA,-nuclear-transcribed-mRNA-catabolic-process
ANIA_1263	Putative-adenosylhomocysteinase-with-a-predicted-role-in-methionine-metabolism;-expression-reduced-after-exposure-to-farnesol
ANIA_0885	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_1001	Ortholog-of-A.-fumigatus-Af293-:-Afu1g12770,-A.-niger-CBS-513.88-:-An08g05540,-A.-oryzae-RIB40-:-AO090012000633,-A.-niger-ATCC-1015-:-198551-mRNA-and-Aspergillus-versicolor-:-Aspve1_0078945
ANIA_0623	Has-domain(s)-with-predicted-flavin-adenine-dinucleotide-binding,-long-chain-alcohol-oxidase-activity-and-role-in-oxidation-reduction-process
ANIA_1925	
ANIA_10166	Ortholog-of-A.-fumigatus-Af293-:-Afu1g11900/gprG,-A.-niger-CBS-513.88-:-An08g04110,-A.-oryzae-RIB40-:-AO090001000374/gprG,-A.-niger-ATCC-1015-:-52722-mRNA-and-Aspergillus-versicolor-:-Aspve1_0036751
ANIA_10051	
ANIA_10019	Ortholog(s)-have-protein-serine/threonine-kinase-activity,-role-in-cellular-ion-homeostasis,-protein-phosphorylation,-regulation-of-nitrogen-utilization-and-cell-division-site,-cell-tip,-cytosol-localization
ANIA_9293	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_0394	Ortholog(s)-have-role-in-positive-regulation-of-apoptotic-process,-response-to-singlet-oxygen-and-mitochondrion,-nucleus-localization
ANIA_0378	Ortholog-of-A.-niger-CBS-513.88-:-An01g06440,-A.-oryzae-RIB40-:-AO090005001321,-Aspergillus-brasiliensis-:-Aspbr1_0040067,-A.-niger-ATCC-1015-:-36035-mRNA-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_01246
ANIA_0365	Ortholog-of-A.-fumigatus-Af293-:-Afu1g01950,-A.-niger-CBS-513.88-:-An01g06340,-A.-oryzae-RIB40-:-AO090005000900,-A.-niger-ATCC-1015-:-51917-mRNA-and-Aspergillus-versicolor-:-Aspve1_0078176
ANIA_0250	Sugar-transporter;-transcriptionally-induced-by-growth-on-xylose
ANIA_0082	Phosducin-like-protein;-positive-regulator-of-G-beta-(SfaD)-and-G-gamma-(GpgA)-activity;-suppressor-of-flbA
ANIA_2575	Ortholog-of-A.-oryzae-RIB40-:-AO090023000042,-A.-niger-ATCC-1015-:-180563-mRNA,-40852-mRNA,-Aspergillus-versicolor-:-Aspve1_0188011-and-Aspergillus-niger-ATCC-1015-:-170793-mRNA
ANIA_2436	Putative-ATP-citrate-synthase-with-a-predicted-role-in-TCA-intermediate-metabolism;-transcript-downregulated-upon-shift-from-glucose-to-ethanol-and-after-exposure-to-farnesol
ANIA_0777	Has-domain(s)-with-predicted-role-in-intracellular-protein-transport-and-intracellular-localization
ANIA_1306	Protein-with-similarity-to-mammalian-gelsolin;-predicted-role-in-actin-filament-severing
ANIA_0928	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_10140	Ortholog-of-A.-fumigatus-Af293-:-Afu1g12900,-A.-niger-CBS-513.88-:-An08g05760,-A.-oryzae-RIB40-:-AO090012000610,-A.-niger-ATCC-1015-:-119224-mRNA-and-Aspergillus-versicolor-:-Aspve1_0122372
ANIA_10124	Beta-glycosidase;-transcriptionally-induced-by-growth-on-xylose
ANIA_1175	Has-domain(s)-with-predicted-role-in-rRNA-processing-and-preribosome,-small-subunit-precursor-localization
ANIA_1060	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity
ANIA_1964	Ortholog-of-S.-cerevisiae-RPS6B-and-RPS6A;-palA-dependent-expression-independent-of-pH
ANIA_2076	Ortholog(s)-have-role-in-ascospore-formation,-autophagy,-cellular-response-to-nitrogen-starvation,-conjugation-with-cellular-fusion-and-cytosol-localization
ANIA_1948	Ortholog-of-A.-fumigatus-Af293-:-Afu4g13320,-A.-niger-CBS-513.88-:-An01g09030,-A.-oryzae-RIB40-:-AO090009000244,-A.-niger-ATCC-1015-:-51834-mRNA-and-Aspergillus-versicolor-:-Aspve1_0050174
ANIA_0364	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_0233	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0182	Small-monomeric-GTPase-of-the-Ras-superfamily-involved-in-regulation-of-development;-involved-in-conidiophore-formation-and-conidial-germination
ANIA_0408	Ortholog(s)-have-cytoplasm-localization
ANIA_0725	Ortholog(s)-have-role-in-late-endosome-to-vacuole-transport-via-multivesicular-body-sorting-pathway-and-endosome-localization
ANIA_0483	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0158177,-Aspergillus-sydowii-:-Aspsy1_0144898,-Aspergillus-terreus-NIH2624-:-ATET_04939-and-Aspergillus-brasiliensis-:-Aspbr1_0204336
ANIA_0709	Putative-zinc-finger-protein;-expression-upregulated-after-exposure-to-farnesol
ANIA_1250	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10220,-A.-niger-CBS-513.88-:-An08g02090,-A.-niger-ATCC-1015-:-52783-mRNA,-Aspergillus-versicolor-:-Aspve1_0119420-and-Aspergillus-sydowii-:-Aspsy1_0063253
ANIA_0682	Ortholog-of-A.-nidulans-FGSC-A4-:-AN1574,-A.-fumigatus-Af293-:-Afu1g13430,-Afu8g05950,-A.-niger-CBS-513.88-:-An09g02840,-A.-oryzae-RIB40-:-AO090012000536-and-A.-niger-ATCC-1015-:-127635-mRNA,-54389-mRNA
ANIA_10217	Ortholog(s)-have-oxidoreductase-activity,-acting-on-CH-OH-group-of-donors-activity,-role-in-oxidation-reduction-process-and-cytosol,-nucleus-localization
ANIA_2225	Has-domain(s)-with-predicted-NAD-binding,-oxidoreductase-activity,-acting-on-the-aldehyde-or-oxo-group-of-donors,-NAD-or-NADP-as-acceptor-activity-and-role-in-cellular-amino-acid-metabolic-process,-oxidation-reduction-process
ANIA_2110	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_7104	Ortholog(s)-have-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity,-role-in-protein-phosphorylation-and-cytoplasm,-nucleus-localization
ANIA_7139	Ortholog-of-A.-fumigatus-Af293-:-Afu4g03730,-A.-niger-CBS-513.88-:-An14g01430,-A.-oryzae-RIB40-:-AO090011000309,-A.-niger-ATCC-1015-:-210957-mRNA-and-Aspergillus-versicolor-:-Aspve1_0088056
ANIA_0225	Ortholog(s)-have-bile-acid-exporting-ATPase-activity,-role-in-bile-acid-and-bile-salt-transport-and-fungal-type-vacuole-localization
ANIA_1297	Ortholog(s)-have-role-in-Golgi-to-endosome-transport-and-Golgi-membrane,-fungal-type-vacuole-membrane-localization
ANIA_9303	Ortholog-of-A.-fumigatus-Af293-:-Afu3g13140,-A.-niger-CBS-513.88-:-An07g06460,-A.-oryzae-RIB40-:-AO090023000147,-Aspergillus-versicolor-:-Aspve1_0066653-and-Aspergillus-sydowii-:-Aspsy1_0163501
ANIA_1182	Beta-tubulin,-highly-conserved-component-of-microtubules;-A.-nidulans-has-two-beta-tubulin-genes,-benA-and-tubC;-temperature-sensitive-mutants-are-blocked-in-mitosis-and-in-nuclear-division
ANIA_1137	Putative-quinate-5-dehydrogenase-with-a-predicted-role-in-aromatic-amino-acid-biosynthesis
ANIA_0902	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_0660	Putative-allantoin-transporter;-transcript-is-induced-by-allantoin-and-by-uric-acid-and-is-repressed-by-ammonium

ANIA_1163	Putative-chaperone;-ortholog-of-S.-cerevisiae-Hsp78p;-expression-upregulated-after-exposure-to-farnesol
ANIA_0670	Protein-required-for-riboflavin-biosynthesis;-putative-GTP-cyclohydrolase;-A.-fumigatus-riboB-complements-the-riboB2-mutant
ANIA_1016	Alpha-subunit-of-a-heterotrimeric-G-protein-composed-of-GanB,-SfaD-and-GpgA-that-controls-conidial-germination-via-cAMP/PKA-pathway-in-response-to-carbon-source-availability;-negatively-regulates-asexual-development;-regulated-by-RgsA
ANIA_0654	Ortholog(s)-have-farnesyltranstransferase-activity,-role-in-terpenoid-biosynthetic-process-and-mitochondrion-localization
ANIA_0833	Ortholog-of-A.-fumigatus-Af293-:-Afu1g14930,-A.-oryzae-RIB40-:-AO090005001239,-A.-niger-ATCC-1015-:-205470-mRNA,-Aspergillus-versicolor-:-Aspve1_0036415-and-Aspergillus-sydowii-:-Aspsy1_0139633
ANIA_0817	Ortholog(s)-have-role-in-positive-regulation-of-ribosomal-protein-gene-transcription-from-RNA-polymerase-II-promoter,-regulation-of-cell-size-and-cytosol,-nucleus-localization
ANIA_0575	Ortholog-of-A.-fumigatus-Af293-:-Afu6g11200,-A.-oryzae-RIB40-:-AO090023000494,-Aspergillus-versicolor-:-Aspve1_0121528,-Aspergillus-sydowii-:-Aspsy1_0144497-and-Aspergillus-terreus-NIH2624-:-ATET_05047
ANIA_10128	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_10898	
ANIA_7640	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5292,-A.-fumigatus-Af293-:-Afu5g12490,-Afu5g13780,-A.-niger-CBS-513.88-:-An14g06730-and-A.-oryzae-RIB40-:-AO090120000374,-AO090020000661
ANIA_10910	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_7632	Putative-dehydrogenase-with-a-predicted-role-in-two-carbon-compound-metabolism
ANIA_0608	Ortholog(s)-have-role-in-ergosterol-biosynthetic-process,-siderophore-biosynthetic-process
ANIA_0235	Putative-serine-threonine-kinase-with-a-predicted-role-in-the-endoplasmic-reticulum-(ER)-unfolded-protein-response-(UPR);-ortholog-of-S.-cerevisiae-Ire1p
ANIA_1192	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10840,-A.-oryzae-RIB40-:-AO090038000328,-A.-niger-ATCC-1015-:-176291-mRNA,-Aspergillus-versicolor-:-Aspve1_0049452-and-Aspergillus-sydowii-:-Aspsy1_0236946
ANIA_1290	Has-domain(s)-with-predicted-solute:hydrogen-antiporter-activity,-role-in-cation-transport,-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0644	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_0988	Ortholog(s)-have-role-in-activation-of-bipolar-cell-growth,-cellular-response-to-oxidative-stress,-negative-regulation-of-filamentous-growth-and-negative-regulation-of-flocculation,-more
ANIA_1251	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_1219	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10600,-A.-niger-CBS-513.88-:-An08g02600,-A.-oryzae-RIB40-:-AO090038000362,-A.-niger-ATCC-1015-:-130459-mRNA-and-Aspergillus-versicolor-:-Aspve1_0294708
ANIA_0857	Ortholog-of-A.-fumigatus-Af293-:-Afu1g15290,-A.-niger-CBS-513.88-:-An01g13320,-A.-oryzae-RIB40-:-AO090005001211,-A.-niger-ATCC-1015-:-171242-mRNA-and-Aspergillus-versicolor-:-Aspve1_0078797
ANIA_9297	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3782,-AN10287,-A.-fumigatus-Af293-:-Afu3g03570,-Afu5g09970,-A.-niger-CBS-513.88-:-An18g01620,-An14g05890-and-A.-oryzae-RIB40-:-AO090026000109
ANIA_10886	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6413,-AN8328,-AN3395,-AN3241,-AN10369,-AN1930,-AN2386,-AN1738,-AN9266,-AN7232,-AN7406,-AN7774,-AN12202
ANIA_7727	Ortholog-of-A.-fumigatus-Af293-:-Afu5g07980,-Afu5g14920,-A.-niger-CBS-513.88-:-An03g03960,-A.-oryzae-RIB40-:-AO090701000712,-A.-niger-ATCC-1015-:-191642-mRNA-and-Aspergillus-versicolor-:-Aspve1_0659470
ANIA_1100	Has-domain(s)-with-predicted-hydrolase-activity
ANIA_0595	Putative-NADPH-cytochrome-P450-reductase-with-a-predicted-role-in-energy-metabolism
ANIA_7047	Ortholog(s)-have-role-in-protein-targeting-to-mitochondrion-and-mitochondrial-outer-membrane-localization
ANIA_10896	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_7753	ATP-dependent-DNA-helicase-II;-70-kDa-subunit-of-Ku70/Ku80;-mutants-display-a-dramatic-increase-in-homologous-integration
ANIA_11022	Ortholog-of-A.-fumigatus-Af293-:-Afu5g07770,-A.-oryzae-RIB40-:-AO090701000684,-A.-niger-ATCC-1015-:-53446-mRNA-and-Aspergillus-terreus-NIH2624-:-ATET_08352
ANIA_0929	Putative-choline-kinase-with-a-predicted-role-in-phospholipid-metabolism
ANIA_11006	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08200,-A.-niger-CBS-513.88-:-An03g04400,-A.-oryzae-RIB40-:-AO090701000738,-A.-niger-ATCC-1015-:-213490-mRNA-and-Aspergillus-sydowii-:-Aspsy1_0046266
ANIA_7382	Putative-salicylate-1-monooxygenase
ANIA_7358	Putative-dihydroxy-acid-dehydratase-with-a-predicted-role-in-branched-chain-amino-acid-biosynthesis;-transcript-is-induced-by-nitrate
ANIA_7286	Has-domain(s)-with-predicted-bile-acid:sodium-symporter-activity,-role-in-sodium-ion-transport-and-membrane-localization
ANIA_9389	Has-domain(s)-with-predicted-role-in-cell-wall-macromolecule-catabolic-process
ANIA_1303	Putative-Zn2-Cys6-binuclear-cluster-domain-transcription-factor;-required-for-transcriptional-activation-of-genes-involved-in-utilization-of-short-chain-fatty-acids;-transcript-repressed-by-nitrogen-limitation
ANIA_0683	Predicted-mariner-transposon-related-ORF
ANIA_10168	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10430,-A.-niger-CBS-513.88-:-An08g02380,-Aspergillus-brasiliensis-:-Aspbr1_0041682,-N.-fischeri-NRRL-181-:-NFIA_015240-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_07725
ANIA_0726	Putative-Sun-family-protein;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_0468	Ortholog-of-A.-fumigatus-Af293-:-Afu1g01350,-N.-fischeri-NRRL-181-:-NFIA_023260,-A.-clavatus-NRRL-1-:-ACLA_033050,-Aspergillus-versicolor-:-Aspve1_0023589-and-Aspergillus-sydowii-:-Aspsy1_0646811
ANIA_9288	Ortholog(s)-have-cytoplasm,-nucleus-localization
ANIA_7591	Ortholog-of-A.-fumigatus-Af293-:-Afu2g15370,-A.-niger-CBS-513.88-:-An09g03630,-A.-oryzae-RIB40-:-AO090012000289,-A.-niger-ATCC-1015-:-212593-mRNA-and-Aspergillus-versicolor-:-Aspve1_0135383
ANIA_7583	Has-domain(s)-with-predicted-zinc-ion-binding-activity-and-intracellular-localization
ANIA_7710	Ortholog(s)-have-intracellular-localization
ANIA_7452	
ANIA_0663	
ANIA_0389	Ortholog-of-A.-fumigatus-Af293-:-Afu1g01570,-A.-niger-CBS-513.88-:-An04g08610,-Aspergillus-versicolor-:-Aspve1_0119805-and-Aspergillus-sydowii-:-Aspsy1_0086024
ANIA_11288	
ANIA_0274	Has-domain(s)-with-predicted-nucleic-acid-binding,-zinc-ion-binding-activity-and-intracellular-localization
ANIA_1333	Dynein-light-chain
ANIA_9336	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1342	Putative-alanine-glyoxylate-transaminase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_1199	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10770,-A.-niger-CBS-513.88-:-An08g02900,-A.-oryzae-RIB40-:-AO090038000339,-A.-niger-ATCC-1015-:-176593-mRNA-and-Aspergillus-versicolor-:-Aspve1_0119396
ANIA_1041	Putative-beta-1,4-endoglucanase
ANIA_0867	Ortholog-of-A.-nidulans-FGSC-A4-:-AN4122,-AN2881,-AN10123,-A.-fumigatus-Af293-:-Afu1g13860,-Afu1g15180,-Afu3g11650-and-A.-niger-CBS-513.88-:-An08g07010,-An02g07440,-An01g13480
ANIA_1114	Has-domain(s)-with-predicted-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7622	Has-domain(s)-with-predicted-ATP-binding,-catalytic-activity
ANIA_7485	Predicted-siderophore-iron-transporter
ANIA_0585	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_0454	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_7661	Ortholog(s)-have-RNA-polymerase-II-core-promoter-proximal-region-sequence-specific-DNA-binding,-sterol-response-element-binding-activity
ANIA_11019	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_7395	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5639,-AN2587,-A.-fumigatus-Af293-:-Afu5g00840,-A.-oryzae-RIB40-:-AO090102000018-and-A.-niger-ATCC-1015-:-134885-mRNA,-194124-mRNA
ANIA_7387	Putative-pyrroline-5-carboxylate-reductase-with-a-predicted-role-in-proline-metabolism
ANIA_7530	Ortholog-of-A.-niger-CBS-513.88-:-An11g07875,-A.-niger-ATCC-1015-:-53021-mRNA,-Aspergillus-versicolor-:-Aspve1_0085875,-Aspergillus-sydowii-:-Aspsy1_0031999-and-Aspergillus-terreus-NIH2624-:-ATET_06692
ANIA_0734	Histone-H4.1,-core-histone-protein;-nearly-identical-to-histone-H4.2
ANIA_10176	
ANIA_10045	Has-domain(s)-with-predicted-nucleic-acid-binding-activity
ANIA_0214	
ANIA_0186	Ortholog-of-A.-fumigatus-Af293-:-Afu5g11190,-A.-niger-ATCC-1015-:-206311-mRNA,-Aspergillus-versicolor-:-Aspve1_0157455,-Aspergillus-sydowii-:-Aspsy1_0055012-and-Aspergillus-terreus-NIH2624-:-ATET_07706
ANIA_0313	Has-domain(s)-with-predicted-hydrolase-activity-and-role-in-metabolic-process
ANIA_0071	Ortholog-of-A.-fumigatus-Af293-:-Afu5g12320,-A.-niger-CBS-513.88-:-An01g02090,-A.-oryzae-RIB40-:-AO090120000349,-A.-niger-ATCC-1015-:-170268-mRNA-and-Aspergillus-sydowii-:-Aspsy1_0027598
ANIA_1356	Ortholog-of-A.-fumigatus-Af293-:-Afu1g09300,-A.-niger-CBS-513.88-:-An08g00850,-A.-oryzae-RIB40-:-AO090005001593,-A.-niger-ATCC-1015-:-176703-mRNA-and-Aspergillus-versicolor-:-Aspve1_0037072
ANIA_1098	
ANIA_7161	Has-domain(s)-with-predicted-ferric-iron-binding,-oxidoreductase-activity,-acting-on-single-donors-with-incorporation-of-molecular-oxygen,-incorporation-of-two-atoms-of-oxygen-activity
ANIA_7030	Polarisome-component-required-for-conidiation-and-vacuolar-fusion;-has-similarity-to-Saccharomyces-cerevisiae-Bem1p
ANIA_7133	
ANIA_10974	
ANIA_0689	Transcription-factor-containing-a-Zn(II)2-Cys6-binuclear-DNA-binding-cluster-domain;-activates-transcription-of-genes-required-for-acetate-utilization;-active-form-is-likely-a-dimer-formed-via-leucine-zipper-like-repeats;-induced-by-acetate
ANIA_0698	Ortholog-of-A.-fumigatus-Af293-:-Afu1g13610,-A.-niger-CBS-513.88-:-An08g06690,-A.-oryzae-RIB40-:-AO090012000513,-A.-niger-ATCC-1015-:-52644-mRNA-and-Aspergillus-versicolor-:-Aspve1_0048949
ANIA_0825	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent

ANIA_0409	Ortholog(s)-have-cytosol,-fungal-type-vacuole-membrane,-nucleus-localization
ANIA_9392	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_7819	Ortholog(s)-have-role-in-aflatoxin-biosynthetic-process,-regulation-of-aflatoxin-biosynthetic-process
ANIA_7704	Ortholog(s)-have-role-in-cellular-response-to-stress,-proteasomal-ubiquitin-dependent-protein-catabolic-process-and-cytoplasm,-nucleus-localization
ANIA_7073	Putative-transcription-factor;-predicted-role-in-secondary-metabolite-production
ANIA_7454	Ortholog-of-S.-cerevisiae-:-TDA6,-A.-fumigatus-Af293-:-Afu2g05980,-A.-niger-CBS-513.88-:-An02g14280,-A.-oryzae-RIB40-:-AO090001000716-and-A.-niger-ATCC-1015-:-52480-mRNA
ANIA_7700	Ortholog(s)-have-role-in-regulation-of-barrier-septum-assembly,-regulation-of-fungal-type-cell-wall-biogenesis-and-cytoplasm-localization
ANIA_0986	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_1233	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10450,-A.-niger-CBS-513.88-:-An08g02400,-A.-oryzae-RIB40-:-AO090038000382,-A.-niger-ATCC-1015-:-119822-mRNA-and-Aspergillus-versicolor-:-Aspve1_0079210
ANIA_1217	Putative-LIM/homeobox-transcription-factor;-transcript-upregulated-in-response-to-camptothecin
ANIA_0736	Ortholog-of-A.-nidulans-FGSC-A4-:-AN2423,-A.-fumigatus-Af293-:-Afu1g14230,-Afu2g13800,-A.-niger-CBS-513.88-:-An01g12240,-An02g05360,-A.-oryzae-RIB40-:-AO090026000195-and-A.-niger-ATCC-1015-:-46361-mRNA
ANIA_0605	Ortholog-of-A.-fumigatus-Af293-:-Afu6g10890,-A.-niger-CBS-513.88-:-An09g02900,-A.-oryzae-RIB40-:-AO090023000527,-A.-niger-ATCC-1015-:-54387-mRNA-and-Aspergillus-terreus-NIH2624-:-ATET_05072
ANIA_0363	Component-of-the-velvet-complex-composed-of-VelB,-VeA,-and-LaeA-that-coordinates-development-and-secondary-metabolism-in-response-to-light
ANIA_7225	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0241	Cu/Zn-superoxide-dismutase;-induced-under-iron-starvation-and-repressed-under-copper-starvation
ANIA_6984	Ortholog-of-A.-fumigatus-Af293-:-Afu4g04690,-A.-niger-CBS-513.88-:-An14g00150,-A.-oryzae-RIB40-:-AO090206000018,-A.-niger-ATCC-1015-:-201307-mRNA-and-Aspergillus-versicolor-:-Aspve1_0140663
ANIA_7088	Has-domain(s)-with-predicted-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1214	
ANIA_0264	
ANIA_0771	Putative-ABC-multidrug-transporter;-confers-resistance-to-azole-antifungal-drugs
ANIA_7110	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0139279,-Aspve1_0834531-and-Aspergillus-sydowii-:-Aspsy1_0091735
ANIA_7665	Putative-exosome-complex-subunit;-transcript-repressed-by-nitrate
ANIA_7657	Putative-1,3-beta-transglycosidase-with-a-predicted-role-in-glucan-processing;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor;-palA-dependent-expression-independent-of-pH
ANIA_9450	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_0405	Ortholog-of-A.-fumigatus-Af293-:-Afu1g05000,-A.-niger-ATCC-1015-:-172299-mRNA,-Aspergillus-versicolor-:-Aspve1_0048685,-Aspergillus-sydowii-:-Aspsy1_0055250-and-Aspergillus-terreus-NIH2624-:-ATET_02569
ANIA_9356	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_0640	Protein-with-a-role-in-sphingoglycolipid-metabolism;-required-for-phytosphingosine-biosynthesis;-depletion-causes-cell-wall-thickening,-reduced-asexual-development,-increased-sexual-development,-increased-levels-of-ppoA-and-steA-transcript
ANIA_1270	Putative-translation-initiation-factor-3,-subunit-h-(eIF-3h);-expression-reduced-after-exposure-to-farnesol
ANIA_1094	Putative-mitochondrial-NADH-dehydrogenase-(ubiquinone)-with-a-predicted-role-in-energy-metabolism
ANIA_9241	Has-domain(s)-with-predicted-zinc-ion-binding-activity-and-role-in-lipid-metabolic-process
ANIA_7266	
ANIA_0919	Has-domain(s)-with-predicted-orotidine-5'-phosphate-decarboxylase-activity-and-role-in-'de-novo'-pyrimidine-nucleobase-biosynthetic-process
ANIA_0820	Ortholog-of-A.-niger-CBS-513.88-:-An01g12850,-N.-fischeri-NRRL-181-:-NFIA_010610,-Aspergillus-flavus-NRRL-3357-:-AFL2T_01176-and-Aspergillus-acidus-:-Aspfo1_0043117
ANIA_0677	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_0562	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_10115	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1173	
ANIA_1110	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_0732	Putative-transporter-of-the-major-facilitator-superfamily-(MFS);-expression-upregulated-after-exposure-to-farnesol
ANIA_0601	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_1379	Putative-nuclear-pore-complex-protein;-extragenic-suppressor-of-nimA1;-similar-to-Schizosaccharomyces-pombe-Rae1-and-Saccharomyces-cerevisiae-Gle2
ANIA_7798	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6764,-AN2660,-A.-fumigatus-Af293-:-Afu8g01960-and-A.-niger-CBS-513.88-:-An15g04120,-An11g05430,-An01g12050,-An11g03480,-An01g01140
ANIA_7364	Has-domain(s)-with-predicted-2-iron,-2-sulfur-cluster-binding,-oxidoreductase-activity,-transition-metal-ion-binding-activity-and-role-in-oxidation-reduction-process
ANIA_0779	Putative-glucan-1,3-beta-glucosidase-with-a-predicted-role-in-glucan-metabolism
ANIA_7649	Ortholog(s)-have-protein-transporter-activity,-unfolded-protein-binding-activity-and-role-in-protein-import-into-mitochondrial-inner-membrane
ANIA_7399	Putative-cytochrome-P450
ANIA_7542	Basic-leucine-zipper-transcription-factor-involved-in-regulation-of-conidiophore-development;-localizes-to-the-most-apical-nucleus-and-the-tip-of-mature-vegetative-hyphae;-required-for-light-dependent-activation-of-brlA-transcription
ANIA_1268	Ortholog-of-A.-fumigatus-Af293-:-Afu1g10012,-N.-fischeri-NRRL-181-:-NFIA_015630,-Aspergillus-versicolor-:-Aspve1_0299082,-Aspergillus-sydowii-:-Aspsy1_0229566-and-Aspergillus-terreus-NIH2624-:-ATET_00188
ANIA_7683	Protein-associated-with-the-nonclassical-protein-export-pathway;-ortholog-of-S.-cerevisiae-Nce102p
ANIA_10945	Has-domain(s)-with-predicted-nucleic-acid-binding-activity
ANIA_7667	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10937	Has-domain(s)-with-predicted-ATP-binding,-protein-kinase-activity-and-role-in-protein-phosphorylation
ANIA_7407	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6148,-A.-fumigatus-Af293-:-Afu2g08500,-Afu5g13710,-A.-niger-CBS-513.88-:-An02g14290,-An12g03860-and-A.-oryzae-RIB40-:-AO090701000324,-AO090011000852
ANIA_7173	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_7149	Ortholog(s)-have-role-in-nucleobase-containing-compound-transport-and-plasma-membrane-localization
ANIA_7566	Ortholog(s)-have-nucleus-localization
ANIA_7701	Ortholog(s)-have-structural-constituent-of-ribosome-activity-and-mitochondrial-small-ribosomal-subunit-localization
ANIA_7451	Putative-NAD-glutamate-dehydrogenase-with-a-predicted-role-in-glutamate-and-glutamine-metabolism
ANIA_7553	Basic-helix-loop-helix-transcription-factor-required-for-normal-conidiophore-development;-mutants-are-infertile-in-self-crosses
ANIA_7545	Component-of-AnCP/AnCF-CCAAT-binding-complex;-hapB-mRNA-is-negatively-regulated-by-AnCP/AnCF-complex
ANIA_7537	Has-domain(s)-with-predicted-ATP-binding,-protein-serine/threonine-kinase-activity,-protein-tyrosine-kinase-activity-and-role-in-protein-phosphorylation
ANIA_8683	Ortholog(s)-have-ferric-chelate-reductase-activity,-role-in-copper-ion-import,-iron-ion-transport-and-plasma-membrane-localization
ANIA_8673	ORF-that-was-absent-from-the-original-release-of-version-4-of-the-A.-nidulans-annotation,-but-present-in-a-previous-version;-reinstated-into-version-4-in-AspGD-as-of-July-2009
ANIA_7262	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5649,-A.-fumigatus-Af293-:-Afu2g17000,-Afu4g13630,-A.-niger-CBS-513.88-:-An01g09380,-An04g09080-and-A.-oryzae-RIB40-:-AO090102000117,-AO090009000212
ANIA_7580	Ortholog-of-A.-fumigatus-Af293-:-Afu2g15110,-A.-niger-CBS-513.88-:-An15g02960,-A.-oryzae-RIB40-:-AO090012000329,-Aspergillus-versicolor-:-Aspve1_0030832-and-Aspergillus-sydowii-:-Aspsy1_0046014
ANIA_7199	Ortholog(s)-have-cytoplasm-localization
ANIA_7131	Putative-cytochrome-P450
ANIA_10964	Has-domain(s)-with-predicted-methyltransferase-activity-and-role-in-metabolic-process
ANIA_10960	Ortholog-of-Aspergillus-versicolor-:-Aspve1_0135933
ANIA_10952	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_10936	Ortholog(s)-have-2,5-diamino-6-ribitylamino-4(3H)-pyrimidinone-5'-phosphate-deaminase-activity,-pseudouridine-synthase-activity,-role-in-riboflavin-biosynthetic-process,-tRNA-pseudouridine-synthesis-and-cytosol-localization
ANIA_7543	Ortholog-of-A.-fumigatus-Af293-:-Afu2g14690,-A.-oryzae-RIB40-:-AO090026000808,-A.-niger-ATCC-1015-:-48751-mRNA,-Aspergillus-versicolor-:-Aspve1_0054583-and-Aspergillus-sydowii-:-Aspsy1_0045967
ANIA_7535	Ortholog-of-A.-fumigatus-Af293-:-Afu2g17320,-A.-oryzae-RIB40-:-AO090023000622,-N.-fischeri-NRRL-181-:-NFIA_092740,-A.-clavatus-NRRL-1-:-ACLA_076190-and-Aspergillus-sydowii-:-Aspsy1_0090170
ANIA_7035	Has-domain(s)-with-predicted-peptidase-activity-and-role-in-proteolysis
ANIA_11008	Ortholog(s)-have-drug-binding,-squalene-monooxygenase-activity,-role-in-cellular-response-to-drug,-ergosterol-biosynthetic-process-and-endoplasmic-reticulum,-fungal-type-vacuole-membrane,-lipid-particle-localization
ANIA_7511	Putative-1,3-beta-transglycosidase-with-a-predicted-role-in-glucan-processing;-predicted-glycosyl-phosphatidylinositol-(GPI)-anchor
ANIA_11570	
ANIA_7159	Ortholog(s)-have-tripeptidyl-peptidase-activity
ANIA_7052	Ortholog(s)-have-mitochondrion-localization
ANIA_7027	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_7388	Putative-catalase-peroxidase-with-a-predicted-role-in-gluconic-acid-and-gluconate-metabolism;-protein-also-identified-as-laccase-II-which-is-expressed-during-sexual-development
ANIA_7507	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent

ANIA_7273	Ortholog-of-A.-fumigatus-Af293-:-Afu2g16990,-A.-oryzae-RIB40-:-AO090102000119,-A.-niger-ATCC-1015-:-194652-mRNA,-Aspergillus-versicolor-:-Aspve1_0026187-and-Aspergillus-sydowii-:-Aspsy1_0027170
ANIA_7400	Ortholog-of-A.-nidulans-FGSC-A4-:-AN9444,-Aspergillus-flavus-NRRL-3357-:-AFL2T_02908,-Aspergillus-acidus-:-Aspfo1_0034827,-Aspergillus-versicolor-:-Aspve1_0037710-and-Aspergillus-sydowii-:-Aspsy1_0038876
ANIA_7463	Major-ammonium-transporter-of-A.-nidulans;-transcript-upregulated-by-nitrate-limitation
ANIA_7334	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_7076	
ANIA_7488	Ortholog(s)-have-endoplasmic-reticulum,-fungal-type-vacuole-localization
ANIA_7631	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_7765	Has-domain(s)-with-predicted-DNA-binding-activity
ANIA_7757	Coiled-coil-protein-involved-in-distribution-of-nuclei-in-hyphae-and-in-conididiophores;-required-for-entry-of-nuclei-into-sterigmata;-mutants-are-nearly-aconidial
ANIA_7189	Ortholog(s)-have-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity
ANIA_7332	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_7074	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_7509	
ANIA_7214	Has-domain(s)-with-predicted-oxidoreductase-activity
ANIA_7785	Ortholog-of-A.-nidulans-FGSC-A4-:-AN5372,-A.-fumigatus-Af293-:-Afu5g07450,-Afu6g14060-and-A.-niger-CBS-513.88-:-An08g08280,-An15g02880,-An12g10360
ANIA_7777	Ortholog-of-A.-fumigatus-Af293-:-Afu2g00310,-A.-niger-CBS-513.88-:-An09g03250,-A.-oryzae-RIB40-:-AO090701000622,-A.-niger-ATCC-1015-:-43345-mRNA-and-Aspergillus-versicolor-:-Aspve1_0133024
ANIA_7670	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01430,-A.-niger-ATCC-1015-:-135788-mRNA,-Aspergillus-versicolor-:-Aspve1_0030702,-Aspergillus-sydowii-:-Aspsy1_0119592-and-Aspergillus-terreus-NIH2624-:-ATET_08186
ANIA_9492	C2H2-zinc-finger-transcription-factor-involved-in-regulation-of-acetamide-catabolism;-regulates-amdS-transcription
ANIA_7229	Transcript-induced-in-response-to-calcium-dichloride-in-a-CrzA-dependent-manner
ANIA_7118	Has-domain(s)-with-predicted-DNA-binding,-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent,-transcription,-DNA-dependent
ANIA_4770	Adenosine-3-phosphate-5-phosphosulfate-(PAPS)-reductase-involved-in-sulfate-assimilation
ANIA_7521	Ortholog-of-A.-fumigatus-Af293-:-Afu3g09230,-A.-niger-CBS-513.88-:-An12g05590,-A.-oryzae-RIB40-:-AO090023000559,-A.-niger-ATCC-1015-:-121874-mRNA-and-Aspergillus-versicolor-:-Aspve1_0135354
ANIA_7247	
ANIA_10977	Ortholog-of-A.-fumigatus-Af293-:-Afu2g00790,-A.-oryzae-RIB40-:-AO090701000343,-A.-niger-ATCC-1015-:-45016-mRNA,-Aspergillus-versicolor-:-Aspve1_0330455-and-Aspergillus-sydowii-:-Aspsy1_0048752
ANIA_7699	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08380,-A.-niger-CBS-513.88-:-An03g04660,-A.-oryzae-RIB40-:-AO090701000761,-A.-niger-ATCC-1015-:-54717-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041716
ANIA_7592	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7269	Ortholog(s)-have-role-in-secondary-metabolic-process
ANIA_7170	Protein-of-unknown-function;-transcript-upregulated-in-response-to-camptothecin
ANIA_7162	Has-domain(s)-with-predicted-FMN-binding,-riboflavin-reductase-(NADPH)-activity-and-role-in-oxidation-reduction-process
ANIA_7138	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_7469	Ortholog(s)-have-riboflavin-kinase-activity,-role-in-FMN-biosynthetic-process-and-cytosol,-mitochondrial-inner-membrane,-nucleus-localization
ANIA_7193	Putative-NADPH-dependent-glycerol-dehydrogenase-with-a-predicted-role-in-carbohydrate-metabolism;-transcript-upregulated-by-growth-in-glycerol,-by-growth-on-xylose-and-after-exposure-to-farnesol
ANIA_7177	Ortholog-of-A.-fumigatus-Af293-:-Afu4g03322,-A.-niger-CBS-513.88-:-An14g01990,-A.-oryzae-RIB40-:-AO090011000139,-A.-niger-ATCC-1015-:-53774-mRNA-and-Aspergillus-versicolor-:-Aspve1_0333372
ANIA_7625	Putative-myo-inositol-1-phosphate-synthase-with-a-predicted-role-in-phospholipid-metabolism;-intracellular,-menadione-stress-induced-protein;-palA-dependent-expression-independent-of-pH
ANIA_8692	Thioredoxin-dependent-peroxidase;-intracellular;-PRX5-like-domain;-highly-similar-to-the-allergen-Aspf3-from-related-fungi;-menadione-stress-repressed-protein;-osmoadaptation-induced-protein;-repressed-by-starvation-induced-autophagy
ANIA_7190	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7174	Has-domain(s)-with-predicted-DNA-binding-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_7166	Ortholog-of-A.-nidulans-FGSC-A4-:-AN3215,-AN8609,-A.-fumigatus-Af293-:-Afu3g14210,-Afu4g03360-and-A.-niger-CBS-513.88-:-An09g04200,-An14g01840
ANIA_7158	Has-domain(s)-with-predicted-hydrolase-activity,-acting-on-ester-bonds-activity-and-role-in-lipid-metabolic-process
ANIA_7714	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08220,-A.-niger-CBS-513.88-:-An03g04430,-A.-oryzae-RIB40-:-AO090701000741,-A.-niger-ATCC-1015-:-191326-mRNA-and-Aspergillus-versicolor-:-Aspve1_0041686
ANIA_10949	Ortholog(s)-have-xenobiotic-transporting-ATPase-activity,-role-in-response-to-drug-and-mitochondrion,-plasma-membrane-localization
ANIA_7576	Predicted-Rho-GTPase-activating-protein
ANIA_7750	Ortholog(s)-have-nucleus-localization
ANIA_7742	Ortholog(s)-have-single-stranded-DNA-binding-activity,-role-in-mitochondrial-genome-maintenance-and-mitochondrial-nucleoid-localization
ANIA_7734	Basic-region-helix-loop-helix-(bHLH)-transcription-factor;-represses-expression-of-the-penicillin-biosynthesis-gene-aatA
ANIA_7383	Ortholog-of-A.-oryzae-RIB40-:-AO090010000377,-Aspergillus-flavus-NRRL-3357-:-AFL2T_11553,-Aspergillus-versicolor-:-Aspve1_0137812-and-Aspergillus-sydowii-:-Aspsy1_0092249
ANIA_7458	Ortholog-of-A.-fumigatus-Af293-:-Afu2g05930,-A.-niger-CBS-513.88-:-An02g14360,-A.-oryzae-RIB40-:-AO090001000711,-A.-niger-ATCC-1015-:-37604-mRNA-and-Aspergillus-versicolor-:-Aspve1_0152895
ANIA_7654	Predicted-glycosylphosphatidylinositol-(GPI)-anchored-protein
ANIA_7476	Ortholog-of-A.-fumigatus-Af293-:-Afu2g05630,-A.-niger-CBS-513.88-:-An02g14010,-A.-oryzae-RIB40-:-AO090001000675,-A.-niger-ATCC-1015-:-37580-mRNA-and-Aspergillus-versicolor-:-Aspve1_0085923
ANIA_7468	Putative-binuclear-zinc-cluster-type-transcriptional-activator-of-gluconeogenesis
ANIA_7725	Protein-required-for-biosynthesis-of-pyridoxine;-highly-conserved-throughout-fungi,-plants-and-bacteria
ANIA_7717	Ortholog-of-A.-fumigatus-Af293-:-Afu5g08190,-A.-oryzae-RIB40-:-AO090701000736,-A.-niger-ATCC-1015-:-213488-mRNA,-Aspergillus-versicolor-:-Aspve1_0041683-and-Aspergillus-sydowii-:-Aspsy1_0046260
ANIA_7610	Predicted-GAL4-type-zinc-finger-transcription-factor-involved-in-regulation-of-genes-of-xylan-degradation;-regulated-by-CreA,-the-mediator-of-carbon-catabolite-repression;-transcriptionally-induced-by-growth-on-xylose
ANIA_6973	Putative-C-4-sterol-methyl-oxidase-with-a-predicted-role-in-sterol-metabolism;-expression-reduced-after-exposure-to-farnesol
ANIA_7232	Ortholog-of-A.-nidulans-FGSC-A4-:-AN6413,-AN8328,-AN3395,-AN3241,-AN10369,-AN1930,-AN2386,-AN1738,-AN9266,-AN10886,-AN7406,-AN7774,-AN12202
ANIA_8677	ORF-that-was-absent-from-the-original-release-of-version-4-of-the-A.-nidulans-annotation,-but-present-in-a-previous-version;-reinstated-into-version-4-in-AspGD-as-of-July-2009
ANIA_8676	Putative-MADS-box-family-transcription-factor;-ORF-that-was-absent-from-the-original-release-of-version-4-of-the-A.-nidulans-annotation,-but-present-in-a-previous-version;-reinstated-into-version-4-in-AspGD-as-of-July-2009
ANIA_7541	Protein-with-cutinase-activity,-involved-in-carbohydrate-catabolism;-activity-induced-by-olive-oil,-some-triacylglycerides-and-fatty-acids;-repressed-by-glucose-and-other-sugars
ANIA_7533	Protein-with-exo-beta-(1,3)-glucanase-activity,-involved-in-degradation-of-glucans
ANIA_7517	Ortholog-of-A.-fumigatus-Af293-:-Afu5g03330,-A.-niger-CBS-513.88-:-An09g05650,-A.-oryzae-RIB40-:-AO090102000538,-A.-niger-ATCC-1015-:-189002-mRNA-and-Aspergillus-versicolor-:-Aspve1_0157647
ANIA_7572	Putative-response-regulator-of-a-two-component-phosphorelay-system
ANIA_7564	Putative-threonine-aldolase-with-a-predicted-role-in-glycine,-serine,-and-threonine-metabolism
ANIA_7697	Response-regulator,-part-of-a-two-component-signal-transducer-involved-in-the-HOG-signaling-pathway-that-regulates-osmotic-stress-response;-transcript-induced-by-hydrogen-peroxide;-null-spores-are-heat-labile-and-lose-viability-at-4-degrees
ANIA_7546	
ANIA_8670	ORF-that-was-absent-from-the-original-release-of-version-4-of-the-A.-nidulans-annotation,-but-present-in-a-previous-version;-reinstated-into-version-4-in-AspGD-as-of-July-2009
ANIA_9500	Has-domain(s)-with-predicted-protein-kinase-binding-activity-and-role-in-regulation-of-cyclin-dependent-protein-kinase-activity
ANIA_11246	ORF-that-was-absent-from-the-original-release-of-version-4-of-the-A.-nidulans-annotation,-but-present-in-a-previous-version;-reinstated-into-version-4-in-AspGD-as-of-July-2009
ANIA_7175	Ortholog(s)-have-cytosol,-nucleus-localization
ANIA_7832	Has-domain(s)-with-predicted-flavin-adenine-dinucleotide-binding,-oxidoreductase-activity,-acting-on-CH-OH-group-of-donors-activity-and-role-in-alcohol-metabolic-process,-oxidation-reduction-process
ANIA_7590	Putative-reductase-with-a-predicted-role-in-carbohydrate-metabolism;-mannitol-2-dehydrogenase;-intracellular,-menadione-stress-induced-protein;-HapX-regulated;-protein-induced-by-farnesol
ANIA_7816	Putative-sterigmatocystin-biosynthesis-lipase/esterase-with-a-predicted-role-in-sterigmatocystin/aflatoxin-biosynthesis;-member-of-the-sterigmatocystin-biosynthesis-gene-cluster
ANIA_7203	
ANIA_7744	Ortholog-of-A.-fumigatus-Af293-:-Afu5g07870,-A.-oryzae-RIB40-:-AO090701000920,-A.-niger-ATCC-1015-:-54693-mRNA,-Aspergillus-versicolor-:-Aspve1_0133353-and-Aspergillus-sydowii-:-Aspsy1_0152961
ANIA_7228	Has-domain(s)-with-predicted-N,N-dimethylaniline-monooxygenase-activity,-NADP-binding,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_7121	Has-domain(s)-with-predicted-metallocarboxypeptidase-activity,-zinc-ion-binding-activity-and-role-in-proteolysis
ANIA_7208	SET-domain-protein;-protein-levels-decrease-in-response-to-farnesol
ANIA_7101	Ortholog-of-A.-fumigatus-Af293-:-Afu4g03820,-A.-niger-CBS-513.88-:-An14g01070,-A.-oryzae-RIB40-:-AO090011000344,-A.-niger-ATCC-1015-:-201415-mRNA-and-Aspergillus-versicolor-:-Aspve1_0140534
ANIA_7779	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_7295	Putative-transmembrane-transporter;-upregulated-in-A.-oryzae-and-A.-nidulans-under-hypoxic-growth-conditions
ANIA_7341	Ortholog-of-A.-niger-CBS-513.88-:-An15g06860,-A.-oryzae-RIB40-:-AO090102000219,-Aspergillus-brasiliensis-:-Aspbr1_0200551,-A.-niger-ATCC-1015-:-210358-mRNA-and-N.-fischeri-NRRL-181-:-NFIA_091700
ANIA_10872	Ortholog-of-A.-fumigatus-Af293-:-Afu4g04650,-A.-niger-CBS-513.88-:-An14g00190,-A.-oryzae-RIB40-:-AO090206000024,-A.-niger-ATCC-1015-:-210842-mRNA-and-Aspergillus-versicolor-:-Aspve1_0140371
ANIA_7594	DUF636-domain-containing-protein;-intracellular,-menadione-stress-induced-protein;-protein-levels-decrease-in-response-to-farnesol

ANIA_7651	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01080,-A.-niger-CBS-513.88-:-An10g00470,-A.-oryzae-RIB40-:-AO090701000377,-A.-niger-ATCC-1015-:-213866-mRNA-and-Aspergillus-versicolor-:-Aspve1_0136028
ANIA_7500	Putative-NADH-dehydrogenase-(ubiquinone)-with-a-predicted-role-in-energy-metabolism;-expression-upregulated-after-exposure-to-farnesol
ANIA_7218	Ortholog-of-A.-nidulans-FGSC-A4-:-AN10534,-A.-fumigatus-Af293-:-Afu1g13000,-Afu7g03950,-A.-niger-CBS-513.88-:-An13g00410,-An06g00970-and-A.-oryzae-RIB40-:-AO090023000035,-AO090026000819
ANIA_7111	Peroxisomal-multifunctional-enzyme-involved-in-fatty-acid-beta-oxidation;-required-for-growth-on-very-long-chain-fatty-acids;-transcription-is-induced-by-fatty-acids
ANIA_7799	Protein-expressed-at-increased-levels-during-osmoadaptation;-short-chain-alcohol-dehydrogenase-domain
ANIA_7279	Has-domain(s)-with-predicted-poly(beta-D-mannuronate)-lyase-activity,-role-in-alginic-acid-catabolic-process-and-periplasmic-space-localization
ANIA_7713	Has-domain(s)-with-predicted-zinc-ion-binding-activity
ANIA_7344	Has-domain(s)-with-predicted-substrate-specific-transmembrane-transporter-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_10914	
ANIA_10906	Has-domain(s)-with-predicted-DNA-binding,-zinc-ion-binding-activity,-role-in-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7103	Protein-with-homology-to-Cockayne's-syndrome-nucleotide-excision-repair-protein;-transcript-upregulated-in-response-to-camptothecin
ANIA_7317	Protein-with-homology-to-GPR1/FUN34/YaaH-family-members
ANIA_7026	Ortholog-of-A.-fumigatus-Af293-:-Afu4g04230,-A.-niger-CBS-513.88-:-An14g00600,-A.-oryzae-RIB40-:-AO090206000070,-A.-niger-ATCC-1015-:-41506-mRNA-and-Aspergillus-versicolor-:-Aspve1_0140914
ANIA_7386	Ortholog-of-A.-nidulans-FGSC-A4-:-AN1127,-A.-fumigatus-Af293-:-Afu1g11740,-A.-niger-CBS-513.88-:-An02g03380,-An08g03700,-A.-oryzae-RIB40-:-AO090026000507-and-A.-niger-ATCC-1015-:-126803-mRNA
ANIA_7187	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity,-acting-on-the-CH-NH2-group-of-donors,-oxygen-as-acceptor-activity-and-role-in-oxidation-reduction-process
ANIA_7322	Ortholog-of-A.-niger-CBS-513.88-:-An01g14820,-Aspergillus-brasiliensis-:-Aspbr1_0145931,-A.-niger-ATCC-1015-:-172038-mRNA-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_05928
ANIA_7773	Putative-cytochrome-P450
ANIA_10899	
ANIA_7772	Putative-cytochrome-P450;-transcript-repressed-by-nitrate
ANIA_10911	Has-domain(s)-with-predicted-sequence-specific-DNA-binding-RNA-polymerase-II-transcription-factor-activity,-zinc-ion-binding-activity,-role-in-regulation-of-transcription,-DNA-dependent-and-nucleus-localization
ANIA_7684	Has-domain(s)-with-predicted-monooxygenase-activity-and-role-in-oxidation-reduction-process
ANIA_9506	Has-domain(s)-with-predicted-amino-acid-transmembrane-transporter-activity,-role-in-amino-acid-transmembrane-transport-and-membrane-localization
ANIA_7148	Ortholog-of-A.-nidulans-FGSC-A4-:-AN11171,-A.-fumigatus-Af293-:-Afu4g03595,-A.-niger-CBS-513.88-:-An02g01320,-An14g01685,-An03g06340-and-A.-oryzae-RIB40-:-AO090026000213,-AO090026000142,-AO090023000130
ANIA_7041	Ortholog-of-A.-fumigatus-Af293-:-Afu4g04070,-A.-niger-CBS-513.88-:-An14g00800,-A.-oryzae-RIB40-:-AO090206000109,-A.-niger-ATCC-1015-:-41522-mRNA-and-Aspergillus-versicolor-:-Aspve1_0056348
ANIA_7033	Ortholog-of-A.-fumigatus-Af293-:-Afu4g04190,-A.-niger-CBS-513.88-:-An14g00640,-A.-oryzae-RIB40-:-AO090206000078,-A.-niger-ATCC-1015-:-201359-mRNA-and-Aspergillus-versicolor-:-Aspve1_0075847
ANIA_8690	Protein-expressed-at-increased-levels-during-osmoadaptation;-palA-dependent-expression-independent-of-pH
ANIA_7329	
ANIA_7453	Ortholog-of-A.-fumigatus-Af293-:-Afu2g05990,-A.-niger-CBS-513.88-:-An02g14270,-Aspergillus-versicolor-:-Aspve1_0031005,-Aspergillus-sydowii-:-Aspsy1_0090031-and-Aspergillus-terreus-NIH2624-:-ATET_06789
ANIA_7017	Ortholog(s)-have-pyridoxal-phosphate-binding-activity-and-cytosol,-nucleus-localization
ANIA_7690	Ortholog-of-A.-fumigatus-Af293-:-Afu2g01610,-A.-niger-CBS-513.88-:-An03g04840,-A.-oryzae-RIB40-:-AO090701000787,-A.-niger-ATCC-1015-:-50710-mRNA-and-Aspergillus-versicolor-:-Aspve1_0136164
ANIA_7336	Ortholog-of-A.-fumigatus-Af293-:-Afu2g16500,-A.-niger-CBS-513.88-:-An15g06925,-A.-niger-ATCC-1015-:-210364-mRNA,-Aspergillus-versicolor-:-Aspve1_0050737-and-Aspergillus-sydowii-:-Aspsy1_0054451
ANIA_6982	Putative-phosphotyrosine-specific-protein-phosphatase-of-the-HOG-signaling-pathway-that-regulates-osmotic-stress-response
ANIA_7221	
ANIA_7205	Ortholog(s)-have-role-in-ribosome-biogenesis-and-cytosol,-nucleolus-localization
ANIA_8797	Ortholog-of-A.-fumigatus-Af293-:-Afu5g09640,-A.-niger-CBS-513.88-:-An07g03220,-A.-oryzae-RIB40-:-AO090020000593,-A.-niger-ATCC-1015-:-209757-mRNA-and-Aspergillus-versicolor-:-Aspve1_0141277
ANIA_12348	Ortholog-of-A.-niger-CBS-513.88-:-An08g00240,-Aspergillus-versicolor-:-Aspve1_0024638,-Aspergillus-sydowii-:-Aspsy1_0025347-and-Aspergillus-terreus-NIH2624-:-ATET_08502
ANIA_12052	
ANIA_12018	
ANIA_11779	
ANIA_11704	Has-domain(s)-with-predicted-RNA-polymerase-II-transcription-cofactor-activity,-role-in-regulation-of-transcription-from-RNA-polymerase-II-promoter-and-mediator-complex-localization
ANIA_20001	Mitochondrially-encoded-subunit-5-of-NADH-dehydrogenase
ANIA_20017	Mitochondrially-encoded-protein-with-similarity-to-subunit-9-of-F1-F0-ATP-synthase;-apparently-does-not-encode-the-functional-subunit-9,-which-is-encoded-by-the-nuclear-oliC-gene
ANIA_20014	Subunit-I-of-cytochrome-c-oxidase,-which-is-the-terminal-member-of-the-mitochondrial-inner-membrane-electron-transport-chain;-one-of-three-mitochondrially-encoded-subunits;-2nd-and-3rd-introns-contain-maturase-related-open-reading-frames
ANIA_12311	
ANIA_11781	
ANIA_12088	Has-domain(s)-with-predicted-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_12279	Putative-chitinase;-glycoside-hydrolase-family-18-(GH18)-protein-with-a-predicted-role-in-chitin-hydrolysis
ANIA_11921	Ortholog-of-A.-fumigatus-Af293-:-Afu8g07200,-A.-niger-CBS-513.88-:-An15g07550,-A.-oryzae-RIB40-:-AO090701000752,-A.-niger-ATCC-1015-:-200874-mRNA-and-Aspergillus-versicolor-:-Aspve1_0131033
ANIA_11751	
ANIA_12270	
ANIA_3734	Possible-pseudogene,-similar-to-autophagy-related-protein
ANIA_2379	Possible-pseudogene
ANIA_11140	Possible-pseudogene
ANIA_0011	Possible-pseudogene
ANIA_1070	Possible-pseudogene,-mariner-element-related
ANIA_0010	Possible-pseudogene,-similar-to-amino-acid-transporter
ANIA_1749	Possible-pseudogene
ANIA_7928	Possible-pseudogene
ANIA_12218	
ANIA_12087	
ANIA_12284	
ANIA_12080	
ANIA_12017	Ortholog(s)-have-polyphosphate-kinase-activity-and-role-in-microautophagy,-polyphosphate-metabolic-process,-vacuolar-transport,-vacuole-fusion,-non-autophagic
ANIA_11748	
ANIA_12183	
ANIA_12015	
ANIA_11695	
ANIA_11891	Has-domain(s)-with-predicted-protein-dimerization-activity,-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_12135	
ANIA_12290	Has-domain(s)-with-predicted-nucleotide-binding,-oxidoreductase-activity-and-role-in-oxidation-reduction-process
ANIA_12199	Ortholog-of-Aspergillus-brasiliensis-:-Aspbr1_0078801,-A.-clavatus-NRRL-1-:-ACLA_074610,-Aspergillus-acidus-:-Aspfo1_0207590-and-Aspergillus-versicolor-:-Aspve1_0080732
ANIA_11782	
ANIA_12031	
ANIA_11785	
ANIA_12054	Ortholog-of-S.-cerevisiae-Ssn6p;-essential-gene-in-A.-nidulans-and-S.-pombe-but-not-in-S.-cerevisiae
ANIA_11886	Has-domain(s)-with-predicted-transferase-activity,-transferring-phosphorus-containing-groups-activity-and-membrane-localization
ANIA_12051	
ANIA_11965	
ANIA_11883	
ANIA_11778	Putative-exoinulinase
ANIA_12460	Has-domain(s)-with-predicted-sequence-specific-DNA-binding,-sequence-specific-DNA-binding-transcription-factor-activity-and-role-in-regulation-of-transcription,-DNA-dependent
ANIA_12077	

ANIA_12305	Ortholog(s)-have-cell-cortex,-spindle-pole-body-localization
ANIA_12114	
ANIA_12414	
ANIA_11684	Ortholog(s)-have-ubiquitin-specific-protease-activity,-role-in-protein-deubiquitination-and-mitochondrial-outer-membrane-localization
ANIA_11877	
ANIA_12386	Ortholog-of-A.-fumigatus-Af293-:-Afu3g04020,-A.-oryzae-RIB40-:-AO090124000070,-A.-niger-ATCC-1015-:-191450-mRNA,-Aspergillus-versicolor-:-Aspve1_0132548-and-Aspergillus-sydowii-:-Aspsy1_0150607
ANIA_12458	Has-domain(s)-with-predicted-catalytic-activity-and-role-in-metabolic-process
ANIA_12016	
ANIA_12360	Has-domain(s)-with-predicted-role-in-response-to-stress
ANIA_11940	
ANIA_12030	
ANIA_11851	
ANIA_12224	
ANIA_12157	
ANIA_12160	
ANIA_11735	
ANIA_12361	
ANIA_12189	
ANIA_11708	
ANIA_11866	
ANIA_11852	
ANIA_11980	
ANIA_12388	Ortholog-of-A.-fumigatus-Af293-:-Afu6g08650,-N.-fischeri-NRRL-181-:-NFIA_054300,-Aspergillus-flavus-NRRL-3357-:-AFL2T_09170,-A.-clavatus-NRRL-1-:-ACLA_083760-and-Aspergillus-versicolor-:-Aspve1_0083813
ANIA_20012	Subunit-III-of-cytochrome-c-oxidase,-which-is-the-terminal-member-of-the-mitochondrial-inner-membrane-electron-transport-chain;-one-of-three-mitochondrially-encoded-subunits
ANIA_20005	Cytochrome-b,-mitochondrially-encoded-subunit-of-the-ubiquinol-cytochrome-c-reductase-complex
ANIA_11844	
ANIA_12230	
ANIA_12207	Ortholog-of-A.-fumigatus-Af293-:-Afu5g04280,-A.-niger-CBS-513.88-:-An09g06750,-A.-oryzae-RIB40-:-AO090102000634,-A.-niger-ATCC-1015-:-142854-mRNA-and-Aspergillus-versicolor-:-Aspve1_0089321
ANIA_12064	
ANIA_12109	
ANIA_11860	
ANIA_11976	
ANIA_11776	Ortholog(s)-have-mitochondrion-localization
ANIA_12084	Ortholog-of-Aspergillus-brasiliensis-:-Aspbr1_0198574,-Aspergillus-acidus-:-Aspfo1_0207812,-Aspergillus-versicolor-:-Aspve1_0052887-and-Aspergillus-sydowii-:-Aspsy1_1045764
ANIA_11884	
ANIA_11907	
ANIA_12129	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_12013	
ANIA_11981	Has-domain(s)-with-predicted-UDP-N-acetylmuramate-dehydrogenase-activity,-flavin-adenine-dinucleotide-binding-activity-and-role-in-oxidation-reduction-process
ANIA_11871	Ortholog-of-A.-fumigatus-Af293-:-Afu1g11260,-Afu6g00270,-A.-niger-CBS-513.88-:-An03g03440,-An04g04460,-A.-niger-ATCC-1015-:-190306-mRNA-and-Aspergillus-versicolor-:-Aspve1_0081045,-Aspve1_0086252,-Aspve1_0198276
ANIA_12159	Ortholog-of-A.-fumigatus-Af293-:-Afu2g10870,-A.-niger-CBS-513.88-:-An02g02720,-A.-oryzae-RIB40-:-AO090011000543,-Aspergillus-sydowii-:-Aspsy1_0044896-and-Aspergillus-terreus-NIH2624-:-ATET_01491
ANIA_11878	
ANIA_12103	
ANIA_11915	Ortholog-of-A.-niger-CBS-513.88-:-An11g00410,-A.-oryzae-RIB40-:-AO090012000154,-A.-niger-ATCC-1015-:-208535-mRNA,-Aspergillus-versicolor-:-Aspve1_0041340-and-Aspergillus-sydowii-:-Aspsy1_0058317
ANIA_11685	Ortholog-of-A.-oryzae-RIB40-:-AO090003000723,-Aspergillus-brasiliensis-:-Aspbr1_0038462,-A.-clavatus-NRRL-1-:-ACLA_039550,-Aspergillus-acidus-:-Aspfo1_0204521-and-Aspergillus-versicolor-:-Aspve1_0026974
ANIA_12461	Ortholog-of-A.-fumigatus-Af293-:-Afu1g05670,-A.-niger-CBS-513.88-:-An18g03360,-A.-oryzae-RIB40-:-AO090009000369,-A.-niger-ATCC-1015-:-42808-mRNA-and-Aspergillus-versicolor-:-Aspve1_0054309,-Aspve1_0072820
ANIA_11869	
ANIA_12353	
ANIA_12261	
ANIA_11978	Ortholog(s)-have-endoplasmic-reticulum-localization
ANIA_12357	
ANIA_12443	Ortholog-of-A.-niger-CBS-513.88-:-An16g02400,-Aspergillus-brasiliensis-:-Aspbr1_0192860,-Aspbr1_0205648,-A.-niger-ATCC-1015-:-125573-mRNA-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_00317
ANIA_12162	
ANIA_11865	
ANIA_11934	Has-domain(s)-with-predicted-ATP-binding,-ATPase-activity,-coupled-to-transmembrane-movement-of-substances-activity,-role-in-transmembrane-transport-and-integral-to-membrane-localization
AN1IA_2449	Has-domain(s)-with-predicted-NAD(P)+-transhydrogenase-(AB-specific)-activity,-NADP-binding-activity,-role-in-oxidation-reduction-process,-proton-transport-and-integral-to-membrane-localization
ANIA_11850	
ANIA_12217	Has-domain(s)-with-predicted-role-in-transmembrane-transport-and-integral-to-membrane-localization
ANIA_12136	
ANIA_12488	Has-domain(s)-with-predicted-nucleotide-binding-activity
ANIA_12481	
ANIA_12480	Ortholog-of-A.-fumigatus-Af293-:-Afu2g08060,-A.-oryzae-RIB40-:-AO090011000895,-Aspergillus-brasiliensis-:-Aspbr1_0661447,-N.-fischeri-NRRL-181-:-NFIA_083710-and-Aspergillus-flavus-NRRL-3357-:-AFL2T_05605
ANIA_12487	

Chapter 4

Supplementary Table 2

Uniprot Cross referenced of unique targets

Entry	Status	Protein names	Gene names	Organism	Length
Q5B6V0_EMENI	unreviewed	1,3-beta-glucanosyltransferase (EC 2.4.1.-)	AN3730.2 ANIA_03730	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	542
Q5AVM3_EMENI	unreviewed	**1,3-beta-glucanosyltransferase (EC 2.4.1.-)**	AN7657.2 ANIA_07657	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	455
Q5AW19_EMENI	unreviewed	1,3-beta-glucanosyltransferase (EC 2.4.1.-)	AN7511.2 ANIA_07511	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	539
Q5B4M9_EMENI	unreviewed	1433_TRIHA 14-3-3 PROTEIN HOMOLOG (TH1433) (ARTA [Source:UniProtKB/TrEMBLAcc:Q9C1D9])	AN4501.2 ANIA_04501	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	261
C8V1C5_EMENI	unreviewed	2-methylcitrate dehydratase (Eurofung)	ANIA_06639	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	635
HSP30_EMENI	reviewed	**30 kDa heat shock protein**	hsp30 AN2530	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	181
Q5AVH9_EMENI	unreviewed	37S ribosomal protein S16 (AFU_orthologue AFUA_5G08350) (Uncharacterized protein)	AN7701.2 ANIA_07701	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	105
C8VN86_EMENI	unreviewed	3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.34)	ANIA_01593	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	416
C8VGU6_EMENI	unreviewed	3-hydroxyacyl-CoA dehydrogenase, putative (AFU_orthologue AFUA_3G00290)	ANIA_05331	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	325
C8VSB3_EMENI	unreviewed	3-hydroxyisobutyrate dehydrogenase (AFU_orthologue AFUA_6G11020)	ANIA_00593	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
Q5B0P4_EMENI	unreviewed	3-isopropylmalate dehydratase (EC 4.2.1.33) (Alpha-IPM isomerase) (Isopropylmalate isomerase)	AN5886.2 ANIA_05886	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	772
C8VQW0_EMENI	unreviewed	3-ketoacyl-acyl carrier protein reductase, putative (AFU_orthologue AFUA_1G14380)	ANIA_10122	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	251
Q5BEI0_EMENI	unreviewed	3-ketoacyl-CoA ketothiolase (Kat1), putative (AFU_orthologue AFUA_1G12650) (Uncharacterized protein)	AN1050.2 ANIA_01050	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	417
PANB_EMENI	reviewed	**3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase)**	panB AN1778	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	349
C8V5G7_EMENI	unreviewed	3-oxo-5-alpha-steroid 4-dehydrogenase, putative (AFU_orthologue AFUA_1G05470)	ANIA_04071	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
C8V9B1_EMENI	unreviewed	3-phosphoglycerate dehydrogenase, hypothetical (Eurofung)	ANIA_08866	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	475
RSSA_EMENI	reviewed	**40S ribosomal protein S0**	rps0 AN3172	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	293
C8V7K1_EMENI	unreviewed	**40S ribosomal protein S10b (AFU_orthologue AFUA_6G12660)**	ANIA_03706	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	153
Q5BBW6_EMENI	unreviewed	40S ribosomal protein S6	AN1964.2 ANIA_01964	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	237
GABAT_EMENI	reviewed	4-aminobutyrate aminotransferase (EC 2.6.1.19) (GABA aminotransferase) (GABA-AT) (Gamma-amino-N-butyrate transaminase) (GABA transaminase)	gatA AN2248	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	498
Q5B731_EMENI	unreviewed	**50S ribosomal protein L2 (AFU_orthologue AFUA_4G12170) (Uncharacterized protein)**	AN3649.2 ANIA_03649	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	405
C8VMW6_EMENI	unreviewed	50S ribosomal subunit L7, putative (AFU_orthologue AFUA_5G06430)	ANIA_02268	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	354
HEM1_EMENI	reviewed	5-aminolevulinate synthase, mitochondrial (EC 2.3.1.37) (5-aminolevulinic acid synthase) (Delta-ALA synthase) (Delta-aminolevulinate synthase)	hemA AN2284	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	648
C8V7X1_EMENI	unreviewed	5-demethoxyubiquinone hydroxylase, mitochondrial (DMQ hydroxylase) (EC 1.14.13.-) (Ubiquinone biosynthesis monooxygenase COQ7)	COQ7 ANIA_04569	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	240
C8V8L0_EMENI	unreviewed	**60S ribosomal protein L22, putative (AFU_orthologue AFUA_3G12300)**	ANIA_05014	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	124
Q5B900_EMENI	unreviewed	60S ribosomal protein L35Ae (AFU_orthologue AFUA_3G08460) (Uncharacterized protein)	AN2980.2 ANIA_02980	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	109
Q5AU54_EMENI	unreviewed	**60S ribosomal protein L4, putative (AFU_orthologue AFUA_5G03020) (Uncharacterized protein)**	AN8176.2 ANIA_08176	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	372
Q5AQY3_EMENI	unreviewed	67 kDa myosin-cross-reactive antigen family protein (AFU_orthologue AFUA_3G03570) (Uncharacterized protein)	AN9297.2 ANIA_09297	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	589
C8V621_EMENI	unreviewed	**6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)**	ANIA_03954	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	490
C8VUB6_EMENI	unreviewed	6-phosphogluconolactonase, putative (AFU_orthologue AFUA_1G02980)	ANIA_00285	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	265
C8VM55_EMENI	unreviewed	AAA family ATPase, putative (AFU_orthologue AFUA_8G04270)	ANIA_10191	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1631
Q5BGV5_EMENI	unreviewed	ABC bile acid transporter (Eurofung) (Uncharacterized protein)	AN0225.2 ANIA_00225	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1667
C8V9M3_EMENI	unreviewed	ABC multidrug transporter (Eurofung)	ANIA_08813	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1480
Q5AYP9_EMENI	unreviewed	ABC multidrug transporter (Eurofung) (Uncharacterized protein)	AN6581.2 ANIA_06581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1517
Q5BFA9_EMENI	unreviewed	**ABC transporter protein [Source:UniProtKB/TrEMBLAcc:Q96VK4] (Uncharacterized protein)**	AN0771.2 ANIA_00771	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1499
C8VBS0_EMENI	unreviewed	ABC transporter protein [Source:UniProtKB/TrEMBLAcc:Q96VK5]	ANIA_10949	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1501
Q5B565_EMENI	unreviewed	ABC transporter, putative (Eurofung) (Uncharacterized protein)	AN4315.2 ANIA_04315	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	751
Q9Y8G1_EMEND	unreviewed	ABC-transporter (Multidrug resistance protein MDR)	atrD abcD	Emericella nidulans (Aspergillus nidulans)	1348
AMDS_EMENI	reviewed	**Acetamidase (EC 3.5.1.4)**	amdS AN8777	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	548
ACPA_EMENI	reviewed	**Acetate permease A (Monocarboxylate transporter acpA)**	acpA AN5226.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	298
C8V916_EMENI	unreviewed	Acetolactate synthase (EC 2.2.1.6)	ANIA_04956	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	687
ACSA_EMENI	reviewed	**Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-activating enzyme)**	facA acuA AN5626	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	670
C8V9S3_EMENI	unreviewed	Acetylglutamate kinase (Eurofung)	ANIA_08770	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	905
Q1HFU0_EMEND	unreviewed	Acetylxylan esterase	AN3294-2	Emericella nidulans (Aspergillus nidulans)	402
TREA_EMENI	reviewed	**Acid trehalase (EC 3.2.1.28) (Alpha,alpha-trehalase) (Alpha,alpha-trehalose glucohydrolase)**	treA AN9340	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1054
Q5BAJ4_EMENI	unreviewed	ACL1_NEUCR Probable ATP-citrate synthase subunit 1 (ATP-citrate (Pro-S-)-lyase 1) (Citrate cleavage enzyme subunit 1) (ATP citrate lyase, subunit 1, putative (AFU_orthologue AFUA_6G10650))	AN2436.2 ANIA_02436	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	655
Q5BH45_EMENI	unreviewed	Actin cytoskeleton organization protein (Cro1), putative (AFU_orthologue AFUA_5G11600) (Uncharacterized protein)	AN0135.2 ANIA_00135	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	832
Q5B0C6_EMENI	unreviewed	Actin cytoskeleton protein (VIP1), putative (AFU_orthologue AFUA_2G10030) (Uncharacterized protein)	AN6004.2 ANIA_06004	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	270
C8V199_EMENI	unreviewed	**AcuM, Zn(II)2Cys6 transcription factor involved in transcription control of gluconeogenisis (Eurofung)**	ANIA_06293	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	522
Q5ATG5_EMENI	unreviewed	Acyl-CoA dehydrogenase (Eurofung) (Uncharacterized protein)	AN8415.2 ANIA_08415	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	438
Q5B5P5_EMENI	unreviewed	Acyl-CoA desaturase (EC 1.14.19.1)	AN4135.2 ANIA_04135	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	449
AAAA_EMENI	reviewed	**Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase 40 kDa form (EC 2.3.1.164) (Isopenicillin-N N-acyltransferase) [Cleaved into: Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase 11 kDa subunit; Acyl-coenzym**	penDE aat AN2623	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	357
C8VJI7_EMENI	unreviewed	ADAM family of metalloprotease ADM-A (AFU_orthologue AFUA_6G14420)	ANIA_02810	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	722
Q5ARJ7_EMENI	unreviewed	Adenine phosphoribosyltransferase 1 (AFU_orthologue AFUA_7G02310) (Uncharacterized protein)	AN9083.2 ANIA_09083	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	214
Q5BDW7_EMENI	unreviewed	Adenosylhomocysteinase (EC 3.3.1.1)	AN1263.2 ANIA_01263	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	449
PURA_EMENI	reviewed	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	adB oxpA AN0893	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	424
Q5B5W6_EMENI	unreviewed	ADP,ATP carrier protein (Broad) (ADT_NEUCR ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT))	AN4064.2 ANIA_04064	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	311
Q5BEA4_EMENI	unreviewed	ADP-ribosylation factor (Broad) (ARF_AJECA ADP-RIBOSYLATION FACTOR)	AN1126.2 ANIA_01126	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	183
C8VC81_EMENI	unreviewed	Alanine racemase family protein, putative (AFU_orthologue AFUA_4G04300)	ANIA_07017	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	272
C8VKU5_EMENI	unreviewed	Alanine transaminase (Eurofung)	ANIA_01923	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	555
ADH1_EMENI	reviewed	**Alcohol dehydrogenase 1 (EC 1.1.1.1) (Alcohol dehydrogenase I) (ADH I)**	alcA AN8979	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	350
ADH3_EMENI	reviewed	**Alcohol dehydrogenase 3 (EC 1.1.1.1) (Alcohol dehydrogenase III) (ADH III)**	alcC adh3 AN2286	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	352
C8VT88_EMENI	unreviewed	**Alcohol dehydrogenase, zinc-containing, putative (AFU_orthologue AFUA_1G04620)**	ANIA_00443	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	348
ALDH_EMENI	reviewed	**Aldehyde dehydrogenase (ALDDH) (ALDH) (EC 1.2.1.3)**	aldA aspA AN0554	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	497
C8VA73_EMENI	unreviewed	**Aldehyde dehydrogenase family protein, putative (AFU_orthologue AFUA_3G03250)**	ANIA_10602	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	493
C8VN10_EMENI	unreviewed	Aldo-keto reductase (AKR13), puatative (AFU_orthologue AFUA_7G00700)	ANIA_10217	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	339
Q5B8E6_EMENI	unreviewed	Aldose 1-epimerase, putative (AFU_orthologue AFUA_3G13240) (Uncharacterized protein)	AN3184.2 ANIA_03184	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	447
Q5B4C7_EMENI	unreviewed	Allantoinase (Eurofung) (Uncharacterized protein)	AN4603.2 ANIA_04603	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	506
Q5B6M6_EMENI	unreviewed	Allergen Asp F4 (AFU_orthologue AFUA_2G03830) (Uncharacterized protein)	AN3804.2 ANIA_03804	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	320
Q5ATB9_EMENI	unreviewed	Allergen Asp F4-like, putative (AFU_orthologue AFUA_3G00710) (Uncharacterized protein)	AN8461.2 ANIA_08461	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
Q5B501_EMENI	unreviewed	Allergen Asp F7 (AFU_orthologue AFUA_4G06670) (Uncharacterized protein)	AN4379.2 ANIA_04379	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	284

C8V4N3_EMENI	unreviewed	Alpha/beta hydrolase, putative (AFU_orthologue AFUA_6G11570)	ANIA_10520	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	545
G5EB12_EMENI	unreviewed	alpha-1,2-Mannosidase (EC 3.2.1.-)	AN3566.2 ANIA_03566	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	586
Q5AXX3_EMENI	unreviewed	Alpha-1,2-mannosyltransferase, putative (AFU_orthologue AFUA_5G13090) (Uncharacterized protein)	AN6857.2 ANIA_06857	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	490
Q5B823_EMENI	unreviewed	Alpha-1,3 glucan synthases (Eurofung) (Uncharacterized protein)	AN3307.2 ANIA_03307	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	2444
C8VU49_EMENI	unreviewed	Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)	ANIA_01015	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	879
AGALC_EMENI	reviewed	Alpha-galactosidase C (EC 3.2.1.22) (Melibiase C)	aglC AN8138	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	750
Q5BB80_EMENI	unreviewed	Alpha-ketoglutarate-dependent taurine dioxygenase (AFU_orthologue AFUA_8G02210) (Uncharacterized protein)	AN2200.2 ANIA_02200	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	383
ABFC_EMENI	reviewed	Alpha-L-arabinofuranosidase C (ABF C) (Arabinosidase C) (EC 3.2.1.55)	abfC AN1277	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	504
AOX_EMENI	reviewed	**Alternative oxidase, mitochondrial (EC 1.-.-.-)**	alxA aod-1 AN2099	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	354
Q5B0N0_EMENI	unreviewed	AMFR protein, putative (AFU_orthologue AFUA_2G11100) (Uncharacterized protein)	AN5900.2 ANIA_05900	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	197
Q5AYA7_EMENI	unreviewed	Amidohydrolase family protein (AFU_orthologue AFUA_7G05840) (Uncharacterized protein)	AN6723.2 ANIA_06723	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	338
C8VPL4_EMENI	unreviewed	Amine oxidase (EC 1.4.3.-)	ANIA_02532	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	674
C8VNK8_EMENI	unreviewed	**Amino acid transporter (Eurofung)**	ANIA_01659	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	467
Q5B6F4_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN3876.2 ANIA_03876	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	547
Q5AT42_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN8538.2 ANIA_08538	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	507
Q5B843_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN3287.2 ANIA_03287	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	562
Q5BB79_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN2201.2 ANIA_02201	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	544
Q5BE31_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN1199.2 ANIA_01199	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	497
Q5AVA3_EMENI	unreviewed	**Amino acid transporter (Eurofung) (Uncharacterized protein)**	AN7777.2 ANIA_07777	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	580
C8V2E0_EMENI	unreviewed	**Amino acid transporter [Source:UniProtKB/TrEMBLAcc:B2M1L6]**	ANIA_06118	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	567
Q5BFA0_EMENI	unreviewed	Aminotransferase, hypothetical (Eurofung) (Uncharacterized protein)	AN0780.2 ANIA_00780	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	437
G5EB09_EMENI	unreviewed	**Ammonium transporter**	AN7463.2 ANIA_07463	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	544
APSA_EMENI	reviewed	**Anucleate primary sterigmata protein A**	apsA AN7757	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1676
Q5B5H3_EMENI	unreviewed	AP-1 adaptor complex subunit gamma, putative (AFU_orthologue AFUA_1G06030) (Uncharacterized protein)	AN4207.2 ANIA_04207	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	839
Q5ARH5_EMENI	unreviewed	Arrestin (Or S-antigen), N-terminal domain protein (AFU_orthologue AFUA_7G02050) (Uncharacterized protein)	AN9105.2 ANIA_09105	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	609
C8VP13_EMENI	unreviewed	**Arrestin domain protein (AFU_orthologue AFUA_6G10550)**	ANIA_02447	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	401
Q5BBT7_EMENI	unreviewed	Aspartate aminotransferase (EC 2.6.1.1)	AN1993.2 ANIA_01993	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	429
Q5B082_EMENI	unreviewed	Aspartate transaminase (Eurofung) (Uncharacterized protein)	AN6048.2 ANIA_06048	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	445
C8V8R7_EMENI	unreviewed	Aspartic-type endopeptidase (CtsD), putative (AFU_orthologue AFUA_4G07040)	ANIA_04422	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	498
Q5AYZ3_EMENI	unreviewed	Aspartic-type endopeptidase (OpsB), putative (AFU_orthologue AFUA_6G05350) (Uncharacterized protein)	AN6487.2 ANIA_06487	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	454
C8VJ72_EMENI	unreviewed	AtfA [Source:UniProtKB/TrEMBLAcc:Q8J0Q4]	ANIA_02911	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	485
ATP9_EMENI	reviewed	ATP synthase subunit 9, mitochondrial (Lipid-binding protein)	atp9 oliC AN1624	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	143
C8VMQ7_EMENI	unreviewed	ATP synthase subunit alpha	ANIA_01523	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	556
Q5AS02_EMENI	unreviewed	ATP-binding cassette multidrug transporter [Source:UniProtKB/TrEMBLAcc:P78576] (Uncharacterized protein)	AN8928.2 ANIA_08928	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1466
Q5B8A7_EMENI	unreviewed	ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	AN3223.2 ANIA_03223	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	795
DED1_EMENI	reviewed	ATP-dependent RNA helicase ded1 (EC 3.6.4.13)	ded1 AN10557	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	668
C8V8N6_EMENI	unreviewed	Aureobasidin-resistance protein [Source:UniProtKB/TrEMBLAcc:Q9Y744]	ANIA_04991	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	439
ATG13_EMENI	reviewed	**Autophagy-related protein 13**	atg13 AN2076	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	974
AT222_EMENI	reviewed	**Autophagy-related protein 22-2**	atg22-2 AN7591	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	593
ATG8_EMENI	reviewed	**Autophagy-related protein 8 (Autophagy-related ubiquitin-like modifier atg8)**	atg8 AN5131	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	118
C8VN24_EMENI	unreviewed	BAR domain protein (AFU_orthologue AFUA_5G06340)	ANIA_02277	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	428
C8V3Q1_EMENI	unreviewed	Basic amino acid transporter (Eurofung)	ANIA_08279	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	527
Q5B4M2_EMENI	unreviewed	Bax Inhibitor family protein (AFU_orthologue AFUA_2G03220) (Uncharacterized protein)	AN4508.2 ANIA_04508	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	335
Q5AWG6_EMENI	unreviewed	Beta-1,4-xylosidase (Eurofung) (Uncharacterized protein)	AN7364.2 ANIA_07364	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	446
C8VQG4_EMENI	unreviewed	**Beta-glucosidase, putative (AFU_orthologue AFUA_1G14710)**	ANIA_10124	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	483
Q5B9B0_EMENI	unreviewed	Beta-N-acetylglucosaminidase, putative (AFU_orthologue AFUA_3G11780) (Uncharacterized protein)	AN2870.2 ANIA_02870	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	366
Q5B0Q3_EMENI	unreviewed	Bifunctional fatty acid transporter/acyl-CoA synthetase (FAT1), putative (AFU_orthologue AFUA_2G11360) (Uncharacterized protein)	AN5877.2 ANIA_05877	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	639
Q5AYI7_EMENI	unreviewed	Biotin synthase (Eurofung) (Uncharacterized protein)	AN6643.2 ANIA_06643	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	393
Q5B2J9_EMENI	unreviewed	BNR/Asp-box repeat domain protein (AFU_orthologue AFUA_7G06430) (Uncharacterized protein)	AN5231.2 ANIA_05231	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	367
C8V2M4_EMENI	unreviewed	BZIP transcription factor (Atf21), putative (AFU_orthologue AFUA_5G12960)	ANIA_06849	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	322
Q5AST7_EMENI	unreviewed	BZIP transcription factor (Atf21), putative (AFU_orthologue AFUA_5G12960) (Uncharacterized protein)	AN8643.2 ANIA_08643	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
Q5BD44_EMENI	unreviewed	B-zip transcription factor (Eurofung) (Uncharacterized protein)	AN1536.2 ANIA_01536	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	627
C8VBM8_EMENI	unreviewed	BZIP-type transcription factor [Source:UniProtKB/TrEMBLAcc:B0B2H8]	flbB ANIA_07542	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	426
Q5B5A7_EMENI	unreviewed	C2 domain protein (AFU_orthologue AFUA_7G03800) (Uncharacterized protein)	AN4273.2 ANIA_04273	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	584
Q5B609_EMENI	unreviewed	C2H2 finger domain protein, putative (AFU_orthologue AFUA_1G03710) (Uncharacterized protein)	AN4021.2 ANIA_04021	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	422
Q5B4E4_EMENI	unreviewed	C2H2 finger domain protein, putative (AFU_orthologue AFUA_2G02080) (Uncharacterized protein)	AN4586.2 ANIA_04586	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	226
Q5B1C1_EMENI	unreviewed	C2H2 finger domain protein, putative (AFU_orthologue AFUA_4G13600) (Uncharacterized protein)	AN5659.2 ANIA_05659	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
Q5ASI9_EMENI	unreviewed	C2H2 finger domain protein, putative (AFU_orthologue AFUA_6G02690) (Uncharacterized protein)	AN8741.2 ANIA_08741	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	311
Q5AY97_EMENI	unreviewed	C2H2 finger domain protein, putative (AFU_orthologue AFUA_7G05960) (Uncharacterized protein)	AN6733.2 ANIA_06733	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1003
C8VSJ0_EMENI	unreviewed	C2H2 transcription factor (Egr2), putative (AFU_orthologue AFUA_1G10230)	ANIA_01251	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	242
Q5BF63_EMENI	unreviewed	C2H2 transcription factor (Sfp1), putative (AFU_orthologue AFUA_1G14750) (Uncharacterized protein)	AN0817.2 ANIA_00817	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	566
Q5BDW5_EMENI	unreviewed	C2H2 transcription factor, putative (AFU_orthologue AFUA_1G10080) (Uncharacterized protein)	AN1265.2 ANIA_01265	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	627
Q5BFN6_EMENI	unreviewed	C2H2 transcription factor, putative (AFU_orthologue AFUA_1G13050) (Uncharacterized protein)	AN0644.2 ANIA_00644	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	264
C8VB91_EMENI	unreviewed	C-4 methyl sterol oxidase Erg25, putative (AFU_orthologue AFUA_4G04820)	ANIA_06973	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	302
C8VLK9_EMENI	unreviewed	C-4 methyl sterol oxidase, putative (AFU_orthologue AFUA_8G02440)	ANIA_08907	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	291
C8V7M7_EMENI	unreviewed	C6 transcription factor, putative (AFU_orthologue AFUA_4G12570)	ANIA_03684	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	624
C8V1J5_EMENI	unreviewed	Calcineurin binding protein, putative (AFU_orthologue AFUA_2G13060)	ANIA_06249	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	301
KCC1_EMENI	reviewed	Calcium/calmodulin-dependent protein kinase (CMPK) (EC 2.7.11.17)	cmkA AN2412	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	414
Q5B3G0_EMENI	unreviewed	**Calcium-transporting ATPase (EC 3.6.3.8)**	AN4920.2 ANIA_04920	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1181
Q5BE41_EMENI	unreviewed	**Calcium-transporting ATPase (EC 3.6.3.8)**	AN1189.2 ANIA_01189	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1432
C8V4M8_EMENI	unreviewed	Calpain-like protein (AFU_orthologue AFUA_6G07970)	ANIA_10513	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	834
CARA_EMENI	reviewed	Carbamoyl-phosphate synthase arginine-specific small chain (CPS-A) (EC 6.3.5.5) (Arginine-specific carbamoyl-phosphate synthetase, glutamine chain)	cpa-1 AN2243	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	454
Q5B0D1_EMENI	unreviewed	Carbamoyl-phosphate synthetase, arginine-specific large chain (Eurofung) (Uncharacterized protein)	AN5999.2 ANIA_05999	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1173

Q5B9T3_EMENI	unreviewed	Carboxylic ester hydrolase (EC 3.1.1.-)	AN2697.2 ANIA_02697	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	584
Q5BA75_EMENI	unreviewed	Carboxypeptidase (EC 3.4.16.-)	AN2555.2 ANIA_02555	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	541
C8V7X8_EMENI	unreviewed	Casein kinase I (Eurofung)	ANIA_04563	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	370
C8V6D9_EMENI	unreviewed	Casein kinase II subunit beta (CK II beta)	ANIA_08079	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	680
Q5B0L2_EMENI	unreviewed	Catalase (EC 1.11.1.6)	AN5918.2 ANIA_05918	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	501
KATG_EMENI	reviewed	Catalase-peroxidase (CP) (EC 1.11.1.21) (Peroxidase/catalase)	katG cpeA AN7388	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	739
Q5BFB6_EMENI	unreviewed	Catechol dioxygenase, putative (AFU_orthologue AFUA_1G14270) (Uncharacterized protein)	AN0764.2 ANIA_00764	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
Q5B4J8_EMENI	unreviewed	Catechol dioxygenase, putative (AFU_orthologue AFUA_2G02910) (Uncharacterized protein)	AN4532.2 ANIA_04532	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	295
Q5B164_EMENI	unreviewed	CBS and PB1 domain protein (AFU_orthologue AFUA_1G06780) (Uncharacterized protein)	AN5716.2 ANIA_05716	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	666
Q5ASD9_EMENI	unreviewed	CDF iron transporter (Eurofung) (Uncharacterized protein)	AN8791.2 ANIA_08791	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	490
C8VGC5_EMENI	unreviewed	CECR1 family adenosine deaminase, putative (AFU_orthologue AFUA_6G13180)	ANIA_05492	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	567
Q5B1R3_EMENI	unreviewed	Cell division control protein Cdc4, putative (AFU_orthologue AFUA_6G13030) (Uncharacterized protein)	AN5517.2 ANIA_05517	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1038
C8VPR9_EMENI	unreviewed	Cell wall biogenesis protein Ecm15, putative (AFU_orthologue AFUA_4G09900)	ANIA_10243	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	108
C8VER3_EMENI	unreviewed	Cell wall cysteine-rich protein (AFU_orthologue AFUA_2G00400)	ANIA_08544	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	291
Q5B952_EMENI	unreviewed	Cell wall protein, putative (AFU_orthologue AFUA_3G08110) (Uncharacterized protein)	AN2928.2 ANIA_02928	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	730
Q5B3I3_EMENI	unreviewed	Cell wall protein, putative (AFU_orthologue AFUA_3G10960) (Uncharacterized protein)	AN4897.2 ANIA_04897	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	271
Q5AYE5_EMENI	unreviewed	Cellular morphogenesis protein (Rax2), putative (AFU_orthologue AFUA_7G05340) (Uncharacterized protein)	AN6685.2 ANIA_06685	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1214
Q5B548_EMENI	unreviewed	Ceramide synthase BarA (Eurofung) (Uncharacterized protein)	AN4332.2 ANIA_04332	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	429
Q5B273_EMENI	unreviewed	CFEM domain protein (AFU_orthologue AFUA_6G14090) (Uncharacterized protein)	AN5357.2 ANIA_05357	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	308
C8V173_EMENI	unreviewed	Chitin synthase [Source:UniProtKB/TrEMBLAcc:Q2L6A0]	ANIA_06317	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1739
CHSB_EMENI	reviewed	Chitin synthase B (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase B) (Class-III chitin synthase B)	chsB AN2523	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	916
CHSC_EMENI	reviewed	Chitin synthase C (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase C) (Class-I chitin synthase C)	chsC chs1 AN4566	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	918
CHSD_EMENI	reviewed	Chitin synthase D (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase D) (Class-V chitin synthase D)	chsD chsE AN1555	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1194
C8VUP2_EMENI	unreviewed	Choline kinase, putative (AFU_orthologue AFUA_1G15930)	ANIA_00929	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	730
Q5ARF0_EMENI	unreviewed	Cholinesterase, putative (AFU_orthologue AFUA_7G01710) (Uncharacterized protein)	AN9130.2 ANIA_09130	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	728
Q5B149_EMENI	unreviewed	Chorismate synthase (EC 4.2.3.5)	AN5731.2 ANIA_05731	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	410
Q5BFG5_EMENI	unreviewed	**Chromosome segregation protein BIR1, putative (AFU_orthologue AFUA_1G14070) (Uncharacterized protein)**	AN0715.2 ANIA_00715	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	833
Q5AUU3_EMENI	unreviewed	CipC protein [Source:UniProtKB/TrEMBLAcc:Q8NKC9] (Uncharacterized protein)	AN7937.2 ANIA_07937	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	110
Q5BAJ5_EMENI	unreviewed	Citrate lyase subunit (Eurofung) (Uncharacterized protein)	AN2435.2 ANIA_02435	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	485
CISY_EMENI	reviewed	Citrate synthase, mitochondrial (EC 2.3.3.16)	citA AN8275	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	474
C8VU97_EMENI	unreviewed	Class V chitinase, putative (AFU_orthologue AFUA_1G02800)	ANIA_00299	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	366
Q5B023_EMENI	unreviewed	CLC channel [Source:UniProtKB/TrEMBLAcc:Q870M6] (Uncharacterized protein)	AN6107.2 ANIA_06107	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	909
Q5ASB3_EMENI	unreviewed	**Clock controled protein (Ccg-8), putative (AFU_orthologue AFUA_5G09420) (Uncharacterized protein)**	AN8817.2 ANIA_08817	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	489
C8V8J7_EMENI	unreviewed	Cobalamin-independent methionine synthase (EC 2.1.1.14) [Source:UniProtKB/TrEMBLAcc:Q9P444]	ANIA_04443	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	774
Q5B6P5_EMENI	unreviewed	**Component of the chromatin assembly complex (Eurofung) (Uncharacterized protein)**	AN3785.2 ANIA_03785	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	684
Q5B5E1_EMENI	unreviewed	Component of the RSC chromatin remodeling complex (Eurofung) (Uncharacterized protein)	AN4239.2 ANIA_04239	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	595
Q5BFE4_EMENI	unreviewed	Conserved fungal protein (AFU_orthologue AFUA_1G14230) (Uncharacterized protein)	AN0736.2 ANIA_00736	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	247
Q5B454_EMENI	unreviewed	Conserved glutamic acid rich protein (AFU_orthologue AFUA_5G09010) (Uncharacterized protein)	AN4676.2 ANIA_04676	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	662
C8VB27_EMENI	unreviewed	Conserved serine proline-rich protein (AFU_orthologue AFUA_2G01790)	ANIA_04650	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	811
Q5BAW4_EMENI	unreviewed	COX5_ASPNG Cytochrome c oxidase polypeptide V, mitochondrial (Uncharacterized protein)	AN2316.2 ANIA_02316	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	197
Q5BG45_EMENI	unreviewed	CRAL/TRIO domain protein (AFU_orthologue AFUA_4G13930) (Uncharacterized protein)	AN0485.2 ANIA_00485	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	471
C8V7J8_EMENI	unreviewed	CRAL/TRIO domain protein (AFU_orthologue AFUA_6G12690)	ANIA_03709	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	585
Q5B978_EMENI	unreviewed	CTD phosphatase-related (Eurofung) (Uncharacterized protein)	AN2902.2 ANIA_02902	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	829
CUTI2_EMENI	reviewed	Cutinase 2 (EC 3.1.1.74) (Cutin hydrolase 2)	AN7541	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	255
C8VHB0_EMENI	unreviewed	Cystathionine gamma-synthase (Eurofung)	ANIA_03456	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	669
Q5B4U1_EMENI	unreviewed	Cytidylyltransferase family protein (AFU_orthologue AFUA_4G07310) (Uncharacterized protein)	AN4439.2 ANIA_04439	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	285
Q5B0V2_EMENI	unreviewed	Cytochrome b5, putative (AFU_orthologue AFUA_2G07720) (Uncharacterized protein)	AN5828.2 ANIA_05828	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	84
C8V1I9_EMENI	unreviewed	Cytochrome c oxidase polypeptide vib (AFU_orthologue AFUA_2G13010)	ANIA_06255	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	84
C8VPK4_EMENI	unreviewed	Cytochrome c oxidase subunit 7A (EC 1.9.3.1) (Cytochrome c oxidase polypeptide VIIA)	ANIA_11347	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	62
Q5AUB2_EMENI	unreviewed	Cytochrome c oxidase subunit Va, putative (AFU_orthologue AFUA_5G02750) (Uncharacterized protein)	AN8118.2 ANIA_08118	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	157
C8V5J7_EMENI	unreviewed	Cytochrome P450, putative (Eurofung)	ANIA_04042	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
C8VAF3_EMENI	unreviewed	Cytochrome P450, putative (Eurofung)	ANIA_08615	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	502
C8VGU2_EMENI	unreviewed	Cytochrome P450, putative (Eurofung)	ANIA_05335	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	432
C8VPF3_EMENI	unreviewed	Cytochrome P450, putative (Eurofung)	ANIA_01794	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
Q5B7I3_EMENI	unreviewed	Cytochrome P450, putative (Eurofung) (Uncharacterized protein)	AN3497.2 ANIA_03497	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	523
Q5AXZ5_EMENI	unreviewed	Cytochrome P450, putative (Eurofung) (Uncharacterized protein)	AN6835.2 ANIA_06835	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1083
Q5AWD1_EMENI	unreviewed	Cytochrome P450, putative (Eurofung) (Uncharacterized protein)	AN7399.2 ANIA_07399	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	543
Q5AX49_EMENI	unreviewed	Cytochrome P450, putative (Eurofung) (Uncharacterized protein)	AN7131.2 ANIA_07131	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	474
Q5AVA7_EMENI	unreviewed	Cytochrome P450, putative (Eurofung) (Uncharacterized protein)	AN7773.2 ANIA_07773	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
Q5BDH3_EMENI	unreviewed	Cytoplasmic protein required for cell viability, putative (AFU_orthologue AFUA_8G03980) (Uncharacterized protein)	AN1407.2 ANIA_01407	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	201
Q5AVI3_EMENI	unreviewed	Cytoplasmic response regulator (Eurofung) (Uncharacterized protein)	sskA AN7697.2 ANIA_07697	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	838
NAR1_EMENI	reviewed	Cytosolic Fe-S cluster assembly factor nar1 (Nuclear architecture-related protein 1)	nar1 AN3632	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	590
Q5B531_EMENI	unreviewed	DDENN domain protein (AFU_orthologue AFUA_4G06480) (Uncharacterized protein)	AN4349.2 ANIA_04349	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1125
PUT2_EMENI	reviewed	**Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial (P5C dehydrogenase) (EC 1.2.1.88) (L-glutamate gamma-semialdehyde dehydrogenase)**	prnC AN1733	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	572
Q5BFV5_EMENI	unreviewed	DENN (AEX-3) domain protein (AFU_orthologue AFUA_6G11200) (Uncharacterized protein)	AN0575.2 ANIA_00575	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	902
C8V613_EMENI	unreviewed	Dephospho-CoA kinase, putative (AFU_orthologue AFUA_5G02060)	ANIA_11040	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	280
VEA_EMENI	reviewed	Developmental and secondary metabolism regulator veA (Velvet complex subunit A)	veA ANIA_01052	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	573
C8VD86_EMENI	unreviewed	Dienelactone hydrolase (AFU_orthologue AFUA_4G03730)	ANIA_07139	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	499
Q5BCR6_EMENI	unreviewed	Dienelactone hydrolase family protein (AFU_orthologue AFUA_4G08790) (Uncharacterized protein)	AN1664.2 ANIA_01664	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	290
Q5ARR8_EMENI	unreviewed	Dihydrodipicolinate synthetase family protein (AFU_orthologue AFUA_8G02270) (Uncharacterized protein)	AN9012.2 ANIA_09012	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	298
Q5BGV6_EMENI	unreviewed	Dipeptidase (EC 3.4.13.19)	AN0224.2 ANIA_00224	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	415
Q5B4W6_EMENI	unreviewed	Diphosphomevalonate decarboxylase (AFU_orthologue AFUA_4G07130) (Uncharacterized protein)	AN4414.2 ANIA_04414	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	404
Q5B8L7_EMENI	unreviewed	DMT family organic anion transporter (Eurofung) (Uncharacterized protein)	AN3113.2 ANIA_03113	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	400

Q5B682_EMENI	unreviewed	DMT family transporter (Eurofung) (Uncharacterized protein)	AN3948.2 ANIA_03948	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	582
Q5B0D8_EMENI	unreviewed	**DNA helicase (EC 3.6.4.12)**	AN5992.2 ANIA_05992	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	811
CREA_EMENI	reviewed	**DNA-binding protein creA (Carbon catabolite repressor A)**	creA AN6195	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	416
C8VCJ6_EMENI	unreviewed	DRAP deaminase (Rib2), putative (AFU_orthologue AFUA_2G16360)	ANIA_10936	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	572
Q5B3X2_EMENI	unreviewed	**DsDNA-binding protein PDCD5, putative (AFU_orthologue AFUA_3G06420) (Uncharacterized protein)**	AN4758.2 ANIA_04758	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	143
C8VU80_EMENI	unreviewed	Dual specificity protein kinase (Eurofung)	ANIA_00988	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	667
Q5AT85_EMENI	unreviewed	DUF1212 domain membrane protein (AFU_orthologue AFUA_3G01440) (Uncharacterized protein)	AN8495.2 ANIA_08495	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	847
Q5B8I7_EMENI	unreviewed	DUF1212 domain membrane protein Prm10, putative (AFU_orthologue AFUA_3G13940) (Uncharacterized protein)	AN3143.2 ANIA_03143	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	869
Q5B3M5_EMENI	unreviewed	DUF1275 domain protein (AFU_orthologue AFUA_3G07550) (Uncharacterized protein)	AN4855.2 ANIA_04855	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	331
Q5BFF5_EMENI	unreviewed	DUF292 domian protein (AFU_orthologue AFUA_1G13960) (Uncharacterized protein)	AN0725.2 ANIA_00725	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	405
Q5B0F0_EMENI	unreviewed	DUF408 domain protein (AFU_orthologue AFUA_2G10310) (Uncharacterized protein)	AN5980.2 ANIA_05980	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	323
Q5AVD0_EMENI	unreviewed	DUF625 domain protein, putative (AFU_orthologue AFUA_5G07830) (Uncharacterized protein)	AN7750.2 ANIA_07750	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	878
Q5AS13_EMENI	unreviewed	DUF636 domain protein (AFU_orthologue AFUA_2G12650) (Uncharacterized protein)	AN8917.2 ANIA_08917	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	361
Q5AVT6_EMENI	unreviewed	DUF636 domain protein (AFU_orthologue AFUA_2G15290) (Uncharacterized protein)	AN7594.2 ANIA_07594	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	136
Q5B5F6_EMENI	unreviewed	DUF887 domain protein (AFU_orthologue AFUA_1G06320) (Uncharacterized protein)	AN4224.2 ANIA_04224	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	390
Q5BDF3_EMENI	unreviewed	DUF895 domain membrane protein (AFU_orthologue AFUA_8G04110) (Uncharacterized protein)	AN1427.2 ANIA_01427	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	508
Q5B2J4_EMENI	unreviewed	DUF914 domain membrane protein (AFU_orthologue AFUA_5G07810) (Uncharacterized protein)	AN5236.2 ANIA_05236	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	399
Q5AWY7_EMENI	unreviewed	D-xylose reductases (Eurofung) (Uncharacterized protein)	AN7193.2 ANIA_07193	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	334
C8VS47_EMENI	unreviewed	Dynein light chain (Eurofung)	ANIA_01333	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	141
Q5AZF0_EMENI	unreviewed	EF2_NEUCR Elongation factor 2 (EF-2) (Colonial temperature-sensitive 3) (Elongation factor 2 (Eurofung))	AN6330.2 ANIA_06330	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	844
Q5BEP9_EMENI	unreviewed	Elongation of fatty acids protein (EC 2.3.1.199) (Very-long-chain 3-oxoacyl-CoA synthase)	AN0981.2 ANIA_00981	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	534
C8VJ25_EMENI	unreviewed	Endo alpha-1,4 polygalactosaminidase, putative (AFU_orthologue AFUA_3G07890)	ANIA_02953	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
EGLX_EMENI	reviewed	Endo-1,3(4)-beta-glucanase xgeA (EC 3.2.1.6) (Mixed-linked glucanase xgeA)	xgeA AN2385	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	626
Q5B9S7_EMENI	unreviewed	Endo-1,3(4)-beta-glucanase, putative (AFU_orthologue AFUA_5G13990) (Uncharacterized protein)	AN2703.2 ANIA_02703	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	407
EGLD_EMENI	reviewed	Endo-beta-1,4-glucanase D (Endoglucanase D) (EC 3.2.1.4) (Carboxymethylcellulase D) (Cellulase D)	eglD AN1602	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	357
CHIA1_EMENI	reviewed	Endochitinase A (EC 3.2.1.14) (Chitinase A)	chiA AN8241	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	961
Q5BEI9_EMENI	unreviewed	Endoglucanase, putative (AFU_orthologue AFUA_1G12560) (Uncharacterized protein)	AN1041.2 ANIA_01041	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	434
PGLRB_EMENI	reviewed	**Endopolygalacturonase B (EC 3.2.1.15) (Pectinase B) (Polygalacturonase B)**	pgaB pecB AN4372	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
ENO_EMENI	reviewed	**Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)**	enoA AN5746	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	438
Q5BGS6_EMENI	unreviewed	Epimerase/dehydratase family protein, putative (AFU_orthologue AFUA_1G03490) (Uncharacterized protein)	AN0254.2 ANIA_00254	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	370
C8VLY9_EMENI	unreviewed	ER membrane protein (Pkr1), putative (AFU_orthologue AFUA_2G05200)	ANIA_10261	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	175
C8VTA6_EMENI	unreviewed	Ethanolamine kinase, putative (AFU_orthologue AFUA_1G11550)	ANIA_10156	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	413
EIF3H_EMENI	reviewed	Eukaryotic translation initiation factor 3 subunit H (eIF3h)	AN1270	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	366
BXLB_EMENI	reviewed	Exo-1,4-beta-xylosidase bxlB (EC 3.2.1.37) (1,4-beta-D-xylan xylohydrolase bxlB) (Beta-xylosidase bxlB) (Xylobiase bxlB)	bxlB AN8401	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	763
C8VQV2_EMENI	unreviewed	Exo-beta-1,3-glucanase, putative (AFU_orthologue AFUA_6G11980)	ANIA_00779	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	781
Q5AVW4_EMENI	unreviewed	Exonuclease, putative (AFU_orthologue AFUA_2G14950) (Uncharacterized protein)	AN7566.2 ANIA_07566	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	723
C8VMJ7_EMENI	unreviewed	Exo-polygalacturonase, putative (AFU_orthologue AFUA_7G06410)	ANIA_10274	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	424
Q5AVL5_EMENI	unreviewed	Exosome complex subunit Rrp46, putative (AFU_orthologue AFUA_2G01330) (Uncharacterized protein)	AN7665.2 ANIA_07665	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	248
C8VUN8_EMENI	unreviewed	Extracellular cell wall glucanase Crf1/allergen Asp F9 (AFU_orthologue AFUA_1G16190)	ANIA_00933	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	405
Q5AX19_EMENI	unreviewed	Extracellular dioxygenase, putative (AFU_orthologue AFUA_6G03070) (Uncharacterized protein)	AN7161.2 ANIA_07161	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	377
Q5B926_EMENI	unreviewed	Extracellular serine-rich protein, putative (AFU_orthologue AFUA_3G07870) (Uncharacterized protein)	AN2954.2 ANIA_02954	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	912
Q5AQX2_EMENI	unreviewed	FAD binding domain protein (AFU_orthologue AFUA_2G00730) (Uncharacterized protein)	AN9308.2 ANIA_09308	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	473
C8VLL8_EMENI	unreviewed	FAD binding domain protein (AFU_orthologue AFUA_4G10100)	ANIA_02042	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	644
Q5ARW3_EMENI	unreviewed	FAD binding domain protein (AFU_orthologue AFUA_6G14300) (Uncharacterized protein)	AN8967.2 ANIA_08967	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	497
C8V013_EMENI	unreviewed	FAD binding oxidoreductase, putative (AFU_orthologue AFUA_4G14630)	ANIA_05846	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	472
Q5AQS4_EMENI	unreviewed	FAD dependent oxidoreductase superfamily (AFU_orthologue AFUA_3G02360) (Uncharacterized protein)	AN9356.2 ANIA_09356	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	436
C8VNG1_EMENI	unreviewed	FAD dependent oxidoreductase, putative (AFU_orthologue AFUA_7G05070)	ANIA_10296	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	484
C8VI28_EMENI	unreviewed	FAD-binding oxidoreductase, putative (AFU_orthologue AFUA_3G03300)	ANIA_10402	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	500
C8VM39_EMENI	unreviewed	FarB [Source:UniProtKB/TrEMBLAcc:Q1WD25]	ANIA_01425	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	853
C8V333_EMENI	unreviewed	Fatty acid activator Faa4, putative (AFU_orthologue AFUA_2G09910)	ANIA_06014	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	698
Q5B4J5_EMENI	unreviewed	F-box domain protein (AFU_orthologue AFUA_2G02860) (Uncharacterized protein)	AN4535.2 ANIA_04535	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	723
Q5B8C7_EMENI	unreviewed	F-box domain protein (AFU_orthologue AFUA_2G14640) (Uncharacterized protein)	AN3203.2 ANIA_03203	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	310
Q5AUD2_EMENI	unreviewed	F-box domain protein (AFU_orthologue AFUA_3G00440) (Uncharacterized protein)	AN8098.2 ANIA_08098	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	276
Q5B2J6_EMENI	unreviewed	Fe-containing alcohol dehydrogenase, putative (AFU_orthologue AFUA_1G06800) (Uncharacterized protein)	AN5234.2 ANIA_05234	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	414
Q5B3H4_EMENI	unreviewed	Ferric-chelate reductase, putative (AFU_orthologue AFUA_3G10820) (Uncharacterized protein)	AN4906.2 ANIA_04906	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	593
C8VIA2_EMENI	unreviewed	Ferric-chelate reductase, putative (AFU_orthologue AFUA_6G13750)	ANIA_03208	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	682
DRE2_EMENI	reviewed	**Fe-S cluster assembly protein dre2 (Anamorsin homolog)**	dre2 AN8485	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	310
C8V2Y7_EMENI	unreviewed	FHA domain protein (AFU_orthologue AFUA_5G13560)	ANIA_06908	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	554
Q5B987_EMENI	unreviewed	FHA domain protein SNIP1, putative (AFU_orthologue AFUA_3G11540) (Uncharacterized protein)	AN2893.2 ANIA_02893	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	351
Q5AWV2_EMENI	unreviewed	Flavin-binding monooxygenase, putative (AFU_orthologue AFUA_2G17490) (Uncharacterized protein)	AN7228.2 ANIA_07228	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	565
Q5ATM9_EMENI	unreviewed	Flavin-binding monooxygenase-like protein (AFU_orthologue AFUA_4G09220) (Uncharacterized protein)	AN8351.2 ANIA_08351	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	614
FDH_EMENI	reviewed	**Formate dehydrogenase (FDH) (EC 1.2.1.2) (Acetate inducible protein A) (NAD-dependent formate dehydrogenase)**	aciA AN6525	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	365
Q5BG35_EMENI	unreviewed	Formyltetrahydrofolate deformylase, putative (AFU_orthologue AFUA_6G11620) (Uncharacterized protein)	AN0495.2 ANIA_00495	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	289
Q5ASM3_EMENI	unreviewed	Fumarate hydratase, putative (AFU_orthologue AFUA_6G02470) (Uncharacterized protein)	AN8707.2 ANIA_08707	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	544
Q5B0Z8_EMENI	unreviewed	Fumarylacetoacetate hydrolase family protein (AFU_orthologue AFUA_6G06460) (Uncharacterized protein)	AN5782.2 ANIA_05782	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	289
C8V965_EMENI	unreviewed	**Fungal specific transcription factor, putative (AFU_orthologue AFUA_4G06190)**	ANIA_10541	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	729
Q5BFQ3_EMENI	unreviewed	FYVE domain protein, putative (AFU_orthologue AFUA_1G17070) (Uncharacterized protein)	AN0627.2 ANIA_00627	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	281
Q5BBE3_EMENI	unreviewed	G2/mitotic-specific cyclin (Clb3), putative (AFU_orthologue AFUA_2G16150) (Uncharacterized protein)	AN2137.2 ANIA_02137	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	629
Q5B918_EMENI	unreviewed	GABA permease [Source:UniProtKB/TrEMBLAcc:Q9Y860] (Uncharacterized protein)	AN2962.2 ANIA_02962	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	520
Q5ASK4_EMENI	unreviewed	GABA transporter (Eurofung) (Uncharacterized protein)	AN8726.2 ANIA_08726	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	514
C8VHU6_EMENI	unreviewed	GABA transporter, putative (Eurofung)	ANIA_03345	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	532
C8VHU4_EMENI	unreviewed	GABA transporter, putative (Eurofung)	ANIA_03347	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	527
Q5ARU0_EMENI	unreviewed	GABA transporter, putative (Eurofung) (Uncharacterized protein)	AN8990.2 ANIA_08990	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	542

C8V226_EMENI	unreviewed	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	ANIA_06182	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	385
Q5B3X1_EMENI	unreviewed	GDP/GTP exchange factor Sec2p, putative (AFU_orthologue AFUA_3G06430) (Uncharacterized protein)	AN4759.2 ANIA_04759	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	605
Q5BFM6_EMENI	unreviewed	Geranylgeranyl diphosphate synthase [Source:UniProtKB/TrEMBLAcc:Q874I1] (Uncharacterized protein)	AN0654.2 ANIA_00654	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	396
EXGD_EMENI	reviewed	Glucan 1,3-beta-glucosidase D (EC 3.2.1.58) (Exo-1,3-beta-glucanase D)	exgD AN7533	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	831
BTGC_EMENI	reviewed	Glucan endo-1,3-beta-glucosidase btgC (EC 3.2.1.39) (Endo-1,3-beta-glucanase btgC) (Laminarinase btgC)	btgC AN4700	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	649
Q5B739_EMENI	unreviewed	**Gluconokinase (EC 2.7.1.12)**	AN3641.2 ANIA_03641	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	251
C8VI35_EMENI	unreviewed	Glucooligosaccharide oxidase, putative (AFU_orthologue AFUA_6G14340)	ANIA_10388	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	471
C8VQN7_EMENI	unreviewed	Glucose repressible protein Grg1, putative (AFU_orthologue AFUA_5G14210)	ANIA_09285	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	71
Q5B093_EMENI	unreviewed	**Glucose-6-phosphate isomerase (EC 5.3.1.9)**	AN6037.2 ANIA_06037	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	553
Q5B1Y3_EMENI	unreviewed	**Glutamate decarboxylase (EC 4.1.1.15)**	AN5447.2 ANIA_05447	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	515
C8VIG5_EMENI	unreviewed	Glutamate-cysteine ligase, catalytic subunit (Eurofung)	ANIA_03150	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	642
C8VFD3_EMENI	unreviewed	Glutamine-fructose-6-phosphate transaminase (EC 2.6.1.16) [Source:UniProtKB/TrEMBLAcc:Q5I6D3] (Glutamine:fructose-6-phosphate amidotransferase)	ANIA_10709	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	694
C8VJD9_EMENI	unreviewed	Glutathione peroxidase	ANIA_02846	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	282
G3P_EMENI	reviewed	**Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12)**	gpdA AN8041	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	336
Q5B6B4_EMENI	unreviewed	Glycerol kinase, putative (AFU_orthologue AFUA_6G08470) (Uncharacterized protein)	AN3916.2 ANIA_03916	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	608
C8VRM5_EMENI	unreviewed	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	ANIA_01396	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	700
C8V6J6_EMENI	unreviewed	Glycosyl hydrolases family 32 superfamily (AFU_orthologue AFUA_6G05000)	ANIA_03837	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	646
Q5BCW0_EMENI	unreviewed	Glycosyl transferase, putative (AFU_orthologue AFUA_8G02040) (Uncharacterized protein)	AN1620.2 ANIA_01620	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	387
Q5B9L9_EMENI	unreviewed	Glyoxalase family protein (AFU_orthologue AFUA_3G06020) (Uncharacterized protein)	AN2760.2 ANIA_02760	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	560
Q5AZ35_EMENI	unreviewed	GMC oxidoreductase, putative (AFU_orthologue AFUA_3G08070) (Uncharacterized protein)	AN6445.2 ANIA_06445	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	611
Q5BDT3_EMENI	unreviewed	Golgi traffic protein SFT2, putative (AFU_orthologue AFUA_1G09680) (Uncharacterized protein)	AN1297.2 ANIA_01297	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	215
Q5BDE8_EMENI	unreviewed	G-patch domain protein, putative (AFU_orthologue AFUA_8G04200) (Uncharacterized protein)	AN1432.2 ANIA_01432	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	354
Q5AVM6_EMENI	unreviewed	GPI anchored cell wall protein (Dan4), putative (AFU_orthologue AFUA_2G01140) (Uncharacterized protein)	AN7654.2 ANIA_07654	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	294
Q5BE70_EMENI	unreviewed	GPI anchored protein, putative (AFU_orthologue AFUA_1G11220) (Uncharacterized protein)	AN1160.2 ANIA_01160	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	158
Q5AX14_EMENI	unreviewed	GPI anchored protein, putative (AFU_orthologue AFUA_4G03360) (Uncharacterized protein)	AN7166.2 ANIA_07166	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	201
Q5AWK8_EMENI	unreviewed	GPI anchored protein, putative (AFU_orthologue AFUA_6G02800) (Uncharacterized protein)	AN7322.2 ANIA_07322	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	289
Q5AY76_EMENI	unreviewed	GPI anchored protein, putative (AFU_orthologue AFUA_7G00450) (Uncharacterized protein)	AN6754.2 ANIA_06754	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	215
Q5BDD1_EMENI	unreviewed	GPI anchored protein, putative (AFU_orthologue AFUA_8G04370) (Uncharacterized protein)	AN1449.2 ANIA_01449	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	232
Q5B5J0_EMENI	unreviewed	GPI anchored serine-rich protein (AFU_orthologue AFUA_1G05790) (Uncharacterized protein)	AN4190.2 ANIA_04190	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	178
BST1_EMENI	reviewed	GPI inositol-deacylase (EC 3.1.-.-)	bst1 AN6702	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1140
SMP3_EMENI	reviewed	GPI mannosyltransferase 4 (EC 2.4.1.-) (GPI mannosyltransferase IV) (GPI-MT-IV)	smp3 AN2303	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	546
Q5BHA9_EMENI	unreviewed	GPI-anchored cell surface glycoprotein, putative (AFU_orthologue AFUA_5G12320) (Uncharacterized protein)	AN0071.2 ANIA_00071	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1119
Q5B4Z1_EMENI	unreviewed	GPI-anchored cell wall organization protein Ecm33 (AFU_orthologue AFUA_4G06820) (Uncharacterized protein)	AN4390.2 ANIA_04390	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	396
Q5B6U5_EMENI	unreviewed	GTPase activating protein (BUD2/CLA2), putative (AFU_orthologue AFUA_6G12340) (Uncharacterized protein)	AN3735.2 ANIA_03735	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1269
GPA1_EMENI	reviewed	Guanine nucleotide-binding protein subunit alpha	fadA AN0651	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
Q5AVH0_EMENI	unreviewed	HAD-superfamily hydrolase (Eurofung) (Uncharacterized protein)	AN7710.2 ANIA_07710	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	251
Q5B0V0_EMENI	unreviewed	Haloacid dehalogenase, type II (AFU_orthologue AFUA_2G07750) (Uncharacterized protein)	AN5830.2 ANIA_05830	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	263
HSP7M_EMENI	reviewed	Heat shock 70 kDa protein	AN6010	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	666
HSP70_EMENI	reviewed	Heat shock 70 kDa protein (HSP70)	hsp70 AN5129	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	644
Q5BEI3_EMENI	unreviewed	Heat shock protein (Eurofung) (Uncharacterized protein)	AN1047.2 ANIA_01047	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	724
HSP60_EMENI	reviewed	Heat shock protein 60 (60 kDa chaperonin) (Protein Cpn60)	hsp60 AN6089	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	588
C8V505_EMENI	unreviewed	Heat shock protein Hsp20/Hsp26, putative (AFU_orthologue AFUA_5G10270)	ANIA_10507	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	181
CRED_EMENI	reviewed	**HECT-type ubiquitin ligase-interacting protein creD (Carbon catabolite repressor D)**	creD cre-34 AN4170	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	597
C8VNW7_EMENI	unreviewed	HET domain protein (AFU_orthologue AFUA_8G07340)	ANIA_01717	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
Q5AX92_EMENI	unreviewed	**Hexose transporter protein (AFU_orthologue AFUA_8G04480) (Uncharacterized protein)**	AN7088.2 ANIA_07088	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	471
Q5B5C8_EMENI	unreviewed	High expression lethality protein Hel10, putative (AFU_orthologue AFUA_1G06580) (Uncharacterized protein)	AN4252.2 ANIA_04252	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	189
C8VPX1_EMENI	unreviewed	Histidine kinase G7 [Source:UniProtKB/TrEMBLAcc:Q6WJ25]	ANIA_02581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1282
C8V8F5_EMENI	unreviewed	Histidine kinase J7 [Source:UniProtKB/TrEMBLAcc:Q6WJ24]	nikA ANIA_04479	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1297
Q5BBS5_EMENI	unreviewed	Histidine-containing phosphotransfer protein (Eurofung) (Uncharacterized protein)	ypdA AN2005.2 ANIA_02005	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	172
C8VTU6_EMENI	unreviewed	**Histone demethylase (Eurofung)**	ANIA_01060	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1405
H2B_EMENI	reviewed	**Histone H2B**	htbA htb1 AN3469	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	140
H41_EMENI	reviewed	**Histone H4.1**	hhfA AN0734	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	103
CYSD_EMENI	reviewed	Homocysteine synthase (EC 2.5.1.49) (O-acetylhomoserine sulfhydrylase) (OAH SHL) (OAH sulfhydrylase)	cysD AN8277	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	437
Q5ATW1_EMENI	unreviewed	HS90_PODAN HEAT SHOCK PROTEIN 90 HOMOLOG (SUPPRESSOR OF VEGETATIVE INCOMPATIBILITY MOD-E) (Heat shock protein 90 (Eurofung))	AN8269.2 ANIA_08269	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	700
C8VQK3_EMENI	unreviewed	Hydroxymethylbilane synthase, putative (AFU_orthologue AFUA_5G11760)	ANIA_00121	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
Q5B3F7_EMENI	unreviewed	Hydroxymethylglutaryl-CoA synthase, expressed (Eurofung) (Uncharacterized protein)	AN4923.2 ANIA_04923	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	459
Q5BED0_EMENI	unreviewed	Hypothetical 5-oxoprolinase (Eurofung) (Uncharacterized protein)	AN1100.2 ANIA_01100	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1355
Q5B7Y6_EMENI	unreviewed	Hypothetical acetyltransferase (Eurofung) (Uncharacterized protein)	AN3344.2 ANIA_03344	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	249
C8VRY8_EMENI	unreviewed	Hypothetical alanine--glyoxylate aminotransferase (Eurofung)	ANIA_01342	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	386
Q5AX42_EMENI	unreviewed	Hypothetical amino acid transporter (Eurofung) (Uncharacterized protein)	AN7138.2 ANIA_07138	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	577
Q5AWH2_EMENI	unreviewed	Hypothetical dihydroxy-acid dehydratase (Eurofung) (Uncharacterized protein)	AN7358.2 ANIA_07358	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	651
Q5ARU8_EMENI	unreviewed	Hypothetical fructosyl amine:oxygen oxidoreductase (Eurofung) (Uncharacterized protein)	AN8982.2 ANIA_08982	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	438
Q5BD37_EMENI	unreviewed	Hypothetical fumarate reductase (Eurofung) (Uncharacterized protein)	AN1543.2 ANIA_01543	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	627
C8VKD7_EMENI	unreviewed	Hypothetical oxidoreductase (Eurofung)	ANIA_02682	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	412
Q5ASB5_EMENI	unreviewed	Hypothetical oxidoreductase (Eurofung) (Uncharacterized protein)	AN8815.2 ANIA_08815	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
Q5BGD6_EMENI	unreviewed	Hypothetical oxidoreductase (Eurofung) (Uncharacterized protein)	AN0394.2 ANIA_00394	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	398
Q5B2L2_EMENI	unreviewed	Hypothetical second sulfur transcription regulator MetZ, bZIP transcription factor (Eurofung) (Uncharacterized protein)	AN5218.2 ANIA_05218	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	279
C8VUL6_EMENI	unreviewed	Hypothetical serine protease (Eurofung)	ANIA_10030	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	477
Q5AXV0_EMENI	unreviewed	Inositol hexakisphosphate kinase (Eurofung) (Uncharacterized protein)	AN6880.2 ANIA_06880	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1357
Q5BGF1_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_1G01760) (Uncharacterized protein)	AN0379.2 ANIA_00379	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	298
Q5B4G5_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_2G01860) (Uncharacterized protein)	AN4565.2 ANIA_04565	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	205
Q5B7U3_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_2G12640) (Uncharacterized protein)	AN3387.2 ANIA_03387	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	427
C8VA77_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_2G17760)	ANIA_10604	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	350

Q5AXN9_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_3G03520) (Uncharacterized protein)	AN6941.2 ANIA_06941	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	405
Q5AZ67_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_4G00600) (Uncharacterized protein)	AN6413.2 ANIA_06413	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	396
C8VI17_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_4G01270)	ANIA_03285	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	406
Q5AR75_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_5G00100) (Uncharacterized protein)	AN9205.2 ANIA_09205	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	260
C8VAW4_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_5G08640)	ANIA_10581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	159
Q5ARV9_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_5G13725) (Uncharacterized protein)	AN8971.2 ANIA_08971	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	423
Q5B2L7_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_6G07470) (Uncharacterized protein)	AN5213.2 ANIA_05213	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	326
Q5BDB5_EMENI	unreviewed	Integral membrane protein (AFU_orthologue AFUA_8G04560) (Uncharacterized protein)	AN1465.2 ANIA_01465	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	443
Q5ARY7_EMENI	unreviewed	Integral membrane protein, putative (AFU_orthologue AFUA_6G11560) (Uncharacterized protein)	AN8943.2 ANIA_08943	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	417
C8V1Y0_EMENI	unreviewed	Integral membrane protein, putative (AFU_orthologue AFUA_7G06040)	ANIA_06740	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	224
G8Z4I7_EMEND	unreviewed	Intracellular beta-galactosidase BgaD	bgaD	Emericella nidulans (Aspergillus nidulans)	1043
C8VL47_EMENI	unreviewed	Iron-sulfur cluster assembly accessory protein Isa1, putative (AFU_orthologue AFUA_4G10690)	ANIA_10237	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	242
Q5B475_EMENI	unreviewed	Iron-sulfur cluster assembly protein	AN4655.2 ANIA_04655	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	173
Q5B9Y2_EMENI	unreviewed	Isoamyl alcohol oxidase, putative (AFU_orthologue AFUA_1G01180) (Uncharacterized protein)	AN2648.2 ANIA_02648	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	566
Q5B064_EMENI	unreviewed	Isochorismatase family hydrolase, putative (AFU_orthologue AFUA_2G08950) (Uncharacterized protein)	AN6066.2 ANIA_06066	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	207
Q5BAA3_EMENI	unreviewed	Isochorismatase family protein family (AFU_orthologue AFUA_3G14500) (Uncharacterized protein)	AN2527.2 ANIA_02527	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	817
C8VIX5_EMENI	unreviewed	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	ANIA_02999	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	493
Q599M3_EMEND	unreviewed	Isocitrate lyase	mclA	Emericella nidulans (Aspergillus nidulans)	604
ACEA_EMENI	reviewed	**Isocitrate lyase (ICL) (Isocitrase) (Isocitratase) (EC 4.1.3.1) (Methylisocitrate lyase) (MICA) (EC 4.1.3.30) (Threo-D(S)-isocitrate glyoxylate-lyase)**	acuD AN5634	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	538
C8VUP5_EMENI	unreviewed	KapC [Source:UniProtKB/TrEMBLAcc:Q2LD07]	ANIA_00926	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	939
Q5B9X2_EMENI	unreviewed	Kelch repeat protein (AFU_orthologue AFUA_4G14350) (Uncharacterized protein)	AN2658.2 ANIA_02658	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	746
Q5BAA4_EMENI	unreviewed	Ketol-acid reductoisomerase, mitochondrial (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacyl reductoisomerase)	AN2526.2 ANIA_02526	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	400
C8V115_EMENI	unreviewed	KH domain protein (AFU_orthologue AFUA_2G13490)	ANIA_10807	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1003
BIMC_EMENI	reviewed	Kinesin-like protein bimC	bimC AN3363	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1184
KMO_EMENI	reviewed	Kynurenine 3-monooxygenase (EC 1.14.13.9) (Biosynthesis of nicotinic acid protein 4) (Kynurenine 3-hydroxylase)	bna4 AN5200	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	506
G8XV57_EMEND	unreviewed	**Lactose permease**	lacpA	Emericella nidulans (Aspergillus nidulans)	533
LAP1_EMENI	reviewed	Leucine aminopeptidase 1 (EC 3.4.11.-) (Leucyl aminopeptidase 1) (LAP1)	lap1 AN7035	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	390
Q5BGC1_EMENI	unreviewed	Leucine Rich Repeat domain protein (AFU_orthologue AFUA_1G04960) (Uncharacterized protein)	AN0409.2 ANIA_00409	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	807
Q5B1L2_EMENI	unreviewed	Leucine Rich Repeat domain protein (AFU_orthologue AFUA_4G11700) (Uncharacterized protein)	AN5568.2 ANIA_05568	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	638
Q5B7S5_EMENI	unreviewed	LipA and NB-ARC domain protein (AFU_orthologue AFUA_7G01150) (Uncharacterized protein)	AN3405.2 ANIA_03405	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	568
Q5BGL7_EMENI	unreviewed	Lipase, putative (AFU_orthologue AFUA_1G02580) (Uncharacterized protein)	AN0313.2 ANIA_00313	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	337
C8V1B2_EMENI	unreviewed	Lipase, putative (AFU_orthologue AFUA_2G12490)	ANIA_10805	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	793
Q5B5C4_EMENI	unreviewed	Lipase, putative (AFU_orthologue AFUA_7G04020) (Uncharacterized protein)	AN4256.2 ANIA_04256	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	78
Q5BFQ7_EMENI	unreviewed	Long chain fatty alcohol oxidase, putative (AFU_orthologue AFUA_1G17110) (Uncharacterized protein)	AN0623.2 ANIA_00623	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	745
SIDA_EMENI	reviewed	L-ornithine N(5)-monooxygenase (OMO) (EC 1.14.13.196) (L-ornithine N(5)-oxygenase) (Siderphore biosynthesis protein A)	sidA AN5823	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	498
Q5B6N1_EMENI	unreviewed	**Low-affinity zinc transporter of the plasma membrane, putative (Eurofung) (Uncharacterized protein)**	AN3799.2 ANIA_03799	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
Q5BCQ5_EMENI	unreviewed	Lysophospholipase (EC 3.1.1.5)	AN1675.2 ANIA_01675	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	628
C8V0H6_EMENI	unreviewed	**Malate dehydrogenase, NAD-dependent (AFU_orthologue AFUA_6G05210)**	ANIA_06499	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	330
C8V9A0_EMENI	unreviewed	Malonyl CoA-acyl carrier protein transacylase, putative (AFU_orthologue AFUA_4G05850)	ANIA_04294	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	390
C8V523_EMENI	unreviewed	**Maltase MalT (AFU_orthologue AFUA_8G07070)**	ANIA_10420	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	585
C8VA95_EMENI	unreviewed	Mandelate racemase/muconate lactonizing enzyme family protein (AFU_orthologue AFUA_1G05520)	ANIA_10599	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	381
C8VFS0_EMENI	unreviewed	Mandelate racemase/muconate lactonizing enzyme family protein (AFU_orthologue AFUA_7G04350)	ANIA_05672	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	425
M2DH_EMENI	reviewed	**Mannitol 2-dehydrogenase (M2DH) (MDH) (EC 1.1.1.67)**	AN2815	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	502
MTLD_EMENI	reviewed	**Mannitol-1-phosphate 5-dehydrogenase (M1PDH) (MPD) (MPDH) (EC 1.1.1.17)**	mpdA AN5975	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	386
MNS1B_EMENI	reviewed	**Mannosyl-oligosaccharide alpha-1,2-mannosidase 1B (EC 3.2.1.113) (Class I alpha-mannosidase 1B) (Man(9)-alpha-mannosidase 1B)**	mns1B msdS AN0787	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	505
Q5BFU9_EMENI	unreviewed	MATE efflux family protein (Eurofung) (Uncharacterized protein)	AN0581.2 ANIA_00581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	622
C8V9H0_EMENI	unreviewed	MEAB protein [Source:UniProtKB/TrEMBLAcc:P87205]	ANIA_04900	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	400
C8V933_EMENI	unreviewed	Meiotic sister chromatid recombination protein Ish1/Msc1, putative (AFU_orthologue AFUA_3G10480)	ANIA_04940	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
C8VK49_EMENI	unreviewed	Membrane bound C2 domain protein (Vp115), putative (AFU_orthologue AFUA_7G01840)	ANIA_09149	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1506
Q5AXD3_EMENI	unreviewed	Membrane-spanning ATPase, putative (AFU_orthologue AFUA_4G03990) (Uncharacterized protein)	AN7047.2 ANIA_07047	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	410
C8VG91_EMENI	unreviewed	Metallo-beta-lactamase domain protein, putative (AFU_orthologue AFUA_6G12940)	ANIA_05524	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	291
Q5BBY3_EMENI	unreviewed	Metallo-beta-lactamase family protein (AFU_orthologue AFUA_5G12770) (Uncharacterized protein)	AN1947.2 ANIA_01947	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	318
Q5BFA7_EMENI	unreviewed	Metalloreductase, putative (AFU_orthologue AFUA_1G14340) (Uncharacterized protein)	AN0773.2 ANIA_00773	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	627
MAP22_EMENI	reviewed	Methionine aminopeptidase 2-2 (MAP 2-2) (MetAP 2-2) (EC 3.4.11.18) (Peptidase M)	AN0369	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	458
C8VQX6_EMENI	unreviewed	Methyltransferase (Ncl1), putative (AFU_orthologue AFUA_1G14180)	ANIA_00757	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	990
C8VNR3_EMENI	unreviewed	Methyltransferase, putative (AFU_orthologue AFUA_2G14390)	ANIA_02405	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	258
C8V9M2_EMENI	unreviewed	**MFS allantoate transporter, putative (AFU_orthologue AFUA_5G09470)**	ANIA_08814	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	529
Q5BAG4_EMENI	unreviewed	**MFS glucose transporter, putative (AFU_orthologue AFUA_3G14170) (Uncharacterized protein)**	AN2466.2 ANIA_02466	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	536
C8VN19_EMENI	unreviewed	**MFS lactose permease, putative (AFU_orthologue AFUA_6G01860)**	ANIA_01577	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	539
Q5BA29_EMENI	unreviewed	**MFS maltose transporter, putative (AFU_orthologue AFUA_4G00150) (Uncharacterized protein)**	AN2601.2 ANIA_02601	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	540
Q5B9N4_EMENI	unreviewed	**MFS monocarboxylate transporter, putative (AFU_orthologue AFUA_1G05170) (Uncharacterized protein)**	AN2746.2 ANIA_02746	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	436
C8VEW6_EMENI	unreviewed	**MFS monosaccharide transporter, putative (AFU_orthologue AFUA_1G07700)**	ANIA_05104	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	576
Q5B4E0_EMENI	unreviewed	**MFS monosaccharide transporter, putative (AFU_orthologue AFUA_2G02110) (Uncharacterized protein)**	AN4590.2 ANIA_04590	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	554
C8VKK5_EMENI	unreviewed	**MFS monosaccharide transporter, putative (AFU_orthologue AFUA_2G05190)**	ANIA_02585	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	499
Q5B5N2_EMENI	unreviewed	**MFS monosaccharide transporter, putative (AFU_orthologue AFUA_4G13080) (Uncharacterized protein)**	AN4148.2 ANIA_04148	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	548
Q5AWN5_EMENI	unreviewed	**MFS multidrug transporter, putative (AFU_orthologue AFUA_2G16860) (Uncharacterized protein)**	AN7295.2 ANIA_07295	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	544
Q5BG32_EMENI	unreviewed	**MFS multidrug transporter, putative (AFU_orthologue AFUA_3G02060) (Uncharacterized protein)**	AN0498.2 ANIA_00498	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	545
C8V9S0_EMENI	unreviewed	**MFS multidrug transporter, putative (AFU_orthologue AFUA_6G03040)**	ANIA_11120	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	608
Q5B866_EMENI	unreviewed	**MFS multidrug transporter, putative (AFU_orthologue AFUA_6G03320) (Uncharacterized protein)**	AN3264.2 ANIA_03264	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	571
Q5ARS0_EMENI	unreviewed	**MFS nicotinic acid transporter Tna1, putative (AFU_orthologue AFUA_3G03820) (Uncharacterized protein)**	AN9010.2 ANIA_09010	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	503
Q5B7S2_EMENI	unreviewed	**MFS peptide transporter Ptr2, putative (AFU_orthologue AFUA_7G01490) (Uncharacterized protein)**	AN3408.2 ANIA_03408	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	587
Q5AS27_EMENI	unreviewed	**MFS peptide transporter, putative (AFU_orthologue AFUA_8G02550) (Uncharacterized protein)**	AN8903.2 ANIA_08903	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	628
Q5B0J5_EMENI	unreviewed	**MFS phosphate transporter, putative (AFU_orthologue AFUA_2G10690) (Uncharacterized protein)**	AN5935.2 ANIA_05935	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	663

Q5B1N1_EMENI	unreviewed	**MFS phospholipid transporter (Git1), putative (AFU_orthologue AFUA_6G07750) (Uncharacterized protein)**	AN5549.2 ANIA_05549	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	488
Q5AZP2_EMENI	unreviewed	**MFS siderophore iron transporter, putative (AFU_orthologue AFUA_3G03440) (Uncharacterized protein)**	AN6238.2 ANIA_06238	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	577
Q5BDV4_EMENI	unreviewed	**MFS sugar transporter, putative (AFU_orthologue AFUA_1G09910) (Uncharacterized protein)**	AN1276.2 ANIA_01276	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	504
C8VEH9_EMENI	unreviewed	**MFS sugar transporter, putative (AFU_orthologue AFUA_1G11050)**	ANIA_08467	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	532
Q5B313_EMENI	unreviewed	**MFS sugar transporter, putative (AFU_orthologue AFUA_5G02840) (Uncharacterized protein)**	AN5067.2 ANIA_05067	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
Q5AUD5_EMENI	unreviewed	MFS toxin efflux pump (AflT), putative (AFU_orthologue AFUA_1G12620) (Uncharacterized protein)	AN8095.2 ANIA_08095	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	539
Q5ARE0_EMENI	unreviewed	**MFS transporter Fmp42, putative (AFU_orthologue AFUA_7G01670) (Uncharacterized protein)**	AN9140.2 ANIA_09140	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	698
Q5BEC0_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_1G11820) (Uncharacterized protein)**	AN1110.2 ANIA_01110	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	493
C8VRB4_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_1G13970)**	ANIA_10115	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	663
Q5B5K0_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_2G08230) (Uncharacterized protein)**	AN4180.2 ANIA_04180	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	561
Q5AT78_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_3G01370) (Uncharacterized protein)**	AN8502.2 ANIA_08502	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	503
Q5B6Q4_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_3G01840) (Uncharacterized protein)**	AN3776.2 ANIA_03776	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	532
Q5B3R3_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_3G07120) (Uncharacterized protein)**	AN4817.2 ANIA_04817	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	731
Q5B8A9_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_4G01000) (Uncharacterized protein)**	AN3221.2 ANIA_03221	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	510
Q5BAT6_EMENI	unreviewed	**MFS transporter, putative (AFU_orthologue AFUA_6G00710) (Uncharacterized protein)**	AN2344.2 ANIA_02344	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	493
MIC19_EMENI	reviewed	MICOS complex subunit mic19	AN8690	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	209
C8V903_EMENI	unreviewed	Microbody (Peroxisome) biogenesis protein peroxin 14 (Eurofung)	ANIA_10610	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	358
C8VJ57_EMENI	unreviewed	Microbody (Peroxisome) biogenesis protein peroxin 6 (Eurofung)	ANIA_02925	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1476
C8VJG9_EMENI	unreviewed	MIP aquaporin (Eurofung)	ANIA_02822	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	449
C8VS86_EMENI	unreviewed	Mitochondrial 2-oxodicarboxylate carrier protein, putative (AFU_orthologue AFUA_1G09660)	ANIA_10172	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	306
Q5BGI4_EMENI	unreviewed	Mitochondrial carrier protein (Rim2), putative (AFU_orthologue AFUA_3G06950) (Uncharacterized protein)	AN0346.2 ANIA_00346	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	351
Q5ASE5_EMENI	unreviewed	Mitochondrial carrier protein, putative (Eurofung) (Uncharacterized protein)	AN8785.2 ANIA_08785	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	707
Q5BBU4_EMENI	unreviewed	Mitochondrial chaperone Frataxin, putative (AFU_orthologue AFUA_4G10510) (Uncharacterized protein)	AN1986.2 ANIA_01986	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	211
C8V6A6_EMENI	unreviewed	Mitochondrial cytochrome b2, putative (AFU_orthologue AFUA_4G03120)	ANIA_03901	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	500
MDM12_EMENI	reviewed	Mitochondrial distribution and morphology protein 12 (Mitochondrial inheritance component mdm12)	mdm12 AN0821	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	436
MDM34_EMENI	reviewed	Mitochondrial distribution and morphology protein 34	mdm34 AN2055	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	561
C8VTP0_EMENI	unreviewed	Mitochondrial hypoxia responsive domain protein (AFU_orthologue AFUA_1G12250)	ANIA_01066	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	268
TIM9_EMENI	reviewed	Mitochondrial import inner membrane translocase subunit tim9	tim9 AN7649	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	90
Q5B984_EMENI	unreviewed	Mitochondrial methylglutaconyl-CoA hydratase (Auh), putative (AFU_orthologue AFUA_3G11480) (Uncharacterized protein)	AN2896.2 ANIA_02896	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	305
Q5BF10_EMENI	unreviewed	Mitochondrial phosphate carrier protein (Mir1), putative (AFU_orthologue AFUA_1G15140) (Uncharacterized protein)	AN0870.2 ANIA_00870	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
Q5B585_EMENI	unreviewed	Mitochondrial protein sorting (Msf1), putative (AFU_orthologue AFUA_4G05920) (Uncharacterized protein)	AN4295.2 ANIA_04295	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	188
C8V7D1_EMENI	unreviewed	Mitogen-activated protein kinase (EC 2.7.11.24)	mpkB ANIA_03719	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	354
MPIP_EMENI	reviewed	**M-phase inducer phosphatase (EC 3.1.3.48)**	nimT AN3941	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	556
C8VF70_EMENI	unreviewed	mRNA splicing factor (Prp17), putative (AFU_orthologue AFUA_6G07300)	ANIA_05196	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
C8V1D8_EMENI	unreviewed	**mRNA-nucleus export ATPase (Elf1), putative (AFU_orthologue AFUA_6G03580)**	ANIA_06651	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1118
Q5B941_EMENI	unreviewed	MRS7 family protein (AFU_orthologue AFUA_3G08230) (Uncharacterized protein)	AN2939.2 ANIA_02939	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	543
Q5AXD9_EMENI	unreviewed	Mucin family signaling protein Msb2, putative (AFU_orthologue AFUA_4G04070) (Uncharacterized protein)	AN7041.2 ANIA_07041	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	821
MBF1_EMENI	reviewed	Multiprotein-bridging factor 1	mbf1 AN2996	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	154
Q5AS18_EMENI	unreviewed	Myo-inositol transporter (AFU_orthologue AFUA_2G07910) (Uncharacterized protein)	AN8912.2 ANIA_08912	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	528
C8VBX3_EMENI	unreviewed	Myo-inositol-1-phosphate synthase (EC 5.5.1.4) [Source:UniProtKB/TrEMBLAcc:B6CK64]	ANIA_07625	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	382
Q5BDF2_EMENI	unreviewed	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	AN1428.2 ANIA_01428	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	430
Q5BF52_EMENI	unreviewed	N-acylethanolamine amidohydrolase, putative (AFU_orthologue AFUA_1G14880) (Uncharacterized protein)	AN0828.2 ANIA_00828	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	619
Q5BAQ2_EMENI	unreviewed	NAD binding Rossmann fold oxidoreductase, putative (AFU_orthologue AFUA_6G09900) (Uncharacterized protein)	AN2378.2 ANIA_02378	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
Q5BBG4_EMENI	unreviewed	NAD dependent epimerase/dehydratase, putative (AFU_orthologue AFUA_7G00180) (Uncharacterized protein)	AN2116.2 ANIA_02116	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	316
Q5AW79_EMENI	unreviewed	NAD dependent glutamate dehydrogenase (EC 1.4.1.2) [Source:UniProtKB/TrEMBLAcc:Q6XNK7] (Uncharacterized protein)	AN7451.2 ANIA_07451	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1096
Q5BED6_EMENI	unreviewed	NADH dehydrogenase (Eurofung) (Uncharacterized protein)	AN1094.2 ANIA_01094	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	570
Q5AU26_EMENI	unreviewed	NADH pyrophosphatase, putative (AFU_orthologue AFUA_5G03360) (Uncharacterized protein)	AN8204.2 ANIA_08204	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	415
Q5AZ94_EMENI	unreviewed	NADH-cytochrome b5 reductase (EC 1.6.2.2)	AN6386.2 ANIA_06386	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	304
NCB5R_EMENI	reviewed	NADH-cytochrome b5 reductase 1 (EC 1.6.2.2) (Microsomal cytochrome b reductase)	cbr1 AN6366	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	310
Q5AY77_EMENI	unreviewed	NADH-dependent flavin oxidoreductase, putative (AFU_orthologue AFUA_7G06420) (Uncharacterized protein)	AN6753.2 ANIA_06753	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	422
Q5B1F1_EMENI	unreviewed	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial (Eurofung) (NUBM_ASPNG NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial (Complex I-51KD) (CI-51KD))	AN5629.2 ANIA_05629	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	497
Q5B5R6_EMENI	unreviewed	NADP(+) coupled glycerol dehydrogenase (Eurofung) (Uncharacterized protein)	AN4114.2 ANIA_04114	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	682
Q5ASV2_EMENI	unreviewed	NADP-dependent alcohol dehydrogenase (AFU_orthologue AFUA_6G00510) (Uncharacterized protein)	AN8628.2 ANIA_08628	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
NCPR_EMENI	reviewed	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	cprA AN0595	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	695
C8VD04_EMENI	unreviewed	NADPH-dependent FMN reductase Lot6, putative (AFU_orthologue AFUA_7G06600)	ANIA_07214	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	463
DHE4_EMENI	reviewed	**NADP-specific glutamate dehydrogenase (NADP-GDH) (EC 1.4.1.4) (NADP-dependent glutamate dehydrogenase)**	gdhA AN4376	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	459
NACA_EMENI	reviewed	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC)	egd2 AN6630	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	203
Q5B4I9_EMENI	unreviewed	Nicotinamide N-methyltransferase, putative (AFU_orthologue AFUA_1G17750) (Uncharacterized protein)	AN4541.2 ANIA_04541	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	350
NIR_EMENI	reviewed	**Nitrite reductase [NAD(P)H] (EC 1.7.1.4)**	niiA AN1007	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1104
NMRA_EMENI	reviewed	Nitrogen metabolite repression protein nmrA (Negative-acting nitrogen regulatory protein nmrA) (Nitrogen metabolite regulation protein)	nmrA AN8168	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	352
NPR3_EMENI	reviewed	Nitrogen permease regulator 3 (Required for meiotic nuclear division protein 11)	npr3 rmd11 AN10171 AN1289	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	816
AREA_EMENI	reviewed	**Nitrogen regulatory protein areA**	areA AN8667	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	876
Q5B4C2_EMENI	unreviewed	NmrA family transcriptional regulator, putative (AFU_orthologue AFUA_7G06920) (Uncharacterized protein)	AN4608.2 ANIA_04608	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	309
Q5BEN8_EMENI	unreviewed	NmrA-like family protein (AFU_orthologue AFUA_8G01860) (Uncharacterized protein)	AN0992.2 ANIA_00992	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	288
Q5AUM1_EMENI	unreviewed	NMT1_ASPPA NMT1 protein homolog (Thiamine biosynthesis protein (Eurofung))	AN8009.2 ANIA_08009	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	341
C8VAZ1_EMENI	unreviewed	Non-biotin containing subunit of 3-methylcrotonyl-CoA carboxylase (EC 6.4.1.4) [Source:UniProtKB/TrEMBLAcc:Q6T5L5]	ANIA_04687	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	588
Q5AVJ7_EMENI	unreviewed	Non-classical export protein Nce102, putative (AFU_orthologue AFUA_2G01590) (Uncharacterized protein)	AN7683.2 ANIA_07683	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	174
NHP6_EMENI	reviewed	**Non-histone chromosomal protein 6**	nhp6 AN2885	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	106
C8VPR1_EMENI	unreviewed	NosA protein [Source:UniProtKB/TrEMBLAcc:Q1XE59]	ANIA_01848	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	675
C8VNR1_EMENI	unreviewed	NRPS-like enzyme, putative (JCVI)	ANIA_10297	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1060
Q5B7T4_EMENI	unreviewed	NRPS-like enzyme, putative (JCVI) (Uncharacterized protein)	AN3396.2 ANIA_03396	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	938
Q5BFD4_EMENI	unreviewed	Nucleoside-diphosphate-sugar epimerase, putative (AFU_orthologue AFUA_1G14210) (Uncharacterized protein)	AN0746.2 ANIA_00746	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	321
Q5BB55_EMENI	unreviewed	Nucleoside-diphosphate-sugar epimerase, putative (AFU_orthologue AFUA_5G07170) (Uncharacterized protein)	AN2225.2 ANIA_02225	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	342

Q5BE67_EMENI	unreviewed	Oligomeric mitochondrial matrix chaperone (Eurofung) (Uncharacterized protein)	AN1163.2 ANIA_01163	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	800
C8VHB7_EMENI	unreviewed	OTU-like cysteine protease, putative (AFU_orthologue AFUA_3G05550)	ANIA_03449	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	323
C8V514_EMENI	unreviewed	Oxidoreductase 2-nitropropane dioxygenase family, putative (AFU_orthologue AFUA_2G17430)	ANIA_04120	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	380
Q5B099_EMENI	unreviewed	Oxidoreductase, 2-nitropropane dioxygenase family, putative (AFU_orthologue AFUA_2G09850) (Uncharacterized protein)	AN6031.2 ANIA_06031	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
Q5BAU5_EMENI	unreviewed	Oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor (AFU_orthologue AFUA_5G10280) (Uncharacterized protein)	AN2335.2 ANIA_02335	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	434
Q5B0A7_EMENI	unreviewed	Oxidoreductase, FAD-binding, putative (AFU_orthologue AFUA_6G07600) (Uncharacterized protein)	AN6023.2 ANIA_06023	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	640
Q5AXA6_EMENI	unreviewed	Oxidoreductase, short chain dehydrogenase/reductase family, putative (AFU_orthologue AFUA_4G00940) (Uncharacterized protein)	AN7074.2 ANIA_07074	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	310
C8VGC7_EMENI	unreviewed	Oxidoreductase, short-chain dehydrogenase/reductase family (AFU_orthologue AFUA_6G13210)	ANIA_05490	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	476
Q5BCL7_EMENI	unreviewed	Patatin-like phospholipase domain-containing protein (EC 3.1.1.-)	AN1713.2 ANIA_01713	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	789
C8V4B0_EMENI	unreviewed	Pathogenesis associated protein Cap20, putative (AFU_orthologue AFUA_1G06350)	ANIA_10518	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	187
PLYH_EMENI	reviewed	**Pectate lyase H (EC 4.2.2.2)**	plyH AN8453	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	260
PELA_EMENI	reviewed	Pectin lyase A (PLA) (EC 4.2.2.10)	pelA AN2331	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	379
C8VDK0_EMENI	unreviewed	PENR2 protein [Source:UniProtKB/TrEMBLAcc:Q8J0E0]	ANIA_07734	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	292
C8VDL9_EMENI	unreviewed	Pentatricopeptide repeat protein (AFU_orthologue AFUA_5G07770)	ANIA_11022	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	975
C8VN59_EMENI	unreviewed	Pentatricopeptide repeat protein (AFU_orthologue AFUA_5G10660)	ANIA_10285	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1272
Q5AZK5_EMENI	unreviewed	Peptidase family M20/M25/M40 protein (AFU_orthologue AFUA_2G12570) (Uncharacterized protein)	AN6275.2 ANIA_06275	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	798
Q5ATD5_EMENI	unreviewed	Peptide hydrolase (EC 3.4.-.-)	AN8445.2 ANIA_08445	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	503
Q5ASX5_EMENI	unreviewed	**Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)**	AN8605.2 ANIA_08605	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	162
Q5BFW8_EMENI	unreviewed	Peroxisomal AMP binding enzyme, putative (AFU_orthologue AFUA_6G11340) (Uncharacterized protein)	AN0562.2 ANIA_00562	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	533
C8VDC2_EMENI	unreviewed	Peroxisomal multifunctional beta-oxidation protein (MFP), putative (AFU_orthologue AFUA_4G03900)	ANIA_07111	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	903
Q5B9N1_EMENI	unreviewed	**PH domain protein (AFU_orthologue AFUA_1G05130) (Uncharacterized protein)**	AN2749.2 ANIA_02749	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1174
C8VFS1_EMENI	unreviewed	PH domain protein (AFU_orthologue AFUA_6G12290)	ANIA_05671	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	828
Q5AU19_EMENI	unreviewed	PHD transcription factor (Rum1), putative (AFU_orthologue AFUA_5G03430) (Uncharacterized protein)	AN8211.2 ANIA_08211	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1717
PHACA_EMEND	reviewed	**Phenylacetate 2-hydroxylase (EC 1.14.13.-)**	phacA	Emericella nidulans (Aspergillus nidulans)	518
Q5B055_EMENI	unreviewed	Phenylalanine ammonia-lyase (EC 4.3.1.24)	AN6075.2 ANIA_06075	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	701
C8V3P3_EMENI	unreviewed	PHO4-like protein [Source:UniProtKB/TrEMBLAcc:Q6PND5]	ANIA_08271	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	707
C8VF25_EMENI	unreviewed	PHO80-like cyclin [Source:UniProtKB/TrEMBLAcc:Q6PND6]	ANIA_05156	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	390
Q5BH98_EMENI	unreviewed	Phosducin-like protein (Eurofung) (Uncharacterized protein)	AN0082.2 ANIA_00082	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	281
Q5B8F3_EMENI	unreviewed	Phosphatidate cytidylyltransferase, putative (AFU_orthologue AFUA_3G13270) (Uncharacterized protein)	AN3177.2 ANIA_03177	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	381
Q5B8P5_EMENI	unreviewed	Phosphatidyl synthase (AFU_orthologue AFUA_3G12330) (Uncharacterized protein)	AN3085.2 ANIA_03085	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	450
Q5B744_EMENI	unreviewed	Phosphatidylinositol phospholipase C (AFU_orthologue AFUA_4G12000) (Uncharacterized protein)	AN3636.2 ANIA_03636	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	485
MET16_EMENI	reviewed	Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (3'-phosphoadenylylsulfate reductase) (PAPS reductase, thioredoxin dependent) (PAdoPS reductase)	sA AN4770	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	306
PCKA_EMENI	reviewed	**Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)**	acuF AN1918	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	600
PGK_EMENI	reviewed	Phosphoglycerate kinase (EC 2.7.2.3)	pgkA pgk AN1246	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	421
C8V1Q0_EMENI	unreviewed	Phospholipase D [Source:UniProtKB/TrEMBLAcc:Q874F2]	ANIA_06712	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	833
Q5B0S3_EMENI	unreviewed	Phospholipid metabolism enzyme regulator, putative (AFU_orthologue AFUA_2G08080) (Uncharacterized protein)	AN5857.2 ANIA_05857	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	903
Q5BBR9_EMENI	unreviewed	Phospholipid-transporting ATPase (EC 3.6.3.1)	AN2011.2 ANIA_02011	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1688
Q5AUA9_EMENI	unreviewed	Phosphoribosylformylglycinamidine synthase (Eurofung) (Uncharacterized protein)	AN8121.2 ANIA_08121	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1360
Q5B5C5_EMENI	unreviewed	**Phosphotransferase (EC 2.7.1.-)**	AN4255.2 ANIA_04255	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
PALF_EMENI	reviewed	pH-response regulator protein palF/RIM8	palF AN1844	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	775
PALI_EMENI	reviewed	pH-response regulator protein palI/RIM9	palI AN4853	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
Q5BA16_EMENI	unreviewed	Plasma membrane hexose transporter, putative (AFU_orthologue AFUA_7G00220) (Uncharacterized protein)	AN2614.2 ANIA_02614	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	528
C8V2S8_EMENI	unreviewed	Polyadenylation factor subunit CstF64, putative (AFU_orthologue AFUA_2G09100)	ANIA_06074	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	293
C8VLC7_EMENI	unreviewed	**Polyubiquitin [Source:UniProtKB/TrEMBLAcc:A2RVC1]**	ANIA_02000	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	305
C8VDG7_EMENI	unreviewed	**Polyubiquitin binding protein (Doa1/Ufd3), putative (AFU_orthologue AFUA_5G08370)**	ANIA_07704	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	811
Q5BDU0_EMENI	unreviewed	Potassium ion/proton antiporter (Eurofung) (Uncharacterized protein)	AN1290.2 ANIA_01290	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	883
C8VTJ9_EMENI	unreviewed	PQ loop repeat protein (AFU_orthologue AFUA_1G11900)	ANIA_10166	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	424
CWC25_EMENI	reviewed	**Pre-mRNA-splicing factor cwc25**	cwc25 AN5949	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	415
Q5B2L3_EMENI	unreviewed	Primary component of eisosomes (Eurofung) (Uncharacterized protein)	AN5217.2 ANIA_05217	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
BTGE_EMENI	reviewed	Probable beta-glucosidase btgE (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase btgE) (Cellobiase btgE) (Gentiobiase btgE)	btgE AN1551	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	555
BGLG_EMENI	reviewed	**Probable beta-glucosidase G (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase G) (Cellobiase G) (Gentiobiase G)**	bglG AN5976	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	819
Q5AYI6_EMENI	unreviewed	Probable bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase (Eurofung) (Uncharacterized protein)	biA AN6644.2 ANIA_06644	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	787
XYL2_EMENI	reviewed	Probable D-xylulose reductase A (EC 1.1.1.9) (Xylitol dehydrogenase A)	xdhA AN9064	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
SCONB_EMENI	reviewed	**Probable E3 ubiquitin ligase complex SCF subunit sconB (Sulfur controller B) (Sulfur metabolite repression control protein B)**	sconB mapB1 AN6359	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	678
FAEB_EMENI	reviewed	Probable feruloyl esterase B (EC 3.1.1.73) (Ferulic acid esterase B) (FAEB)	faeB AN1772	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	527
EGLC_EMENI	reviewed	**Probable glucan endo-1,3-beta-glucosidase eglC (EC 3.2.1.39) (Endo-1,3-beta-glucanase eglC) (Laminarinase eglC)**	eglC AN7950	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	465
PLYD_EMENI	reviewed	**Probable pectate lyase D (EC 4.2.2.2)**	plyD AN2542	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	264
C8VPA8_EMENI	unreviewed	Profilin	ANIA_02484	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	131
Q5B551_EMENI	unreviewed	Progesterone binding protein, putative (AFU_orthologue AFUA_4G06240) (Uncharacterized protein)	AN4329.2 ANIA_04329	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	125
Q5BCJ9_EMENI	unreviewed	**Proline oxidase [Source:UniProtKB/TrEMBLAcc:Q9P8H9] (Uncharacterized protein)**	prnD AN1731.2 ANIA_01731	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	478
BCP1_EMENI	reviewed	Protein bcp1	bcp1 AN6865	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	290
FMP52_EMENI	reviewed	Protein fmp52, mitochondrial	fmp52 AN1753	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	233
Q5BBU6_EMENI	unreviewed	Protein involved in transcription initiation at TATA-containing promoters (Eurofung) (Uncharacterized protein)	AN1984.2 ANIA_01984	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	808
Q5AXF0_EMENI	unreviewed	Protein kinase activator Bem1, putative (AFU_orthologue AFUA_4G04120) (Uncharacterized protein)	AN7030.2 ANIA_07030	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	616
Q5B8X9_EMENI	unreviewed	Protein kinase domain-containing protein (AFU_orthologue AFUA_3G08710) (Uncharacterized protein)	AN3001.2 ANIA_03001	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	394
Q5AZD3_EMENI	unreviewed	Protein kinase, putative (AFU_orthologue AFUA_2G14200) (Uncharacterized protein)	AN6347.2 ANIA_06347	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	674
C8VQK9_EMENI	unreviewed	Protein kinase, putative (AFU_orthologue AFUA_5G11840)	ANIA_10019	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	826
C8VCH9_EMENI	unreviewed	Protein kinase, putative (AFU_orthologue AFUA_7G00740)	ANIA_10937	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	460
C8VJZ5_EMENI	unreviewed	Protein mitochondrial targeting protein (Mas1), putative (AFU_orthologue AFUA_1G05040)	ANIA_02731	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	412
C8V9D0_EMENI	unreviewed	Protein serine/threonine kinase (Ran1), putative (AFU_orthologue AFUA_3G10530)	ANIA_04935	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	436
SEY1_EMENI	reviewed	Protein sey1 (EC 3.6.5.-)	sey1 AN1085	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	858
Q5B4E1_EMENI	unreviewed	Protein translocation complex subunit Sss1, putative (AFU_orthologue AFUA_3G06901) (Uncharacterized protein)	AN4589.2 ANIA_04589	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	70
Q5BH51_EMENI	unreviewed	Protein tyrosine phosphatase Pps1, putative (AFU_orthologue AFUA_5G11690) (Uncharacterized protein)	AN0129.2 ANIA_00129	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	689

Q5AT82_EMENI	unreviewed	Proteinase, putative (AFU_orthologue AFUA_3G01350) (Uncharacterized protein)	AN8498.2 ANIA_08498	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	678
Q5B4I6_EMENI	unreviewed	Protein-tyrosine phosphatase, putative (AFU_orthologue AFUA_2G02760) (Uncharacterized protein)	AN4544.2 ANIA_04544	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	702
UAPC_EMENI	reviewed	**Purine permease**	uapC AN6730	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	580
FCY2_EMENI	reviewed	Purine-cytosine permease fcyB (PCP fcyB) (Cytosine/purine transport protein fcyB) (Fluorocytosine resistance protein fcyB)	fcyB AN10767	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	508
C8V200_EMENI	unreviewed	Putative 1,6-beta-glucan synthetase (Eurofung)	ANIA_10779	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	632
C8VD53_EMENI	unreviewed	Putative bHLH transcription factor (Eurofung)	ANIA_07170	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	277
Q5BEB6_EMENI	unreviewed	Putative bHLH transcription factor (Eurofung) (Uncharacterized protein)	AN1114.2 ANIA_01114	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	393
C8VNE8_EMENI	unreviewed	Putative b-zip transcription factor (Eurofung)	ANIA_10295	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	469
Q5B8B4_EMENI	unreviewed	Putative b-zip transcription factor (Eurofung) (Uncharacterized protein)	AN3216.2 ANIA_03216	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	791
Q5AR40_EMENI	unreviewed	Putative C2H2 finger domain transcription factor (Eurofung) (Uncharacterized protein)	AN5252.2 AN9240.2 ANIA_05252 ANIA_0924	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	197
CCPR2_EMENI	reviewed	Putative heme-binding peroxidase (EC 1.11.1.-)	AN5440	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	312
Q5B0S0_EMENI	unreviewed	**Putative low affinity glucose transporter MstE [Source:UniProtKB/TrEMBLAcc:Q400D8] (Uncharacterized protein)**	AN5860.2 ANIA_05860	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	562
Q5F2L5_EMEND	unreviewed	**Putative monosaccharide sugar transporter**	mstF	Emericella nidulans (Aspergillus nidulans)	547
Q5B4K6_EMENI	unreviewed	Putative Myb-like transcription factor (Eurofung) (Uncharacterized protein)	AN4524.2 ANIA_04524	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	332
Q5AX06_EMENI	unreviewed	Putative Myb-like transcription factor (Eurofung) (Uncharacterized protein)	AN7174.2 ANIA_07174	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	305
PMP20_EMENI	reviewed	Putative peroxiredoxin pmp20 (EC 1.11.1.15) (Peroxisomal membrane protein pmp20) (Thioredoxin reductase)	AN8692	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	168
Q5B1C0_EMENI	unreviewed	Putative plasma membrane sensor transducer (Eurofung) (Uncharacterized protein)	AN5660.2 ANIA_05660	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	280
C8V4B8_EMENI	unreviewed	Putative TeaA receptor TeaR (Eurofung)	teaR ANIA_04214	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	524
KAPC_EMENI	reviewed	**Putative transcription factor kapC**	kapC AN10378	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	278
C8V9Y2_EMENI	unreviewed	Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung)	ANIA_11112	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	446
C8VCY7_EMENI	unreviewed	Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung)	ANIA_10910	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	913
Q5ARQ5_EMENI	unreviewed	Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung) (Uncharacterized protein)	AN9025.2 ANIA_09025	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	891
Q5AX62_EMENI	unreviewed	Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung) (Uncharacterized protein)	AN7118.2 ANIA_07118	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	991
C8V664_EMENI	unreviewed	Putative transglycosidase, GH16 family (Eurofung)	ANIA_03914	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	375
Q5B4L5_EMENI	unreviewed	Putative transglycosidase, GH16 family (Eurofung) (Uncharacterized protein)	AN4515.2 ANIA_04515	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	435
Q5B8S7_EMENI	unreviewed	Putative transglycosidase, GH16 family (Eurofung) (Uncharacterized protein)	AN3053.2 ANIA_03053	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
Y0176_EMENI	reviewed	Putative uncharacterized protein AN10176	AN10176	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	60
C8V1L9_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_06684	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	748
C8VAH1_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_11099	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	713
C8V6J8_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_03835	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	594
C8V8Z3_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_10548	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1160
C8V692_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_10491	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	759
C8V3N0_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_07872	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	610
C8VAN3_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_04785	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	687
C8VFU5_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_05651	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	677
C8V955_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_10550	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	797
C8VJP0_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_02763	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	736
C8VLJ4_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_08918	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	618
C8VJD2_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_02852	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1018
C8VI22_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_03280	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	442
C8VF97_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_05220	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	962
C8VNN2_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_02375	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	568
C8VK48_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung)**	ANIA_11169	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	683
C8VI55_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_03250	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	460
C8VNR0_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_10300	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	596
C8VNM3_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_02367	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	528
C8VN09_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_01569	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	681
C8VRL9_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_01402	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	692
C8VMQ2_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_01518	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	825
C8VQV9_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_10120	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	733
C8VTS3_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_00364	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	396
C8VD32_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_07190	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	581
C8VD11_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung)	ANIA_10911	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	509
C8VKQ5_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Fragment)	ANIA_09043	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	517
Q5B0H5_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN5955.2 ANIA_05955	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	613
Q5AXY4_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN6846.2 ANIA_06846	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	681
Q5AUV7_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN7923.2 ANIA_07923	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	383
Q5B5D3_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN4247.2 ANIA_04247	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	634
Q5B7P7_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN3433.2 ANIA_03433	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	311
Q5BBE4_EMENI	unreviewed	**Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)**	AN2136.2 ANIA_02136	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	687
Q5B7W1_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN3369.2 ANIA_03369	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	773
Q5AS45_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN8885.2 ANIA_08885	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	915
Q5ARN0_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN9050.2 ANIA_09050	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	538
Q5AQY7_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN9293.2 ANIA_09293	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	564
Q5BEV2_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN0928.2 ANIA_00928	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	574
Q5BEX8_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN0902.2 ANIA_00902	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	609
Q5BFU5_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN0585.2 ANIA_00585	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	556
Q5AXA7_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor (Eurofung) (Uncharacterized protein)	AN7073.2 ANIA_07073	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	321
Q5BEZ5_EMENI	unreviewed	Putative Zn(II)2Cys6 transcription factor and homeobox domain transcription factor (Eurofung) (Uncharacterized protein)	AN0885.2 ANIA_00885	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	848
C8VJ33_EMENI	unreviewed	PX domain protein (AFU_orthologue AFUA_3G08020)	ANIA_10350	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	910
PDX1_EMENI	reviewed	Pyridoxal 5'-phosphate synthase subunit pyroA (PLP synthase subunit pyroA) (EC 4.3.3.6) (Pdx1)	pyroA AN7725	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	304
G5EB79_EMENI	unreviewed	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	AN7387.2 ANIA_07387	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	283
Q5B4R8_EMENI	unreviewed	Pyruvate carboxylase (EC 6.4.1.1)	AN4462.2 ANIA_04462	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1196

PDC_EMENI	reviewed	**Pyruvate decarboxylase (EC 4.1.1.1)**	pdcA AN4888	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	568
DHQA_EMENI	reviewed	**Quinate dehydrogenase (EC 1.1.1.24)**	qutB AN1137	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
Q5BAF6_EMENI	unreviewed	Ras-like GTP-binding protein, putative (AFU_orthologue AFUA_4G03100) (Uncharacterized protein)	AN2474.2 ANIA_02474	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	307
RAS_EMENI	reviewed	**Ras-like protein**	rasA AN0182	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	212
ALCR_EMENI	reviewed	**Regulatory protein alcR**	alcR AN8978	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	821
Q5AS44_EMENI	unreviewed	Repressor protein (AFU_orthologue AFUA_8G02700) (Uncharacterized protein)	AN8886.2 ANIA_08886	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	804
RRG9_EMENI	reviewed	Required for respiratory growth protein 9, mitochondrial	rrg9 AN6290	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	271
C8VLD7_EMENI	unreviewed	RfeB [Source:UniProtKB/TrEMBLAcc:Q8J178]	ANIA_02009	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	604
C8VLE0_EMENI	unreviewed	RfeF [Source:UniProtKB/TrEMBLAcc:Q8J174]	ANIA_02012	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	524
C8VAZ8_EMENI	unreviewed	RfeG [Source:UniProtKB/TrEMBLAcc:Q8J173]	ANIA_04680	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	270
C8V794_EMENI	unreviewed	Rho guanyl nucleotide exchange factor, putative (AFU_orthologue AFUA_7G04600)	ANIA_10442	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1921
C8V019_EMENI	unreviewed	**Ribosomal protein L19**	ANIA_10740	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	190
Q5B7R7_EMENI	unreviewed	**Ribosomal protein S5 (AFU_orthologue AFUA_7G01460) (Uncharacterized protein)**	AN3413.2 ANIA_03413	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	259
Q5BE55_EMENI	unreviewed	Ribosomal RNA processing protein, putative (AFU_orthologue AFUA_1G10990) (Uncharacterized protein)	AN1175.2 ANIA_01175	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	331
C8VD17_EMENI	unreviewed	Ribosome biogenesis protein (Rrb1), putative (AFU_orthologue AFUA_6G10320)	ANIA_07205	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	492
Q5BEL7_EMENI	unreviewed	RL5_NEUCR 60S ribosomal protein L5 (CPR4) (Uncharacterized protein)	AN1013.2 ANIA_01013	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	301
Q5AVI0_EMENI	unreviewed	RNA binding protein (AFU_orthologue AFUA_5G08330) (Uncharacterized protein)	AN7700.2 ANIA_07700	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	628
Q5B8Q8_EMENI	unreviewed	**RNA binding protein, putative (AFU_orthologue AFUA_3G09620) (Uncharacterized protein)**	AN3072.2 ANIA_03072	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	856
Q5B677_EMENI	unreviewed	RNP domain protein (AFU_orthologue AFUA_6G08040) (Uncharacterized protein)	AN3953.2 ANIA_03953	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
Q5B7W4_EMENI	unreviewed	RPEL repeat protein (AFU_orthologue AFUA_7G01340) (Uncharacterized protein)	AN3366.2 ANIA_03366	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	104
Q5B3G8_EMENI	unreviewed	RTA1 domain protein, putative (AFU_orthologue AFUA_3G10770) (Uncharacterized protein)	AN4912.2 ANIA_04912	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	311
Q5AVP8_EMENI	unreviewed	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	AN7632.2 ANIA_07632	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	379
Q5BE08_EMENI	unreviewed	S-adenosylmethionine synthase (EC 2.5.1.6)	AN1222.2 ANIA_01222	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	388
Q5BCW6_EMENI	unreviewed	S-adenosyl-methionine-sterol-C-methyltransferas (AFU_orthologue AFUA_4G09190) (Uncharacterized protein)	AN1614.2 ANIA_01614	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	387
Q5BBG6_EMENI	unreviewed	Salicylate hydroxylase, putative (AFU_orthologue AFUA_2G05260) (Uncharacterized protein)	AN2114.2 ANIA_02114	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	448
Q5AWE8_EMENI	unreviewed	Salicylate hydroxylase, putative (AFU_orthologue AFUA_3G01460) (Uncharacterized protein)	AN7382.2 ANIA_07382	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	422
C8VS78_EMENI	unreviewed	ScfA [Source:UniProtKB/TrEMBLAcc:Q1WD27]	ANIA_01303	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	729
Q5BEH2_EMENI	unreviewed	SCP-like extracellular protein, putative (AFU_orthologue AFUA_1G12350) (Uncharacterized protein)	AN1058.2 ANIA_01058	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
C8VHD2_EMENI	unreviewed	Sec7 domain protein (AFU_orthologue AFUA_3G05700)	ANIA_03438	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1475
LAEA_EMENI	reviewed	**Secondary metabolism regulator laeA (Methyltransferase laeA) (EC 2.1.1.-) (Velvet complex subunit laeA)**	laeA ANIA_00807	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	374
Q5BCD1_EMENI	unreviewed	Secretory lipase, putative (AFU_orthologue AFUA_7G00110) (Uncharacterized protein)	AN1799.2 ANIA_01799	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	450
C8VAK9_EMENI	unreviewed	Septin [Source:UniProtKB/TrEMBLAcc:Q9C1M0]	ANIA_10595	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	587
C8V028_EMENI	unreviewed	Serine hydroxymethyltransferase (EC 2.1.2.1)	ANIA_10745	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	600
C8VIR5_EMENI	unreviewed	Serine hydroxymethyltransferase (EC 2.1.2.1)	ANIA_03058	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	471
Q5BEC8_EMENI	unreviewed	Serine palmitoyl transferase subunit [Source:UniProtKB/TrEMBLAcc:Q7ZA40] (Uncharacterized protein)	AN1102.2 ANIA_01102	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	672
Q5B7S3_EMENI	unreviewed	**Serine protease (EC 3.4.21.-)**	AN3407.2 ANIA_03407	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	712
Q5B0F7_EMENI	unreviewed	**Serine/threonine protein kinase (YPK1), putative (AFU_orthologue AFUA_2G10620) (Uncharacterized protein)**	AN5973.2 ANIA_05973	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	640
Q5B8M0_EMENI	unreviewed	Serine/threonine protein kinase, putative (AFU_orthologue AFUA_3G12670) (Uncharacterized protein)	AN3110.2 ANIA_03110	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	813
ATG1_EMENI	reviewed	**Serine/threonine-protein kinase atg1 (EC 2.7.11.1) (Autophagy-related protein 1)**	atg1 AN1632	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	935
STE20_EMENI	reviewed	**Serine/threonine-protein kinase ste20 (EC 2.7.11.1)**	ste20 AN2067	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	848
G5EB04_EMENI	unreviewed	**Serine/threonine-protein phosphatase (EC 3.1.3.16)**	AN3793.2 ANIA_03793	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	512
PP1_EMENI	reviewed	**Serine/threonine-protein phosphatase PP1 (EC 3.1.3.16)**	bimG AN0410	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	323
Q5AXK8_EMENI	unreviewed	Serine-leucine-rich repeat protein (AFU_orthologue AFUA_8G02230) (Uncharacterized protein)	AN6972.2 ANIA_06972	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	448
C8VUM1_EMENI	unreviewed	Serine-threonine kinase and endoribonuclease (Eurofung)	ANIA_00235	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1121
C8V6P1_EMENI	unreviewed	SfgA [Source:UniProtKB/TrEMBLAcc:Q3I5F3]	ANIA_08129	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	601
Q5BFI2_EMENI	unreviewed	SH3 domain protein (AFU_orthologue AFUA_1G13610) (Uncharacterized protein)	AN0698.2 ANIA_00698	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	726
C8VNZ3_EMENI	unreviewed	SH3 domain protein (AFU_orthologue AFUA_2G13880)	ANIA_10307	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	914
Q5BCQ3_EMENI	unreviewed	Short chain dehydrogenase, putative (AFU_orthologue AFUA_4G08710) (Uncharacterized protein)	AN1677.2 ANIA_01677	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	287
Q5BBA3_EMENI	unreviewed	Short chain dehydrogenase/oxidoreductase, putative (AFU_orthologue AFUA_2G15740) (Uncharacterized protein)	AN2177.2 ANIA_02177	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	337
Q5AS34_EMENI	unreviewed	Short-chain dehydrogenase/reductase 2, putative (AFU_orthologue AFUA_8G02600) (Uncharacterized protein)	AN8896.2 ANIA_08896	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	337
C8VHU0_EMENI	unreviewed	Short-chain dehydrogenase/reductase, putative (AFU_orthologue AFUA_6G03370)	ANIA_10399	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	285
Q5B6R7_EMENI	unreviewed	**Siderochrome-iron transporter, putative (AFU_orthologue AFUA_7G04730) (Uncharacterized protein)**	AN3763.2 ANIA_03763	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	604
MIRB_EMENI	reviewed	**Siderophore iron transporter mirB (Major facilitator iron-regulated transporter B) (Triacetylfusarinine C permease)**	mirB AN8540	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	604
MIRC_EMENI	reviewed	**Siderophore iron transporter mirC (Major facilitator iron-regulated transporter C)**	mirC AN7485	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	607
C8VLE2_EMENI	unreviewed	Signal recognition particle subunit SRP72	ANIA_02014	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	649
Q5BFB3_EMENI	unreviewed	Small nuclear ribonucleoprotein (LSM7), putative (AFU_orthologue AFUA_1G14290) (Uncharacterized protein)	AN0767.2 ANIA_00767	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	136
Q5B6N6_EMENI	unreviewed	Small nucleolar ribonucleoprotein complex subunit, putative (AFU_orthologue AFUA_2G03930) (Uncharacterized protein)	AN3794.2 ANIA_03794	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	938
Q5AW72_EMENI	unreviewed	Small nucleolar ribonucleoprotein complex subunit, putative (AFU_orthologue AFUA_2G05930) (Uncharacterized protein)	AN7458.2 ANIA_07458	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	579
C8V2M6_EMENI	unreviewed	**Snf1 protein kinase complex subunit Snf4, putative (AFU_orthologue AFUA_5G12990)**	ANIA_10854	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	431
Q5AXR0_EMENI	unreviewed	**SNF7 family protein (AFU_orthologue AFUA_5G13890) (Uncharacterized protein)**	AN6920.2 ANIA_06920	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	228
Q5BFP0_EMENI	unreviewed	Sphinganine hydroxylase BasA (Eurofung) (Uncharacterized protein)	AN0640.2 ANIA_00640	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	430
Q5B7N3_EMENI	unreviewed	Spindle poison sensitivity protein Scp3, putative (AFU_orthologue AFUA_3G05570) (Uncharacterized protein)	AN3447.2 ANIA_03447	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
C8VEV9_EMENI	unreviewed	Splicing factor 3b, subunit 2, 145kD (AFU_orthologue AFUA_5G04420)	ANIA_05098	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
C8VDL8_EMENI	unreviewed	Squalene epoxidase [Source:UniProtKB/TrEMBLAcc:Q27PP1]	ANIA_11008	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	483
Q5B527_EMENI	unreviewed	Sterol carrier protein, putative (AFU_orthologue AFUA_4G06380) (Uncharacterized protein)	AN4353.2 ANIA_04353	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	458
C8VIF1_EMENI	unreviewed	Stomatin family protein (AFU_orthologue AFUA_3G13440)	ANIA_03163	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	344
Q5AVP0_EMENI	unreviewed	Stress response protein Rds1, putative (AFU_orthologue AFUA_5G12490) (Uncharacterized protein)	AN7640.2 ANIA_07640	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	486
C8V7M0_EMENI	unreviewed	**Stress response regulator SrrA [Source:UniProtKB/TrEMBLAcc:Q8J0P7]**	srrA ANIA_03688	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	558
Q5B3R0_EMENI	unreviewed	Succinate semialdehyde dehydrogenase (Eurofung) (Uncharacterized protein)	AN4820.2 ANIA_04820	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	499
C8VT00_EMENI	unreviewed	Succinyl-CoA synthetase subunit alpha, putative (AFU_orthologue AFUA_1G10830)	ANIA_01193	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	703
C8V5Q9_EMENI	unreviewed	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)	ANIA_10495	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	506
C8VFS4_EMENI	unreviewed	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)	ANIA_05669	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	519
Q5AYC7_EMENI	unreviewed	**Sugar transporter family protein (AFU_orthologue AFUA_7G05550) (Uncharacterized protein)**	AN6703.2 ANIA_06703	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	495

C8VK66_EMENI	unreviewed	**Sugar transporter, putative (AFU_orthologue AFUA_7G01740)**	ANIA_11167	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	521
Q5AWV1_EMENI	unreviewed	Sulfatase domain protein (AFU_orthologue AFUA_2G17610) (Uncharacterized protein)	AN7229.2 ANIA_07229	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	925
MET3_EMENI	reviewed	**Sulfate adenylyltransferase (EC 2.7.7.4) (ATP-sulfurylase) (Sulfate adenylate transferase) (SAT)**	met3 sC AN4769	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	574
Q5BFF4_EMENI	unreviewed	SUN domain protein (Adg3), putative (AFU_orthologue AFUA_1G13940) (Uncharacterized protein)	AN0726.2 ANIA_00726	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	451
Q5AYD3_EMENI	unreviewed	SUN domain protein (Eurofung) (Uncharacterized protein)	AN6697.2 ANIA_06697	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	410
SODC_EMENI	reviewed	**Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)**	sodA AN0241	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	154
C8VEW0_EMENI	unreviewed	SWIRM domain protein Fun19, putative (AFU_orthologue AFUA_1G07750)	ANIA_05099	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	392
TBP_EMENI	reviewed	**TATA-box-binding protein (TATA sequence-binding protein) (TBP) (TATA-binding factor) (TATA-box factor) (Transcription initiation factor TFIID TBP subunit)**	tbpA tbp AN4976	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	268
Q5B5L1_EMENI	unreviewed	**Telomere silencing protein Zds1, putative (AFU_orthologue AFUA_6G07890) (Uncharacterized protein)**	AN4169.2 ANIA_04169	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	839
Q5B016_EMENI	unreviewed	Terminal deoxynucleotidyl transferase, putative (AFU_orthologue AFUA_2G08840) (Uncharacterized protein)	AN6114.2 ANIA_06114	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	665
Q5AR85_EMENI	unreviewed	Thermolabile L-asparaginase, putative (AFU_orthologue AFUA_3G11890) (Uncharacterized protein)	AN9195.2 ANIA_09195	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	356
C8VI66_EMENI	unreviewed	Thermophilic desulfurizing enzyme family protein (AFU_orthologue AFUA_8G01010)	ANIA_03239	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
THI4_EMENI	reviewed	Thiamine thiazole synthase (Thiazole biosynthetic enzyme)	thiA thi4 thiF AN3928	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	331
C8V4E8_EMENI	unreviewed	Thioredoxin reductase (EC 1.8.1.9)	ANIA_03581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	339
Q5AU12_EMENI	unreviewed	Thioredoxin reductase, putative (AFU_orthologue AFUA_5G03540) (Uncharacterized protein)	AN8218.2 ANIA_08218	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	385
Q5BCU1_EMENI	unreviewed	Thioredoxin, putative (AFU_orthologue AFUA_4G09090) (Uncharacterized protein)	AN1639.2 ANIA_01639	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	330
C8VBQ1_EMENI	unreviewed	Threonine aldolase or alanine racemase, putative (Eurofung)	ANIA_07564	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	411
C8V7M6_EMENI	unreviewed	TIM complex componenet Tim54 (AFU_orthologue AFUA_4G11900)	ANIA_10453	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	476
Q5B5Z6_EMENI	unreviewed	**Transcription factor HapC (Eurofung) (Uncharacterized protein)**	AN4034.2 ANIA_04034	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	219
STE12_EMENI	reviewed	**Transcription factor steA**	steA ste12 AN2290	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	692
Q5AT29_EMENI	unreviewed	Transketolase (EC 2.2.1.1)	AN8551.2 ANIA_08551	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	696
C8VRQ4_EMENI	unreviewed	Transketolase (EC 2.2.1.1)	ANIA_00688	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	684
C8V7L9_EMENI	unreviewed	Translation initiation factor eif-2b epsilon subunit, putative (AFU_orthologue AFUA_6G12530)	ANIA_10459	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	704
Q5BAM0_EMENI	unreviewed	Translation initiation factor eIF-2B subunit family protein (AFU_orthologue AFUA_2G14290) (Uncharacterized protein)	AN2410.2 ANIA_02410	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	548
C8VL87_EMENI	unreviewed	Transporter	ANIA_08966	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	675
C8V6K4_EMENI	unreviewed	Transposase Tan1-Aspergillus niger (ANG_orthologue An07g09460)	ANIA_11044	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	461
Q5BF54_EMENI	unreviewed	Transposase Tan1-Aspergillus niger (ANG_orthologue An07g09460) (Uncharacterized protein)	AN0826.2 ANIA_00826	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	553
Q5ARJ4_EMENI	unreviewed	TRAPP complex component Bet3, putative (Eurofung) (Uncharacterized protein)	AN9086.2 ANIA_09086	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	188
Q5B2E7_EMENI	unreviewed	TRI7-like toxin biosynthesis protein, putative (AFU_orthologue AFUA_8G02360) (Uncharacterized protein)	AN5283.2 ANIA_05283	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	420
Q5B0M2_EMENI	unreviewed	Triosephosphate isomerase (EC 5.3.1.1)	AN5908.2 ANIA_05908	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	284
C8V6D2_EMENI	unreviewed	Tryptophanyl-tRNA synthetase (AFU_orthologue AFUA_2G01640)	ANIA_10475	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	424
TBB1_EMENI	reviewed	**Tubulin beta-1 chain (Beta-1-tubulin)**	benA rhiA AN1182	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	447
TBB2_EMENI	reviewed	**Tubulin beta-2 chain (Beta-2-tubulin)**	tubC AN6838	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	449
TCSA_EMENI	reviewed	Two-component system protein A (EC 2.7.13.3)	tcsA AN5296	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	682
TCSB_EMENI	reviewed	Two-component system protein B (EC 2.7.13.3) (Protein NHK1) (SLN1 homolog)	tcsB AN1800	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1065
C8VH61_EMENI	unreviewed	U5 snRNP complex subunit, putative (AFU_orthologue AFUA_7G02280)	ANIA_09085	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
Q5AT68_EMENI	unreviewed	UbiD family decarboxylase, putative (AFU_orthologue AFUA_7G00920) (Uncharacterized protein)	AN8512.2 ANIA_08512	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	375
C8VD48_EMENI	unreviewed	UbiE/COQ5 methyltransferase, putative (AFU_orthologue AFUA_4G03321)	ANIA_07175	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	313
UBP16_EMENI	reviewed	**Ubiquitin carboxyl-terminal hydrolase 16 (EC 3.4.19.12) (Deubiquitinating enzyme 16) (Ubiquitin thioesterase 16) (Ubiquitin-specific-processing protease 16)**	ubp16 AN11684	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	624
CREB_EMENI	reviewed	**Ubiquitin carboxyl-terminal hydrolase creB (EC 3.4.19.12) (Carbon catabolite repression protein B) (Deubiquitinating enzyme creB) (Ubiquitin thioesterase creB) (Ubiquitin-hydrolyzing enzyme creB) (Ubiquitin-specific-proces**	creB molB AN3587	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	766
C8VP63_EMENI	unreviewed	**Ubiquitin conjugating enzyme Ubc8, putative (AFU_orthologue AFUA_6G09160)**	ANIA_01761	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	181
C8VGS5_EMENI	unreviewed	**Ubiquitin conjugating enzyme, putative (AFU_orthologue AFUA_6G14130)**	ANIA_05351	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	168
Q5AZC6_EMENI	unreviewed	**Ubiquitin C-terminal hydrolase, putative (AFU_orthologue AFUA_2G14130) (Uncharacterized protein)**	AN6354.2 ANIA_06354	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1418
Q5BE57_EMENI	unreviewed	**Ubiquitin domain protein, putative (AFU_orthologue AFUA_1G11060) (Uncharacterized protein)**	AN1173.2 ANIA_01173	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
C8VAN4_EMENI	unreviewed	**Ubiquitin thiolesterase (OtuB1), putative (AFU_orthologue AFUA_3G06710)**	ANIA_04784	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	509
ATG12_EMENI	reviewed	**Ubiquitin-like protein ATG12 (Autophagy-related protein 12)**	atg12 AN1760	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	166
C8VGA1_EMENI	unreviewed	UDP-galactose transporter (Eurofung)	ANIA_10676	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	450
C8VAU8_EMENI	unreviewed	UDP-glucose 4-epimerase (Eurofung)	ANIA_04727	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	371
C8VK50_EMENI	unreviewed	UDP-glucose pyrophosphorylase (EC 2.7.7.9) [Source:UniProtKB/TrEMBLAcc:Q5I6D1]	ANIA_09148	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	514
Y7799_EMENI	reviewed	Uncharacterized oxidoreductase AN7799 (EC 1.-.-.-)	AN7799	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	255
Q5AZW1_EMENI	unreviewed	Uncharacterized protein	AN6169.2 ANIA_06169	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	734
G5EB78_EMENI	unreviewed	Uncharacterized protein	AN9451.2 ANIA_09451	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	216
C8V1Z0_EMENI	unreviewed	Uncharacterized protein	ANIA_06749	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	291
Q5B070_EMENI	unreviewed	Uncharacterized protein	AN6060.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1447
Q5B0J1_EMENI	unreviewed	Uncharacterized protein	AN5939.2 ANIA_05939	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	582
Q5AYN3_EMENI	unreviewed	Uncharacterized protein	AN6597.2 ANIA_06597	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	452
C8UZZ9_EMENI	unreviewed	Uncharacterized protein	ANIA_10751	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	321
Q5B026_EMENI	unreviewed	Uncharacterized protein	AN6104.2 ANIA_06104	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	264
C8V2N6_EMENI	unreviewed	Uncharacterized protein	ANIA_06859	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	309
G5EB22_EMENI	unreviewed	Uncharacterized protein	AN5822.2 ANIA_05822	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1050
C8V1V6_EMENI	unreviewed	Uncharacterized protein	ANIA_10853	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	904
C8V1K0_EMENI	unreviewed	Uncharacterized protein	ANIA_06245	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	260
Q5AZF3_EMENI	unreviewed	Uncharacterized protein	AN6327.2 ANIA_06327	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	576
Q5AYU2_EMENI	unreviewed	Uncharacterized protein	AN6538.2 ANIA_06538	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1285
Q5AZ57_EMENI	unreviewed	Uncharacterized protein	AN6423.2 ANIA_06423	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	173
Q5AYS0_EMENI	unreviewed	Uncharacterized protein	AN6560.2 ANIA_06560	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	459
C8V1J8_EMENI	unreviewed	Uncharacterized protein	ANIA_06247	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	621
C8V1V2_EMENI	unreviewed	Uncharacterized protein	ANIA_10847	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	142
Q5AYG1_EMENI	unreviewed	Uncharacterized protein	AN6669.2 ANIA_06669	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	534
Q5AYL7_EMENI	unreviewed	Uncharacterized protein	AN6613.2 ANIA_06613	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	244
Q5AZA9_EMENI	unreviewed	Uncharacterized protein	AN6371.2 ANIA_06371	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	387
Q5B0E2_EMENI	unreviewed	Uncharacterized protein	AN5988.2 ANIA_05988	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1142
C8V1F0_EMENI	unreviewed	Uncharacterized protein	ANIA_10843	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	242

C8UZY2_EMENI	unreviewed	Uncharacterized protein	ANIA_10742	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	107
G5EAT9_EMENI	unreviewed	Uncharacterized protein	AN6126.2 ANIA_06126	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	2288
C8V064_EMENI	unreviewed	Uncharacterized protein	ANIA_10819	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	752
Q5AXL7_EMENI	unreviewed	Uncharacterized protein	AN6963.2 ANIA_06963	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	387
C8V1G2_EMENI	unreviewed	Uncharacterized protein	ANIA_06280	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	929
Q5AZD8_EMENI	unreviewed	Uncharacterized protein	AN6342.2 ANIA_06342	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	968
Q5B6F0_EMENI	unreviewed	Uncharacterized protein	AN3880.2 ANIA_03880	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	458
C8V3H6_EMENI	unreviewed	Uncharacterized protein	ANIA_05943	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	374
Q5B0T2_EMENI	unreviewed	Uncharacterized protein	AN5848.2 ANIA_05848	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	582
Q5AUJ9_EMENI	unreviewed	Uncharacterized protein	AN8031.2 ANIA_08031	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	853
Q5AY25_EMENI	unreviewed	Uncharacterized protein	AN6805.2 ANIA_06805	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
Q5AYG6_EMENI	unreviewed	Uncharacterized protein	AN6664.2 ANIA_06664	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	450
Q5AUY8_EMENI	unreviewed	Uncharacterized protein	AN7892.2 ANIA_07892	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	184
Q5AUJ6_EMENI	unreviewed	Uncharacterized protein	AN8034.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	566
C8V6E2_EMENI	unreviewed	Uncharacterized protein	ANIA_11046	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	202
Q5B632_EMENI	unreviewed	Uncharacterized protein	AN3998.2 ANIA_03998	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	335
G5EAX9_EMENI	unreviewed	Uncharacterized protein	AN8251.2 ANIA_08251	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	475
Q5B6D9_EMENI	unreviewed	Uncharacterized protein	AN3891.2 ANIA_03891	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	290
Q5B6I5_EMENI	unreviewed	Uncharacterized protein	AN3845.2 ANIA_03845	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	149
G5EB86_EMENI	unreviewed	Uncharacterized protein	AN3729.2 ANIA_03729	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1905
Q5B634_EMENI	unreviewed	Uncharacterized protein	AN3996.2 ANIA_03996	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	221
C8V4F6_EMENI	unreviewed	Uncharacterized protein	ANIA_03573	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	446
Q5B740_EMENI	unreviewed	Uncharacterized protein	AN3640.2 ANIA_03640	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	534
Q5B635_EMENI	unreviewed	Uncharacterized protein	AN3995.2 ANIA_03995	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	357
Q5B0H4_EMENI	unreviewed	Uncharacterized protein	AN5956.2 ANIA_05956	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	442
Q5AXZ9_EMENI	unreviewed	Uncharacterized protein	AN6831.2 ANIA_06831	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	536
C8UZY7_EMENI	unreviewed	Uncharacterized protein	ANIA_10752	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	383
Q5AZV8_EMENI	unreviewed	Uncharacterized protein	AN6172.2 ANIA_06172	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	412
Q5AZ54_EMENI	unreviewed	Uncharacterized protein	AN6426.2 ANIA_06426	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	333
G5EAS7_EMENI	unreviewed	Uncharacterized protein	AN6534.2 ANIA_06534	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
Q5AZJ6_EMENI	unreviewed	Uncharacterized protein	AN6284.2 ANIA_06284	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	926
Q5AZ43_EMENI	unreviewed	Uncharacterized protein	AN6437.2 ANIA_06437	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	330
Q5AZL8_EMENI	unreviewed	Uncharacterized protein	AN6262.2 ANIA_06262	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	451
Q5AYH3_EMENI	unreviewed	Uncharacterized protein	AN6657.2 ANIA_06657	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	96
Q5AXL6_EMENI	unreviewed	Uncharacterized protein	AN6964.2 ANIA_06964	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	217
C8V3A5_EMENI	unreviewed	Uncharacterized protein	ANIA_05989	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	280
Q5AYD8_EMENI	unreviewed	Uncharacterized protein	AN6692.2 ANIA_06692	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	176
Q5AXV3_EMENI	unreviewed	Uncharacterized protein	AN6877.2 ANIA_06877	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	287
Q5AY36_EMENI	unreviewed	Uncharacterized protein	AN6794.2 ANIA_06794	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	159
C8V1V8_EMENI	unreviewed	Uncharacterized protein	ANIA_10844	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	443
C8V257_EMENI	unreviewed	Uncharacterized protein	ANIA_06768	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	902
C8V0X4_EMENI	unreviewed	Uncharacterized protein	ANIA_06365	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	208
C8V0C3_EMENI	unreviewed	Uncharacterized protein	ANIA_06460	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	357
Q5AXM0_EMENI	unreviewed	Uncharacterized protein	AN6960.2 ANIA_06960	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1878
Q5AYG4_EMENI	unreviewed	Uncharacterized protein	AN6666.2 ANIA_06666	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	253
Q5AZ74_EMENI	unreviewed	Uncharacterized protein	AN6406.2 ANIA_06406	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	102
Q5AZA1_EMENI	unreviewed	Uncharacterized protein	AN6379.2 ANIA_06379	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	155
C8V745_EMENI	unreviewed	Uncharacterized protein	ANIA_11053	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	337
Q5AUW6_EMENI	unreviewed	Uncharacterized protein	AN7914.2 ANIA_07914	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	348
Q5ATU1_EMENI	unreviewed	Uncharacterized protein	AN8289.2 ANIA_08289	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	619
Q5B685_EMENI	unreviewed	Uncharacterized protein	AN3945.2 ANIA_03945	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	658
C8V3T3_EMENI	unreviewed	Uncharacterized protein	ANIA_10458	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	118
Q5B6A5_EMENI	unreviewed	Uncharacterized protein	AN3925.2 ANIA_03925	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	279
Q5AV06_EMENI	unreviewed	Uncharacterized protein	AN7874.2 ANIA_07874	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	306
C8V578_EMENI	unreviewed	Uncharacterized protein	ANIA_07943	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	330
Q5B7J8_EMENI	unreviewed	Uncharacterized protein	AN3482.2 ANIA_03482	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	277
C8V749_EMENI	unreviewed	Uncharacterized protein	ANIA_08188	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
C8V5F3_EMENI	unreviewed	Uncharacterized protein	ANIA_07975	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	235
Q5B476_EMENI	unreviewed	Uncharacterized protein	AN4654.2 ANIA_04654	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	580
Q5B716_EMENI	unreviewed	Uncharacterized protein	AN3664.2 ANIA_03664	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
Q5B7G3_EMENI	unreviewed	Uncharacterized protein	AN3517.2 ANIA_03517	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	356
Q5AST6_EMENI	unreviewed	Uncharacterized protein	AN8644.2 ANIA_08644	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	367
Q5B6W7_EMENI	unreviewed	Uncharacterized protein	AN3713.2 ANIA_03713	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	157
Q5AU84_EMENI	unreviewed	Uncharacterized protein	AN8146.2 ANIA_08146	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	346
Q5B589_EMENI	unreviewed	Uncharacterized protein	AN4291.2 ANIA_04291	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	162
Q5B7G0_EMENI	unreviewed	Uncharacterized protein	AN3520.2 ANIA_03520	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	593
Q5B6N4_EMENI	unreviewed	Uncharacterized protein	AN3796.2 ANIA_03796	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	67
Q5B5X9_EMENI	unreviewed	Uncharacterized protein	AN4051.2 ANIA_04051	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	286
C8V489_EMENI	unreviewed	Uncharacterized protein	ANIA_10528	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	99
Q5B656_EMENI	unreviewed	Uncharacterized protein	AN3974.2 ANIA_03974	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	320
Q5AUS7_EMENI	unreviewed	Uncharacterized protein	AN7953.2 ANIA_07953	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	338
C8V400_EMENI	unreviewed	Uncharacterized protein	ANIA_04276	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	506
C8V6T9_EMENI	unreviewed	Uncharacterized protein	ANIA_10461	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	147

Q5B5B6_EMENI	unreviewed	Uncharacterized protein	AN4264.2 ANIA_04264	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	494
Q5AUX3_EMENI	unreviewed	Uncharacterized protein	AN7907.2 ANIA_07907	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	162
Q5B5M6_EMENI	unreviewed	Uncharacterized protein	AN4154.2 ANIA_04154	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
Q5B6Q7_EMENI	unreviewed	Uncharacterized protein	AN3773.2 ANIA_03773	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	295
Q5B6R5_EMENI	unreviewed	Uncharacterized protein	AN3765.2 ANIA_03765	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	439
Q5B7D2_EMENI	unreviewed	Uncharacterized protein	AN3548.2 ANIA_03548	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	223
Q5B5V2_EMENI	unreviewed	Uncharacterized protein	AN4078.2 ANIA_04078	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	186
C8V3X4_EMENI	unreviewed	Uncharacterized protein	ANIA_03639	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	471
C8V1S7_EMENI	unreviewed	Uncharacterized protein	ANIA_11504 ANIA_11582	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	90
Q5AU82_EMENI	unreviewed	Uncharacterized protein	AN8148.2 ANIA_08148	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	299
C8V7F1_EMENI	unreviewed	Uncharacterized protein	ANIA_11061	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	476
Q5AUU7_EMENI	unreviewed	Uncharacterized protein	AN7933.2 ANIA_07933	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	335
Q5ATW4_EMENI	unreviewed	Uncharacterized protein	AN8266.2 ANIA_08266	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	398
Q5B7C8_EMENI	unreviewed	Uncharacterized protein	AN3552.2 ANIA_03552	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	486
C8V5C1_EMENI	unreviewed	Uncharacterized protein	ANIA_10509	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	114
C8V764_EMENI	unreviewed	Uncharacterized protein	ANIA_11597	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	74
Q5ATZ5_EMENI	unreviewed	Uncharacterized protein	AN8235.2 ANIA_08235	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1539
Q5B6N9_EMENI	unreviewed	Uncharacterized protein	AN3791.2 ANIA_03791	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	312
Q5B5Q9_EMENI	unreviewed	Uncharacterized protein	AN4121.2 ANIA_04121	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
Q5B7I7_EMENI	unreviewed	Uncharacterized protein	AN3493.2 ANIA_03493	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	215
C8V641_EMENI	unreviewed	Uncharacterized protein	ANIA_03935	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	139
C8V3M9_EMENI	unreviewed	Uncharacterized protein	ANIA_11581	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	47
C8V4I9_EMENI	unreviewed	Uncharacterized protein	ANIA_07891	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	363
Q5AUZ7_EMENI	unreviewed	Uncharacterized protein	AN7883.2 ANIA_07883	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	156
Q5ATZ3_EMENI	unreviewed	Uncharacterized protein	AN8237.2 ANIA_08237	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	359
C8V4K8_EMENI	unreviewed	Uncharacterized protein	ANIA_11431	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	90
Q5B674_EMENI	unreviewed	Uncharacterized protein	AN3956.2 ANIA_03956	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	557
Q5AUW0_EMENI	unreviewed	Uncharacterized protein	AN7920.2 ANIA_07920	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	358
Q5B5K8_EMENI	unreviewed	Uncharacterized protein	AN4172.2 ANIA_04172	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	378
Q5B5N3_EMENI	unreviewed	Uncharacterized protein	AN4147.2 ANIA_04147	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	228
Q5B5Y9_EMENI	unreviewed	Uncharacterized protein	AN4041.2 ANIA_04041	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	193
Q5AU49_EMENI	unreviewed	Uncharacterized protein	AN8181.2 ANIA_08181	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	475
Q5AU65_EMENI	unreviewed	Uncharacterized protein	AN8165.2 ANIA_08165	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	635
Q5AUU1_EMENI	unreviewed	Uncharacterized protein	AN7939.2 ANIA_07939	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	411
C8V5H6_EMENI	unreviewed	Uncharacterized protein	ANIA_04062	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	365
Q5B429_EMENI	unreviewed	Uncharacterized protein	AN4701.2 ANIA_04701	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	322
C8VA14_EMENI	unreviewed	Uncharacterized protein	ANIA_11108	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
Q5B4A8_EMENI	unreviewed	Uncharacterized protein	AN4622.2 ANIA_04622	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	433
Q5B4B6_EMENI	unreviewed	Uncharacterized protein	AN4614.2 ANIA_04614	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	310
Q5AYS1_EMENI	unreviewed	Uncharacterized protein	AN4391.2 AN6559.2 ANIA_04391 ANIA_0655	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	554
Q5B3P6_EMENI	unreviewed	Uncharacterized protein	AN4834.2 ANIA_04834	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
Q5B4F5_EMENI	unreviewed	Uncharacterized protein	AN4575.2 ANIA_04575	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	357
Q5B312_EMENI	unreviewed	Uncharacterized protein	AN5068.2 ANIA_05068	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
C8VAX8_EMENI	unreviewed	Uncharacterized protein	ANIA_04698	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	615
Q5B3N2_EMENI	unreviewed	Uncharacterized protein	AN4848.2 ANIA_04848	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	440
C8V7U1_EMENI	unreviewed	Uncharacterized protein	ANIA_04598	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	457
C8V8A0_EMENI	unreviewed	Uncharacterized protein	ANIA_11442	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	72
Q5B408_EMENI	unreviewed	Uncharacterized protein	AN4722.2 ANIA_04722	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	339
Q5ASE9_EMENI	unreviewed	Uncharacterized protein	AN8781.2 ANIA_08781	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	126
Q5B392_EMENI	unreviewed	Uncharacterized protein	AN4988.2 ANIA_04988	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	435
Q5B3J9_EMENI	unreviewed	Uncharacterized protein	AN4881.2 ANIA_04881	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	361
Q5ASW9_EMENI	unreviewed	Uncharacterized protein	AN8611.2 ANIA_08611	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	343
Q5ASA0_EMENI	unreviewed	Uncharacterized protein	AN8830.2 ANIA_08830	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	524
C8VAS4_EMENI	unreviewed	Uncharacterized protein	ANIA_04750	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	365
Q5B5V3_EMENI	unreviewed	Uncharacterized protein	AN4077.2 ANIA_04077	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	539
C8V6A8_EMENI	unreviewed	Uncharacterized protein	ANIA_10483	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	315
C8VAJ3_EMENI	unreviewed	Uncharacterized protein	ANIA_11097	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	320
Q5B3F1_EMENI	unreviewed	Uncharacterized protein	AN4929.2 ANIA_04929	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	947
Q5AST2_EMENI	unreviewed	Uncharacterized protein	AN8648.2 ANIA_08648	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1581
C8V4M5_EMENI	unreviewed	Uncharacterized protein	ANIA_10530	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	418
Q5B6L2_EMENI	unreviewed	Uncharacterized protein	AN3818.2 ANIA_03818	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	348
G5EAW6_EMENI	unreviewed	Uncharacterized protein	AN4361.2 ANIA_04361	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	294
Q5B5E3_EMENI	unreviewed	Uncharacterized protein	AN4237.2 ANIA_04237	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	776
C8V528_EMENI	unreviewed	Uncharacterized protein	ANIA_10422	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	165
Q5AU55_EMENI	unreviewed	Uncharacterized protein	AN8175.2 ANIA_08175	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	418
Q5AU63_EMENI	unreviewed	Uncharacterized protein	AN8167.2 ANIA_08167	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	507
Q5AV16_EMENI	unreviewed	Uncharacterized protein	AN7864.2 ANIA_07864	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	540
C8V4L2_EMENI	unreviewed	Uncharacterized protein	ANIA_04195	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	598
Q5B4V7_EMENI	unreviewed	Uncharacterized protein	AN4423.2 ANIA_04423	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	250
Q5B5A5_EMENI	unreviewed	Uncharacterized protein	AN4275.2 ANIA_04275	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	109
Q5B4S9_EMENI	unreviewed	Uncharacterized protein	AN4451.2 ANIA_04451	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	117
Q5B127_EMENI	unreviewed	Uncharacterized protein	AN5753.2 ANIA_05753	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	120
C8VEU6_EMENI	unreviewed	Uncharacterized protein	ANIA_11622	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	77

Q5B2A8_EMENI	unreviewed	Uncharacterized protein	AN5322.2 ANIA_05322	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	103
Q5B1W5_EMENI	unreviewed	Uncharacterized protein	AN5465.2 ANIA_05465	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	690
C8VEM3_EMENI	unreviewed	Uncharacterized protein	ANIA_11670	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	79
G5EAZ6_EMENI	unreviewed	Uncharacterized protein	AN5604.2 ANIA_05604	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
Q5B154_EMENI	unreviewed	Uncharacterized protein	AN5726.2 ANIA_05726	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	730
Q5B2B6_EMENI	unreviewed	Uncharacterized protein	AN5314.2 ANIA_05314	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	529
Q5B1Y1_EMENI	unreviewed	Uncharacterized protein	AN5449.2 ANIA_05449	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	594
Q5B2B2_EMENI	unreviewed	Uncharacterized protein	AN5318.2 ANIA_05318	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1270
C8VH32_EMENI	unreviewed	Uncharacterized protein	ANIA_05257	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	342
C8VGQ1_EMENI	unreviewed	Uncharacterized protein	ANIA_05373	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	274
C8VEQ4_EMENI	unreviewed	Uncharacterized protein	ANIA_08537	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	568
Q5AT07_EMENI	unreviewed	Uncharacterized protein	AN8573.2 ANIA_08573	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	377
Q5B3L4_EMENI	unreviewed	Uncharacterized protein	AN4866.2 ANIA_04866	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	439
Q5AS91_EMENI	unreviewed	Uncharacterized protein	AN8839.2 ANIA_08839	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	801
C8V7Q1_EMENI	unreviewed	Uncharacterized protein	ANIA_10575	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	113
C8V8T2_EMENI	unreviewed	Uncharacterized protein	ANIA_04410	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	278
Q5ASJ2_EMENI	unreviewed	Uncharacterized protein	AN8738.2 ANIA_08738	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	230
Q5B2Z1_EMENI	unreviewed	Uncharacterized protein	AN5089.2 ANIA_05089	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	204
Q5B3L0_EMENI	unreviewed	Uncharacterized protein	AN4870.2 ANIA_04870	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	180
Q5B3Y5_EMENI	unreviewed	Uncharacterized protein	AN4745.2 ANIA_04745	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	665
C8VAN2_EMENI	unreviewed	Uncharacterized protein	ANIA_04786	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
C8V7Z8_EMENI	unreviewed	Uncharacterized protein	ANIA_10625	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	486
Q5B555_EMENI	unreviewed	Uncharacterized protein	AN4325.2 ANIA_04325	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	185
Q5B320_EMENI	unreviewed	Uncharacterized protein	AN5060.2 ANIA_05060	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	343
C8VA67_EMENI	unreviewed	Uncharacterized protein	ANIA_10603	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	815
Q5B378_EMENI	unreviewed	Uncharacterized protein	AN5002.2 ANIA_05002	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	122
Q5B488_EMENI	unreviewed	Uncharacterized protein	AN4642.2 ANIA_04642	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	427
C8V8Q2_EMENI	unreviewed	Uncharacterized protein	ANIA_11438	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	93
C8VAQ3_EMENI	unreviewed	Uncharacterized protein	ANIA_04768	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	588
Q5AS97_EMENI	unreviewed	Uncharacterized protein	AN8833.2 ANIA_08833	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	372
Q5B516_EMENI	unreviewed	Uncharacterized protein	AN4364.2 ANIA_04364	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	405
Q5B381_EMENI	unreviewed	Uncharacterized protein	AN4999.2 ANIA_04999	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	139
C8V9S1_EMENI	unreviewed	Uncharacterized protein	ANIA_11119	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	399
C8VGV3_EMENI	unreviewed	Uncharacterized protein	ANIA_05324	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
C8VE39_EMENI	unreviewed	Uncharacterized protein	ANIA_08346	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	442
C8VFI3_EMENI	unreviewed	Uncharacterized protein	ANIA_05756	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	139
Q5AR81_EMENI	unreviewed	Uncharacterized protein	AN9199.2 ANIA_09199	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	493
C8VJ69_EMENI	unreviewed	Uncharacterized protein	ANIA_02912	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	136
Q5ARK4_EMENI	unreviewed	Uncharacterized protein	AN9076.2 ANIA_09076	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	352
Q5B1U1_EMENI	unreviewed	Uncharacterized protein	AN5489.2 ANIA_05489	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	390
Q5B9I4_EMENI	unreviewed	Uncharacterized protein	AN2796.2 ANIA_02796	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	686
C8VJ38_EMENI	unreviewed	Uncharacterized protein	ANIA_02943	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	448
Q5B9U5_EMENI	unreviewed	Uncharacterized protein	AN2685.2 ANIA_02685	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	90
G5EB48_EMENI	unreviewed	Uncharacterized protein	AN3075.2 ANIA_03075	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	637
Q5B869_EMENI	unreviewed	Uncharacterized protein	AN3261.2 ANIA_03261	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	524
Q5AT57_EMENI	unreviewed	Uncharacterized protein	AN8523.2 ANIA_08523	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	385
Q5B7Y2_EMENI	unreviewed	Uncharacterized protein	AN3348.2 ANIA_03348	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	381
Q5ARE9_EMENI	unreviewed	Uncharacterized protein	AN9131.2 ANIA_09131	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	408
Q5ATF3_EMENI	unreviewed	Uncharacterized protein	AN8427.2 ANIA_08427	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	198
Q5B2Q9_EMENI	unreviewed	Uncharacterized protein	AN5171.2 ANIA_05171	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	146
Q5B2R7_EMENI	unreviewed	Uncharacterized protein	AN5163.2 ANIA_05163	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	628
Q5B8Q2_EMENI	unreviewed	Uncharacterized protein	AN3078.2 ANIA_03078	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	136
C8VHH7_EMENI	unreviewed	Uncharacterized protein	ANIA_11356	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	97
G5EB00_EMENI	unreviewed	Uncharacterized protein	azgA AN8534.2 ANIA_08534	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	580
Q5B2H6_EMENI	unreviewed	Uncharacterized protein	AN5254.2 ANIA_05254	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1010
C8VGR8_EMENI	unreviewed	Uncharacterized protein	ANIA_11476	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	54
Q5B1K0_EMENI	unreviewed	Uncharacterized protein	AN5580.2 ANIA_05580	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	309
Q5B1J8_EMENI	unreviewed	Uncharacterized protein	AN5582.2 ANIA_05582	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	257
Q5ATQ9_EMENI	unreviewed	Uncharacterized protein	AN8321.2 ANIA_08321	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	153
C8VEH4_EMENI	unreviewed	Uncharacterized protein	ANIA_08462	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	285
Q5B2K5_EMENI	unreviewed	Uncharacterized protein	AN5225.2 ANIA_05225	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	699
C8VF10_EMENI	unreviewed	Uncharacterized protein	ANIA_05144	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	700
Q5AQF7_EMENI	unreviewed	Uncharacterized protein	AN9473.2 ANIA_09473	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	566
Q5B2N9_EMENI	unreviewed	Uncharacterized protein	AN5191.2 ANIA_05191	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	376
Q5B943_EMENI	unreviewed	Uncharacterized protein	AN2937.2 ANIA_02937	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	519
Q5ATE1_EMENI	unreviewed	Uncharacterized protein	AN8439.2 ANIA_08439	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	216
C8VGW6_EMENI	unreviewed	Uncharacterized protein	ANIA_11475	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	59
G5EB84_EMENI	unreviewed	Uncharacterized protein	esdC AN9121.2 ANIA_09121	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	266
Q5AQC9_EMENI	unreviewed	Uncharacterized protein	AN9501.2 ANIA_09501	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	434
C8VFP6_EMENI	unreviewed	Uncharacterized protein	ANIA_11489	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	23
C8V9Z5_EMENI	unreviewed	Uncharacterized protein	ANIA_11115	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	427
Q5AQF4_EMENI	unreviewed	Uncharacterized protein	AN9476.2 ANIA_09476	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	194
C8VG45_EMENI	unreviewed	Uncharacterized protein	ANIA_10694	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	623

Q5AR93_EMENI	unreviewed	Uncharacterized protein	AN9187.2 ANIA_09187	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	747
C8VGZ6_EMENI	unreviewed	Uncharacterized protein	ANIA_10657	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	550
Q5B200_EMENI	unreviewed	Uncharacterized protein	AN5430.2 ANIA_05430	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	440
Q5B2W3_EMENI	unreviewed	Uncharacterized protein	AN5117.2 ANIA_05117	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	176
Q5B109_EMENI	unreviewed	Uncharacterized protein	AN5771.2 ANIA_05771	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	158
C8VFE8_EMENI	unreviewed	Uncharacterized protein	ANIA_10717	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	78
Q5B258_EMENI	unreviewed	Uncharacterized protein	AN5372.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	348
G5EB24_EMENI	unreviewed	Uncharacterized protein	AN5356.2 ANIA_05356	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	326
Q5B1Y5_EMENI	unreviewed	Uncharacterized protein	AN5445.2 ANIA_05445	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	200
Q5B255_EMENI	unreviewed	Uncharacterized protein	AN5375.2 ANIA_05375	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	317
Q5B7N8_EMENI	unreviewed	Uncharacterized protein	AN3442.2 ANIA_03442	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	514
C8VMG4_EMENI	unreviewed	Uncharacterized protein	ANIA_10196	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	404
Q5ARK7_EMENI	unreviewed	Uncharacterized protein	AN9073.2 ANIA_09073	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	150
C8VJ14_EMENI	unreviewed	Uncharacterized protein	ANIA_10370	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	411
Q5BCP3_EMENI	unreviewed	Uncharacterized protein	AN1687.2 ANIA_01687	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	149
Q5BDG3_EMENI	unreviewed	Uncharacterized protein	AN1417.2 ANIA_01417	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	222
Q5B8C4_EMENI	unreviewed	Uncharacterized protein	AN3206.2 ANIA_03206	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	575
C8VIN5_EMENI	unreviewed	Uncharacterized protein	ANIA_03087	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	581
G5EAZ8_EMENI	unreviewed	Uncharacterized protein	AN2944.2 ANIA_02944	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	739
C8VKD3_EMENI	unreviewed	Uncharacterized protein	ANIA_02686	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	94
Q5B9I6_EMENI	unreviewed	Uncharacterized protein	AN2794.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	555
Q5B8I8_EMENI	unreviewed	Uncharacterized protein	AN3142.2 ANIA_03142	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	631
C8VJ68_EMENI	unreviewed	Uncharacterized protein	ANIA_02913	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	267
Q5B9Q1_EMENI	unreviewed	Uncharacterized protein	AN2729.2 ANIA_02729	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	465
Q5BA00_EMENI	unreviewed	Uncharacterized protein	AN2630.2 ANIA_02630	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	141
Q5B9T8_EMENI	unreviewed	Uncharacterized protein	AN2692.2 ANIA_02692	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	505
Q5BC28_EMENI	unreviewed	Uncharacterized protein	AN1902.2 ANIA_01902	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	574
Q5AR96_EMENI	unreviewed	Uncharacterized protein	AN9184.2 ANIA_09184	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	531
Q5BAP0_EMENI	unreviewed	Uncharacterized protein	AN2390.2 ANIA_02390	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	341
Q5B924_EMENI	unreviewed	Uncharacterized protein	AN2956.2 ANIA_02956	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	654
Q5ARV3_EMENI	unreviewed	Uncharacterized protein	AN8977.2 ANIA_08977	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
Q5B8Q4_EMENI	unreviewed	Uncharacterized protein	AN3076.2 ANIA_03076	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	149
C8VJI8_EMENI	unreviewed	Uncharacterized protein	ANIA_02809	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	299
Q5B803_EMENI	unreviewed	Uncharacterized protein	AN3327.2 ANIA_03327	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	353
C8VEC1_EMENI	unreviewed	Uncharacterized protein	ANIA_11609	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	81
Q5B8I5_EMENI	unreviewed	Uncharacterized protein	AN3145.2 ANIA_03145	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	573
C8VFU6_EMENI	unreviewed	Uncharacterized protein	ANIA_05650	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	489
C8VHW7_EMENI	unreviewed	Uncharacterized protein	ANIA_11387	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	70
Q5B7V1_EMENI	unreviewed	Uncharacterized protein	AN3379.2 ANIA_03379	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	442
Q5B822_EMENI	unreviewed	Uncharacterized protein	AN3308.2 ANIA_03308	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	552
Q5AT32_EMENI	unreviewed	Uncharacterized protein	AN8548.2 ANIA_08548	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	370
Q5B2F4_EMENI	unreviewed	Uncharacterized protein	AN5276.2 ANIA_05276	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	492
Q5B7S1_EMENI	unreviewed	Uncharacterized protein	AN3409.2 ANIA_03409	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	287
Q5B9Q0_EMENI	unreviewed	Uncharacterized protein	AN2730.2 ANIA_02730	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	827
Q5B7T3_EMENI	unreviewed	Uncharacterized protein	AN3397.2 ANIA_03397	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	461
Q5B879_EMENI	unreviewed	Uncharacterized protein	AN3251.2 ANIA_03251	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	306
Q5ARB3_EMENI	unreviewed	Uncharacterized protein	AN9167.2 ANIA_09167	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	358
Q5B989_EMENI	unreviewed	Uncharacterized protein	AN2891.2 ANIA_02891	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	250
Q5B9A5_EMENI	unreviewed	Uncharacterized protein	AN2875.2 ANIA_02875	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	360
Q5B9X0_EMENI	unreviewed	Uncharacterized protein	AN2660.2 ANIA_02660	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	505
Q5AR64_EMENI	unreviewed	Uncharacterized protein	AN9216.2 ANIA_09216	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	567
C8VHE1_EMENI	unreviewed	Uncharacterized protein	ANIA_02659	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	834
Q5B1J1_EMENI	unreviewed	Uncharacterized protein	AN5589.2 ANIA_05589	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	567
C8VHI2_EMENI	unreviewed	Uncharacterized protein	ANIA_10329	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
C8VNW6_EMENI	unreviewed	Uncharacterized protein	ANIA_01716	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	311
C8VM32_EMENI	unreviewed	Uncharacterized protein	ANIA_11301	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	58
C8VEU8_EMENI	unreviewed	Uncharacterized protein	ANIA_11623	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	89
Q5B8B7_EMENI	unreviewed	Uncharacterized protein	AN3213.2 ANIA_03213	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	354
Q5B9D7_EMENI	unreviewed	Uncharacterized protein	AN2843.2 ANIA_02843	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	143
Q5AQH3_EMENI	unreviewed	Uncharacterized protein	AN9457.2 ANIA_09457	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	486
C8VK54_EMENI	unreviewed	Uncharacterized protein	ANIA_11181	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1118
C8VHG1_EMENI	unreviewed	Uncharacterized protein	ANIA_10332	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	461
Q5B8Z1_EMENI	unreviewed	Uncharacterized protein	AN2989.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	118
Q5BAC8_EMENI	unreviewed	Uncharacterized protein	AN2502.2 ANIA_02502	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	227
C8VLD0_EMENI	unreviewed	Uncharacterized protein	ANIA_10252	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	148
Q5BCX5_EMENI	unreviewed	Uncharacterized protein	AN1605.2 ANIA_01605	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	344
C8VM03_EMENI	unreviewed	Uncharacterized protein	ANIA_11867	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	601
Q5BDA9_EMENI	unreviewed	Uncharacterized protein	AN1471.2 ANIA_01471	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	121
Q5BD60_EMENI	unreviewed	Uncharacterized protein	AN1520.2 ANIA_01520	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	538
Q5AS03_EMENI	unreviewed	Uncharacterized protein	AN8927.2 ANIA_08927	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	355
Q5BBE6_EMENI	unreviewed	Uncharacterized protein	AN2134.2 ANIA_02134	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	397
Q5BA42_EMENI	unreviewed	Uncharacterized protein	AN2588.2 ANIA_02588	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	448
Q5BDE1_EMENI	unreviewed	Uncharacterized protein	AN1439.2 ANIA_01439	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	107

C8VPW9_EMENI	unreviewed	Uncharacterized protein	ANIA_10327	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	431
Q5BC64_EMENI	unreviewed	Uncharacterized protein	AN1866.2 ANIA_01866	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
Q5BBB6_EMENI	unreviewed	Uncharacterized protein	AN2164.2 ANIA_02164	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1034
Q5BAE2_EMENI	unreviewed	Uncharacterized protein	AN2488.2 ANIA_02488	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	173
Q5B8D7_EMENI	unreviewed	Uncharacterized protein	AN3193.2 ANIA_03193	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
Q5B996_EMENI	unreviewed	Uncharacterized protein	AN2884.2 ANIA_02884	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	525
Q5BAW1_EMENI	unreviewed	Uncharacterized protein	AN2319.2 ANIA_02319	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	298
C8VMB6_EMENI	unreviewed	Uncharacterized protein	ANIA_10268	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	447
Q5BA48_EMENI	unreviewed	Uncharacterized protein	AN2582.2 ANIA_02582	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	441
Q5BA56_EMENI	unreviewed	Uncharacterized protein	AN2574.2 ANIA_02574	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
C8VLC3_EMENI	unreviewed	Uncharacterized protein	ANIA_11321	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	87
Q5BBA9_EMENI	unreviewed	Uncharacterized protein	AN2171.2 ANIA_02171	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	199
C8VKQ7_EMENI	unreviewed	Uncharacterized protein	ANIA_09041	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	295
Q5BBH9_EMENI	unreviewed	Uncharacterized protein	AN2101.2 ANIA_02101	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1010
Q5BCY4_EMENI	unreviewed	Uncharacterized protein	AN1596.2 ANIA_01596	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	333
Q5B981_EMENI	unreviewed	Uncharacterized protein	AN2899.2 ANIA_02899	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	495
Q5B9G2_EMENI	unreviewed	Uncharacterized protein	AN2818.2 ANIA_02818	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	679
Q5BC20_EMENI	unreviewed	Uncharacterized protein	AN1910.2 ANIA_01910	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	290
Q5BC50_EMENI	unreviewed	Uncharacterized protein	AN1880.2 ANIA_01880	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	470
Q5BD07_EMENI	unreviewed	Uncharacterized protein	AN1573.2 ANIA_01573	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	545
C8VKB6_EMENI	unreviewed	Uncharacterized protein	ANIA_02702	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	172
C8VI80_EMENI	unreviewed	Uncharacterized protein	ANIA_03226	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	312
C8VJF6_EMENI	unreviewed	Uncharacterized protein	ANIA_10372	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	373
C8VPW7_EMENI	unreviewed	Uncharacterized protein	ANIA_02578	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	266
Q5BB83_EMENI	unreviewed	Uncharacterized protein	AN2197.2 ANIA_02197	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	480
Q5BDD7_EMENI	unreviewed	Uncharacterized protein	AN1443.2 ANIA_01443	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1309
Q5BBX2_EMENI	unreviewed	Uncharacterized protein	AN1958.2 ANIA_01958	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	122
Q5BGB4_EMENI	unreviewed	Uncharacterized protein	AN0416.2 ANIA_00416	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	335
Q5BGM9_EMENI	unreviewed	Uncharacterized protein	AN0301.2 ANIA_00301	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	322
Q5BEQ1_EMENI	unreviewed	Uncharacterized protein	AN0979.2 ANIA_00979	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	733
C8VQU0_EMENI	unreviewed	Uncharacterized protein	ANIA_00789	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	484
Q5BGB8_EMENI	unreviewed	Uncharacterized protein	AN0412.2 ANIA_00412	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	731
Q5AQY5_EMENI	unreviewed	Uncharacterized protein	AN9295.2 ANIA_09295	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	512
C8VUU8_EMENI	unreviewed	Uncharacterized protein	ANIA_00213	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	315
C8VLF5_EMENI	unreviewed	Uncharacterized protein	ANIA_10256	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1311
Q5BC36_EMENI	unreviewed	Uncharacterized protein	AN1894.2 ANIA_01894	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	503
Q5BGJ6_EMENI	unreviewed	Uncharacterized protein	AN0334.2 ANIA_00334	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	395
Q5BFR8_EMENI	unreviewed	Uncharacterized protein	AN0612.2 ANIA_00612	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	216
G5EB11_EMENI	unreviewed	Uncharacterized protein	AN8953.2 ANIA_08953	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	955
Q5BGK6_EMENI	unreviewed	Uncharacterized protein	AN0324.2 ANIA_00324	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	216
G5EB62_EMENI	unreviewed	Uncharacterized protein	fphA AN9008.2 ANIA_09008	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1280
G5EB40_EMENI	unreviewed	Uncharacterized protein	AN2350.2 ANIA_02350	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	685
C8VPL8_EMENI	unreviewed	Uncharacterized protein	ANIA_10318	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	130
Q5ARQ2_EMENI	unreviewed	Uncharacterized protein	AN9028.2 ANIA_09028	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	376
Q5BA81_EMENI	unreviewed	Uncharacterized protein	AN2549.2 ANIA_02549	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	565
Q5BDV5_EMENI	unreviewed	Uncharacterized protein	AN1275.2 ANIA_01275	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	233
Q5ARQ6_EMENI	unreviewed	Uncharacterized protein	AN9024.2 ANIA_09024	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	281
Q5BAN0_EMENI	unreviewed	Uncharacterized protein	AN2400.2 ANIA_02400	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	341
Q5BGD3_EMENI	unreviewed	Uncharacterized protein	AN0397.2 ANIA_00397	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	115
Q5BGR4_EMENI	unreviewed	Uncharacterized protein	AN0266.2 ANIA_00266	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	475
Q5BBX8_EMENI	unreviewed	Uncharacterized protein	AN1952.2 ANIA_01952	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	163
C8VLI7_EMENI	unreviewed	Uncharacterized protein	ANIA_08924	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	424
G5EB21_EMENI	unreviewed	Uncharacterized protein	AN2270.2 ANIA_02270	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	880
C8VR23_EMENI	unreviewed	Uncharacterized protein	ANIA_10014	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	78
Q5BBG1_EMENI	unreviewed	Uncharacterized protein	AN2119.2 ANIA_02119	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1271
Q5AQA7_EMENI	unreviewed	Uncharacterized protein	AN9523.2 ANIA_09523	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	491
Q5AS07_EMENI	unreviewed	Uncharacterized protein	AN8923.2 ANIA_08923	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	793
Q5BB97_EMENI	unreviewed	Uncharacterized protein	AN2183.2 ANIA_02183	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	345
Q5BC13_EMENI	unreviewed	Uncharacterized protein	AN1917.2 ANIA_01917	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	314
G5EB33_EMENI	unreviewed	Uncharacterized protein	AN2037.2 ANIA_02037	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	336
C8VNR6_EMENI	unreviewed	Uncharacterized protein	ANIA_11337	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	97
Q5BD71_EMENI	unreviewed	Uncharacterized protein	AN1509.2 ANIA_01509	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	232
C8VKW2_EMENI	unreviewed	Uncharacterized protein	ANIA_01940	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1192
C8VMY0_EMENI	unreviewed	Uncharacterized protein	ANIA_11306	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	54
Q5BCV8_EMENI	unreviewed	Uncharacterized protein	AN1622.2 ANIA_01622	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	551
Q5BC95_EMENI	unreviewed	Uncharacterized protein	AN1835.2 ANIA_01835	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	428
Q5BDQ0_EMENI	unreviewed	Uncharacterized protein	AN1330.2 ANIA_01330	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	470
C8VRB5_EMENI	unreviewed	Uncharacterized protein	ANIA_10116	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	587
G5EB14_EMENI	unreviewed	Uncharacterized protein	AN8881.2 ANIA_08881	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	326
Q5BBR5_EMENI	unreviewed	Uncharacterized protein	AN2015.2 ANIA_02015	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	503
C8VMB7_EMENI	unreviewed	Uncharacterized protein	ANIA_11329	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	61
C8VS61_EMENI	unreviewed	Uncharacterized protein	ANIA_01320	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	255
Q5BDS6_EMENI	unreviewed	Uncharacterized protein	AN1304.2 ANIA_01304	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	156

Q5BET8_EMENI	unreviewed	Uncharacterized protein	AN0942.2 ANIA_00942	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	386
C8VMC5_EMENI	unreviewed	Uncharacterized protein	ANIA_11304	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	77
Q5BCX2_EMENI	unreviewed	Uncharacterized protein	AN1608.2 ANIA_01608	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	176
Q5BAU2_EMENI	unreviewed	Uncharacterized protein	AN2338.2 ANIA_02338	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	304
Q5ARU4_EMENI	unreviewed	Uncharacterized protein	AN8986.2 ANIA_08986	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	417
C8VSC5_EMENI	unreviewed	Uncharacterized protein	ANIA_11276	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	56
Q5BGL9_EMENI	unreviewed	Uncharacterized protein	AN0311.2 ANIA_00311	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	247
G5EB03_EMENI	unreviewed	Uncharacterized protein	AN2017.2 ANIA_02017	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	992
Q5BBL0_EMENI	unreviewed	Uncharacterized protein	AN2070.2 ANIA_02070	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	652
Q5BE17_EMENI	unreviewed	Uncharacterized protein	AN1213.2 ANIA_01213	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	994
Q5BFZ5_EMENI	unreviewed	Uncharacterized protein	AN0535.2 ANIA_00535	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	191
Q5BGJ8_EMENI	unreviewed	Uncharacterized protein	AN0332.2 ANIA_00332	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	523
Q5BE46_EMENI	unreviewed	Uncharacterized protein	AN1184.2 ANIA_01184	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	445
C8VQ40_EMENI	unreviewed	Uncharacterized protein	ANIA_00169	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	112
C8VTD4_EMENI	unreviewed	Uncharacterized protein	ANIA_01112	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	110
C8VSV8_EMENI	unreviewed	Uncharacterized protein	ANIA_10104	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	544
Q5BGE0_EMENI	unreviewed	Uncharacterized protein	AN0390.2 ANIA_00390	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	287
Q5BFT0_EMENI	unreviewed	Uncharacterized protein	AN0600.2 ANIA_00600	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	259
Q5AQQ9_EMENI	unreviewed	Uncharacterized protein	AN9371.2 ANIA_09371	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1630
G5EB20_EMENI	unreviewed	Uncharacterized protein	AN0176.2 ANIA_00176	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	549
C8VRM1_EMENI	unreviewed	Uncharacterized protein	ANIA_01400	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	188
C8VTR9_EMENI	unreviewed	Uncharacterized protein	ANIA_00368	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1054
Q5BGB7_EMENI	unreviewed	Uncharacterized protein	AN0413.2 ANIA_00413	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	281
Q5AQQ0_EMENI	unreviewed	Uncharacterized protein	AN9380.2 ANIA_09380	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	237
Q5BGJ9_EMENI	unreviewed	Uncharacterized protein	AN0331.2 ANIA_00331	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	119
Q5BGY0_EMENI	unreviewed	Uncharacterized protein	AN0200.2 ANIA_00200	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	252
G5EAS5_EMENI	unreviewed	Uncharacterized protein	AN1812.2 ANIA_01812	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	258
C8VS22_EMENI	unreviewed	Uncharacterized protein	ANIA_00633	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	533
Q5BEK3_EMENI	unreviewed	Uncharacterized protein	AN1027.2 ANIA_01027	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	318
Q5BCB3_EMENI	unreviewed	Uncharacterized protein	AN1817.2 ANIA_01817	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	85
C8VT75_EMENI	unreviewed	Uncharacterized protein	ANIA_10090	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	468
Q5BGR7_EMENI	unreviewed	Uncharacterized protein	AN0263.2 ANIA_00263	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	381
Q5BAA8_EMENI	unreviewed	Uncharacterized protein	AN2522.2 ANIA_02522	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	428
C8VRB6_EMENI	unreviewed	Uncharacterized protein	ANIA_00723	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	285
Q5BEB7_EMENI	unreviewed	Uncharacterized protein	AN1113.2 ANIA_01113	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	133
C8VSS5_EMENI	unreviewed	Uncharacterized protein	ANIA_10177	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	112
Q5BE10_EMENI	unreviewed	Uncharacterized protein	AN1220.2 ANIA_01220	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	218
C8VQ42_EMENI	unreviewed	Uncharacterized protein	ANIA_11261	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	74
Q5BFE0_EMENI	unreviewed	Uncharacterized protein	AN0740.2 ANIA_00740	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	479
Q5BEM9_EMENI	unreviewed	Uncharacterized protein	AN1001.2 ANIA_01001	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	728
Q5BC05_EMENI	unreviewed	Uncharacterized protein	AN1925.2 ANIA_01925	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	99
C8VUB9_EMENI	unreviewed	Uncharacterized protein	ANIA_10051	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	47
Q5BGF2_EMENI	unreviewed	Uncharacterized protein	AN0378.2 ANIA_00378	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	279
Q5BGG5_EMENI	unreviewed	Uncharacterized protein	AN0365.2 ANIA_00365	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	133
C8VQV4_EMENI	unreviewed	Uncharacterized protein	ANIA_00777	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	435
Q5BBY2_EMENI	unreviewed	Uncharacterized protein	AN1948.2 ANIA_01948	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1595
Q5BG48_EMENI	unreviewed	Uncharacterized protein	AN0483.2 ANIA_00483	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	115
Q5BDY1_EMENI	unreviewed	Uncharacterized protein	AN1250.2 ANIA_01250	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	622
Q5BBH0_EMENI	unreviewed	Uncharacterized protein	AN2110.2 ANIA_02110	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	399
G5EB53_EMENI	unreviewed	Uncharacterized protein	ganB AN1016.2 ANIA_01016	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	356
C8VQE2_EMENI	unreviewed	Uncharacterized protein	ANIA_00833	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	117
C8VDE0_EMENI	unreviewed	Uncharacterized protein	ANIA_10898	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	466
Q5BFS2_EMENI	unreviewed	Uncharacterized protein	AN0608.2 ANIA_00608	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	443
C8VT01_EMENI	unreviewed	Uncharacterized protein	ANIA_01192	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	231
Q5BE11_EMENI	unreviewed	Uncharacterized protein	AN1219.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	694
C8VQ13_EMENI	unreviewed	Uncharacterized protein	ANIA_00857	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	392
C8VDF5_EMENI	unreviewed	Uncharacterized protein	ANIA_10886	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	371
C8VDD4_EMENI	unreviewed	Uncharacterized protein	ANIA_10896	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	236
Q5AQP1_EMENI	unreviewed	Uncharacterized protein	AN9389.2 ANIA_09389	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	589
Q5BFJ7_EMENI	unreviewed	Uncharacterized protein	AN0683.2 AN9381.2 ANIA_00683 ANIA_0938	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	393
C8VSQ5_EMENI	unreviewed	Uncharacterized protein	ANIA_10168	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	233
C8VT61_EMENI	unreviewed	Uncharacterized protein	ANIA_00468	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	177
Q5AQZ2_EMENI	unreviewed	Uncharacterized protein	AN9288.2 ANIA_09288	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	382
Q5AW78_EMENI	unreviewed	Uncharacterized protein	AN7452.2 ANIA_07452	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	182
Q5BGE1_EMENI	unreviewed	Uncharacterized protein	AN0389.2 ANIA_00389	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	308
C8VTX4_EMENI	unreviewed	Uncharacterized protein	ANIA_11288	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	19
Q5BF13_EMENI	unreviewed	Uncharacterized protein	AN0867.2 ANIA_00867	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	366
Q5AVQ8_EMENI	unreviewed	Uncharacterized protein	AN7622.2 ANIA_07622	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	494
C8VDK7_EMENI	unreviewed	Uncharacterized protein	ANIA_11019	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	223
Q5AW00_EMENI	unreviewed	Uncharacterized protein	AN7530.2 ANIA_07530	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	219
C8VUM8_EMENI	unreviewed	Uncharacterized protein	ANIA_10045	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	247
Q5BDM4_EMENI	unreviewed	Uncharacterized protein	AN1356.2 ANIA_01356	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	415
Q5BED2_EMENI	unreviewed	Uncharacterized protein	AN1098.2 ANIA_01098	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	79

C8VBW6_EMENI	unreviewed	Uncharacterized protein	ANIA_10974	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	329
G5EB36_EMENI	unreviewed	Uncharacterized protein	AN0689.2 ANIA_00689	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	867
C8VDU3_EMENI	unreviewed	Uncharacterized protein	ANIA_07819	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	389
Q5AW76_EMENI	unreviewed	Uncharacterized protein	AN7454.2 ANIA_07454	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	641
Q5AXJ6_EMENI	unreviewed	Uncharacterized protein	AN6984.2 ANIA_06984	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	198
Q5BE16_EMENI	unreviewed	Uncharacterized protein	AN1214.2 ANIA_01214	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	116
Q5BGR6_EMENI	unreviewed	Uncharacterized protein	AN0264.2 ANIA_00264	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	235
Q5AX70_EMENI	unreviewed	Uncharacterized protein	AN7110.2 ANIA_07110	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	190
Q5AQI0_EMENI	unreviewed	Uncharacterized protein	AN9450.2 ANIA_09450	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	193
Q5BGC5_EMENI	unreviewed	Uncharacterized protein	AN0405.2 ANIA_00405	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	143
C8VCU4_EMENI	unreviewed	Uncharacterized protein	ANIA_07266	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	61
Q5BEW1_EMENI	unreviewed	Uncharacterized protein	AN0919.2 ANIA_00919	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	458
Q5BF60_EMENI	unreviewed	Uncharacterized protein	AN0820.2 ANIA_00820	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	78
Q5BFK3_EMENI	unreviewed	Uncharacterized protein	AN0677.2 ANIA_00677	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	72
G5EAY2_EMENI	unreviewed	Uncharacterized protein	AN0732.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	614
G5EAY9_EMENI	unreviewed	Uncharacterized protein	AN1379.2 ANIA_01379	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	362
Q5AV82_EMENI	unreviewed	Uncharacterized protein	AN7798.2 ANIA_07798	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	463
C8VBJ7_EMENI	unreviewed	Uncharacterized protein	ANIA_10945	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	289
Q5AVL3_EMENI	unreviewed	Uncharacterized protein	AN7667.2 ANIA_07667	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	512
C8VD76_EMENI	unreviewed	Uncharacterized protein	ANIA_07149	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	438
Q5ASP7_EMENI	unreviewed	Uncharacterized protein	AN8683.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	801
C8VBL4_EMENI	unreviewed	Uncharacterized protein	ANIA_10960	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	395
C8VBM9_EMENI	unreviewed	Uncharacterized protein	ANIA_07543	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	416
Q5AVZ5_EMENI	unreviewed	Uncharacterized protein	AN7535.2 ANIA_07535	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	479
C8VBZ8_EMENI	unreviewed	Uncharacterized protein	ANIA_11570	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	52
Q5AXC8_EMENI	unreviewed	Uncharacterized protein	AN7052.2 ANIA_07052	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	321
Q5AWQ7_EMENI	unreviewed	Uncharacterized protein	AN7273.2 ANIA_07273	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	259
C8VDN4_EMENI	unreviewed	Uncharacterized protein	ANIA_07765	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	174
Q5AW21_EMENI	unreviewed	Uncharacterized protein	AN7509.2 ANIA_07509	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	269
Q5AV95_EMENI	unreviewed	Uncharacterized protein	AN7785.2 ANIA_07785	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	364
Q5AWT3_EMENI	unreviewed	Uncharacterized protein	AN7247.2 ANIA_07247	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	292
C8VBZ7_EMENI	unreviewed	Uncharacterized protein	ANIA_10977	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	126
Q5AVI1_EMENI	unreviewed	Uncharacterized protein	AN7699.2 ANIA_07699	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	395
C8VBT4_EMENI	unreviewed	Uncharacterized protein	ANIA_07592	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	913
C8VCU1_EMENI	unreviewed	Uncharacterized protein	ANIA_07269	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	474
Q5AX18_EMENI	unreviewed	Uncharacterized protein	AN7162.2 ANIA_07162	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	241
Q5AWE7_EMENI	unreviewed	Uncharacterized protein	AN7383.2 ANIA_07383	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	505
Q5AW54_EMENI	unreviewed	Uncharacterized protein	AN7476.2 ANIA_07476	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	308
Q5AVG3_EMENI	unreviewed	Uncharacterized protein	AN7717.2 ANIA_07717	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	411
Q5AWU8_EMENI	unreviewed	Uncharacterized protein	AN7232.2 ANIA_07232	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	386
Q5ASQ4_EMENI	unreviewed	Uncharacterized protein	AN8676.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	224
Q5AVY4_EMENI	unreviewed	Uncharacterized protein	AN7546.2 ANIA_07546	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	163
Q5AVU0_EMENI	unreviewed	Uncharacterized protein	AN7590.2 ANIA_07590	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	266
Q5AWX7_EMENI	unreviewed	Uncharacterized protein	AN7203.2 ANIA_07203	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	369
Q5AX59_EMENI	unreviewed	Uncharacterized protein	AN7121.2 ANIA_07121	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	541
Q5AWX2_EMENI	unreviewed	Uncharacterized protein	AN7208.2 ANIA_07208	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	188
Q5AX79_EMENI	unreviewed	Uncharacterized protein	AN7101.2 ANIA_07101	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	289
C8VCL0_EMENI	unreviewed	Uncharacterized protein	ANIA_07341	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	334
C8VCB4_EMENI	unreviewed	Uncharacterized protein	ANIA_10872	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	579
Q5AWI6_EMENI	unreviewed	Uncharacterized protein	AN7344.2 ANIA_07344	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	567
C8VD00_EMENI	unreviewed	Uncharacterized protein	ANIA_10914	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	467
C8VC71_EMENI	unreviewed	Uncharacterized protein	ANIA_07026	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	383
Q5AWE4_EMENI	unreviewed	Uncharacterized protein	AN7386.2 ANIA_07386	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	280
C8VDA2_EMENI	unreviewed	Uncharacterized protein	ANIA_10899	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	249
Q5AQC4_EMENI	unreviewed	Uncharacterized protein	AN9506.2	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	498
Q5AX32_EMENI	unreviewed	Uncharacterized protein	AN7148.2 ANIA_07148	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	162
Q5AXE7_EMENI	unreviewed	Uncharacterized protein	AN7033.2 ANIA_07033	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	294
C8VCM4_EMENI	unreviewed	Uncharacterized protein	ANIA_07329	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	164
Q5AVJ0_EMENI	unreviewed	Uncharacterized protein	AN7690.2 ANIA_07690	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	269
Q5AWV9_EMENI	unreviewed	Uncharacterized protein	AN7221.2 ANIA_07221	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	122
Q5ATW8_EMENI	unreviewed	Uncharacterized protein (cAMP receptor-like protein, putative (AFU_orthologue AFUA_5G04135))	AN8262.2 ANIA_08262	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	404
Q5BCN3_EMENI	unreviewed	Uncharacterized protein (mRNA capping nucleoside-triphosphatase, putative (AFU_orthologue AFUA_4G08510))	AN1697.2 ANIA_01697	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	765
Q5BGB2_EMENI	unreviewed	Uncharacterized protein (Urea transporter (Dur3), putative (AFU_orthologue AFUA_1G04870))	AN0418.2 ANIA_00418	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	693
Q5B069_EMENI	unreviewed	Uncharacterized protein (Usp (Universal stress protein) family protein (Eurofung))	AN6061.2 ANIA_06061	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	439
Q5B738_EMENI	unreviewed	Uncharacterized protein (Vacuolar protein sorting-associated protein 26, putative (AFU_orthologue AFUA_4G12060))	AN3642.2 ANIA_03642	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	347
Q5B8I6_EMENI	unreviewed	Uncharacterized protein (Vacuolar segregation protein (Pep7), putative (AFU_orthologue AFUA_3G13770))	AN3144.2 ANIA_03144	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	675
Q5BDP6_EMENI	unreviewed	Uncharacterized protein (Vacuolar transporter chaperon Vtc1, putative (AFU_orthologue AFUA_1G09540))	AN1334.2 ANIA_01334	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	123
Q5B2R3_EMENI	unreviewed	Uncharacterized protein (von Willebrand and RING finger domain protein (AFU_orthologue AFUA_6G06990))	AN5167.2 ANIA_05167	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1166
Q5B9S9_EMENI	unreviewed	Uncharacterized protein (WD domain, G-beta repeat protein (AFU_orthologue AFUA_5G13970))	AN2701.2 ANIA_02701	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1570
Q5AX03_EMENI	unreviewed	Uncharacterized protein (WW domain protein (AFU_orthologue AFUA_4G03322))	AN7177.2 ANIA_07177	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	231
Q5ARS6_EMENI	unreviewed	Uncharacterized protein (Xenobiotic compound monooxygenase, DszA family, putative (AFU_orthologue AFUA_1G17580))	AN9004.2 ANIA_09004	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	482
Q5BBT4_EMENI	unreviewed	Uncharacterized protein (YagE family protein (AFU_orthologue AFUA_4G10390))	AN1996.2 ANIA_01996	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	655
Y1006_EMENI	reviewed	Uncharacterized protein AN11006	AN11006	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	255

Q5B3R6_EMENI	unreviewed	UPF0016 domain protein, putative (AFU_orthologue AFUA_3G07080) (Uncharacterized protein)	AN4814.2 ANIA_04814	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	516
Q5B7I1_EMENI	unreviewed	UPF0075 domain protein (AFU_orthologue AFUA_4G14600) (Uncharacterized protein)	AN3499.2 ANIA_03499	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	438
Q5BB29_EMENI	unreviewed	UPF0187 domain membrane protein (AFU_orthologue AFUA_5G06660) (Uncharacterized protein)	AN2251.2 ANIA_02251	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	499
VELB_EMENI	reviewed	**Velvet complex subunit B**	velB ANIA_00363	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	369
C8VUB4_EMENI	unreviewed	**WD repeat-containing protein (AFU_orthologue AFUA_1G02990)**	ANIA_00287	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	1089
C8VKG9_EMENI	unreviewed	Xylosidase/arabinosidase, putative (AFU_orthologue AFUA_2G04480)	ANIA_01870	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	344
C8VHJ1_EMENI	unreviewed	ZZ type zinc finger domain protein (AFU_orthologue AFUA_3G05820)	ANIA_10407	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46	800