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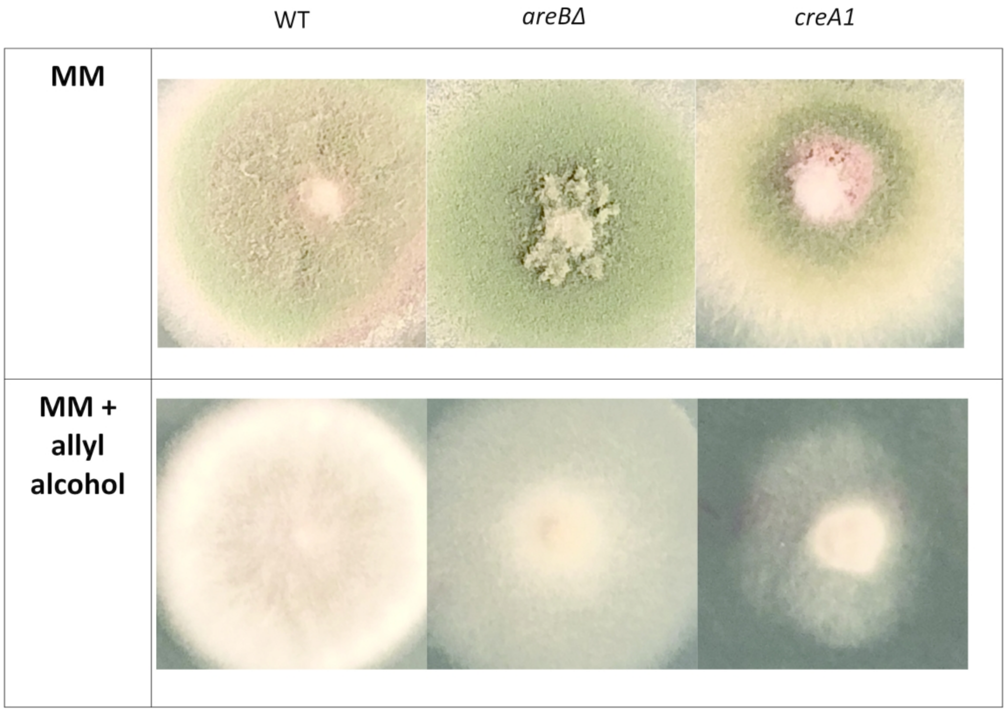

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The role of the GATA transcription factor AreB in regulation of nitrogen and carbon metabolism in *Aspergillus nidulans*.

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Key words

Nitrogen metabolite repression, carbon catabolite repression, RNA-Seq, AreB, AreA, CreA

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Abstract

In *Aspergillus nidulans,* nitrogen and carbon metabolism are under the control of wide-domain regulatory systems, including nitrogen metabolite repression, carbon catabolite repression and the nutrient starvation response. Transcriptomic analysis of the wild type strain grown under different combinations of carbon and nitrogen regimes was performed, to identify differentially regulated genes. Carbon metabolism predominates as the most important regulatory signal but for many genes, both carbon and nitrogen metabolisms coordinate regulation. To identify mechanisms coordinating nitrogen and carbon metabolism, we tested the role of AreB, previously identified as a regulator of genes involved in nitrogen metabolism. Deletion of *areB* has significant phenotypic effects on the utilization of specific carbon sources, confirming its role in the regulation of carbon metabolism. AreB was shown to regulate the expression of *areA*, *tamA, creA, xprG* and *cpcA* regulatory genes suggesting *areB* has a range of indirect, regulatory effects. Different isoforms of AreB are produced as a result of differential splicing and use of two promoters. These are differentially regulated by carbon and nitrogen conditions. These are likely to be functionally distinct and thus contributing to the modulation of AreB activity.

Introduction

Fungi can utilize a wide variety of compounds as a source of carbon and/or nitrogen. Coordinated regulation of carbon and nitrogen metabolism is crucial for a quick adaptation of their physiology in response to the quality and concentration of available nutrients. Generally, these catabolic processes are under the control of two main global regulatory systems, carbon catabolite repression and nitrogen metabolite repression, in addition to pathway specific induction. These general regulatory systems are responsible for a preferential utilization of the most economical source of carbon or nitrogen available, thus enabling fungi to optimally utilize a wide variety of compounds (Kelly & Katz, 2010) (Wong *et al.*, 2008).

In the model filamentous fungus, *Aspergillus nidulans,* carbon catabolite repression is mediated by the transcriptional repressor CreA (Dowzer & Kelly, 1991, Cubero & Scazzocchio, 1994), which also participates in the response to carbon starvation (Katz *et al.*, 2008). Ubiquitination/deubiquitination processes mediated by CreB, CreC and CreD are important in this regulation (Lockington & Kelly, 2002, Boase & Kelly, 2004), although CreA itself is not ubiquitinated (Alam & Kelly, 2017). Response to nutrient stress, like carbon or nitrogen starvation, is also meditated by XprG, the p53-like transcription factor (Katz *et al.*, 2006, Katz *et al.*, 2013).

Nitrogen metabolite repression modulates the expression of genes participating in uptake and catabolism of various nitrogen sources (Arst & Cove, 1973). The respective genes are transcribed only when there is limiting glutamine or ammonium in the environment, with intracellular glutamine levels being a key signal (Morozov *et al.*, 2001). In *A. nidulans*, nitrogen metabolite repression is mediated primarily by the GATA transcriptional activator, AreA (Kudla *et al.*, 1990, Ravagnani *et al.*, 1997). AreA mediates chromatin remodeling, increases histone acetylation and directly stimulates binding of specific transcriptional activators (Muro-Pastor *et al.*, 1999, Berger *et al.*, 2006, Berger *et al.*, 2008). AreA activity is modulated by both posttranscriptional and posttranslational mechanisms, in response to nitrogen source and availability. The stability of the *areA* transcript reflects intracellular glutamine levels, resulting in instability and low levels of the transcription factor under conditions of nitrogen sufficiency (Platt *et al.*, 1996, Morozov *et al.*, 2001). This signaling is mediated by the

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RrmA protein, which regulates the rate of *areA* transcript deadenylation (Morozov *et al.*, 2000, Morozov *et al.*, 2001, Krol *et al.*, 2013). The activity of AreA is also regulated at the protein level by a co-repressor, NmrA, and co-activator TamA. In the presence of ammonium or glutamine NmrA interacts with the zinc finger and the highly conserved C terminus of AreA, repressing its activity (Platt *et al.*, 1996, Andrianopoulos *et al.*, 1998, Lamb *et al.*, 2004, Kotaka *et al.*, 2008). TamA interacts with the same part of AreA and co-activates the expression of target genes (Small *et al.*, 1999, Small *et al.*, 2001, Downes *et al.*, 2014). *nmrA* transcription is partially regulated by the bZIP transcription factor MeaB (Polley & Caddick, 1996). MeaB and AreA coordinately mediate nitrogen metabolite repression, however, they can also function independently (Wong *et al.*, 2007, Wagner *et al.*, 2010). It is interestingly to note that for *meaB* the regulatory role of the antisense transcript was demonstrated (Sibthorp *et al.*, 2013). AreA is evenly distributed in the cell except under nitrogen starvation, when it accumulates in the nucleus. It exits the nucleus when nitrogen is added to the growth medium, or under carbon starvation, and this is mediated by multiple nuclear localization signals (Todd *et al.*, 2005, Hunter *et al.*, 2014).

AreB is the second GATA factor participating in nitrogen metabolite repression in *A. nidulans,* containing an N-terminal GATA type DNA binding domain and C-terminal leucine zipper dimerization domain (Tollervey & Arst, 1982, Conlon *et al.*, 2001). The *areB* gene encodes three protein isoforms, all of which include both the GATA and dimerization domain. These three AreB variants differ at their N-termini, as a result of differential splicing and the utilization of two different promoter regions. The two *areB* promoters are differentially regulated in response to nitrogen regime, and this is probably mediated, at least in part, by GATA factors as GATA elements are present in both *areB* promoters (Conlon *et al.*, 2001). Similarly in, *F. fujikuroi areB* encodes three protein

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isoforms. These differ in their subcellular localization, depending on nitrogen conditions and the longest AreB isoform was shown to interact with AreA in the nucleus under nitrogen starvation (Michielse *et al.*, 2014).

Many AreA target genes have been identified and their regulation characterized (Caddick, 1994). Much less is known about the role of AreB in nitrogen metabolism. *fmdS,* coding for formamidase (Wong *et al.*, 2009), and the arginine catabolism genes, *agaA* and *otaA* (Dzikowska *et al.*, 2003, Macios *et al.*, 2012), were the first AreB target genes identified in *A. nidulans*. In these cases AreB functions as a repressor, however, the resulting regulation is different: in the presence of ammonium AreB represses *agaA* and *otaA* expression while the expression of the *fmdS* gene is repressed by AreB under nitrogen limiting and nitrogen starvation conditions.

In the presence of ammonium, the expression of arginine catabolism genes is also negatively regulated by AreA, which is at variance with most other characterized examples where AreA functions as the activator under nitrogen derepressing conditions. With respect to arginine catabolism, the activity of both AreA and AreB was shown to depend on carbon source: AreA being necessary for the ammonium repression of *agaA* and *otaA* under carbon repressing conditions while AreB is primarily responsible under non-repressing, carbon-limiting conditions. Carbon signaling via AreA and AreB does not depend on the main carbon catabolite repressor CreA (Macios *et al.*, 2012).

In *F. fujikuroi* both GATA factors, AreA and AreB, were shown to function as positive and negative transcriptional regulators, participating not only in regulating nitrogen metabolism but also secondary metabolism (Mihlan *et al.*, 2003, Michielse *et al.*, 2014, Pfannmuller *et al.*, 2017). Nitrogen metabolism is also subjected to transcriptional regulation by CpcA, which mediates cross-pathway control in response to amino acid limitation and stress (Hoffmann *et al.*, 2001, Busch *et al.*, 2003).

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In most cases, carbon and nitrogen regulation are studied separately. In order to define how both carbon and nitrogen conditions influence the expression profile of *A. nidulans* genes, we undertook transcriptomic analysis of the wild type strain grown under different carbon and nitrogen regimes. We tested the role of AreB as a potential global transcription factor linking nitrogen and carbon metabolism and investigated the differential regulation of its isoforms.

Materials and Methods

A. nidulans strains and growth condition

biA1 (wild type), *areBΔ* (*areBΔ::Af-pyrG, (pyrG89), argB2, pabaB22, nkuAΔ::argB, riboB2*) (Macios *et al.*, 2012) and *creA1, paba1* (Shroff *et al.*, 1996) strains were employed. Strains were grown for 10-12 hours in 37˚C in minimal medium, under the following nitrogen and carbon regimes:

- carbon and nitrogen repression (CR/NR), comprised 1% glucose, 10 mM ammonium tartrate (GNH_4)
- carbon and nitrogen derepression (CD/ND), comprised 0.1% fructose, 10 mM urea (FU)
- carbon repression and nitrogen derepression (CR/ND), comprised 1% glucose, 10 mM urea (GU)
- carbon derepression and nitrogen repression (CD/NR), comprised 0.1% fructose,10 mM ammonium tartrate (FNH_4)

Glucose and fructose were filter sterilised and added to the medium after autoclaving. Carbon derepression observed on 0.1% fructose results from the low concentration of the sugar. Growth tests were performed using 5 mM allyl alcohol which was added to the cooled minimal medium.

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To compare the growth of *areBΔ* and the wild type on different carbon sources, conidia of both strains were suspended in 0.25% Phytagel, 0.03% Tween 20 (final concentration 10^4/ml) and grown on FF MicroPlate^{TM} (BIOLOG) microtiter plates, comprising 126 selected carbon sources. This is a standard biology plate used as a fungi identification test panel. Strains were grown at 30°C in VICTOR3™ Multilabel Counter (Perkin Elmer). Turbidity was measured at 650 nm after 40 hours. Three independent biological experiments were performed.

Preparation of RNA-Seq libraries and Illumina HiSeq 2000 sequencing

Total RNA for RNA-Seq was isolated from the wild type strain using mirVana^{TM} miRNA Isolation Kit (Ambion) according to the protocol for total RNA isolation. Ribosomal RNA was depleted with RiboZero Magnetic kit from Epicentre and, additionally, Ribo Minus^{TM} Concentrarion Module (Invitrogen). The success of depletion and sample quality was assessed using an Agilent 2100 Bioanalyzer.

RNA-Seq was performed by the Centre for Genomic Research, The University of Liverpool. RNA–Seq libraries were prepared using the Epicentre ScriptSeq v2 RNA-Seq Library Preparation Kit. 17.5 ng of rRNA-depleted RNA, according to quantification by Bioanalyzer, was used as input and following 10 cycles of amplification, libraries were purified using AMPure XP beads. Each library was quantified using a Qubit fluorimeter and the size distribution assessed using the Bioanalyzer. Libraries were pooled in equimolar amounts, based on the Qubit and Bioanalyzer data. The quantity and quality of each pool was assessed by Bioanalyzer and subsequently by qPCR using the Illumina Library Quantification Kit from Kapa on a Roche Light Cycler LC480II. The pool of libraries was sequenced on one lane of the HiSeq 2000 at 2x100 bp paired-end sequencing with v3 chemistry.

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Bioinformatics and statistical analysis

Paired-end reads were aligned to the *A. nidulans* reference genome sequence A_nidulans_FGSC_A4 version “s09-m04-r07”, downloaded from the *Aspergillus* Genome Database (AspGD) website (http://www.aspergillusgenome.org/). Alignment was done using Tophat v1.3.2 (Trapnell *et al.*, 2009) with default parameters except for those regarding mapping across spliced introns, where the minimum (option ‘-i’) and maximum (option ‘-I’) allowed intron sizes were set to 10 and 4000 nucleotides, respectively.

Mapped reads were filtered to retain only those where both reads of the pair (R1 and R2) aligned in the correct relative orientation. These were used to estimate expression levels for annotated loci by counting fragments (two reads, R1 and R2, represent one fragment of a transcript) mapped to each locus. Fragment counting was done using htseq-count (http://www-huber.embl.de/users/anders/HTSeq/doc/count.html#count). Alignment data is summarized in Supplementary Table 1.

Fragment counts were used to assess differential gene expression, after normalization for library size, using the R package edgeR (Robinson *et al.*, 2010, Robinson & Oshlack, 2010). As there was only one sequence library for each carbon/nitrogen regime (although it consisted of three pooled replicates), normalisation was done using a nominal value of 0.3 for the ‘biological coefficient of variation’ (BCV). Gene expression was regarded as significantly changed if the P-value was <0.05 and the $|FC| > 2$.The data discussed in this publication have been deposited in NCBI’s Gene Expression Omnibus (Edgar *et al.*, 2002) and are accessible through GEO Series accession number GSE115021

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(https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE115021). Gene Ontology (GO) enrichment analysis was performed using the 'GO-term-finder' tool on the AspGD website and protein function annotation was performed using the AspGD (Cerqueira *et al.*, 2013) and FungiDB (http://fungidb.org/fungidb/) (Stajich *et al.*, 2012, Basenko *et al.*, 2018) databases. Venn diagrams were prepared using BioVenn (Hulsen *et al.*, 2008).

RT-qPCR analysis

For RT-qPCR analysis, total RNA was isolated from *areBΔ* and the wild type strains (Schmitt *et al.*, 1990),using the FastPrep®-24 instrument (MP Biomedicals) for mycelium homogenization. RNA was treated with Turbo DNase (Thermo Fisher Scientific). RNA quality and concentration were measured using an RNA Nano chip on Bioanalyzer. cDNA was synthesized using 2 µg of total RNA using SuperScript® III Reverse Transcriptase (Invitrogen, Life Technologies) and a mixture of oligo-dT and random hexamer primers. Real-time RT-PCR was performed using the LightCycler® 480 II System (Roche Diagnostics) with specific primers for *creA*, *tamA, areA, meaB, cpcA, xprG*; or *areBα*, *areBβ*, *areBγ* transcripts (Supplementary Table 2) and LightCycler®480 SYBR Green I Master mix (Roche Laboratories). Three biological replicates were analyzed for both strains with three technical replicates for each. Efficiency (E) and specificity of each pair of primers were tested in RT-qPCR reactions using 6-point standard curves of 5-fold diluted cDNA of the control strain. E-value for all primer pairs used was in the range of 1.89–2.00. Cp values were calculated using LightCycler®480 Software 1.5 (Roche Diagnostics), based on the Second Derivative Maximum Method. Cp values were normalized using 18S rRNA as an endogenous control. Expression levels were compared between the wild type and *areBΔ* strains.

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Results and Discussion

Carbon and nitrogen regulated genes in the wild type strain

To identify genes regulated in response to different carbon and nitrogen regimes, we conducted global transcriptomic analysis of the wild type strain grown under four conditions, combining nitrogen metabolite repression (ammonium as N source) or derepression (urea as N source) with carbon catabolite repression (glucose as C source) or derepression (fructose as C source). This analysis showed that the expression of 3491, out of 10987 annotated *A. nidulans* genes are differentially regulated by carbon (fructose v glucose) and/or nitrogen (urea v ammonium) source, under at least one of the four growth conditions tested (Supplementary Table 3a-d). We identified genes regulated by ammonium under different carbon conditions and/or regulated by glucose under different nitrogen conditions (Fig.1A). 53% (1842) of the differentially regulated genes identified in the wild type responded specifically to changes in the carbon source while 39% (1357) responded to both carbon and nitrogen source. Genes regulated only by nitrogen source represent merely 8% (292) of all differentially regulated genes.

We classified all differentially regulated genes into 34 groups defined by their expression profile, i.e. up or down regulation under specific conditions (Fig.1B). 16 of these groups have at least 10 genes. Supplementary Table 4 comprises a full list of genes in each group.

For several previously characterized genes, these expression profiles correlate well with published data. For example, *ureA* (Abreu *et al.*, 2010)*, mepA* (Monahan *et al.*, 2002)*, agtA* (Apostolaki *et al.*, 2009)*, otaA* (Dzikowska *et al.*, 1999) were all repressed by ammonium*; alcR, alcA* (Fillinger *et al.*, 1995)*, acuG* (Hynes *et al.*, 2007)*, xlnD* (Tamayo *et al.*, 2008) and *creA* (Strauss *et al.*, 1999) were all subject to carbon catabolite repression and *amdS* was repressed by both ammonium and glucose (Hynes, 1994).

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To assess the interdependence of the nitrogen and carbon regulatory mechanisms, we compared the groups of genes repressed or derepressed by ammonium and under the two carbon regimes (Fig. 2 A), and similarly those repressed or derepressed by glucose under the two nitrogen regimes (Fig. 2 B). Results show that for the vast majority of genes, both positive and negative effects of ammonium depend on the carbon regime, with the majority only being observed under carbon derepressing conditions (fructose). Similarly, although to a lesser degree, the effects of glucose depend on nitrogen regime and were observable mainly under nitrogen derepressing conditions (urea).

Functional enrichment analysis was performed for all genes differentially expressed under the four carbon/nitrogen conditions tested. For genes affected by ammonium, the analysis indicated an over representation of genes involved in nitrogen and/or carbon metabolism, amino acids and nucleotides metabolism, ribosome biogenesis and metal ion homeostasis (Supplementary Fig. 1 and Supplementary Table 5a-b). Genes participating in carbon and/or nitrogen metabolism, organic acids and carbohydrate metabolism, ribosome assembly, RNA metabolism and translation are over-represented among glucose regulated genes (Supplementary Fig. 2 and Supplementary Table 5c-d).

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AreB is involved in both nitrogen and carbon regulation

Transcriptomic analysis of the wild type strain showed that nitrogen regulation of several *A. nidulans* genes depends on carbon conditions. As the previously published results suggest that AreB might be involved in the regulation of not only nitrogen but also carbon metabolism (Macios *et al.*, 2012), we utilized growth profiling using the Biolog FF MicroPlate to determine if deletion of *areB* changes the ability of the fungus to utilize different carbon sources. As shown in Figure 3 and supplementary Fig. 3, the growth of the *areBΔ* strain was significantly different from wild type on several carbon sources tested. The mutant strain grew more poorly than wild type on 63 carbon sources tested, with only three exceptions of better growth. The reduced growth of the mutant on several amino acids suggests that AreB might regulate their catabolism, as shown previously for arginine (Macios *et al.*, 2012). Among compounds for which deletion of *areB* most dramatically impaired growth are four tricarboxylic acids from the TCA cycle: α-ketoglutaric, succinic, fumaric and malic acid. Reduced efficiency of the TCA cycle might explain the previously described phenotype of slower growth of *areBΔ* (Wong *et al.*, 2009, Macios *et al.*, 2012). These data confirm that AreB plays an important role in carbon metabolism. It is worth noting that in the plant pathogen, *F. fujikuroi,* analysis of *areB* deletion mutant also showed that AreB is involved in regulation of not only nitrogen, but also carbon and secondary metabolism (Pfannmuller *et al.*, 2017).

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Deletion of *areB* affects the expression of several downstream regulators

To assess the potential role of AreB in the coordination of carbon and nitrogen metabolism we performed the transcriptional analysis of genes coding for key carbon/nitrogen regulators: *areA*, *tamA, meaB, creA*, *xprG* and *cpcA* (Fig. 4B). qPCR analysis was performed using total RNA from mycelia of the *areBΔ* and wild type strains grown under the four carbon/nitrogen regimes used for the transcriptomic analysis. With only one exception, *meaB*, deletion of *areB* results in significant changes in transcript levels (Fig. 4A). These effects depend on carbon/nitrogen conditions and are specific for each gene analyzed. Decreased level of expression in *areBΔ* strain was observed for *areA* (about 0.5 fold under all conditions tested except carbon repressing and nitrogen derepressing conditions)*, tamA* (till 3-fold under carbon and nitrogen derepressing conditions)*, creA* (about 2-fold under carbon derepressing conditions) and *xprG* (about 2-fold under carbon repressing conditions), suggesting a positive regulatory function for

AreB. For *cpcA* its function is negative as deletion of *areB* results in increased level of expression (till 3-fold under carbon and nitrogen repressing conditions). Potential GATA factor binding sites were found in promoter regions of all these five genes (Fig. 4B), suggesting that AreB might directly regulate their transcription.

A strong decrease in *tamA* transcript level in the *areBΔ* strain grown under nitrogen repressing conditions was also shown in *F. fujikuroi* (Pfannmuller *et al.*, 2017), suggesting that AreB might also regulate AreA activity indirectly by modulating the level of its co-activator, TamA. However, it is worth noting, that in a few cases TamA was shown to activate gene expression as a DNA-binding activator (Downes *et al.*, 2014). The activity of *xprG* might be regulated by AreB both directly and indirectly, as *xprG* was proposed to be regulated by CreA (Katz *et al.*, 2008).

Deletion of *areB* results also in increased sensitivity to allyl alcohol, similarly as in the case of the *creA1* mutant (Fig. 4C), what is consistent with decreased level of *creA* transcription in *areBΔ* (Fig. 4A). This *creA* mutation relieves the catabolite repression of several genes, including *alcA,* which codes for catabolic alcohol dehydrogenase converting allyl alcohol to a toxic acrolein (Bailey & Arst, 1975, Shroff *et al.*, 1996). This growth effect doesn't depend on nitrogen source but is not observable under carbon derepressing conditions (on fructose) where derepression of *alcA* results in similar sensitivity also of the wild type.

All these data suggest an important, global regulatory function for AreB which appears to act both positively and negatively. A significant proportion of the regulatory effects are likely to be indirect, as AreB plays a significant role in regulating key wide domain transcriptional factors.

Analysis of areB transcripts

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areB encodes three different protein isoforms which differ at their N-terminus. This results from alternative splicing, the presence of two different promoter regions and three start codons (Fig. 5A) (Conlon *et al.*, 2001). Such variation in a transcript sequence of a specific gene is rather rare in *A. nidulans* (Sibthorp *et al.*, 2013). The longest transcript, *areB*γ, is synthesized after three introns are removed and it can potentially produce two different proteins (AreBγ and/or AreBβ) depending on which start codon is used. Translation from the first AUG would produce AreBβ (320 aa), whereas translation from a highly conserved, non-canonical GUG start codon would result in AreBγ (436 aa), with a unique 116 amino-acid extension at the N terminus. The *areB*β transcript is obtained when only two introns are removed. Retention of the first intron disrupts the ORF of the AreBγ isoform. Consequently, *areB*β mRNA can produce only the AreBβ protein. *areB*α is the shortest *areB* transcript resulting from the selection of an alternative downstream promoter, located within the second intron of the longer transcripts. This transcript includes an alternative AUG start codon which would produce AreBα (312 aa), the shortest version of the protein with a unique 14 amino-acids at the N-terminus.

RT-qPCR analysis was performed to analyze proportions of the three *areB* transcripts under the four carbon/nitrogen regimes used for the transcriptomic analysis. We compared levels of these three transcripts under specific conditions (Fig. 5B) and the levels of each specific transcript under different conditions (Fig. 5C). Under all conditions tested the *areB*γ mRNA is synthesized at the highest level (Fig. 5B). This transcript has a capacity to code for two AreB isoforms, differing at the N terminus that creates an additional possibility of regulation at the level of translational initiation via selection of the standard AUG or the non-canonical GUG start codon.

Only under carbon and nitrogen derepressing conditions (F/U), was the level of *areB*γ and *areB*α mRNA comparable (Fig. 5B). Moreover, under these conditions, the

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expression level of *areB*γ transcript is lowest, while *areB*α transcript levels were similar under all the conditions tested (Fig. 5C). This shows that the differential expression of the three AreB isoforms is regulated by carbon and nitrogen regimes. It is possible that the function of these proteins will differ due to the variation at the N-terminus, as was suggested for AreB isoforms in *F. fujikuroi* (Michielse *et al.*, 2014). Consequently, this variation may have a direct role in the observed differences in AreB functionality under different growth regimes.

Conclusions

Transcriptome analysis of the wild type strain showed that carbon metabolism predominates as the most important regulatory signal but for a large proportion of genes both carbon and nitrogen metabolism coordinates regulation. The nitrogen regime affects the expression of far more genes under carbon derepressing conditions. Genes affected by nitrogen metabolite repression independently of the carbon regime, are relatively rare. Similarly, the effect of carbon was more prevalent under nitrogen derepressing conditions.

AreB is the wide-domain regulator in *A. nidulans*, involved in mediating a regulatory response to changes in both nitrogen and carbon conditions. Although originally considered as a gene involved in regulation of nitrogen metabolism, we have shown that the deletion of *areB* has significant phenotypic effects on carbon utilisation, consistent with a broader role.

AreB positively regulates key regulatory genes mediating nitrogen metabolite repression (*areA, tamA*), carbon catabolite repression (*creA*), response to nutrient starvation (*xprG*), and negatively - *cpcA*, the main regulator of amino acid biosynthesis. Consequently, the regulatory effect of AreB on the transcription is likely

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to be extended by a range of indirect effects mediated by these wide-domain regulators which, in turn, regulate the expression of several pathway specific transcription factor.

We confirmed that the three transcripts encoded by *areB* are differentially regulated in response to carbon and nitrogen regime. We propose that three AreB isoforms differ in their specific functions or activity, contributing to modulation of AreB activity. These results underline the complex interplay between carbon and nitrogen regulation and the potential for the differential use of transcription factors under different regimes.

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Conflict of interest. None declared.

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Figure Legends

Fig.1. Nitrogen and carbon regulated genes in *A. nidulans* wild type strain.

A. Effect of ammonium or glucose on the wild type strain transcriptome under carbon or nitrogen repressing / derepressing conditions, respectively.

Expression of genes under two different carbon/nitrogen conditions was compared. Number of up or down regulated genes is shown. CR - carbon repression; CD - carbon derepression; NR - nitrogen repression; ND - nitrogen derepression. For detailed lists of differentially expressed genes see Supplementary Table 3 a-d.

B. Expression profile codes for groups of genes regulated by nitrogen and/or carbon source in the wild type strain.

Expressions decreased (↓), increased (↑) or not changed (-) in the presence of ammonium or glucose, respectively. GU vs. GNH_4 - effect of ammonium under carbon repressing conditions (glucose as a carbon source); FU vs. FNH_4 - effect of ammonium under carbon derepressing conditions (fructose as a carbon source); FU vs. GU - effect of glucose under nitrogen derepressing conditions (urea as a nitrogen source); FNH_4 vs. GNH_4 - effect of glucose under nitrogen repressing conditions (ammonium as a nitrogen source).

Number of genes in each group is shown. For detailed lists of genes in each group see Supplementary Table 4.

Fig. 2. Effect of ammonium and glucose in the wild type strain grown under different carbon or nitrogen conditions, respectively.

A. Number of genes induced or repressed by ammonium under carbon derepressing (yellow), repressing (pink) or independently on carbon conditions (orange).

B. Number of genes induced or repressed by glucose under nitrogen derepressing (yellow), repressing (pink) or independently on nitrogen conditions (orange)

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Fig.3 Deletion of *areBΔ* influences the growth on several carbon sources.

Growth of *areBΔ* and the wild type strain on glucose, fructose and some other selected carbon sources. Amino acids (in green); tricarboxylic acids from TCA (Krebs) cycle (in blue); compounds utilised by *areBΔ* as a carbon source better than by the wild type (in red). For detailed lists of carbon sources utilised less effectively by *areBΔ* see Supplementary Figure 3.

Fig. 4. Deletion of *areB* influences the expression of the wide-domain regulatory genes *areA*, *tamA, creA, xprG* and *cpcA*.

A. Quantitative transcriptional analysis of *areA*, *tamA, creA, xprG* and *cpcA* in *areB* deletion strain. Relative expression in *areBΔ* mutant in comparison with the control wild type strain was calculated by RT-qPCR analysis. * - P-value<0,1; ** - P-value <0,05; FC - fold change *areBΔ/ wt*.

B. Number of GATA sites in potential promoter regions of *areA*, *tamA, creA, xprG* and *cpcA*. GATA pair was defined as two sites at a distance of less than 30 bp. Potential promoter region was defined as 1kb upstream of ATG for *tamA, creA* and *xprG* or 1,5 kb for *areA* and *cpcA* that comprise much longer 5' UTR.

C. Deletion of *areB* decreases the expression of the CreA, the carbon catabolite repressor. Sensitivity of the wild type, *areBΔ* and *creA1* strains was tested on minimal medium with 10 mM sodium nitrate and 1% glucose (MM) or with other carbon/nitrogen sources, as described in Materials and Methods.

Fig.5. Transcriptional analysis of the *areB* gene under different carbon and nitrogen regimes.

A. Structure of *areB* gene and its three transcripts (based on Conlon et al., 2011). Differential RT- qPCR analysis of *areB* transcripts was performed using primers specific for each mRNA. Introns are marked in red. Amplified fragments, specific for α, β or γ *areB*

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mRNA are marked with blue arrows. Left primer for *areBγ* mRNA amplification is complementary to exon - exon junction in the spliced transcript.

B. Comparison of expression levels of three *areB* transcripts in the wild type strain grown under specific carbon/nitrogen repressing and / or derepressing conditions.

The level of *areBβ* mRNA was arbitrarily set to 1. *- P-value<0,1; **- P-value <0,05

C. Comparison of expression levels of each specific *areB* transcript, in the wild type strain grown under different carbon/nitrogen repressing and / or derepressing conditions.

The level of each mRNA under nitrogen and carbon de-repressing conditions (FU) was arbitrarily set to 1. *- P-value<0,1; **- P-value <0,05. NS - difference not significant.

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Supplementary Fig.1. Functional enrichment analysis for genes affected by ammonium in the wild type strain.

Cluster frequency for groups of genes affected by ammonium under carbon derepressing (A) or repressing (B) conditions. For detailed lists of genes in each cluster see Supplementary Table 5a-b.

Supplementary Fig.2. Functional enrichment analysis for genes affected by glucose in the wild type strain.

Cluster frequency for groups of genes affected by glucose under nitrogen derepressing (A) or repressing (B) conditions. For detailed lists of genes in each cluster see Supplementary Table 5c-d.

Supplementary Fig.3. Results of growth tests on BIOLOG FF MicroPlate^{TM} identification panel for the wild type and *areBΔ* mutant strain.

From carbon sources present on the plate, all these are shown for which the difference in growth between the two strains is at least 25%. Compounds utilised by *areBΔ* as a carbon source better than by the wild type (in red); amino acids (in green); tricarboxylic acids from TCA (Krebs) cycle (in blue).

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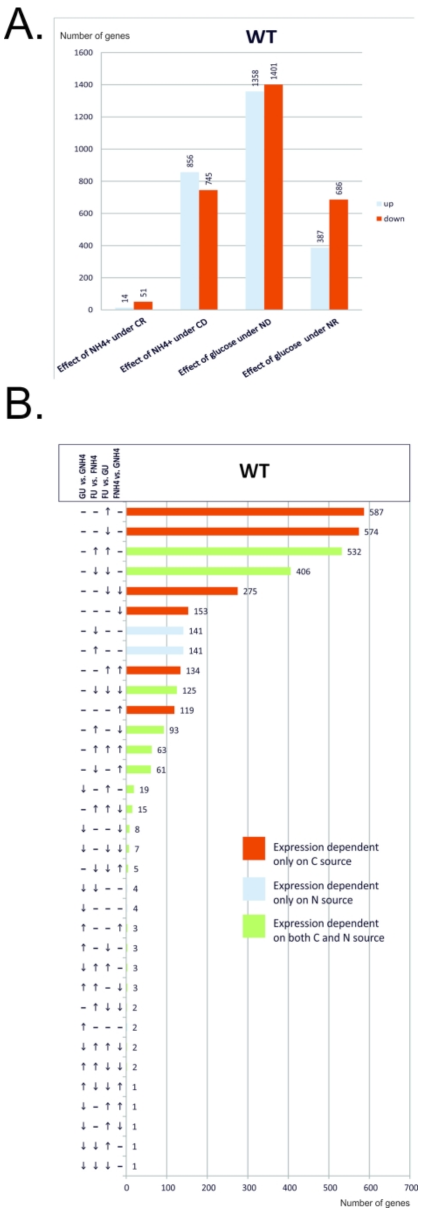

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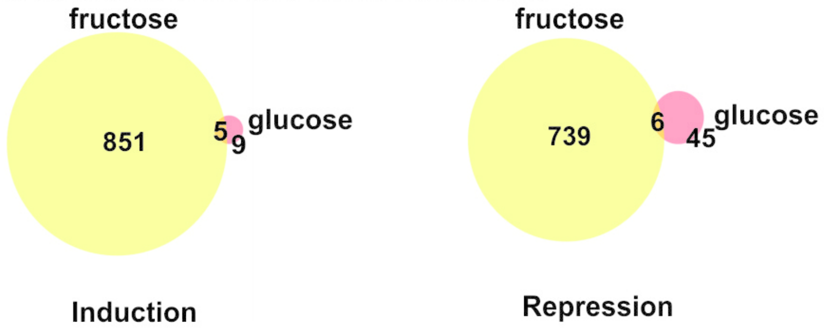
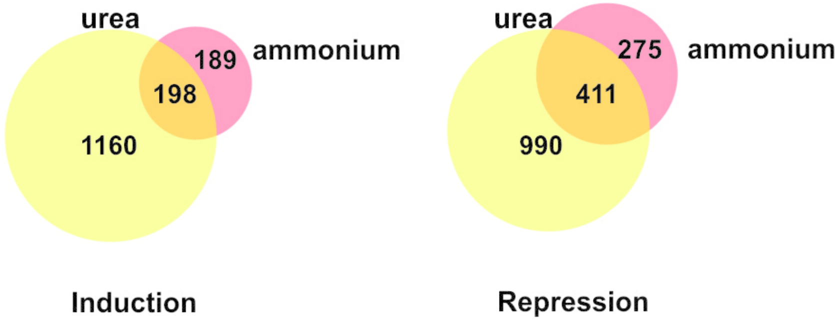
A. Effect of ammonium under different carbon conditions



B. Effect of glucose under diferent nitrogen conditions.



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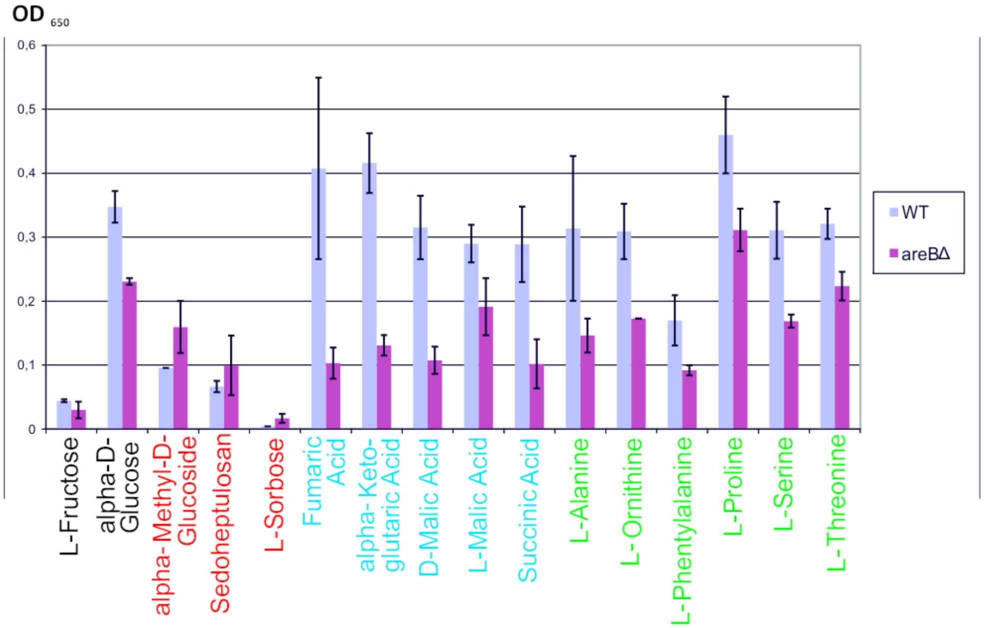

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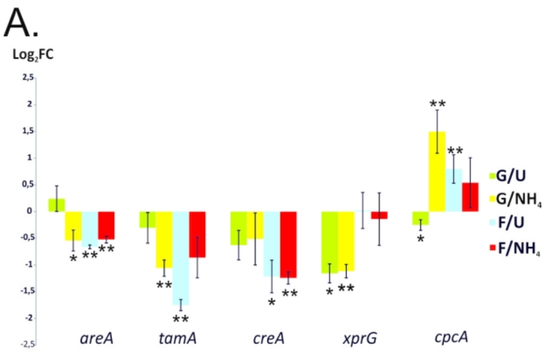
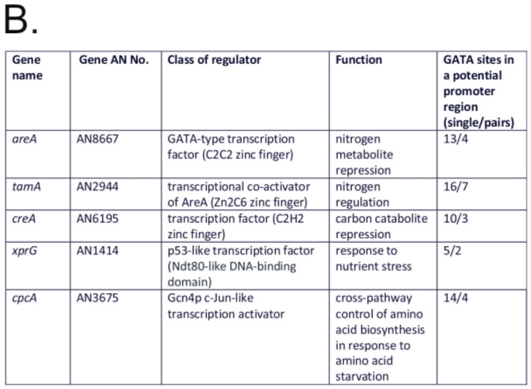
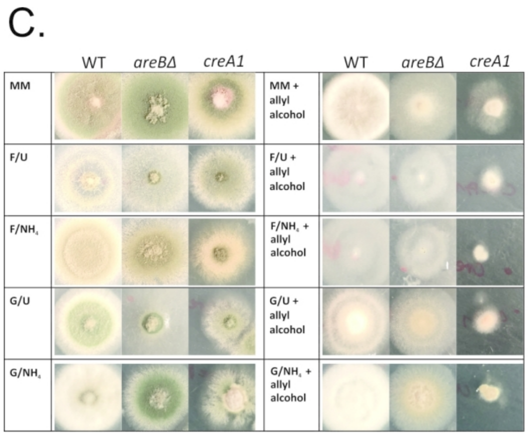




Gene name	**Gene AN No.**	**Class of regulator**	**Function**	**GATA sites in a potential promoter region (single/pairs)**
areA	AN8667	GATA-type transcription factor (C2C2 zinc finger)	nitrogen metabolite repression	13/4
tamA	AN2944	transcriptional co-activator of AreA (Zn2C6 zinc finger)	nitrogen regulation	16/7
creA	AN6195	transcription factor (C2H2 zinc finger)	carbon catabolite repression	10/3
xprG	AN1414	p53-like transcription factor (Ndt80-like DNA-binding domain)	response to nutrient stress	5/2
cpcA	AN3675	Gcn4p c-Jun-like transcription activator	cross-pathway control of amino acid biosynthesis in response to amino acid starvation	14/4



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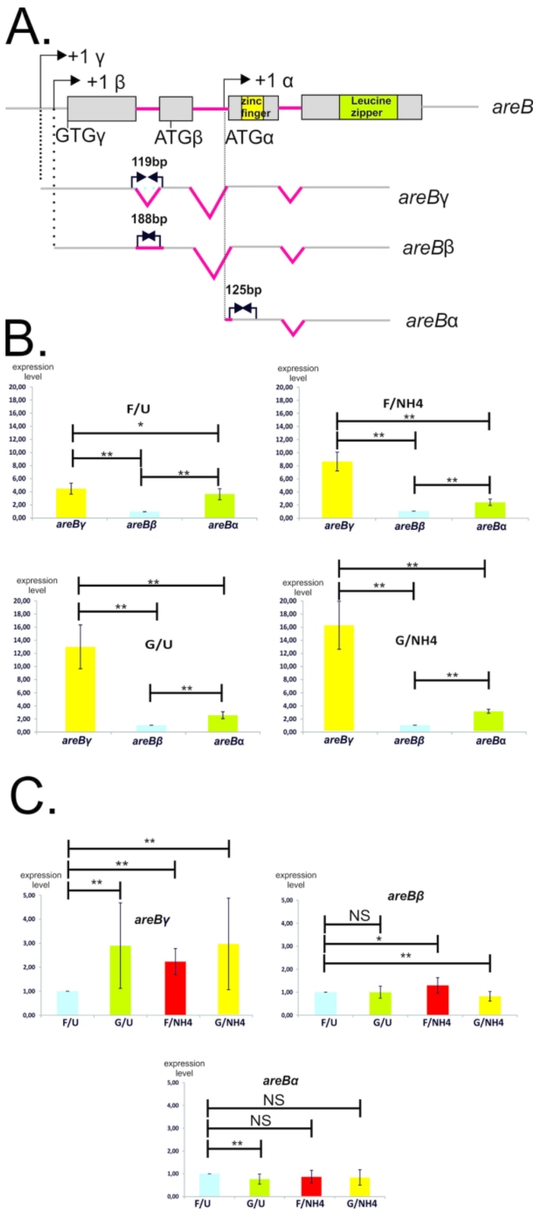

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Chudzicka-Orrmaniec et al. - Supplementary files information

Supplementary Fig.1. - diagram showing results of the functional enrichment analysis for genes affected by ammonium in the wild type strain.

Supplementary Fig.2. - diagram showing results of the functional enrichment analysis for genes affected by glucose in the wild type strain.

Supplementary Fig.3. - extended data set for growth tests on BIOLOG FF MicroPlate^{TM} identification panel for the wild type and *areBΔ* mutant strain.

Supplementary Table 1 - alignment summary data for RNA-Seq analysis

Supplementary Table 2 - primer sequences

Supplementary Table 3 (a-d) - complete results for differential gene expression analysis

Supplementary Table 4 - complete lists of genes in groups differentially regulated by carbon and nitrogen

Supplementary Table 5 - complete lists of genes in groups selected after functional enrichment analysis.

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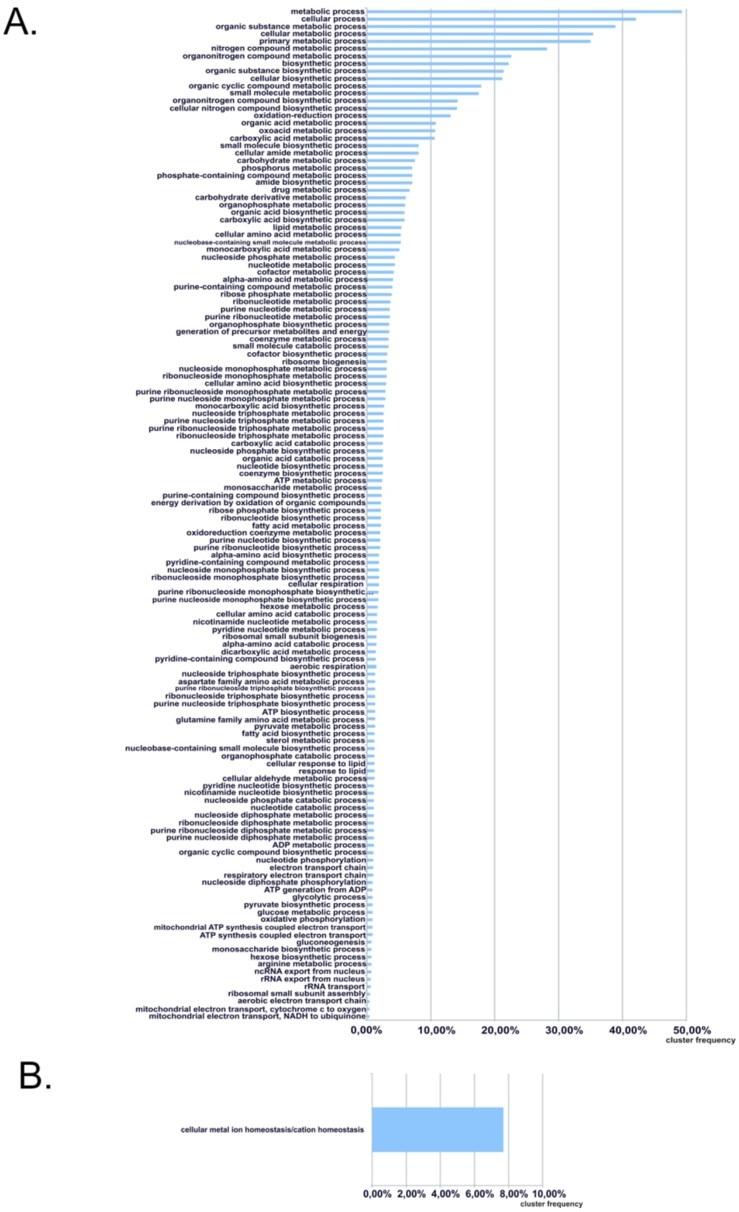

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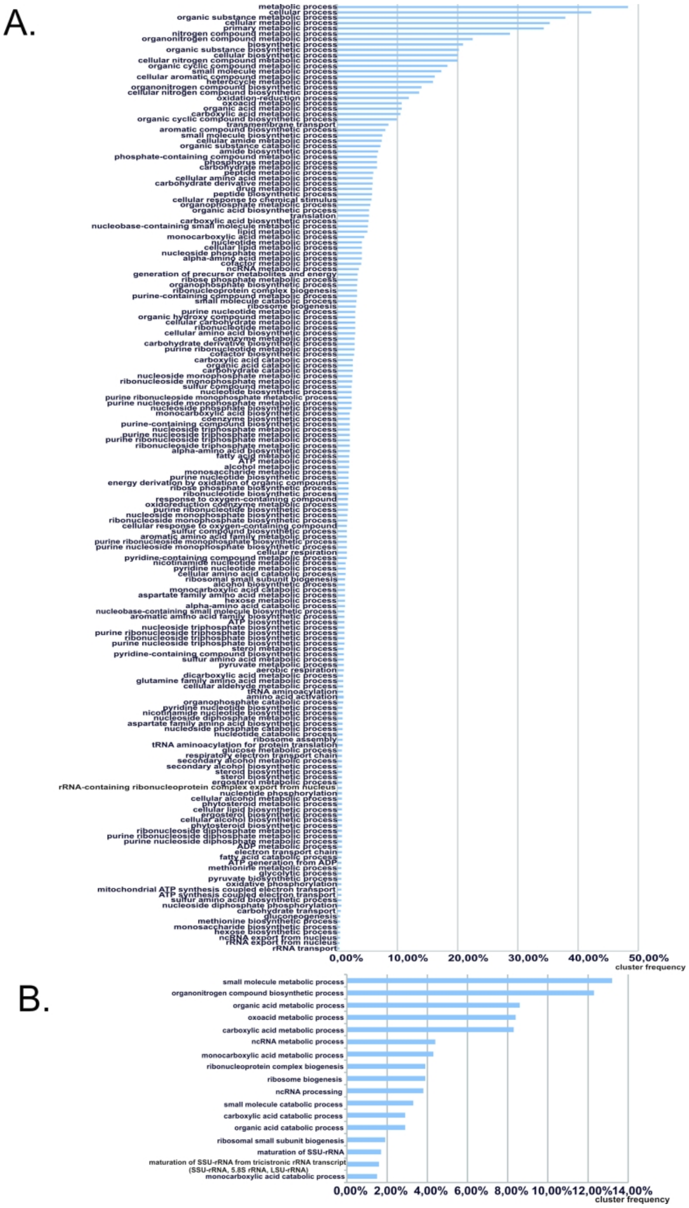

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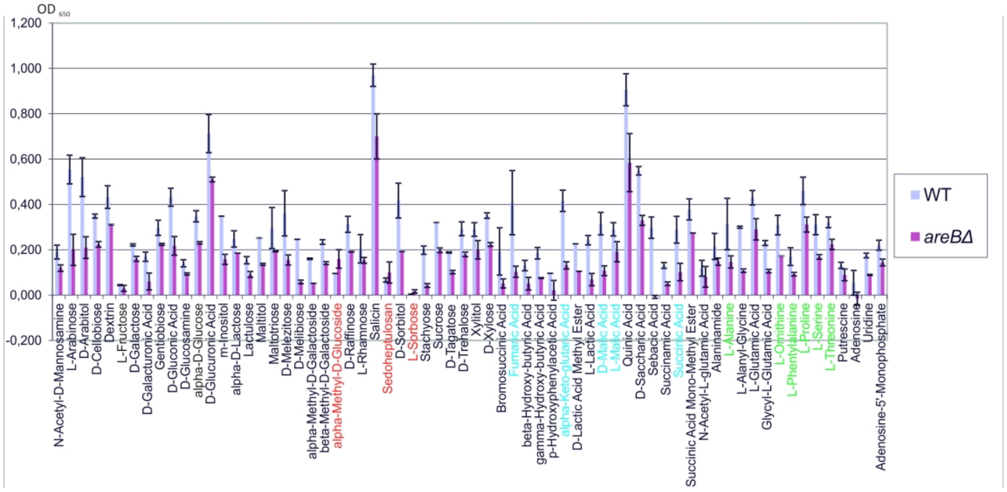

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Sample (conditions)	Total R1 reads	Total R2 reads	Mapped R1 reads	Mapped R2 reads	Both Mates Mapped	Singletons
WT (CD/NR)	18438502	18438502	1477194 (8.01%)	1390158 (7.54%)	2304714 (6.25%)	562638 (1.53%)
WT (CD/ND)	23667805	23667805	1998490 (8.44%)	1883235 (8.00%)	3231508 (6.83%)	650217 (1.37%)
WT (CR/NR)	21462084	21462084	5930574 (27.63%)	5652621 (26.34%)	9360788 (21.81%)	2222407 (5.18%)
WT (CR/ND)	19146665	19146665	4002901 (20.91%)	3849171 (20.10%)	6720258 (17.55%)	1131814 (3.00%)

Supplementary Table 1.

Alignment summary for RNA-Seq analysis of the wild type strain grown under different nitrogen and carbon repressing/derepressing conditions.

Counts of total forward (R1) and reverse (R2) reads in the sequence library and the numbers and proportions of reads mapped to the reference genome sequence are shown.

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Name	Sequence
creAF1	5’ TGGATTCCGCTCTGGTCAAC 3’
creAR1	5’ GACGCGATGTGACGCATAAG 3’
tamAF2	5’ AGACTCTACCACCGACCTCT 3’
tamAR2	5’ GGAATCTGGAGAGAGGGAGC 3’
alphaF2	5’ AACGCCCTCAATTACAGC 3’
alphaR2	5’ TCTGCCATGGAGCTTTAGG 3’
betaF3	5’ TAGTCGTGATAAGGCTGGCA 3’
betaR3	5’ GTTCACTTTATTAGCCGGCG 3’
gammaF2	5’ GTATCGTCGCAGTACTTCGC 3’
gammaR2	5’ GCATCGCCACTTGAGGTACG 3’
18RNA_1L	5’ CAGCGAGTACATCACCTTGG 3’
18RNA_1P	5’ TAGTAGCGACAGGCGGTGTG 3’
areAF1	5’ GACCCGGATTTCTCACATGC 3’
areAR1	5’ TGGAAGGATAGGATCGTCGC 3’
meaBF3	5’ CCCAAATGCTCACTCACTCG 3’
meaBR3	5’ TAGTACGCAGAAGGGAGACG 3’
cpcAF1	5’ CTGACCTCAGCACACCTTCA 3’
cpcAR1	5’ CATCGACATTCCATCATTCG 3’
xprGF2	5’ ATGGACCTTCCTGATCAACG 3’
xprGR2	5’ AGTGACCATCTCTGGGAACG 3’

Supplementary Table 2. Primer sequences

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Supplementary Table 3a.

Effect of ammonium under carbon repressing conditions (glucose as a carbon source) in the wild type strain

Differentially expressed genes (GU vs. GNH4)are shown.

Gene expression was regarded as significantly changed if the FDR was <0.05 and the fold change |FC| >2

65 differentially regulated genes were identified under these conditions: 14 upregulated and 51 downregulated

gene	**Description**	**Name**	**log$_2$FC**	**PValue**	**FDR**
AN4822	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	7.226425	2.16E-17	1.39E-13
AN7539	Putative hydrophobin; transcript is induced by nitrate	null	-7.38779	9.53E-15	3.07E-11
AN0300	Putative asparaginase with a predicted role in asparagine metabolism	null	-7.63375	4.00E-13	8.60E-10
AN0418	Putative high-affinity urea/H+ symporter; regulated by nitrogen catabolite repression; transcript upregulated by nitrate limitation	ureA	-7.52357	8.77E-13	1.41E-09
AN1181	Putative transporter with a predicted role in small molecule transport; ammonium permease	mepA	-9.3063	8.54E-12	1.10E-08
AN8539	Ortholog of A. fumigatus sidG; GNAT family acetyltransferase; transcript induced by light in in developmentally competent mycelia	ngn26	-5.79574	1.22E-11	1.31E-08
AN7322	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	null	-5.26276	7.27E-11	6.70E-08
AN8540	Siderophore iron transporter	mirB	-4.20205	2.82E-09	2.27E-06
AN7323	Covalently-bound cell wall protein; predicted glycosyl phosphatidylinositol (GPI)-anchor	null	-5.33968	1.71E-08	1.23E-05
AN8913	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-4.34244	2.41E-07	0.000156
AN1832	N-glycosylated membrane protein, immunodominant antigen in sera from aspergilloma patients; repressed by bafilomycin; production increases under zinc-limiting conditions	aspnd1	-3.65199	2.74E-07	0.000161
AN8652	null	null	-5.50028	5.13E-07	0.000276
AN1831	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.42054	8.91E-07	0.000442
AN7990	Ortholog of A. niger CBS 513.88 : An11g06780, A. niger ATCC 1015 : 208909-mRNA, Aspergillus versicolor : Aspve1_0045473, Aspergillus sydowii : Aspsy1_0047960 and Aspergillus terreus NIH2624 : ATET_06661	null	-4.47441	1.51E-06	0.000695
AN3160	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.46399	1.82E-06	0.000783
AN3400	Ortholog(s) have tetrahydroxynaphthalene reductase activity, role in melanin biosynthetic process and intracellular localization	null	-4.01696	2.35E-06	0.000947
AN8647	High-affinity nitrite transporter; transcription is induced by nitrite and nitrate, and repressed by ammonium; regulated by NirA and AreA	nitA	-7.24084	3.63E-06	0.001318

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AN11233	Has domain(s) with predicted cation binding, chitin binding, chitinase activity and role in carbohydrate metabolic process, chitin catabolic process	null	5.2318	3.68E-06	0.001318
AN7800	Siderophore iron transporter	mirA	-3.07167	6.05E-06	0.002052
AN7108	Ortholog(s) have ATP binding activity and cytosol, nucleus localization	null	3.305134	7.71E-06	0.002484
AN0374	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.05547	8.62E-06	0.002646
AN0701	Has domain(s) with predicted NAD binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	-4.93827	1.12E-05	0.00327
AN2390	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	null	-3.41432	1.37E-05	0.003828
AN10626	Has domain(s) with predicted ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism activity	null	-3.61261	1.82E-05	0.004901
AN7801	Ortholog(s) have hydrolase activity, acting on ester bonds activity, role in iron assimilation and cytoplasm localization	null	-3.72742	1.99E-05	0.005002
AN8490	Ortholog of Aspergillus versicolor : Aspve1_0369297 and Aspergillus sydowii : Aspsy1_0471403	null	4.916467	2.02E-05	0.005002
AN11064	Putative alpha-1,3-glucanase	agnD	-3.32409	2.72E-05	0.006244
AN6005	Ortholog of A. fumigatus Af293 : Afu2g10020, A. niger CBS 513.88 : An16g05030, Aspergillus versicolor : Aspve1_0040814 and Aspergillus sydowii : Aspsy1_0089381	null	-3.32409	2.72E-05	0.006244
AN11121	Protein of unknown function; transcript repressed by nitrate	null	-4.33111	2.85E-05	0.006244
AN4339	null	null	-6.84532	3.00E-05	0.006244
AN4870	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	null	-6.84532	3.00E-05	0.006244
AN7937	Protein responsive to Concanamycin A	cipC	2.789097	3.19E-05	0.006422
AN3479	Ortholog of A. nidulans FGSC A4 : AN8495, A. fumigatus Af293 : Afu3g01440, Afu4g03340, Afu5g07620, A. niger CBS 513.88 : An13g02880, A. oryzae RIB40 : AO090009000050 and A. niger ATCC 1015 : 129924-mRNA	null	4.812081	3.37E-05	0.006578
AN5489	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	null	-6.7788	3.90E-05	0.007396
AN3159	Has domain(s) with predicted guanyl-nucleotide exchange factor activity, role in regulation of small GTPase mediated signal transduction, small GTPase mediated signal transduction and intracellular localization	null	-4.03968	4.02E-05	0.007396
AN0403	Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.73718	4.16E-05	0.007448

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AN9285	Ortholog of A. fumigatus grg1; homologous to ccg-1 from N. crassa; transcript induced by light in developmentally competent mycelia	null	-2.95575	4.67E-05	0.00814
AN10638	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	null	6.672128	5.10E-05	0.008586
AN7324	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.76801	5.19E-05	0.008586
AN4949	Ortholog(s) have chromatin insulator sequence binding, core RNA polymerase III binding transcription factor activity, tDNA binding activity and role in transcription initiation from RNA polymerase III promoter	null	4.08765	5.74E-05	0.009259
AN1792	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	6.625294	6.72E-05	0.010069
AN3531	Putative D-sorbitol dehydrogenase (acceptor) with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism	null	6.576888	6.72E-05	0.010069
AN6274	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-6.70907	6.72E-05	0.010069
AN3079	Secreted thaumatin-like protein; role in early conidial germination; localized to the cell wall of germinating conidia but not to germ tubes; cetA transcript is repressed by glucose	cetA	-3.9072	8.36E-05	0.011971
AN8011	null	null	4.63981	8.36E-05	0.011971
AN1628	Putative membrane ATPase with a predicted role in energy metabolism	enaB	-2.96598	8.88E-05	0.012451
AN5941	null	null	-6.5586	0.000119	0.015731
AN9288	Ortholog(s) have cytoplasm, nucleus localization	null	-6.5586	0.000119	0.015731
AN6525	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	aciA	2.55477	0.00012	0.015731
AN6881	Ortholog of A. fumigatus Af293 : Afu8g07160, A. niger CBS 513.88 : An03g01630, A. niger ATCC 1015 : 137513-mRNA, Aspergillus versicolor : Aspve1_0035247 and Aspergillus sydowii : Aspsy1_0040388	null	-2.98459	0.000135	0.017451
AN3357	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.74912	0.000147	0.018551
AN0609	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	null	-2.4974	0.000171	0.021156
AN5939	Putative 5'-nucleotidase with a predicted role in nucleotide salvage pathways; predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.54251	0.000187	0.02224

AN5056	Homologous to ccg-1 from N. crassa; transcript induced by light in in developmentally competent mycelia	null	-2.65028	0.000189	0.02224
AN0402	Ortholog of Aspergillus versicolor : Aspve1_0048646 and Aspergillus sydowii : Aspsy1_0055229	null	-2.56392	0.00019	0.02224
AN0319	Ortholog of A. fumigatus Af293 : Afu1g02490, A. niger CBS 513.88 : An01g05680, A. oryzae RIB40 : AO090005000843, A. niger ATCC 1015 : 122243-mRNA and Aspergillus versicolor : Aspve1_0067268	null	-3.57157	0.000221	0.025425
AN3961	Ortholog of Aspergillus versicolor : Aspve1_0054191	null	2.867313	0.000225	0.025425
AN0404	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	null	-2.42909	0.000249	0.027553
AN6729	Has domain(s) with predicted catalytic activity, molybdenum ion binding, pyridoxal phosphate binding activity	null	3.356405	0.000252	0.027553
AN7922	Has domain(s) with predicted FMN binding, riboflavin reductase (NADPH) activity and role in oxidation-reduction process	null	-3.52604	0.000265	0.028119
AN0483	Ortholog of Aspergillus versicolor : Aspve1_0158177, Aspergillus sydowii : Aspsy1_0144898, Aspergillus terreus NIH2624 : ATET_04939 and Aspergillus brasiliensis : Aspbr1_0204336	null	-3.04201	0.000266	0.028119
AN6118	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	agtA	-3.47903	0.000318	0.033044
AN3627	Ortholog(s) have intracellular localization	null	-2.38082	0.000386	0.039452
AN1515	Ortholog of A. nidulans FGSC A4 : AN2922, AN7536, A. niger CBS 513.88 : An12g10030, A. oryzae RIB40 : AO090701000305, AO090102000038, AO090124000043 and A. niger ATCC 1015 : 55190-mRNA	null	-3.79934	0.000455	0.045794
AN0960	Has domain(s) with predicted role in mitosis and chromosome, centromeric region, nucleus localization	null	-2.64498	0.00048	0.047606

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Supplementary Table 3b

Effect of ammonium under carbon derepressing conditions (fructose as a carbon source) in the wild type strain

Differentially expressed genes (FU vs. FNH_4) are shown.

Gene expression was regarded as significantly changed if the FDR was <0.05 and the fold change |FC| >2

1601 differentially regulated genes were identified under these conditions: 856 upregulated and 745 downregulated

gene	Description	Name	log_2FC	PValue	FDR
AN2831	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	11.812532	1.17E-26	8.74E-23
AN4822	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	9.0393845	2.84E-24	1.06E-20
AN9297	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	null	7.8808206	1.56E-19	3.89E-16
AN4003	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	8.3628918	2.45E-19	4.57E-16
AN3961	Ortholog of Aspergillus versicolor : Aspve1_0054191	null	8.8183929	8.94E-17	1.33E-13
AN5030	Has domain(s) with predicted NAD binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	8.7505257	1.49E-16	1.85E-13
AN8907	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism	null	6.58827	2.59E-16	2.56E-13
AN4127	Ortholog(s) have intracellular localization	null	8.670153	2.74E-16	2.56E-13
AN7108	Ortholog(s) have ATP binding activity and cytosol, nucleus localization	null	6.9810149	5.07E-16	4.21E-13
AN2653	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-10.93566	6.38E-16	4.76E-13
AN11233	Has domain(s) with predicted cation binding, chitin binding, chitinase activity and role in carbohydrate metabolic process, chitin catabolic process	null	7.3890645	7.86E-16	5.34E-13
AN10296	Ortholog(s) have fumarate reductase (NADH) activity, role in cellular response to anoxia and cytosol, mitochondrion, plasma membrane, ribosome localization	null	6.4164737	1.02E-14	6.32E-12
AN11006	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	null	6.3276807	2.17E-14	1.25E-11
AN5031	Putative malate dehydrogenase with a predicted role in the methylglyoxal bypass or the TCA cycle	mdhB	10.014554	5.51E-14	2.94E-11
AN4809	Putative glutaminase A with a predicted role in glutamate and glutamine metabolism	gtaA	-6.589726	1.82E-13	9.04E-11

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AN6723	Putative 2,3-dihydroxybenzoate carboxylyase	dhbD	-6.058283	2.19E-13	9.64E-11
AN8084	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-10.13061	2.27E-13	9.64E-11
AN4871	Class V chitinase; glycoside hydrolase family 18 (GH18) protein with a role in the age-dependent autolysis	chiB	-5.790829	2.32E-13	9.64E-11
AN2583	Putative glyceraldehyde-3-phosphate dehydrogenase with a predicted role in gluconeogenesis and glycolysis	gpdC	5.610477	5.07E-13	1.99E-10
AN10482	Putative beta-glucosidase	bglF	-6.79015	1.24E-12	4.64E-10
AN7053	Ortholog of Aspergillus versicolor : Aspve1_0054863	null	6.1239346	1.61E-12	5.72E-10
AN4135	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	sdeB	5.7156992	1.87E-12	6.34E-10
AN2584	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	5.8458204	2.66E-12	8.63E-10
AN2286	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	alcC	5.3194708	3.42E-12	1.07E-09
AN5130	Ortholog(s) have coproporphyrinogen oxidase activity, role in heme biosynthetic process and cytosol, nucleus localization	null	5.2661011	4.03E-12	1.20E-09
AN4480	null	null	9.3920752	5.08E-12	1.46E-09
AN1549	Ortholog of A. fumigatus Af293 : Afu8g05600, A. niger CBS 513.88 : An16g07080, A. oryzae RIB40 : AO090005000583, A. niger ATCC 1015 : 205017-mRNA and Aspergillus versicolor : Aspve1_0037356	null	5.3540287	5.44E-12	1.51E-09
AN1857	Putative kynureninase with a predicted role in aromatic amino acid biosynthesis	null	-5.66801	6.33E-12	1.69E-09
AN0214	null	null	5.2864083	2.07E-11	5.34E-09
AN11965	null	null	9.1387315	3.03E-11	7.55E-09
AN1772	Type B feruloyl esterase	null	-5.230789	3.38E-11	8.13E-09
AN6789	null	null	7.0355325	3.80E-11	8.87E-09
AN1883	Putative argininosuccinate synthase with a predicted role in arginine metabolism; intracellular; protein abundance decreased by menadione stress	null	5.8422622	6.00E-11	1.36E-08
AN12135	null	null	6.9473431	7.10E-11	1.56E-08
AN4055	Putative acid phosphatase with a predicted role in gluconic acid and gluconate metabolism	null	-4.821439	8.49E-11	1.81E-08
AN1433	Ortholog of A. fumigatus Af293 : Afu1g01310, Afu8g04210, A. niger CBS 513.88 : An16g08870, An08g11860, An13g01880, A. oryzae RIB40 : AO090701000542, AO090103000036 and A. niger ATCC 1015 : 193610-mRNA	null	-4.921327	8.74E-11	1.81E-08

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AN3555	Small heat-shock protein; Hsp30p ortholog/paralog; expression upregulated after exposure to farnesol; palA-dependent expression independent of pH	null	4.9205635	9.73E-11	1.96E-08
AN10507	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	null	6.4066215	1.04E-10	2.05E-08
AN1792	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	5.1306037	1.15E-10	2.20E-08
AN0913	Putative phosphatidylinositol synthase with a predicted role in phospholipid metabolism	null	5.6283339	1.45E-10	2.70E-08
AN8046	Putative triacylglycerol lipase with a predicted role in glycerolipid metabolism	null	-4.769401	1.52E-10	2.77E-08
AN0553	null	null	6.8040454	1.79E-10	3.12E-08
AN10910	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	null	4.8246826	1.80E-10	3.12E-08
AN4051	Has domain(s) with predicted heme binding, iron ion binding, oxygen binding activity and role in oxygen transport	null	4.8187479	1.85E-10	3.15E-08
AN3282	Has domain(s) with predicted catalytic activity, nucleotide binding activity and role in biosynthetic process	null	5.2074723	1.91E-10	3.16E-08
AN3223	Putative 6-phosphofructokinase with a predicted role in gluconeogenesis and glycolysis; upregulated under hypoxic growth conditions	pfkA	4.6040034	2.55E-10	4.13E-08
AN5823	L-ornithine N5-monooxygenase; involved in siderophore biosynthesis; null mutant inviable unless medium is supplemented with siderophores	sidA	4.8009228	2.85E-10	4.53E-08
AN11574	null	null	8.7965303	3.35E-10	5.22E-08
AN7026	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	null	5.4910033	3.72E-10	5.66E-08
AN5742	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.510593	3.97E-10	5.93E-08
AN9323	Ortholog of A. niger CBS 513.88 : An02g00370, An06g00670, A. oryzae RIB40 : AO090102000655, Aspergillus brasiliensis : Aspbr1_0192788, Aspbr1_0199838 and Aspergillus acidus : Aspfo1_0076240, Aspfo1_0078934	null	-5.950012	4.64E-10	6.79E-08
AN8351	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-5.059179	4.75E-10	6.82E-08
AN0231	Conidiophore-specific phenol oxidase; mutant conidiophores, metulae and phialides lack pigmentation; ivoB mutants accumulate the substrate N-acetyl-6-hydroxytryptophan (AHT); repressed by light in developmentally competent mycelia	ivoB	-5.045714	5.26E-10	7.34E-08

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AN1896	Fumarylacetoacetate hydrolase, catalyzes the last step in the phenylalanine catabolic pathway; intracellular; protein abundance decreased by menadione stress; mutation in human ortholog causes type I hereditary tyrosinaemia	fahA	-5.253516	5.35E-10	7.34E-08
AN4821	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	6.1762428	5.40E-10	7.34E-08
AN20013	Putative mitochondrial ribosomal protein S5, encoded within the intron of the large mitochondrial ribosomal rRNA gene (L-rRNA); similar to open reading frames in the introns of N. crassa and Penicillium sp. mt rRNA genes	null	5.3842344	7.76E-10	1.03E-07
AN7359	Putative cytochrome P450	CYP5078A3	-8.963311	8.00E-10	1.03E-07
AN9380	Putative chitin deacetylase; catalyzes the conversion of chitin to chitosan by the deacetylation of N-acetyl-D-glucosamine residues	null	-8.963311	8.00E-10	1.03E-07
AN7386	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	null	4.6923398	8.49E-10	1.07E-07
AN4888	Putative pyruvate decarboxylase with a predicted role in pyruvate metabolism or penicillin biosynthesis; intracellular; protein abundance decreased by menadione stress	pdcA	4.3831009	9.81E-10	1.22E-07
AN12070	Ortholog(s) have cytosol, nucleus localization	null	5.2627349	1.08E-09	1.30E-07
AN8007	Protein with arabinan endo-1,5-alpha-L-arabinosidase activity, involved in degradation of pectin	abnC	-4.47319	1.08E-09	1.30E-07
AN3347	Putative amino acid transporter; expression reduced after exposure to farnesol	null	5.7982043	1.19E-09	1.41E-07
AN8602	Ortholog of A. fumigatus Af293 : Afu2g00500, A. oryzae RIB40 : AO090023000371, Aspergillus versicolor : Aspve1_0031494 and Aspergillus sydowii : Aspsy1_0060228	null	5.4044722	1.27E-09	1.48E-07
AN7211	Putative C-8,7 sterol isomerase with a predicted role in ergosterol biosynthesis	null	8.5481139	1.64E-09	1.87E-07
AN4825	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	null	-4.747484	1.65E-09	1.87E-07
AN0875	Has domain(s) with predicted O-acetyltransferase activity and cytoplasm localization	null	-4.434638	1.73E-09	1.93E-07
AN8661	Ortholog of A. nidulans FGSC A4 : AN5943, AN8548, AN4642, A. fumigatus Af293 : Afu3g00850, Afu4g08850 and A. niger CBS 513.88 : An02g13470, An11g00090, An03g01430, An12g09260	null	-6.414293	1.82E-09	1.98E-07
AN7307	Ortholog(s) have endoplasmic reticulum localization	null	-8.838876	1.83E-09	1.98E-07
AN3399	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-6.405896	1.96E-09	2.09E-07
AN5781	Putative 30 kilodalton heat shock protein; transcript levels increase during the unfolded-protein response (UPR); palA-dependent expression independent of pH	null	4.3440216	2.01E-09	2.11E-07

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AN6923	Putative high-affinity hexose transporter with a predicted role in hexose transport; induced upon starvation and during sexual development	hxtA	-4.448147	2.15E-09	2.23E-07
AN9184	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	4.3482587	2.21E-09	2.23E-07
AN8544	Ortholog of Aspergillus versicolor : Aspve1_0033877 and Aspergillus sydowii : Aspsy1_0466900	null	4.5635438	2.21E-09	2.23E-07
AN6657	Ortholog of A. fumigatus Af293 : Afu6g03400, A. niger CBS 513.88 : An15g02040, Aspergillus versicolor : Aspve1_0086179 and Aspergillus sydowii : Aspsy1_0157063	null	4.7263924	2.28E-09	2.27E-07
AN7170	Protein of unknown function; transcript upregulated in response to camptothecin	null	4.5995662	2.57E-09	2.53E-07
AN2779	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, iron-sulfur cluster binding activity	null	-5.227296	2.70E-09	2.61E-07
AN7892	Small heat-shock protein; molecular chaperone; expression upregulated after exposure to farnesol	null	4.4863049	2.73E-09	2.61E-07
AN4807	Ortholog of A. niger CBS 513.88 : An02g13800, A. oryzae RIB40 : AO090020000293, A. niger ATCC 1015 : 207448-mRNA, Aspergillus versicolor : Aspve1_0040098 and Aspergillus sydowii : Aspsy1_0087808	null	-5.012183	3.51E-09	3.32E-07
AN10326	Ortholog of Aspergillus versicolor : Aspve1_0081330 and Aspergillus sydowii : Aspsy1_0148173	null	-4.764368	3.63E-09	3.39E-07
AN10921	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity, role in GPI anchor metabolic process, intracellular protein transport and intrinsic to endoplasmic reticulum membrane localization	null	5.0790271	3.73E-09	3.41E-07
AN4245	Putative ceramidase	null	-4.690087	3.74E-09	3.41E-07
AN5719	Ortholog(s) have cytosol localization	null	8.4172364	4.00E-09	3.59E-07
AN2455	Ortholog(s) have cytosol, nucleus localization	null	4.6362205	4.04E-09	3.59E-07
AN6382	Has domain(s) with predicted phospholipase C activity and role in intracellular signal transduction, lipid metabolic process	null	-5.143981	4.84E-09	4.25E-07
AN6750	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	5.0202222	5.71E-09	4.96E-07
AN2704	Putative aryl-alcohol oxidase-related protein	null	4.7518358	5.92E-09	5.08E-07
AN4077	Has domain(s) with predicted DNA binding activity, role in regulation of transcription, DNA-dependent and chromosome, centromeric region localization	null	-8.612004	7.97E-09	6.77E-07
AN4094	Putative C-14 sterol reductase with a predicted role in sterol metabolism	null	4.3986806	1.02E-08	8.59E-07
AN1982	Ortholog of A. fumigatus Af293 : Afu4g10570, A. niger CBS 513.88 : An04g06100, A. oryzae RIB40 : AO090003001154, A. niger ATCC 1015 : 193413-mRNA and Aspergillus versicolor : Aspve1_0465099	null	6.1867921	1.05E-08	8.71E-07
AN8043	null	null	4.1774615	1.20E-08	9.82E-07

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AN7625	Putative myo-inositol-1-phosphate synthase with a predicted role in phospholipid metabolism; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH	null	4.039566	1.26E-08	1.02E-06
AN9142	Ortholog of A. fumigatus Af293 : Afu7g01570, A. niger ATCC 1015 : 189733-mRNA, Aspergillus versicolor : Aspve1_0057650, Aspergillus sydowii : Aspsy1_0093879 and Aspergillus terreus NIH2624 : ATET_01773	null	-6.107596	1.32E-08	1.06E-06
AN1510	Ortholog(s) have protein disulfide oxidoreductase activity, thiol oxidase activity, role in protein thiol-disulfide exchange and endoplasmic reticulum membrane localization	null	4.0584868	1.35E-08	1.07E-06
AN7484	Protein expressed at increased levels during osmoadaptation; contains a DUF1349 domain	null	4.6471083	1.36E-08	1.07E-06
AN0500	null	null	-4.776512	1.70E-08	1.33E-06
AN4757	Ortholog(s) have role in ubiquinone biosynthetic process and mitochondrial inner membrane localization	null	4.7839424	1.85E-08	1.42E-06
AN0565	Multifunctional enzyme with carbamoyl-phosphate synthase (CPSase) and aspartate carbamoyltransferase (ATCase) activities that catalyze the first two steps in pyrimidine biosynthesis	pyrABCN	4.1804558	2.00E-08	1.52E-06
AN8374	Ortholog(s) have oligopeptide transporter activity and role in oligopeptide transport, vacuole fusion, non-autophagic	null	8.168673	2.01E-08	1.52E-06
AN5591	Putative aminotransferase; protein expressed at decreased levels in a hapX mutant versus wild-type	null	4.9676675	2.25E-08	1.68E-06
AN6693	Protein of unknown function; transcript repressed by nitrate	null	4.8001982	2.45E-08	1.81E-06
AN1426	Ortholog(s) have serine-type carboxypeptidase activity	null	-5.343959	2.50E-08	1.83E-06
AN2530	Heat shock protein 30; expression and protein levels upregulated after exposure to farnesol	hsp30	4.0480125	2.52E-08	1.83E-06
AN12331	Putative polyketide synthase (PKS)-like enzyme	null	8.1412887	2.64E-08	1.89E-06
AN1609	null	null	4.8385433	2.93E-08	2.08E-06
AN2533	Putative alpha-L-arabinofuranosidase	null	6.0238628	3.03E-08	2.09E-06
AN7402	Putative glucoamylase with a predicted role in starch metabolism	glaB	6.0238628	3.03E-08	2.09E-06
AN8495	Ortholog(s) have endoplasmic reticulum localization	null	8.0849095	3.03E-08	2.09E-06
AN6973	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism; expression reduced after exposure to farnesol	null	3.8611858	3.13E-08	2.15E-06
AN7092	Ortholog of Aspergillus aculeatus ATCC16872 : Aacu16872_053301	null	-8.384367	3.46E-08	2.35E-06
AN7800	Siderophore iron transporter	mirA	4.6828231	3.74E-08	2.51E-06
AN3344	Putative GNAT-type acetyltransferase	ngn27	5.5173053	4.34E-08	2.89E-06
AN3031	Putative threonine synthase with a predicted role in glycine, serine, and threonine metabolism	null	4.6988486	4.72E-08	3.09E-06

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AN8692	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	prxA	4.6988486	4.72E-08	3.09E-06
AN3239	Has domain(s) with predicted acyl-CoA dehydrogenase activity and role in oxidation-reduction process	null	5.9349345	5.35E-08	3.47E-06
AN2316	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	4.7380654	5.71E-08	3.68E-06
AN1699	Putative acyl-coA dehydrogenase; expression upregulated after exposure to farnesol	null	-4.349652	5.95E-08	3.80E-06
AN11476	Ortholog of A. fumigatus Af293 : Afu2g03190, Aspergillus versicolor : Aspve1_0086542, Aspve1_0089117, Aspergillus sydowii : Aspsy1_0093985 and Aspergillus brasiliensis : Aspbr1_0045764, Aspbr1_0201559	null	5.4459701	6.15E-08	3.89E-06
AN12192	Ortholog of A. nidulans FGSC A4 : AN3979, Aspergillus flavus NRRL 3357 : AFL2T_09411, Aspergillus versicolor : Aspve1_0043435 and Aspergillus sydowii : Aspsy1_0051867	null	7.9650772	6.20E-08	3.89E-06
AN3741	Alcohol dehydrogenase II, has a predicted role in two-carbon compound metabolism	alcB	-4.331465	6.69E-08	4.16E-06
AN2544	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-8.27039	6.93E-08	4.27E-06
AN4150	Ortholog(s) have biotin transporter activity, role in biotin transport and Golgi apparatus localization	null	4.7936027	7.08E-08	4.31E-06
AN7169	NirA-dependent flavohemoprotein; required for nitrate and nitrite reductase enzyme activity, regulates sexual development; menadione stress-induced protein; induced by nitrate; palA-dependent, pH-independent expression	fhbA	4.2067094	7.09E-08	4.31E-06
AN7225	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.1989769	7.24E-08	4.36E-06
AN9108	Has domain(s) with predicted heme binding activity	null	-4.307286	7.69E-08	4.59E-06
AN6543	Ortholog(s) have adenyl-nucleotide exchange factor activity, role in cytoplasmic translation and cytosolic ribosome, nucleus localization	null	4.6850743	8.10E-08	4.80E-06
AN0443	Putative zinc containing alcohol dehydrogenase; protein expressed at decreased levels in a hapX mutant versus wild-type	null	4.1763751	8.69E-08	5.11E-06
AN9384	Putative cytochrome P450 alkane hydroxylase	CYP584E1	-8.225215	8.81E-08	5.14E-06
AN3345	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	4.5898376	9.46E-08	5.43E-06
AN2445	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	4.7518942	9.63E-08	5.43E-06
AN5665	Putative cytochrome P450	CYP531D2	-5.796796	9.63E-08	5.43E-06
AN3205	Putative aldehyde dehydrogenase; ortholog of A. fumigatus Afu4g02830	null	-5.128408	9.69E-08	5.43E-06

AN1542	Protein with oligoxyloglucan reducing end-specific cellobiohydrolase activity, involved in degradation of xyloglucans	xgcA	7.9012093	9.75E-08	5.43E-06
AN7836	Ortholog of A. fumigatus Af293 : Afu7g01060, A. oryzae RIB40 : AO090003000833, Aspergillus brasiliensis : Aspbr1_0035748, N. fischeri NRRL 181 : NFIA_113770 and Aspergillus flavus NRRL 3357 : AFL2T_02186	null	7.9012093	9.75E-08	5.43E-06
AN5435	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	null	5.1109135	1.07E-07	5.91E-06
AN9183	Putative beta-glucosidase with a predicted role in polysaccharide degradation	bglR	4.5735698	1.11E-07	6.10E-06
AN8012	Putative bifunctional enzyme with a predicted role in sterol metabolism	null	4.3168462	1.22E-07	6.66E-06
AN0858	Putative chaperone	hsp104	3.6361442	1.23E-07	6.68E-06
AN0943	Putative mitochondrial F1F0-ATP synthase subunit g; ortholog of S. cerevisiae Atp20p; expression reduced after exposure to farnesol	atp20	3.8971111	1.33E-07	7.17E-06
AN4659	Putative acyl-CoA synthetase/AMP-binding domain protein; has a predicted mitochondrial localization signal	null	-3.821382	1.49E-07	7.97E-06
AN8483	Ortholog of A. niger CBS 513.88 : An13g02730, Aspergillus brasiliensis : Aspbr1_0180212, N. fischeri NRRL 181 : NFIA_001870, Aspergillus flavus NRRL 3357 : AFL2T_10566 and A. clavatus NRRL 1 : ACLA_063590	null	-3.935373	1.52E-07	8.06E-06
AN1397	Putative cytochrome P450 monooxygenase involved in the catabolism of aromatic compounds; transcript induced by phenylacetate and repressed by glucose	phacB	-4.404271	1.55E-07	8.14E-06
AN7396	Putative beta-glucosidase	bglM	-8.113958	1.65E-07	8.62E-06
AN3058	Putative glycine hydroxymethyltransferase with a predicted role in glycine, serine, and threonine metabolism	null	4.1908117	1.80E-07	9.32E-06
AN1298	Has domain(s) with predicted role in regulation of transcription, DNA-dependent and nucleus localization	null	-3.955749	1.92E-07	9.85E-06
AN8777	Acetamidase, produces ammonium and acetate from acetamide, allowing utilization of acetamide as sole carbon or nitrogen source; transcript induced under low nitrogen conditions	amdS	-3.855782	1.93E-07	9.85E-06
AN5497	Ortholog(s) have 3,4-dihydroxy-2-butanone-4-phosphate synthase activity, role in aerobic respiration, riboflavin biosynthetic process and cytosol, mitochondrial intermembrane space, nucleus localization	null	3.9427455	2.11E-07	1.07E-05
AN3565	Has domain(s) with predicted hydrolase activity	null	-8.080528	2.14E-07	1.07E-05
AN7884	Putative nonribosomal peptide synthase (NRPS) similar to ferrichrome peptide synthetases involved in siderophore biosynthesis	null	5.2643731	2.14E-07	1.07E-05
AN20003	Ortholog(s) have endonuclease activity	null	7.7643092	2.17E-07	1.07E-05
AN5445	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	null	5.7032624	2.17E-07	1.07E-05

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AN1160	Predicted glycosylphosphatidylinositol (GPI)-anchored protein; S. cerevisiae ortholog Srl1p has role in cell wall organization	null	3.8574384	2.48E-07	1.22E-05
AN2801	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-5.648094	2.55E-07	1.24E-05
AN7865	Putative beta-glucosidase	bglJ	7.7279534	2.56E-07	1.24E-05
AN7722	Putative N-acetyltransferase with a predicted role in arginine metabolism	null	3.8015425	2.58E-07	1.24E-05
AN0942	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	ladA	-4.207303	2.65E-07	1.27E-05
AN2436	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	aclB	3.5611009	2.93E-07	1.39E-05
AN0884	Ortholog of A. fumigatus Af293 : Afu1g15560, A. niger CBS 513.88 : An01g13780, A. oryzae RIB40 : AO090005001164, A. niger ATCC 1015 : 171062-mRNA and Aspergillus versicolor : Aspve1_0049145	null	4.1336709	2.96E-07	1.40E-05
AN4504	Putative endo-mannanase GH76 family protein	dfgG	-3.603445	3.20E-07	1.50E-05
AN5088	Putative potassium-transporting ATPase with a predicted role in energy metabolism	null	-8.01125	3.21E-07	1.50E-05
AN5996	Ortholog(s) have cytosol localization	null	3.5934035	3.42E-07	1.59E-05
AN10024	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-4.721898	3.59E-07	1.65E-05
AN6386	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	4.143549	3.59E-07	1.65E-05
AN8396	Putative pyruvate decarboxylase with a predicted role in pyruvate metabolism	pdcB	-3.756932	3.71E-07	1.69E-05
AN4594	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosolic small ribosomal subunit localization	null	3.5920361	3.90E-07	1.77E-05
AN2895	Has domain(s) with predicted ADP binding, ATP binding activity and role in apoptotic process	null	-7.957017	4.23E-07	1.90E-05
AN1605	Ortholog of Aspergillus sydowii : Aspsy1_0679421	null	4.4082456	4.54E-07	2.02E-05
AN7349	Protein with alpha-1,3-glucanase (mutanase) activity, involved in carbohydrate catabolism; highly expressed during sexual development, specifically expressed in Hulle cells	mutA	-4.888034	4.54E-07	2.02E-05
AN5762	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-4.019304	4.79E-07	2.11E-05
AN20008	Mitochondrially encoded subunit 4 of NADH dehydrogenase; sequence in AspGD is truncated at the 3' end	ndhD	3.4576892	4.81E-07	2.11E-05
AN10358	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-4.670667	4.99E-07	2.18E-05

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AN3763	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.4726241	5.13E-07	2.22E-05
AN5924	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	null	-5.529427	5.13E-07	2.22E-05
AN1614	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	4.3241635	5.30E-07	2.27E-05
AN8019	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	4.0610726	5.47E-07	2.33E-05
AN6636	Ortholog(s) have role in reciprocal meiotic recombination and cytosol, endoplasmic reticulum, nucleus localization	null	3.5969997	6.00E-07	2.55E-05
AN2981	Putative glucose 6-phosphate 1-dehydrogenase with a predicted role in the pentose-phosphate shunt; intracellular, menadione stress-induced protein; transcript downregulated by growth in ethanol	gsdA	3.7120404	6.36E-07	2.68E-05
AN0451	Putative C-8 sterol isomerase with a predicted role in sterol metabolism	null	4.4467151	6.55E-07	2.75E-05
AN6500	Ortholog(s) have cytosol localization	null	3.5046158	6.86E-07	2.86E-05
AN1608	Ortholog of A. fumigatus Af293 : Afu4g09250, A. niger CBS 513.88 : An04g04280, A. oryzae RIB40 : AO090023000611 and A. niger ATCC 1015 : 213011-mRNA	null	3.4876174	7.11E-07	2.94E-05
AN1163	Putative chaperone; ortholog of S. cerevisiae Hsp78p; expression upregulated after exposure to farnesol	null	3.4001443	7.13E-07	2.94E-05
AN5715	Putative 40s ribosomal protein S26; ortholog of S. cerevisiae Rps26Bp which has role in rRNA export from nucleus; expression reduced after exposure to farnesol	null	3.5386071	7.17E-07	2.94E-05
AN2613	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	7.5726117	7.39E-07	3.01E-05
AN2675	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.8006669	7.41E-07	3.01E-05
AN1624	Subunit 9 of the mitochondrial inner membrane F1F0-ATPase complex; mutation confers oligomycin resistance; palA-dependent expression independent of pH	oliC	4.0128092	7.46E-07	3.01E-05
AN4803	Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), positive regulation of translational fidelity	null	3.6833042	7.85E-07	3.14E-05
AN4474	Ortholog of A. niger CBS 513.88 : An04g02110, A. oryzae RIB40 : AO090023000799, A. niger ATCC 1015 : 203625-mRNA, Aspergillus versicolor : Aspve1_0133959 and Aspergillus sydowii : Aspsy1_0095044	null	-3.60879	7.85E-07	3.14E-05
AN10547	Ortholog of A. fumigatus Af293 : Afu4g06220, A. oryzae RIB40 : AO090023000968, Aspergillus sydowii : Aspsy1_0051149 and Aspergillus carbonarius ITEM 5010 : Acar5010_403603	null	3.6233683	7.92E-07	3.15E-05

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AN1810	Ornithine transaminase, involved in utilization of arginine as a proline source; arginine-induced expression and activity; subject to carbon-catabolite and nitrogen-metabolite repression; regulated by CreA and AreA; stress-induced protein	otaA	-3.427102	8.05E-07	3.18E-05
AN4020	Has domain(s) with predicted membrane localization	null	3.4268043	8.11E-07	3.19E-05
AN1524	Putative methylenetetrahydrofolate dehydrogenase (NAD+) with a predicted role in one-carbon metabolism	null	4.3934582	8.40E-07	3.28E-05
AN3954	Putative phosphogluconate dehydrogenase (decarboxylating) with a predicted role in the pentose-phosphate shunt	null	3.5058243	8.80E-07	3.42E-05
AN0224	Ortholog(s) have Golgi apparatus, cytosol, nucleus localization	null	7.5310144	8.91E-07	3.45E-05
AN3559	Ortholog of Aspergillus brasiliensis : Aspbr1_0209810, Aspergillus versicolor : Aspve1_0043449, Aspergillus sydowii : Aspsy1_0176892 and Aspergillus aculeatus ATCC16872 : Aacu16872_044955	null	-7.821934	1.02E-06	3.87E-05
AN3790	Putative alpha-1,3-glucanase	agnB	-7.821934	1.02E-06	3.87E-05
AN6684	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	null	-7.801561	1.02E-06	3.87E-05
AN0282	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	-7.780897	1.18E-06	4.48E-05
AN1723	Ortholog(s) have cell septum, hyphal tip localization	null	-3.426337	1.21E-06	4.55E-05
AN2941	Ortholog of A. nidulans FGSC A4 : AN5437, A. fumigatus Af293 : Afu3g08250, Afu6g13630, A. niger CBS 513.88 : An08g08620, An02g11860, A. oryzae RIB40 : AO090103000325 and A. niger ATCC 1015 : 175401-mRNA	null	-4.097183	1.22E-06	4.55E-05
AN4522	Ortholog(s) have cytosol localization	null	3.7653677	1.22E-06	4.55E-05
AN6209	Putative 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase with a predicted role in purine metabolism; adenylosuccinate lyase; expression reduced after exposure to farnesol	null	4.7184942	1.23E-06	4.58E-05
AN0640	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	basA	3.7517166	1.30E-06	4.81E-05
AN0843	Ortholog(s) have structural constituent of ribosome activity, role in rRNA export from nucleus and 90S preribosome, cytosolic small ribosomal subunit, nucleolus localization	null	3.4100337	1.51E-06	5.54E-05
AN12306	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	4.0925141	1.56E-06	5.70E-05
AN10506	Ortholog of A. fumigatus Af293 : Afu5g14780, A. niger CBS 513.88 : An18g01640, A. oryzae RIB40 : AO090103000417, A. niger ATCC 1015 : 42671-mRNA and Aspergillus versicolor : Aspve1_0173600	null	7.444039	1.59E-06	5.79E-05

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AN11693	Ortholog of A. fumigatus Af293 : Afu3g08370, A. niger ATCC 1015 : 37428-mRNA, Aspergillus versicolor : Aspve1_0070387 and Aspergillus sydowii : Aspsy1_0066686	null	4.9228557	1.62E-06	5.83E-05
AN8164	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	null	-7.738657	1.62E-06	5.83E-05
AN6005	Ortholog of A. fumigatus Af293 : Afu2g10020, A. niger CBS 513.88 : An16g05030, Aspergillus versicolor : Aspve1_0040814 and Aspergillus sydowii : Aspsy1_0089381	null	-4.212733	1.83E-06	6.57E-05
AN6424	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	null	3.4441801	1.84E-06	6.57E-05
AN8905	Putative cytochrome P450	CYP537B1	3.6006489	1.86E-06	6.62E-05
AN2037	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	null	4.8873936	1.90E-06	6.64E-05
AN5408	Has domain(s) with predicted RNA binding, ribonuclease III activity and role in RNA processing	null	4.8873936	1.90E-06	6.64E-05
AN10223	Putative 1-Cys peroxiredoxin; intracellular; protein abundance decreased by menadione stress; expression reduced after exposure to farnesol	null	4.1719256	1.90E-06	6.64E-05
AN5049	Has domain(s) with predicted cation transmembrane transporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	4.1719256	1.90E-06	6.64E-05
AN4336	Putative L-arabinitol 4-dehydrogenase with a predicted role in L-arabinose/arabitol and D-xylose/D,L-xylulose/xylitol metabolism	ladB	5.3374558	1.94E-06	6.75E-05
AN3068	Ortholog of A. fumigatus Af293 : Afu3g09570, A. niger CBS 513.88 : An16g03070, A. niger ATCC 1015 : 49047-mRNA, Aspergillus versicolor : Aspve1_0128162 and Aspergillus sydowii : Aspsy1_0029214	null	3.3386942	1.96E-06	6.76E-05
AN4064	Putative ADP/ATP carrier protein with a predicted role in energy metabolism; palA-dependent expression independent of pH	null	3.2531275	2.04E-06	7.01E-05
AN8041	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	gpdA	3.2243491	2.09E-06	7.17E-05
AN5032	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.631357	2.10E-06	7.17E-05
AN9007	Putative cytochrome P450	CYP548D1	-3.23243	2.11E-06	7.17E-05
AN11174	Ortholog of A. fumigatus Af293 : Afu7g02120, A. niger CBS 513.88 : An12g00530, A. oryzae RIB40 : AO090038000590, N. fischeri NRRL 181 : NFIA_114850 and Aspergillus flavus NRRL 3357 : AFL2T_07916	null	-4.615329	2.14E-06	7.24E-05
AN1432	Ortholog(s) have cytoplasm, nucleus localization	null	-7.672884	2.23E-06	7.49E-05

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AN0366	Has domain(s) with predicted membrane localization	null	5.2904351	2.38E-06	7.94E-05
AN1597	Ortholog of N. fischeri NRRL 181 : NFIA_009820	null	7.3514819	2.38E-06	7.94E-05
AN7961	Ortholog of A. fumigatus Af293 : Afu4g13760, A. oryzae RIB40 : AO090010000492, Aspergillus versicolor : Aspve1_0045462, Aspergillus sydowii : Aspsy1_1151790 and Aspergillus terreus NIH2624 : ATET_04942	null	-3.631164	2.39E-06	7.94E-05
AN3797	Ortholog(s) have role in cellular response to UV, postreplication repair, recombinational repair and nucleus, spindle pole body localization	null	4.2207665	2.41E-06	7.95E-05
AN0893	Putative adenylosuccinate synthase with a predicted role in purine metabolism; induced by ammonium and adenosine	adB	4.1460167	2.42E-06	7.95E-05
AN6881	Ortholog of A. fumigatus Af293 : Afu8g07160, A. niger CBS 513.88 : An03g01630, A. niger ATCC 1015 : 137513-mRNA, Aspergillus versicolor : Aspve1_0035247 and Aspergillus sydowii : Aspsy1_0040388	null	-4.408289	2.49E-06	8.16E-05
AN5422	Putative beta-lactamase family protein; intracellular; protein abundance decreased by menadione stress	null	-3.518716	2.64E-06	8.60E-05
AN8277	Putative bifunctional enzyme with a predicted role in methionine metabolism; O-acetlyhomoserine (homocysteine synthase)	cysD	3.1851546	2.75E-06	8.93E-05
AN3027	Ortholog(s) have flavin-linked sulfhydryl oxidase activity and role in cellular iron ion homeostasis, cellular response to oxidative stress, protein import into mitochondrial intermembrane space	null	4.1898625	2.77E-06	8.96E-05
AN20011	Mitochondrially encoded subunit 6 of NADH dehydrogenase	ndhF	3.7827203	2.83E-06	9.09E-05
AN1749	Possible pseudogene	null	7.3028768	2.93E-06	9.32E-05
AN6821	Ortholog of Aspergillus sydowii : Aspsy1_0091668	null	7.3028768	2.93E-06	9.32E-05
AN8204	Ortholog(s) have NAD+ diphosphatase activity, role in NADH metabolic process and cytosol, nucleus, peroxisome localization	null	5.2418301	2.93E-06	9.32E-05
AN5222	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	3.2928044	2.96E-06	9.36E-05
AN20002	Mitochondrially encoded subunit 2 of NADH dehydrogenase; note that the sequence represented in AspGD is N-terminally truncated relative to orthologous genes in other species	ndhB	3.2842859	2.98E-06	9.39E-05
AN8078	Phenylacetate 2-hydroxylase; cytochrome P450 monooxygenase involved in phenylacetate utilization; transcript is induced by phenylacetate	phacA	-7.627309	3.10E-06	9.73E-05
AN5935	Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	3.3784743	3.21E-06	0.000100303
AN1901	Putative sterol 14 alpha-demethylase with a predicted role in sterol metabolism	pdmA	3.2902329	3.24E-06	0.000100701
AN5669	Putative succinyl-CoA:3-ketoacid-coenzyme A transferase	null	-3.17256	3.28E-06	0.000101737

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AN10838	Has domain(s) with predicted cation binding, chitin binding, chitinase activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, chitin catabolic process	null	3.9982667	3.63E-06	0.00011188
AN5852	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.181427	3.68E-06	0.000112621
AN2435	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	aclA	3.7626157	3.68E-06	0.000112621
AN9004	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	null	3.7438234	3.70E-06	0.000112621
AN0472	Putative 1,3-beta-glucosidase with a role in carbon starvation-induced autolytic cell wall degradation	engA	-3.161925	3.72E-06	0.000112924
AN5206	Putative homoisocitrate dehydrogenase with a predicted role in lysine metabolism	lysB	3.7406513	4.07E-06	0.00012307
AN20000	Mitochondrially encoded subunit 4L of NADH dehydrogenase	ndhDL	4.7361276	4.36E-06	0.000130495
AN7217	null	null	4.7361276	4.36E-06	0.000130495
AN8866	Putative phosphoglycerate dehydrogenase with a predicted role in glycine, serine, and threonine metabolism	null	3.3484281	4.37E-06	0.000130495
AN11751	null	null	7.252577	4.50E-06	0.000131336
AN12341	Has domain(s) with predicted 5-(carboxyamino)imidazole ribonucleotide mutase activity, phosphoribosylaminoimidazole carboxylase activity and role in 'de novo' IMP biosynthetic process	null	-7.16772	4.50E-06	0.000131336
AN1310	Ortholog(s) have role in secondary metabolic process	null	7.252577	4.50E-06	0.000131336
AN1593	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	null	7.252577	4.50E-06	0.000131336
AN3396	Putative non-ribosomal peptide synthase (NRPS) responsible for microperfuranone biosynthesis; transcript repressed by nitrogen limitation	micA	5.1915303	4.50E-06	0.000131336
AN12368	Putative alpha-L-rhamnosidase	rhaB	-4.304561	4.50E-06	0.000131336
AN5997	Ortholog(s) have role in rRNA export from nucleus and nucleolus localization	null	3.234416	4.65E-06	0.000134997
AN2663	Ortholog(s) have pantothenate transmembrane transporter activity, role in endocytosis, pantothenate transmembrane transport and plasma membrane localization	null	-5.141524	4.92E-06	0.000142468
AN8746	Possible pseudogene; transcript upregulated in response to camptothecin	null	3.0740432	4.96E-06	0.000143079
AN5204	Ortholog of A. fumigatus Af293 : Afu6g07370, A. niger CBS 513.88 : An07g09060, A. oryzae RIB40 : AO090005001564, Aspergillus versicolor : Aspve1_0154324 and Aspergillus sydowii : Aspsy1_0156764	null	-4.465633	5.09E-06	0.000146117

AN4732	Ortholog of A. fumigatus Af293 : Afu5g10730, A. niger CBS 513.88 : An14g03950, A. oryzae RIB40 : AO090010000468, A. niger ATCC 1015 : 184967-mRNA and Aspergillus versicolor : Aspve1_0718613	null	-7.531597	5.19E-06	0.000147952
AN4770	Adenosine 3-phosphate 5-phosphosulfate (PAPS) reductase involved in sulfate assimilation	sA	3.5297467	5.19E-06	0.000147952
AN3114	Ortholog of A. fumigatus Af293 : Afu3g12710, A. niger CBS 513.88 : An02g08680, A. oryzae RIB40 : AO090012000852, A. niger ATCC 1015 : 52342-mRNA and Aspergillus versicolor : Aspve1_0026716	null	-7.102598	5.61E-06	0.000155663
AN5029	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	7.20046	5.61E-06	0.000155663
AN5838	Has domain(s) with predicted FMN binding, NADPH-hemoprotein reductase activity, iron ion binding activity and role in oxidation-reduction process	null	5.1394132	5.61E-06	0.000155663
AN6624	Has domain(s) with predicted zinc ion binding activity	null	-7.135526	5.61E-06	0.000155663
AN6954	null	null	5.1394132	5.61E-06	0.000155663
AN8551	Putative transferase with a predicted role in the pentose-phosphate shunt or xylulose metabolism	null	-7.102598	5.61E-06	0.000155663
AN9263	Ortholog of A. oryzae RIB40 : AO090011000236, N. fischeri NRRL 181 : NFIA_029940, A. clavatus NRRL 1 : ACLA_055010, Aspergillus versicolor : Aspve1_0042688 and Aspergillus sydowii : Aspsy1_0047416	null	7.20046	5.61E-06	0.000155663
AN0570	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	3.2540812	5.65E-06	0.000156388
AN1110	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.447999	5.79E-06	0.000159503
AN3220	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.825188	6.13E-06	0.000167
AN20010	Mitochondrially encoded subunit 6 of the F0 sector of mitochondrial F1F0 ATP synthase; can mutate to confer oligomycin resistance	oliA	3.0627792	6.18E-06	0.000167
AN6578	Ortholog(s) have role in positive regulation of gluconate transmembrane transport and cytosol, nucleus localization	null	-3.535029	6.19E-06	0.000167
AN11062	Ortholog(s) have role in mitochondrial genome maintenance and cytosol, mitochondrial matrix, nucleus localization	null	-7.506642	6.20E-06	0.000167
AN7864	Putative beta-1,4-xylosidase	bxlD	-7.506642	6.20E-06	0.000167
AN8890	Has domain(s) with predicted carbohydrate binding, catalytic activity and role in carbohydrate catabolic process	null	-7.506642	6.20E-06	0.000167
AN8415	Putative acyl-coA dehydrogenase; member of the aspyridone (apd) gene cluster	apdG	-4.430147	6.60E-06	0.000177175
AN0433	Ortholog(s) have cytosol, nucleolus localization	null	3.4795635	6.71E-06	0.000179702

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AN0437	Ortholog of A. fumigatus Af293 : Afu1g04570, A. niger CBS 513.88 : An01g03540, Aspergillus versicolor : Aspve1_0243211, Aspergillus sydowii : Aspsy1_0642698 and Aspergillus terreus NIH2624 : ATET_03749	null	-7.0689	7.02E-06	0.00018458
AN10026	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	null	-7.0689	7.02E-06	0.00018458
AN2612	Putative beta-glucosidase with a predicted role in degradation of glucans	bglK	5.0853427	7.02E-06	0.00018458
AN9173	Sugar transporter; transcriptionally induced by growth on xylose	null	5.0853427	7.02E-06	0.00018458
AN9241	Has domain(s) with predicted zinc ion binding activity and role in lipid metabolic process	null	7.1463894	7.02E-06	0.00018458
AN6778	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.323311	7.12E-06	0.00018661
AN10416	Putative 60s ribosomal protein similar to subunits L15 and L27; ortholog of S. cerevisiae RPL28; expression reduced after exposure to farnesol; palA-dependent expression independent of pH	null	3.4585735	7.23E-06	0.000188867
AN4739	Putative phosphoribosyl amino imidazolesuccinocarbozamide synthetase with a predicted role in purine metabolism	null	3.950324	7.53E-06	0.000195858
AN1898	Ortholog(s) have role in melanin biosynthetic process from tyrosine, tyrosine catabolic process and cytoplasm localization	null	-3.556845	8.20E-06	0.000212642
AN0628	Putative D-lactate dehydrogenase with a role in pyruvate-acetyl-coA metabolism; transcript is induced by nitrate	null	3.1175466	8.34E-06	0.000215377
AN1923	Putative alanine transaminase with a predicted role in alanine and aspartate metabolism; intracellular, menadione stress-induced protein	null	3.0561333	8.45E-06	0.000217604
AN4901	Putative glutaminase A with a predicted role in glutamate and glutamine metabolism	null	-3.070781	8.49E-06	0.000217895
AN2387	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	3.5585632	8.77E-06	0.000222741
AN0649	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	null	-3.636029	8.79E-06	0.000222741
AN5014	Ortholog(s) have cytosol, nucleolus localization	null	3.2384718	8.80E-06	0.000222741
AN10122	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-7.034397	8.83E-06	0.000222741
AN5381	null	null	-7.034397	8.83E-06	0.000222741
AN6541	Putative ligase with a predicted role in purine metabolism	null	4.3694289	9.02E-06	0.000226686
AN1246	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	pgkA	2.9885842	9.17E-06	0.000229313

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AN4394	Ortholog(s) have role in asexual sporulation resulting in formation of a cellular spore, positive regulation of asexual sporulation resulting in formation of a cellular spore, regulation of transcription, DNA-dependent	null	-3.469046	9.18E-06	0.000229313
AN4762	Ortholog(s) have mitochondrion localization	null	3.1789451	9.32E-06	0.000232027
AN3990	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.178193	9.36E-06	0.000232224
AN20007	Mitochondrially encoded subunit 1 of NADH dehydrogenase	ndhA	3.1894598	9.44E-06	0.00023258
AN5172	Ortholog of A. fumigatus Af293 : Afu4g09700, Afu6g07000, A. niger CBS 513.88 : An04g07430, A. oryzae RIB40 : AO090012000946, AO090003001270 and A. niger ATCC 1015 : 53150-mRNA, 57315-mRNA	null	-3.61696	9.45E-06	0.00023258
AN10059	Putative Zn(II)C6 domain containing transcription factor; predicted NirA binding site in promoter; transcript repressed by nitrate	null	-3.937248	9.49E-06	0.00023258
AN8399	Putative potassium-transporting ATPase with a predicted role in energy metabolism; transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	3.5430565	9.50E-06	0.00023258
AN4042	Putative C-22 sterol desaturase with a predicted role in sterol metabolism; putative cytochrome P450	CYP61A1	3.2693745	9.53E-06	0.00023258
AN6202	Putative ribosomal protein L3	rpl3	3.0263051	9.58E-06	0.000232987
AN7661	Ortholog(s) have RNA polymerase II core promoter proximal region sequence-specific DNA binding, sterol response element binding activity	null	3.0628999	9.77E-06	0.000236766
AN1726	Putative 3-methyl-2-oxobutanoate dehydrogenase	null	-3.03254	9.91E-06	0.000239158
AN8280	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism; transcript induced in the presence of short and long chain fatty acids	faaB	-3.335155	9.93E-06	0.000239158
AN8683	Ortholog(s) have ferric-chelate reductase activity, role in copper ion import, iron ion transport and plasma membrane localization	null	-3.17159	9.96E-06	0.000239158
AN3499	Has domain(s) with predicted ATP binding, phosphotransferase activity, alcohol group as acceptor activity and role in amino sugar metabolic process, peptidoglycan turnover	null	3.8166697	1.03E-05	0.000245566
AN11094	Putative zinc-binding oxidoreductase; intracellular, menadione stress-induced protein; expression upregulated after exposure to farnesol	null	3.039336	1.10E-05	0.000259587
AN1197	Has domain(s) with predicted catalytic activity	null	-6.999048	1.12E-05	0.000259587
AN12386	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	null	-6.999048	1.12E-05	0.000259587
AN1681	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.962812	1.12E-05	0.000259587

AN5707	Ortholog of A. niger CBS 513.88 : An18g05710, Aspergillus versicolor : Aspve1_0053485, Aspergillus sydowii : Aspsy1_0043729 and Aspergillus terreus NIH2624 : ATET_02952	null	-6.962812	1.12E-05	0.000259587
AN5888	Ortholog(s) have UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase activity, role in aerobic respiration, protein N-linked glycosylation and UDP-N-acetylglucosamine transferase complex localization	null	-6.962812	1.12E-05	0.000259587
AN7539	Putative hydrophobin; transcript is induced by nitrate	null	-6.962812	1.12E-05	0.000259587
AN8314	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in defense response, lipid metabolic process	null	5.0291664	1.12E-05	0.000259587
AN8376	null	null	7.0902132	1.12E-05	0.000259587
AN1860	Ortholog(s) have mitochondrion localization	null	3.1667517	1.12E-05	0.000260681
AN4073	Putative cytosolic small ribosomal subunit protein S12; expression reduced after exposure to farnesol	null	3.1420804	1.14E-05	0.000264044
AN2958	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.275895	1.16E-05	0.000267242
AN20018	Mitochondrially encoded subunit 3 of NADH dehydrogenase	ndhC	2.9632581	1.23E-05	0.000281989
AN10710	Ortholog(s) have phosphomannomutase activity, role in ER to Golgi vesicle-mediated transport, nuclear envelope organization, protein targeting to ER and cytosol, nucleus localization	null	3.5156209	1.25E-05	0.00028733
AN5979	Ortholog(s) have role in ribosomal small subunit assembly and cytosol localization	null	3.216402	1.27E-05	0.000290153
AN7907	Putative glyoxylate-bleomycin resistance protein; member of the F9775 secondary metabolite gene cluster	null	-4.118269	1.30E-05	0.000296008
AN7138	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	3.0514857	1.30E-05	0.000296008
AN3172	Ortholog of S. cerevisiae RPS0A and RPS0B; expression reduced after exposure to farnesol	null	3.2732541	1.34E-05	0.000304179
AN2161	Putative GNAT-type acetyltransferase	ngn1	-2.931177	1.36E-05	0.000305769
AN7107	Ortholog(s) have nucleolus localization	null	3.017552	1.38E-05	0.000310243
AN7950	Putative glucan endo-1,3-beta-D-glucosidase with predicted role in degradation of glucans; glycosyl phosphatidylinositol (GPI)-linked protein	eglC	3.1045886	1.38E-05	0.000310243
AN10491	Putative transcription factor; predicted role in secondary metabolite production	null	3.3601912	1.41E-05	0.000315025
AN6366	Ortholog(s) have endoplasmic reticulum localization	null	3.5088414	1.42E-05	0.000315025
AN7648	Ortholog(s) have endoplasmic reticulum localization	null	-6.925641	1.42E-05	0.000315025
AN5746	Putative phosphopyruvate hydratase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; protein induced by farnesol	acuN	2.9199245	1.43E-05	0.000316588

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AN10585	Ortholog(s) have cytochrome-c oxidase activity, enzyme regulator activity, role in aerobic respiration, mitochondrial respiratory chain supercomplex assembly and mitochondrial respiratory chain complex IV localization	null	3.0344998	1.44E-05	0.000317648
AN6263	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	4.2957775	1.45E-05	0.00031842
AN6412	Ortholog(s) have endoplasmic reticulum localization	null	4.2957775	1.45E-05	0.00031842
AN0948	Has domain(s) with predicted ATP binding, ATPase activity	null	3.5262957	1.45E-05	0.00031842
AN5846	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	3.1946516	1.49E-05	0.000325932
AN1825	Putative sulfide:quinone oxidoreductase; transcript repressed by nitrogen limitation	null	3.342086	1.53E-05	0.000332671
AN7590	Putative reductase with a predicted role in carbohydrate metabolism; mannitol 2-dehydrogenase; intracellular, menadione stress-induced protein; HapX-regulated; protein induced by farnesol	null	-3.139309	1.59E-05	0.000346031
AN10075	Putative permease of the major facilitator superfamily (MFS)	null	-3.638223	1.66E-05	0.00035871
AN8930	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	null	-3.159554	1.70E-05	0.000367369
AN2974	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	4.2574921	1.71E-05	0.00036781
AN8768	Ortholog(s) have COPI-coated vesicle, clathrin-coated vesicle localization	null	-4.258683	1.72E-05	0.000369255
AN2228	Ortholog of A. fumigatus Af293 : Afu5g07200, A. niger CBS 513.88 : An17g00620, A. oryzae RIB40 : AO090701000236, A. niger ATCC 1015 : 45103-mRNA and Aspergillus versicolor : Aspve1_0124231	null	-6.887488	1.81E-05	0.000387305
AN8870	Expression increased in salt-adapted strains	null	2.8640927	1.90E-05	0.00040504
AN4122	Ortholog of A. nidulans FGSC A4 : AN2881, AN10123, AN0867, A. fumigatus Af293 : Afu1g13860, Afu1g15180, Afu3g11650 and A. niger CBS 513.88 : An08g07010, An02g07440, An01g13480	null	-7.289757	1.91E-05	0.00040504
AN7764	Has domain(s) with predicted ligase activity	null	-7.260202	1.91E-05	0.00040504
AN2835	Has domain(s) with predicted D-arabinono-1,4-lactone oxidase activity, UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity, role in oxidation-reduction process and membrane localization	null	-3.009824	1.92E-05	0.000405399
AN2238	Ortholog(s) have cytosol, nucleus localization	null	2.8651153	1.92E-05	0.000405399
AN3586	Ortholog(s) have mitochondrion localization	null	3.0689218	1.93E-05	0.000406397
AN0362	Ortholog of A. fumigatus Af293 : Afu6g00430, Afu6g03560, A. niger CBS 513.88 : An10g01040, An01g06280, A. oryzae RIB40 : AO090005000897 and A. niger ATCC 1015 : 36048-mRNA	null	3.2070131	1.96E-05	0.000411226

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AN9273	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_00195, Aspergillus versicolor : Aspve1_0083996, Aspergillus sydowii : Aspsy1_0900274 and Aspergillus terreus NIH2624 : ATET_04373	null	-2.961205	1.98E-05	0.000414077
AN20004	Protein of unknown function, encoded on the mitochondrial genome; N terminus is similar to the transmembrane domain of Atp8p	URFA3	3.7584693	1.99E-05	0.00041448
AN5169	Has domain(s) with predicted phospholipid binding activity	null	-3.099818	2.02E-05	0.000419314
AN5663	Ortholog of A. fumigatus Af293 : Afu4g13710, A. niger CBS 513.88 : An01g09510, A. oryzae RIB40 : AO090010000145, AO090009000200 and A. niger ATCC 1015 : 171254-mRNA	null	3.1455426	2.06E-05	0.000427869
AN6399	Putative bleomycin hydrolase	null	-3.208276	2.10E-05	0.000434152
AN4569	Ortholog(s) have role in ubiquinone biosynthetic process and mitochondrial inner membrane localization	null	2.9580149	2.14E-05	0.000440843
AN4525	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	3.0877245	2.19E-05	0.000450384
AN3221	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.978841	2.20E-05	0.000451531
AN2901	Arginase, catalyzes hydrolysis of arginine to urea and ornithine in the arginine catabolic pathway; induced by arginine and repressed by ammonium	agaA	-2.930309	2.29E-05	0.000468129
AN1071	Has domain(s) with predicted ADP binding, ATP binding, microtubule motor activity, role in apoptotic process, nucleoside metabolic process and kinesin complex localization	null	-6.848298	2.32E-05	0.000470228
AN1422	Ortholog of Aspergillus brasiliensis : Aspbr1_0125634, Aspergillus acidus : Aspfo1_0134032, Aspergillus versicolor : Aspve1_0037180 and Aspergillus sydowii : Aspsy1_0041970	null	-6.848298	2.32E-05	0.000470228
AN2526	Putative ketol-acid reductoisomerase with a predicted role in Coenzyme A and pantothenate biosynthesis or amino acid metabolism	null	6.9072317	2.32E-05	0.000470228
AN6057	Putative cytochrome P450	CYP52G1	4.8461849	2.32E-05	0.000470228
AN5843	Putative pyruvate, water dikinase	pdkA	4.4259613	2.33E-05	0.000470228
AN0856	Putative amino acid transporter; expression reduced after exposure to farnesol	null	2.9451543	2.38E-05	0.00047861
AN10714	Ortholog of A. fumigatus Af293 : Afu1g06650, A. oryzae RIB40 : AO090001000464, N. fischeri NRRL 181 : NFIA_018040, Aspergillus flavus NRRL 3357 : AFL2T_09110 and A. clavatus NRRL 1 : ACLA_027920	null	-3.373468	2.38E-05	0.00047861
AN11337	Ortholog of A. niger CBS 513.88 : An18g01250, Aspergillus brasiliensis : Aspbr1_0322983, Aspergillus acidus : Aspfo1_0209416 and Aspergillus versicolor : Aspve1_0038289	null	3.4073975	2.44E-05	0.00048905
AN7354	Ortholog(s) have cytosol, nucleus localization	null	3.0526833	2.54E-05	0.000506317

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AN0365	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	null	2.962823	2.67E-05	0.000532402
AN9010	Ortholog(s) have nicotinamide mononucleotide transmembrane transporter activity, role in nicotinamide mononucleotide transport and mitochondrion localization	null	-3.285285	2.71E-05	0.000538787
AN8978	Transcription factor involved in positive regulation of the ethanol regulon; contains Zn(II)2Cys6 DNA-binding domain	alcR	-3.015686	2.78E-05	0.000551257
AN0935	null	null	4.1777315	2.83E-05	0.00055634
AN11112	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	null	-4.800839	2.83E-05	0.00055634
AN5734	Putative MFS-type quinate transporter	null	-4.826232	2.83E-05	0.00055634
AN3866	Putative dehydratase with a predicted role in glycine, serine, and threonine metabolism	null	-2.799081	2.85E-05	0.000559234
AN9103	Putative apoptosis-inducing factor (AIF)-like mitochondrial oxidoreductase; mutants display decreased survival in the presence of farnesol or menadione, decreased electron transport; expression upregulated after exposure to farnesol	aifA	-3.216768	2.87E-05	0.000561206
AN2042	Ortholog(s) have cytosol localization	null	2.8353879	2.91E-05	0.000566465
AN10771	Ortholog(s) have cytosol, nucleus localization	null	-6.808013	3.00E-05	0.00058076
AN10805	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-6.766572	3.00E-05	0.00058076
AN9363	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	null	-6.766572	3.00E-05	0.00058076
AN4131	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	3.688396	3.09E-05	0.000597053
AN4688	Putative acyl-coA dehydrogenase	ivdA	-2.819394	3.21E-05	0.000618297
AN7691	Putative phospholipase	plcB	-3.512008	3.24E-05	0.000622327
AN7159	Ortholog(s) have tripeptidyl-peptidase activity	null	3.33981	3.27E-05	0.000626099
AN8235	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	null	-3.532647	3.29E-05	0.000628348
AN4013	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-3.708938	3.30E-05	0.000628348
AN3926	Ortholog(s) have role in histone H3-K4 methylation and Set1C/COMPASS complex, cytosol localization	null	-3.388661	3.48E-05	0.000659742
AN6423	Ortholog of A. fumigatus Af293 : Afu3g00960, A. niger CBS 513.88 : An16g08680, A. oryzae RIB40 : AO090009000250 and A. niger ATCC 1015 : 194055-mRNA	null	3.2007053	3.48E-05	0.000659742

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AN0354	Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with a predicted role in aromatic amino acid family biosynthesis; protein expressed at increased levels in a hapX mutant versus wild-type; feedback-inhibited by phenylalanine	aroG	4.3756615	3.51E-05	0.000663124
AN7600	Ortholog(s) have sulfite reductase (NADPH) activity, role in oxidation-reduction process, sulfate assimilation, sulfur amino acid biosynthetic process and cytosol, sulfite reductase complex (NADPH) localization	null	3.3181751	3.59E-05	0.000676934
AN5421	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.916343	3.66E-05	0.000687127
AN9468	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, cytosol localization	null	2.967047	3.66E-05	0.000687127
AN9075	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-3.693394	3.68E-05	0.000689259
AN2968	Putative inorganic diphosphatase with a predicted role in energy metabolism; intracellular; protein abundance decreased by menadione stress; protein expressed at increased levels during osmoadaptation	ippA	3.5482208	3.71E-05	0.000690072
AN5569	Ortholog(s) have phosphatidylinositol-3-phosphate binding, phosphatidylinositol-5-phosphate binding activity	null	-3.939358	3.71E-05	0.000690072
AN2567	Ortholog(s) have endoplasmic reticulum, mitochondrion localization	null	2.9139126	3.77E-05	0.000700749
AN10131	Dihydroorotase, catalyzes the third step in pyrimidine biosynthesis	pyrD	4.779643	3.90E-05	0.000717465
AN2677	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	null	-6.723905	3.90E-05	0.000717465
AN5520	Has domain(s) with predicted role in ribosome biogenesis and ribonucleoprotein complex localization	null	4.779643	3.90E-05	0.000717465
AN5616	Ortholog(s) have cytosol, nucleus localization	null	6.8406897	3.90E-05	0.000717465
AN9065	Ortholog(s) have translation regulator activity and role in mitochondrial respiratory chain complex IV biogenesis, positive regulation of mitochondrial translation	null	2.815922	3.93E-05	0.000720084
AN5228	Putative NADH:flavin oxidoreductase/NADH oxidase; intracellular, menadione stress-induced protein	null	3.2962107	3.94E-05	0.000720084
AN6320	Fatty acid oxygenase involved in oxylipin biosynthesis; null mutant overproduces sterigmatocystin and penicillin, displays increased conidial production and decreased ascospore production, accumulation of psiBbeta decreased	ppoB	3.2962107	3.94E-05	0.000720084
AN10863	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	null	3.0860077	3.99E-05	0.000725065

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AN8704	60S ribosomal protein L24a; PalA-dependent expression independent of pH	null	3.1761815	4.00E-05	0.000725065
AN20012	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	oxiC	2.740267	4.00E-05	0.000725065
AN6900	Putative triose-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; protein induced by farnesol	tpiA	2.9026514	4.13E-05	0.000747156
AN5819	Ortholog(s) have GTP binding, signal recognition particle binding activity, role in protein targeting to ER and integral to endoplasmic reticulum membrane localization	null	2.7916102	4.19E-05	0.000753695
AN4087	Putative 40S ribosomal protein subunit; ortholog of S. cerevisiae Rps3p; expression reduced after exposure to farnesol	null	3.5191829	4.19E-05	0.000753695
AN4727	UDP-glucose 4-epimerase, involved in galactose metabolism; converts UDP-galactose to UDP-glucose; intracellular; protein abundance decreased by menadione stress	ugeA	3.2806554	4.21E-05	0.000755448
AN10959	Has domain(s) with predicted catalytic activity	null	-3.071364	4.22E-05	0.000755448
AN4163	Protein with seven WD repeats, involved in cross-pathway control of the response to amino acid starvation; required for sexual development; palA-dependent expression independent of pH; protein induced by farnesol	cpcB	4.3235444	4.33E-05	0.000773292
AN7388	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	cpeA	-2.73056	4.37E-05	0.000778046
AN10681	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation, regulation of translational fidelity and cytosolic large ribosomal subunit localization	null	2.8008754	4.38E-05	0.000778046
AN1841	Has domain(s) with predicted nucleotide binding activity	null	3.2599519	4.60E-05	0.000816639
AN2301	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	3.053692	4.69E-05	0.0008307
AN5575	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	null	-4.721861	4.80E-05	0.000847584
AN10298	3-phosphoserine aminotransferase; intracellular; protein abundance decreased by menadione stress	null	3.5435639	4.85E-05	0.000854949
AN0248	Putative protein disulfide isomerase; pdiB mRNA levels increase in the presence of farnesol	pdiB	-4.064058	4.91E-05	0.00086191
AN8931	Ortholog of A. fumigatus Af293 : Afu1g10120, A. niger CBS 513.88 : An08g01940, A. oryzae RIB40 : AO090038000421, A. niger ATCC 1015 : 38532-mRNA and Aspergillus versicolor : Aspve1_0132736	null	-3.133344	4.97E-05	0.000871668
AN2343	Putative nitroreductase; intracellular, menadione stress-induced protein	null	2.9052507	5.01E-05	0.000871668

AN0554	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	aldA	-2.687198	5.08E-05	0.000871668
AN2980	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	2.9011201	5.10E-05	0.000871668
AN10193	Ortholog(s) have role in vacuolar protein processing and Golgi apparatus, endoplasmic reticulum, fungal-type vacuole membrane localization	null	-6.679937	5.10E-05	0.000871668
AN2912	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	null	-6.679937	5.10E-05	0.000871668
AN3480	Ortholog of A. niger CBS 513.88 : An11g08860, Aspergillus brasiliensis : Aspbr1_0114065, A. niger ATCC 1015 : 48080-mRNA, N. fischeri NRRL 181 : NFIA_008010 and Aspergillus acidus : Aspfo1_0124719	null	-6.679937	5.10E-05	0.000871668
AN3704	Has domain(s) with predicted 1-aminocyclopropane-1-carboxylate synthase activity, pyridoxal phosphate binding, transferase activity, transferring nitrogenous groups activity	null	-6.679937	5.10E-05	0.000871668
AN3881	Has domain(s) with predicted ADP binding, ATP binding, nucleoside-triphosphatase activity and role in apoptotic process, nucleoside metabolic process	null	-6.679937	5.10E-05	0.000871668
AN5942	Ortholog of Aspergillus versicolor : Aspve1_0148858 and Aspergillus sydowii : Aspsy1_0029071	null	4.7098829	5.10E-05	0.000871668
AN6736	Ortholog(s) have unfolded protein binding activity	null	4.7098829	5.10E-05	0.000871668
AN8805	Ortholog(s) have role in cellular response to oxidative stress, response to osmotic stress, ribosomal small subunit biogenesis and cytosol, nucleus localization	null	4.7098829	5.10E-05	0.000871668
AN4367	Putative chitin synthase III with a predicted role in chitin biosynthesis; transcript is induced by nitrate	chsF	3.2832935	5.16E-05	0.000879645
AN4990	Ortholog(s) have ferrous iron transmembrane transporter activity, manganese ion transmembrane transporter activity	null	-2.882733	5.36E-05	0.000910198
AN8068	Putative beta-1,4-endoglucanase	null	4.2694739	5.36E-05	0.000910198
AN9392	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.066266	5.39E-05	0.000912075
AN20001	Mitochondrially-encoded subunit 5 of NADH dehydrogenase	ndhE	2.7457327	5.45E-05	0.000920209
AN7725	Protein required for biosynthesis of pyridoxine; highly conserved throughout fungi, plants and bacteria	pyroA	2.9587833	5.69E-05	0.000958658
AN1798	Ortholog(s) have sterol esterase activity, role in cell wall mannoprotein biosynthetic process, sterol metabolic process and integral to membrane, plasma membrane localization	null	-2.923854	5.93E-05	0.000997081

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AN6236	Putative nonribosomal peptide synthetase	null	2.6690605	6.03E-05	0.001009459
AN2875	Putative fructose-bisphosphate aldolase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH	fbaA	2.6751123	6.03E-05	0.001009459
AN0465	Ortholog of S. cerevisiae RPS8A and RPS8B; palA-dependent expression independent of pH	null	2.7150253	6.06E-05	0.001011276
AN9304	Glutathione S-transferase; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.6617751	6.07E-05	0.001011276
AN0013	Possible pseudogene	null	-3.831531	6.10E-05	0.001014161
AN7181	Ortholog of A. fumigatus Af293 : Afu4g03200, A. oryzae RIB40 : AO090011000112, N. fischeri NRRL 181 : NFIA_030260, Aspergillus flavus NRRL 3357 : AFL2T_04908 and A. clavatus NRRL 1 : ACLA_055410	null	-2.998601	6.12E-05	0.001014994
AN5828	Has domain(s) with predicted heme binding activity	null	-2.784322	6.37E-05	0.001055102
AN0262	Ortholog(s) have role in ribosomal large subunit assembly and cytosol, nucleolus localization	null	2.8873371	6.46E-05	0.001066628
AN8444	Protein with similarity to cellulose synthase; predicted role in beta-glucan synthesis	celA	2.9297371	6.66E-05	0.001092512
AN1137	Putative quinate 5-dehydrogenase with a predicted role in aromatic amino acid biosynthesis	qutB	4.6365774	6.72E-05	0.001092512
AN2554	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	null	-6.634587	6.72E-05	0.001092512
AN2780	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	null	-6.634587	6.72E-05	0.001092512
AN3139	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	6.6976242	6.72E-05	0.001092512
AN5565	Ortholog(s) have lipase activity	null	-6.634587	6.72E-05	0.001092512
AN7183	Protein of unknown function; transcript upregulated by nitrate limitation	null	-6.634587	6.72E-05	0.001092512
AN0859	null	null	2.9367766	6.74E-05	0.001094559
AN5792	Ortholog of A. niger CBS 513.88 : An18g06780, A. oryzae RIB40 : AO090003000006, A. niger ATCC 1015 : 43055-mRNA, Aspergillus versicolor : Aspve1_0132738 and Aspergillus sydowii : Aspsy1_0150121	null	-4.638309	6.93E-05	0.001120177
AN11897	Has domain(s) with predicted RNA binding, ribonuclease T2 activity	null	-3.812749	6.93E-05	0.001120177
AN0186	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	null	2.8387475	7.00E-05	0.001129122

AN4842	Ortholog(s) have copper ion binding activity, role in copper ion transport, protein complex assembly and mitochondrial inner membrane localization	null	2.9812255	7.08E-05	0.001137135
AN10964	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	-2.686651	7.08E-05	0.001137135
AN11797	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-2.755954	7.28E-05	0.001166994
AN3639	Putative dihydrolipoamide transacylase; alpha keto acid dehydrogenase E2 subunit	null	-2.656434	7.44E-05	0.001190321
AN3218	Ortholog of A. oryzae RIB40 : AO090701000492 and Aspergillus flavus NRRL 3357 : AFL2T_06113	null	-3.051959	7.50E-05	0.001196956
AN4702	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.726732	7.60E-05	0.001209578
AN6731	Putative delta-9-stearic acid desaturase; converts palmitic acid and stearic acid to palmitoleic acid and oleic acid; null mutant has increased fatty acid content; synthetically lethal with sdeB mutation; expression reduced by farnesol	sdeA	2.6240229	7.93E-05	0.001259728
AN2914	Putative argininosuccinate lyase with a predicted role in arginine metabolism	null	2.7900163	8.16E-05	0.001293048
AN11771	null	null	-4.579792	8.36E-05	0.001313484
AN3430	Ortholog of A. fumigatus Af293 : Afu3g05790, A. niger CBS 513.88 : An11g10810, A. oryzae RIB40 : AO090020000047, Aspergillus versicolor : Aspve1_0040463 and Aspergillus sydowii : Aspsy1_0056861	null	3.9566016	8.36E-05	0.001313484
AN4676	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	null	-4.579792	8.36E-05	0.001313484
AN4810	Has domain(s) with predicted metallocarboxypeptidase activity and role in proteolysis	null	-4.609347	8.36E-05	0.001313484
AN1993	Putative aspartate transaminase with a predicted role in alanine, aspartate, and aromatic amino acid metabolism	null	2.6513694	8.73E-05	0.001365068
AN1899	Putative 4-hydroxyphenylpyruvate dioxygenase with a predicted role in aromatic amino acid biosynthesis; expression induced by phenylalanine and repressed by glucose; mutants unable to use phenylalanine as a sole carbon source	hpdA	-2.629626	8.73E-05	0.001365068
AN1045	Has domain(s) with predicted RNA binding, nucleotide binding activity, role in RNA processing and nucleus, ribonucleoprotein complex localization	null	3.0390943	8.74E-05	0.001365068
AN20019	Subunit II of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; one of three mitochondrially-encoded subunits	oxiB	2.6481357	8.76E-05	0.001366132
AN0776	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit localization	null	3.0218387	8.82E-05	0.001372619
AN10898	null	null	-3.119731	8.88E-05	0.001373566
AN3310	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	4.5593469	8.90E-05	0.001373566

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AN7986	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity and role in protein phosphorylation	null	-6.539373	8.90E-05	0.001373566
AN8020	Putative protein of unknown function; expression upregulated after exposure to farnesol	null	-6.539373	8.90E-05	0.001373566
AN11151	Ortholog of A. oryzae RIB40 : AO090010000656, Aspergillus versicolor : Aspve1_0047516 and Aspergillus terreus NIH2624 : ATET_04818	null	-3.754891	8.99E-05	0.001384278
AN1136	Putative myo-inositol-1(or 4)-monophosphatase with a predicted role in phospholipid metabolism; transcript inducible by quinate	qutG	-3.510351	9.26E-05	0.001422762
AN6842	Putative ortholog of S. cerevisiae Mrpl35p which is a mitochondrial large ribosomal subunit; expression reduced after exposure to farnesol	null	3.1630541	9.43E-05	0.001446256
AN3028	Ortholog of A. fumigatus Af293 : Afu3g08860, A. niger CBS 513.88 : An16g02480, A. oryzae RIB40 : AO090005001356, A. niger ATCC 1015 : 49077-mRNA and Aspergillus versicolor : Aspve1_0070326	null	2.8691494	9.52E-05	0.00145413
AN4687	Beta subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccB	-2.963067	9.52E-05	0.00145413
AN10903	Ortholog(s) have guanine deaminase activity and cytosol localization	null	-3.009477	9.55E-05	0.001455437
AN3920	Ortholog(s) have cytosol, nucleus localization	null	2.9276323	9.62E-05	0.001462869
AN6674	Ortholog of A. oryzae RIB40 : AO090005000271, A. niger ATCC 1015 : 56237-mRNA, Aspergillus versicolor : Aspve1_0154959, Aspergillus sydowii : Aspsy1_0049346 and Aspergillus terreus NIH2624 : ATET_06449	null	-3.196522	9.64E-05	0.001462869
AN7736	Ortholog(s) have cytosol localization	null	2.7912502	9.80E-05	0.00148425
AN3764	Has domain(s) with predicted catalytic activity	null	-2.794649	9.90E-05	0.001496886
AN12088	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.564863	9.95E-05	0.00150121
AN1637	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	hxB	-3.000829	0.0001015	0.001528504
AN10983	Ortholog(s) have cytosol, mitochondrion, nucleus localization	null	2.9074	0.0001044	0.00156518
AN2432	Ortholog(s) have chaperone binding, unfolded protein binding activity, role in protein refolding and mitochondrial matrix localization	null	3.1408578	0.0001045	0.00156518
AN1826	Has domain(s) with predicted hydrolase activity	null	4.154845	0.0001047	0.00156518
AN4008	Has domain(s) with predicted O-methyltransferase activity	null	-2.657176	0.0001048	0.00156518
AN10544	Has domain(s) with predicted 3-dehydroquinate dehydratase activity and role in metabolic process	null	-3.32036	0.0001054	0.00156518
AN10712	Has domain(s) with predicted pseudouridine synthase activity, snoRNA binding activity, role in ribosome biogenesis, snRNA pseudouridine synthesis and box H/ACA snoRNP complex localization	null	2.8080361	0.0001055	0.00156518
AN3452	Ortholog(s) have endoplasmic reticulum localization	null	-3.292242	0.0001056	0.00156518

AN4616	Putative 70 kilodalton heat shock protein; protein induced by farnesol	ssz1	3.1060589	0.0001056	0.00156518
AN10078	Ortholog(s) have ATPase activity, coupled to transmembrane movement of substances activity, role in fatty acid transport and integral to peroxisomal membrane localization	null	-2.898167	0.0001063	0.001571053
AN20006	Group I intron maturase encoded by the first exon and part of the intron of the mitochondrial cobA gene; facilitates the splicing of the cobA group I intron; also has DNA endonuclease activity	I-AniI	2.8441639	0.000108	0.001593295
AN1947	Has domain(s) with predicted hydrolase activity	null	-3.89215	0.0001105	0.001623988
AN6506	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism	null	3.4551012	0.0001105	0.001623988
AN11003	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	null	-3.083606	0.0001142	0.001674716
AN0688	Putative transketolase with a predicted role in the pentose-phosphate shunt or xylulose metabolism	null	2.6847874	0.0001148	0.001680136
AN10290	Has domain(s) with predicted FMN binding, pyridoxamine-phosphate oxidase activity and role in oxidation-reduction process, pyridoxine biosynthetic process	null	2.7570757	0.0001151	0.001680904
AN1814	null	null	2.9788885	0.0001153	0.001680904
AN0828	Putative amidase; expression upregulated after exposure to farnesol	null	-2.839346	0.0001176	0.001704213
AN3830	L-threonine dehydratase with a predicted role in glycine, serine, and threonine metabolism	ileA	3.3046941	0.000118	0.001704213
AN0301	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	null	-2.619769	0.0001187	0.001704213
AN12246	Ortholog(s) have cytosol localization	null	2.6834954	0.0001187	0.001704213
AN0551	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	null	6.6203936	0.0001189	0.001704213
AN11076	Ortholog of A. fumigatus Af293 : Afu3g02220, A. niger CBS 513.88 : An01g02020, A. niger ATCC 1015 : 128447-mRNA, Aspergillus versicolor : Aspve1_0056749 and Aspergillus sydowii : Aspsy1_0093720	null	-6.489301	0.0001189	0.001704213
AN3259	Ortholog of A. oryzae RIB40 : AO090011000035, Aspergillus flavus NRRL 3357 : AFL2T_04841, Aspergillus versicolor : Aspve1_0040331 and Aspergillus sydowii : Aspsy1_0029969	null	6.6203936	0.0001189	0.001704213
AN5684	Ortholog(s) have endoplasmic reticulum, fungal-type vacuole membrane localization	null	-6.489301	0.0001189	0.001704213
AN8357	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	null	-6.489301	0.0001189	0.001704213

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AN4202	Predicted ribosomal protein of the large (60S) ribosomal subunit; differentially expressed during sexual development	rpl16a	2.5646367	0.0001195	0.00170892
AN5021	Has domain(s) with predicted role in biosynthetic process	null	2.6281757	0.0001216	0.001736141
AN0360	Ortholog(s) have cytoplasm, nucleolus localization	null	-4.5188	0.0001228	0.001749608
AN2952	Ortholog of A. fumigatus Af293 : Afu3g07900, Afu8g00900, A. niger CBS 513.88 : An02g11330, An03g05560, A. oryzae RIB40 : AO090120000471 and A. niger ATCC 1015 : 213572-mRNA, 47124-mRNA	null	2.8637824	0.0001303	0.001849046
AN8639	Putative alpha,alpha-trehalose-phosphate synthase (UDP-forming) with a predicted role in trehalose biosynthesis	null	2.8637824	0.0001303	0.001849046
AN3348	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	null	3.4122689	0.0001309	0.001854602
AN4916	Ortholog(s) have role in ribosome biogenesis and cytosol, nucleolus, small-subunit processome localization	null	2.5909828	0.0001331	0.001880533
AN0870	Putative transporter with a predicted role in small molecule transport	null	3.1106018	0.0001335	0.001880533
AN10159	Ortholog of Aspergillus brasiliensis : Aspbr1_0205897, Aspergillus flavus NRRL 3357 : AFL2T_07527, A. clavatus NRRL 1 : ACLA_023190 and Aspergillus acidus : Aspfo1_0217083	null	3.2744382	0.0001335	0.001880533
AN2386	Ortholog of A. nidulans FGSC A4 : AN6413, AN8328, AN3395, AN3241, AN10369, AN1930, AN1738, AN9266, AN10886, AN7232, AN7406, AN7774, AN12202	null	3.2976937	0.0001344	0.001885932
AN8657	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.67395	0.0001344	0.001885932
AN6649	Putative fatty acyl-CoA synthetase	fatC	-3.046553	0.0001353	0.001896107
AN2585	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	2.5379475	0.0001367	0.001911122
AN8118	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	3.0588961	0.0001413	0.001971657
AN4802	60S ribosomal protein L21; ortholog of S. cerevisiae Rpl21Ap; expression reduced after exposure to farnesol	null	2.6024382	0.0001471	0.002049486
AN5990	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	null	-3.033988	0.0001475	0.002051107
AN2284	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	hemA	2.7082426	0.0001487	0.0020639
AN10875	Ortholog(s) have Golgi apparatus, endoplasmic reticulum, fungal-type vacuole membrane localization	null	-4.48731	0.0001496	0.002072147
AN3998	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.7847927	0.0001511	0.002088804

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AN1868	Putative glycerol dehydrogenase with a predicted role in glycerol metabolism; protein expressed at decreased levels in a hapX mutant versus wild-type	null	-2.909643	0.0001549	0.002134568
AN2248	Putative 4-aminobutyrate transaminase, required for utilization of gamma-aminobutyric acid (GABA); transcriptionally regulated by AmdR	gatA	-2.899541	0.0001549	0.002134568
AN0678	Ortholog(s) have nucleus localization	null	-3.83902	0.0001555	0.002137844
AN11009	Putative mitochondrial pyruvate carboxylase	null	-6.437428	0.0001601	0.002176913
AN12339	Ortholog of A. fumigatus Af293 : Afu8g01800, A. niger CBS 513.88 : An03g05910, A. oryzae RIB40 : AO090010000636, A. niger ATCC 1015 : 126296-mRNA and Aspergillus versicolor : Aspve1_0046675	null	6.5387938	0.0001601	0.002176913
AN3390	Protein with pectinesterase activity, involved in degradation of pectin	pmeA	6.5387938	0.0001601	0.002176913
AN5395	Ortholog of Aspergillus brasiliensis : Aspbr1_0032446, Aspergillus versicolor : Aspve1_0086456 and Aspergillus sydowii : Aspsy1_0092345	null	6.5387938	0.0001601	0.002176913
AN6518	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in carbohydrate metabolic process	null	-6.437428	0.0001601	0.002176913
AN7817	Putative protein with a predicted role in sterigmatocystin/aflatoxin biosynthesis	null	-6.437428	0.0001601	0.002176913
AN4465	Ortholog(s) have unfolded protein binding activity, role in negative regulation of ergosterol biosynthetic process, sterol biosynthetic process and endoplasmic reticulum localization	null	-3.021312	0.0001609	0.002183981
AN8540	Siderophore iron transporter	mirB	2.4759065	0.0001614	0.002186923
AN4222	Ortholog(s) have cytosol, nucleus localization	null	2.5535377	0.0001674	0.002264719
AN10512	Putative mitochondrial ketoacyl-CoA thiolase with a role in fatty acid beta-oxidation	mthA	-2.626232	0.0001701	0.002296201
AN4800	Ortholog of A. fumigatus Af293 : Afu3g06910, A. niger CBS 513.88 : An11g09440, A. oryzae RIB40 : AO090020000302, A. niger ATCC 1015 : 48103-mRNA and Aspergillus versicolor : Aspve1_0040110	null	-3.205926	0.0001722	0.002320484
AN10950	Cytochrome P450, member of CYP53A3 family; ortholog of A. niger bphA; required for utilization of benzamide and benzoate; transcription is inducible by benzoate and subject to carbon catabolite repression mediated by CreA	bzuA	-2.767521	0.0001737	0.0023374
AN8709	Putative aspartate transaminase with a predicted role in alanine and aspartate metabolism	null	-2.572958	0.0001753	0.002353587
AN7967	Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport and membrane localization	null	-3.631711	0.000177	0.002373262
AN2236	Ortholog of A. fumigatus Af293 : Afu5g07310, A. niger CBS 513.88 : An17g00750, A. oryzae RIB40 : AO090701000224, A. niger ATCC 1015 : 213970-mRNA and Aspergillus versicolor : Aspve1_0050602	null	-2.798812	0.0001788	0.002387913
AN7331	Has domain(s) with predicted DNA binding, cyanate hydratase activity, hydro-lyase activity and role in cyanate metabolic process	null	-2.807358	0.0001788	0.002387913

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AN6157	Orotidine-5'-phosphate decarboxylase, enzyme of the pyrimidine biosynthesis pathway	pyrG	2.6183737	0.0001799	0.002398298
AN1166	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation, ribosomal large subunit assembly and cytosolic large ribosomal subunit, nucleolus localization	null	2.5814653	0.0001805	0.002402023
AN3413	Protein with homology to ribosomal protein S2 and S5; ortholog of S. cerevisiae Rps2p; expression reduced after exposure to farnesol	null	2.5653147	0.0001812	0.002407031
AN6659	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	3.2884242	0.0001821	0.002410542
AN7523	Ortholog of A. nidulans FGSC A4 : AN0171, A. niger CBS 513.88 : An18g01570, A. oryzae RIB40 : AO090010000737, A. niger ATCC 1015 : 134538-mRNA and Aspergillus versicolor : Aspve1_0077940	null	3.2884242	0.0001821	0.002410542
AN1941	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-4.455116	0.0001829	0.002416586
AN4060	Putative ribosomal protein S16	rps16	2.6319283	0.0001843	0.002431491
AN7469	Ortholog(s) have riboflavin kinase activity, role in FMN biosynthetic process and cytosol, mitochondrial inner membrane, nucleus localization	null	2.5102497	0.0001889	0.002487062
AN12360	Has domain(s) with predicted role in response to stress	null	-2.614438	0.0001952	0.002565553
AN6940	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	2.7359851	0.0001976	0.002592977
AN1007	Putative nitrite reductase with a predicted role in nitrogen metabolism; transcript stabilized by intracellular nitrate	niiA	2.6222901	0.0001997	0.002615519
AN8079	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	null	-2.583168	0.0002021	0.002642282
AN1855	Has domain(s) with predicted phosphoric diester hydrolase activity and role in lipid metabolic process	null	2.6654253	0.0002087	0.002724828
AN4872	Fusion protein consisting of N-terminal ubiquitin and C-terminal extension protein (CEP) of the small ribosomal subunit; transcript upregulated in response to camptothecin	ubi1	2.4453814	0.0002092	0.002725929
AN1703	Putative cytochrome P450	CYP5128A1	2.9937442	0.0002096	0.002726603
AN0912	Putative Beta-isopropylmalate dehydrogenase with a predicted role in valine, leucine, and isoleucine metabolism	null	2.9851287	0.0002105	0.002733986
AN2951	Putative UDP-glucose 4-epimerase with a predicted role in galactose and galactitol metabolism	null	2.5443822	0.0002122	0.002744426
AN8523	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	null	3.2479928	0.000213	0.002744426

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AN7228	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.472971	0.0002142	0.002744426
AN0507	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	null	-6.38362	0.0002172	0.002744426
AN10627	Has domain(s) with predicted GTP binding, GTPase activity, structural molecule activity, role in GTP catabolic process, microtubule-based movement, protein polymerization and microtubule localization	null	-6.38362	0.0002172	0.002744426
AN12121	Ortholog(s) have protein tag activity and role in cell budding, cellular response to oxidative stress, invasive growth in response to glucose limitation, protein urmylation, tRNA wobble position uridine thiolation	null	-6.327728	0.0002172	0.002744426
AN2040	Putative cytochrome P450	CYP552A2	-6.327728	0.0002172	0.002744426
AN2057	Ortholog(s) have role in aerobic respiration and mitochondrial nucleoid localization	null	6.4523004	0.0002172	0.002744426
AN4877	Predicted DDE1 transposon-related ORF	null	6.4523004	0.0002172	0.002744426
AN6321	Putative cytochrome P450	CYP656A1	-6.327728	0.0002172	0.002744426
AN6704	null	null	-6.327728	0.0002172	0.002744426
AN7898	Major facilitator superfamily (MFS) transporter with a role in secondary metabolism; member of the dba gene cluster	dbaD	-6.38362	0.0002172	0.002744426
AN8292	Ortholog of A. oryzae RIB40 : AO090124000092, Aspergillus brasiliensis : Aspbr1_0118961, N. fischeri NRRL 181 : NFIA_006570, Aspergillus acidus : Aspfo1_0178460 and Aspergillus versicolor : Aspve1_0086706	null	-6.38362	0.0002172	0.002744426
AN8412	Putative hybrid polyketide synthase-nonribosomal peptide synthase (PKS-NRPS); aspyridone synthetase; member of the aspyridone (apd) gene cluster	apdA	6.4523004	0.0002172	0.002744426
AN8453	Protein with pectate lyase activity, involved in degradation of pectin	plyH	-6.327728	0.0002172	0.002744426
AN8481	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin	null	-6.327728	0.0002172	0.002744426
AN5611	Putative carbonic anhydrase	canA	2.6363701	0.0002191	0.002763047
AN4975	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	3.6232878	0.000221	0.002783394
AN4690	Alpha subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccA	-2.504541	0.0002252	0.002830583
AN8083	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.755305	0.000227	0.002848583
AN4332	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	barA	-3.165296	0.000236	0.002951796

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AN8823	Ortholog of A. fumigatus Af293 : Afu5g06020, A. niger CBS 513.88 : An17g01805, A. oryzae RIB40 : AO090009000658, A. niger ATCC 1015 : 51067-mRNA and Aspergillus versicolor : Aspve1_0088214	null	-3.14699	0.000236	0.002951796
AN5800	Ortholog(s) have cytosol localization	null	2.4884304	0.0002385	0.002978183
AN3832	Ortholog(s) have role in mitochondrial translation and mitochondrion localization	null	2.6547692	0.0002411	0.003005924
AN20017	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	atp9	2.3976856	0.0002428	0.003017844
AN4787	Putative ribosomal protein L37; palA-dependent expression independent of pH	rpl37	2.4442548	0.0002429	0.003017844
AN2872	null	null	2.58308	0.0002444	0.003032044
AN8912	Ortholog(s) have role in ascospore formation, conjugation with cellular fusion and Golgi apparatus, fungal-type vacuole membrane localization	null	-2.709076	0.0002453	0.003037467
AN5170	Putative Zn(II)2Cys6 transcription factor; negative regulator of sexual development	rosA	-2.573188	0.0002466	0.003049063
AN1915	Ortholog(s) have electron carrier activity, oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor activity, role in electron transport chain, heme a biosynthetic process and mitochondrial inner membrane localization	null	2.8372037	0.0002506	0.003082793
AN3606	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	null	-2.929318	0.0002506	0.003082793
AN6476	null	null	-2.929318	0.0002506	0.003082793
AN0840	Putative alpha-isopropylmalate synthase with a predicted role in valine, leucine, and isoleucine metabolism	null	2.6813815	0.0002551	0.003133195
AN4848	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	null	-2.691933	0.0002601	0.003188659
AN10229	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity and role in oxidation-reduction process	null	3.2755687	0.0002647	0.00322911
AN1304	null	null	3.5762671	0.0002647	0.00322911
AN6834	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.726506	0.0002647	0.00322911
AN0918	Putative ceramide hydroxylase with a predicted role in sphingoglycolipid metabolism	null	2.3995361	0.0002674	0.003257775
AN8163	Putative short-chain dehydrogenase/reductase	null	-2.862601	0.0002695	0.003277552
AN1584	Ortholog(s) have transcription cofactor activity, role in negative regulation of calcium ion-dependent exocytosis and nucleus localization	null	-3.54333	0.0002711	0.003291942

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AN9123	Ortholog of Aspergillus brasiliensis : Aspbr1_0040215, Aspbr1_0678615, Aspergillus versicolor : Aspve1_0140141, Aspergillus niger ATCC 1015 : 183284-mRNA and Aspergillus sydowii : Aspsy1_0158152	null	3.9637742	0.0002727	0.003305766
AN0833	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	null	2.3640863	0.0002838	0.003434158
AN4018	Ortholog(s) have role in protein targeting to vacuole	null	-2.917305	0.0002863	0.003459049
AN5566	Putative GMP synthase (glutamine-hydrolyzing) with a predicted role in purine metabolism	null	2.949003	0.0002876	0.003469015
AN6091	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	null	2.4697643	0.0002924	0.003521726
AN10005	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-6.269582	0.0002974	0.003541409
AN12373	null	null	4.2992422	0.0002974	0.003541409
AN3190	Ortholog of A. fumigatus Af293 : Afu4g02920, A. niger CBS 513.88 : An14g02990, A. oryzae RIB40 : AO090001000192, A. niger ATCC 1015 : 201534-mRNA and Aspergillus versicolor : Aspve1_0140942	null	-6.269582	0.0002974	0.003541409
AN3276	Putative Type II fatty acid synthase with a predicted role in mitochondrial fatty acid formation	null	6.3602889	0.0002974	0.003541409
AN3658	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.269582	0.0002974	0.003541409
AN7739	Has domain(s) with predicted DNA binding activity	null	6.3602889	0.0002974	0.003541409
AN7942	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	null	4.2992422	0.0002974	0.003541409
AN2876	Ortholog of A. clavatus NRRL 1 : ACLA_039650, Aspergillus versicolor : Aspve1_0051465, Aspergillus sydowii : Aspsy1_0146596 and Aspergillus terreus NIH2624 : ATET_04728	null	-3.109669	0.0003003	0.003568789
AN5134	Glutamate synthase, NAD(+)-dependent (GOGAT) with a predicted role in glutamate and glutamine metabolism; required for ammonium uptake in the absence of NADP-glutamate dehydrogenase GdhA; transcript upregulated by nitrate limitation	gltA	2.3921255	0.0003006	0.003568789
AN5339	Ortholog of A. oryzae RIB40 : AO090103000416, A. niger ATCC 1015 : 47268-mRNA, Aspergillus versicolor : Aspve1_0044729, Aspergillus sydowii : Aspsy1_0050291 and Aspergillus terreus NIH2624 : ATET_00936	null	-2.796132	0.0003024	0.003584518
AN10174	Ortholog of A. fumigatus Af293 : Afu1g10090, A. oryzae RIB40 : AO090038000427, A. niger ATCC 1015 : 52788-mRNA, Aspergillus sydowii : Aspsy1_0139584 and Aspergillus terreus NIH2624 : ATET_00177	null	2.6609609	0.0003054	0.003614031

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AN4159	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	glnA	2.3745901	0.0003103	0.003666295
AN8995	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.520362	0.0003136	0.003699646
AN4172	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	null	-3.696951	0.0003178	0.003740086
AN1743	Putative methyltransferase with a predicted role in histidine metabolism	null	2.5783299	0.0003181	0.003740086
AN0485	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	null	-2.499937	0.0003192	0.00374746
AN5906	Has domain(s) with predicted ubiquitin-protein ligase activity, role in protein ubiquitination and ubiquitin ligase complex localization	null	2.4229858	0.0003204	0.003755423
AN10993	Ortholog of A. fumigatus Af293 : Afu2g01310, A. niger CBS 513.88 : An03g05110, A. oryzae RIB40 : AO090701000405, A. niger ATCC 1015 : 50726-mRNA and Aspergillus versicolor : Aspve1_0043704	null	-2.539419	0.0003209	0.003755596
AN4777	Ortholog(s) have structural constituent of ribosome activity	null	2.4156706	0.0003254	0.003802299
AN1754	Putative protein of unknown function; expression upregulated after exposure to farnesol	null	-3.259032	0.0003285	0.00383227
AN11303	Ortholog(s) have proton-transporting ATPase activity, rotational mechanism, structural molecule activity and role in ATP synthesis coupled proton transport, cristae formation, protein oligomerization	null	2.4936561	0.0003315	0.003862099
AN4500	Putative mitochondrial ATPase inhibitor; expression upregulated after exposure to farnesol	null	2.3473863	0.0003344	0.003889574
AN8275	Mitochondrial citrate synthase with a predicted role in the TCA cycle	citA	2.3767195	0.0003365	0.003906051
AN6785	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	null	-2.621485	0.0003369	0.003906051
AN11802	Ortholog(s) have N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity and role in dolichol-linked oligosaccharide biosynthetic process	null	-3.090639	0.0003394	0.003916855
AN10746	MOSC-domain containing protein; transcript repressed by nitrate	null	-4.282402	0.0003415	0.003916855
AN2270	C2H2 zinc-finger transcription factor involved in regulation of structural genes for acetamidase (amdS), formate dehydrogenase (aciA), and alcohol dehydrogenase II (alcB)	amdA	-4.318638	0.0003415	0.003916855

AN2305	Ortholog of A. fumigatus Af293 : Afu5g06030, A. niger CBS 513.88 : An17g01795, A. niger ATCC 1015 : 192595-mRNA, Aspergillus versicolor : Aspve1_0124892 and Aspergillus sydowii : Aspsy1_0139055	null	-4.318638	0.0003415	0.003916855
AN5885	Putative catalytic subunit of the alpha-1,3 glucan synthase complex; locus contains the conserved upstream open reading frame (uORF) AN5885-uORF	agsA	-4.282402	0.0003415	0.003916855
AN8223	Protein with a putative role in carbon-starvation response; two ABM motifs; induced by carbon starvation-induced autophagy	null	-4.282402	0.0003415	0.003916855
AN8741	Has domain(s) with predicted DNA binding, zinc ion binding activity and intracellular localization	null	-4.282402	0.0003415	0.003916855
AN10651	Ortholog(s) have cytosol localization	null	2.880511	0.0003536	0.004047407
AN6985	Putative ribulokinase with a predicted role in ribulose metabolism	null	-2.417897	0.0003548	0.004047407
AN1694	Ortholog(s) have cytosol, nucleus localization	null	2.5117885	0.000355	0.004047407
AN3829	Putative succinate-semialdehyde dehydrogenase [NAD(P)+] with a predicted role in 4-aminobutyrate (GABA) shunt	null	-2.561094	0.000355	0.004047407
AN9339	Hyphal catalase with a predicted role in gluconic acid and gluconate metabolism	catB	2.7680204	0.0003582	0.004077384
AN9407	Fatty acid synthase, alpha subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid biosynthesis	fasA	2.3449069	0.0003596	0.004086765
AN1037	Oleate delta-12 desaturase; transcriptionally regulated by low temperature and by light	odeA	2.6718941	0.000368	0.004175979
AN1964	Ortholog of S. cerevisiae RPS6B and RPS6A; palA-dependent expression independent of pH	null	2.6152373	0.00037	0.004192876
AN6436	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	null	3.0782281	0.0003757	0.004250978
AN3431	Ortholog(s) have nicotinate-nucleotide diphosphorylase (carboxylating) activity, role in de novo NAD biosynthetic process from tryptophan and cytoplasm, nucleus localization	null	2.4389824	0.000382	0.004314815
AN10619	Has domain(s) with predicted carboxy-lyase activity, pyridoxal phosphate binding activity and role in carboxylic acid metabolic process	null	3.4773623	0.0003827	0.004316346
AN11419	Ortholog(s) have cytosol localization	null	2.41674	0.0003852	0.00433794
AN2147	Putative ribosomal RNA processing protein; ortholog of S. cerevisiae Rrp5p; expression reduced after exposure to farnesol	rrp5	2.5003586	0.0003901	0.004379713
AN8406	Putative alcohol dehydrogenase; intracellular, menadione stress-induced protein; protein expressed at decreased levels in a hapX mutant versus wild-type	null	2.5003586	0.0003901	0.004379713
AN1109	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.654706	0.0003956	0.004435563
AN7430	Putative glutamine amidotransferase with a predicted role in histidine metabolism	hisHF	2.6049843	0.000397	0.004444508
AN4494	Ortholog(s) have mitochondrion, nucleus localization	null	2.4533721	0.0003977	0.004445715

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AN4277	Ortholog(s) have glucose transmembrane transporter activity and plasma membrane localization	null	-2.393618	0.0004042	0.004511534
AN0015	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	null	-6.208994	0.0004109	0.004558646
AN10952	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-6.208994	0.0004109	0.004558646
AN4124	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-6.208994	0.0004109	0.004558646
AN8005	Putative GNAT-type acetyltransferase	ngn9	-6.208994	0.0004109	0.004558646
AN2932	Putative eukaryotic initiation factor 4A; expression reduced after exposure to farnesol	null	2.3607085	0.0004126	0.004571448
AN9117	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-2.509882	0.0004143	0.004583428
AN20005	Cytochrome b, mitochondrially encoded subunit of the ubiquinol-cytochrome c reductase complex	cobA	2.3256161	0.0004157	0.004591883
AN8445	Putative aminopeptidase Y; transcript is induced by nitrate	null	-2.316553	0.0004216	0.004647327
AN5601	Putative saccharopine dehydrogenase (NADP+, L-glutamate-forming) with a predicted role in lysine metabolism	null	3.0763544	0.000422	0.004647327
AN11085	Putative D-arabinitol 4-dehydrogenaset	null	-2.682339	0.0004234	0.004656292
AN0404	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	null	2.3667699	0.0004298	0.004713201
AN6567	Ortholog(s) have role in histone acetylation and NuA4 histone acetyltransferase complex localization	null	-3.194244	0.0004305	0.004713201
AN6996	Ortholog(s) have mitochondrion localization	null	-3.216165	0.0004305	0.004713201
AN5129	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	hsp70	2.2895767	0.0004339	0.004743827
AN2837	Ortholog of A. nidulans FGSC A4 : AN5509, AN2029, A. fumigatus Af293 : Afu4g00200, A. oryzae RIB40 : AO090023000015, AO090113000086 and N. fischeri NRRL 181 : NFIA_003110, NFIA_045440	null	-3.031997	0.0004351	0.004750184
AN3573	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	null	-3.016064	0.0004379	0.004773854
AN1805	Putative carbonic anhydrase; required for growth in ambient CO2 conditions; protein expressed at increased levels during osmoadaptation	canB	2.4330837	0.000443	0.004821459

AN0788	Ortholog of A. niger CBS 513.88 : An09g02430, An03g05960, An09g00710, An09g01710 and A. oryzae RIB40 : AO090003000250, AO090010000570, AO090023000882, AO090120000022, AO090012000900	null	-2.520789	0.0004467	0.004854757
AN4475	Ortholog(s) have role in ribosomal large subunit assembly and cytosol localization	null	2.4574769	0.0004476	0.004857766
AN2538	Ortholog of Aspergillus versicolor : Aspve1_0026536 and Aspergillus sydowii : Aspsy1_0028980	null	-2.662206	0.0004525	0.004903867
AN11880	null	null	3.8207086	0.0004546	0.004905373
AN5890	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	3.8207086	0.0004546	0.004905373
AN6794	null	null	3.8207086	0.0004546	0.004905373
AN0034	Putative glycerone kinase with a predicted role in glycerol metabolism; transcript upregulated by growth in glycerol	null	-2.430851	0.0004555	0.004907831
AN5399	Ortholog of A. fumigatus Af293 : Afu2g15280, A. niger CBS 513.88 : An18g02600, A. oryzae RIB40 : AO090003001548, A. niger ATCC 1015 : 42737-mRNA and Aspergillus versicolor : Aspve1_0045700	null	-3.604468	0.0004622	0.004973054
AN7771	Ortholog of A. fumigatus Af293 : Afu5g07480, A. niger CBS 513.88 : An15g02850, A. oryzae RIB40 : AO090701000657, A. niger ATCC 1015 : 48718-mRNA and Aspergillus versicolor : Aspve1_0072039	null	2.4176081	0.0004653	0.004998619
AN11347	Ortholog(s) have cytochrome-c oxidase activity, role in mitochondrial electron transport, cytochrome c to oxygen and mitochondrial respiratory chain complex IV localization	null	2.4430103	0.0004681	0.005021805
AN7708	Ortholog(s) have alditol:NADP+ 1-oxidoreductase activity, role in D-xylose catabolic process, arabinose catabolic process, cellular response to oxidative stress and cytosol, nucleus localization	null	2.3454896	0.0004785	0.005125908
AN1215	Putative GTPase; S. cerevisiae ortholog Nug1p has role in rRNA processing; expression reduced after exposure to farnesol	null	2.5034909	0.0004837	0.005175002
AN9138	Putative amidase/acetamidase	null	-2.287372	0.0004921	0.00525424
AN4577	Putative kynurenine formamidase with a predicted role in aromatic amino acid biosynthesis; transcript induced under low nitrogen conditions	fmdS	-3.171985	0.000494	0.00525424
AN6246	Cytochrome C	cycA	2.3339913	0.0004946	0.00525424
AN1122	Ortholog(s) have cytosol localization	null	2.4600743	0.0004952	0.00525424
AN2395	Putative beta-glucuronidase with a predicted role in polysaccharide degradation	null	-2.475225	0.0004954	0.00525424
AN9465	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus localization	null	2.4225545	0.0004954	0.00525424
AN6205	Ortholog of A. fumigatus Af293 : Afu6g11420, A. niger CBS 513.88 : An05g02520, An02g13310, An08g07320, A. oryzae RIB40 : AO090010000327, AO090103000241, AO090023000470 and A. niger ATCC 1015 : 37520-mRNA	null	2.5495968	0.0005003	0.005299431

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AN5763	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.547513	0.0005165	0.005462877
AN11374	null	null	-4.207078	0.0005281	0.005574035
AN5441	Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), rRNA export from nucleus	null	2.3757298	0.0005285	0.005574035
AN1228	Ortholog(s) have role in maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, nucleolus, preribosome, large subunit precursor localization	null	2.482454	0.0005321	0.005603549
AN9069	Ortholog of A. fumigatus Af293 : Afu7g02500, A. niger CBS 513.88 : An12g00100, A. oryzae RIB40 : AO090038000626, A. niger ATCC 1015 : 56966-mRNA and Aspergillus versicolor : Aspve1_0144824	null	-2.669212	0.0005405	0.005684618
AN10834	Protein with an acyl-CoA dehydrogenase domain	acdB	2.3158312	0.0005434	0.005700956
AN10108	Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.96442	0.0005445	0.005700956
AN5673	Possible pseudogene	null	-2.96442	0.0005445	0.005700956
AN0191	Ortholog(s) have ATPase activity, tRNA binding activity, role in regulation of transcription from RNA polymerase II promoter, tRNA wobble uridine modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	-3.539347	0.00056	0.005700956
AN1539	Subunit 4 of the COP9 signalosome; required for light-dependent asexual and sexual development and cleistothecia production; regulates secondary metabolite production, mutant hyphae are aberrant with abnormal red pigmentation	csnD	-3.539347	0.00056	0.005700956
AN9032	Ortholog of A. nidulans FGSC A4 : AN10883, A. fumigatus Af293 : Afu7g06950, Afu8g02470, A. niger CBS 513.88 : An03g06330, An03g00350, An05g02580 and A. oryzae RIB40 : AO090010000660	null	3.4252452	0.00056	0.005700956
AN6747	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	null	-2.97087	0.0005609	0.005700956
AN3207	Ortholog of A. nidulans FGSC A4 : AN1505, A. fumigatus Af293 : Afu2g15470, Afu8g00720, Afu8g05070 and A. niger CBS 513.88 : An07g04980, An16g07680, An14g02720, An14g07130, An15g05540	null	-2.537355	0.0005716	0.005700956
AN4316	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.546921	0.0005716	0.005700956
AN7992	Ortholog of A. fumigatus Af293 : Afu5g02500, A. niger CBS 513.88 : An02g10280, A. niger ATCC 1015 : 173308-mRNA, Aspergillus versicolor : Aspve1_0064892 and Aspergillus sydowii : Aspsy1_0047959	null	-3.374303	0.0005721	0.005700956
AN0694	Ortholog(s) have intracellular localization	null	-6.079606	0.0005733	0.005700956

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AN0878	Extracellular laccase, a copper-containing enzyme that oxidizes phenolic substrates	lccD	6.262007	0.0005733	0.005700956
AN0949	Has domain(s) with predicted iron ion binding, oxidoreductase activity and role in fatty acid biosynthetic process, oxidation-reduction process	null	-6.079606	0.0005733	0.005700956
AN10254	Ortholog of A. fumigatus Af293 : Afu4g10530, A. niger CBS 513.88 : An04g06150, A. niger ATCC 1015 : 193550-mRNA, Aspergillus versicolor : Aspve1_0050207 and Aspergillus sydowii : Aspsy1_0053923	null	6.262007	0.0005733	0.005700956
AN10812	Protein of unknown function; transcript repressed by nitrate	null	4.2009603	0.0005733	0.005700956
AN11872	null	null	6.262007	0.0005733	0.005700956
AN12269	Ortholog of A. fumigatus Af293 : Afu5g12450, A. niger CBS 513.88 : An14g06770, A. oryzae RIB40 : AO090120000369, A. niger ATCC 1015 : 121597-mRNA and Aspergillus versicolor : Aspve1_0035337	null	-6.079606	0.0005733	0.005700956
AN1600	Has domain(s) with predicted nucleotide binding activity	null	6.262007	0.0005733	0.005700956
AN1858	Putative tryptophan 2,3-dioxygenase with a predicted role in aromatic amino acid biosynthesis	null	-6.14575	0.0005733	0.005700956
AN1958	null	null	-6.14575	0.0005733	0.005700956
AN2235	Ortholog of A. fumigatus Af293 : Afu5g07270, A. niger CBS 513.88 : An17g00710, A. oryzae RIB40 : AO090701000228, A. niger ATCC 1015 : 192711-mRNA and Aspergillus versicolor : Aspve1_0038524	null	6.262007	0.0005733	0.005700956
AN4351	Protein involved in a signaling pathway that activates PacC transcription factor in response to alkaline ambient pH	palA	-6.079606	0.0005733	0.005700956
AN4720	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-6.079606	0.0005733	0.005700956
AN5112	Ortholog of A. fumigatus Af293 : Afu1g07620, A. niger CBS 513.88 : An07g10250, A. oryzae RIB40 : AO090012001014, A. niger ATCC 1015 : 39574-mRNA and Aspergillus versicolor : Aspve1_0045822	null	-6.079606	0.0005733	0.005700956
AN5274	Ortholog(s) have sequence-specific DNA binding activity	null	-6.079606	0.0005733	0.005700956
AN5731	Putative chorismate synthase with a predicted role in aromatic amino acid biosynthesis	null	6.262007	0.0005733	0.005700956
AN5855	Has domain(s) with predicted ATP adenylyltransferase activity	null	-6.079606	0.0005733	0.005700956
AN6128	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity, role in carbohydrate metabolic process and membrane localization	null	6.262007	0.0005733	0.005700956
AN6324	Putative alpha-amylase with a predicted role in starch metabolism; predicted glycosylphosphatidylinositol (GPI)-anchored protein	amyE	-6.079606	0.0005733	0.005700956
AN6398	Ortholog(s) have intracellular localization	null	-6.14575	0.0005733	0.005700956
AN6401	Putative hydrophobin	null	-6.079606	0.0005733	0.005700956

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AN6460	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	null	4.2009603	0.0005733	0.005700956
AN7135	Protein with rhamnogalacturonan lyase activity, involved in degradation of pectin	rglA	-6.14575	0.0005733	0.005700956
AN7240	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.14575	0.0005733	0.005700956
AN7278	Putative glutamate decarboxylase with a predicted role in the 4-aminobutyrate (GABA) shunt	null	6.262007	0.0005733	0.005700956
AN7557	Has domain(s) with predicted transporter activity, role in transmembrane transport and membrane localization	null	6.262007	0.0005733	0.005700956
AN8309	Putative cytochrome P450	CYP682B1	-6.14575	0.0005733	0.005700956
AN8473	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	null	-6.14575	0.0005733	0.005700956
AN8793	Putative succinate dehydrogenase (ubiquinone) with a predicted role in the TCA cycle; palA-dependent expression independent of pH	carC	4.2009603	0.0005733	0.005700956
AN8940	Ortholog of Aspergillus terreus NIH2624 : ATET_03481	null	-6.079606	0.0005733	0.005700956
AN4268	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	2.4352392	0.0005734	0.005700956
AN10166	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	null	-2.409356	0.000575	0.005702383
AN1049	Putative zinc metalloproteinase; PalA-dependent expression independent of pH	null	2.3861427	0.000575	0.005702383
AN4361	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	metR	2.4245328	0.0005817	0.00576106
AN0403	Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	2.4131151	0.0005907	0.005842373
AN10305	Has domain(s) with predicted hydrogen ion transmembrane transporter activity, role in ATP hydrolysis coupled proton transport and proton-transporting V-type ATPase, V0 domain localization	null	3.7434781	0.0005922	0.005848802
AN5833	Putative acetyl-CoA synthase with a predicted role in two-carbon metabolism or the methylcitrate pathway; transcript induced by heptadecanoic acid	pcsA	-2.403234	0.0005983	0.005901131
AN1402	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	null	-2.315285	0.0006028	0.005937587
AN1084	Putative elongation factor EF-Tu; intracellular, menadione stress-induced protein	null	2.4045978	0.0006035	0.005937587

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AN8269	90 kilodalton heat shock protein; physically associates with importin-alpha, KapA; palA-dependent expression independent of pH	hsp90	2.2251987	0.0006118	0.006011314
AN4234	Putative phosphoacetylglucosamine mutase with a predicted role in chitin biosynthesis	pcmA	2.6531186	0.0006248	0.006130567
AN5413	Ortholog of Aspergillus acidus : Aspfo1_0061846	null	-2.494204	0.0006442	0.006310311
AN6181	Ortholog(s) have cytosol localization	null	2.324595	0.0006448	0.006310311
AN4233	Ortholog(s) have cytosol, nucleus localization	null	3.5123514	0.0006609	0.006442627
AN5179	Ortholog(s) have role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and cytosol localization	null	3.5123514	0.0006609	0.006442627
AN8891	Putative exopolygalacturonase	pgxB	-4.167888	0.0006609	0.006442627
AN8899	Ortholog(s) have cytosol, nucleus localization	null	2.9943257	0.0006681	0.006504386
AN10177	null	null	3.0268629	0.000679	0.006601578
AN6394	Putative acyl-coA dehydrogenase	null	-2.608491	0.0006835	0.006636863
AN7687	Ortholog(s) have mitochondrion localization	null	2.2309053	0.0006956	0.006745933
AN8557	Protein of unknown function; transcript is induced by nitrate	null	2.4969811	0.0006974	0.006754554
AN0705	Ortholog(s) have isoleucine-tRNA ligase activity, role in isoleucyl-tRNA aminoacylation and cytosol localization	null	2.30159	0.0007119	0.006885299
AN5568	Putative F-box protein	null	2.2310072	0.0007188	0.006934924
AN5764	Transcript induced by light in in developmentally competent mycelia	null	-2.419919	0.0007195	0.006934924
AN8273	Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism; hapX-repressed; protein levels decrease in response to farnesol	null	2.2494712	0.0007198	0.006934924
AN6909	Putative bestrophin-like protein; similar to plasma membrane anion channels	BEST2	-2.345793	0.0007286	0.007010616
AN7860	Ortholog of A. nidulans FGSC A4 : AN9318, A. fumigatus Af293 : Afu8g01270 and A. oryzae RIB40 : AO090010000599, AO090005000383, AO090011000082, AO090020000631	null	2.6081042	0.0007324	0.007038253
AN2208	Putative galactose 1-dehydrogenase with a predicted role in galactonic acid and galactonate metabolism; NAD binding Rossmann fold oxidoreductase; intracellular, menadione stress-induced protein	null	2.4685079	0.0007399	0.007101159
AN1087	Putative cytochrome P450	CYP578B1	-2.411367	0.0007428	0.007120194
AN0653	Ortholog(s) have cytosol, nucleus localization	null	2.7669929	0.0007537	0.007206028
AN8356	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	null	-3.10307	0.0007537	0.007206028
AN12408	Ortholog(s) have Golgi apparatus, fungal-type vacuole membrane localization	null	-2.340446	0.0007547	0.007206028
AN10982	Putative P-type ATPase sodium pump	enaC	-2.220213	0.0007707	0.007350103

AN6048	Putative aspartate transaminase with a predicted role in amino acid metabolism; palA-dependent expression independent of pH; induced by carbon starvation-induced autophagy	null	2.1890237	0.0007753	0.007383854
AN8856	Ortholog(s) have RNA binding activity, role in ribosomal large subunit assembly and cytosol localization	null	2.2423583	0.0007779	0.00739934
AN1752	Putative sulfite reductase with a predicted role in sulfur metabolism	null	2.7352256	0.0007928	0.007522142
AN2621	Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase, nonribosomal peptide synthase, the first enzyme of the penicillin biosynthesis pathway	acvA	2.7352256	0.0007928	0.007522142
AN7949	Ortholog of A. fumigatus Af293 : Afu7g05200, A. oryzae RIB40 : AO090011000198, AO090003000528, Aspergillus versicolor : Aspve1_0087362 and Aspergillus sydowii : Aspsy1_0033753	null	2.4591054	0.0008063	0.007524876
AN0804	Ortholog(s) have cytosol, nucleus localization	null	-6.010283	0.0008082	0.007524876
AN11187	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-6.010283	0.0008082	0.007524876
AN12152	Ortholog(s) have 4-hydroxybenzoate octaprenyltransferase activity, antioxidant activity and role in polyprenol biosynthetic process, ubiquinone biosynthetic process	null	4.0954904	0.0008082	0.007524876
AN1596	Putative short-chain dehydrogenase; member of the PbcR-activated diterpene cluster	null	6.1565371	0.0008082	0.007524876
AN1734	Ortholog of A. fumigatus Af293 : Afu6g08740, A. niger CBS 513.88 : An11g06130, A. oryzae RIB40 : AO090001000548, A. niger ATCC 1015 : 39163-mRNA and Aspergillus versicolor : Aspve1_0124562	null	-6.010283	0.0008082	0.007524876
AN2312	Has domain(s) with predicted integral to membrane localization	null	-6.010283	0.0008082	0.007524876
AN2590	Has domain(s) with predicted FMN binding, heme binding, oxidoreductase activity and role in oxidation-reduction process	null	4.0954904	0.0008082	0.007524876
AN3574	null	null	-6.010283	0.0008082	0.007524876
AN3822	Has domain(s) with predicted hydrolase activity	null	-6.010283	0.0008082	0.007524876
AN4801	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	4.0954904	0.0008082	0.007524876
AN6831	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	6.1565371	0.0008082	0.007524876
AN7378	Ortholog of A. fumigatus Af293 : Afu4g14205, A. niger CBS 513.88 : An15g07560, A. oryzae RIB40 : AO090103000092, A. niger ATCC 1015 : 40862-mRNA and Aspergillus versicolor : Aspve1_0187655	null	4.0954904	0.0008082	0.007524876
AN7825	Putative polyketide synthase with a predicted role in sterigmatocystin/aflatoxin biosynthesis; member of the sterigmatocystin biosynthesis gene cluster	stcA	6.1565371	0.0008082	0.007524876
AN8928	Putative plasma membrane ATP-binding cassette (ABC) transporter with a predicted role in multidrug resistance; transcript induced by the fungicide imazalil	atrA	6.1565371	0.0008082	0.007524876
AN5372	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.4129102	0.0008094	0.007526822

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AN3024	Ortholog of A. fumigatus Af293 : Afu3g08880, A. oryzae RIB40 : AO090005001351, N. fischeri NRRL 181 : NFIA_068240, A. clavatus NRRL 1 : ACLA_036860 and Aspergillus versicolor : Aspve1_0039444	null	-2.782834	0.0008141	0.007560401
AN1520	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	null	2.7318161	0.0008293	0.007630032
AN1262	Ortholog of A. fumigatus Af293 : Afu1g10170, A. oryzae RIB40 : AO090038000416, A. niger ATCC 1015 : 38529-mRNA, Aspergillus versicolor : Aspve1_0121257 and Aspergillus sydowii : Aspsy1_0025487	null	3.0143	0.00083	0.007630032
AN2054	Ortholog(s) have histone kinase activity (H3-T3 specific) activity and role in mitotic sister chromatid segregation, regulation of histone H3-T3 phosphorylation involved in chromosome passenger complex localization to kinetochore	null	3.0143	0.00083	0.007630032
AN5383	null	null	-3.471146	0.00083	0.007630032
AN5648	Has domain(s) with predicted Rho GTPase binding, actin binding activity and role in actin cytoskeleton organization	null	-3.471146	0.00083	0.007630032
AN8662	Ortholog of A. nidulans FGSC A4 : AN11201, A. niger CBS 513.88 : An12g09180, A. oryzae RIB40 : AO090023000027, A. niger ATCC 1015 : 42065-mRNA and Aspergillus versicolor : Aspve1_0031400, Aspve1_0153960	null	3.3149984	0.00083	0.007630032
AN9047	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	null	3.3149984	0.00083	0.007630032
AN10523	Ortholog(s) have role in double-strand break repair via homologous recombination, meiotic DNA double-strand break processing, mitotic sister chromatid segregation, replication fork protection and Smc5-Smc6 complex, nucleus localization	null	-4.086162	0.0008308	0.007630032
AN1423	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane, plasma membrane localization	null	-4.127603	0.0008308	0.007630032
AN5919	Ortholog(s) have role in ascospore formation, cellular response to nitrogen starvation, multivesicular body membrane disassembly, piecemeal microautophagy of nucleus, vacuolar protein processing	null	-2.627427	0.0008322	0.007633647
AN3706	S. cerevisiae ortholog RPS10A has role in rRNA export from nucleus; palA-dependent expression independent of pH	null	2.4108269	0.0008371	0.007669273
AN5092	Putative RecQ protein; telomere linked helicase	null	2.595185	0.0008521	0.00779768
AN8044	Ortholog(s) have metalloendopeptidase activity, role in peptide pheromone maturation and cytosol, extrinsic to membrane localization	null	2.2140394	0.0008595	0.00785523
AN3681	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	null	-2.693521	0.0008673	0.007916781

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AN0132	Ortholog of A. fumigatus Af293 : Afu5g11630, A. niger CBS 513.88 : An18g03110, A. oryzae RIB40 : AO090026000663, A. niger ATCC 1015 : 42787-mRNA and Aspergillus versicolor : Aspve1_0035450	null	2.8915001	0.0008707	0.007918586
AN11843	Ortholog of A. fumigatus Af293 : Afu1g11535, A. niger ATCC 1015 : 138318-mRNA, Aspergillus versicolor : Aspve1_0289755 and Aspergillus sydowii : Aspsy1_0083601	null	2.8915001	0.0008707	0.007918586
AN6206	Ortholog of A. fumigatus Af293 : Afu2g11880, A. oryzae RIB40 : AO090026000453, Aspergillus brasiliensis : Aspbr1_0203997, N. fischeri NRRL 181 : NFIA_087110 and A. clavatus NRRL 1 : ACLA_070820	null	2.7276637	0.0008707	0.007918586
AN8365	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.2073282	0.0009085	0.008252918
AN2427	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.9073503	0.0009169	0.008318582
AN3072	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	-2.48397	0.0009263	0.008393604
AN5960	Ortholog(s) have mRNA binding activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	2.1876575	0.0009282	0.008401028
AN7532	Ortholog of A. niger CBS 513.88 : An11g07940, A. oryzae RIB40 : AO090001000606, Aspergillus brasiliensis : Aspbr1_0050895, N. fischeri NRRL 181 : NFIA_054950 and A. clavatus NRRL 1 : ACLA_083130	null	-2.186686	0.0009313	0.00841852
AN3145	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	null	-2.862858	0.0009475	0.008534495
AN5853	Has domain(s) with predicted transferase activity, transferring acyl groups other than amino-acyl groups activity and role in metabolic process	null	-2.885117	0.0009475	0.008534495
AN7283	Ortholog of A. fumigatus Af293 : Afu2g16980, A. niger ATCC 1015 : 51412-mRNA, Aspergillus versicolor : Aspve1_0123900, Aspergillus sydowii : Aspsy1_0140978 and Aspergillus terreus NIH2624 : ATET_10101	null	-2.885117	0.0009475	0.008534495
AN10803	Ortholog of Aspergillus brasiliensis : Aspbr1_0204155, Aspergillus flavus NRRL 3357 : AFL2T_06924, Aspergillus acidus : Aspfo1_0055346 and Aspergillus versicolor : Aspve1_0130960	null	2.2603949	0.0009627	0.008654817
AN5490	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	null	-2.512808	0.0009635	0.008654817
AN3481	Ortholog of A. fumigatus Af293 : Afu1g02290, A. niger CBS 513.88 : An01g05960, A. oryzae RIB40 : AO090026000175, A. niger ATCC 1015 : 51930-mRNA and Aspergillus versicolor : Aspve1_0039102	null	2.2030948	0.0009644	0.008654817
AN4833	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	2.2771596	0.0009862	0.008840303

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AN5917	Ortholog(s) have alpha-glucoside:hydrogen symporter activity, maltose:hydrogen symporter activity, trehalose transmembrane transporter activity and role in disaccharide catabolic process, maltose transport, trehalose transport	null	-2.232798	0.0009907	0.008865564
AN0048	Ortholog of A. fumigatus Af293 : Afu5g12560, A. niger CBS 513.88 : An14g06630, A. oryzae RIB40 : AO090120000382, A. niger ATCC 1015 : 201783-mRNA and Aspergillus versicolor : Aspve1_0035341	null	-2.473269	0.0009914	0.008865564
AN7670	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	null	-3.030698	0.0010075	0.008998596
AN9383	Putative unsaturated rhamnogalacturonan hydrolase	urhC	-3.435797	0.0010156	0.009056155
AN6227	Ortholog(s) have cytosol, nucleus localization	null	-2.229442	0.0010163	0.009056155
AN0661	Has domain(s) with predicted RNA binding, RNA-directed DNA polymerase activity and role in RNA-dependent DNA replication	null	3.6618782	0.0010241	0.009103522
AN5467	Ortholog of Aspergillus terreus NIH2624 : ATET_07601	null	3.6618782	0.0010241	0.009103522
AN6644	Putative bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase, enzyme of the biotin biosynthesis pathway; common mutation in laboratory strains	biA	2.2954554	0.0010344	0.009183982
AN10483	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	null	3.4458095	0.001049	0.009236875
AN10726	null	null	3.4458095	0.001049	0.009236875
AN1269	Ortholog of A. fumigatus Af293 : Afu1g09980, Afu8g01400, A. niger CBS 513.88 : An08g01800, A. oryzae RIB40 : AO090038000434, AO090011000869 and A. niger ATCC 1015 : 177364-mRNA	null	-4.043495	0.001049	0.009236875
AN1429	Putative choline oxidase; intracellular, menadione stress-induced protein	codA	3.4458095	0.001049	0.009236875
AN3630	Ortholog of A. fumigatus Af293 : Afu5g01370, N. fischeri NRRL 181 : NFIA_040730, A. clavatus NRRL 1 : ACLA_003850, Aspergillus versicolor : Aspve1_0032027 and Aspergillus sydowii : Aspsy1_0046672	null	-4.043495	0.001049	0.009236875
AN7002	Ortholog of A. fumigatus Af293 : Afu4g04465, A. niger CBS 513.88 : An14g00360, A. niger ATCC 1015 : 41483-mRNA, Aspergillus versicolor : Aspve1_0075872 and Aspergillus sydowii : Aspsy1_0034671	null	-4.043495	0.001049	0.009236875
AN8162	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-4.043495	0.001049	0.009236875
AN8764	Protein of unknown function; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.2795987	0.0010527	0.009254417
AN10552	Ortholog of A. fumigatus Af293 : Afu4g07060, A. niger CBS 513.88 : An04g01460, A. oryzae RIB40 : AO090023000870, A. niger ATCC 1015 : 44254-mRNA and Aspergillus versicolor : Aspve1_0085132	null	2.4023637	0.0010535	0.009254417

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AN4164	Ortholog of A. fumigatus Af293 : Afu4g13180, A. niger CBS 513.88 : An01g08860, A. niger ATCC 1015 : 196273-mRNA and Aspergillus terreus NIH2624 : ATET_03201	null	2.3750837	0.0010657	0.009350871
AN2424	Has domain(s) with predicted beta-N-acetylhexosaminidase activity, cation binding activity and role in carbohydrate metabolic process	null	-2.836202	0.0010728	0.009391084
AN3731	Ortholog of A. fumigatus Af293 : Afu6g12420, A. niger CBS 513.88 : An06g01580, A. oryzae RIB40 : AO090009000171, A. niger ATCC 1015 : 177882-mRNA and Aspergillus versicolor : Aspve1_0084038	null	2.6453347	0.0010728	0.009391084
AN6237	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	null	2.16536	0.0010748	0.009397534
AN12477	Has domain(s) with predicted GTP binding, GTPase activity	null	-2.167716	0.0011006	0.009600806
AN3591	Protein with similarity to bacterial propionyl-CoA-yielding methylmalonate semialdehyde dehydrogenase; may be involved in isoleucine and valine catabolism	null	-2.167716	0.0011006	0.009600806
AN4264	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	null	-2.142339	0.0011205	0.009762504
AN12127	Ortholog of A. fumigatus Af293 : Afu3g07310, A. niger CBS 513.88 : An02g13400, A. oryzae RIB40 : AO090020000191 and A. niger ATCC 1015 : 173674-mRNA	null	2.2865864	0.0011284	0.009809594
AN11278	Ortholog(s) have role in cristae formation and integral to mitochondrial inner membrane, mitochondrial crista junction localization	null	2.2885658	0.0011471	0.009809594
AN7214	Has domain(s) with predicted oxidoreductase activity	null	2.1723912	0.0011476	0.009809594
AN10553	Has domain(s) with predicted cytochrome-c oxidase activity	null	2.6337875	0.0011495	0.009809594
AN10287	Ortholog of A. nidulans FGSC A4 : AN3782, AN9297, A. fumigatus Af293 : Afu3g03570, Afu5g09970, A. niger CBS 513.88 : An18g01620, An14g05890 and A. oryzae RIB40 : AO090026000109	null	6.0427443	0.0011521	0.009809594
AN10313	Ortholog(s) have role in ER to Golgi vesicle-mediated transport, Golgi to endosome transport and ER to Golgi transport vesicle, Golgi membrane, endoplasmic reticulum localization	null	6.0427443	0.0011521	0.009809594
AN1169	Ortholog of A. fumigatus Af293 : Afu1g11100, A. niger CBS 513.88 : An08g03390, A. oryzae RIB40 : AO090038000299, Aspergillus versicolor : Aspve1_0291494 and Aspergillus sydowii : Aspsy1_0239888	null	-5.93746	0.0011521	0.009809594
AN2035	Putative polyketide synthase; involved in secondary metabolite production	pkhB	6.0427443	0.0011521	0.009809594
AN2402	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	6.0427443	0.0011521	0.009809594
AN3086	Ortholog of A. fumigatus Af293 : Afu3g12340, A. niger CBS 513.88 : An02g08040, A. niger ATCC 1015 : 174757-mRNA, Aspergillus versicolor : Aspve1_0538833 and Aspergillus sydowii : Aspsy1_0087243	null	-5.93746	0.0011521	0.009809594

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AN4521	Forkhead domain protein with a possible role in sexual development	fhpA	6.0427443	0.0011521	0.009809594
AN4830	Ortholog(s) have role in coenzyme A biosynthetic process and cytosol, nucleus localization	null	-5.93746	0.0011521	0.009809594
AN6549	Ortholog(s) have RNA polymerase II transcription coactivator activity involved in preinitiation complex assembly activity	null	-5.93746	0.0011521	0.009809594
AN6865	Ortholog(s) have endoplasmic reticulum, nuclear envelope localization	null	3.9816975	0.0011521	0.009809594
AN6917	Ortholog of A. nidulans FGSC A4 : AN7927, A. niger CBS 513.88 : An12g02480, Aspergillus versicolor : Aspve1_0045429, Aspve1_0208268 and Aspergillus sydowii : Aspsy1_0091967, Aspsy1_0587056	null	3.9816975	0.0011521	0.009809594
AN7400	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	null	6.0427443	0.0011521	0.009809594
AN7847	Has domain(s) with predicted role in cell wall macromolecule catabolic process	null	6.0427443	0.0011521	0.009809594
AN8132	Has domain(s) with predicted metalloendopeptidase activity, zinc ion binding activity, role in proteolysis and extracellular matrix localization	null	6.0427443	0.0011521	0.009809594
AN8392	Putative alpha-glycosidase distantly related to bacterial alpha-galactosidase; predicted role in polysaccharide degradation	aglE	-5.93746	0.0011521	0.009809594
AN8802	Ortholog of Aspergillus versicolor : Aspve1_0088238 and Aspergillus sydowii : Aspsy1_0035041	null	-5.93746	0.0011521	0.009809594
AN3803	Ortholog(s) have cytosol, nucleus localization	null	2.3118649	0.0011541	0.009809609
AN11209	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.266936	0.0011557	0.009809609
AN20014	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	oxiA	2.1127405	0.0011561	0.009809609
AN1733	Putative delta-1-pyrroline-5-carboxylate dehydrogenase with a predicted role in glutamate and glutamine metabolism; expression is negatively regulated by CreA	prnC	-2.244954	0.0011644	0.009868975
AN6418	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.98035	0.0011679	0.009887242
AN1102	Putative serine C-palmitoyltransferase with a predicted role in sphingoglycolipid metabolism	null	2.18259	0.0011876	0.010042425
AN10148	Cysteine- and histidine-rich-domain [CHORD]-containing protein; required for maintenance of the diploid state	chpA	2.1906598	0.0011949	0.01009312
AN5216	Ortholog(s) have role in nucleotide-excision repair and nucleus localization	null	-2.492306	0.0012037	0.010155571
AN6126	Putative acetyl-CoA carboxylase with a predicted role in cytosolic fatty acid formation	accA	2.149341	0.0012279	0.010348693

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AN3117	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, metal ion binding activity and role in ATP biosynthetic process, metal ion transport	null	2.1514778	0.0012338	0.010380073
AN1870	Putative beta-1,4-xylosidase	null	-2.385688	0.0012411	0.010380073
AN1079	Ortholog of N. fischeri NRRL 181 : NFIA_013390	null	-2.817282	0.0012424	0.010380073
AN0195	Ortholog of A. nidulans FGSC A4 : AN8020, A. fumigatus Af293 : Afu5g02380, A. niger CBS 513.88 : An03g04900, An02g10420 and A. oryzae RIB40 : AO090001000067, AO090102000350	null	-3.36239	0.0012469	0.010380073
AN2374	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in metabolic process	null	2.9558474	0.0012469	0.010380073
AN2465	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.39956	0.0012469	0.010380073
AN4445	Ortholog(s) have role in histone exchange and NuA4 histone acetyltransferase complex, Swr1 complex localization	null	-3.39956	0.0012469	0.010380073
AN4795	Has domain(s) with predicted guanyl-nucleotide exchange factor activity, role in small GTPase mediated signal transduction and intracellular localization	null	-3.39956	0.0012469	0.010380073
AN6297	Ortholog(s) have copper ion binding activity, role in aerobic respiration, protein complex assembly and mitochondrial inner membrane, mitochondrial ribosome localization	null	3.2565458	0.0012469	0.010380073
AN6753	Putative NADH-dependent flavin oxidoreductase; menadione stress-induced protein	null	2.9558474	0.0012469	0.010380073
AN8346	Ortholog(s) have role in cellular cadmium ion homeostasis, cellular response to cadmium ion, regulation of sulfur metabolic process and mitochondrion localization	null	3.2565458	0.0012469	0.010380073
AN8660	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.265689	0.0012746	0.010598151
AN2731	Ortholog(s) have ATPase activator activity, unfolded protein binding activity	null	2.1261414	0.0012761	0.010598806
AN3598	Putative peptidyl-prolyl cis-trans isomerase; FKBP12 homolog; mutant displays reduced growth on 2-pyrrolidone and enhanced growth on threonine	fprA	-2.455467	0.0012836	0.010649416
AN9097	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, mitochondrion, nucleolus localization	null	2.1904067	0.0012991	0.010764097
AN1306	Protein with similarity to mammalian gelsolin; predicted role in actin filament severing	null	2.2959558	0.0013003	0.010764097
AN1222	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	sasA	2.3782479	0.0013061	0.010800075
AN2847	Ortholog(s) have RNA binding, single-stranded telomeric DNA binding activity and cytosol, nucleus localization	null	-3.999527	0.0013308	0.01096849

AN3973	Putative peroxiredoxin	null	3.3760494	0.0013308	0.01096849
AN6426	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	null	3.3760494	0.0013308	0.01096849
AN8737	Putative sugar transporter	mstA	-2.213282	0.0013331	0.010974516
AN0528	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.954502	0.0013563	0.011106987
AN7206	Ortholog(s) have role in barrier septum assembly involved in cell cycle cytokinesis, cellular protein localization, septation initiation signaling cascade and spindle pole body localization	spgA	-2.954502	0.0013563	0.011106987
AN10819	Has domain(s) with predicted ATP binding, protein kinase activity and role in protein phosphorylation	null	-2.77756	0.0013566	0.011106987
AN5610	Putative L-aminoadipate-semialdehyde dehydrogenase with a predicted role in lysine metabolism	null	2.6130473	0.0013566	0.011106987
AN7506	Has domain(s) with predicted role in intracellular signal transduction	null	-2.77756	0.0013566	0.011106987
AN5076	Has domain(s) with predicted role in cell wall macromolecule catabolic process	null	3.5753849	0.0013605	0.011114404
AN7705	Ortholog of A. fumigatus Af293 : Afu5g08320, A. oryzae RIB40 : AO090701000755, A. niger ATCC 1015 : 191332-mRNA, Aspergillus versicolor : Aspve1_0133270 and Aspergillus sydowii : Aspsy1_0090398	null	3.5753849	0.0013605	0.011114404
AN4750	null	null	2.8758411	0.0013912	0.011353458
AN8559	Putative branched chain alpha-keto acid dehydrogenase E1, beta subunit	null	-2.163275	0.0013986	0.01140098
AN2997	Ortholog(s) have role in cellular response to osmotic stress, translational initiation	null	2.2418179	0.001411	0.011489186
AN0895	Predicted NAD-dependent oxidoreductase; intracellular; expression upregulated after exposure to farnesol	null	2.2032591	0.0014131	0.011493931
AN2734	Ortholog(s) have LSU rRNA binding activity, role in ribosomal large subunit assembly and 90S preribosome, cytosol, preribosome, large subunit precursor localization	null	2.4069535	0.0014218	0.011543296
AN6897	Ortholog(s) have GTPase activity, protein homodimerization activity, role in mitochondrial fusion and integral to mitochondrial outer membrane, mitochondrial inner membrane localization	null	2.1780415	0.0014222	0.011543296
AN1461	Ortholog of A. fumigatus Af293 : Afu8g04530, A. niger CBS 513.88 : An16g08470, A. oryzae RIB40 : AO090023000334, A. niger ATCC 1015 : 45507-mRNA and Aspergillus versicolor : Aspve1_0125562	null	-2.77022	0.0014259	0.011560374
AN7287	Putative mitochondrial succinate/fumarate antiporter	acuL	2.1135121	0.001438	0.011645887
AN10444	Ortholog(s) have gamma-glutamyltransferase activity, role in cellular response to nitrogen starvation and endoplasmic reticulum localization	null	-2.120906	0.0014441	0.01167863

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AN3957	Amidase, similar to A. nidulans AmdS; probable A. niger AmdS ortholog; required for benzamide or phenylacetamide utilization; transcription is activated by AreA in low-nitrogen conditions and repressed during carbon starvation	gmdA	-2.40854	0.0014452	0.01167863
AN3222	Ortholog(s) have IMP 5'-nucleotidase activity and role in inosine salvage, nicotinamide riboside biosynthetic process, nicotinic acid riboside biosynthetic process	null	-2.199018	0.0014484	0.011692434
AN5482	Putative Ran GTPase, GTP binding protein; protein abundance decreased by menadione stress; palA-dependent expression independent of pH	ran	2.2204637	0.0014717	0.01186736
AN8347	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.30576	0.0014803	0.011923804
AN6526	Ortholog(s) have leucine-tRNA ligase activity, mRNA binding activity, role in Group I intron splicing, leucyl-tRNA aminoacylation, mitochondrial translation and mitochondrion localization	null	2.5983255	0.0014821	0.011925605
AN1047	Putative heat shock protein	null	2.0653092	0.0014881	0.011960774
AN2139	Ortholog(s) have DNA 5'-adenosine monophosphate hydrolase activity, role in response to DNA damage stimulus and cytosol, nucleus localization	null	-3.182811	0.0014979	0.011988006
AN3713	null	null	2.8147931	0.0014979	0.011988006
AN4214	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	teaR	-3.182811	0.0014979	0.011988006
AN5933	Ortholog of A. fumigatus Af293 : Afu2g10720, A. niger CBS 513.88 : An02g02500, A. niger ATCC 1015 : 173949-mRNA, Aspergillus versicolor : Aspve1_0052165 and Aspergillus sydowii : Aspsy1_0044922	null	-3.182811	0.0014979	0.011988006
AN5984	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	2.5800208	0.0015281	0.012177325
AN7814	Putative polyketide synthase/fatty acid synthase beta; required for sterigmatocystin biosynthesis; member of the sterigmatocystin biosynthesis gene cluster	stcK	2.4673865	0.0015281	0.012177325
AN8832	Ortholog(s) have aminoacyl-tRNA hydrolase activity, role in mitochondrial translation and mitochondrion localization	null	2.4673865	0.0015281	0.012177325
AN9400	Putative amidase with a predicted role in arginine metabolism	null	2.5800208	0.0015281	0.012177325
AN12279	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin hydrolysis	null	3.1956246	0.0015365	0.012231595
AN0787	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	mns1B	-2.079639	0.0015407	0.012240094
AN4218	Ortholog(s) have GDP binding, GTP binding, translation elongation factor activity, role in tRNA export from nucleus, translational elongation and cytosol, mitochondrion, nucleus localization	null	2.0959852	0.0015409	0.012240094

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AN0278	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	2.3146149	0.0015466	0.012272627
AN8138	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	aglC	-2.243697	0.001562	0.0123817
AN4052	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	exgC	2.766639	0.001578	0.012495015
AN4654	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	null	2.2373295	0.0016074	0.012714443
AN10378	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	null	2.0968619	0.0016152	0.012720588
AN5973	Protein with sequence similarity to protein kinase C	pkcB	-2.276748	0.0016227	0.012720588
AN1640	Ortholog of N. fischeri NRRL 181 : NFIA_028180, Aspergillus versicolor : Aspve1_0122087 and Aspergillus sydowii : Aspsy1_0135110, Aspsy1_0638682	null	-2.462356	0.0016245	0.012720588
AN2128	Ortholog(s) have role in cellular protein localization, cytokinesis checkpoint, dynein-driven meiotic oscillatory nuclear movement, microtubule bundle formation, mitotic spindle elongation, spindle midzone assembly involved in mitosis	null	2.4473492	0.0016245	0.012720588
AN5807	Ortholog of A. fumigatus Af293 : Afu2g07470, A. niger CBS 513.88 : An05g00010, A. oryzae RIB40 : AO090011000945, A. niger ATCC 1015 : 186864-mRNA and Aspergillus versicolor : Aspve1_0130354	null	-2.7461	0.001639	0.012720588
AN4443	Putative methionine synthase with a predicted role in methionine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type	metH	2.0859168	0.0016558	0.012720588
AN0518	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	null	-5.860765	0.0016619	0.012720588
AN10259	Putative cytochrome P450	CYP532A4	-5.860765	0.0016619	0.012720588
AN10331	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	null	-5.860765	0.0016619	0.012720588
AN10517	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	3.8581547	0.0016619	0.012720588
AN10555	Has domain(s) with predicted nucleic acid binding activity	null	5.9192015	0.0016619	0.012720588
AN10715	Ortholog of A. fumigatus Af293 : Afu6g06560, A. niger CBS 513.88 : An03g03300, A. oryzae RIB40 : AO090003000028, A. niger ATCC 1015 : 57126-mRNA and Aspergillus versicolor : Aspve1_0133004	null	5.9192015	0.0016619	0.012720588
AN11288	null	null	3.8581547	0.0016619	0.012720588
AN11987	null	null	5.9192015	0.0016619	0.012720588

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AN1382	Ortholog(s) have role in cellular zinc ion homeostasis, endoplasmic reticulum inheritance, protein targeting to nuclear inner membrane, septin ring assembly	null	-5.860765	0.0016619	0.012720588
AN1656	Ortholog of A. fumigatus Af293 : Afu6g03025, Aspergillus brasiliensis : Aspbr1_0036761, N. fischeri NRRL 181 : NFIA_049360, Aspergillus acidus : Aspfo1_0052667 and Aspergillus versicolor : Aspve1_0037520	null	-5.860765	0.0016619	0.012720588
AN1920	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	-5.860765	0.0016619	0.012720588
AN20016	null	null	3.8581547	0.0016619	0.012720588
AN2720	Has domain(s) with predicted catalytic activity	null	5.9192015	0.0016619	0.012720588
AN2778	Has domain(s) with predicted heme binding activity	null	-5.860765	0.0016619	0.012720588
AN3255	Ortholog(s) have glutathione peroxidase activity, glutathione transferase activity, phosphoprotein binding, protein heterodimerization activity, protein homodimerization activity, transcription corepressor activity	null	-5.860765	0.0016619	0.012720588
AN3377	Has domain(s) with predicted aspartic-type endopeptidase activity and role in proteolysis	null	5.9192015	0.0016619	0.012720588
AN3640	Ortholog of N. fischeri NRRL 181 : NFIA_060750	null	3.8581547	0.0016619	0.012720588
AN3889	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	5.9192015	0.0016619	0.012720588
AN5976	Putative beta-glucosidase	bglG	-5.860765	0.0016619	0.012720588
AN6114	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	null	-5.860765	0.0016619	0.012720588
AN6396	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	null	-5.860765	0.0016619	0.012720588
AN7385	Putative phosphatidylserine decarboxylase with a predicted role in phospholipid metabolism	null	5.9192015	0.0016619	0.012720588
AN7577	Has domain(s) with predicted acid-amino acid ligase activity and role in post-translational protein modification	null	-5.860765	0.0016619	0.012720588
AN9090	Putative RNA binding protein with homology to Saccharomyces cerevisiae Nam8p; involved in the regulation of arginine catabolism	rrmA	-5.860765	0.0016619	0.012720588
AN9249	Protein required for austinol and dehydroaustinol biosynthesis	ausH	-5.860765	0.0016619	0.012720588
AN3823	Ortholog(s) have structural constituent of ribosome activity	null	2.0548341	0.0016627	0.012720588
AN5948	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.286817	0.001665	0.012724904
AN1345	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), regulation of translational fidelity	null	2.0321132	0.001683	0.012838959
AN4046	Ortholog(s) have Golgi apparatus, endoplasmic reticulum localization	null	2.2912262	0.0016833	0.012838959

AN11982	null	null	-3.954177	0.0016967	0.012875319
AN1793	Has domain(s) with predicted magnesium ion binding, terpene synthase activity	null	3.3027439	0.0016967	0.012875319
AN5621	Ortholog of A. fumigatus Af293 : Afu4g11130, A. niger CBS 513.88 : An04g05550, A. niger ATCC 1015 : 214353-mRNA, Aspergillus versicolor : Aspve1_0053400 and Aspergillus sydowii : Aspsy1_0088403	null	-3.907355	0.0016967	0.012875319
AN5842	Putative L-lactate dehydrogenase with a predicted role in the methylglyoxal bypass	ldhA	3.3027439	0.0016967	0.012875319
AN6437	Ortholog of Aspergillus versicolor : Aspve1_0052718 and Aspergillus sydowii : Aspsy1_0031878	null	3.3027439	0.0016967	0.012875319
AN4603	Putative allantoinase with a predicted role in purine metabolism	null	-2.146162	0.0017172	0.013017382
AN1673	Has domain(s) with predicted 3-deoxy-7-phosphoheptulonate synthase activity and role in aromatic amino acid family biosynthetic process	null	-2.395751	0.0017216	0.01303695
AN4189	Putative mitogen-activated protein kinase kinase (MAPKK)	mkkA	-2.716433	0.0017232	0.01303695
AN0116	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.7661881	0.0017721	0.013366152
AN0349	Ortholog(s) have role in protein refolding and mitochondrial matrix localization	null	-3.153255	0.0017721	0.013366152
AN6039	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.7661881	0.0017721	0.013366152
AN4837	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	null	-2.445545	0.0017949	0.01352397
AN11795	Has domain(s) with predicted acyl-CoA hydrolase activity and role in acyl-CoA metabolic process	null	3.4833734	0.0018203	0.013674154
AN12378	null	null	3.4833734	0.0018203	0.013674154
AN6146	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	3.4833734	0.0018203	0.013674154
AN2062	Putative ER-resident chaperone of the HSP70 family; unfolded-protein response (UPR) target gene; transcript levels increase during the UPR	bipA	-2.025014	0.0018279	0.013717806
AN6301	Ortholog of A. niger CBS 513.88 : An02g04310, Aspergillus brasiliensis : Aspbr1_0192484, Aspergillus acidus : Aspfo1_0176079 and Aspergillus versicolor : Aspve1_0052461	null	-2.901372	0.0018394	0.013748537
AN6405	Has domain(s) with predicted cation binding, lysozyme activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, peptidoglycan catabolic process	null	2.5586596	0.0018394	0.013748537
AN7482	Ortholog of A. fumigatus Af293 : Afu2g05690, A. oryzae RIB40 : AO090001000684, A. niger ATCC 1015 : 197971-mRNA, Aspergillus versicolor : Aspve1_0197052 and Aspergillus sydowii : Aspsy1_0152978	null	2.7224959	0.0018394	0.013748537
AN8814	Ortholog(s) have endoplasmic reticulum localization	null	-2.901372	0.0018394	0.013748537

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AN5879	Ortholog(s) have role in intracellular sterol transport and fungal-type vacuole lumen localization	null	-2.371156	0.0018548	0.013835731
AN8262	Secretin-like G-protein coupled receptor	gprH	-2.371156	0.0018548	0.013835731
AN6061	Has domain(s) with predicted role in response to stress	null	2.2455827	0.0018597	0.013858823
AN6089	Putative 60 kilodalton heat shock protein	null	2.0751315	0.0018746	0.013955839
AN6231	Tryptophan synthase involved in tryptophan biosynthesis; transcription is regulated by the cross-pathway control of amino acid biosynthesis; repressed by starvation-induced autophagy; protein induced by farnesol	trpB	2.5401187	0.0018871	0.014034548
AN0720	Putative diphthine synthase with a predicted role in methionine metabolism	null	2.8313185	0.0019004	0.014091308
AN6141	Ortholog(s) have role in negative regulation of apoptotic process, pyridoxine metabolic process and cytoplasm localization	null	3.1320169	0.0019004	0.014091308
AN8641	Transcript induced by light in in developmentally competent mycelia	null	3.1320169	0.0019004	0.014091308
AN6847	Ortholog(s) have cytosol, nucleus localization	null	2.5246741	0.0019211	0.014231266
AN1972	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.145745	0.0019554	0.014470936
AN4473	Ortholog of A. nidulans FGSC A4 : AN5608, A. fumigatus Af293 : Afu4g07720, A. niger CBS 513.88 : An14g07030, An04g02100 and A. oryzae RIB40 : AO090023000800, AO090009000070	null	-2.600698	0.0019632	0.014511397
AN8953	Putative alpha-glucosidase with a predicted role in maltose metabolism; transcriptionally induced by isomaltose; induced by rapamycin-induced autophagy	agdB	2.1318736	0.0019648	0.014511397
AN6653	Malate synthase, required for utilization of acetate as carbon source; transcription induction by acetate mediated by FacB; carbon catabolite repression mediated by CreA; transcription induction by long-chain fatty acids mediated by FarA	acuE	-2.059836	0.0019678	0.014519601
AN6082	Ortholog(s) have pre-mRNA 5'-splice site binding, structural constituent of ribosome activity, role in negative regulation of mRNA splicing, via spliceosome, rRNA processing and cytosol localization	null	2.1428661	0.001973	0.014543177
AN8502	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.428535	0.0019847	0.014615257
AN7479	Putative asparaginyl-tRNA synthetase with a predicted role in tRNA charging for translation	null	2.163971	0.0019881	0.014625735
AN3200	Putative beta-glucuronidase with a predicted role in polysaccharide degradation; the predicted pseudogene AN10383 and predicted ORF AN3200 occupy overlapping chromosomal locations in version 4 of the A. nidulans annotation	null	-2.456351	0.001995	0.014661883
AN4258	Putative kinase with a predicted role in nucleotide or phospholipid metabolism	null	2.2257337	0.0019983	0.014665026
AN4401	Putative asparagine synthase with a predicted role in asparagine metabolism	null	2.2751644	0.0019993	0.014665026
AN1730	Protein of the prn gene cluster; predicted to be involved in proline metabolism	prnX	2.7655942	0.0020249	0.014837919

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AN1716	Ortholog of Aspergillus versicolor : Aspve1_0037607, Aspergillus sydowii : Aspsy1_0084105 and Aspergillus terreus NIH2624 : ATET_05357	null	-2.093206	0.0020303	0.014863034
AN9403	Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism	pdhC	2.0176457	0.0020557	0.015034219
AN1848	Zinc(II)2Cys6 putative transcription factor involved in the regulation of sexual development; mutant produces immature cleistothecia and reduced numbers of ascospores	nosA	-2.021538	0.0020744	0.015156213
AN6031	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-2.096182	0.0020776	0.015159095
AN7324	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.061268	0.0020789	0.015159095
AN10130	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit localization	null	2.0004428	0.0020872	0.015204687
AN5602	Ortholog(s) have ATPase activator activity, chaperone binding activity, role in protein folding, response to stress and cytosol localization	null	2.0321025	0.0020895	0.015206757
AN4794	Putative ribosomal protein; expression increased in salt-adapted strains	null	2.0348691	0.0020927	0.015215624
AN5583	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-3.092264	0.0021015	0.015264195
AN7437	Ortholog(s) have role in amino acid export from vacuole, cellular response to nitrogen starvation and integral to fungal-type vacuolar membrane localization	null	-2.228445	0.0021133	0.015335372
AN8102	Putative pepsin-like aspartic protease; predicted glycosyl phosphatidylinositol (GPI)-anchor	pepAc	2.0085964	0.0021389	0.015506071
AN6255	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	2.0552079	0.0021418	0.015511849
AN3422	MAP kinase kinase (MAPKK), component of a signaling module SteD-SteC-MkkB-MpkB that controls coordination of development and secondary metabolism	ste7	-2.874056	0.0021482	0.015513511
AN4019	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.874056	0.0021482	0.015513511
AN5484	Has domain(s) with predicted sterol binding activity	null	-2.874056	0.0021482	0.015513511
AN0053	Ortholog of A. fumigatus Af293 : Afu5g12500, A. oryzae RIB40 : AO090120000375, A. niger ATCC 1015 : 185165-mRNA, Aspergillus versicolor : Aspve1_0048292 and Aspergillus sydowii : Aspsy1_0144467	null	3.2255134	0.0021741	0.015609825
AN2890	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-3.858963	0.0021741	0.015609825
AN4126	Putative dehydrogenase with a predicted role in metabolism or penicillin biosynthesis	null	3.2255134	0.0021741	0.015609825
AN5279	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	null	-3.858963	0.0021741	0.015609825

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AN5690	Has domain(s) with predicted copper ion binding, primary amine oxidase activity, quinone binding activity and role in amine metabolic process, oxidation-reduction process	null	-3.858963	0.0021741	0.015609825
AN5968	Ortholog(s) have fungal-type vacuole localization	null	-3.858963	0.0021741	0.015609825
AN8532	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.069994	0.002177	0.015613145
AN5373	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.142499	0.0021788	0.015613145
AN2289	Ortholog(s) have alpha-glucoside transmembrane transporter activity, role in carbohydrate transmembrane transport and Golgi apparatus, fungal-type vacuole membrane localization	null	-2.212373	0.0021852	0.015631364
AN11776	Ortholog(s) have mitochondrion localization	null	2.3079085	0.0021911	0.015631364
AN1685	Putative phytase with a predicted role in phytic acid catabolism	null	-2.495404	0.0021911	0.015631364
AN0330	NADH:flavin oxidoreductase; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.3051475	0.0021964	0.015631364
AN3236	Has domain(s) with predicted O-methyltransferase activity	null	2.3051475	0.0021964	0.015631364
AN10880	Ortholog(s) have cytoplasm, nucleus localization	null	1.9889253	0.0021966	0.015631364
AN6311	Has domain(s) with predicted voltage-gated chloride channel activity, role in chloride transport, transmembrane transport and membrane localization	null	-2.674193	0.0021993	0.015631364
AN4982	Ortholog of A. fumigatus Af293 : Afu3g10065, A. niger CBS 513.88 : An16g03820, A. oryzae RIB40 : AO090003000540, A. niger ATCC 1015 : 49011-mRNA and Aspergillus versicolor : Aspve1_0039817	null	-2.488335	0.0022002	0.015631364
AN6885	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	null	-2.488335	0.0022002	0.015631364
AN6346	Putative dihydroxy-acid dehydratase with a predicted role in valine, leucine, and isoleucine metabolism; intracellular, menadione stress-induced protein	null	2.1600921	0.0022128	0.015706015
AN5027	Ortholog of A. fumigatus Af293 : Afu3g12130, A. niger CBS 513.88 : An11g08400, An02g07940, A. oryzae RIB40 : AO090023000019, AO090138000194, AO090003000773 and A. niger ATCC 1015 : 52322-mRNA	null	-2.004081	0.0022249	0.015777259
AN9408	Fatty acid synthase, beta subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid formation	fasB	1.9747044	0.0022524	0.015957245
AN3141	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.181312	0.0022859	0.016179109
AN1990	Putative homocitrate synthase with a predicted role in pyruvate metabolism	null	2.1509016	0.0023238	0.016431442
AN9303	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	null	2.0807114	0.0023457	0.016541489
AN4464	Putative bifunctional enzyme with a predicted role in purine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type	purH	2.225082	0.0023583	0.016541489

AN0257	Putative peroxisomal ATP carrier protein with a predicted role in fatty acid beta-oxidation	antA	-3.244762	0.0023593	0.016541489
AN1090	Ortholog of A. fumigatus Af293 : Afu1g12010, A. oryzae RIB40 : AO090001000352, A. niger ATCC 1015 : 47560-mRNA, Aspergillus versicolor : Aspve1_0036731 and Aspergillus terreus NIH2624 : ATET_00399	null	-3.244762	0.0023593	0.016541489
AN11841	Putative GNAT-type acetyltransferase	ngn18	-3.244762	0.0023593	0.016541489
AN5503	null	null	2.7647765	0.0023593	0.016541489
AN7051	Cystathionine beta-lyase, enzyme of the methionine biosynthesis pathway; mutants show a reduced rate of DNA damage repair	metG	2.7647765	0.0023593	0.016541489
AN7435	Ortholog(s) have uracil DNA N-glycosylase activity, role in DNA repair and mitochondrion, nucleus localization	null	-3.244762	0.0023593	0.016541489
AN8514	Asterriquinone prenyltransferase; member of the tdi gene cluster; required for terrequinone A production; catalyzes the reverse prenylation event during terrequinone A biosynthesis; lacks canonical prenyl diphosphate binding motif (D/N)DXXD	tdiB	3.065475	0.0023593	0.016541489
AN3743	Ortholog of A. nidulans FGSC A4 : AN5603, A. fumigatus Af293 : Afu4g11320, Afu7g04400, A. niger CBS 513.88 : An13g00980, An04g05280 and A. oryzae RIB40 : AO090005000127	null	-2.13259	0.0023715	0.016555611
AN2867	Putative phosphoglucomutase with a predicted role in carbohydrate metabolism; intracellular; protein abundance decreased by menadione stress; transcript levels increase during asexual development	pgmB	2.0345211	0.0023983	0.016555611
AN3359	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	1.9601196	0.0024163	0.016555611
AN11045	Ortholog(s) have D-lactate dehydrogenase (cytochrome) activity, actin binding activity and mitochondrial matrix localization	null	2.2035094	0.0024214	0.016555611
AN0087	Ortholog(s) have cell division site, cell tip, cytoplasm localization	null	-5.779762	0.0024278	0.016555611
AN0159	Ortholog of Aspergillus versicolor : Aspve1_0023174 and Aspergillus sydowii : Aspsy1_0054986	null	-5.693939	0.0024278	0.016555611
AN0482	Putative ubiquitin-conjugating enzyme; transcript repressed by nitrate	null	-5.693939	0.0024278	0.016555611
AN11127	Ortholog of A. fumigatus Af293 : Afu5g05910, A. oryzae RIB40 : AO090009000671, Aspergillus terreus NIH2624 : ATET_09443 and Aspergillus carbonarius ITEM 5010 : Acar5010_009107	null	-5.779762	0.0024278	0.016555611
AN11177	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-5.779762	0.0024278	0.016555611
AN11222	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	null	-5.693939	0.0024278	0.016555611

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AN1751	Has domain(s) with predicted methyltransferase activity, nucleic acid binding activity and role in RNA methylation	null	-5.779762	0.0024278	0.016555611
AN2187	null	null	-5.693939	0.0024278	0.016555611
AN2393	Ortholog(s) have cytosol localization	null	-5.779762	0.0024278	0.016555611
AN3305	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.779762	0.0024278	0.016555611
AN3400	Ortholog(s) have tetrahydroxynaphthalene reductase activity, role in melanin biosynthetic process and intracellular localization	null	-5.779762	0.0024278	0.016555611
AN3951	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	null	-5.779762	0.0024278	0.016555611
AN4125	Ortholog of Aspergillus brasiliensis : Aspbr1_0028583, Aspergillus versicolor : Aspve1_0040328, Aspve1_0732669 and Aspergillus sydowii : Aspsy1_0029968, Aspsy1_0033388	null	-5.779762	0.0024278	0.016555611
AN4154	Has domain(s) with predicted 1-alkyl-2-acetylglycerophosphocholine esterase activity and role in lipid catabolic process	null	-5.779762	0.0024278	0.016555611
AN4511	Ortholog of A. fumigatus Af293 : Afu2g03160, A. niger CBS 513.88 : An07g07590, A. oryzae RIB40 : AO090120000270, A. niger ATCC 1015 : 39770-mRNA and Aspergillus versicolor : Aspve1_0030098	null	-5.693939	0.0024278	0.016555611
AN4953	Putative Rho-like GTPase	null	-5.693939	0.0024278	0.016555611
AN5000	Ortholog(s) have enoyl-CoA hydratase activity, role in sphingolipid biosynthetic process, vacuolar transport and fungal-type vacuole membrane, integral to endoplasmic reticulum membrane localization	null	-5.779762	0.0024278	0.016555611
AN5086	Conidium-specific RNA of unknown function; member of the SpoC1 gene cluster	SpoC1-C1D	-5.693939	0.0024278	0.016555611
AN5207	Ortholog(s) have cytosol, nucleus localization	null	-5.779762	0.0024278	0.016555611
AN5391	Has domain(s) with predicted zinc ion binding activity and role in intracellular signal transduction	null	-5.779762	0.0024278	0.016555611
AN5941	null	null	-5.693939	0.0024278	0.016555611
AN6043	null	null	-5.779762	0.0024278	0.016555611
AN6062	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	null	-5.693939	0.0024278	0.016555611
AN6555	Ortholog(s) have role in medium-chain fatty acid biosynthetic process	null	-5.779762	0.0024278	0.016555611
AN6582	Ortholog of A. oryzae RIB40 : AO090011000564, Aspergillus brasiliensis : Aspbr1_0050325, Aspergillus flavus NRRL 3357 : AFL2T_05315 and Aspergillus versicolor : Aspve1_0808994	null	-5.779762	0.0024278	0.016555611
AN8610	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.693939	0.0024278	0.016555611

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AN3157	Ortholog(s) have endoplasmic reticulum, fungal-type vacuole membrane localization	null	2.2761096	0.0024327	0.016573934
AN0316	Alpha-tubulin, forms a heterodimer with beta-tubulin that promotes microtubule assembly	tubA	2.191775	0.0024627	0.016763026
AN1414	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	xprG	-2.265686	0.0024855	0.01688708
AN7604	Putative phospholipase with a predicted role in phospholipid metabolism	null	-2.265686	0.0024855	0.01688708
AN0470	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.3635129	0.0024891	0.016891109
AN7304	Ortholog(s) have coenzyme A transmembrane transporter activity, role in coenzyme A transport and mitochondrial inner membrane localization	null	-2.219089	0.0024906	0.016891109
AN6817	Predicted NAD-dependent oxidoreductase; expression upregulated after exposure to farnesol	null	-2.645374	0.0025136	0.017002832
AN8857	Ortholog(s) have role in cellular bud site selection, mRNA splicing, via spliceosome and U2 snRNP, spliceosomal complex localization	null	-2.645374	0.0025136	0.017002832
AN10213	Ortholog(s) have 1-phosphatidylinositol-3-kinase activity	null	-2.81782	0.0025139	0.017002832
AN10678	Ortholog of A. fumigatus Af293 : Afu4g11810, A. oryzae RIB40 : AO090003001035, A. niger ATCC 1015 : 127472-mRNA, Aspergillus sydowii : Aspsy1_0043963 and Aspergillus terreus NIH2624 : ATET_03902	null	-2.179075	0.0025425	0.017181093
AN3034	Suppressor of prgA1 mutation; involved in regulation of penicillin biosynthesis; null mutation results in decreased expression of ipnA and acvA, and reduced penicillin production	suAprgA1	2.185174	0.0025851	0.017452595
AN1763	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.183182	0.0026113	0.017614043
AN6193	Ortholog(s) have ATP-dependent peptidase activity, role in chaperone-mediated protein complex assembly, misfolded or incompletely synthesized protein catabolic process and mitochondrial matrix localization	null	1.9912267	0.0026404	0.017794198
AN3818	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	null	-2.111465	0.0026571	0.017890515
AN0423	Putative D-xylose reductase with a predicted role in carbohydrate metabolism; transcriptionally induced by growth on xylose	null	-2.029273	0.0026635	0.017905097
AN11900	Ortholog(s) have Golgi apparatus localization	null	2.0234592	0.0026641	0.017905097
AN8770	Putative bifunctional enzyme with a predicted role in arginine metabolism; putative acetylglutamate kinase	null	2.0903468	0.002702	0.018143748
AN10117	Ortholog of A. fumigatus Af293 : Afu1g14050/fbpA, A. oryzae RIB40 : AO090012000463, A. niger ATCC 1015 : 205573-mRNA, Aspergillus versicolor : Aspve1_0048993 and Aspergillus sydowii : Aspsy1_0086500	null	-2.294748	0.00271	0.018180849

AN5403	Ortholog of A. fumigatus Af293 : Afu6g13660, A. niger CBS 513.88 : An08g08590, A. oryzae RIB40 : AO090103000319, A. niger ATCC 1015 : 38046-mRNA and Aspergillus versicolor : Aspve1_0199259	null	2.0449644	0.0027262	0.018273692
AN5969	Ortholog of A. niger CBS 513.88 : An02g05900, Aspergillus flavus NRRL 3357 : AFL2T_05331, A. clavatus NRRL 1 : ACLA_069580, Aspergillus acidus : Aspfo1_0039232 and Aspergillus versicolor : Aspve1_0040765	null	2.0604295	0.0027758	0.018581525
AN2283	Ortholog(s) have nucleolus localization	null	2.3291122	0.0027772	0.018581525
AN0824	Putative mitochondrial acyl-coA dehydrogenase involved in short-chain fatty acid beta-oxidation; required for growth on short-chain fatty acids	scdA	-2.004694	0.0027984	0.01870677
AN1003	Putative isocitrate dehydrogenase (NAD+) with a predicted role in the TCA cycle; intracellular, menadione stress-induced protein	null	2.0843268	0.0028027	0.018718935
AN2456	Ortholog of A. fumigatus Af293 : Afu6g10360, A. niger CBS 513.88 : An11g00830, A. oryzae RIB40 : AO090023000231, Aspergillus versicolor : Aspve1_0038224 and Aspergillus sydowii : Aspsy1_0141642	null	2.3271571	0.0028204	0.018803664
AN9496	Has domain(s) with predicted cholestenol delta-isomerase activity, role in sterol metabolic process and endoplasmic reticulum, integral to membrane localization	null	2.3271571	0.0028204	0.018803664
AN1013	Putative 60S ribosomal protein L5; ortholog of S. cerevisiae Rpl5p which is an RNA binding protein with a role in ribosomal large subunit assembly	null	2.007082	0.0028265	0.018827144
AN5880	Ortholog(s) have cytosol, nucleus localization	null	-2.306014	0.0028328	0.018852691
AN4255	Non-catalytic atypical hexokinase involved in regulation of extracellular proteases in response to carbon starvation; associates with mitochondria	hxkC	1.9482628	0.0028433	0.018905855
AN0847	Putative chaperone of the endoplasmic reticulum (ER) lumen	null	-2.027486	0.002867	0.019046041
AN3595	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.1993814	0.0028805	0.019089405
AN3752	Has domain(s) with predicted Rab GTPase activator activity, role in regulation of Rab GTPase activity and intracellular localization	null	-2.240663	0.0028805	0.019089405
AN8894	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	null	-2.362551	0.0028812	0.019089405
AN7177	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	null	1.971949	0.0029456	0.019477736
AN2889	Ortholog of A. fumigatus Af293 : Afu3g11570, A. niger CBS 513.88 : An02g07370, A. oryzae RIB40 : AO090003000716, A. niger ATCC 1015 : 37091-mRNA and Aspergillus sydowii : Aspsy1_0029412	null	2.4661024	0.0029476	0.019477736
AN3084	Ortholog(s) have lipid particle localization	null	-2.788858	0.0029476	0.019477736
AN0382	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.02858	0.0029764	0.019529899

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AN0714	Ortholog(s) have role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex localization	null	-2.995651	0.0029764	0.019529899
AN10164	Ortholog(s) have mRNA binding, poly(U) RNA binding activity and role in nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, regulation of mRNA stability, stress granule assembly	null	-2.995651	0.0029764	0.019529899
AN12429	Has domain(s) with predicted role in lipid metabolic process	null	-2.995651	0.0029764	0.019529899
AN3626	Putative phosphoribosylamino-imidazole-carboxylase with a predicted role in purine metabolism	null	2.6637712	0.0029764	0.019529899
AN4383	Ortholog of A. fumigatus Af293 : Afu4g06730, A. niger CBS 513.88 : An04g01110, A. oryzae RIB40 : AO090023000913, A. niger ATCC 1015 : 134018-mRNA and Aspergillus versicolor : Aspve1_0043227	null	-3.02858	0.0029764	0.019529899
AN5508	Putative G-protein coupled receptor	gprN	-2.995651	0.0029764	0.019529899
AN6873	null	null	-2.995651	0.0029764	0.019529899
AN11090	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	2.7071416	0.0029823	0.019533751
AN12164	null	null	2.7071416	0.0029823	0.019533751
AN1715	Putative mannose-6-phosphate isomerase with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism	null	-2.340339	0.0029917	0.019561402
AN2421	Putative C2H2 zinc finger transcription factor; involved in regulation of conidiophore development; required for light-dependent activation of brlA transcription	flbC	-2.340339	0.0029917	0.019561402
AN3590	Ortholog of A. nidulans FGSC A4 : AN7906, A. fumigatus Af293 : Afu4g12880, A. niger CBS 513.88 : An01g08440, A. oryzae RIB40 : AO090009000315 and A. niger ATCC 1015 : 51857-mRNA	null	-1.985167	0.0029956	0.01956954
AN1601	Putative cytochrome P450; O-methylsterigmatocystin oxidoreductase with a predicted role in sterigmatocystin/aflatoxin biosynthesis	CYP620E1	-2.4127	0.0030549	0.019922511
AN3387	Putative G-protein coupled receptor	gprD	2.2985225	0.0030549	0.019922511
AN6234	Ortholog(s) have role in ergosterol biosynthetic process, siderophore biosynthetic process and cytosol, nucleus localization	null	2.0763703	0.0030776	0.020052763
AN0736	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	null	-2.290636	0.0030961	0.020155406
AN8537	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	2.1780661	0.003103	0.020183227
AN2426	Histone H4.2, core histone protein; nearly identical to histone H4.1	H4.2	-2.069961	0.0031462	0.020446125
AN7320	Putative acyl-coA dehydrogenase	null	-2.346307	0.0031638	0.020524679
AN7554	Ortholog(s) have poly(A) RNA binding activity	null	2.2312132	0.0031638	0.020524679

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AN9025	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	null	-1.970737	0.0031798	0.020610472
AN0033	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-2.585813	0.0031999	0.02068698
AN10648	Ortholog(s) have delta24(24-1) sterol reductase activity	null	2.4024958	0.0031999	0.02068698
AN11898	Ortholog of A. fumigatus Af293 : Afu7g05420, A. niger ATCC 1015 : 209812-mRNA, Aspergillus versicolor : Aspve1_0355367, Aspergillus sydowii : Aspsy1_0159682 and Aspergillus terreus NIH2624 : ATET_06393	null	2.2898615	0.0031999	0.02068698
AN0907	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus localization	null	2.1399022	0.0032103	0.020736382
AN0770	Ortholog(s) have endoplasmic reticulum localization	null	-2.043752	0.0032495	0.020971235
AN2509	Putative tryptophan 2,3-dioxygenase with a predicted role in aromatic amino acid biosynthesis	null	1.9734991	0.003324	0.021433756
AN11869	null	null	3.3850915	0.0033341	0.021443077
AN5598	Ortholog(s) have cytosol, nucleus localization	null	3.3850915	0.0033341	0.021443077
AN6934	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	3.3850915	0.0033341	0.021443077
AN2853	Ortholog(s) have cytosol, nucleus localization	null	-2.202297	0.0033441	0.021489416
AN7540	Ortholog(s) have role in ascospore formation, cellular response to caffeine, eukaryotic translation initiation factor 3 complex assembly, gamma-tubulin complex localization	null	2.0261222	0.0033644	0.02160071
AN10079	Urease, involved in utilization of urea as a nitrogen source	ureB	-2.373341	0.0034146	0.021885917
AN8208	Has domain(s) with predicted nucleus localization	null	-2.373341	0.0034146	0.021885917
AN5916	Mitochondrial enoyl-CoA hydratase, involved in fatty acid beta-oxidation; required for growth on short-chain fatty acids and for catabolism of isoleucine and valine; transcription is induced by fatty acids	echA	-1.95976	0.0034373	0.022012471
AN6210	Ortholog(s) have Rho GTPase binding, phosphatidylinositol-4,5-bisphosphate binding activity and role in Golgi to plasma membrane transport, exocyst assembly, exocyst localization	null	-2.125583	0.003452	0.022083564
AN1149	Protein of unknown function; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.0107556	0.0034616	0.022083564
AN10845	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.759303	0.0034632	0.022083564
AN2748	Ortholog(s) have cytosol, nucleus localization	null	-2.759303	0.0034632	0.022083564

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AN6306	Ortholog(s) have protein transporter activity, role in protein import into mitochondrial inner membrane and cytosol, mitochondrial intermembrane space protein transporter complex, nucleus localization	null	2.5813337	0.0034632	0.022083564
AN4477	Ortholog(s) have role in cellular response to nitrogen starvation and endoplasmic reticulum localization	null	-2.329878	0.0034765	0.022149091
AN3974	Ortholog of Aspergillus versicolor : Aspve1_0135108, Aspergillus sydowii : Aspsy1_0057545 and Aspergillus terreus NIH2624 : ATET_08256	null	-2.025785	0.0034967	0.022258974
AN4151	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-1.970262	0.0035333	0.022295655
AN4898	null	null	-2.961954	0.0035554	0.022295655
AN5748	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	null	-2.961954	0.0035554	0.022295655
AN5785	Ortholog(s) have unfolded protein binding activity	null	-2.961954	0.0035554	0.022295655
AN7778	null	null	-2.961954	0.0035554	0.022295655
AN0413	null	null	5.7840801	0.003595	0.022295655
AN0737	Possible pseudogene, similar to Zn(II)2Cys6 transcription factor	null	-5.602687	0.003595	0.022295655
AN10293	Ortholog of A. fumigatus Af293 : Afu5g09950, N. fischeri NRRL 181 : NFIA_077320, Aspergillus flavus NRRL 3357 : AFL2T_11694 and Aspergillus versicolor : Aspve1_0025761	null	5.7840801	0.003595	0.022295655
AN11060	Ortholog(s) have 4 iron, 4 sulfur cluster binding activity, role in iron-sulfur cluster assembly, tRNA wobble uridine modification and cytoplasm localization	null	3.7230333	0.003595	0.022295655
AN11161	Has domain(s) with predicted phosphatidylserine decarboxylase activity and role in phospholipid biosynthetic process	null	-5.602687	0.003595	0.022295655
AN12353	null	null	5.7840801	0.003595	0.022295655
AN1320	Has domain(s) with predicted serine-type peptidase activity and role in proteolysis	null	-5.602687	0.003595	0.022295655
AN2346	null	null	-5.602687	0.003595	0.022295655
AN2586	Has domain(s) with predicted catalytic activity and role in metabolic process	null	5.7840801	0.003595	0.022295655
AN2821	Ortholog of A. fumigatus Af293 : Afu2g00180, Afu2g17480, A. niger CBS 513.88 : An03g05360, An04g09420, A. oryzae RIB40 : AO090102000063, AO090009000716 and A. niger ATCC 1015 : 191223-mRNA	null	-5.602687	0.003595	0.022295655
AN3290	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	null	5.7840801	0.003595	0.022295655
AN3318	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding, zinc ion binding activity and role in lipid metabolic process	null	-5.602687	0.003595	0.022295655

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AN3398	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.602687	0.003595	0.022295655
AN3997	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.7840801	0.003595	0.022295655
AN5733	Ortholog of A. fumigatus Af293 : Afu6g06970, A. oryzae RIB40 : AO090003000079, N. fischeri NRRL 181 : NFIA_052620, Aspergillus flavus NRRL 3357 : AFL2T_02868 and A. clavatus NRRL 1 : ACLA_088750	null	-5.602687	0.003595	0.022295655
AN6296	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	null	5.7840801	0.003595	0.022295655
AN6759	Has domain(s) with predicted sequence-specific DNA binding transcription factor activity, zinc ion binding activity, role in regulation of transcription, DNA-dependent and nucleus localization	null	3.7230333	0.003595	0.022295655
AN7150	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	5.7840801	0.003595	0.022295655
AN7257	Ortholog of Aspergillus versicolor : Aspve1_0050844 and Aspergillus sydowii : Aspsy1_0040033	null	3.7230333	0.003595	0.022295655
AN7392	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	3.7230333	0.003595	0.022295655
AN7797	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.7840801	0.003595	0.022295655
AN7952	Has domain(s) with predicted hydrolase activity	null	-5.602687	0.003595	0.022295655
AN8098	null	null	5.7840801	0.003595	0.022295655
AN8099	Putative oxalate decarboxylase with a predicted role in oxalic acid metabolism	null	5.7840801	0.003595	0.022295655
AN9072	Ortholog(s) have cytosol, nucleus localization	null	-5.602687	0.003595	0.022295655
AN9365	Protein with endo-1,4-beta-xylanase activity, involved in degradation of xylans	xlnB	5.7840801	0.003595	0.022295655
AN6525	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	aciA	-1.978311	0.0036102	0.022364078
AN7436	Putative protein disulfide isomerase; pdiA mRNA expression increased in the presence of farnesol	pdiA	-1.889083	0.0036263	0.022364078
AN10249	Ortholog(s) have aminoacyl-tRNA hydrolase activity, role in negative regulation of proteasomal ubiquitin-dependent protein catabolic process and mitochondrial outer membrane localization	null	3.1439135	0.0036271	0.022364078
AN3113	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	ugtA	-3.757018	0.0036271	0.022364078

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AN3868	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	null	-3.757018	0.0036271	0.022364078
AN8999	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin hydrolysis	null	-3.757018	0.0036271	0.022364078
AN1162	Ortholog(s) have guanyl-nucleotide exchange factor activity and cytosol, eukaryotic translation elongation factor 1 complex localization	null	1.9265948	0.0036306	0.022364078
AN7677	Ortholog(s) have role in peroxisome organization and peroxisomal membrane localization	null	-2.562845	0.0036349	0.022364078
AN11391	null	null	2.6462204	0.003636	0.022364078
AN5963	Possible pseudogene, Mariner element-related	null	2.6462204	0.003636	0.022364078
AN8561	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.10739	0.0036605	0.022484152
AN0227	Ortholog of A. niger CBS 513.88 : An14g03700, A. oryzae RIB40 : AO090010000440, Aspergillus brasiliensis : Aspbr1_0190452 and Aspergillus flavus NRRL 3357 : AFL2T_11608	null	-3.116686	0.0036796	0.022484152
AN10532	Has domain(s) with predicted hydrolase activity	null	-3.116686	0.0036796	0.022484152
AN1505	Ortholog of A. nidulans FGSC A4 : AN3207, A. fumigatus Af293 : Afu2g15470, Afu8g00720, Afu8g05070 and A. niger CBS 513.88 : An07g04980, An16g07680, An14g02720, An14g07130, An15g05540	null	2.9957148	0.0036796	0.022484152
AN4177	Has domain(s) with predicted catalytic activity, coenzyme binding, nucleotide binding activity and role in cellular metabolic process	null	-3.116686	0.0036796	0.022484152
AN8135	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity and role in metabolic process	null	2.9957148	0.0036796	0.022484152
AN8668	Ortholog(s) have role in rRNA processing, ribosomal large subunit assembly and nucleoplasm, spindle pole body localization	null	2.9957148	0.0036796	0.022484152
AN9446	Putative pantothenate kinase with a predicted role in Coenzyme A and pantothenate biosynthesis	panK	2.6950164	0.0036796	0.022484152
AN4461	Has domain(s) with predicted nucleic acid binding activity and intracellular localization	null	-2.243492	0.003705	0.02262092
AN6068	Ortholog(s) have role in chromatin remodeling and ASTRA complex, mitochondrion localization	null	-2.442178	0.0037659	0.022974034
AN4323	Putative branched chain amino acid aminotransferase with a predicted role in valine, leucine, and isoleucine metabolism	null	2.0430553	0.0037932	0.023121294
AN8488	Ortholog(s) have SNAP receptor activity, palmitoyltransferase activity, role in vacuole fusion, non-autophagic, vesicle fusion and Golgi apparatus, SNARE complex, cytosol, endosome, fungal-type vacuole, mitochondrion, nucleus localization	null	-2.353252	0.0038204	0.023268119

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AN8705	Ortholog(s) have cytoplasmic stress granule, cytosol, nucleus localization	null	1.863275	0.0038435	0.023389882
AN7208	SET domain protein; protein levels decrease in response to farnesol	null	2.3660095	0.0039131	0.023794098
AN1693	Putative F-box protein	null	-1.977754	0.0039458	0.023973427
AN0964	Ortholog of A. fumigatus Af293 : Afu1g16640, A. niger CBS 513.88 : An01g10620, A. oryzae RIB40 : AO090005001050, A. niger ATCC 1015 : 136898-mRNA and Aspergillus versicolor : Aspve1_0036577	null	-1.923047	0.0039576	0.024025469
AN6168	Putative malate dehydrogenase with a predicted role in oxidation of malate to pyruvate	maeA	1.8682278	0.0039726	0.024097123
AN9419	Ortholog(s) have alanine-tRNA ligase activity, role in alanyl-tRNA aminoacylation and cytosol, mitochondrion localization	null	1.9309928	0.0040545	0.024553393
AN0716	Ortholog(s) have role in cardiolipin biosynthetic process, protein import into mitochondrial matrix and extrinsic to mitochondrial inner membrane, mitochondrial matrix localization	null	2.0549637	0.0040631	0.024553393
AN8344	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of substances activity, role in transport and integral to membrane localization	null	2.0122964	0.0040631	0.024553393
AN0335	Ortholog of A. fumigatus Af293 : Afu1g02330, A. niger CBS 513.88 : An01g05850, A. oryzae RIB40 : AO090005000867, A. niger ATCC 1015 : 205986-mRNA and Aspergillus versicolor : Aspve1_0048589	null	2.5310339	0.0040774	0.024553393
AN10618	Ortholog(s) have RNA binding activity	null	2.3671976	0.0040774	0.024553393
AN1127	Ortholog of A. nidulans FGSC A4 : AN7386, A. fumigatus Af293 : Afu1g11740, A. niger CBS 513.88 : An02g03380, An08g03700, A. oryzae RIB40 : AO090026000507 and A. niger ATCC 1015 : 126803-mRNA	null	2.5310339	0.0040774	0.024553393
AN2983	Putative Rho GTPase-activating protein (Rho-GAP); null mutants form normal septa	msb1	2.3671976	0.0040774	0.024553393
AN3085	Ortholog(s) have mitochondrion localization	null	-2.698311	0.0040774	0.024553393
AN5010	null	null	2.3671976	0.0040774	0.024553393
AN8233	Ortholog(s) have phosphatidylinositol transporter activity	null	2.0039923	0.0041724	0.025105192
AN2013	Has domain(s) with predicted nucleotide binding, oxidoreductase activity	null	-2.927451	0.0042578	0.025577397
AN3198	null	null	2.5535244	0.0042578	0.025577397
AN4482	Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.332879	0.0042785	0.025681296
AN5596	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.107888	0.0042868	0.025710193
AN12324	null	null	-2.390937	0.0043274	0.02591251
AN6812	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in nitrogen compound metabolic process	null	-2.416785	0.0043274	0.02591251

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AN1290	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	-1.920514	0.0043712	0.026153845
AN0836	Ortholog(s) have D-arabinono-1,4-lactone oxidase activity, role in cellular response to oxidative stress, dehydro-D-arabinono-1,4-lactone biosynthetic process and integral to mitochondrial outer membrane localization	null	1.9505462	0.0043906	0.026248607
AN4908	Putative eukaryotic translation initiation factor subunit; PalA-dependent expression independent of pH	null	1.8329858	0.0044432	0.026459697
AN0589	Putative ATP-dependent RNA helicase with a predicted role in rRNA processing; ortholog of S. cerevisiae Hca4p; expression reduced after exposure to farnesol	null	-2.741351	0.0044472	0.026459697
AN2741	Has domain(s) with predicted selenium binding activity and role in cell redox homeostasis	null	2.5826127	0.0044472	0.026459697
AN5163	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	null	-2.741351	0.0044472	0.026459697
AN5700	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.741351	0.0044472	0.026459697
AN6245	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	null	2.5826127	0.0044472	0.026459697
AN10351	Ortholog(s) have aminopeptidase activity, role in chaperone-mediated protein folding, proteolysis and cytosol, fungal-type vacuole lumen, ribosome localization	null	-2.090382	0.0044662	0.026530436
AN11597	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	null	2.0059652	0.0044662	0.026530436
AN2282	Putative MFS transporter; PalA-dependent expression independent of pH	null	-1.951918	0.0044935	0.026671649
AN2933	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	null	1.971012	0.0045247	0.026807564
AN1050	Putative 3-ketoacyl-CoA thiolase with a predicted role in fatty acid metabolism; protein is mislocalized in a pexG mutant	null	-1.912494	0.0045274	0.026807564
AN2165	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	null	-1.847727	0.0045303	0.026807564
AN10297	Protein with similarity to nonribosomal peptide synthases (NRPS-like); putative acyl CoA synthetase with an NAD-binding domain	null	-2.135994	0.0045308	0.026807564
AN1424	Ortholog of A. fumigatus Af293 : Afu8g04140, A. niger CBS 513.88 : An16g08950, A. oryzae RIB40 : AO090103000029, A. niger ATCC 1015 : 214466-mRNA and Aspergillus versicolor : Aspve1_0049699	null	3.2796216	0.0045674	0.027002761
AN3578	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity	null	-2.226854	0.0045711	0.027003389

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AN2768	Ortholog of A. fumigatus Af293 : Afu3g06100, A. oryzae RIB40 : AO090020000083, A. niger ATCC 1015 : 179806-mRNA, Aspergillus versicolor : Aspve1_0149606 and Aspergillus terreus NIH2624 : ATET_08860	null	1.9677314	0.0046174	0.027099064
AN0687	Putative spermine or spermidine synthase with a predicted role in arginine metabolism; transcript upregulated in response to camptothecin; protein induced by farnesol	spdA	2.621711	0.0046236	0.027099064
AN1021	Ortholog of A. fumigatus Af293 : Afu1g12980, A. oryzae RIB40 : AO090012000595, A. niger ATCC 1015 : 208023-mRNA, Aspergillus versicolor : Aspve1_0280973 and Aspergillus sydowii : Aspsy1_0053349	null	2.9224094	0.0046236	0.027099064
AN10518	Protein of unknown function; protein induced by farnesol	null	2.621711	0.0046236	0.027099064
AN11212	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-3.071336	0.0046236	0.027099064
AN1368	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	null	-3.071336	0.0046236	0.027099064
AN4902	Ortholog of A. niger CBS 513.88 : An02g06740, A. oryzae RIB40 : AO090003001585, N. fischeri NRRL 181 : NFIA_066360, Aspergillus flavus NRRL 3357 : AFL2T_02363 and A. clavatus NRRL 1 : ACLA_038800	null	2.9224094	0.0046236	0.027099064
AN6487	Putative aspartyl protease; ortholog of S. cerevisiae BAR1; expression reduced after exposure to farnesol	null	-3.071336	0.0046236	0.027099064
AN7255	Ortholog of A. oryzae RIB40 : AO090102000108, Aspergillus brasiliensis : Aspbr1_0200327, A. niger ATCC 1015 : 194648-mRNA, Aspergillus acidus : Aspfo1_0206622 and Aspergillus versicolor : Aspve1_0038807	null	2.621711	0.0046236	0.027099064
AN7286	Has domain(s) with predicted bile acid:sodium symporter activity, role in sodium ion transport and membrane localization	null	2.621711	0.0046236	0.027099064
AN2149	Putative chaperonin complex component, TCP-1 alpha subunit; ortholog of S. cerevisiae Tcp1p; expression reduced after exposure to farnesol	cct1	1.8457036	0.0046734	0.027369717
AN2995	Ortholog(s) have cytoplasm, nucleus localization	null	-2.491663	0.0047085	0.027493866
AN4786	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	null	2.3248812	0.0047085	0.027493866
AN0276	Ortholog of A. niger CBS 513.88 : An01g04950, A. oryzae RIB40 : AO090005000773, A. niger ATCC 1015 : 36142-mRNA, Aspergillus versicolor : Aspve1_0157671 and Aspergillus sydowii : Aspsy1_0085871	null	-3.70321	0.0047241	0.027493866
AN11991	Has domain(s) with predicted identical protein binding activity	null	-3.647318	0.0047241	0.027493866
AN1565	Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation and endoplasmic reticulum localization	null	-3.647318	0.0047241	0.027493866
AN1571	Protein with alpha-arabinofuranosidase activity, involved in degradation of pectin	abfB	3.0574202	0.0047241	0.027493866

AN1604	Putative alpha-1,3-glucanase; predicted glycosyl phosphatidylinositol (GPI)-anchor	agnE	-3.647318	0.0047241	0.027493866
AN8025	Ortholog of A. fumigatus Af293 : Afu1g01450, A. niger CBS 513.88 : An11g08050, An05g01890, An11g03950, A. oryzae RIB40 : AO090010000064, AO090701000602 and A. niger ATCC 1015 : 195287-mRNA, 39295-mRNA	null	-3.70321	0.0047241	0.027493866
AN5458	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	null	-2.112131	0.0047286	0.027498751
AN7008	Putative mitochondrial hydroxyacyl-CoA dehydrogenase involved in short-chain fatty acid beta-oxidation	hadA	-1.840079	0.0047355	0.027517299
AN6058	DUF833 domain-containing protein; intracellular, menadione stress-induced protein	null	1.835186	0.0048015	0.027879069
AN8979	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	alcA	-1.965348	0.0048333	0.028042367
AN12201	Ortholog(s) have oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor activity, role in heme a biosynthetic process, iron-sulfur cluster assembly, ubiquinone biosynthetic process and mitochondrial matrix localization	null	1.8723586	0.004849	0.028111145
AN10663	Ortholog of A. fumigatus Af293 : Afu6g14320, A. niger CBS 513.88 : An08g08150, A. oryzae RIB40 : AO090103000451, Aspergillus brasiliensis : Aspbr1_0053618 and N. fischeri NRRL 181 : NFIA_060200	null	1.9829207	0.0048835	0.028289211
AN0445	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	1.8628925	0.0048907	0.028309321
AN4016	Possible pseudogene, similar to 60S ribosomal protein L40	null	1.8333513	0.0049363	0.028550929
AN9444	Ortholog of A. nidulans FGSC A4 : AN7400, Aspergillus flavus NRRL 3357 : AFL2T_02908, Aspergillus acidus : Aspfo1_0034827, Aspergillus versicolor : Aspve1_0037710 and Aspergillus sydowii : Aspsy1_0038876	null	-2.364617	0.0049801	0.028782102
AN0781	Ortholog of A. fumigatus Af293 : Afu1g14500, A. oryzae RIB40 : AO090011000360, A. niger ATCC 1015 : 46347-mRNA, Aspergillus versicolor : Aspve1_0036344 and Aspergillus sydowii : Aspsy1_0145580	null	-2.369593	0.0050592	0.029216484
AN0409	Ortholog(s) have cytosol, fungal-type vacuole membrane, nucleus localization	null	-2.099988	0.0050656	0.029230783
AN1780	Ortholog(s) have aminopeptidase activity, role in protein processing, protein stabilization and extrinsic to mitochondrial inner membrane, nucleus localization	null	2.0247666	0.0050799	0.029290866
AN7158	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	1.9224847	0.0050914	0.029318146
AN0981	Has domain(s) with predicted integral to membrane localization	null	2.077476	0.0050925	0.029318146

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AN2273	Ortholog of A. fumigatus Af293 : Afu5g06380, A. niger CBS 513.88 : An17g01340, A. oryzae RIB40 : AO090009000618, A. niger ATCC 1015 : 45156-mRNA and Aspergillus versicolor : Aspve1_0162627	null	-2.22717	0.0051037	0.029337218
AN8407	Ortholog of Aspergillus brasiliensis : Aspbr1_0177798, Aspergillus versicolor : Aspve1_0046756, Aspergillus sydowii : Aspsy1_0210366 and A. fumigatus A1163 : AFUB_071580	null	2.1184118	0.0051037	0.029337218
AN10475	Ortholog(s) have cytosol localization	null	2.0164931	0.0052581	0.030099552
AN5104	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-1.80118	0.005316	0.030099552
AN6629	Putative ribosomal protein L14; ortholog of S. cerevisiae Rpl14Ap; expression reduced after exposure to farnesol	null	1.9395213	0.0053367	0.030099552
AN1274	Ortholog(s) have alditol:NADP+ 1-oxidoreductase activity, mRNA binding activity, role in D-xylose catabolic process, arabinose catabolic process, cellular response to oxidative stress and cytoplasm, nucleus localization	null	2.1043127	0.0053698	0.030099552
AN2794	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	2.1043127	0.0053698	0.030099552
AN0126	Ortholog(s) have ATP binding, ATPase activity, dinucleotide insertion or deletion binding, loop DNA binding, single-stranded DNA binding activity	null	5.6349831	0.0054016	0.030099552
AN0187	null	null	5.6349831	0.0054016	0.030099552
AN0402	Ortholog of Aspergillus versicolor : Aspve1_0048646 and Aspergillus sydowii : Aspsy1_0055229	null	5.6349831	0.0054016	0.030099552
AN0826	Predicted DDE1 transposon-related ORF	null	5.6349831	0.0054016	0.030099552
AN0965	null	null	-5.50527	0.0054016	0.030099552
AN0993	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.6349831	0.0054016	0.030099552
AN1034	Putative polyketide synthase; required for asperfuranone biosynthesis; transcriptionally induced by scrP overexpression	afoE	5.6349831	0.0054016	0.030099552
AN10957	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	null	3.5739363	0.0054016	0.030099552
AN11008	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	null	5.6349831	0.0054016	0.030099552
AN11080	Putative dimethyl-allyl-tryptophan synthase (DMATS)-type aromatic prenyltransferase	null	5.6349831	0.0054016	0.030099552
AN11110	Has domain(s) with predicted ATP binding, ligase activity, forming aminoacyl-tRNA and related compounds activity, role in tRNA aminoacylation, translation and cytoplasm localization	null	-5.50527	0.0054016	0.030099552

AN11703	null	null	5.6349831	0.0054016	0.030099552
AN12330	Has domain(s) with predicted catalytic activity and role in biosynthetic process	null	5.6349831	0.0054016	0.030099552
AN12484	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.50527	0.0054016	0.030099552
AN1865	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	3.5739363	0.0054016	0.030099552
AN1951	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and nucleus localization	null	-5.50527	0.0054016	0.030099552
AN2197	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	5.6349831	0.0054016	0.030099552
AN3143	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	null	5.6349831	0.0054016	0.030099552
AN4117	Putative cytochrome P450	CYP660A1	-5.50527	0.0054016	0.030099552
AN4451	null	null	5.6349831	0.0054016	0.030099552
AN4682	Ortholog of A. fumigatus Af293 : Afu5g08980, A. niger CBS 513.88 : An07g04180, A. niger ATCC 1015 : 209689-mRNA, Aspergillus versicolor : Aspve1_0084718 and Aspergillus sydowii : Aspsy1_0155159	null	-5.50527	0.0054016	0.030099552
AN5759	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity and role in protein phosphorylation	null	3.5739363	0.0054016	0.030099552
AN6417	Ortholog(s) have cell cortex localization	null	-5.50527	0.0054016	0.030099552
AN6648	Has domain(s) with predicted catalytic activity, pyridoxal phosphate binding activity and role in metabolic process	null	3.5739363	0.0054016	0.030099552
AN6884	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	null	-5.50527	0.0054016	0.030099552
AN7215	null	null	5.6349831	0.0054016	0.030099552
AN7292	Has domain(s) with predicted catalytic activity	null	-5.50527	0.0054016	0.030099552
AN7305	Ortholog(s) have ATPase activator activity, RNA binding activity	null	-5.50527	0.0054016	0.030099552
AN7651	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	null	-5.50527	0.0054016	0.030099552
AN7779	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.6349831	0.0054016	0.030099552
AN8030	Has domain(s) with predicted NAD binding, adenosylhomocysteinase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	-5.50527	0.0054016	0.030099552

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AN8112	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	5.6349831	0.0054016	0.030099552
AN8136	Ortholog of Aspergillus versicolor : Aspve1_0202914 and Aspergillus sydowii : Aspsy1_0072548	null	3.5739363	0.0054016	0.030099552
AN8186	Predicted mariner transposon-related ORF	null	3.5739363	0.0054016	0.030099552
AN8199	Ortholog(s) have role in fumiquinazoline A biosynthetic process, secondary metabolic process	null	5.6349831	0.0054016	0.030099552
AN9320	Has domain(s) with predicted zinc ion binding activity	null	3.5739363	0.0054016	0.030099552
AN4446	Ortholog(s) have role in ER to Golgi vesicle-mediated transport and ER to Golgi transport vesicle, Golgi apparatus, endoplasmic reticulum, mitochondrion localization	null	-1.951691	0.005445	0.030295299
AN1536	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	null	-2.659626	0.005457	0.030295299
AN3043	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.701067	0.005457	0.030295299
AN8193	Ortholog of A. niger CBS 513.88 : An09g05410, A. niger ATCC 1015 : 143341-mRNA, Aspergillus versicolor : Aspve1_0047160, Aspergillus sydowii : Aspsy1_0211762 and Aspergillus terreus NIH2624 : ATET_08095	null	-2.659626	0.005457	0.030295299
AN8752	Ortholog of A. fumigatus Af293 : Afu6g02845, A. niger CBS 513.88 : An12g07700, Aspergillus versicolor : Aspve1_0086213, Aspergillus sydowii : Aspsy1_0092097 and Aspergillus terreus NIH2624 : ATET_07166	null	-2.659626	0.005457	0.030295299
AN12419	Ortholog(s) have role in mRNA export from nucleus, nucleolus organization, protein localization to nucleolar rDNA repeats and cytosol localization	null	1.9545672	0.0055269	0.030660539
AN6014	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	faaA	-1.793817	0.0055835	0.030951965
AN8603	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.04962	0.0055916	0.030973458
AN3840	Putative tetrahydrofolylpolyglutamate synthase with a predicted role in folate biosynthesis	null	2.0887774	0.0056278	0.031150796
AN1144	Has domain(s) with predicted peptidase activity	null	2.0884208	0.00568	0.031367695
AN0695	Putative snoRNP component with a predicted role in ribosomal RNA pseudouridinylation; ortholog of S. cerevisiae Nhp2p; expression reduced after exposure to farnesol	null	2.3150805	0.0056879	0.031367695
AN6038	Ortholog of A. fumigatus Af293 : Afu2g09780, A. niger CBS 513.88 : An16g05430, A. oryzae RIB40 : AO090011000660, A. niger ATCC 1015 : 184220-mRNA and Aspergillus versicolor : Aspve1_0627568	null	2.4789169	0.0056879	0.031367695

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AN8368	Ortholog of A. fumigatus Af293 : Afu4g14080, N. fischeri NRRL 181 : NFIA_102240, A. fumigatus A1163 : AFUB_071230 and Aspergillus carbonarius ITEM 5010 : Acar5010_209519	null	2.4789169	0.0056879	0.031367695
AN8977	Putative gluconolactonase with a predicted role in gluconic acid and gluconate metabolism; transcript upregulated by exposure to ethanol	alcP	-2.634627	0.0056879	0.031367695
AN3226	HAS domain protein; protein levels decrease in response to farnesol	null	1.8142005	0.0056925	0.031369535
AN3258	Ortholog of A. fumigatus Af293 : Afu8g07090, A. niger CBS 513.88 : An05g02250, A. oryzae RIB40 : AO090001000070, A. niger ATCC 1015 : 127335-mRNA and Aspergillus carbonarius ITEM 5010 : Acar5010_211879	null	1.987212	0.0057162	0.03147705
AN1124	Ortholog of A. fumigatus Af293 : Afu1g11720, A. niger CBS 513.88 : An08g03680, A. oryzae RIB40 : AO090038000251, A. niger ATCC 1015 : 208202-mRNA and Aspergillus versicolor : Aspve1_0288823	null	-1.897993	0.0057393	0.031538037
AN4112	Ortholog of A. fumigatus Af293 : Afu1g05840, A. niger CBS 513.88 : An18g03610, A. oryzae RIB40 : AO090009000350, A. niger ATCC 1015 : 131259-mRNA and Aspergillus versicolor : Aspve1_0135838	null	2.2780553	0.0057399	0.031538037
AN4418	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-2.337808	0.0057399	0.031538037
AN10090	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	null	-1.942728	0.0057522	0.031561531
AN6060	Has domain(s) with predicted DNA binding, RNA binding activity and role in RNA metabolic process	null	1.9145308	0.0057566	0.031561531
AN0891	Zn(2)-Cys(6) binuclear cluster domain transcription factor required for positive regulation of genes involved in purine degradation pathway in response to uric acid; homology to Neurospora crassa pco-1	uaY	1.9189238	0.0057569	0.031561531
AN7146	Putative S-adenosyl-methionine delta-24-sterol-C-methyltransferase with a predicted role in sterol metabolism	null	1.9603486	0.0058195	0.031845875
AN0128	Ortholog(s) have tRNA methyltransferase activity, role in tRNA methylation, wybutosine biosynthetic process and cytosol, mitochondrion, nucleus localization	null	2.8451788	0.0058344	0.031845875
AN12110	null	null	-2.976122	0.0058344	0.031845875
AN3366	Ortholog of Aspergillus versicolor : Aspve1_0051963 and Aspergillus sydowii : Aspsy1_0088131	null	-2.976122	0.0058344	0.031845875
AN4600	Ortholog of A. fumigatus Af293 : Afu2g02210, A. niger CBS 513.88 : An07g06630, A. niger ATCC 1015 : 180337-mRNA, Aspergillus versicolor : Aspve1_0134605 and Aspergillus sydowii : Aspsy1_0180963	null	2.5444804	0.0058344	0.031845875
AN7344	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.024514	0.0058344	0.031845875
AN6208	Ortholog of A. fumigatus Af293 : Afu2g11920, A. niger CBS 513.88 : An02g04010, A. oryzae RIB40 : AO090026000451, A. niger ATCC 1015 : 134131-mRNA and Aspergillus versicolor : Aspve1_0130633	null	1.9546409	0.0059806	0.032620268

AN9168	Ortholog(s) have solute:hydrogen symporter activity, role in glycerol transport, transmembrane transport and plasma membrane localization	null	-2.248382	0.0060456	0.032950585
AN5231	Putative exo-arabinanase	null	2.089067	0.006094	0.033190446
AN6823	Ortholog of A. fumigatus Af293 : Afu5g12860, A. niger CBS 513.88 : An14g06360, A. oryzae RIB40 : AO090120000406, A. niger ATCC 1015 : 201762-mRNA and Aspergillus versicolor : Aspve1_0122523	null	-1.948314	0.0061519	0.033418602
AN1892	Ortholog(s) have protein channel activity, role in mitochondrial genome maintenance, protein import into mitochondrial matrix and mitochondrial inner membrane presequence translocase complex localization	null	-2.855865	0.0061538	0.033418602
AN2020	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	null	-2.855865	0.0061538	0.033418602
AN2144	Ortholog(s) have cytosol, nucleus localization	null	-2.818695	0.0061538	0.033418602
AN7035	Has domain(s) with predicted peptidase activity and role in proteolysis	null	-1.98567	0.0061781	0.033510352
AN2271	Ortholog of A. fumigatus Af293 : Afu5g06400, A. niger CBS 513.88 : An17g01320, A. niger ATCC 1015 : 214021-mRNA, Aspergillus versicolor : Aspve1_0050563 and Aspergillus sydowii : Aspsy1_0054275	null	-2.450175	0.0061886	0.033510352
AN0844	Protein required for actin cytoskeleton organization and cell cycle progression; ortholog of S. cerevisiae Sda1p;	null	2.9654087	0.0061887	0.033510352
AN2798	Has domain(s) with predicted role in response to stress and integral to membrane localization	null	2.9654087	0.0061887	0.033510352
AN3013	Ortholog(s) have cytoplasm localization	null	-1.853722	0.0061981	0.033537013
AN3421	Has domain(s) with predicted nucleotide binding activity	null	3.1658288	0.006311	0.03412308
AN7913	Protein of unknown function; member of the F9775 secondary metabolite gene cluster	null	1.9798086	0.0063627	0.034378096
AN2879	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	null	-2.013495	0.0063988	0.034548213
AN10172	Ortholog(s) have dicarboxylic acid transmembrane transporter activity, role in mitochondrial transport and mitochondrial inner membrane localization	null	1.7720552	0.0064176	0.034622919
AN4900	Putative bZIP DNA-binding protein involved in regulating nitrogen metabolite repression	meaB	-2.005063	0.006422	0.034622919
AN6843	Mitochondrial ribosomal protein L4; this locus is reported to contain an upstream open reading frame (uORF)	null	1.939451	0.0064369	0.034678353
AN3865	Ortholog(s) have mitochondrion localization	null	1.8751555	0.0064465	0.034705085
AN1019	Putative Scf complex protein; NeddH-associated protein; transcript upregulated in response to camptothecin	culA	-1.808294	0.0064882	0.034904584

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AN3075	Zinc finger protein of unknown function; overexpression confers the "fluffy" phenotype	oefC	-1.807963	0.0065918	0.035436428
AN8875	Ortholog(s) have cell tip, endoplasmic reticulum localization	null	-2.282647	0.0066259	0.035593945
AN6037	Putative glucose-6-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; mutant defective in hyphal polarity and conidiation	swoM	1.876407	0.0066545	0.035708869
AN10922	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	1.9955384	0.0066664	0.035708869
AN1143	Has domain(s) with predicted zinc ion binding activity	null	2.0616827	0.0066664	0.035708869
AN3687	Ortholog(s) have cytosol, nucleus localization	null	1.9955384	0.0066664	0.035708869
AN10568	null	null	1.9015279	0.0066925	0.03582301
AN5679	Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex, U6 snRNP, nucleolus, small nucleolar ribonucleoprotein complex localization	null	-2.616958	0.0067183	0.035895717
AN12358	Ortholog(s) have mitochondrion localization	null	1.7613985	0.006727	0.035895717
AN4980	Ortholog(s) have cytosol localization	null	-2.568001	0.0067398	0.035895717
AN5116	Ortholog(s) have alpha-tubulin binding activity and cytosol, nucleus localization	null	2.26101	0.0067398	0.035895717
AN6593	Ortholog(s) have unfolded protein binding activity, role in aerobic respiration, mitochondrial respiratory chain complex IV assembly and integral to mitochondrial inner membrane localization	null	2.26101	0.0067398	0.035895717
AN6610	Putative phosphatidylglycerol phosphate phosphatase with a predicted role in phospholipid metabolism	null	-2.568001	0.0067398	0.035895717
AN8882	Ortholog of A. fumigatus Af293 : Afu8g02740, A. niger CBS 513.88 : An03g06840, A. niger ATCC 1015 : 191330-mRNA, Aspergillus versicolor : Aspve1_0047604 and Aspergillus sydowii : Aspsy1_0522885	null	-2.568001	0.0067398	0.035895717
AN3455	Ortholog(s) have role in rRNA processing and CURI complex, UTP-C complex, small-subunit processome localization	null	1.9865528	0.0068712	0.036517781
AN6630	Putative nascent polypeptide-associated complex subunit alpha; induced by rapamycin-induced autophagy	null	1.9865528	0.0068712	0.036517781
AN8565	Putative serine O-acetyltransferase with a predicted role in cysteine metabolism	cysA	1.9865528	0.0068712	0.036517781
AN12335	Protein with an acyl-CoA dehydrogenase domain	acdA	-1.79222	0.0069553	0.036938403
AN1674	Has domain(s) with predicted DNA binding activity and intracellular localization	null	1.862756	0.006966	0.036968664
AN5614	Ortholog(s) have role in plasma membrane fusion involved in cytogamy, response to pheromone and cytoplasm, mating projection tip localization	null	-1.96802	0.0069943	0.037092431
AN6718	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	-2.083894	0.0070624	0.037423362
AN3014	Ortholog(s) have cytosol localization	null	-1.776146	0.0070667	0.037423362

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AN8886	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	null	1.9090426	0.0070845	0.03747254
AN6201	Ortholog of A. fumigatus Af293 : Afu2g11830, A. oryzae RIB40 : AO090026000461, Aspergillus versicolor : Aspve1_0052426, Aspergillus sydowii : Aspsy1_0151758 and Aspergillus terreus NIH2624 : ATET_01122	null	-2.092048	0.007086	0.03747254
AN1959	Nuclear protein involved in spore formation and trehalose accumulation; potential transcription-activating domain; mutants have low spore viability; two overlapping transcripts; VosA-VelB form a dimeric complex in hyphae grown in the dark	vosA	-2.024906	0.0071853	0.037970596
AN8390	GPR1/FUN34/YaaH family member; ethanol- and ethylacetate-induced gene	null	-1.787685	0.00722	0.038126921
AN10762	Ortholog(s) have cytosol localization	null	-2.037732	0.0072412	0.038212189
AN5122	Putative kinase with a predicted role in nucleotide salvage pathways	null	1.8370548	0.0072678	0.038325528
AN6767	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-2.037783	0.0072969	0.038415474
AN6699	Ortholog(s) have mitochondrion localization	null	-1.745464	0.0072978	0.038415474
AN4741	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	null	1.7918819	0.0073003	0.038415474
AN3112	UDP-galactopyranose mutase, a flavoenzyme that converts UDP-galactopyranose to UDP-galactofuranose, a central enzyme in in galactofuranose biosynthesis; involved in cell wall biogenesis	ugmA	1.9135268	0.0073325	0.038557751
AN10790	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.92605	0.0073943	0.038800355
AN11861	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	null	-2.92605	0.0073943	0.038800355
AN2129	Subunit 5 of the COP9 signalosome (CSN) responsible for cleaving the ubiquitin-like protein Nedd8 from cullin-RING E3 ubiquitin ligases; required for normal cleistothecia development; mutants impaired in secondary metabolism	csnE	-2.92605	0.0073943	0.038800355
AN20009	Putative mitochondrial ATP synthase subunit 8	atp8	2.4341506	0.0074277	0.038893954
AN7128	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.780541	0.0074277	0.038893954
AN7781	Putative alpha-L-arabinofuranosidase	null	2.4341506	0.0074277	0.038893954
AN5836	APSES domain transcription factor involved in regulation of conidiophore development; represses abaA and other developmentally regulated genes; locus consists of stuA-alpha and stuA-beta transcriptional units; stuA-alpha contains a uORF	stuA	-1.881103	0.007471	0.039093351

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AN4209	Has domain(s) with predicted sugar:hydrogen symporter activity, role in carbohydrate transport and Golgi membrane, integral to membrane localization	null	-1.891093	0.0076235	0.039835245
AN5414	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity, role in carbohydrate metabolic process and membrane localization	null	-1.891093	0.0076235	0.039835245
AN0392	Ortholog of A. fumigatus Af293 : Afu1g01540, A. oryzae RIB40 : AO090102000263, N. fischeri NRRL 181 : NFIA_023120, A. clavatus NRRL 1 : ACLA_032940 and Aspergillus versicolor : Aspve1_0157964	null	-2.254255	0.0076605	0.040000611
AN7367	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in nitrogen compound metabolic process	null	-1.733013	0.0076956	0.040152191
AN1061	Putative GABA permease; transcript is induced by nitrate	null	-1.816328	0.0077003	0.040152191
AN6797	null	null	-2.074196	0.007794	0.040612505
AN7770	Ortholog(s) have 2,4-dienoyl-CoA reductase (NADPH) activity, role in ascospore formation, fatty acid catabolic process and peroxisomal matrix localization	null	-2.008383	0.0078423	0.040769208
AN5338	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	1.8762491	0.0078484	0.040769208
AN12027	Ortholog(s) have cytosol, nucleus localization	null	-1.963877	0.0078533	0.040769208
AN0179	Putative oxidoreductase; protein induced by farnesol	null	1.8172404	0.0078885	0.040769208
AN8366	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-1.780023	0.0079131	0.040769208
AN8827	Ca2+/calmodulin-dependent protein kinase, involved in nuclear division; required for normal timing of NimX activation at G1/S transition	cmkC	-1.931895	0.0079847	0.040769208
AN0094	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	null	2.3686701	0.0080037	0.040769208
AN11794	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	2.2048337	0.0080037	0.040769208
AN1230	Ortholog(s) have unfolded protein binding activity, role in mitochondrial proton-transporting ATP synthase complex assembly and integral to mitochondrial membrane, mitochondrial inner membrane localization	null	2.2048337	0.0080037	0.040769208
AN4452	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.3686701	0.0080037	0.040769208
AN7701	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	2.3686701	0.0080037	0.040769208
AN4017	Ortholog(s) have endoplasmic reticulum localization	null	-1.863898	0.0080321	0.040769208

AN0401	Ortholog of A. fumigatus Af293 : Afu2g02490, Aspergillus flavus NRRL 3357 : AFL2T_08730, A. clavatus NRRL 1 : ACLA_092310, Aspergillus versicolor : Aspve1_0035846 and Aspergillus sydowii : Aspsy1_0143520	null	2.8671268	0.0081561	0.040769208
AN3360	Has domain(s) with predicted hydrolase activity, hydrolyzing O-glycosyl compounds activity and role in carbohydrate metabolic process	null	2.8671268	0.0081561	0.040769208
AN3863	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	null	-3.528584	0.0081561	0.040769208
AN6809	Ortholog of A. fumigatus Af293 : Afu5g00680, A. niger CBS 513.88 : An16g00250, A. oryzae RIB40 : AO090010000081, A. niger ATCC 1015 : 210803-mRNA and Aspergillus terreus NIH2624 : ATET_09248	null	2.8671268	0.0081561	0.040769208
AN2846	Putative glutathione peroxidase with a predicted role in glutathione biosynthesis; protein induced by farnesol	gpxA	1.8047322	0.0081604	0.040769208
AN3214	Putative histidine-containing phosphotransfer protein	null	1.7660703	0.008189	0.040769208
AN5162	Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism	pdhB	1.7080556	0.0081993	0.040769208
AN0841	null	null	-1.729008	0.0082008	0.040769208
AN3843	Ortholog(s) have role in cristae formation, protein import into mitochondrial intermembrane space and integral to mitochondrial inner membrane, mitochondrial crista, mitochondrial crista junction localization	null	1.7164082	0.0082121	0.040769208
AN0018	Possible pseudogene	null	-5.288162	0.0082445	0.040769208
AN0577	null	null	-5.288162	0.0082445	0.040769208
AN0666	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-5.288162	0.0082445	0.040769208
AN0774	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	null	-5.400796	0.0082445	0.040769208
AN10033	Ortholog(s) have role in vesicle-mediated transport and COPI-coated vesicle, integral to Golgi membrane localization	null	3.4076358	0.0082445	0.040769208
AN10505	Putative unsaturated rhamnogalacturonan hydrolase	null	-5.400796	0.0082445	0.040769208
AN10628	Conidium-specific RNA of unknown function; member of the SpoC1 gene cluster	SpoC1-C1C	-5.288162	0.0082445	0.040769208
AN10631	Ortholog(s) have cytosol, nucleus localization	null	-5.400796	0.0082445	0.040769208
AN1067	Has domain(s) with predicted oxidoreductase activity, role in antibiotic biosynthetic process and cytoplasm localization	null	-5.288162	0.0082445	0.040769208
AN10896	Has domain(s) with predicted nucleotide binding activity	null	-5.288162	0.0082445	0.040769208
AN11015	Has domain(s) with predicted S-(hydroxymethyl)glutathione synthase activity, zinc ion binding activity and role in formaldehyde catabolic process	null	-5.288162	0.0082445	0.040769208
AN11207	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	5.4686825	0.0082445	0.040769208

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AN11622	null	null	5.4686825	0.0082445	0.040769208
AN11714	Has domain(s) with predicted cell outer membrane, integral to membrane localization	null	5.4686825	0.0082445	0.040769208
AN11738	Ortholog of Aspergillus versicolor : Aspve1_0035989, Aspergillus sydowii : Aspsy1_0129331 and Aspergillus terreus NIH2624 : ATET_05766	null	-5.400796	0.0082445	0.040769208
AN1186	Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport and membrane localization	null	-5.288162	0.0082445	0.040769208
AN11959	Putative acylglycerone-phosphate reductase with a predicted role in phospholipid metabolism	null	-5.400796	0.0082445	0.040769208
AN12012	null	null	-5.288162	0.0082445	0.040769208
AN12061	null	null	-5.288162	0.0082445	0.040769208
AN1477	Putative beta-1,4-xylosidase	null	-5.288162	0.0082445	0.040769208
AN2118	Has domain(s) with predicted catalytic activity and role in metabolic process	null	5.4686825	0.0082445	0.040769208
AN2280	Ortholog(s) have role in ascospore formation, meiosis and cytosol, nucleus localization	null	5.4686825	0.0082445	0.040769208
AN2325	Ortholog of A. nidulans FGSC A4 : AN3054, A. fumigatus Af293 : Afu5g10520, A. niger CBS 513.88 : An14g04240, An16g02910, A. oryzae RIB40 : AO090010000486 and A. niger ATCC 1015 : 41807-mRNA, 49061-mRNA	null	-5.400796	0.0082445	0.040769208
AN2328	Ortholog of Aspergillus versicolor : Aspve1_0486502 and Aspergillus sydowii : Aspsy1_0026790	null	5.4686825	0.0082445	0.040769208
AN2605	null	null	5.4686825	0.0082445	0.040769208
AN2628	Predicted mariner transposon-related ORF	null	-5.288162	0.0082445	0.040769208
AN2685	Ortholog of A. niger ATCC 1015 : 184563-mRNA, Aspergillus versicolor : Aspve1_0134218, Aspergillus sydowii : Aspsy1_0155644 and Aspergillus terreus NIH2624 : ATET_06110	null	-5.400796	0.0082445	0.040769208
AN3181	Protein kinase domain-containing protein; transcript is induced by nitrate; predicted NirA binding site in promoter	null	-5.400796	0.0082445	0.040769208
AN3275	Putative cytochrome P450	CYP567E1	5.4686825	0.0082445	0.040769208
AN3304	Putative GABA transporter; transcript repressed by light in developmentally competent mycelia	null	-5.400796	0.0082445	0.040769208
AN3380	Putative fatty-acyl-CoA synthase with a predicted role in cytosolic fatty acid formation; involved in secondary metabolite production	pkiB	-5.288162	0.0082445	0.040769208
AN3724	Ortholog of A. fumigatus Af293 : Afu6g12460, A. niger CBS 513.88 : An06g01620, A. oryzae RIB40 : AO090009000166, A. niger ATCC 1015 : 177709-mRNA and Aspergillus versicolor : Aspve1_0131430	null	-5.400796	0.0082445	0.040769208
AN3845	null	null	-5.288162	0.0082445	0.040769208
AN3987	Tetratricopeptide repeat domain-containing protein; intracellular, menadione stress-induced protein	null	5.4686825	0.0082445	0.040769208

AN4524	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	-5.288162	0.0082445	0.040769208
AN5002	null	null	-5.288162	0.0082445	0.040769208
AN5053	Has domain(s) with predicted N-acetyltransferase activity and role in metabolic process	null	5.4686825	0.0082445	0.040769208
AN5070	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	null	3.4076358	0.0082445	0.040769208
AN5117	null	null	5.4686825	0.0082445	0.040769208
AN5305	Has domain(s) with predicted catalytic activity	null	-5.288162	0.0082445	0.040769208
AN5691	Ortholog(s) have cytosol, nucleus localization	null	-5.288162	0.0082445	0.040769208
AN5845	Has domain(s) with predicted zinc ion binding activity	null	5.4686825	0.0082445	0.040769208
AN5934	Ortholog(s) have role in budding cell bud growth, microtubule cytoskeleton organization, tRNA wobble uridine modification and cytosol, nucleus localization	null	5.4686825	0.0082445	0.040769208
AN6156	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	5.4686825	0.0082445	0.040769208
AN6431	Putative polyketide synthase	null	-5.400796	0.0082445	0.040769208
AN6877	null	null	3.4076358	0.0082445	0.040769208
AN7186	Ortholog of A. fumigatus Af293 : Afu5g14180, A. niger CBS 513.88 : An14g05580, A. oryzae RIB40 : AO090001000217, A. niger ATCC 1015 : 185461-mRNA and Aspergillus versicolor : Aspve1_0186358	null	-5.288162	0.0082445	0.040769208
AN7275	Putative beta-1,4-xylosidase	null	-5.288162	0.0082445	0.040769208
AN7366	null	null	-5.288162	0.0082445	0.040769208
AN8026	Ortholog of A. fumigatus Af293 : Afu3g00120, A. niger CBS 513.88 : An12g05610, A. oryzae RIB40 : AO090010000524, AO090166000107 and A. niger ATCC 1015 : 186000-mRNA, 50976-mRNA	null	-5.400796	0.0082445	0.040769208
AN8414	Putative transcription factor; member of the aspyridone (apd) gene cluster; role in aspyridone production	apdR	5.4686825	0.0082445	0.040769208
AN8685	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	null	-5.400796	0.0082445	0.040769208
AN8956	Has domain(s) with predicted inorganic phosphate transmembrane transporter activity, role in phosphate ion transport and membrane localization	null	5.4686825	0.0082445	0.040769208
AN8968	Putative isoflavone reductase; ortholog of A. fumigatus Afu1g12510	null	-5.400796	0.0082445	0.040769208
AN9015	null	null	5.4686825	0.0082445	0.040769208
AN9031	Has domain(s) with predicted catalytic activity and role in metabolic process	null	3.4076358	0.0082445	0.040769208

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AN6679	Ortholog(s) have SSU rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	null	1.8125249	0.0082546	0.040792246
AN0751	Ortholog of A. fumigatus Af293 : Afu1g14080, A. niger CBS 513.88 : An01g11940, A. oryzae RIB40 : AO090012000449, A. niger ATCC 1015 : 171119-mRNA and Aspergillus versicolor : Aspve1_0122011	null	-2.572991	0.0082992	0.040904276
AN0808	Putative WD40 repeat protein; ortholog of S. cerevisiae Swd1p which has role in histone H3-K4 methylation; expression reduced after exposure to farnesol	null	-2.572991	0.0082992	0.040904276
AN5177	Ortholog(s) have role in ribosomal large subunit biogenesis and nucleolus localization	null	2.4463107	0.0082992	0.040904276
AN8062	Has domain(s) with predicted outer membrane localization	null	-2.572991	0.0082992	0.040904276
AN5447	Putative glutamate decarboxylase with a predicted role in 4-aminobutyrate (GABA) shunt	null	1.7881057	0.0083209	0.040984214
AN11317	Ortholog of A. niger CBS 513.88 : An04g07180, Aspergillus brasiliensis : Aspbr1_0196407, A. niger ATCC 1015 : 204621-mRNA, N. fischeri NRRL 181 : NFIA_106180 and Aspergillus flavus NRRL 3357 : AFL2T_01814	null	1.7749043	0.0083316	0.041009862
AN0286	Ortholog of A. fumigatus Af293 : Afu1g02985, A. niger CBS 513.88 : An01g05160, A. oryzae RIB40 : AO090005000790, A. niger ATCC 1015 : 196559-mRNA and Aspergillus versicolor : Aspve1_0121399	null	1.8576777	0.0083377	0.041012731
AN10588	Ortholog of A. fumigatus Af293 : Afu5g08870, A. niger CBS 513.88 : An07g04510, A. oryzae RIB40 : AO090020000457 and Aspergillus carbonarius ITEM 5010 : Acar5010_507640	null	-1.732403	0.0083682	0.0411356
AN1962	Has domain(s) with predicted DNA binding activity	null	-2.116586	0.0083807	0.041170346
AN5210	Putative pyruvate kinase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein	pkiA	1.7563828	0.0084351	0.041410241
AN0740	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	null	-1.798215	0.0084414	0.041413937
AN10160	Ortholog of A. nidulans FGSC A4 : AN2370, AN0323, A. fumigatus Af293 : Afu1g02440, Afu4g02760, A. niger CBS 513.88 : An01g05750, An12g09350, An13g03290 and A. oryzae RIB40 : AO090020000719, AO090005000852	null	1.7916207	0.0084553	0.041454688
AN10994	Ortholog(s) have ubiquitin-protein ligase activity, role in protein autoubiquitination, protein import into peroxisome matrix, receptor recycling, protein monoubiquitination and cytosol, nucleus, peroxisome localization	null	-1.993481	0.0084972	0.041605743
AN2954	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	null	1.8896705	0.0084972	0.041605743
AN3592	Putative calnexin with a predicted role in protein folding and protein quality control on the endoplasmic reticulum (ER) membrane	clxA	-1.849274	0.0085304	0.041740593

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AN4692	null	null	-1.742391	0.0085812	0.04194789
AN0574	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-1.809435	0.008584	0.04194789
AN8174	Ortholog of A. oryzae RIB40 : AO090102000187, AO090102000186, Aspergillus flavus NRRL 3357 : AFL2T_09624, Aspergillus versicolor : Aspve1_0089187 and Aspergillus sydowii : Aspsy1_0064970, Aspsy1_0505144	null	-1.832498	0.0086027	0.042011815
AN6295	Has domain(s) with predicted role in regulation of transcription, DNA-dependent and nucleus localization	null	-2.158626	0.0086208	0.042073098
AN4216	Ortholog(s) have mitochondrion localization	null	1.7182138	0.0086662	0.042266873
AN6217	Putative F-box protein	null	-1.887894	0.0087299	0.042549719
AN11961	Ortholog(s) have role in nucleotide-excision repair, phosphorylation of RNA polymerase II C-terminal domain, transcription from RNA polymerase II promoter and core TFIIH complex, cytosol, holo TFIIH complex localization	null	3.042286	0.0087991	0.04280304
AN8173	Ortholog(s) have actin monomer binding, protein kinase inhibitor activity, ribosome binding activity, role in negative regulation of protein phosphorylation and cytoplasm, nucleus, polysome, ribosome localization	null	3.042286	0.0087991	0.04280304
AN8933	Has domain(s) with predicted acyl-CoA hydrolase activity and role in acyl-CoA metabolic process	null	3.042286	0.0087991	0.04280304
AN0142	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	2.0703697	0.0088653	0.043066498
AN0704	Ortholog of A. fumigatus Af293 : Afu1g13700, A. niger CBS 513.88 : An08g06760, A. oryzae RIB40 : AO090012000507, A. niger ATCC 1015 : 47444-mRNA and Aspergillus versicolor : Aspve1_0182850	null	2.1854982	0.0088705	0.043066498
AN3030	Alcohol dehydrogenase, class V; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.1854982	0.0088705	0.043066498
AN0089	Putative small GTPase involved in endosomal maturation and vacuolar biogenesis	avaA	-1.747043	0.0089275	0.043313296
AN6107	Putative voltage-gated anion channel protein with a role in copper homeostasis	clcA	-1.692129	0.008933	0.043313296
AN10382	null	null	2.3705429	0.0089896	0.043531593
AN7505	Protein with alpha-xylosidase activity, involved in degradation of xyloglucans	agdD	2.3705429	0.0089896	0.043531593
AN2440	Putative ribose-5-phosphate isomerase with a predicted role in the pentose-phosphate shunt	null	1.8532272	0.0090477	0.043738625
AN4728	Ortholog(s) have endoplasmic reticulum localization	null	1.8532272	0.0090477	0.043738625
AN5674	MAP kinase, kinase, kinase, kinase (MAPKKKK) with similarity to Ste20p	ste20	-1.808896	0.00905	0.043738625
AN12208	Ortholog(s) have role in regulation of mitotic cell cycle and cell division site, cytosol, nucleus, spindle pole body localization	null	1.9736179	0.0090819	0.043864437
AN3733	Putative alpha-1,2 mannosidase with a predicted role in mannose polymer metabolism	mns1A	-1.894842	0.009127	0.044053622

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AN0591	Ortholog(s) have cytosol, nucleus localization	null	2.155877	0.0092014	0.044327174
AN10906	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	2.0432427	0.0092014	0.044327174
AN7662	Putative metalloreductase with a predicted role in iron homeostasis; regulated by iron independently of SreA	freA	2.155877	0.0092014	0.044327174
AN4841	Putative molybdopterin synthase large subunit involved in molybdenum cofactor biosynthesis; molybdopterin cofactor required for the activity of nitrate reductase	cnxH	1.9637495	0.009275	0.044652546
AN4753	Ortholog(s) have unfolded protein binding activity, role in aerobic respiration, mitochondrial respiratory chain complex IV assembly and integral to membrane, mitochondrial inner membrane localization	null	1.7525406	0.0092856	0.04467519
AN7111	Peroxisomal multifunctional enzyme involved in fatty acid beta-oxidation; required for growth on very long-chain fatty acids; transcription is induced by fatty acids	foxA	-1.833093	0.0093253	0.044836982
AN4996	Ortholog(s) have role in cellular response to pheromone, chromatin remodeling at centromere, mitotic sister chromatid segregation and NMS complex, condensed chromosome kinetochore, cytosol, nucleus, spindle pole body localization	null	1.7950169	0.0093698	0.044940193
AN7459	Putative hexokinase with a predicted role in carbohydrate metabolism	hxkA	1.7552369	0.0093913	0.044940193
AN0458	Ortholog of A. fumigatus Af293 : Afu1g04410, A. niger CBS 513.88 : An01g03270, A. oryzae RIB40 : AO090003000909, A. niger ATCC 1015 : 206228-mRNA and Aspergillus versicolor : Aspve1_0121756	null	2.4628806	0.0094129	0.044940193
AN0938	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.874177	0.0094129	0.044940193
AN11093	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	null	2.4628806	0.0094129	0.044940193
AN11903	Has domain(s) with predicted aminopeptidase activity, dipeptidyl-peptidase activity and role in proteolysis	null	2.763579	0.0094129	0.044940193
AN12032	Ortholog of Aspergillus versicolor : Aspve1_0087631 and Aspergillus sydowii : Aspsy1_1136647	null	-2.874177	0.0094129	0.044940193
AN4824	Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and membrane localization	null	-2.874177	0.0094129	0.044940193
AN5780	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	null	2.4628806	0.0094129	0.044940193
AN6319	Ortholog of Aspergillus versicolor : Aspve1_0645540 and Aspergillus sydowii : Aspsy1_0995740	null	2.763579	0.0094129	0.044940193
AN7043	Ortholog(s) have holo-[acyl-carrier-protein] synthase activity and mitochondrion localization	null	2.4628806	0.0094129	0.044940193
AN10873	Ortholog(s) have mitochondrion localization	null	1.723296	0.0094444	0.045061596

AN10408	Ortholog of A. fumigatus Af293 : Afu3g05850, A. niger CBS 513.88 : An11g10750, A. oryzae RIB40 : AO090020000054, N. fischeri NRRL 181 : NFIA_071380 and Aspergillus flavus NRRL 3357 : AFL2T_11218	null	2.0257442	0.0094825	0.045185474
AN9464	Has domain(s) with predicted electron carrier activity, protein disulfide oxidoreductase activity and role in cell redox homeostasis	null	2.0257442	0.0094825	0.045185474
AN8533	null	null	-1.844175	0.0095089	0.045282545
AN4014	Putative vacuolar sorting protein; ortholog of S. cerevisiae Vps52p; expression reduced after exposure to farnesol	vps52	2.3102175	0.0095257	0.045333743
AN6835	Putative cytochrome P450; expression upregulated after exposure to farnesol	CYP505A8	-1.945701	0.0095661	0.04549666
AN8202	Ortholog of A. fumigatus Af293 : Afu5g03340, A. niger CBS 513.88 : An09g05655, A. oryzae RIB40 : AO090102000539, A. niger ATCC 1015 : 212456-mRNA and Aspergillus versicolor : Aspve1_0089228	null	1.798176	0.0095837	0.045551563
AN9492	C2H2 zinc-finger transcription factor involved in regulation of acetamide catabolism; regulates amdS transcription	amdX	-1.799645	0.0096358	0.045770268
AN7148	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	null	1.6865952	0.009666	0.045884396
AN10258	Ortholog(s) have anaphase-promoting complex, cytosol localization	null	2.0496855	0.0097234	0.046098085
AN4836	Ortholog(s) have Golgi apparatus localization	null	-2.135287	0.0097234	0.046098085
AN2866	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-1.882277	0.0097626	0.046239689
AN0593	Putative dehydrogenase; expression reduced after exposure to farnesol	null	-1.67814	0.0097656	0.046239689
AN11908	Has domain(s) with predicted hydrolase activity, acting on ester bonds, zinc ion binding activity and nucleus localization	null	-1.807431	0.0098672	0.046661523
AN6055	Ortholog(s) have biotin-[acetyl-CoA-carboxylase] ligase activity, biotin-[pyruvate-carboxylase] ligase activity, role in protein biotinylation and cytoplasm, nucleus localization	null	-1.807431	0.0098672	0.046661523
AN10703	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-2.037901	0.0099316	0.046906696
AN3191	Ortholog(s) have lipase activity	null	-2.06016	0.0099316	0.046906696
AN3917	Putative cytochrome P450	CYP539D1	-2.325499	0.0099489	0.046958479
AN1976	Ortholog(s) have histone acetyltransferase activity	null	-1.801566	0.0099578	0.046970728
AN6632	Putative 40S ribosomal protein S28; ortholog of S. cerevisiae Rps28Bp; expression reduced after exposure to farnesol	null	1.7939427	0.0099887	0.047087057
AN1420	Ortholog of A. fumigatus Af293 : Afu8g04180, A. niger CBS 513.88 : An16g08910/srpB, A. oryzae RIB40 : AO090103000033, A. niger ATCC 1015 : 55055-mRNA and Aspergillus versicolor : Aspve1_0024681	null	-1.755204	0.0100063	0.04713988

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AN1979	Ortholog of A. fumigatus Af293 : Afu4g10610, A. niger CBS 513.88 : An04g06070, A. niger ATCC 1015 : 214295-mRNA, Aspergillus versicolor : Aspve1_0080153 and Aspergillus sydowii : Aspsy1_0053917	null	-1.850969	0.010085	0.047481126
AN4537	Has domain(s) with predicted Rab GTPase activator activity, role in regulation of Rab GTPase activity and intracellular localization	null	-1.910101	0.0100964	0.04750467
AN11133	Has domain(s) with predicted peptidase activity, role in signal peptide processing and integral to membrane, signal peptidase complex localization	null	-2.527641	0.0102874	0.04821409
AN4752	Ortholog(s) have nucleus, spindle pole body localization	null	2.3730052	0.0102874	0.04821409
AN5090	Predicted ADP ribosylation factor (Arf) GTPase	null	-2.527641	0.0102874	0.04821409
AN7826	Ortholog of Aspergillus versicolor : Aspve1_0045384 and Aspergillus sydowii : Aspsy1_0165058	null	-2.527641	0.0102874	0.04821409
AN0675	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.165564	0.010288	0.04821409
AN1449	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.165564	0.010288	0.04821409
AN9124	Ortholog(s) have ATPase inhibitor activity, Hsp70 protein binding, Hsp90 protein binding, mRNA binding activity, role in protein folding and cytosol, nucleus localization	null	1.7640039	0.0102924	0.04821409
AN1854	Putative inositol pentakisphosphate 2-kinase; locus contains the conserved upstream open reading frame (uORF) AN1854-uORF	null	-1.794005	0.0103773	0.048581595
AN2555	Ortholog(s) have role in conjugation with cellular fusion and cytosol, nucleus localization	null	1.8258567	0.010446	0.048872143
AN8567	null	null	1.7016253	0.0104899	0.049047039
AN1056	Ortholog(s) have cytosol, nucleus localization	null	1.880487	0.0105374	0.049238347
AN0270	Ortholog(s) have role in cellular bud site selection, pyridoxal phosphate biosynthetic process and cytosol, nucleus localization	null	1.9977063	0.0105635	0.049329158
AN6239	Ortholog of A. nidulans FGSC A4 : AN6793, A. fumigatus Af293 : Afu3g03390, Afu7g00330, A. niger CBS 513.88 : An03g03530 and A. oryzae RIB40 : AO090103000170, AO090701000114	null	1.7634014	0.0105864	0.049405593
AN2937	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	null	-1.852726	0.0106473	0.049658512

Supplementary Table 3c

Effect of glucose under nitrogen derepressing conditions (urea as a nitrogen source) in the wild type strain

Differentially expressed genes (FU vs. GU) are shown.

Gene expression was regarded as significantly changed if the FDR was <0.05 and the fold change |FC| >2

2759 differentially regulated genes were identified under these conditions: 1358 upregulated and 1401 downregulated

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gene	Description	Name	log$_2$FC	PValue	FDR
AN7388	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	cpeA	-13.23	1.67E-24	8.25E-21
AN8007	Protein with arabinan endo-1,5-alpha-L-arabinosidase activity, involved in degradation of pectin	abnC	-13.193	2.24E-24	8.25E-21
AN12088	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-9.4712	3.35E-24	8.25E-21
AN8046	Putative triacylglycerol lipase with a predicted role in glycerolipid metabolism	null	-10.415	1.34E-23	2.47E-20
AN9007	Putative cytochrome P450	CYP548D1	-9.5151	2.31E-23	3.41E-20
AN6923	Putative high-affinity hexose transporter with a predicted role in hexose transport; induced upon starvation and during sexual development	hxtA	-10.483	3.33E-22	3.55E-19
AN8445	Putative aminopeptidase Y; transcript is induced by nitrate	null	-9.2406	3.36E-22	3.55E-19
AN8781	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	null	-8.0651	1.34E-20	1.24E-17
AN1897	Homogentisate 1,2-dioxygenase, enzyme in phenylalanine catabolism; required for growth on phenylalanine or phenylacetate as the sole carbon source; mutation in human ortholog results in alkaptonuria	hmgA	-11.997	2.06E-20	1.69E-17
AN3866	Putative dehydratase with a predicted role in glycine, serine, and threonine metabolism	null	-8.1305	2.99E-20	2.21E-17
AN6723	Putative 2,3-dihydroxybenzoate carboxylyase	dhbD	-8.5612	5.97E-20	4.02E-17
AN12477	Has domain(s) with predicted GTP binding, GTPase activity	null	-11.819	7.92E-20	4.88E-17
AN0301	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	null	-11.728	1.58E-19	8.78E-17
AN2653	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-11.721	1.66E-19	8.78E-17
AN10588	Ortholog of A. fumigatus Af293 : Afu5g08870, A. niger CBS 513.88 : An07g04510, A. oryzae RIB40 : AO090020000457 and Aspergillus carbonarius ITEM 5010 : Acar5010_507640	null	-11.615	3.73E-19	1.84E-16
AN1899	Putative 4-hydroxyphenylpyruvate dioxygenase with a predicted role in aromatic amino acid biosynthesis; expression induced by phenylalanine and repressed by glucose; mutants unable to use phenylalanine as a sole carbon source	hpdA	-8.1204	6.10E-19	2.82E-16

AN1433	Ortholog of A. fumigatus Af293 : Afu1g01310, Afu8g04210, A. niger CBS 513.88 : An16g08870, An08g11860, An13g01880, A. oryzae RIB40 : AO090701000542, AO090103000036 and A. niger ATCC 1015 : 193610-mRNA	null	-7.803	9.73E-19	4.23E-16
AN8611	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	-11.438	1.42E-18	5.83E-16
AN8907	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism	null	7.20786	2.00E-18	7.77E-16
AN8351	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-11.314	3.62E-18	1.34E-15
AN1772	Type B feruloyl esterase	null	-7.6645	4.73E-18	1.66E-15
AN11874	Ortholog of Aspergillus versicolor : Aspve1_0141900 and Aspergillus sydowii : Aspsy1_0035361	null	-8.0695	5.23E-18	1.76E-15
AN8483	Ortholog of A. niger CBS 513.88 : An13g02730, Aspergillus brasiliensis : Aspbr1_0180212, N. fischeri NRRL 181 : NFIA_001870, Aspergillus flavus NRRL 3357 : AFL2T_10566 and A. clavatus NRRL 1 : ACLA_063590	null	-11.26	5.48E-18	1.76E-15
AN2388	Putative beta-1,4-endoglucanase	null	-8.3878	8.35E-18	2.58E-15
AN5421	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-11.146	1.27E-17	3.76E-15
AN8390	GPR1/FUN34/YaaH family member; ethanol- and ethylacetate-induced gene	null	-9.0675	1.52E-17	4.33E-15
AN5444	Putative tryptophan synthase with a predicted role in aromatic amino acid biosynthesis	null	-7.4615	1.79E-17	4.92E-15
AN8559	Putative branched chain alpha-keto acid dehydrogenase E1, beta subunit	null	-11.034	2.96E-17	7.83E-15
AN10326	Ortholog of Aspergillus versicolor : Aspve1_0081330 and Aspergillus sydowii : Aspsy1_0148173	null	-8.9647	3.30E-17	8.42E-15
AN0964	Ortholog of A. fumigatus Af293 : Afu1g16640, A. niger CBS 513.88 : An01g10620, A. oryzae RIB40 : AO090005001050, A. niger ATCC 1015 : 136898-mRNA and Aspergillus versicolor : Aspve1_0036577	null	-8.4291	4.71E-17	1.16E-14
AN1553	Has domain(s) with predicted role in fruiting body development, hemolysis by symbiont of host erythrocytes	null	-8.4006	5.85E-17	1.40E-14
AN4809	Putative glutaminase A with a predicted role in glutamate and glutamine metabolism	gtaA	-7.5607	6.56E-17	1.52E-14
AN8084	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-10.916	7.24E-17	1.62E-14
AN7532	Ortholog of A. niger CBS 513.88 : An11g07940, A. oryzae RIB40 : AO090001000606, Aspergillus brasiliensis : Aspbr1_0050895, N. fischeri NRRL 181 : NFIA_054950 and A. clavatus NRRL 1 : ACLA_083130	null	-7.2624	8.00E-17	1.71E-14
AN0875	Has domain(s) with predicted O-acetyltransferase activity and cytoplasm localization	null	-6.9821	8.07E-17	1.71E-14
AN0231	Conidiophore-specific phenol oxidase; mutant conidiophores, metulae and phialides lack pigmentation; ivoB mutants accumulate the substrate N-acetyl-6-hydroxytryptophan (AHT); repressed by light in developmentally competent mycelia	ivoB	-7.6999	8.47E-17	1.73E-14
AN1726	Putative 3-methyl-2-oxobutanoate dehydrogenase	null	-7.2097	8.65E-17	1.73E-14

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AN10482	Putative beta-glucosidase	bglF	-8.2702	1.54E-16	3.01E-14
AN5742	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-10.797	1.77E-16	3.36E-14
AN5169	Has domain(s) with predicted phospholipid binding activity	null	-10.793	1.82E-16	3.36E-14
AN5170	Putative Zn(II)2Cys6 transcription factor; negative regulator of sexual development	rosA	-10.71	3.39E-16	6.09E-14
AN4659	Putative acyl-CoA synthetase/AMP-binding domain protein; has a predicted mitochondrial localization signal	null	-7.0951	3.46E-16	6.09E-14
AN10982	Putative P-type ATPase sodium pump	enaC	-6.8727	4.07E-16	7.00E-14
AN3557	Ortholog of Aspergillus versicolor : Aspve1_0145302 and Aspergillus aculeatus ATCC16872 : Aacu16872_053773	null	-8.5936	5.23E-16	8.80E-14
AN6778	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-10.648	5.38E-16	8.85E-14
AN4127	Ortholog(s) have intracellular localization	null	8.50213	6.01E-16	9.47E-14
AN10993	Ortholog of A. fumigatus Af293 : Afu2g01310, A. niger CBS 513.88 : An03g05110, A. oryzae RIB40 : AO090701000405, A. niger ATCC 1015 : 50726-mRNA and Aspergillus versicolor : Aspve1_0043704	null	-8.5738	6.02E-16	9.47E-14
AN4807	Ortholog of A. niger CBS 513.88 : An02g13800, A. oryzae RIB40 : AO090020000293, A. niger ATCC 1015 : 207448-mRNA, Aspergillus versicolor : Aspve1_0040098 and Aspergillus sydowii : Aspsy1_0087808	null	-8.5537	6.93E-16	1.07E-13
AN9108	Has domain(s) with predicted heme binding activity	null	-10.561	1.01E-15	1.53E-13
AN4055	Putative acid phosphatase with a predicted role in gluconic acid and gluconate metabolism	null	-6.4154	1.05E-15	1.55E-13
AN1896	Fumarylacetoacetate hydrolase, catalyzes the last step in the phenylalanine catabolic pathway; intracellular; protein abundance decreased by menadione stress; mutation in human ortholog causes type I hereditary tyrosinaemia	fahA	-7.3371	1.27E-15	1.82E-13
AN8737	Putative sugar transporter	mstA	-10.53	1.28E-15	1.82E-13
AN4150	Ortholog(s) have biotin transporter activity, role in biotin transport and Golgi apparatus localization	null	7.18353	2.07E-15	2.87E-13
AN5669	Putative succinyl-CoA:3-ketoacid-coenzyme A transferase	null	-6.3382	2.09E-15	2.87E-13
AN5422	Putative beta-lactamase family protein; intracellular; protein abundance decreased by menadione stress	null	-7.8877	2.71E-15	3.64E-13
AN4688	Putative acyl-coA dehydrogenase	ivdA	-6.3832	4.25E-15	5.61E-13
AN4135	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	sdeB	6.40313	5.20E-15	6.75E-13

AN7961	Ortholog of A. fumigatus Af293 : Afu4g13760, A. oryzae RIB40 : AO090010000492, Aspergillus versicolor : Aspve1_0045462, Aspergillus sydowii : Aspsy1_1151790 and Aspergillus terreus NIH2624 : ATET_04942	null	-10.336	5.44E-15	6.93E-13
AN1883	Putative argininosuccinate synthase with a predicted role in arginine metabolism; intracellular; protein abundance decreased by menadione stress	null	7.04744	5.67E-15	7.07E-13
AN8683	Ortholog(s) have ferric-chelate reductase activity, role in copper ion import, iron ion transport and plasma membrane localization	null	-7.0365	5.74E-15	7.07E-13
AN9323	Ortholog of A. niger CBS 513.88 : An02g00370, An06g00670, A. oryzae RIB40 : AO090102000655, Aspergillus brasiliensis : Aspbr1_0192788, Aspbr1_0199838 and Aspergillus acidus : Aspfo1_0076240, Aspfo1_0078934	null	-10.299	7.18E-15	8.70E-13
AN2395	Putative beta-glucuronidase with a predicted role in polysaccharide degradation	null	-10.292	7.43E-15	8.87E-13
AN4871	Class V chitinase; glycoside hydrolase family 18 (GH18) protein with a role in the age-dependent autolysis	chiB	-6.1184	7.89E-15	9.26E-13
AN5762	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-10.273	8.57E-15	9.90E-13
AN4825	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	null	-6.5761	1.35E-14	1.54E-12
AN3741	Alcohol dehydrogenase II, has a predicted role in two-carbon compound metabolism	alcB	-6.9854	1.74E-14	1.95E-12
AN4264	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	null	-6.1208	2.12E-14	2.34E-12
AN8175	Has domain(s) with predicted viral capsid localization	null	-6.0676	2.45E-14	2.67E-12
AN10959	Has domain(s) with predicted catalytic activity	null	-8.0646	2.54E-14	2.72E-12
AN6382	Has domain(s) with predicted phospholipase C activity and role in intracellular signal transduction, lipid metabolic process	null	-7.5614	2.99E-14	3.16E-12
AN2835	Has domain(s) with predicted D-arabinono-1,4-lactone oxidase activity, UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity, role in oxidation-reduction process and membrane localization	null	-6.4815	3.34E-14	3.48E-12
AN5222	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	5.90296	3.41E-14	3.50E-12
AN4692	null	null	-6.7181	3.49E-14	3.54E-12
AN3639	Putative dihydrolipoamide transacylase; alpha keto acid dehydrogenase E2 subunit	null	-5.9887	4.26E-14	4.26E-12
AN5823	L-ornithine N5-monooxygenase; involved in siderophore biosynthesis; null mutant inviable unless medium is supplemented with siderophores	sidA	5.95255	4.44E-14	4.37E-12
AN0500	null	null	-7.503	4.56E-14	4.37E-12

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AN3130	Ortholog of A. fumigatus Af293 : Afu3g12990, A. niger CBS 513.88 : An02g08890, A. niger ATCC 1015 : 207115-mRNA, Aspergillus versicolor : Aspve1_0026699 and Aspergillus sydowii : Aspsy1_0029142	null	-6.389	4.61E-14	4.37E-12
AN1848	Zinc(II)2Cys6 putative transcription factor involved in the regulation of sexual development; mutant produces immature cleistothecia and reduced numbers of ascospores	nosA	-6.0072	4.63E-14	4.37E-12
AN7181	Ortholog of A. fumigatus Af293 : Afu4g03200, A. oryzae RIB40 : AO090011000112, N. fischeri NRRL 181 : NFIA_030260, Aspergillus flavus NRRL 3357 : AFL2T_04908 and A. clavatus NRRL 1 : ACLA_055410	null	-10.046	4.66E-14	4.37E-12
AN4394	Ortholog(s) have role in asexual sporulation resulting in formation of a cellular spore, positive regulation of asexual sporulation resulting in formation of a cellular spore, regulation of transcription, DNA-dependent	null	-10.038	4.86E-14	4.49E-12
AN7722	Putative N-acetyltransferase with a predicted role in arginine metabolism	null	5.93605	5.01E-14	4.58E-12
AN9273	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_00195, Aspergillus versicolor : Aspve1_0083996, Aspergillus sydowii : Aspsy1_0900274 and Aspergillus terreus NIH2624 : ATET_04373	null	-6.216	5.18E-14	4.67E-12
AN4690	Alpha subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccA	-6.3289	6.14E-14	5.47E-12
AN4691	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.7536	7.31E-14	6.44E-12
AN1898	Ortholog(s) have role in melanin biosynthetic process from tyrosine, tyrosine catabolic process and cytoplasm localization	null	-9.9769	7.44E-14	6.47E-12
AN4888	Putative pyruvate decarboxylase with a predicted role in pyruvate metabolism or penicillin biosynthesis; intracellular; protein abundance decreased by menadione stress	pdcA	5.67156	8.26E-14	7.11E-12
AN1723	Ortholog(s) have cell septum, hyphal tip localization	null	-5.8854	1.14E-13	9.69E-12
AN10296	Ortholog(s) have fumarate reductase (NADH) activity, role in cellular response to anoxia and cytosol, mitochondrion, plasma membrane, ribosome localization	null	5.98175	1.32E-13	1.11E-11
AN4008	Has domain(s) with predicted O-methyltransferase activity	null	-6.0881	1.34E-13	1.11E-11
AN4474	Ortholog of A. niger CBS 513.88 : An04g02110, A. oryzae RIB40 : AO090023000799, A. niger ATCC 1015 : 203625-mRNA, Aspergillus versicolor : Aspve1_0133959 and Aspergillus sydowii : Aspsy1_0095044	null	-6.0863	1.51E-13	1.24E-11
AN2161	Putative GNAT-type acetyltransferase	ngn1	-5.6637	1.64E-13	1.33E-11
AN3399	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-9.8713	1.67E-13	1.34E-11
AN7521	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	null	6.01631	1.71E-13	1.36E-11
AN5860	Low affinity glucose transporter of the major facilitator superfamily (MFS); transcriptionally repressed by growth on xylose	mstE	5.76271	1.81E-13	1.41E-11

AN8912	Ortholog(s) have role in ascospore formation, conjugation with cellular fusion and Golgi apparatus, fungal-type vacuole membrane localization	null	-9.8543	1.84E-13	1.41E-11
AN9010	Ortholog(s) have nicotinamide mononucleotide transmembrane transporter activity, role in nicotinamide mononucleotide transport and mitochondrion localization	null	-9.8543	1.84E-13	1.41E-11
AN7800	Siderophore iron transporter	mirA	6.23238	1.90E-13	1.45E-11
AN9138	Putative amidase/acetamidase	null	-5.6501	2.07E-13	1.56E-11
AN4594	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosolic small ribosomal subunit localization	null	5.61539	2.14E-13	1.60E-11
AN9121	Protein with a glycogen binding domain involved in sexual development; regulated by VeA and FlbA	esdC	-5.7613	2.21E-13	1.63E-11
AN9380	Putative chitin deacetylase; catalyzes the conversion of chitin to chitosan by the deacetylation of N-acetyl-D-glucosamine residues	null	-9.7482	4.00E-13	2.93E-11
AN7211	Putative C-8,7 sterol isomerase with a predicted role in ergosterol biosynthesis	null	10.0501	4.26E-13	3.09E-11
AN8347	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.711	5.17E-13	3.71E-11
AN4990	Ortholog(s) have ferrous iron transmembrane transporter activity, manganese ion transmembrane transporter activity	null	-6.1021	5.38E-13	3.82E-11
AN0649	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	null	-7.6476	5.44E-13	3.83E-11
AN1109	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.7015	5.73E-13	3.94E-11
AN2941	Ortholog of A. nidulans FGSC A4 : AN5437, A. fumigatus Af293 : Afu3g08250, Afu6g13630, A. niger CBS 513.88 : An08g08620, An02g11860, A. oryzae RIB40 : AO090103000325 and A. niger ATCC 1015 : 175401-mRNA	null	-7.6381	5.73E-13	3.94E-11
AN0942	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	ladA	-6.5067	5.75E-13	3.94E-11
AN5172	Ortholog of A. fumigatus Af293 : Afu4g09700, Afu6g07000, A. niger CBS 513.88 : An04g07430, A. oryzae RIB40 : AO090012000946, AO090003001270 and A. niger ATCC 1015 : 53150-mRNA, 57315-mRNA	null	-7.6285	6.04E-13	4.10E-11
AN1659	Putative amino acid transporter; transcript is induced by nitrate	null	-6.0099	6.40E-13	4.29E-11
AN9392	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-7.1391	6.44E-13	4.29E-11
AN5435	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	null	6.64098	7.22E-13	4.77E-11

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AN3031	Putative threonine synthase with a predicted role in glycine, serine, and threonine metabolism	null	6.12571	9.86E-13	6.45E-11
AN4702	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-5.707	1.06E-12	6.90E-11
AN0570	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	5.44057	1.18E-12	7.61E-11
AN5603	Ortholog of A. nidulans FGSC A4 : AN3743, A. fumigatus Af293 : Afu4g11320, Afu7g04400, A. niger CBS 513.88 : An13g00980, An04g05280 and A. oryzae RIB40 : AO090005000127	null	-6.4009	1.23E-12	7.88E-11
AN9142	Ortholog of A. fumigatus Af293 : Afu7g01570, A. niger ATCC 1015 : 189733-mRNA, Aspergillus versicolor : Aspve1_0057650, Aspergillus sydowii : Aspsy1_0093879 and Aspergillus terreus NIH2624 : ATET_01773	null	-9.5727	1.44E-12	9.13E-11
AN10358	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-9.5623	1.53E-12	9.58E-11
AN4803	Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), positive regulation of translational fidelity	null	5.50216	1.66E-12	1.03E-10
AN11006	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	null	5.65552	1.78E-12	1.10E-10
AN7552	Ortholog of A. fumigatus Af293 : Afu2g14790, A. oryzae RIB40 : AO090026000798, A. niger ATCC 1015 : 119038-mRNA, Aspergillus versicolor : Aspve1_0085801 and Aspergillus sydowii : Aspsy1_0058559	null	-6.2188	2.28E-12	1.40E-10
AN0841	null	null	-5.5266	2.38E-12	1.44E-10
AN5060	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_03090, Aspergillus versicolor : Aspve1_0144439, Aspergillus sydowii : Aspsy1_0061440 and Aspergillus terreus NIH2624 : ATET_06090	null	-9.4983	2.43E-12	1.46E-10
AN1895	Maleyl-acetoacetate isomerase, enzyme involved in phenylalanine catabolism	maiA	-6.9334	2.84E-12	1.69E-10
AN5715	Putative 40s ribosomal protein S26; ortholog of S. cerevisiae Rps26Bp which has role in rRNA export from nucleus; expression reduced after exposure to farnesol	null	5.31097	2.85E-12	1.69E-10
AN3205	Putative aldehyde dehydrogenase; ortholog of A. fumigatus Afu4g02830	null	-9.4763	2.91E-12	1.71E-10
AN4094	Putative C-14 sterol reductase with a predicted role in sterol metabolism	null	5.48352	2.94E-12	1.71E-10
AN6426	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	null	6.42699	3.40E-12	1.96E-10
AN3310	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	7.3169	3.44E-12	1.96E-10
AN20013	Putative mitochondrial ribosomal protein S5, encoded within the intron of the large mitochondrial ribosomal rRNA gene (L-rRNA); similar to open reading frames in the introns of N. crassa and Penicillium sp. mt rRNA genes	null	6.10301	3.45E-12	1.96E-10

AN6438	Ortholog(s) have dipeptidyl-peptidase activity and role in proteolysis involved in cellular protein catabolic process	null	-5.2874	4.07E-12	2.30E-10
AN3220	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.4198	4.21E-12	2.36E-10
AN1857	Putative kynureninase with a predicted role in aromatic amino acid biosynthesis	null	-5.3316	4.28E-12	2.38E-10
AN2937	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	null	-9.4082	4.48E-12	2.47E-10
AN1677	Short-chain dehydrogenase; transcriptionally induced by growth on xylose	null	-5.3484	4.52E-12	2.48E-10
AN3591	Protein with similarity to bacterial propionyl-CoA-yielding methylmalonate semialdehyde dehydrogenase; may be involved in isoleucine and valine catabolism	null	-5.3905	4.68E-12	2.55E-10
AN4077	Has domain(s) with predicted DNA binding activity, role in regulation of transcription, DNA-dependent and chromosome, centromeric region localization	null	-7.3426	4.77E-12	2.57E-10
AN5413	Ortholog of Aspergillus acidus : Aspfo1_0061846	null	-6.2104	4.82E-12	2.57E-10
AN2779	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, iron-sulfur cluster binding activity	null	-5.9859	4.82E-12	2.57E-10
AN9025	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	null	-5.4889	5.25E-12	2.78E-10
AN9468	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, cytosol localization	null	5.2606	5.40E-12	2.83E-10
AN0554	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	aldA	-5.0918	5.95E-12	3.10E-10
AN8495	Ortholog(s) have endoplasmic reticulum localization	null	9.66941	6.30E-12	3.26E-10
AN6500	Ortholog(s) have cytosol localization	null	5.11983	8.04E-12	4.12E-10
AN9117	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-5.7291	8.07E-12	4.12E-10
AN0262	Ortholog(s) have role in ribosomal large subunit assembly and cytosol, nucleolus localization	null	5.2416	8.17E-12	4.14E-10
AN10964	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	-5.2257	8.33E-12	4.19E-10
AN0593	Putative dehydrogenase; expression reduced after exposure to farnesol	null	-5.2755	8.54E-12	4.27E-10
AN5996	Ortholog(s) have cytosol localization	null	5.10316	8.66E-12	4.30E-10
AN6649	Putative fatty acyl-CoA synthetase	fatC	-9.2997	9.77E-12	4.82E-10
AN5719	Ortholog(s) have cytosol localization	null	9.60078	1.01E-11	4.96E-10

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AN12070	Ortholog(s) have cytosol, nucleus localization	null	5.79863	1.06E-11	5.15E-10
AN11143	Putative glucoamylase with a predicted role in starch metabolism	glaA	-7.2077	1.20E-11	5.79E-10
AN3068	Ortholog of A. fumigatus Af293 : Afu3g09570, A. niger CBS 513.88 : An16g03070, A. niger ATCC 1015 : 49047-mRNA, Aspergillus versicolor : Aspve1_0128162 and Aspergillus sydowii : Aspsy1_0029214	null	5.06328	1.21E-11	5.82E-10
AN3344	Putative GNAT-type acetyltransferase	ngn27	6.638	1.23E-11	5.87E-10
AN3349	Putative cytochrome P450	CYP659A1	-6.7245	1.26E-11	5.97E-10
AN5014	Ortholog(s) have cytosol, nucleolus localization	null	5.18837	1.34E-11	6.30E-10
AN9297	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	null	5.30879	1.35E-11	6.30E-10
AN4051	Has domain(s) with predicted heme binding, iron ion binding, oxygen binding activity and role in oxygen transport	null	5.14751	1.38E-11	6.43E-10
AN10090	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	null	-5.9636	1.44E-11	6.65E-10
AN1166	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation, ribosomal large subunit assembly and cytosolic large ribosomal subunit, nucleolus localization	null	5.03826	1.48E-11	6.79E-10
AN6399	Putative bleomycin hydrolase	null	-5.8261	1.53E-11	6.97E-10
AN7349	Protein with alpha-1,3-glucanase (mutanase) activity, involved in carbohydrate catabolism; highly expressed during sexual development, specifically expressed in Hulle cells	mutA	-9.2356	1.58E-11	7.17E-10
AN10681	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation, regulation of translational fidelity and cytosolic large ribosomal subunit localization	null	5.01644	1.60E-11	7.22E-10
AN4245	Putative ceramidase	null	-5.3316	1.64E-11	7.34E-10
AN11419	Ortholog(s) have cytosol localization	null	5.00049	1.65E-11	7.34E-10
AN8083	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.4158	1.70E-11	7.51E-10
AN7463	Major ammonium transporter of A. nidulans; transcript upregulated by nitrate limitation	meaA	5.60306	1.71E-11	7.51E-10
AN3221	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.2555	1.77E-11	7.74E-10
AN8910	Putative polyketide synthase (PKS)	null	-6.6725	1.86E-11	8.11E-10
AN4522	Ortholog(s) have cytosol localization	null	5.32837	1.90E-11	8.24E-10
AN2157	Putative aspartic endopeptidase	pepAa	-5.2357	2.03E-11	8.74E-10
AN8533	null	null	-6.3891	2.06E-11	8.81E-10

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AN10297	Protein with similarity to nonribosomal peptide synthases (NRPS-like); putative acyl CoA synthetase with an NAD-binding domain	null	-7.1284	2.10E-11	8.93E-10
AN6804	Predicted transporter of the major facilitator superfamily (MFS); expression upregulated after exposure to farnesol	null	-5.0282	2.16E-11	9.09E-10
AN6158	Ortholog of A. fumigatus Af293 : Afu2g08370, A. niger CBS 513.88 : An12g03580, A. niger ATCC 1015 : 128428-mRNA, Aspergillus versicolor : Aspve1_0634305 and Aspergillus sydowii : Aspsy1_0089574	null	7.05679	2.16E-11	9.09E-10
AN6476	null	null	-9.1823	2.26E-11	9.44E-10
AN8174	Ortholog of A. oryzae RIB40 : AO090102000187, AO090102000186, Aspergillus flavus NRRL 3357 : AFL2T_09624, Aspergillus versicolor : Aspve1_0089187 and Aspergillus sydowii : Aspsy1_0064970, Aspsy1_0505144	null	-5.9019	2.28E-11	9.46E-10
AN2860	Ortholog(s) have alcohol dehydrogenase (NADP+) activity, hydroxymethylfurfural reductase (NADH) activity, hydroxymethylfurfural reductase (NADPH) activity and role in alcohol metabolic process, furaldehyde metabolic process	null	-5.5327	2.32E-11	9.58E-10
AN3764	Has domain(s) with predicted catalytic activity	null	-5.5275	2.46E-11	1.01E-09
AN0843	Ortholog(s) have structural constituent of ribosome activity, role in rRNA export from nucleus and 90S preribosome, cytosolic small ribosomal subunit, nucleolus localization	null	4.98385	2.49E-11	1.02E-09
AN7053	Ortholog of Aspergillus versicolor : Aspve1_0054863	null	5.5506	2.63E-11	1.07E-09
AN0402	Ortholog of Aspergillus versicolor : Aspve1_0048646 and Aspergillus sydowii : Aspsy1_0055229	null	9.46581	2.64E-11	1.07E-09
AN5130	Ortholog(s) have coproporphyrinogen oxidase activity, role in heme biosynthetic process and cytosol, nucleus localization	null	4.96616	2.75E-11	1.11E-09
AN1979	Ortholog of A. fumigatus Af293 : Afu4g10610, A. niger CBS 513.88 : An04g06070, A. niger ATCC 1015 : 214295-mRNA, Aspergillus versicolor : Aspve1_0080153 and Aspergillus sydowii : Aspsy1_0053917	null	-6.6075	2.80E-11	1.12E-09
AN8692	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	prxA	5.64053	3.26E-11	1.30E-09
AN5558	Broad specificity thermostable alkaline protease; extracellular; regulated by nitrogen, carbon and sulfur metabolite repression; transcript repressed by light in developmentally competent mycelia	prtA	-4.9925	3.60E-11	1.42E-09
AN7727	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	null	-5.3286	3.66E-11	1.44E-09
AN8079	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	null	-5.215	3.77E-11	1.47E-09

AN5601	Putative saccharopine dehydrogenase (NADP+, L-glutamate-forming) with a predicted role in lysine metabolism	null	5.49779	3.83E-11	1.49E-09
AN8163	Putative short-chain dehydrogenase/reductase	null	-6.5624	4.01E-11	1.55E-09
AN2549	Putative acyl-CoA ligase; required for emericellamide biosynthesis	easD	-5.2979	4.56E-11	1.76E-09
AN3058	Putative glycine hydroxymethyltransferase with a predicted role in glycine, serine, and threonine metabolism	null	5.23962	4.73E-11	1.81E-09
AN5997	Ortholog(s) have role in rRNA export from nucleus and nucleolus localization	null	4.9043	4.80E-11	1.83E-09
AN1733	Putative delta-1-pyrroline-5-carboxylate dehydrogenase with a predicted role in glutamate and glutamine metabolism; expression is negatively regulated by CreA	prnC	-5.2823	5.10E-11	1.93E-09
AN2828	Putative beta-glucosidase with a predicted role in polysaccharide degradation	bglL	-6.2571	5.12E-11	1.93E-09
AN3990	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.0693	5.17E-11	1.94E-09
AN2544	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.0545	5.59E-11	2.09E-09
AN7430	Putative glutamine amidotransferase with a predicted role in histidine metabolism	hisHF	4.9997	5.61E-11	2.09E-09
AN10898	null	null	-6.5041	5.82E-11	2.15E-09
AN8467	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-6.2372	6.00E-11	2.21E-09
AN9032	Ortholog of A. nidulans FGSC A4 : AN10883, A. fumigatus Af293 : Afu7g06950, Afu8g02470, A. niger CBS 513.88 : An03g06330, An03g00350, An05g02580 and A. oryzae RIB40 : AO090010000660	null	5.76694	6.10E-11	2.23E-09
AN0912	Putative Beta-isopropylmalate dehydrogenase with a predicted role in valine, leucine, and isoleucine metabolism	null	5.21489	6.18E-11	2.25E-09
AN3706	S. cerevisiae ortholog RPS10A has role in rRNA export from nucleus; palA-dependent expression independent of pH	null	4.97355	6.28E-11	2.28E-09
AN5833	Putative acetyl-CoA synthase with a predicted role in two-carbon metabolism or the methylcitrate pathway; transcript induced by heptadecanoic acid	pcsA	-5.2411	6.59E-11	2.38E-09
AN8365	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.77022	7.05E-11	2.53E-09
AN3347	Putative amino acid transporter; expression reduced after exposure to farnesol	null	5.99907	7.16E-11	2.56E-09
AN2994	Ortholog of A. niger CBS 513.88 : An02g12350, A. niger ATCC 1015 : 52433-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_01318 and Aspergillus terreus NIH2624 : ATET_01608	null	-6.94	7.70E-11	2.74E-09

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AN0736	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	null	-8.9939	8.35E-11	2.96E-09
AN2366	Putative trypsin-like protease with a role in the proteolytic cleavage of NmrA	null	-4.8825	8.56E-11	3.01E-09
AN0451	Putative C-8 sterol isomerase with a predicted role in sterol metabolism	null	5.7187	8.59E-11	3.01E-09
AN0472	Putative 1,3-beta-glucosidase with a role in carbon starvation-induced autolytic cell wall degradation	engA	-4.7671	8.73E-11	3.05E-09
AN0787	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	mns1B	-4.8231	9.19E-11	3.19E-09
AN7107	Ortholog(s) have nucleolus localization	null	4.76649	9.59E-11	3.32E-09
AN3988	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-6.9087	9.85E-11	3.39E-09
AN7354	Ortholog(s) have cytosol, nucleus localization	null	4.90916	1.03E-10	3.51E-09
AN2436	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	aclB	4.70439	1.06E-10	3.61E-09
AN8308	Ortholog of A. oryzae RIB40 : AO090001000393 and Aspergillus flavus NRRL 3357 : AFL2T_09046	null	-5.7748	1.10E-10	3.72E-09
AN10416	Putative 60s ribosomal protein similar to subunits L15 and L27; ortholog of S. cerevisiae RPL28; expression reduced after exposure to farnesol; palA-dependent expression independent of pH	null	5.01361	1.10E-10	3.73E-09
AN5168	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding activity	null	-4.875	1.15E-10	3.88E-09
AN4073	Putative cytosolic small ribosomal subunit protein S12; expression reduced after exposure to farnesol	null	4.81873	1.16E-10	3.89E-09
AN10950	Cytochrome P450, member of CYP53A3 family; ortholog of A. niger bphA; required for utilization of benzamide and benzoate; transcription is inducible by benzoate and subject to carbon catabolite repression mediated by CreA	bzuA	-5.5971	1.17E-10	3.89E-09
AN8396	Putative pyruvate decarboxylase with a predicted role in pyruvate metabolism	pdcB	-4.9392	1.17E-10	3.89E-09
AN6209	Putative 5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lyase with a predicted role in purine metabolism; adenylosuccinate lyase; expression reduced after exposure to farnesol	null	5.92792	1.18E-10	3.91E-09
AN4687	Beta subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccB	-5.5889	1.22E-10	4.01E-09
AN3342	Has domain(s) with predicted zinc ion binding activity	null	-5.2676	1.35E-10	4.42E-09
AN4087	Putative 40S ribosomal protein subunit; ortholog of S. cerevisiae Rps3p; expression reduced after exposure to farnesol	null	5.30928	1.47E-10	4.80E-09
AN7386	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	null	4.90865	1.52E-10	4.94E-09

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AN8012	Putative bifunctional enzyme with a predicted role in sterol metabolism	null	5.2917	1.56E-10	5.05E-09
AN4603	Putative allantoinase with a predicted role in purine metabolism	null	-5.1024	1.62E-10	5.22E-09
AN7396	Putative beta-glucosidase	bglM	-8.8979	1.64E-10	5.25E-09
AN4802	60S ribosomal protein L21; ortholog of S. cerevisiae Rpl21Ap; expression reduced after exposure to farnesol	null	4.68817	1.66E-10	5.30E-09
AN6541	Putative ligase with a predicted role in purine metabolism	null	5.87551	1.70E-10	5.38E-09
AN0943	Putative mitochondrial F1F0-ATP synthase subunit g; ortholog of S. cerevisiae Atp20p; expression reduced after exposure to farnesol	atp20	4.83824	1.70E-10	5.38E-09
AN6985	Putative ribulokinase with a predicted role in ribulose metabolism	null	-4.8559	1.74E-10	5.48E-09
AN20012	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	oxiC	4.60469	1.76E-10	5.51E-09
AN4590	Sugar transporter; transcriptionally induced by growth on xylose	null	-5.0988	1.91E-10	5.95E-09
AN8561	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.596	1.96E-10	6.10E-09
AN2286	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	alcC	4.70282	1.97E-10	6.10E-09
AN0776	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit localization	null	4.9546	1.99E-10	6.15E-09
AN8870	Expression increased in salt-adapted strains	null	4.58454	2.01E-10	6.17E-09
AN7509	null	null	-5.6761	2.08E-10	6.35E-09
AN6767	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-8.8644	2.13E-10	6.49E-09
AN3606	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	null	-6.3135	2.22E-10	6.73E-09
AN8502	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-8.8473	2.33E-10	7.04E-09
AN3265	Arrestin domains and PY motif-containing protein with homology to Saccharomyces cerevisiae Rod1p and Rog3p proteins	apyA	9.14278	2.39E-10	7.15E-09
AN6785	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	null	-5.2279	2.39E-10	7.15E-09
AN12246	Ortholog(s) have cytosol localization	null	4.69199	2.45E-10	7.31E-09

AN4345	Has domain(s) with predicted magnesium ion binding, thiamine pyrophosphate binding, transferase activity	null	-8.8301	2.55E-10	7.55E-09
AN11085	Putative D-arabinitol 4-dehydrogenaset	null	-5.5566	2.55E-10	7.55E-09
AN1624	Subunit 9 of the mitochondrial inner membrane F1F0-ATPase complex; mutation confers oligomycin resistance; palA-dependent expression independent of pH	oliC	5.1357	2.58E-10	7.61E-09
AN1549	Ortholog of A. fumigatus Af293 : Afu8g05600, A. niger CBS 513.88 : An16g07080, A. oryzae RIB40 : AO090005000583, A. niger ATCC 1015 : 205017-mRNA and Aspergillus versicolor : Aspve1_0037356	null	4.7541	2.67E-10	7.83E-09
AN1131	Putative cytosolic Cu/Zn superoxide dismutase; transcript repressed by light in developmentally competent mycelia	null	-5.0444	2.72E-10	7.95E-09
AN4277	Ortholog(s) have glucose transmembrane transporter activity and plasma membrane localization	null	-4.745	2.87E-10	8.36E-09
AN1832	N-glycosylated membrane protein, immunodominant antigen in sera from aspergilloma patients; repressed by bafilomycin; production increases under zinc-limiting conditions	aspnd1	5.32218	3.03E-10	8.79E-09
AN8235	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	null	-6.2581	3.19E-10	9.22E-09
AN4727	UDP-glucose 4-epimerase, involved in galactose metabolism; converts UDP-galactose to UDP-glucose; intracellular; protein abundance decreased by menadione stress	ugeA	4.98215	3.21E-10	9.25E-09
AN8138	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	aglC	-5.1843	3.25E-10	9.33E-09
AN5960	Ortholog(s) have mRNA binding activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	4.53675	3.32E-10	9.46E-09
AN1160	Predicted glycosylphosphatidylinositol (GPI)-anchored protein; S. cerevisiae ortholog Srl1p has role in cell wall organization	null	4.74812	3.33E-10	9.46E-09
AN20008	Mitochondrially encoded subunit 4 of NADH dehydrogenase; sequence in AspGD is truncated at the 3' end	ndhD	4.5188	3.34E-10	9.46E-09
AN8415	Putative acyl-coA dehydrogenase; member of the aspyridone (apd) gene cluster	apdG	-6.7232	3.35E-10	9.47E-09
AN2301	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	4.82789	3.64E-10	1.02E-08
AN2466	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.5675	3.66E-10	1.02E-08
AN6797	null	null	-8.7771	3.68E-10	1.02E-08
AN8093	Ortholog of A. nidulans FGSC A4 : AN12197, A. fumigatus Af293 : Afu4g13910, Afu5g12760, A. niger CBS 513.88 : An15g06460, An13g02370, A. oryzae RIB40 : AO090012000187 and A. niger ATCC 1015 : 40780-mRNA	null	-8.7771	3.68E-10	1.02E-08

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AN10356	Ortholog of A. oryzae RIB40 : AO090012000821, Aspergillus flavus NRRL 3357 : AFL2T_03687, A. clavatus NRRL 1 : ACLA_040800, Aspergillus versicolor : Aspve1_0164205 and Aspergillus sydowii : Aspsy1_0087183	null	-4.4956	3.79E-10	1.05E-08
AN8661	Ortholog of A. nidulans FGSC A4 : AN5943, AN8548, AN4642, A. fumigatus Af293 : Afu3g00850, Afu4g08850 and A. niger CBS 513.88 : An02g13470, An11g00090, An03g01430, An12g09260	null	-5.352	4.32E-10	1.19E-08
AN1524	Putative methylenetetrahydrofolate dehydrogenase (NAD+) with a predicted role in one-carbon metabolism	null	5.48133	4.48E-10	1.23E-08
AN1122	Ortholog(s) have cytosol localization	null	4.61537	4.50E-10	1.23E-08
AN5763	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.1588	4.51E-10	1.23E-08
AN1731	Putative proline dehydrogenase with a predicted role in proline metabolism; expression is regulated by carbon and nitrogen repression; negatively regulated by CreA	prnD	-4.9682	4.55E-10	1.23E-08
AN6750	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	5.26389	4.55E-10	1.23E-08
AN0740	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	null	-4.9562	4.86E-10	1.31E-08
AN2980	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	4.64627	4.87E-10	1.31E-08
AN2895	Has domain(s) with predicted ADP binding, ATP binding activity and role in apoptotic process	null	-8.7407	4.89E-10	1.31E-08
AN6394	Putative acyl-coA dehydrogenase	null	-5.9257	5.29E-10	1.41E-08
AN0013	Possible pseudogene	null	-8.7221	5.38E-10	1.43E-08
AN3223	Putative 6-phosphofructokinase with a predicted role in gluconeogenesis and glycolysis; upregulated under hypoxic growth conditions	pfkA	4.47581	5.63E-10	1.49E-08
AN2958	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.9201	5.79E-10	1.53E-08
AN1866	null	null	-6.1708	5.84E-10	1.54E-08
AN2876	Ortholog of A. clavatus NRRL 1 : ACLA_039650, Aspergillus versicolor : Aspve1_0051465, Aspergillus sydowii : Aspsy1_0146596 and Aspergillus terreus NIH2624 : ATET_04728	null	-6.6494	5.93E-10	1.55E-08
AN3818	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	null	-5.0737	5.97E-10	1.56E-08
AN10710	Ortholog(s) have phosphomannomutase activity, role in ER to Golgi vesicle-mediated transport, nuclear envelope organization, protein targeting to ER and cytosol, nucleus localization	null	4.93413	6.35E-10	1.65E-08
AN1962	Has domain(s) with predicted DNA binding activity	null	-6.6303	6.54E-10	1.70E-08

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AN4916	Ortholog(s) have role in ribosome biogenesis and cytosol, nucleolus, small-subunit processome localization	null	4.4559	6.90E-10	1.79E-08
AN6202	Putative ribosomal protein L3	rpl3	4.44157	6.93E-10	1.79E-08
AN3763	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.40834	7.35E-10	1.88E-08
AN1050	Putative 3-ketoacyl-CoA thiolase with a predicted role in fatty acid metabolism; protein is mislocalized in a pexG mutant	null	-4.7232	7.36E-10	1.88E-08
AN3172	Ortholog of S. cerevisiae RPS0A and RPS0B; expression reduced after exposure to farnesol	null	4.66116	7.68E-10	1.96E-08
AN6973	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism; expression reduced after exposure to farnesol	null	4.38157	8.11E-10	2.06E-08
AN4163	Protein with seven WD repeats, involved in cross-pathway control of the response to amino acid starvation; required for sexual development; palA-dependent expression independent of pH; protein induced by farnesol	cpcB	6.02859	8.27E-10	2.10E-08
AN4197	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	null	-4.7611	9.32E-10	2.35E-08
AN10059	Putative Zn(II)C6 domain containing transcription factor; predicted NirA binding site in promoter; transcript repressed by nitrate	null	-5.456	9.64E-10	2.42E-08
AN4757	Ortholog(s) have role in ubiquinone biosynthetic process and mitochondrial inner membrane localization	null	5.03706	9.64E-10	2.42E-08
AN4246	Ortholog of A. fumigatus Af293 : Afu1g06480, A. niger CBS 513.88 : An18g05510, A. oryzae RIB40 : AO090001000450, A. niger ATCC 1015 : 54213-mRNA and Aspergillus versicolor : Aspve1_0845556	null	-6.5715	9.75E-10	2.44E-08
AN5979	Ortholog(s) have role in ribosomal small subunit assembly and cytosol localization	null	4.64256	9.86E-10	2.46E-08
AN0800	null	null	-6.0938	1.02E-09	2.53E-08
AN10819	Has domain(s) with predicted ATP binding, protein kinase activity and role in protein phosphorylation	null	-8.6255	1.08E-09	2.64E-08
AN2629	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-8.6255	1.08E-09	2.64E-08
AN2663	Ortholog(s) have pantothenate transmembrane transporter activity, role in endocytosis, pantothenate transmembrane transport and plasma membrane localization	null	-6.5514	1.08E-09	2.64E-08
AN6727	Ortholog of A. nidulans FGSC A4 : AN8146, A. fumigatus Af293 : Afu6g03180, Afu7g05880, A. niger CBS 513.88 : An07g02000, An01g14710 and Aspergillus versicolor : Aspve1_0079826	null	-6.5514	1.08E-09	2.64E-08
AN7264	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	-8.6255	1.08E-09	2.64E-08

AN10512	Putative mitochondrial ketoacyl-CoA thiolase with a role in fatty acid beta-oxidation	mthA	-4.6737	1.09E-09	2.64E-08
AN7359	Putative cytochrome P450	CYP5078A3	-5.2205	1.09E-09	2.64E-08
AN5709	null	null	-5.3411	1.11E-09	2.68E-08
AN5028	Fatty acid oxygenase that plays a role in oxylipin biosynthesis; responsible for the formation of the psi-factor component psiB-beta; expression reduced after exposure to farnesol	ppoC	-4.365	1.12E-09	2.71E-08
AN3790	Putative alpha-1,3-glucanase	agnB	-8.6053	1.20E-09	2.88E-08
AN0278	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	4.60435	1.28E-09	3.07E-08
AN8930	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	null	-4.7144	1.29E-09	3.07E-08
AN10949	Ortholog(s) have xenobiotic-transporting ATPase activity, role in response to drug and mitochondrion, plasma membrane localization	null	-4.5895	1.33E-09	3.15E-08
AN10691	Has domain(s) with predicted GTP binding, GTPase activity	null	-8.5849	1.33E-09	3.15E-08
AN0433	Ortholog(s) have cytosol, nucleolus localization	null	4.69447	1.36E-09	3.21E-08
AN7092	Ortholog of Aspergillus aculeatus ATCC16872 : Aacu16872_053301	null	-5.7822	1.37E-09	3.22E-08
AN3823	Ortholog(s) have structural constituent of ribosome activity	null	4.30488	1.46E-09	3.43E-08
AN0282	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	-8.5642	1.64E-09	3.83E-08
AN6747	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	null	-8.5642	1.64E-09	3.83E-08
AN0553	null	null	6.40793	1.82E-09	4.23E-08
AN7962	Extracellular deuterolysin-type metallo-proteinase	pepJ	-8.5432	1.83E-09	4.24E-08
AN10518	Protein of unknown function; protein induced by farnesol	null	5.19414	2.03E-09	4.68E-08
AN3075	Zinc finger protein of unknown function; overexpression confers the "fluffy" phenotype	oefC	-4.4843	2.06E-09	4.75E-08
AN8314	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in defense response, lipid metabolic process	null	6.38288	2.10E-09	4.83E-08
AN1007	Putative nitrite reductase with a predicted role in nitrogen metabolism; transcript stabilized by intracellular nitrate	niiA	4.381	2.15E-09	4.93E-08
AN2387	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	4.69378	2.19E-09	4.99E-08
AN0913	Putative phosphatidylinositol synthase with a predicted role in phospholipid metabolism	null	5.18094	2.19E-09	4.99E-08
AN0465	Ortholog of S. cerevisiae RPS8A and RPS8B; palA-dependent expression independent of pH	null	4.27371	2.25E-09	5.10E-08

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AN7508	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	null	-5.712	2.27E-09	5.12E-08
AN0362	Ortholog of A. fumigatus Af293 : Afu6g00430, Afu6g03560, A. niger CBS 513.88 : An10g01040, An01g06280, A. oryzae RIB40 : AO090005000897 and A. niger ATCC 1015 : 36048-mRNA	null	4.54421	2.60E-09	5.87E-08
AN10703	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-6.4021	2.84E-09	6.38E-08
AN0214	null	null	4.53043	2.85E-09	6.38E-08
AN10166	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	null	-4.5957	2.95E-09	6.59E-08
AN1228	Ortholog(s) have role in maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, nucleolus, preribosome, large subunit precursor localization	null	4.38617	2.98E-09	6.63E-08
AN5665	Putative cytochrome P450	CYP531D2	-5.1945	3.04E-09	6.76E-08
AN6082	Ortholog(s) have pre-mRNA 5'-splice site binding, structural constituent of ribosome activity, role in negative regulation of mRNA splicing, via spliceosome, rRNA processing and cytosol localization	null	4.32991	3.11E-09	6.89E-08
AN4475	Ortholog(s) have role in ribosomal large subunit assembly and cytosol localization	null	4.31758	3.19E-09	7.05E-08
AN4787	Putative ribosomal protein L37; palA-dependent expression independent of pH	rpl37	4.2117	3.25E-09	7.15E-08
AN6650	Methylcitrate synthase with a predicted role in the methylcitrate pathway or the TCA cycle; transcript upregulated by exposure to ethanol	mcsA	-5.2731	3.30E-09	7.24E-08
AN2993	Ortholog of A. fumigatus Af293 : Afu3g08610, A. niger CBS 513.88 : An02g12330, A. oryzae RIB40 : AO090005001411, A. niger ATCC 1015 : 173126-mRNA and Aspergillus versicolor : Aspve1_0081680	null	-4.5773	3.31E-09	7.24E-08
AN4202	Predicted ribosomal protein of the large (60S) ribosomal subunit; differentially expressed during sexual development	rpl16a	4.19238	3.43E-09	7.47E-08
AN6181	Ortholog(s) have cytosol localization	null	4.26574	3.43E-09	7.47E-08
AN0601	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.61222	3.98E-09	8.63E-08
AN1584	Ortholog(s) have transcription cofactor activity, role in negative regulation of calcium ion-dependent exocytosis and nucleus localization	null	-8.4333	4.00E-09	8.64E-08
AN0779	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	null	-4.5497	4.02E-09	8.67E-08
AN5267	Protein with ferulic acid esterase activity, involved in degradation of xylans	faeC	-5.0241	4.10E-09	8.81E-08
AN1860	Ortholog(s) have mitochondrion localization	null	4.31437	4.40E-09	9.43E-08

AN8995	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-8.4103	4.49E-09	9.60E-08
AN12135	null	null	6.26903	4.50E-09	9.60E-08
AN5441	Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), rRNA export from nucleus	null	4.24146	4.53E-09	9.64E-08
AN9465	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus localization	null	4.26432	4.90E-09	1.04E-07
AN9097	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, mitochondrion, nucleolus localization	null	4.19879	4.94E-09	1.04E-07
AN7484	Protein expressed at increased levels during osmoadaptation; contains a DUF1349 domain	null	4.78782	5.02E-09	1.06E-07
AN1699	Putative acyl-coA dehydrogenase; expression upregulated after exposure to farnesol	null	-4.3958	5.21E-09	1.09E-07
AN2455	Ortholog(s) have cytosol, nucleus localization	null	4.52374	5.31E-09	1.11E-07
AN4494	Ortholog(s) have mitochondrion, nucleus localization	null	4.22356	5.34E-09	1.12E-07
AN10060	Putative alpha-amylase; glycogen debranching enzyme	null	-4.2862	5.66E-09	1.18E-07
AN8777	Acetamidase, produces ammonium and acetate from acetamide, allowing utilization of acetamide as sole carbon or nitrogen source; transcript induced under low nitrogen conditions	amdS	-4.2862	5.66E-09	1.18E-07
AN6629	Putative ribosomal protein L14; ortholog of S. cerevisiae Rpl14Ap; expression reduced after exposure to farnesol	null	4.22918	5.87E-09	1.22E-07
AN5053	Has domain(s) with predicted N-acetyltransferase activity and role in metabolic process	null	8.65998	5.96E-09	1.23E-07
AN4794	Putative ribosomal protein; expression increased in salt-adapted strains	null	4.12517	6.02E-09	1.24E-07
AN8746	Possible pseudogene; transcript upregulated in response to camptothecin	null	4.08946	6.03E-09	1.24E-07
AN1608	Ortholog of A. fumigatus Af293 : Afu4g09250, A. niger CBS 513.88 : An04g04280, A. oryzae RIB40 : AO090023000611 and A. niger ATCC 1015 : 213011-mRNA	null	4.18957	6.08E-09	1.25E-07
AN10024	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-4.7373	6.91E-09	1.41E-07
AN0354	Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with a predicted role in aromatic amino acid family biosynthesis; protein expressed at increased levels in a hapX mutant versus wild-type; feedback-inhibited by phenylalanine	aroG	5.53219	6.93E-09	1.41E-07
AN2236	Ortholog of A. fumigatus Af293 : Afu5g07310, A. niger CBS 513.88 : An17g00750, A. oryzae RIB40 : AO090701000224, A. niger ATCC 1015 : 213970-mRNA and Aspergillus versicolor : Aspve1_0050602	null	-4.6889	7.36E-09	1.50E-07
AN5800	Ortholog(s) have cytosol localization	null	4.1194	7.46E-09	1.51E-07
AN4060	Putative ribosomal protein S16	rps16	4.19295	7.93E-09	1.60E-07

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AN5490	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	null	-4.7414	8.01E-09	1.61E-07
AN4739	Putative phosphoribosyl amino imidazolesuccinocarbozamide synthetase with a predicted role in purine metabolism	null	4.99228	8.04E-09	1.62E-07
AN1290	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	-4.2962	8.10E-09	1.62E-07
AN7670	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	null	-8.3144	8.18E-09	1.64E-07
AN3141	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-4.5455	8.32E-09	1.66E-07
AN6157	Orotidine-5'-phosphate decarboxylase, enzyme of the pyrimidine biosynthesis pathway	pyrG	4.16556	8.38E-09	1.67E-07
AN5520	Has domain(s) with predicted role in ribosome biogenesis and ribonucleoprotein complex localization	null	6.16514	8.61E-09	1.71E-07
AN4353	Has domain(s) with predicted 3-oxoacyl-[acyl-carrier-protein] synthase activity and role in fatty acid biosynthetic process	null	-4.218	8.99E-09	1.78E-07
AN4901	Putative glutaminase A with a predicted role in glutamate and glutamine metabolism	null	-4.1104	9.04E-09	1.78E-07
AN2646	Has domain(s) with predicted ATP binding activity	null	-8.2894	9.26E-09	1.81E-07
AN7864	Putative beta-1,4-xylosidase	bxlD	-8.2894	9.26E-09	1.81E-07
AN8890	Has domain(s) with predicted carbohydrate binding, catalytic activity and role in carbohydrate catabolic process	null	-8.2894	9.26E-09	1.81E-07
AN1719	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	null	-4.9035	9.53E-09	1.86E-07
AN4872	Fusion protein consisting of N-terminal ubiquitin and C-terminal extension protein (CEP) of the small ribosomal subunit; transcript upregulated in response to camptothecin	ubi1	4.03153	9.63E-09	1.88E-07
AN10223	Putative 1-Cys peroxiredoxin; intracellular; protein abundance decreased by menadione stress; expression reduced after exposure to farnesol	null	4.95657	1.01E-08	1.96E-07
AN1810	Ornithine transaminase, involved in utilization of arginine as a proline source; arginine-induced expression and activity; subject to carbon-catabolite and nitrogen-metabolite repression; regulated by CreA and AreA; stress-induced protein	otaA	-4.0533	1.02E-08	1.98E-07
AN7322	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	null	4.68784	1.04E-08	2.01E-07

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AN20002	Mitochondrially encoded subunit 2 of NADH dehydrogenase; note that the sequence represented in AspGD is N-terminally truncated relative to orthologous genes in other species	ndhB	4.11408	1.08E-08	2.08E-07
AN3565	Has domain(s) with predicted hydrolase activity	null	-5.478	1.11E-08	2.13E-07
AN4837	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	null	-5.0979	1.11E-08	2.13E-07
AN0485	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	null	-4.2189	1.12E-08	2.15E-07
AN1087	Putative cytochrome P450	CYP578B1	-4.3968	1.14E-08	2.17E-07
AN0824	Putative mitochondrial acyl-coA dehydrogenase involved in short-chain fatty acid beta-oxidation; required for growth on short-chain fatty acids	scdA	-4.1854	1.16E-08	2.21E-07
AN1918	Putative phosphoenolpyruvate carboxykinase with a predicted role in gluconeogenesis and glycolysis; transcriptionally induced by acetate and after exposure to farnesol	acuF	-4.0442	1.17E-08	2.21E-07
AN6632	Putative 40S ribosomal protein S28; ortholog of S. cerevisiae Rps28Bp; expression reduced after exposure to farnesol	null	4.11955	1.24E-08	2.34E-07
AN4401	Putative asparagine synthase with a predicted role in asparagine metabolism	null	4.22091	1.27E-08	2.40E-07
AN8704	60S ribosomal protein L24a; PalA-dependent expression independent of pH	null	4.36847	1.27E-08	2.40E-07
AN4222	Ortholog(s) have cytosol, nucleus localization	null	4.05541	1.31E-08	2.45E-07
AN6657	Ortholog of A. fumigatus Af293 : Afu6g03400, A. niger CBS 513.88 : An15g02040, Aspergillus versicolor : Aspve1_0086179 and Aspergillus sydowii : Aspsy1_0157063	null	4.44111	1.31E-08	2.45E-07
AN0528	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-8.238	1.36E-08	2.53E-07
AN5614	Ortholog(s) have role in plasma membrane fusion involved in cytogamy, response to pheromone and cytoplasm, mating projection tip localization	null	-4.6604	1.36E-08	2.54E-07
AN4975	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	4.97497	1.38E-08	2.57E-07
AN4064	Putative ADP/ATP carrier protein with a predicted role in energy metabolism; palA-dependent expression independent of pH	null	3.9956	1.44E-08	2.67E-07
AN20010	Mitochondrially encoded subunit 6 of the F0 sector of mitochondrial F1F0 ATP synthase; can mutate to confer oligomycin resistance	oliA	3.97941	1.46E-08	2.70E-07
AN0609	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	null	4.22164	1.50E-08	2.77E-07

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AN7691	Putative phospholipase	plcB	-4.6485	1.54E-08	2.83E-07
AN1852	Putative chitin deacetylase	null	-8.2116	1.54E-08	2.83E-07
AN5458	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	null	-4.6364	1.63E-08	2.99E-07
AN6024	Protein with glutathione S-transferase and glutathione peroxidase activities; intracellular, menadione stress-induced protein	gstB	-4.9422	1.69E-08	3.08E-07
AN5088	Putative potassium-transporting ATPase with a predicted role in energy metabolism	null	-5.0285	1.71E-08	3.12E-07
AN8969	Has domain(s) with predicted cation binding, lysozyme activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, peptidoglycan catabolic process	null	-4.5635	1.76E-08	3.20E-07
AN7111	Peroxisomal multifunctional enzyme involved in fatty acid beta-oxidation; required for growth on very long-chain fatty acids; transcription is induced by fatty acids	foxA	-4.4249	1.76E-08	3.20E-07
AN7967	Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport and membrane localization	null	-5.6531	1.80E-08	3.25E-07
AN10921	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity, role in GPI anchor metabolic process, intracellular protein transport and intrinsic to endoplasmic reticulum membrane localization	null	4.72255	1.80E-08	3.25E-07
AN8400	Sugar transporter; transcriptionally induced by growth on xylose	null	-5.3907	1.87E-08	3.37E-07
AN4464	Putative bifunctional enzyme with a predicted role in purine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type	purH	4.18296	1.93E-08	3.47E-07
AN4792	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-4.5597	1.99E-08	3.57E-07
AN11046	Protein of unknown function; transcript is induced by nitrate	null	-8.1848	2.01E-08	3.58E-07
AN8814	Ortholog(s) have endoplasmic reticulum localization	null	-8.1848	2.01E-08	3.58E-07
AN5566	Putative GMP synthase (glutamine-hydrolyzing) with a predicted role in purine metabolism	null	4.49872	2.04E-08	3.63E-07
AN3481	Ortholog of A. fumigatus Af293 : Afu1g02290, A. niger CBS 513.88 : An01g05960, A. oryzae RIB40 : AO090026000175, A. niger ATCC 1015 : 51930-mRNA and Aspergillus versicolor : Aspve1_0039102	null	3.96503	2.09E-08	3.70E-07
AN7287	Putative mitochondrial succinate/fumarate antiporter	acuL	-4.5996	2.09E-08	3.71E-07
AN10789	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	null	-4.8392	2.13E-08	3.76E-07
AN2545	Putative nonribosomal peptide synthetase; emericellamide synthetase; required for emericellamide biosynthesis; present in an emericellamide gene cluster	easA	-4.2974	2.19E-08	3.85E-07

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AN2057	Ortholog(s) have role in aerobic respiration and mitochondrial nucleoid localization	null	8.44192	2.23E-08	3.90E-07
AN9168	Ortholog(s) have solute:hydrogen symporter activity, role in glycerol transport, transmembrane transport and plasma membrane localization	null	-5.6315	2.23E-08	3.90E-07
AN9263	Ortholog of A. oryzae RIB40 : AO090011000236, N. fischeri NRRL 181 : NFIA_029940, A. clavatus NRRL 1 : ACLA_055010, Aspergillus versicolor : Aspve1_0042688 and Aspergillus sydowii : Aspsy1_0047416	null	8.44192	2.23E-08	3.90E-07
AN4339	null	null	-4.2294	2.25E-08	3.93E-07
AN1502	Extracellular N-acetyl-beta-glucosaminidase with a predicted role in chitin hydrolysis	nagA	-4.087	2.35E-08	4.09E-07
AN6693	Protein of unknown function; transcript repressed by nitrate	null	4.68123	2.36E-08	4.10E-07
AN5990	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	null	-4.7594	2.38E-08	4.12E-07
AN20016	null	null	6.01021	2.46E-08	4.25E-07
AN10298	3-phosphoserine aminotransferase; intracellular; protein abundance decreased by menadione stress	null	4.67071	2.59E-08	4.46E-07
AN0403	Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	4.04938	2.67E-08	4.59E-07
AN2037	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	null	5.3293	2.70E-08	4.63E-07
AN2844	Ortholog of A. fumigatus Af293 : Afu3g12255, A. niger CBS 513.88 : An02g08130, A. oryzae RIB40 : AO090003000790, A. niger ATCC 1015 : 37157-mRNA and Aspergillus versicolor : Aspve1_0080524	null	5.3293	2.70E-08	4.63E-07
AN5162	Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism	pdhB	3.87868	2.74E-08	4.68E-07
AN10159	Ortholog of Aspergillus brasiliensis : Aspbr1_0205897, Aspergillus flavus NRRL 3357 : AFL2T_07527, A. clavatus NRRL 1 : ACLA_023190 and Aspergillus acidus : Aspfo1_0217083	null	4.52649	2.96E-08	5.04E-07
AN2435	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	aclA	4.52207	2.96E-08	5.04E-07
AN3282	Has domain(s) with predicted catalytic activity, nucleotide binding activity and role in biosynthetic process	null	4.29238	3.23E-08	5.49E-07
AN6865	Ortholog(s) have endoplasmic reticulum, nuclear envelope localization	null	5.96593	3.25E-08	5.50E-07
AN2701	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	null	-4.2383	3.26E-08	5.50E-07
AN2601	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.5645	3.46E-08	5.83E-07
AN9162	Putative acyl-coA dehydrogenase	null	-8.101	3.48E-08	5.85E-07

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AN8204	Ortholog(s) have NAD+ diphosphatase activity, role in NADH metabolic process and cytosol, nucleus, peroxisome localization	null	5.94326	3.57E-08	5.98E-07
AN0445	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	3.88633	3.57E-08	5.98E-07
AN1425	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	farB	-3.9283	3.65E-08	6.09E-07
AN3413	Protein with homology to ribosomal protein S2 and S5; ortholog of S. cerevisiae Rps2p; expression reduced after exposure to farnesol	null	3.90963	3.70E-08	6.17E-07
AN4504	Putative endo-mannanase GH76 family protein	dfgG	-3.8757	3.73E-08	6.18E-07
AN0401	Ortholog of A. fumigatus Af293 : Afu2g02490, Aspergillus flavus NRRL 3357 : AFL2T_08730, A. clavatus NRRL 1 : ACLA_092310, Aspergillus versicolor : Aspve1_0035846 and Aspergillus sydowii : Aspsy1_0143520	null	5.0681	3.74E-08	6.18E-07
AN2675	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	5.0681	3.74E-08	6.18E-07
AN4376	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	gdhA	3.86247	3.74E-08	6.18E-07
AN11243	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	4.48172	3.89E-08	6.41E-07
AN1345	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), regulation of translational fidelity	null	3.81178	3.90E-08	6.42E-07
AN6231	Tryptophan synthase involved in tryptophan biosynthesis; transcription is regulated by the cross-pathway control of amino acid biosynthesis; repressed by starvation-induced autophagy; protein induced by farnesol	trpB	4.32537	3.94E-08	6.46E-07
AN6630	Putative nascent polypeptide-associated complex subunit alpha; induced by rapamycin-induced autophagy	null	4.05394	3.97E-08	6.49E-07
AN11771	null	null	-5.9884	4.01E-08	6.55E-07
AN1716	Ortholog of Aspergillus versicolor : Aspve1_0037607, Aspergillus sydowii : Aspsy1_0084105 and Aspergillus terreus NIH2624 : ATET_05357	null	-3.9965	4.15E-08	6.76E-07
AN4119	Putative major facilitator superfamily protein; transcript upregulated in response to camptothecin	null	4.48058	4.17E-08	6.78E-07
AN1693	Putative F-box protein	null	-4.1359	4.36E-08	7.07E-07

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AN12368	Putative alpha-L-rhamnosidase	rhaB	-4.4833	4.57E-08	7.39E-07
AN6658	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-4.2833	5.02E-08	8.12E-07
AN2914	Putative argininosuccinate lyase with a predicted role in arginine metabolism	null	3.95375	5.08E-08	8.19E-07
AN11797	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-3.9135	5.18E-08	8.33E-07
AN8262	Secretin-like G-protein coupled receptor	gprH	-4.4358	5.29E-08	8.49E-07
AN1013	Putative 60S ribosomal protein L5; ortholog of S. cerevisiae Rpl5p which is an RNA binding protein with a role in ribosomal large subunit assembly	null	3.84117	5.68E-08	9.09E-07
AN8068	Putative beta-1,4-endoglucanase	null	5.2006	5.71E-08	9.13E-07
AN8866	Putative phosphoglycerate dehydrogenase with a predicted role in glycine, serine, and threonine metabolism	null	3.97238	5.80E-08	9.25E-07
AN2818	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	null	4.04691	6.09E-08	9.69E-07
AN6761	Putative acyl-coA dehydrogenase	null	-8.0121	6.20E-08	9.84E-07
AN5497	Ortholog(s) have 3,4-dihydroxy-2-butanone-4-phosphate synthase activity, role in aerobic respiration, riboflavin biosynthetic process and cytosol, mitochondrial intermembrane space, nucleus localization	null	4.04166	6.38E-08	1.01E-06
AN10891	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.8184	6.41E-08	1.01E-06
AN0048	Ortholog of A. fumigatus Af293 : Afu5g12560, A. niger CBS 513.88 : An14g06630, A. oryzae RIB40 : AO090120000382, A. niger ATCC 1015 : 201783-mRNA and Aspergillus versicolor : Aspve1_0035341	null	-4.3631	6.55E-08	1.03E-06
AN2316	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	4.67201	6.55E-08	1.03E-06
AN1136	Putative myo-inositol-1(or 4)-monophosphatase with a predicted role in phospholipid metabolism; transcript inducible by quinate	qutG	-4.7279	6.80E-08	1.07E-06
AN7528	Ortholog of Aspergillus brasiliensis : Aspbr1_0191334, Aspergillus versicolor : Aspve1_0789753, Aspergillus sydowii : Aspsy1_1018139 and Aspergillus terreus NIH2624 : ATET_06707	null	-4.7279	6.80E-08	1.07E-06
AN7170	Protein of unknown function; transcript upregulated in response to camptothecin	null	4.04215	6.89E-08	1.08E-06
AN7003	Ortholog(s) have cytosol localization	null	3.84393	6.92E-08	1.08E-06
AN8905	Putative cytochrome P450	CYP537B1	4.03921	7.07E-08	1.10E-06
AN1868	Putative glycerol dehydrogenase with a predicted role in glycerol metabolism; protein expressed at decreased levels in a hapX mutant versus wild-type	null	-4.222	7.09E-08	1.10E-06
AN7523	Ortholog of A. nidulans FGSC A4 : AN0171, A. niger CBS 513.88 : An18g01570, A. oryzae RIB40 : AO090010000737, A. niger ATCC 1015 : 134538-mRNA and Aspergillus versicolor : Aspve1_0077940	null	4.51478	7.09E-08	1.10E-06
AN1917	Putative mitochondrial dicarboxylate-tricarboxylate carrier	dicB	-7.9812	7.19E-08	1.11E-06

AN3085	Ortholog(s) have mitochondrion localization	null	-7.9812	7.19E-08	1.11E-06
AN7304	Ortholog(s) have coenzyme A transmembrane transporter activity, role in coenzyme A transport and mitochondrial inner membrane localization	null	-4.2055	7.59E-08	1.17E-06
AN3203	Putative F-box protein	null	-3.7478	7.62E-08	1.17E-06
AN9130	Has domain(s) with predicted cholinesterase activity	null	-4.2193	7.70E-08	1.18E-06
AN6823	Ortholog of A. fumigatus Af293 : Afu5g12860, A. niger CBS 513.88 : An14g06360, A. oryzae RIB40 : AO090120000406, A. niger ATCC 1015 : 201762-mRNA and Aspergillus versicolor : Aspve1_0122523	null	-4.1091	7.77E-08	1.19E-06
AN8931	Ortholog of A. fumigatus Af293 : Afu1g10120, A. niger CBS 513.88 : An08g01940, A. oryzae RIB40 : AO090038000421, A. niger ATCC 1015 : 38532-mRNA and Aspergillus versicolor : Aspve1_0132736	null	-4.1096	7.83E-08	1.20E-06
AN6636	Ortholog(s) have role in reciprocal meiotic recombination and cytosol, endoplasmic reticulum, nucleus localization	null	3.84803	8.14E-08	1.24E-06
AN12341	Has domain(s) with predicted 5-(carboxyamino)imidazole ribonucleotide mutase activity, phosphoribosylaminoimidazole carboxylase activity and role in 'de novo' IMP biosynthetic process	null	-7.9496	8.37E-08	1.27E-06
AN2640	Ortholog of A. fumigatus Af293 : Afu5g14080, A. niger CBS 513.88 : An12g05640, A. niger ATCC 1015 : 49626-mRNA, Aspergillus versicolor : Aspve1_0040725 and Aspergillus sydowii : Aspsy1_0031225	null	-7.9496	8.37E-08	1.27E-06
AN6386	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	4.27689	8.41E-08	1.27E-06
AN4452	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	4.36333	8.45E-08	1.28E-06
AN0443	Putative zinc containing alcohol dehydrogenase; protein expressed at decreased levels in a hapX mutant versus wild-type	null	4.10716	8.78E-08	1.33E-06
AN1993	Putative aspartate transaminase with a predicted role in alanine, aspartate, and aromatic amino acid metabolism	null	3.73582	8.83E-08	1.33E-06
AN10444	Ortholog(s) have gamma-glutamyltransferase activity, role in cellular response to nitrogen starvation and endoplasmic reticulum localization	null	-3.7775	9.21E-08	1.38E-06
AN9193	Ortholog of A. nidulans FGSC A4 : AN3975, AN2891 and A. fumigatus Af293 : Afu1g10150, Afu2g04380, Afu3g15150, Afu3g15280, Afu6g03300	null	-4.7554	9.63E-08	1.44E-06
AN6679	Ortholog(s) have SSU rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	null	3.77923	9.82E-08	1.47E-06
AN3390	Protein with pectinesterase activity, involved in degradation of pectin	pmeA	8.20048	9.96E-08	1.49E-06
AN8913	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	8.20048	9.96E-08	1.49E-06
AN8641	Transcript induced by light in in developmentally competent mycelia	null	4.66612	1.00E-07	1.49E-06
AN6503	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-3.9188	1.03E-07	1.52E-06

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AN3222	Ortholog(s) have IMP 5'-nucleotidase activity and role in inosine salvage, nicotinamide riboside biosynthetic process, nicotinic acid riboside biosynthetic process	null	-3.9268	1.04E-07	1.53E-06
AN8705	Ortholog(s) have cytoplasmic stress granule, cytosol, nucleus localization	null	3.66438	1.06E-07	1.56E-06
AN6873	null	null	-7.8843	1.14E-07	1.68E-06
AN8551	Putative transferase with a predicted role in the pentose-phosphate shunt or xylulose metabolism	null	-7.8843	1.14E-07	1.68E-06
AN8280	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism; transcript induced in the presence of short and long chain fatty acids	faaB	-3.9023	1.14E-07	1.68E-06
AN4779	Ortholog of A. fumigatus Af293 : Afu3g06660, A. niger CBS 513.88 : An11g09650, A. oryzae RIB40 : AO090020000332, A. niger ATCC 1015 : 209032-mRNA and Aspergillus versicolor : Aspve1_0051759	null	-4.0405	1.24E-07	1.83E-06
AN0565	Multifunctional enzyme with carbamoyl-phosphate synthase (CPSase) and aspartate carbamoyltransferase (ATCase) activities that catalyze the first two steps in pyrimidine biosynthesis	pyrABCN	3.87281	1.27E-07	1.86E-06
AN5946	Ortholog(s) have cell division site, cytosol localization	null	8.16922	1.28E-07	1.87E-06
AN7307	Ortholog(s) have endoplasmic reticulum localization	null	-4.1275	1.29E-07	1.89E-06
AN11510	Has domain(s) with predicted role in defense response	null	-4.7118	1.32E-07	1.92E-06
AN10026	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	null	-7.8505	1.33E-07	1.93E-06
AN10638	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	null	-7.8505	1.33E-07	1.93E-06
AN4980	Ortholog(s) have cytosol localization	null	-7.8505	1.33E-07	1.93E-06
AN20011	Mitochondrially encoded subunit 6 of NADH dehydrogenase	ndhF	4.20683	1.38E-07	2.00E-06
AN5315	Ortholog of A. niger CBS 513.88 : An01g01450, A. oryzae RIB40 : AO090001000269, Aspergillus brasiliensis : Aspbr1_0053207, A. niger ATCC 1015 : 36402-mRNA and N. fischeri NRRL 181 : NFIA_044920	null	-4.1175	1.39E-07	2.01E-06
AN10507	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	null	5.05928	1.40E-07	2.01E-06
AN11476	Ortholog of A. fumigatus Af293 : Afu2g03190, Aspergillus versicolor : Aspve1_0086542, Aspve1_0089117, Aspergillus sydowii : Aspsy1_0093985 and Aspergillus brasiliensis : Aspbr1_0045764, Aspbr1_0201559	null	5.07065	1.40E-07	2.01E-06

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AN0640	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	basA	4.03207	1.43E-07	2.04E-06
AN0893	Putative adenylosuccinate synthase with a predicted role in purine metabolism; induced by ammonium and adenosine	adB	4.54723	1.43E-07	2.04E-06
AN2390	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	null	8.13728	1.45E-07	2.07E-06
AN3830	L-threonine dehydratase with a predicted role in glycine, serine, and threonine metabolism	ileA	4.19607	1.46E-07	2.08E-06
AN1919	null	null	-5.0696	1.47E-07	2.09E-06
AN9306	Ortholog of Aspergillus versicolor : Aspve1_0087504 and Aspergillus sydowii : Aspsy1_0134418	null	-5.0696	1.47E-07	2.09E-06
AN3959	Has domain(s) with predicted metalloendopeptidase activity and role in proteolysis	null	-7.8158	1.56E-07	2.20E-06
AN5381	null	null	-7.8158	1.56E-07	2.20E-06
AN5383	null	null	-7.8158	1.56E-07	2.20E-06
AN6116	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	null	-7.8158	1.56E-07	2.20E-06
AN10075	Putative permease of the major facilitator superfamily (MFS)	null	-4.0957	1.63E-07	2.30E-06
AN5373	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.8417	1.64E-07	2.31E-06
AN1542	Protein with oligoxyloglucan reducing end-specific cellobiohydrolase activity, involved in degradation of xyloglucans	xgcA	8.12103	1.65E-07	2.31E-06
AN4848	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	null	-3.9856	1.78E-07	2.49E-06
AN6653	Malate synthase, required for utilization of acetate as carbon source; transcription induction by acetate mediated by FacB; carbon catabolite repression mediated by CreA; transcription induction by long-chain fatty acids mediated by FarA	acuE	-3.6825	1.82E-07	2.54E-06
AN6460	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	null	5.68095	1.83E-07	2.54E-06
AN2683	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	null	4.23845	1.94E-07	2.69E-06
AN8813	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of substances activity, role in transport and integral to membrane localization	null	-3.8953	1.94E-07	2.69E-06

AN7091	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	-4.0699	2.02E-07	2.80E-06
AN2837	Ortholog of A. nidulans FGSC A4 : AN5509, AN2029, A. fumigatus Af293 : Afu4g00200, A. oryzae RIB40 : AO090023000015, AO090113000086 and N. fischeri NRRL 181 : NFIA_003110, NFIA_045440	null	-4.5584	2.04E-07	2.82E-06
AN2704	Putative aryl-alcohol oxidase-related protein	null	4.13652	2.12E-07	2.92E-06
AN0224	Ortholog(s) have Golgi apparatus, cytosol, nucleus localization	null	8.08799	2.14E-07	2.95E-06
AN1197	Has domain(s) with predicted catalytic activity	null	-7.7804	2.17E-07	2.98E-06
AN2305	Ortholog of A. fumigatus Af293 : Afu5g06030, A. niger CBS 513.88 : An17g01795, A. niger ATCC 1015 : 192595-mRNA, Aspergillus versicolor : Aspve1_0124892 and Aspergillus sydowii : Aspsy1_0139055	null	-7.7804	2.17E-07	2.98E-06
AN8356	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	null	-4.6204	2.28E-07	3.12E-06
AN11045	Ortholog(s) have D-lactate dehydrogenase (cytochrome) activity, actin binding activity and mitochondrial matrix localization	null	3.72834	2.54E-07	3.47E-06
AN5942	Ortholog of Aspergillus versicolor : Aspve1_0148858 and Aspergillus sydowii : Aspsy1_0029071	null	5.62509	2.55E-07	3.48E-06
AN0907	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus localization	null	3.74163	2.56E-07	3.49E-06
AN4795	Has domain(s) with predicted guanyl-nucleotide exchange factor activity, role in small GTPase mediated signal transduction and intracellular localization	null	-7.744	2.56E-07	3.49E-06
AN2901	Arginase, catalyzes hydrolysis of arginine to urea and ornithine in the arginine catabolic pathway; induced by arginine and repressed by ammonium	agaA	-3.6027	2.62E-07	3.56E-06
AN8216	Putative nucleoside diphosphate kinase with a predicted role in phospholipid metabolism; required for normal hyphal growth and conidiation; mutants display increased hyphal cell lysis; transcript upregulated in response to camptothecin	swoH	3.66896	2.65E-07	3.59E-06
AN1426	Ortholog(s) have serine-type carboxypeptidase activity	null	-3.9215	2.68E-07	3.63E-06
AN6031	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-3.6873	2.70E-07	3.64E-06
AN6506	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism	null	4.44785	2.73E-07	3.68E-06
AN7320	Putative acyl-coA dehydrogenase	null	-4.2018	2.82E-07	3.80E-06
AN1611	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-3.6988	2.95E-07	3.95E-06
AN8978	Transcription factor involved in positive regulation of the ethanol regulon; contains Zn(II)2Cys6 DNA-binding domain	alcR	-3.6707	2.99E-07	4.00E-06

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AN7081	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	4.94029	3.02E-07	4.04E-06
AN0195	Ortholog of A. nidulans FGSC A4 : AN8020, A. fumigatus Af293 : Afu5g02380, A. niger CBS 513.88 : An03g04900, An02g10420 and A. oryzae RIB40 : AO090001000067, AO090102000350	null	-7.7067	3.04E-07	4.04E-06
AN2678	Ortholog of A. oryzae RIB40 : AO090103000184, Aspergillus flavus NRRL 3357 : AFL2T_12195, Aspergillus versicolor : Aspve1_0053637 and Aspergillus sydowii : Aspsy1_0206329	null	-7.7067	3.04E-07	4.04E-06
AN7648	Ortholog(s) have endoplasmic reticulum localization	null	-7.7067	3.04E-07	4.04E-06
AN5836	APSES domain transcription factor involved in regulation of conidiophore development; represses abaA and other developmentally regulated genes; locus consists of stuA-alpha and stuA-beta transcriptional units; stuA-alpha contains a uORF	stuA	-3.8325	3.04E-07	4.04E-06
AN1805	Putative carbonic anhydrase; required for growth in ambient CO2 conditions; protein expressed at increased levels during osmoadaptation	canB	3.632	3.06E-07	4.05E-06
AN3748	Putative ATP phosphoribosyltransferase with a predicted role in histidine metabolism	null	4.16939	3.10E-07	4.10E-06
AN5415	Has domain(s) with predicted O-methyltransferase activity	null	-3.9912	3.10E-07	4.10E-06
AN4122	Ortholog of A. nidulans FGSC A4 : AN2881, AN10123, AN0867, A. fumigatus Af293 : Afu1g13860, Afu1g15180, Afu3g11650 and A. niger CBS 513.88 : An08g07010, An02g07440, An01g13480	null	-5.2032	3.21E-07	4.23E-06
AN6708	Putative dihydrolipoamide S-acetyltransferase with a predicted role in pyruvate metabolism	pdhA	3.5345	3.27E-07	4.31E-06
AN7051	Cystathionine beta-lyase, enzyme of the methionine biosynthesis pathway; mutants show a reduced rate of DNA damage repair	metG	4.29284	3.39E-07	4.45E-06
AN8363	Has domain(s) with predicted acid phosphatase activity	null	3.56308	3.43E-07	4.50E-06
AN5423	Ortholog of A. oryzae RIB40 : AO090003001412, Aspergillus flavus NRRL 3357 : AFL2T_01664, Aspergillus versicolor : Aspve1_0083396 and Aspergillus carbonarius ITEM 5010 : Acar5010_169601	null	-3.6194	3.53E-07	4.62E-06
AN4042	Putative C-22 sterol desaturase with a predicted role in sterol metabolism; putative cytochrome P450	CYP61A1	3.74248	3.56E-07	4.65E-06
AN0638	Ortholog of A. fumigatus Af293 : Afu1g16870, A. oryzae RIB40 : AO090005000988, A. niger ATCC 1015 : 170269-mRNA, Aspergillus versicolor : Aspve1_0119892 and Aspergillus sydowii : Aspsy1_0129541	null	-3.9693	3.58E-07	4.67E-06
AN1006	Nitrate reductase (NADPH) with a predicted role in nitrogen metabolism; transcript stabilized by intracellular nitrate, destabilized by glutamine; predicted NirA binding site in promoter; hypoxia downregulated	niaD	5.58173	3.60E-07	4.68E-06
AN9187	Putative F-box protein	null	5.56698	3.60E-07	4.68E-06
AN5303	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	null	-3.8012	3.64E-07	4.73E-06
AN5467	Ortholog of Aspergillus terreus NIH2624 : ATET_07601	null	4.90259	3.70E-07	4.79E-06

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AN12052	null	null	-4.5229	4.05E-07	5.23E-06
AN1124	Ortholog of A. fumigatus Af293 : Afu1g11720, A. niger CBS 513.88 : An08g03680, A. oryzae RIB40 : AO090038000251, A. niger ATCC 1015 : 208202-mRNA and Aspergillus versicolor : Aspve1_0288823	null	-3.7103	4.14E-07	5.35E-06
AN2228	Ortholog of A. fumigatus Af293 : Afu5g07200, A. niger CBS 513.88 : An17g00620, A. oryzae RIB40 : AO090701000236, A. niger ATCC 1015 : 45103-mRNA and Aspergillus versicolor : Aspve1_0124231	null	-7.6684	4.30E-07	5.54E-06
AN0495	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	null	4.01942	4.32E-07	5.56E-06
AN5746	Putative phosphopyruvate hydratase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; protein induced by farnesol	acuN	3.46932	4.33E-07	5.56E-06
AN1964	Ortholog of S. cerevisiae RPS6B and RPS6A; palA-dependent expression independent of pH	null	3.70849	4.41E-07	5.66E-06
AN0860	Ortholog of A. fumigatus Af293 : Afu1g15260, A. niger CBS 513.88 : An01g13370, A. oryzae RIB40 : AO090103000449, AO090005001207 and A. niger ATCC 1015 : 205440-mRNA	null	-3.6354	4.46E-07	5.71E-06
AN0688	Putative transketolase with a predicted role in the pentose-phosphate shunt or xylulose metabolism	null	3.55999	4.49E-07	5.74E-06
AN8903	Putative peptide transporter; transcript upregulated by nitrate limitation	null	-3.5224	4.55E-07	5.80E-06
AN0867	Ortholog of A. nidulans FGSC A4 : AN4122, AN2881, AN10123, A. fumigatus Af293 : Afu1g13860, Afu1g15180, Afu3g11650 and A. niger CBS 513.88 : An08g07010, An02g07440, An01g13480	null	-3.5406	4.59E-07	5.84E-06
AN1901	Putative sterol 14 alpha-demethylase with a predicted role in sterol metabolism	pdmA	3.55266	4.72E-07	6.00E-06
AN6593	Ortholog(s) have unfolded protein binding activity, role in aerobic respiration, mitochondrial respiratory chain complex IV assembly and integral to mitochondrial inner membrane localization	null	4.013	4.76E-07	6.04E-06
AN10130	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit localization	null	3.44499	4.80E-07	6.08E-06
AN7479	Putative asparaginyl-tRNA synthetase with a predicted role in tRNA charging for translation	null	3.6118	4.84E-07	6.12E-06
AN5204	Ortholog of A. fumigatus Af293 : Afu6g07370, A. niger CBS 513.88 : An07g09060, A. oryzae RIB40 : AO090005001564, Aspergillus versicolor : Aspve1_0154324 and Aspergillus sydowii : Aspsy1_0156764	null	-4.2849	4.99E-07	6.30E-06
AN1071	Has domain(s) with predicted ADP binding, ATP binding, microtubule motor activity, role in apoptotic process, nucleoside metabolic process and kinesin complex localization	null	-5.5752	5.13E-07	6.43E-06
AN4123	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	null	-7.6291	5.13E-07	6.43E-06
AN5700	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-7.6291	5.13E-07	6.43E-06

AN8891	Putative exopolygalacturonase	pgxB	-7.6291	5.13E-07	6.43E-06
AN6418	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.8775	5.13E-07	6.43E-06
AN8979	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	alcA	-3.6645	5.21E-07	6.52E-06
AN1298	Has domain(s) with predicted role in regulation of transcription, DNA-dependent and nucleus localization	null	-3.5573	5.35E-07	6.68E-06
AN3218	Ortholog of A. oryzae RIB40 : AO090701000492 and Aspergillus flavus NRRL 3357 : AFL2T_06113	null	-3.7432	5.51E-07	6.86E-06
AN10553	Has domain(s) with predicted cytochrome-c oxidase activity	null	3.85224	5.58E-07	6.94E-06
AN0370	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.1124	5.62E-07	6.96E-06
AN5583	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-5.1124	5.62E-07	6.96E-06
AN4793	Putative aspartate semialdehyde dehydrogenase with a predicted role in glycine, serine, and threonine metabolism	null	3.7516	5.68E-07	7.03E-06
AN3328	Has domain(s) with predicted GTP binding, nucleoside-triphosphatase activity	null	-3.7374	5.88E-07	7.27E-06
AN0856	Putative amino acid transporter; expression reduced after exposure to farnesol	null	3.53527	6.01E-07	7.41E-06
AN0903	Ortholog of A. fumigatus Af293 : Afu1g15690, A. niger CBS 513.88 : An01g14030, A. oryzae RIB40 : AO090005001138, A. niger ATCC 1015 : 172402-mRNA and Aspergillus versicolor : Aspve1_0049163	null	-5.5348	6.15E-07	7.57E-06
AN9003	Has domain(s) with predicted aspartic-type endopeptidase activity, zinc ion binding activity and role in proteolysis	null	-3.5622	6.23E-07	7.65E-06
AN1605	Ortholog of Aspergillus sydowii : Aspsy1_0679421	null	4.19115	6.31E-07	7.74E-06
AN3595	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	3.62515	6.35E-07	7.77E-06
AN4258	Putative kinase with a predicted role in nucleotide or phospholipid metabolism	null	3.60072	6.55E-07	8.01E-06
AN10544	Has domain(s) with predicted 3-dehydroquinate dehydratase activity and role in metabolic process	null	-4.038	6.90E-07	8.42E-06
AN7725	Protein required for biosynthesis of pyridoxine; highly conserved throughout fungi, plants and bacteria	pyroA	3.65868	7.18E-07	8.75E-06
AN8856	Ortholog(s) have RNA binding activity, role in ribosomal large subunit assembly and cytosol localization	null	3.41046	7.32E-07	8.91E-06
AN1941	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-5.0485	7.52E-07	9.13E-06
AN6912	Ortholog of A. fumigatus Af293 : Afu5g13610, A. niger CBS 513.88 : An14g05140, A. niger ATCC 1015 : 127881-mRNA, Aspergillus versicolor : Aspve1_0048190 and Aspergillus sydowii : Aspsy1_0075810	null	7.87203	7.52E-07	9.13E-06

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AN4576	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-3.6745	8.34E-07	1.01E-05
AN7907	Putative glyoxylate-bleomycin resistance protein; member of the F9775 secondary metabolite gene cluster	null	-3.9859	8.41E-07	1.02E-05
AN10313	Ortholog(s) have role in ER to Golgi vesicle-mediated transport, Golgi to endosome transport and ER to Golgi transport vesicle, Golgi membrane, endoplasmic reticulum localization	null	7.85249	8.73E-07	1.05E-05
AN5355	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	null	7.85249	8.73E-07	1.05E-05
AN1246	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	pgkA	3.35763	8.82E-07	1.06E-05
AN3954	Putative phosphogluconate dehydrogenase (decarboxylating) with a predicted role in the pentose-phosphate shunt	null	3.45675	8.88E-07	1.07E-05
AN5765	Ortholog of A. fumigatus Af293 : Afu2g09480, A. oryzae RIB40 : AO090011000718, N. fischeri NRRL 181 : NFIA_084970, Aspergillus flavus NRRL 3357 : AFL2T_05450 and Aspergillus versicolor : Aspve1_0072730	null	-7.5471	8.91E-07	1.07E-05
AN8752	Ortholog of A. fumigatus Af293 : Afu6g02845, A. niger CBS 513.88 : An12g07700, Aspergillus versicolor : Aspve1_0086213, Aspergillus sydowii : Aspsy1_0092097 and Aspergillus terreus NIH2624 : ATET_07166	null	-5.4932	8.91E-07	1.07E-05
AN5819	Ortholog(s) have GTP binding, signal recognition particle binding activity, role in protein targeting to ER and integral to endoplasmic reticulum membrane localization	null	3.40959	8.99E-07	1.07E-05
AN4013	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-3.9705	9.04E-07	1.08E-05
AN11181	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	null	-3.7212	9.32E-07	1.11E-05
AN4019	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.771	9.53E-07	1.13E-05
AN8127	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.3909	9.53E-07	1.13E-05
AN10475	Ortholog(s) have cytosol localization	null	3.53834	9.57E-07	1.13E-05
AN7668	Ortholog(s) have methionine-R-sulfoxide reductase activity, role in cellular response to oxidative stress and cytoplasm, nucleus localization	null	4.7411	9.61E-07	1.14E-05
AN1662	Ortholog(s) have cytosol, nucleus, ribosome localization	null	3.68369	9.91E-07	1.17E-05

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AN7708	Ortholog(s) have alditol:NADP+ 1-oxidoreductase activity, role in D-xylose catabolic process, arabinose catabolic process, cellular response to oxidative stress and cytosol, nucleus localization	null	3.38599	9.99E-07	1.18E-05
AN11574	null	null	7.81259	1.02E-06	1.19E-05
AN6821	Ortholog of Aspergillus sydowii : Aspsy1_0091668	null	7.81259	1.02E-06	1.19E-05
AN8132	Has domain(s) with predicted metalloendopeptidase activity, zinc ion binding activity, role in proteolysis and extracellular matrix localization	null	7.81259	1.02E-06	1.19E-05
AN10568	null	null	3.49372	1.02E-06	1.20E-05
AN3024	Ortholog of A. fumigatus Af293 : Afu3g08880, A. oryzae RIB40 : AO090005001351, N. fischeri NRRL 181 : NFIA_068240, A. clavatus NRRL 1 : ACLA_036860 and Aspergillus versicolor : Aspve1_0039444	null	-3.971	1.03E-06	1.20E-05
AN10182	Putative translation initiation factor 3, subunit f (eIF-3f); expression reduced after exposure to farnesol	null	3.49166	1.03E-06	1.20E-05
AN10903	Ortholog(s) have guanine deaminase activity and cytosol localization	null	-3.5768	1.07E-06	1.25E-05
AN1756	Ortholog of A. fumigatus Af293 : Afu6g08950, A. niger ATCC 1015 : 48025-mRNA, Aspergillus versicolor : Aspve1_0025102, Aspergillus sydowii : Aspsy1_0138552 and Aspergillus brasiliensis : Aspbr1_0254359	null	-7.5042	1.08E-06	1.25E-05
AN2674	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.4503	1.08E-06	1.25E-05
AN2677	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	null	-7.5042	1.08E-06	1.25E-05
AN3530	Ortholog of A. nidulans FGSC A4 : AN2658, A. fumigatus Af293 : Afu1g13760, Afu4g00490, Afu4g14350, A. niger CBS 513.88 : An09g01580, A. oryzae RIB40 : AO090166000071 and A. niger ATCC 1015 : 188861-mRNA	null	-7.5042	1.08E-06	1.25E-05
AN8092	Ortholog of Aspergillus versicolor : Aspve1_0034535, Aspergillus sydowii : Aspsy1_0038908, Aspsy1_0527520 and Aspergillus terreus NIH2624 : ATET_08397	null	-7.5042	1.08E-06	1.25E-05
AN9028	Has domain(s) with predicted catalytic activity, coenzyme binding, nucleotide binding activity and role in cellular metabolic process	null	-7.5042	1.08E-06	1.25E-05
AN1972	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.5308	1.08E-06	1.25E-05
AN12307	Ortholog of A. nidulans FGSC A4 : AN4261, A. fumigatus Af293 : Afu5g13200, Afu7g03960, A. oryzae RIB40 : AO090020000704, AO090026000818 and A. niger ATCC 1015 : 44684-mRNA	null	-4.7431	1.08E-06	1.25E-05
AN2997	Ortholog(s) have role in cellular response to osmotic stress, translational initiation	null	3.48071	1.10E-06	1.27E-05
AN6039	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	3.96226	1.14E-06	1.32E-05
AN8275	Mitochondrial citrate synthase with a predicted role in the TCA cycle	citA	3.32656	1.15E-06	1.32E-05

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AN6642	Putative potassium-transporting ATPase with a predicted role in energy metabolism; locus contains the conserved upstream open reading frames (uORFs) AN6642-uORF and AN6642-uORF.2	enaA	-3.777	1.22E-06	1.40E-05
AN8256	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	3.5403	1.22E-06	1.40E-05
AN1952	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	null	-3.4498	1.28E-06	1.46E-05
AN10165	Has domain(s) with predicted outer membrane localization	null	-7.4601	1.31E-06	1.48E-05
AN3881	Has domain(s) with predicted ADP binding, ATP binding, nucleoside-triphosphatase activity and role in apoptotic process, nucleoside metabolic process	null	-5.4062	1.31E-06	1.48E-05
AN4922	Ortholog of A. fumigatus Af293 : Afu3g10670, A. niger CBS 513.88 : An02g06330, A. oryzae RIB40 : AO090003000612, A. niger ATCC 1015 : 120930-mRNA and Aspergillus versicolor : Aspve1_0129208	null	-7.4601	1.31E-06	1.48E-05
AN5564	Putative phosphatidyl synthase; intracellular, menadione stress-induced protein; transcript and protein upregulated after exposure to farnesol	null	3.77722	1.31E-06	1.48E-05
AN8346	Ortholog(s) have role in cellular cadmium ion homeostasis, cellular response to cadmium ion, regulation of sulfur metabolic process and mitochondrion localization	null	4.25191	1.31E-06	1.48E-05
AN0418	Putative high-affinity urea/H+ symporter; regulated by nitrogen catabolite repression; transcript upregulated by nitrate limitation	ureA	4.07224	1.31E-06	1.49E-05
AN11985	Ortholog of A. fumigatus Af293 : Afu3g01210, A. niger CBS 513.88 : An01g10950, A. oryzae RIB40 : AO090026000081, A. niger ATCC 1015 : 46404-mRNA and Aspergillus versicolor : Aspve1_0088529	null	3.36355	1.32E-06	1.49E-05
AN0870	Putative transporter with a predicted role in small molecule transport	null	3.8468	1.32E-06	1.49E-05
AN4777	Ortholog(s) have structural constituent of ribosome activity	null	3.32414	1.33E-06	1.49E-05
AN12449	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	null	-3.6607	1.34E-06	1.51E-05
AN11751	null	null	7.77155	1.38E-06	1.55E-05
AN4259	Ortholog(s) have role in translational initiation and cytosol, eukaryotic 43S preinitiation complex, eukaryotic translation initiation factor 3 complex, eIF3m, nucleus localization	null	7.77155	1.38E-06	1.55E-05
AN8098	null	null	7.75059	1.38E-06	1.55E-05
AN11411	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus localization	null	3.43256	1.39E-06	1.55E-05
AN4201	Putative acyl-CoA synthetase/AMP-binding domain protein	null	-3.6576	1.39E-06	1.56E-05

AN7169	NirA-dependent flavohemoprotein; required for nitrate and nitrite reductase enzyme activity, regulates sexual development; menadione stress-induced protein; induced by nitrate; palA-dependent, pH-independent expression	fhbA	3.67039	1.42E-06	1.58E-05
AN8953	Putative alpha-glucosidase with a predicted role in maltose metabolism; transcriptionally induced by isomaltose; induced by rapamycin-induced autophagy	agdB	3.38114	1.42E-06	1.58E-05
AN10714	Ortholog of A. fumigatus Af293 : Afu1g06650, A. oryzae RIB40 : AO090001000464, N. fischeri NRRL 181 : NFIA_018040, Aspergillus flavus NRRL 3357 : AFL2T_09110 and A. clavatus NRRL 1 : ACLA_027920	null	-3.533	1.44E-06	1.60E-05
AN6843	Mitochondrial ribosomal protein L4; this locus is reported to contain an upstream open reading frame (uORF)	null	3.41181	1.47E-06	1.63E-05
AN8399	Putative potassium-transporting ATPase with a predicted role in energy metabolism; transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	3.70794	1.50E-06	1.66E-05
AN6718	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	-3.7455	1.51E-06	1.67E-05
AN5853	Has domain(s) with predicted transferase activity, transferring acyl groups other than amino-acyl groups activity and role in metabolic process	null	-4.1626	1.55E-06	1.71E-05
AN4016	Possible pseudogene, similar to 60S ribosomal protein L40	null	3.27239	1.56E-06	1.72E-05
AN1428	Has domain(s) with predicted N-acetylglucosamine-6-phosphate deacetylase activity and role in N-acetylglucosamine metabolic process	null	-3.6377	1.58E-06	1.74E-05
AN2780	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	null	-5.3606	1.59E-06	1.75E-05
AN7826	Ortholog of Aspergillus versicolor : Aspve1_0045384 and Aspergillus sydowii : Aspsy1_0165058	null	-5.3606	1.59E-06	1.75E-05
AN4810	Has domain(s) with predicted metallocarboxypeptidase activity and role in proteolysis	null	-4.3054	1.61E-06	1.76E-05
AN11693	Ortholog of A. fumigatus Af293 : Afu3g08370, A. niger ATCC 1015 : 37428-mRNA, Aspergillus versicolor : Aspve1_0070387 and Aspergillus sydowii : Aspsy1_0066686	null	4.65303	1.69E-06	1.85E-05
AN5457	Putative oxidoreductase with a predicted role in energy metabolism; NADPH oxidase; involved in the generation of reactive oxygen species (ROS); mutation blocks cleistothecia formation; homology to p91phox	noxA	-3.7186	1.71E-06	1.87E-05
AN1637	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	hxB	-3.51	1.74E-06	1.89E-05
AN9384	Putative cytochrome P450 alkane hydroxylase	CYP584E1	-3.8524	1.74E-06	1.89E-05

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AN5916	Mitochondrial enoyl-CoA hydratase, involved in fatty acid beta-oxidation; required for growth on short-chain fatty acids and for catabolism of isoleucine and valine; transcription is induced by fatty acids	echA	-3.3551	1.74E-06	1.89E-05
AN1297	Ortholog(s) have role in Golgi to endosome transport and Golgi membrane, fungal-type vacuole membrane localization	null	-3.497	1.78E-06	1.93E-05
AN4323	Putative branched chain amino acid aminotransferase with a predicted role in valine, leucine, and isoleucine metabolism	null	3.39165	1.79E-06	1.94E-05
AN2932	Putative eukaryotic initiation factor 4A; expression reduced after exposure to farnesol	null	3.27462	1.81E-06	1.96E-05
AN8602	Ortholog of A. fumigatus Af293 : Afu2g00500, A. oryzae RIB40 : AO090023000371, Aspergillus versicolor : Aspve1_0031494 and Aspergillus sydowii : Aspsy1_0060228	null	4.19879	1.83E-06	1.98E-05
AN10845	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.6559	1.84E-06	1.98E-05
AN3396	Putative non-ribosomal peptide synthase (NRPS) responsible for microperfuranone biosynthesis; transcript repressed by nitrogen limitation	micA	5.28999	1.84E-06	1.98E-05
AN10614	Ortholog(s) have telomeric DNA binding, triplex DNA binding activity	null	3.31679	1.84E-06	1.98E-05
AN11212	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-7.4146	1.94E-06	2.09E-05
AN9069	Ortholog of A. fumigatus Af293 : Afu7g02500, A. niger CBS 513.88 : An12g00100, A. oryzae RIB40 : AO090038000626, A. niger ATCC 1015 : 56966-mRNA and Aspergillus versicolor : Aspve1_0144824	null	-3.6024	1.97E-06	2.11E-05
AN9075	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-3.6993	2.01E-06	2.15E-05
AN4500	Putative mitochondrial ATPase inhibitor; expression upregulated after exposure to farnesol	null	3.1957	2.22E-06	2.38E-05
AN1681	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.8752	2.23E-06	2.38E-05
AN1724	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.8752	2.23E-06	2.38E-05
AN4646	Ortholog of A. niger CBS 513.88 : An07g05420, Aspergillus brasiliensis : Aspbr1_0123980, A. niger ATCC 1015 : 39924-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_05197 and Aspergillus acidus : Aspfo1_0040987	null	7.6858	2.23E-06	2.38E-05
AN8041	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	gpdA	3.20808	2.28E-06	2.43E-05
AN0890	Ortholog(s) have fungal-type vacuole membrane localization	null	-3.2774	2.35E-06	2.50E-05

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AN8043	null	null	3.31607	2.47E-06	2.62E-05
AN0935	null	null	4.39617	2.49E-06	2.64E-05
AN4218	Ortholog(s) have GDP binding, GTP binding, translation elongation factor activity, role in tRNA export from nucleus, translational elongation and cytosol, mitochondrion, nucleus localization	null	3.21772	2.52E-06	2.67E-05
AN6558	Ortholog(s) have DNA-directed RNA polymerase activity and role in tRNA transcription from RNA polymerase III promoter, transcription from RNA polymerase I promoter	null	3.53488	2.54E-06	2.68E-05
AN1714	Ortholog of A. nidulans FGSC A4 : AN1718, A. fumigatus Af293 : Afu4g08380, Afu4g08420, A. niger CBS 513.88 : An04g03190, An04g03210 and A. oryzae RIB40 : AO090023000718	null	-4.8379	2.63E-06	2.76E-05
AN7144	Ortholog(s) have role in mitochondrial respiratory chain complex III assembly and mitochondrial matrix localization	null	7.64094	2.63E-06	2.76E-05
AN8338	Putative cytochrome P450	CYP671A1	-4.8379	2.63E-06	2.76E-05
AN1743	Putative methyltransferase with a predicted role in histidine metabolism	null	3.34178	2.63E-06	2.77E-05
AN0057	Ortholog(s) have cytosol localization	null	3.50246	2.74E-06	2.87E-05
AN4786	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	null	3.61076	2.76E-06	2.90E-05
AN6113	Has domain(s) with predicted catalytic activity and role in carbohydrate metabolic process	null	-4.5948	2.77E-06	2.90E-05
AN6789	null	null	5.23508	2.77E-06	2.90E-05
AN20006	Group I intron maturase encoded by the first exon and part of the intron of the mitochondrial cobA gene; facilitates the splicing of the cobA group I intron; also has DNA endonuclease activity	I-AniI	3.39173	2.84E-06	2.96E-05
AN0720	Putative diphthine synthase with a predicted role in methionine metabolism	null	3.94264	2.88E-06	3.00E-05
AN2272	Putative kinase with a predicted role in ribose metabolism or nucleotide salvage pathways	null	3.344	2.90E-06	3.02E-05
AN2567	Ortholog(s) have endoplasmic reticulum, mitochondrion localization	null	3.30086	2.93E-06	3.03E-05
AN3366	Ortholog of Aspergillus versicolor : Aspve1_0051963 and Aspergillus sydowii : Aspsy1_0088131	null	-7.3189	2.93E-06	3.03E-05
AN4529	Ortholog of A. niger CBS 513.88 : An07g07320, A. niger ATCC 1015 : 123881-mRNA, Aspergillus versicolor : Aspve1_0739308, Aspergillus sydowii : Aspsy1_1180454 and Aspergillus terreus NIH2624 : ATET_09597	null	-7.3189	2.93E-06	3.03E-05
AN5300	Putative aconitate hydratase with a predicted role in the TCA cycle	null	-7.3189	2.93E-06	3.03E-05
AN7986	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity and role in protein phosphorylation	null	-7.3189	2.93E-06	3.03E-05
AN0470	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	3.54636	3.01E-06	3.10E-05
AN2248	Putative 4-aminobutyrate transaminase, required for utilization of gamma-aminobutyric acid (GABA); transcriptionally regulated by AmdR	gatA	-3.467	3.04E-06	3.13E-05

AN0046	Putative histidyl-tRNA synthetase with a predicted role in tRNA aminoacylation; intracellular, menadione stress-induced protein; expression reduced after exposure to farnesol	null	3.1869	3.08E-06	3.17E-05
AN20004	Protein of unknown function, encoded on the mitochondrial genome; N terminus is similar to the transmembrane domain of Atp8p	URFA3	3.93217	3.12E-06	3.21E-05
AN1990	Putative homocitrate synthase with a predicted role in pyruvate metabolism	null	3.2993	3.19E-06	3.27E-05
AN12306	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	3.78052	3.34E-06	3.43E-05
AN3916	Putative glycerol kinase with a predicted role in glycerol metabolism	null	-3.3164	3.37E-06	3.45E-05
AN7271	null	null	-3.2652	3.40E-06	3.48E-05
AN4020	Has domain(s) with predicted membrane localization	null	3.17192	3.43E-06	3.50E-05
AN2968	Putative inorganic diphosphatase with a predicted role in energy metabolism; intracellular; protein abundance decreased by menadione stress; protein expressed at increased levels during osmoadaptation	ippA	3.77207	3.57E-06	3.64E-05
AN0539	Ortholog of Aspergillus acidus : Aspfo1_0142555	null	-7.2686	3.63E-06	3.68E-05
AN8357	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	null	-7.2686	3.63E-06	3.68E-05
AN8503	Ortholog of A. niger CBS 513.88 : An13g03080, Aspergillus brasiliensis : Aspbr1_0044529, Aspergillus flavus NRRL 3357 : AFL2T_10601 and Aspergillus acidus : Aspfo1_0328979	null	-7.2686	3.63E-06	3.68E-05
AN5036	Ortholog(s) have endoplasmic reticulum localization	null	-4.5309	3.68E-06	3.72E-05
AN8977	Putative gluconolactonase with a predicted role in gluconic acid and gluconate metabolism; transcript upregulated by exposure to ethanol	alcP	-4.5309	3.68E-06	3.72E-05
AN6297	Ortholog(s) have copper ion binding activity, role in aerobic respiration, protein complex assembly and mitochondrial inner membrane, mitochondrial ribosome localization	null	4.0863	3.70E-06	3.73E-05
AN10740	Ortholog(s) have cytosol localization	null	3.14437	3.70E-06	3.74E-05
AN6095	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.296	3.71E-06	3.74E-05
AN11347	Ortholog(s) have cytochrome-c oxidase activity, role in mitochondrial electron transport, cytochrome c to oxygen and mitochondrial respiratory chain complex IV localization	null	3.25874	3.81E-06	3.84E-05
AN5935	Has domain(s) with predicted transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	3.26934	3.82E-06	3.84E-05
AN5843	Putative pyruvate, water dikinase	pdkA	4.50994	3.95E-06	3.96E-05

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AN1510	Ortholog(s) have protein disulfide oxidoreductase activity, thiol oxidase activity, role in protein thiol-disulfide exchange and endoplasmic reticulum membrane localization	null	3.16722	4.00E-06	4.01E-05
AN8277	Putative bifunctional enzyme with a predicted role in methionine metabolism; O-acetlylhomoserine (homocysteine synthase)	cysD	3.11318	4.01E-06	4.01E-05
AN6405	Has domain(s) with predicted cation binding, lysozyme activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, peptidoglycan catabolic process	null	3.66608	4.08E-06	4.08E-05
AN10585	Ortholog(s) have cytochrome-c oxidase activity, enzyme regulator activity, role in aerobic respiration, mitochondrial respiratory chain supercomplex assembly and mitochondrial respiratory chain complex IV localization	null	3.20689	4.10E-06	4.09E-05
AN4569	Ortholog(s) have role in ubiquinone biosynthetic process and mitochondrial inner membrane localization	null	3.19407	4.12E-06	4.11E-05
AN5021	Has domain(s) with predicted role in biosynthetic process	null	3.17815	4.14E-06	4.12E-05
AN7208	SET domain protein; protein levels decrease in response to farnesol	null	3.58655	4.22E-06	4.20E-05
AN2873	Putative saccharopine dehydrogenase (NAD+, L-lysine-forming) with a predicted role in lysine metabolism	lysA	3.1893	4.23E-06	4.20E-05
AN0240	Putative transaldolase with a predicted role in the pentose-phosphate shunt; intracellular, menadione stress-induced protein; protein induced by farnesol	pppA	3.18771	4.29E-06	4.25E-05
AN20003	Ortholog(s) have endonuclease activity	null	7.54679	4.36E-06	4.31E-05
AN5616	Ortholog(s) have cytosol, nucleus localization	null	7.54679	4.36E-06	4.31E-05
AN3559	Ortholog of Aspergillus brasiliensis : Aspbr1_0209810, Aspergillus versicolor : Aspve1_0043449, Aspergillus sydowii : Aspsy1_0176892 and Aspergillus aculeatus ATCC16872 : Aacu16872_044955	null	-3.729	4.43E-06	4.38E-05
AN11795	Has domain(s) with predicted acyl-CoA hydrolase activity and role in acyl-CoA metabolic process	null	4.47612	4.48E-06	4.41E-05
AN7323	Covalently-bound cell wall protein; predicted glycosyl phosphatidylinositol (GPI)-anchor	null	4.47612	4.48E-06	4.41E-05
AN11062	Ortholog(s) have role in mitochondrial genome maintenance and cytosol, mitochondrial matrix, nucleus localization	null	-3.9737	4.53E-06	4.46E-05
AN10174	Ortholog of A. fumigatus Af293 : Afu1g10090, A. oryzae RIB40 : AO090038000427, A. niger ATCC 1015 : 52788-mRNA, Aspergillus sydowii : Aspsy1_0139584 and Aspergillus terreus NIH2624 : ATET_00177	null	3.32738	4.57E-06	4.49E-05
AN5508	Putative G-protein coupled receptor	gprN	-4.1177	4.92E-06	4.83E-05
AN1870	Putative beta-1,4-xylosidase	null	-3.3942	4.93E-06	4.83E-05
AN5626	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	facA	-3.0698	4.97E-06	4.87E-05

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AN7822	Ortholog of A. fumigatus Af293 : Afu5g00770, Aspergillus brasiliensis : Aspbr1_0058805, N. fischeri NRRL 181 : NFIA_041410, Aspergillus flavus NRRL 3357 : AFL2T_07218 and A. clavatus NRRL 1 : ACLA_004530	null	-3.9056	4.98E-06	4.87E-05
AN12213	Ortholog(s) have ubiquinol-cytochrome-c reductase activity, role in aerobic respiration, mitochondrial electron transport, ubiquinol to cytochrome c and mitochondrial respiratory chain complex III localization	null	3.19304	5.08E-06	4.96E-05
AN9403	Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism	pdhC	3.08316	5.15E-06	5.02E-05
AN12015	null	null	-4.7199	5.19E-06	5.05E-05
AN7779	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	7.52226	5.19E-06	5.05E-05
AN6255	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	3.11495	5.21E-06	5.06E-05
AN0840	Putative alpha-isopropylmalate synthase with a predicted role in valine, leucine, and isoleucine metabolism	null	3.3401	5.22E-06	5.07E-05
AN0884	Ortholog of A. fumigatus Af293 : Afu1g15560, A. niger CBS 513.88 : An01g13780, A. oryzae RIB40 : AO090005001164, A. niger ATCC 1015 : 171062-mRNA and Aspergillus versicolor : Aspve1_0049145	null	3.55217	5.24E-06	5.07E-05
AN11337	Ortholog of A. niger CBS 513.88 : An18g01250, Aspergillus brasiliensis : Aspbr1_0322983, Aspergillus acidus : Aspfo1_0209416 and Aspergillus versicolor : Aspve1_0038289	null	3.55217	5.24E-06	5.07E-05
AN5155	Ortholog(s) have cytosol, nucleus localization	null	3.70266	5.37E-06	5.18E-05
AN7204	Putative oleoyl-delta12 desaturase	an2	3.70266	5.37E-06	5.18E-05
AN1902	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	null	-3.1117	5.41E-06	5.21E-05
AN12027	Ortholog(s) have cytosol, nucleus localization	null	-3.4355	5.43E-06	5.23E-05
AN8118	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	3.50054	5.52E-06	5.31E-05
AN0708	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	aromA	3.54519	5.54E-06	5.31E-05
AN7228	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-3.0736	5.59E-06	5.35E-05
AN12487	null	null	-7.2165	5.61E-06	5.35E-05
AN7817	Putative protein with a predicted role in sterigmatocystin/aflatoxin biosynthesis	null	-7.2165	5.61E-06	5.35E-05
AN8999	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin hydrolysis	null	-7.2165	5.61E-06	5.35E-05
AN3226	HAS domain protein; protein levels decrease in response to farnesol	null	3.07426	5.79E-06	5.52E-05

AN6900	Putative triose-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; protein induced by farnesol	tpiA	3.17889	5.84E-06	5.56E-05
AN8544	Ortholog of Aspergillus versicolor : Aspve1_0033877 and Aspergillus sydowii : Aspsy1_0466900	null	3.2857	5.87E-06	5.58E-05
AN6535	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-3.1812	6.00E-06	5.69E-05
AN1402	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	null	-3.1132	6.00E-06	5.69E-05
AN6644	Putative bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase, enzyme of the biotin biosynthesis pathway; common mutation in laboratory strains	biA	3.17052	6.01E-06	5.69E-05
AN0807	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	laeA	-3.5132	6.17E-06	5.83E-05
AN9433	Ortholog of A. fumigatus Af293 : Afu4g07600, A. niger CBS 513.88 : An04g01960, A. niger ATCC 1015 : 190605-mRNA, Aspergillus versicolor : Aspve1_0743999 and Aspergillus sydowii : Aspsy1_0062370	null	3.77906	6.49E-06	6.13E-05
AN7661	Ortholog(s) have RNA polymerase II core promoter proximal region sequence-specific DNA binding, sterol response element binding activity	null	3.10477	6.50E-06	6.14E-05
AN2879	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	null	-3.3357	6.54E-06	6.15E-05
AN6842	Putative ortholog of S. cerevisiae Mrpl35p which is a mitochondrial large ribosomal subunit; expression reduced after exposure to farnesol	null	3.51695	6.54E-06	6.15E-05
AN1397	Putative cytochrome P450 monooxygenase involved in the catabolism of aromatic compounds; transcript induced by phenylacetate and repressed by glucose	phacB	-3.1944	6.54E-06	6.15E-05
AN4172	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	null	-3.9752	6.60E-06	6.19E-05
AN4842	Ortholog(s) have copper ion binding activity, role in copper ion transport, protein complex assembly and mitochondrial inner membrane localization	null	3.32234	6.60E-06	6.19E-05
AN3369	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	null	-4.4295	6.64E-06	6.21E-05
AN3034	Suppressor of prgA1 mutation; involved in regulation of penicillin biosynthesis; null mutation results in decreased expression of ipnA and acvA, and reduced penicillin production	suAprgA1	3.20574	6.64E-06	6.21E-05

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AN6338	Putative aromatic-amino-acid transaminase with a predicted role in aromatic amino acid biosynthesis	null	-3.0619	6.66E-06	6.22E-05
AN8219	Putative plasma membrane ATPase with a predicted role in energy metabolism	null	-3.6415	6.68E-06	6.23E-05
AN2936	Putative Class 2C alpha-mannosidase with a predicted role in mannose polymer metabolism	null	-3.0574	6.73E-06	6.27E-05
AN8943	Ortholog of A. fumigatus Af293 : Afu2g00900, Afu6g11560, A. niger CBS 513.88 : An01g11690, An05g02420, An03g01300 and A. oryzae RIB40 : AO090113000175, AO090023000422	null	3.31264	6.85E-06	6.38E-05
AN6909	Putative bestrophin-like protein; similar to plasma membrane anion channels	BEST2	-3.1367	6.98E-06	6.45E-05
AN10555	Has domain(s) with predicted nucleic acid binding activity	null	7.05958	7.02E-06	6.45E-05
AN11281	Ortholog of A. fumigatus Af293 : Afu3g01196, Aspergillus sydowii : Aspsy1_0281282, Aspergillus terreus NIH2624 : ATET_06475 and Aspergillus carbonarius ITEM 5010 : Acar5010_212232	null	7.05958	7.02E-06	6.45E-05
AN12170	Ortholog of Aspergillus carbonarius ITEM 5010 : Acar5010_128508 and Aspergillus aculeatus ATCC16872 : Aacu16872_031140	null	-7.1624	7.02E-06	6.45E-05
AN1526	Ortholog(s) have cytosol localization	null	7.05958	7.02E-06	6.45E-05
AN1725	Ortholog of S. cerevisiae : YEL023C, A. fumigatus Af293 : Afu2g14400, A. niger CBS 513.88 : An12g01310, An02g00780, A. oryzae RIB40 : AO090012000862, AO090023000064 and A. niger ATCC 1015 : 133532-mRNA	null	-7.1624	7.02E-06	6.45E-05
AN3322	Ortholog of A. fumigatus Af293 : Afu5g14570, N. fischeri NRRL 181 : NFIA_072390 and A. fumigatus A1163 : AFUB_062250	null	-7.1624	7.02E-06	6.45E-05
AN3991	Putative unsaturated glucuronyl hydrolase; transcript upregulated by nitrate limitation	null	-7.1624	7.02E-06	6.45E-05
AN4338	Ortholog of A. niger ATCC 1015 : 203785-mRNA, N. fischeri NRRL 181 : NFIA_109840, A. clavatus NRRL 1 : ACLA_045620, Aspergillus versicolor : Aspve1_0755913 and Aspergillus sydowii : Aspsy1_0540484	null	-7.1624	7.02E-06	6.45E-05
AN8147	Ortholog of A. nidulans FGSC A4 : AN1625, A. fumigatus Af293 : Afu3g01080, Afu3g12760, A. niger CBS 513.88 : An02g08740 and A. oryzae RIB40 : AO090012000846, AO090023000643	null	-5.1085	7.02E-06	6.45E-05
AN7011	Ortholog of A. fumigatus Af293 : Afu4g04318, A. niger CBS 513.88 : An14g00530, A. niger ATCC 1015 : 210876-mRNA, Aspergillus versicolor : Aspve1_0339449 and Aspergillus sydowii : Aspsy1_0184132	null	-3.2196	7.14E-06	6.55E-05
AN10399	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.3845	7.17E-06	6.56E-05
AN0016	Putative nonribosomal peptide synthase	null	-3.8959	7.18E-06	6.56E-05
AN5333	Putative pectate lyase, involved in degradation of pectin	plyC	-3.8959	7.18E-06	6.56E-05
AN3296	Has domain(s) with predicted 2 iron, 2 sulfur cluster binding, oxidoreductase activity and role in oxidation-reduction process	null	7.47191	7.42E-06	6.77E-05
AN7131	Putative cytochrome P450	CYP52H1	-4.6783	7.42E-06	6.77E-05
AN6794	null	null	4.38793	7.53E-06	6.86E-05

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AN8019	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	3.55494	7.73E-06	7.02E-05
AN7590	Putative reductase with a predicted role in carbohydrate metabolism; mannitol 2-dehydrogenase; intracellular, menadione stress-induced protein; HapX-regulated; protein induced by farnesol	null	-3.1027	7.73E-06	7.02E-05
AN2964	Putative pyruvate dehydrogenase complex component	pdhX	3.95151	7.81E-06	7.08E-05
AN8242	Putative lipase	null	-3.624	7.81E-06	7.08E-05
AN1181	Putative transporter with a predicted role in small molecule transport; ammonium permease	mepA	3.76529	7.97E-06	7.22E-05
AN5948	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-3.2639	8.07E-06	7.30E-05
AN11278	Ortholog(s) have role in cristae formation and integral to mitochondrial inner membrane, mitochondrial crista junction localization	null	3.1454	8.11E-06	7.32E-05
AN1614	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	3.74938	8.14E-06	7.35E-05
AN10548	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	null	-3.461	8.20E-06	7.38E-05
AN6306	Ortholog(s) have protein transporter activity, role in protein import into mitochondrial inner membrane and cytosol, mitochondrial intermembrane space protein transporter complex, nucleus localization	null	3.54103	8.20E-06	7.38E-05
AN7459	Putative hexokinase with a predicted role in carbohydrate metabolism	hxkA	3.06554	8.35E-06	7.50E-05
AN6556	Ortholog(s) have mRNA binding activity	null	4.36963	8.60E-06	7.71E-05
AN3295	Ortholog of A. fumigatus Af293 : Afu8g00470, A. oryzae RIB40 : AO090010000638, A. niger ATCC 1015 : 212733-mRNA, Aspergillus versicolor : Aspve1_0044578 and Aspergillus sydowii : Aspsy1_0207819	null	3.9386	8.60E-06	7.71E-05
AN8135	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity and role in metabolic process	null	3.9386	8.60E-06	7.71E-05
AN2866	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.286	8.67E-06	7.76E-05
AN3855	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-3.3577	8.71E-06	7.78E-05
AN6885	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	null	-3.4616	8.77E-06	7.82E-05
AN10332	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	7.02508	8.83E-06	7.82E-05
AN1300	Putative cytochrome P450; possibly a pseudogene	CYP548G2P	-7.1062	8.83E-06	7.82E-05
AN1597	Ortholog of N. fischeri NRRL 181 : NFIA_009820	null	7.02508	8.83E-06	7.82E-05
AN1604	Putative alpha-1,3-glucanase; predicted glycosyl phosphatidylinositol (GPI)-anchor	agnE	-7.1062	8.83E-06	7.82E-05

AN6321	Putative cytochrome P450	CYP656A1	-7.1062	8.83E-06	7.82E-05
AN8453	Protein with pectate lyase activity, involved in degradation of pectin	plyH	-7.1062	8.83E-06	7.82E-05
AN5132	Ortholog(s) have guanine nucleotide transmembrane transporter activity, role in cellular iron ion homeostasis, guanine nucleotide transport, mitochondrial genome maintenance, transmembrane transport and mitochondrion localization	null	3.22228	8.90E-06	7.87E-05
AN4909	null	null	-4.6354	8.90E-06	7.87E-05
AN1855	Has domain(s) with predicted phosphoric diester hydrolase activity and role in lipid metabolic process	null	3.19516	8.96E-06	7.91E-05
AN12152	Ortholog(s) have 4-hydroxybenzoate octaprenyltransferase activity, antioxidant activity and role in polyprenol biosynthetic process, ubiquinone biosynthetic process	null	5.01367	9.02E-06	7.95E-05
AN7214	Has domain(s) with predicted oxidoreductase activity	null	3.02189	9.11E-06	8.02E-05
AN4923	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	null	3.71907	9.50E-06	8.36E-05
AN6146	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	4.3323	9.85E-06	8.65E-05
AN6934	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	4.35109	9.85E-06	8.65E-05
AN1263	Putative adenosylhomocysteinase with a predicted role in methionine metabolism; expression reduced after exposure to farnesol	null	3.17703	1.00E-05	8.81E-05
AN12335	Protein with an acyl-CoA dehydrogenase domain	acdA	-3.0339	1.04E-05	9.10E-05
AN10910	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	null	3.13293	1.04E-05	9.10E-05
AN1429	Putative choline oxidase; intracellular, menadione stress-induced protein	codA	4.13887	1.04E-05	9.10E-05
AN3605	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.7867	1.04E-05	9.10E-05
AN9446	Putative pantothenate kinase with a predicted role in Coenzyme A and pantothenate biosynthesis	panK	3.72946	1.04E-05	9.10E-05
AN10746	MOSC-domain containing protein; transcript repressed by nitrate	null	-3.9775	1.05E-05	9.16E-05
AN5885	Putative catalytic subunit of the alpha-1,3 glucan synthase complex; locus contains the conserved upstream open reading frame (uORF) AN5885-uORF	agsA	-4.3576	1.05E-05	9.16E-05
AN6404	Has domain(s) with predicted zinc ion binding activity	null	-3.9775	1.05E-05	9.16E-05
AN2526	Putative ketol-acid reductoisomerase with a predicted role in Coenzyme A and pantothenate biosynthesis or amino acid metabolism	null	7.39294	1.07E-05	9.29E-05

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AN4177	Has domain(s) with predicted catalytic activity, coenzyme binding, nucleotide binding activity and role in cellular metabolic process	null	-4.5913	1.07E-05	9.29E-05
AN7498	Ortholog(s) have deoxyhypusine monooxygenase activity, role in microtubule cytoskeleton organization, microtubule-based movement, mitochondrion distribution, peptidyl-lysine modification to hypusine and cytosol, nucleus localization	null	3.20181	1.08E-05	9.34E-05
AN2682	Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process	null	3.23256	1.10E-05	9.48E-05
AN0034	Putative glycerone kinase with a predicted role in glycerol metabolism; transcript upregulated by growth in glycerol	null	-3.0615	1.10E-05	9.50E-05
AN0574	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.1005	1.11E-05	9.59E-05
AN1593	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	null	6.98973	1.12E-05	9.61E-05
AN10487	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.8825	1.13E-05	9.72E-05
AN2343	Putative nitroreductase; intracellular, menadione stress-induced protein	null	3.13536	1.13E-05	9.72E-05
AN6470	Protein with lysozyme activity, involved in carbohydrate catabolism	null	-3.1391	1.15E-05	9.87E-05
AN10803	Ortholog of Aspergillus brasiliensis : Aspbr1_0204155, Aspergillus flavus NRRL 3357 : AFL2T_06924, Aspergillus acidus : Aspfo1_0055346 and Aspergillus versicolor : Aspve1_0130960	null	3.03338	1.16E-05	9.95E-05
AN5734	Putative MFS-type quinate transporter	null	-3.7617	1.16E-05	9.97E-05
AN12443	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	null	-3.094	1.17E-05	0.0001
AN11303	Ortholog(s) have proton-transporting ATPase activity, rotational mechanism, structural molecule activity and role in ATP synthesis coupled proton transport, cristae formation, protein oligomerization	null	3.03785	1.19E-05	0.000101
AN8763	Ortholog of A. fumigatus Af293 : Afu6g02960, A. niger CBS 513.88 : An12g07520, A. niger ATCC 1015 : 201966-mRNA, Aspergillus versicolor : Aspve1_0054921 and Aspergillus sydowii : Aspsy1_0387317	null	3.02876	1.21E-05	0.000103
AN2424	Has domain(s) with predicted beta-N-acetylhexosaminidase activity, cation binding activity and role in carbohydrate metabolic process	null	-3.5274	1.23E-05	0.000105
AN10489	FKBP-type peptidyl-prolyl cis-trans isomerase; expression reduced after exposure to farnesol	FKBP5	3.07495	1.23E-05	0.000105
AN7950	Putative glucan endo-1,3-beta-D-glucosidase with predicted role in degradation of glucans; glycosyl phosphatidylinositol (GPI)-linked protein	eglC	3.06159	1.24E-05	0.000105
AN3901	Putative lactic acid dehydrogenase with a predicted role in energy metabolism	null	-4.3203	1.24E-05	0.000105

AN4196	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity and role in protein phosphorylation	null	-4.3203	1.24E-05	0.000105
AN9031	Has domain(s) with predicted catalytic activity and role in metabolic process	null	4.94688	1.24E-05	0.000105
AN9042	Putative alpha-1,3-glucanase	agnC	-3.9402	1.24E-05	0.000105
AN7269	Ortholog(s) have role in secondary metabolic process	null	-3.2364	1.24E-05	0.000105
AN0311	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	null	-2.9968	1.26E-05	0.000106
AN2547	Putative polyketide synthase; required for emericellamide biosynthesis	easB	-3.2293	1.27E-05	0.000107
AN1628	Putative membrane ATPase with a predicted role in energy metabolism	enaB	-3.0043	1.28E-05	0.000108
AN3902	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-3.8502	1.30E-05	0.000109
AN0051	Putative dioxygenase	null	-3.7853	1.31E-05	0.00011
AN1162	Ortholog(s) have guanyl-nucleotide exchange factor activity and cytosol, eukaryotic translation elongation factor 1 complex localization	null	2.9538	1.35E-05	0.000114
AN8366	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.0105	1.38E-05	0.000116
AN20019	Subunit II of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; one of three mitochondrially-encoded subunits	oxiB	2.94138	1.39E-05	0.000117
AN10619	Has domain(s) with predicted carboxy-lyase activity, pyridoxal phosphate binding activity and role in carboxylic acid metabolic process	null	3.8449	1.42E-05	0.000117
AN5610	Putative L-aminoadipate-semialdehyde dehydrogenase with a predicted role in lysine metabolism	null	3.33462	1.42E-05	0.000117
AN10005	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-7.0478	1.42E-05	0.000117
AN11197	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-4.9939	1.42E-05	0.000117
AN12291	Ortholog of A. nidulans FGSC A4 : AN8528, A. fumigatus Af293 : Afu5g09790, A. niger CBS 513.88 : An15g05030, A. oryzae RIB40 : AO090010000330 and A. niger ATCC 1015 : 53484-mRNA	null	-4.9939	1.42E-05	0.000117
AN2957	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	null	-7.0478	1.42E-05	0.000117
AN5149	Ortholog of A. fumigatus Af293 : Afu6g07200, A. niger CBS 513.88 : An07g09260, A. oryzae RIB40 : AO090005001581, A. niger ATCC 1015 : 39654-mRNA and Aspergillus versicolor : Aspve1_0176077	null	-7.0478	1.42E-05	0.000117
AN6683	Ortholog of A. nidulans FGSC A4 : AN8537, AN5260, A. fumigatus Af293 : Afu4g06200 and A. niger CBS 513.88 : An12g04370, An11g06510, An14g01260	null	-7.0478	1.42E-05	0.000117

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AN7557	Has domain(s) with predicted transporter activity, role in transmembrane transport and membrane localization	null	6.9535	1.42E-05	0.000117
AN8037	null	null	6.91633	1.42E-05	0.000117
AN8265	null	null	6.91633	1.42E-05	0.000117
AN11123	Putative transmenbrane-containing nuclear pore complex protein with homology to Schizosaccharomyces pombe Pom34	pom34	4.07832	1.45E-05	0.00012
AN3973	Putative peroxiredoxin	null	4.09369	1.45E-05	0.00012
AN2019	Ortholog of A. oryzae RIB40 : AO090011000511, A. niger ATCC 1015 : 37117-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_05272 and Aspergillus sydowii : Aspsy1_0046222	null	-3.4985	1.51E-05	0.000125
AN4841	Putative molybdopterin synthase large subunit involved in molybdenum cofactor biosynthesis; molybdopterin cofactor required for the activity of nitrate reductase	cnxH	3.16832	1.52E-05	0.000125
AN1045	Has domain(s) with predicted RNA binding, nucleotide binding activity, role in RNA processing and nucleus, ribonucleoprotein complex localization	null	3.27392	1.52E-05	0.000125
AN3832	Ortholog(s) have role in mitochondrial translation and mitochondrion localization	null	3.08763	1.53E-05	0.000126
AN9355	Has domain(s) with predicted protein tyrosine phosphatase activity and role in dephosphorylation	null	7.30939	1.57E-05	0.000129
AN4652	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and large ribosomal subunit localization	null	3.01607	1.57E-05	0.000129
AN5604	Putative fructose-bisphosphatase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; expression upregulated after exposure to farnesol	acuG	-2.9988	1.60E-05	0.000131
AN6061	Has domain(s) with predicted role in response to stress	null	3.07638	1.62E-05	0.000132
AN4762	Ortholog(s) have mitochondrion localization	null	3.02776	1.66E-05	0.000136
AN1276	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.7563	1.68E-05	0.000137
AN1550	Ortholog of A. nidulans FGSC A4 : AN5689, A. niger CBS 513.88 : An18g00740, A. oryzae RIB40 : AO090038000176, Aspergillus brasiliensis : Aspbr1_0078015 and A. niger ATCC 1015 : 54080-mRNA	null	-4.2821	1.71E-05	0.000139
AN7128	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-4.2821	1.71E-05	0.000139
AN11794	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	3.41768	1.72E-05	0.00014
AN1505	Ortholog of A. nidulans FGSC A4 : AN3207, A. fumigatus Af293 : Afu2g15470, Afu8g00720, Afu8g05070 and A. niger CBS 513.88 : An07g04980, An16g07680, An14g02720, An14g07130, An15g05540	null	3.80281	1.74E-05	0.000141

AN5339	Ortholog of A. oryzae RIB40 : AO090103000416, A. niger ATCC 1015 : 47268-mRNA, Aspergillus versicolor : Aspve1_0044729, Aspergillus sydowii : Aspsy1_0050291 and Aspergillus terreus NIH2624 : ATET_00936	null	-3.1436	1.75E-05	0.000142
AN8074	Has domain(s) with predicted ubiquitin thiolesterase activity, zinc ion binding activity and role in ubiquitin-dependent protein catabolic process	null	-2.9575	1.76E-05	0.000142
AN6239	Ortholog of A. nidulans FGSC A4 : AN6793, A. fumigatus Af293 : Afu3g03390, Afu7g00330, A. niger CBS 513.88 : An03g03530 and A. oryzae RIB40 : AO090103000170, AO090701000114	null	2.97959	1.78E-05	0.000144
AN0160	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in carbohydrate metabolic process	null	3.0578	1.80E-05	0.000145
AN1566	Ortholog(s) have cytosol, nucleus localization	null	3.61319	1.80E-05	0.000145
AN5613	Xanthine dehydrogenase (purine hydroxylase I) involved in purine catabolism; requires a molybdenum cofactor for function; induction by uric acid requires the product of the uaY regulatory gene	hxA	-2.8696	1.81E-05	0.000145
AN0015	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	null	-6.9869	1.81E-05	0.000145
AN10952	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-6.9869	1.81E-05	0.000145
AN1101	Ortholog of A. fumigatus Af293 : Afu5g09120, A. niger CBS 513.88 : An07g03970, A. oryzae RIB40 : AO090701000548 and A. niger ATCC 1015 : 181047-mRNA	null	-6.9869	1.81E-05	0.000145
AN3409	Protein of unknown function; transcript repressed by nitrate	null	6.87818	1.81E-05	0.000145
AN4124	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-6.9869	1.81E-05	0.000145
AN4480	null	null	6.87818	1.81E-05	0.000145
AN8154	null	null	-6.9869	1.81E-05	0.000145
AN8652	null	null	6.87818	1.81E-05	0.000145
AN6325	Ortholog(s) have nucleotidase activity and role in pyrimidine nucleobase metabolic process	null	4.04706	1.82E-05	0.000146
AN12360	Has domain(s) with predicted role in response to stress	null	-2.9666	1.93E-05	0.000154
AN11898	Ortholog of A. fumigatus Af293 : Afu7g05420, A. niger ATCC 1015 : 209812-mRNA, Aspergillus versicolor : Aspve1_0355367, Aspergillus sydowii : Aspsy1_0159682 and Aspergillus terreus NIH2624 : ATET_06393	null	3.23427	1.96E-05	0.000156
AN5828	Has domain(s) with predicted heme binding activity	null	-2.9093	1.98E-05	0.000158
AN5104	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.8497	1.99E-05	0.000159
AN8233	Ortholog(s) have phosphatidylinositol transporter activity	null	2.97323	1.99E-05	0.000159

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AN1752	Putative sulfite reductase with a predicted role in sulfur metabolism	null	3.26294	2.01E-05	0.000159
AN0561	Ortholog(s) have mitochondrion localization	null	3.61632	2.01E-05	0.000159
AN3191	Ortholog(s) have lipase activity	null	-3.4549	2.01E-05	0.000159
AN6543	Ortholog(s) have adenyl-nucleotide exchange factor activity, role in cytoplasmic translation and cytosolic ribosome, nucleus localization	null	3.60318	2.01E-05	0.000159
AN2093	Ortholog(s) have role in autophagy, protein targeting to vacuole, vesicle docking and Mon1-Ccz1 complex, cell division site, cytosol, fungal-type vacuole membrane, nucleus localization	null	4.03117	2.05E-05	0.000162
AN0483	Ortholog of Aspergillus versicolor : Aspve1_0158177, Aspergillus sydowii : Aspsy1_0144898, Aspergillus terreus NIH2624 : ATET_04939 and Aspergillus brasiliensis : Aspbr1_0204336	null	-2.9966	2.05E-05	0.000162
AN0705	Ortholog(s) have isoleucine-tRNA ligase activity, role in isoleucyl-tRNA aminoacylation and cytosol localization	null	2.91575	2.06E-05	0.000163
AN20001	Mitochondrially-encoded subunit 5 of NADH dehydrogenase	ndhE	2.88776	2.10E-05	0.000165
AN7583	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-3.2127	2.11E-05	0.000167
AN3593	Ortholog(s) have role in L-methionine salvage from methylthioadenosine and cytoplasm localization	null	3.08048	2.14E-05	0.000169
AN1198	Putative aminomethyltransferase with a predicted role in glycine, serine, and threonine metabolism	null	-2.8642	2.16E-05	0.000169
AN5969	Ortholog of A. niger CBS 513.88 : An02g05900, Aspergillus flavus NRRL 3357 : AFL2T_05331, A. clavatus NRRL 1 : ACLA_069580, Aspergillus acidus : Aspfo1_0039232 and Aspergillus versicolor : Aspve1_0040765	null	2.93447	2.17E-05	0.000171
AN20007	Mitochondrially encoded subunit 1 of NADH dehydrogenase	ndhA	3.02466	2.19E-05	0.000172
AN3072	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	-3.1025	2.19E-05	0.000172
AN4025	Has domain(s) with predicted hydrolase activity, tubulin-tyrosine ligase activity and role in cellular protein modification process	null	2.87599	2.22E-05	0.000174
AN8657	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.2852	2.27E-05	0.000177
AN1424	Ortholog of A. fumigatus Af293 : Afu8g04140, A. niger CBS 513.88 : An16g08950, A. oryzae RIB40 : AO090103000029, A. niger ATCC 1015 : 214466-mRNA and Aspergillus versicolor : Aspve1_0049699	null	4.19351	2.30E-05	0.000179
AN0498	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.83899	2.32E-05	0.000179
AN10698	null	null	-6.9232	2.32E-05	0.000179
AN1858	Putative tryptophan 2,3-dioxygenase with a predicted role in aromatic amino acid biosynthesis	null	-6.9232	2.32E-05	0.000179
AN3337	Protein with pectate lyase activity, involved in degradation of pectin	plyE	-6.9232	2.32E-05	0.000179

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AN5037	Has domain(s) with predicted electron carrier activity, flavin adenine dinucleotide binding, oxidoreductase activity, acting on CH-OH group of donors activity and role in oxidation-reduction process	null	-6.9232	2.32E-05	0.000179
AN5584	null	null	-6.9232	2.32E-05	0.000179
AN7058	null	null	-6.9232	2.32E-05	0.000179
AN7135	Protein with rhamnogalacturonan lyase activity, involved in degradation of pectin	rglA	-6.9232	2.32E-05	0.000179
AN7400	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	null	6.83899	2.32E-05	0.000179
AN8473	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	null	-6.9232	2.32E-05	0.000179
AN9458	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	null	-6.9232	2.32E-05	0.000179
AN1100	Has domain(s) with predicted hydrolase activity	null	-4.4501	2.33E-05	0.000179
AN2890	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-4.4501	2.33E-05	0.000179
AN5690	Has domain(s) with predicted copper ion binding, primary amine oxidase activity, quinone binding activity and role in amine metabolic process, oxidation-reduction process	null	-4.4501	2.33E-05	0.000179
AN5845	Has domain(s) with predicted zinc ion binding activity	null	7.25088	2.33E-05	0.000179
AN10712	Has domain(s) with predicted pseudouridine synthase activity, snoRNA binding activity, role in ribosome biogenesis, snRNA pseudouridine synthesis and box H/ACA snoRNP complex localization	null	3.02606	2.38E-05	0.000182
AN7008	Putative mitochondrial hydroxyacyl-CoA dehydrogenase involved in short-chain fatty acid beta-oxidation	hadA	-2.8379	2.38E-05	0.000183
AN8403	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-4.2023	2.39E-05	0.000183
AN3920	Ortholog(s) have cytosol, nucleus localization	null	3.08906	2.40E-05	0.000184
AN3814	Putative peptidyl-prolyl cis-trans isomerase (PPIase); cyclophilin	cypA	2.88378	2.44E-05	0.000186
AN0687	Putative spermine or spermidine synthase with a predicted role in arginine metabolism; transcript upregulated in response to camptothecin; protein induced by farnesol	spdA	3.57654	2.44E-05	0.000187
AN7540	Ortholog(s) have role in ascospore formation, cellular response to caffeine, eukaryotic translation initiation factor 3 complex assembly, gamma-tubulin complex localization	null	2.91586	2.45E-05	0.000187

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AN0116	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	3.44019	2.53E-05	0.000193
AN2042	Ortholog(s) have cytosol localization	null	2.83598	2.67E-05	0.000203
AN20009	Putative mitochondrial ATP synthase subunit 8	atp8	3.41871	2.74E-05	0.000208
AN0453	Putative G1/S cyclin; physically interacts with nimX; expression is transcriptionally regulated by BrlA and AbaA; mutants produce abnormal conidiophores with extra layers of phialides	pclA	-3.7806	2.83E-05	0.000215
AN10221	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane, plasma membrane localization	null	-3.7806	2.83E-05	0.000215
AN10599	Has domain(s) with predicted catalytic activity and role in cellular amino acid catabolic process	null	-3.7806	2.83E-05	0.000215
AN9363	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	null	-3.7806	2.83E-05	0.000215
AN1338	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.8347	2.84E-05	0.000215
AN1596	Putative short-chain dehydrogenase; member of the PbcR-activated diterpene cluster	null	7.18989	2.85E-05	0.000215
AN2235	Ortholog of A. fumigatus Af293 : Afu5g07270, A. niger CBS 513.88 : An17g00710, A. oryzae RIB40 : AO090701000228, A. niger ATCC 1015 : 192711-mRNA and Aspergillus versicolor : Aspve1_0038524	null	7.18989	2.85E-05	0.000215
AN7856	Has domain(s) with predicted enoyl-[acyl-carrier-protein] reductase (NADH) activity, role in fatty acid biosynthetic process, oxidation-reduction process and fatty acid synthase complex localization	null	7.2207	2.85E-05	0.000215
AN9424	Ortholog(s) have role in regulation of cyclin-dependent protein kinase activity, regulation of mitotic cell cycle and cytosol, nucleus localization	null	7.18989	2.85E-05	0.000215
AN0695	Putative snoRNP component with a predicted role in ribosomal RNA pseudouridinylation; ortholog of S. cerevisiae Nhp2p; expression reduced after exposure to farnesol	null	3.32136	2.91E-05	0.000219
AN4645	null	null	-3.1438	2.93E-05	0.00022
AN8690	Protein expressed at increased levels during osmoadaptation; palA-dependent expression independent of pH	null	2.8541	2.94E-05	0.000221
AN3499	Has domain(s) with predicted ATP binding, phosphotransferase activity, alcohol group as acceptor activity and role in amino sugar metabolic process, peptidoglycan turnover	null	3.52251	2.97E-05	0.000223
AN0694	Ortholog(s) have intracellular localization	null	-4.8028	3.00E-05	0.000225
AN11948	null	null	-4.8028	3.00E-05	0.000225
AN1831	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	6.79871	3.00E-05	0.000225
AN8412	Putative hybrid polyketide synthase-nonribosomal peptide synthase (PKS-NRPS); aspyridone synthetase; member of the aspyridone (apd) gene cluster	apdA	6.79871	3.00E-05	0.000225
AN3840	Putative tetrahydrofolylpolyglutamate synthase with a predicted role in folate biosynthesis	null	3.04774	3.04E-05	0.000227

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AN4929	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	null	-2.8449	3.13E-05	0.000234
AN6578	Ortholog(s) have role in positive regulation of gluconate transmembrane transport and cytosol, nucleus localization	null	-2.9144	3.16E-05	0.000235
AN10108	Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.1279	3.18E-05	0.000237
AN0865	Ortholog(s) have cytosol, nucleus localization	null	3.3969	3.21E-05	0.000239
AN6731	Putative delta-9-stearic acid desaturase; converts palmitic acid and stearic acid to palmitoleic acid and oleic acid; null mutant has increased fatty acid content; synthetically lethal with sdeB mutation; expression reduced by farnesol	sdeA	2.77539	3.24E-05	0.000241
AN1112	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	null	-3.3885	3.28E-05	0.000244
AN5179	Ortholog(s) have role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and cytosol localization	null	3.932	3.28E-05	0.000244
AN3635	Ortholog of A. fumigatus Af293 : Afu4g11990, A. niger CBS 513.88 : An01g07270, A. oryzae RIB40 : AO090003001010, A. niger ATCC 1015 : 35965-mRNA and Aspergillus versicolor : Aspve1_0045171	null	3.07882	3.30E-05	0.000244
AN3876	Ortholog(s) have carnitine transmembrane transporter activity, polyamine transmembrane transporter activity	null	-3.3876	3.30E-05	0.000244
AN9116	Ortholog(s) have nicotinate phosphoribosyltransferase activity, role in chromatin silencing at rDNA, chromatin silencing at telomere, nicotinate nucleotide salvage, replicative cell aging and mitochondrion, nucleus localization	null	3.69952	3.30E-05	0.000244
AN3239	Has domain(s) with predicted acyl-CoA dehydrogenase activity and role in oxidation-reduction process	null	4.75201	3.37E-05	0.000248
AN8805	Ortholog(s) have role in cellular response to oxidative stress, response to osmotic stress, ribosomal small subunit biogenesis and cytosol, nucleus localization	null	4.77786	3.37E-05	0.000248
AN9409	Putative ortholog of S. cerevisiae Hgh1p; expression reduced after exposure to farnesol	null	4.77786	3.37E-05	0.000248
AN10981	Putative bifunctional GTP cyclohydrolase II; intracellular; protein abundance decreased by menadione stress	null	-2.8368	3.39E-05	0.00025
AN11377	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity and mitochondrion localization	null	2.90181	3.44E-05	0.000253
AN7159	Ortholog(s) have tripeptidyl-peptidase activity	null	3.16689	3.45E-05	0.000253

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AN0559	Ortholog(s) have mitochondrion targeting sequence binding, protein channel activity and role in mitochondrial outer membrane translocase complex assembly, protein import into mitochondrial matrix, tRNA import into mitochondrion	null	2.84733	3.49E-05	0.000256
AN4800	Ortholog of A. fumigatus Af293 : Afu3g06910, A. niger CBS 513.88 : An11g09440, A. oryzae RIB40 : AO090020000302, A. niger ATCC 1015 : 48103-mRNA and Aspergillus versicolor : Aspve1_0040110	null	-3.1263	3.50E-05	0.000257
AN5122	Putative kinase with a predicted role in nucleotide salvage pathways	null	2.82848	3.53E-05	0.000259
AN6366	Ortholog(s) have endoplasmic reticulum localization	null	3.29393	3.56E-05	0.000261
AN5027	Ortholog of A. fumigatus Af293 : Afu3g12130, A. niger CBS 513.88 : An11g08400, An02g07940, A. oryzae RIB40 : AO090023000019, AO090138000194, AO090003000773 and A. niger ATCC 1015 : 52322-mRNA	null	-2.7635	3.58E-05	0.000262
AN1609	null	null	3.49354	3.64E-05	0.000266
AN2054	Ortholog(s) have histone kinase activity (H3-T3 specific) activity and role in mitotic sister chromatid segregation, regulation of histone H3-T3 phosphorylation involved in chromosome passenger complex localization to kinetochore	null	3.49354	3.64E-05	0.000266
AN3037	Has domain(s) with predicted cholinesterase activity	null	-3.3617	3.68E-05	0.000268
AN8506	Putative transcription factor; predicted role in secondary metabolite production	null	3.68414	3.68E-05	0.000268
AN7137	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.6016	3.69E-05	0.000269
AN1409	Putative acetyl-CoA C-acetyltransferase with a predicted role in fatty acid metabolism; intracellular; protein abundance decreased by menadione stress	null	2.72939	3.74E-05	0.000272
AN1274	Ortholog(s) have alditol:NADP+ 1-oxidoreductase activity, mRNA binding activity, role in D-xylose catabolic process, arabinose catabolic process, cellular response to oxidative stress and cytoplasm, nucleus localization	null	3.0386	3.76E-05	0.000273
AN6046	Putative p67phox regulatory subunit homolog with a predicted role in regulating hyphal reactive oxygen species (ROS) production; required for normal sexual and asexual development	null	-2.7917	3.79E-05	0.000275
AN0325	Ortholog(s) have mitochondrion localization	null	6.71461	3.90E-05	0.000279
AN10600	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	null	-6.8567	3.90E-05	0.000279
AN12269	Ortholog of A. fumigatus Af293 : Afu5g12450, A. niger CBS 513.88 : An14g06770, A. oryzae RIB40 : AO090120000369, A. niger ATCC 1015 : 121597-mRNA and Aspergillus versicolor : Aspve1_0035337	null	-6.8567	3.90E-05	0.000279
AN1747	Ortholog(s) have mitochondrion localization	null	6.75727	3.90E-05	0.000279

AN2010	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity and role in metabolic process	null	6.71461	3.90E-05	0.000279
AN4022	Ortholog of A. fumigatus Af293 : Afu1g03700, A. oryzae RIB40 : AO090003000976, A. niger ATCC 1015 : 49873-mRNA, Aspergillus versicolor : Aspve1_0135585 and Aspergillus sydowii : Aspsy1_0057572	null	-6.8567	3.90E-05	0.000279
AN4348	Has domain(s) with predicted catalytic activity and role in metabolic process	null	6.75727	3.90E-05	0.000279
AN4769	ATP sulfurylase involved in sulfate assimilation; mutants are resistant to selenate	sC	6.75727	3.90E-05	0.000279
AN5274	Ortholog(s) have sequence-specific DNA binding activity	null	-6.8567	3.90E-05	0.000279
AN5756	null	null	-6.8567	3.90E-05	0.000279
AN6401	Putative hydrophobin	null	-6.8567	3.90E-05	0.000279
AN7278	Putative glutamate decarboxylase with a predicted role in the 4-aminobutyrate (GABA) shunt	null	6.71461	3.90E-05	0.000279
AN8134	Has domain(s) with predicted transferase activity, transferring acyl groups other than amino-acyl groups activity	null	6.71461	3.90E-05	0.000279
AN8893	Has domain(s) with predicted nucleotide binding activity	null	-6.8567	3.90E-05	0.000279
AN8940	Ortholog of Aspergillus terreus NIH2624 : ATET_03481	null	-6.8567	3.90E-05	0.000279
AN1509	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	null	-3.1993	3.94E-05	0.000282
AN3895	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-3.3214	3.94E-05	0.000282
AN4616	Putative 70 kilodalton heat shock protein; protein induced by farnesol	ssz1	3.15478	3.96E-05	0.000282
AN5342	Protein expressed at increased levels during osmoadaptation	null	-3.0963	3.99E-05	0.000284
AN8536	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-2.8856	3.99E-05	0.000284
AN5192	Putative fatty acyl-CoA synthetase with a predicted role in very long-chain fatty acid metabolism	fatA	-3.1836	4.00E-05	0.000284
AN4015	Ortholog(s) have ribosome binding, translation elongation factor activity, translation initiation factor activity	null	2.71718	4.01E-05	0.000285
AN10147	Putative pectin lyase with a predicted role in the degradation of pectin	pelC	-3.7377	4.02E-05	0.000285
AN2205	null	null	4.7257	4.02E-05	0.000285
AN3387	Putative G-protein coupled receptor	gprD	3.08312	4.04E-05	0.000286
AN10765	Ortholog(s) have cytosol, eukaryotic 43S preinitiation complex, eukaryotic translation initiation factor 3 complex, eIF3e, eukaryotic translation initiation factor 3 complex, eIF3m, nucleus localization	null	2.7794	4.10E-05	0.00029
AN11903	Has domain(s) with predicted aminopeptidase activity, dipeptidyl-peptidase activity and role in proteolysis	null	3.65289	4.12E-05	0.000291

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AN2594	Ortholog of A. nidulans FGSC A4 : AN7988, A. fumigatus Af293 : Afu6g03330, A. oryzae RIB40 : AO090020000705, N. fischeri NRRL 181 : NFIA_049690 and Aspergillus flavus NRRL 3357 : AFL2T_10650	null	-3.5443	4.19E-05	0.000296
AN3793	Catalytic subunit of protein phosphatase Z (PPZ); role in resistance to oxidative stress	ppzA	-2.8283	4.28E-05	0.000302
AN6889	Ortholog(s) have nucleic acid binding transcription factor activity, sequence-specific DNA binding activity and role in aromatic amino acid family catabolic process, positive regulation of transcription from RNA polymerase II promoter	null	-3.1655	4.32E-05	0.000304
AN11008	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	null	7.12621	4.33E-05	0.000304
AN11872	null	null	7.12621	4.33E-05	0.000304
AN7801	Ortholog(s) have hydrolase activity, acting on ester bonds activity, role in iron assimilation and cytoplasm localization	null	7.12621	4.33E-05	0.000304
AN3948	Ortholog(s) have Golgi apparatus localization	null	-2.7827	4.35E-05	0.000305
AN1194	Adenylyl phosphosulfate kinase involved in sulfate assimilation	sD	3.02934	4.35E-05	0.000305
AN5116	Ortholog(s) have alpha-tubulin binding activity and cytosol, nucleus localization	null	3.24703	4.38E-05	0.000307
AN2208	Putative galactose 1-dehydrogenase with a predicted role in galactonic acid and galactonate metabolism; NAD binding Rossmann fold oxidoreductase; intracellular, menadione stress-induced protein	null	2.97122	4.44E-05	0.000311
AN20005	Cytochrome b, mitochondrially encoded subunit of the ubiquinol-cytochrome c reductase complex	cobA	2.7144	4.48E-05	0.000313
AN5200	Putative kynurenine 3-monooxygenase with a predicted role in aromatic amino acid biosynthesis	null	2.81883	4.54E-05	0.000318
AN6049	Has domain(s) with predicted zinc ion binding activity	null	-2.9684	4.56E-05	0.000319
AN7526	Ortholog(s) have role in rRNA processing and 90S preribosome, nucleolus localization	null	3.4382	4.60E-05	0.000321
AN2275	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus localization	null	2.87399	4.67E-05	0.000326
AN6512	Ortholog(s) have cytosol, nucleus localization	null	3.12381	4.70E-05	0.000327
AN10249	Ortholog(s) have aminoacyl-tRNA hydrolase activity, role in negative regulation of proteasomal ubiquitin-dependent protein catabolic process and mitochondrial outer membrane localization	null	3.87973	4.74E-05	0.000329
AN12256	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	-3.3298	4.74E-05	0.000329
AN4233	Ortholog(s) have cytosol, nucleus localization	null	3.87973	4.74E-05	0.000329
AN5777	Has domain(s) with predicted triglyceride lipase activity and role in lipid metabolic process	null	-2.8889	4.75E-05	0.00033
AN0033	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-3.2765	4.77E-05	0.000331

AN2912	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	null	-3.6936	4.80E-05	0.000332
AN6736	Ortholog(s) have unfolded protein binding activity	null	4.69889	4.80E-05	0.000332
AN2149	Putative chaperonin complex component, TCP-1 alpha subunit; ortholog of S. cerevisiae Tcp1p; expression reduced after exposure to farnesol	cct1	2.70767	4.83E-05	0.000334
AN1539	Subunit 4 of the COP9 signalosome; required for light-dependent asexual and sexual development and cleistothecia production; regulates secondary metabolite production, mutant hyphae are aberrant with abnormal red pigmentation	csnD	-3.5686	4.85E-05	0.000335
AN10525	Ortholog of A. fumigatus Af293 : Afu1g05820, A. niger ATCC 1015 : 143807-mRNA, Aspergillus versicolor : Aspve1_0138953 and Aspergillus sydowii : Aspsy1_0046943	null	2.74913	5.01E-05	0.000346
AN10311	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	mnpA	-6.7869	5.10E-05	0.000349
AN11749	null	null	-6.7869	5.10E-05	0.000349
AN1415	null	null	-6.7869	5.10E-05	0.000349
AN3341	Has domain(s) with predicted chromate transmembrane transporter activity and role in chromate transport	null	-6.7869	5.10E-05	0.000349
AN3574	null	null	-6.7869	5.10E-05	0.000349
AN6281	Ortholog of Aspergillus versicolor : Aspve1_0028217 and Aspergillus sydowii : Aspsy1_0151548	null	6.67064	5.10E-05	0.000349
AN6667	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	null	-6.7869	5.10E-05	0.000349
AN8374	Ortholog(s) have oligopeptide transporter activity and role in oligopeptide transport, vacuole fusion, non-autophagic	null	6.67064	5.10E-05	0.000349
AN6071	Has domain(s) with predicted membrane localization	null	-2.7788	5.22E-05	0.000357
AN0507	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	null	-4.2936	5.36E-05	0.000366
AN10907	Ortholog of A. fumigatus Af293 : Afu5g00975, A. oryzae RIB40 : AO090005000951, Aspergillus brasiliensis : Aspbr1_0198422, Aspergillus acidus : Aspfo1_0081662 and Aspergillus versicolor : Aspve1_0069870	null	7.09328	5.36E-05	0.000366
AN6253	Putative phenylalanine tRNA synthetase alpha subunit	podG	2.85036	5.40E-05	0.000369

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AN8067	Ortholog of A. fumigatus Af293 : Afu5g01840, A. niger CBS 513.88 : An16g01550, A. oryzae RIB40 : AO090003001340, A. niger ATCC 1015 : 41339-mRNA and Aspergillus versicolor : Aspve1_0055861	null	-2.8086	5.57E-05	0.00038
AN4495	Ortholog(s) have role in ER to Golgi vesicle-mediated transport and endoplasmic reticulum localization	null	2.94912	5.59E-05	0.000381
AN10901	Ortholog(s) have glycine dehydrogenase (decarboxylating) activity, role in glycine decarboxylation via glycine cleavage system, one-carbon metabolic process and mitochondrion localization	null	-2.6923	5.62E-05	0.000383
AN8078	Phenylacetate 2-hydroxylase; cytochrome P450 monooxygenase involved in phenylacetate utilization; transcript is induced by phenylacetate	phacA	-3.2535	5.79E-05	0.000394
AN1640	Ortholog of N. fischeri NRRL 181 : NFIA_028180, Aspergillus versicolor : Aspve1_0122087 and Aspergillus sydowii : Aspsy1_0135110, Aspsy1_0638682	null	-3.0297	5.80E-05	0.000394
AN5674	MAP kinase, kinase, kinase, kinase (MAPKKKK) with similarity to Ste20p	ste20	-2.8026	5.86E-05	0.000398
AN3752	Has domain(s) with predicted Rab GTPase activator activity, role in regulation of Rab GTPase activity and intracellular localization	null	-2.9127	6.12E-05	0.000415
AN2981	Putative glucose 6-phosphate 1-dehydrogenase with a predicted role in the pentose-phosphate shunt; intracellular, menadione stress-induced protein; transcript downregulated by growth in ethanol	gsdA	2.87078	6.12E-05	0.000415
AN10996	Ortholog(s) have cytosol, nucleus localization	null	-2.9208	6.20E-05	0.00042
AN0981	Has domain(s) with predicted integral to membrane localization	null	2.88622	6.22E-05	0.000421
AN10547	Ortholog of A. fumigatus Af293 : Afu4g06220, A. oryzae RIB40 : AO090023000968, Aspergillus sydowii : Aspsy1_0051149 and Aspergillus carbonarius ITEM 5010 : Acar5010_403603	null	2.83969	6.31E-05	0.000426
AN4770	Adenosine 3-phosphate 5-phosphosulfate (PAPS) reductase involved in sulfate assimilation	sA	3.02556	6.37E-05	0.00043
AN5867	Ortholog(s) have acetyl-CoA:L-glutamate N-acetyltransferase activity, role in ornithine biosynthetic process and mitochondrial matrix localization	null	2.85488	6.39E-05	0.000431
AN10570	Ortholog(s) have role in regulation of mitotic cell cycle and cytosol, nucleus localization	null	3.17551	6.41E-05	0.000432
AN2064	Putative nonribosomal peptide synthase (NRPS)-like enzyme	null	-3.5001	6.43E-05	0.000433
AN7600	Ortholog(s) have sulfite reductase (NADPH) activity, role in oxidation-reduction process, sulfate assimilation, sulfur amino acid biosynthetic process and cytosol, sulfite reductase complex (NADPH) localization	null	3.05508	6.47E-05	0.000435
AN3357	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	3.37481	6.61E-05	0.000444
AN8430	Ortholog of A. fumigatus Af293 : Afu5g12780, A. niger CBS 513.88 : An18g00330, A. oryzae RIB40 : AO090010000134, A. niger ATCC 1015 : 187859-mRNA and Aspergillus versicolor : Aspve1_0142146	null	3.37481	6.61E-05	0.000444

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AN0788	Ortholog of A. niger CBS 513.88 : An09g02430, An03g05960, An09g00710, An09g01710 and A. oryzae RIB40 : AO090003000250, AO090010000570, AO090023000882, AO090120000022, AO090012000900	null	-2.781	6.66E-05	0.000447
AN12126	null	null	-4.2374	6.67E-05	0.000447
AN11149	Has domain(s) with predicted arylsulfatase activity and role in phenol-containing compound metabolic process	null	-4.6597	6.72E-05	0.000448
AN1169	Ortholog of A. fumigatus Af293 : Afu1g11100, A. niger CBS 513.88 : An08g03390, A. oryzae RIB40 : AO090038000299, Aspergillus versicolor : Aspve1_0291494 and Aspergillus sydowii : Aspsy1_0239888	null	-6.7136	6.72E-05	0.000448
AN7865	Putative beta-glucosidase	bglJ	6.62529	6.72E-05	0.000448
AN7922	Has domain(s) with predicted FMN binding, riboflavin reductase (NADPH) activity and role in oxidation-reduction process	null	6.62529	6.72E-05	0.000448
AN8392	Putative alpha-glycosidase distantly related to bacterial alpha-galactosidase; predicted role in polysaccharide degradation	aglE	-6.7136	6.72E-05	0.000448
AN8802	Ortholog of Aspergillus versicolor : Aspve1_0088238 and Aspergillus sydowii : Aspsy1_0035041	null	-6.7136	6.72E-05	0.000448
AN3931	Putative conserved eisosome protein	pilB	-3.562	6.74E-05	0.000449
AN4131	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	3.39025	6.81E-05	0.000453
AN4164	Ortholog of A. fumigatus Af293 : Afu4g13180, A. niger CBS 513.88 : An01g08860, A. niger ATCC 1015 : 196273-mRNA and Aspergillus terreus NIH2624 : ATET_03201	null	2.81045	6.87E-05	0.000456
AN6263	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	3.78818	6.93E-05	0.00046
AN0480	null	null	3.16422	6.95E-05	0.000461
AN5917	Ortholog(s) have alpha-glucoside:hydrogen symporter activity, maltose:hydrogen symporter activity, trehalose transmembrane transporter activity and role in disaccharide catabolic process, maltose transport, trehalose transport	null	-2.6733	7.04E-05	0.000466
AN5999	Carbamoyl-phosphate synthase, large subunit; predicted role in arginine or pyrimidine metabolism; protein induced by farnesol	null	3.00215	7.14E-05	0.000473
AN11094	Putative zinc-binding oxidoreductase; intracellular, menadione stress-induced protein; expression upregulated after exposure to farnesol	null	2.69826	7.16E-05	0.000473
AN1414	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	xprG	-2.884	7.25E-05	0.00048
AN0963	Has domain(s) with predicted oxidoreductase activity and role in lipid metabolic process, oxidation-reduction process	null	3.23426	7.41E-05	0.000489

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AN6563	Putative translation elongation factor EF-1 gamma; ortholog of S. cerevisiae Cam1p; expression reduced after exposure to farnesol	null	2.64312	7.50E-05	0.000495
AN0823	Ortholog of A. fumigatus Af293 : Afu1g14830, A. niger CBS 513.88 : An01g12940, A. oryzae RIB40 : AO090005001249, A. niger ATCC 1015 : 55261-mRNA and Aspergillus versicolor : Aspve1_0036404	null	-2.7064	7.52E-05	0.000496
AN6753	Putative NADH-dependent flavin oxidoreductase; menadione stress-induced protein	null	3.35933	7.58E-05	0.000499
AN4397	Ortholog of S. cerevisiae Pcs60p	fatD	-2.9786	7.73E-05	0.000509
AN6161	Putative peroxisome biogenesis protein	null	-2.9786	7.73E-05	0.000509
AN10267	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.8399	7.75E-05	0.000509
AN10974	null	null	-3.2371	7.89E-05	0.000517
AN4608	Has domain(s) with predicted nucleotide binding activity	null	-3.4219	7.89E-05	0.000517
AN8215	Putative methylenetetrahydrofolate reductase (NADPH) with a predicted role in one-carbon metabolism; metA expression is induced by homocysteine; mutation causes methionine auxotrophy	metA	3.76915	7.89E-05	0.000517
AN4212	Putative aryl-alcohol oxidase-related protein	null	-3.5216	7.93E-05	0.000519
AN7172	Ortholog of A. nidulans FGSC A4 : AN10292, A. fumigatus Af293 : Afu5g10460, A. niger CBS 513.88 : An14g02030, An14g04320 and A. oryzae RIB40 : AO090011000125, AO090010000491	null	-3.5216	7.93E-05	0.000519
AN4577	Putative kynurenine formamidase with a predicted role in aromatic amino acid biosynthesis; transcript induced under low nitrogen conditions	fmdS	-3.0644	7.96E-05	0.00052
AN1016	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	ganB	-2.9701	8.26E-05	0.000539
AN5977	Ortholog(s) have carbonyl reductase (NADPH) activity and cytosol, nucleus localization	null	-2.9701	8.26E-05	0.000539
AN8444	Protein with similarity to cellulose synthase; predicted role in beta-glucan synthesis	celA	2.81072	8.52E-05	0.000555
AN0902	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	null	-2.7762	8.53E-05	0.000555
AN0759	Ortholog of A. fumigatus Af293 : Afu1g14190, A. niger CBS 513.88 : An01g12200, A. niger ATCC 1015 : 172849-mRNA, Aspergillus versicolor : Aspve1_0078668 and Aspergillus sydowii : Aspsy1_0041575	null	-2.6498	8.65E-05	0.000563
AN4774	Ortholog(s) have uroporphyrin-III C-methyltransferase activity and role in methionine biosynthetic process, siroheme biosynthetic process	null	3.20945	8.82E-05	0.000569
AN7625	Putative myo-inositol-1-phosphate synthase with a predicted role in phospholipid metabolism; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH	null	2.61889	8.87E-05	0.000569

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AN10259	Putative cytochrome P450	CYP532A4	-6.6364	8.90E-05	0.000569
AN10287	Ortholog of A. nidulans FGSC A4 : AN3782, AN9297, A. fumigatus Af293 : Afu3g03570, Afu5g09970, A. niger CBS 513.88 : An18g01620, An14g05890 and A. oryzae RIB40 : AO090026000109	null	6.57848	8.90E-05	0.000569
AN11121	Protein of unknown function; transcript repressed by nitrate	null	6.53009	8.90E-05	0.000569
AN1617	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	6.53009	8.90E-05	0.000569
AN2033	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	6.53009	8.90E-05	0.000569
AN2352	null	null	-6.6364	8.90E-05	0.000569
AN2586	Has domain(s) with predicted catalytic activity and role in metabolic process	null	6.53009	8.90E-05	0.000569
AN2778	Has domain(s) with predicted heme binding activity	null	-6.6364	8.90E-05	0.000569
AN5664	Ortholog of A. nidulans FGSC A4 : AN6419, AN6946, AN5312, AN8984, AN8971, AN9387, AN1317 and A. fumigatus Af293 : Afu5g13725	null	-6.6364	8.90E-05	0.000569
AN5976	Putative beta-glucosidase	bglG	-4.5825	8.90E-05	0.000569
AN6846	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	null	-4.5825	8.90E-05	0.000569
AN7577	Has domain(s) with predicted acid-amino acid ligase activity and role in post-translational protein modification	null	-6.6364	8.90E-05	0.000569
AN7906	Ortholog of A. nidulans FGSC A4 : AN3590, A. fumigatus Af293 : Afu4g12880, A. niger CBS 513.88 : An01g08440, A. oryzae RIB40 : AO090009000315 and A. niger ATCC 1015 : 51857-mRNA	null	-6.6364	8.90E-05	0.000569
AN8549	null	null	-6.6364	8.90E-05	0.000569
AN8647	High-affinity nitrite transporter; transcription is induced by nitrite and nitrate, and repressed by ammonium; regulated by NirA and AreA	nitA	6.53009	8.90E-05	0.000569
AN9027	Has domain(s) with predicted hydrolase activity	null	-4.5825	8.90E-05	0.000569
AN9249	Protein required for austinol and dehydroaustinol biosynthesis	ausH	-6.6364	8.90E-05	0.000569
AN9351	Ortholog of Aspergillus versicolor : Aspve1_0048024 and Aspergillus sydowii : Aspsy1_0163543	null	-6.6364	8.90E-05	0.000569
AN5776	Ortholog(s) have role in hypotonic response and barrier septum localization	null	-2.667	8.92E-05	0.00057
AN6714	Ortholog(s) have cytosol, nucleus localization	null	2.8653	8.94E-05	0.000571
AN2463	Putative beta-galactosidase with a predicted role in lactose metabolism	lacF	-2.8986	8.99E-05	0.000573
AN6624	Has domain(s) with predicted zinc ion binding activity	null	-3.3896	8.99E-05	0.000573
AN4864	Putative glucosyltransferase; locus contains the conserved upstream open reading frame (uORF) AN4864-uORF	alg6	2.77623	9.10E-05	0.00058
AN6834	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.1957	9.26E-05	0.000589

AN10805	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-3.48	9.35E-05	0.000594
AN0608	Ortholog(s) have role in ergosterol biosynthetic process, siderophore biosynthetic process	null	2.89078	9.41E-05	0.000597
AN11252	Ortholog(s) have 3-hydroxyanthranilate 3,4-dioxygenase activity, role in de novo NAD biosynthetic process from tryptophan and cytoplasm localization	null	2.63138	9.41E-05	0.000597
AN2733	Ortholog(s) have uroporphyrinogen decarboxylase activity, role in heme biosynthetic process and cytosol, nucleus localization	null	3.32773	9.43E-05	0.000597
AN2836	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	null	-3.1614	9.43E-05	0.000597
AN7295	Putative transmembrane transporter; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.90451	9.49E-05	0.000601
AN11699	Ortholog(s) have nucleus, ribosome localization	null	2.9817	9.60E-05	0.000607
AN6237	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	null	2.60311	9.65E-05	0.00061
AN1573	Putative aspartic-type protease; predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.6743	9.67E-05	0.000611
AN6891	Ortholog of A. fumigatus Af293 : Afu5g13330, A. niger CBS 513.88 : An14g04740, A. oryzae RIB40 : AO090120000478, A. niger ATCC 1015 : 211185-mRNA and Aspergillus versicolor : Aspve1_0120830	null	2.63897	9.80E-05	0.000618
AN6911	Ortholog(s) have cytosol, nucleus localization	vps16	-2.7096	9.91E-05	0.000625
AN0137	Ortholog(s) have glycerophosphocholine phosphodiesterase activity, role in glycerophospholipid catabolic process and cytosol, ribosome localization	null	-2.7746	0.000101	0.000636
AN5968	Ortholog(s) have fungal-type vacuole localization	null	-3.5524	0.000101	0.000636
AN6383	Ortholog of A. fumigatus Af293 : Afu1g03300, Afu5g00450, Afu6g10780, A. niger CBS 513.88 : An03g05860, A. oryzae RIB40 : AO090003001528, AO090023001010 and A. niger ATCC 1015 : 47798-mRNA	null	-3.9325	0.000101	0.000636
AN7177	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	null	2.60716	0.000102	0.000638
AN3059	Putative phosphoglycerate mutase with a predicted role in gluconeogenesis and glycolysis; expression upregulated after exposure to farnesol	pgmA	2.60141	0.000102	0.000639
AN8122	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	3.73033	0.000103	0.000643
AN10618	Ortholog(s) have RNA binding activity	null	3.09642	0.000104	0.000651
AN7764	Has domain(s) with predicted ligase activity	null	-3.166	0.000104	0.000654

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AN8789	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.179	0.000105	0.000654
AN2209	Ortholog of A. fumigatus Af293 : Afu5g07010, A. niger CBS 513.88 : An17g00230, A. oryzae RIB40 : AO090701000283, A. niger ATCC 1015 : 45070-mRNA and Aspergillus versicolor : Aspve1_0125550	null	-2.6981	0.000105	0.000655
AN4086	Ortholog(s) have phenylalanine-tRNA ligase activity and cytosol, nucleus, phenylalanine-tRNA ligase complex localization	null	2.77087	0.000105	0.000655
AN5663	Ortholog of A. fumigatus Af293 : Afu4g13710, A. niger CBS 513.88 : An01g09510, A. oryzae RIB40 : AO090010000145, AO090009000200 and A. niger ATCC 1015 : 171254-mRNA	null	2.79011	0.000106	0.000657
AN1179	Protein with a predicted role in negative regulation of gluconeogenesis and protein targeting to vacuole; protein is translationally repressed by the conserved upstream open reading frame (uORF) AN1179-uORF	null	-3.0187	0.000106	0.000657
AN6295	Has domain(s) with predicted role in regulation of transcription, DNA-dependent and nucleus localization	null	-3.0187	0.000106	0.000657
AN7677	Ortholog(s) have role in peroxisome organization and peroxisomal membrane localization	null	-3.0187	0.000106	0.000657
AN2440	Putative ribose-5-phosphate isomerase with a predicted role in the pentose-phosphate shunt	null	2.68884	0.000108	0.000671
AN7770	Ortholog(s) have 2,4-dienoyl-CoA reductase (NADPH) activity, role in ascospore formation, fatty acid catabolic process and peroxisomal matrix localization	null	-2.8548	0.000108	0.000671
AN7711	Ortholog(s) have ADP-ribose diphosphatase activity, role in ribose phosphate metabolic process and cytosol, mitochondrion, nucleus localization	null	3.0858	0.000112	0.000695
AN8004	Putative cytochrome P450	CYP541B1	-2.7712	0.000114	0.000706
AN7701	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	3.0706	0.000114	0.000707
AN10368	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-3.391	0.000115	0.000713
AN12201	Ortholog(s) have oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor activity, role in heme a biosynthetic process, iron-sulfur cluster assembly, ubiquinone biosynthetic process and mitochondrial matrix localization	null	2.59507	0.000115	0.000713
AN2690	Has domain(s) with predicted hydrolase activity, hydrolyzing O-glycosyl compounds activity and role in carbohydrate metabolic process	null	-3.1718	0.000117	0.000725
AN8627	Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and membrane localization	null	3.69042	0.000117	0.000725
AN6526	Ortholog(s) have leucine-tRNA ligase activity, mRNA binding activity, role in Group I intron splicing, leucyl-tRNA aminoacylation, mitochondrial translation and mitochondrion localization	null	2.94356	0.000118	0.000726
AN9076	Transcript repressed by light in developmentally competent mycelia	null	-3.1358	0.000118	0.000728

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AN6831	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	6.48002	0.000119	0.000732
AN8274	Ortholog(s) have DNA binding, tricarboxylate secondary active transmembrane transporter activity and role in alpha-ketoglutarate transport, mitochondrial citrate transport, mitochondrial genome maintenance	null	2.54877	0.00012	0.000741
AN9288	Ortholog(s) have cytoplasm, nucleus localization	null	-2.8891	0.000121	0.000742
AN4018	Ortholog(s) have role in protein targeting to vacuole	null	-2.7583	0.000121	0.000744
AN4151	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.5946	0.000122	0.000748
AN6864	Ortholog(s) have enzyme regulator activity, guanyl-nucleotide exchange factor activity, translation initiation factor activity and role in regulation of translational initiation	null	2.9581	0.000122	0.000748
AN5231	Putative exo-arabinanase	null	2.7902	0.000122	0.000748
AN10019	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	null	-3.5021	0.000123	0.000748
AN11076	Ortholog of A. fumigatus Af293 : Afu3g02220, A. niger CBS 513.88 : An01g02020, A. niger ATCC 1015 : 128447-mRNA, Aspergillus versicolor : Aspve1_0056749 and Aspergillus sydowii : Aspsy1_0093720	null	-3.8822	0.000123	0.000748
AN11861	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	null	-3.8822	0.000123	0.000748
AN2612	Putative beta-glucosidase with a predicted role in degradation of glucans	bglK	4.49583	0.000123	0.000748
AN5720	Putative G-protein coupled receptor; has a PQ loop repeat	gprJ	4.49583	0.000123	0.000748
AN5862	Putative ortholog of S. cerevisiae Erg28p; expression reduced after exposure to farnesol	null	4.52665	0.000123	0.000748
AN9049	Ortholog of A. nidulans FGSC A4 : AN5422, A. fumigatus Af293 : Afu1g16890, Afu5g00920, Afu5g07500 and A. niger CBS 513.88 : An05g01650, An12g06440, An08g09770	null	-3.8822	0.000123	0.000748
AN5596	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.7606	0.000124	0.000755
AN3425	Ortholog(s) have cytosol localization	null	-2.9822	0.000126	0.000768
AN4234	Putative phosphoacetylglucosamine mutase with a predicted role in chitin biosynthesis	pcmA	2.84147	0.000127	0.000774
AN9395	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	null	-2.8381	0.000128	0.000777

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AN6245	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	null	3.23901	0.000128	0.000778
AN1915	Ortholog(s) have electron carrier activity, oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor activity, role in electron transport chain, heme a biosynthetic process and mitochondrial inner membrane localization	null	2.87499	0.000129	0.000784
AN0316	Alpha-tubulin, forms a heterodimer with beta-tubulin that promotes microtubule assembly	tubA	2.72678	0.00013	0.000788
AN3200	Putative beta-glucuronidase with a predicted role in polysaccharide degradation; the predicted pseudogene AN10383 and predicted ORF AN3200 occupy overlapping chromosomal locations in version 4 of the A. nidulans annotation	null	-2.8248	0.00013	0.000788
AN7217	null	null	3.84171	0.000131	0.000792
AN5688	Has domain(s) with predicted role in lipid biosynthetic process	null	2.69203	0.000132	0.000795
AN3430	Ortholog of A. fumigatus Af293 : Afu3g05790, A. niger CBS 513.88 : An11g10810, A. oryzae RIB40 : AO090020000047, Aspergillus versicolor : Aspve1_0040463 and Aspergillus sydowii : Aspsy1_0056861	null	3.67005	0.000134	0.000811
AN5846	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	2.72655	0.000135	0.000812
AN4443	Putative methionine synthase with a predicted role in methionine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type	metH	2.54583	0.000141	0.000849
AN4510	F-box protein; mutant shows increased resistance to 2-deoxyglucose; BLAST indicates no apparent homologs in higher eukaryotes	fbxA	-2.8102	0.000141	0.000851
AN9157	Ortholog(s) have cytosol localization	null	2.64195	0.000141	0.000851
AN10922	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.74057	0.000142	0.000854
AN10290	Has domain(s) with predicted FMN binding, pyridoxamine-phosphate oxidase activity and role in oxidation-reduction process, pyridoxine biosynthetic process	null	2.66095	0.000143	0.000859
AN4159	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	glnA	2.51038	0.000143	0.000861
AN1222	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	sasA	2.71163	0.000145	0.000867
AN1911	Putative mannose-1-phosphate guanyltransferase	null	3.0214	0.000148	0.000884
AN1110	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.7939	0.000148	0.000887

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AN0128	Ortholog(s) have tRNA methyltransferase activity, role in tRNA methylation, wybutosine biosynthetic process and cytosol, mitochondrion, nucleus localization	null	3.39401	0.000151	0.000903
AN5591	Putative aminotransferase; protein expressed at decreased levels in a hapX mutant versus wild-type	null	3.39401	0.000151	0.000903
AN9426	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	null	-3.1049	0.000151	0.000903
AN3957	Amidase, similar to A. nidulans AmdS; probable A. niger AmdS ortholog; required for benzamide or phenylacetamide utilization; transcription is activated by AreA in low-nitrogen conditions and repressed during carbon starvation	gmdA	-2.7556	0.000152	0.000906
AN7617	Ortholog of A. fumigatus Af293 : Afu4g00235, A. niger CBS 513.88 : An16g01350, A. niger ATCC 1015 : 49148-mRNA, Aspergillus versicolor : Aspve1_0054503 and Aspergillus sydowii : Aspsy1_0046081	null	3.02037	0.000152	0.000906
AN3112	UDP-galactopyranose mutase, a flavoenzyme that converts UDP-galactopyranose to UDP-galactofuranose, a central enzyme in in galactofuranose biosynthesis; involved in cell wall biogenesis	ugmA	2.66104	0.000153	0.000911
AN3998	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.72365	0.000154	0.000916
AN3480	Ortholog of A. niger CBS 513.88 : An11g08860, Aspergillus brasiliensis : Aspbr1_0114065, A. niger ATCC 1015 : 48080-mRNA, N. fischeri NRRL 181 : NFIA_008010 and Aspergillus acidus : Aspfo1_0124719	null	-3.393	0.000155	0.000925
AN4582	Ortholog of A. fumigatus Af293 : Afu2g01970, A. niger CBS 513.88 : An07g05780, A. oryzae RIB40 : AO090011000467, A. niger ATCC 1015 : 133628-mRNA and Aspergillus versicolor : Aspve1_0053889	null	-3.393	0.000155	0.000925
AN20018	Mitochondrially encoded subunit 3 of NADH dehydrogenase	ndhC	2.50807	0.000157	0.000934
AN10042	null	null	6.42815	0.00016	0.00094
AN1174	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of substances activity, role in transport and integral to membrane localization	null	-4.5009	0.00016	0.00094
AN1218	Ortholog of A. nidulans FGSC A4 : AN4653, A. fumigatus Af293 : Afu1g10590, Afu2g01840, A. niger CBS 513.88 : An08g02590, An07g05280 and A. oryzae RIB40 : AO090011000442, AO090038000364	null	6.42815	0.00016	0.00094
AN12331	Putative polyketide synthase (PKS)-like enzyme	null	6.42815	0.00016	0.00094
AN1749	Possible pseudogene	null	6.42815	0.00016	0.00094
AN2613	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.42815	0.00016	0.00094
AN3276	Putative Type II fatty acid synthase with a predicted role in mitochondrial fatty acid formation	null	6.42815	0.00016	0.00094
AN3377	Has domain(s) with predicted aspartic-type endopeptidase activity and role in proteolysis	null	6.42815	0.00016	0.00094

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AN3951	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	null	-6.5548	0.00016	0.00094
AN4125	Ortholog of Aspergillus brasiliensis : Aspbr1_0028583, Aspergillus versicolor : Aspve1_0040328, Aspve1_0732669 and Aspergillus sydowii : Aspsy1_0029968, Aspsy1_0033388	null	-6.5548	0.00016	0.00094
AN4527	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	-4.5009	0.00016	0.00094
AN6638	Protein with homology to cytosine methyltransferases; required for early sexual development and formation of viable ascospores; dmtA locus also encodes an anti-sense transcript tmdA	dmtA	-6.5548	0.00016	0.00094
AN8146	Ortholog of A. nidulans FGSC A4 : AN6727, A. fumigatus Af293 : Afu6g03180, Afu7g05880, A. niger CBS 513.88 : An07g02000, An01g14710 and Aspergillus versicolor : Aspve1_0079826	null	-6.5548	0.00016	0.00094
AN8654	Putative aminomethyltransferase with a predicted role in glycine, serine, and threonine metabolism	null	-6.5548	0.00016	0.00094
AN9015	null	null	6.42815	0.00016	0.00094
AN12482	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_05996	null	-2.9326	0.000161	0.000943
AN12408	Ortholog(s) have Golgi apparatus, fungal-type vacuole membrane localization	null	-2.5584	0.000162	0.000949
AN3695	Putative anthranilate synthase with a predicted role in aromatic amino acid biosynthesis	null	2.61345	0.000163	0.000955
AN7736	Ortholog(s) have cytosol localization	null	2.63226	0.000165	0.000966
AN6126	Putative acetyl-CoA carboxylase with a predicted role in cytosolic fatty acid formation	accA	2.51011	0.000169	0.000988
AN2734	Ortholog(s) have LSU rRNA binding activity, role in ribosomal large subunit assembly and 90S preribosome, cytosol, preribosome, large subunit precursor localization	null	2.71696	0.00017	0.000994
AN4149	Protein of unknown function; NeddH-associated protein	null	3.37498	0.000171	0.001
AN8637	Conidia-specific catalase; predicted role in gluconic acid and gluconate metabolism	catA	-3.0733	0.000171	0.001
AN3638	Putative C-4 sterol methyl oxidase with a predicted role in sterol metabolism	null	3.19565	0.000172	0.001004
AN0300	Putative asparaginase with a predicted role in asparagine metabolism	null	2.83548	0.000173	0.00101
AN6088	Predicted metal ion transmembrane transporter; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	-2.5076	0.000174	0.00101
AN3627	Ortholog(s) have intracellular localization	null	-2.4698	0.000175	0.001018
AN5850	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.0679	0.000177	0.001028
AN9383	Putative unsaturated rhamnogalacturonan hydrolase	urhC	-3.0679	0.000177	0.001028
AN4905	theta class glutathione S-transferase; involved in resistance to a variety of xenobiotics and metals; confers susceptibility to the systemic fungicide carboxin	gstA	-2.5075	0.000177	0.00103

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AN10690	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.6791	0.000179	0.001035
AN11174	Ortholog of A. fumigatus Af293 : Afu7g02120, A. niger CBS 513.88 : An12g00530, A. oryzae RIB40 : AO090038000590, N. fischeri NRRL 181 : NFIA_114850 and Aspergillus flavus NRRL 3357 : AFL2T_07916	null	-2.7628	0.000179	0.001035
AN6768	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity and role in protein phosphorylation	null	-3.0279	0.000179	0.001035
AN1026	Ortholog of A. fumigatus Af293 : Afu1g12670, A. niger CBS 513.88 : An08g05420, A. oryzae RIB40 : AO090012000717, A. niger ATCC 1015 : 175597-mRNA and Aspergillus versicolor : Aspve1_0036653	null	4.43215	0.000183	0.001056
AN12032	Ortholog of Aspergillus versicolor : Aspve1_0087631 and Aspergillus sydowii : Aspsy1_1136647	null	-3.8301	0.000183	0.001056
AN6518	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in carbohydrate metabolic process	null	-3.8301	0.000183	0.001056
AN6579	Ortholog of A. fumigatus Af293 : Afu6g04470, A. niger CBS 513.88 : An15g01120, A. oryzae RIB40 : AO090701000109, A. niger ATCC 1015 : 40387-mRNA and Aspergillus versicolor : Aspve1_0197429	null	-3.3475	0.000185	0.001068
AN11093	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	null	3.19393	0.000186	0.001075
AN4346	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	2.64534	0.00019	0.001092
AN10651	Ortholog(s) have cytosol localization	null	2.86751	0.000191	0.001097
AN12489	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-2.4976	0.000192	0.001102
AN3917	Putative cytochrome P450	CYP539D1	-3.041	0.000195	0.001119
AN12473	Putative heat shock protein	hscA	2.45086	0.000196	0.001126
AN3733	Putative alpha-1,2 mannosidase with a predicted role in mannose polymer metabolism	mns1A	-2.6744	0.000198	0.001134
AN9407	Fatty acid synthase, alpha subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid biosynthesis	fasA	2.44566	0.0002	0.001148
AN3208	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	null	2.7649	0.000201	0.001154
AN10335	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.7469	0.000203	0.001164
AN11778	Putative exoinulinase	null	-2.5256	0.000204	0.001168
AN0653	Ortholog(s) have cytosol, nucleus localization	null	2.96348	0.000208	0.001187
AN4532	Putative catechol oxygenase	null	-2.5619	0.000209	0.001195

AN0712	Protein with beta-glucosidase activity, involved in degradation of glucans	bglB	-3.9879	0.000213	0.001214
AN3992	Ortholog of A. nidulans FGSC A4 : AN8424, AN7089, A. fumigatus Af293 : Afu7g05085, A. oryzae RIB40 : AO090005000321 and N. fischeri NRRL 181 : NFIA_026200	null	-3.9879	0.000213	0.001214
AN6324	Putative alpha-amylase with a predicted role in starch metabolism; predicted glycosylphosphatidylinositol (GPI)-anchored protein	amyE	-3.9879	0.000213	0.001214
AN7093	Ortholog of Aspergillus sydowii : Aspsy1_0438481	null	-2.7939	0.000214	0.001215
AN4290	Ortholog(s) have S-methyl-5-thioribose-1-phosphate isomerase activity, role in L-methionine salvage from methylthioadenosine and cytosol, nucleus localization	null	2.73748	0.000215	0.001215
AN4899	Ortholog(s) have peroxisome membrane targeting sequence binding activity	null	-2.5201	0.000216	0.001215
AN0139	Putative asparaginase with a predicted role in asparagine metabolism	null	-6.4683	0.000217	0.001215
AN0482	Putative ubiquitin-conjugating enzyme; transcript repressed by nitrate	null	-6.4683	0.000217	0.001215
AN0701	Has domain(s) with predicted NAD binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	6.31846	0.000217	0.001215
AN0973	C2H2 zinc finger transcription factor, fphA- and lreB-dependent light induced regulator of conidiophore development; locus has 2 overlapping transcriptional units called brlA alpha and brlA beta; see 5' brlA micro-ORF, AN0974	brlA	-6.4683	0.000217	0.001215
AN10353	Protein with similarity to seryl tRNA synthase; required for conidial germination; expression reduced after exposure to farnesol	sgdB	6.31846	0.000217	0.001215
AN10420	Putative alpha-glucosidase with a predicted role in starch metabolism; transcriptionally induced by isomaltose in an amyR-dependent manner	agdF	-6.4683	0.000217	0.001215
AN10970	RNA polymerase I transcription factor TFIIS, subunit A12.2; ortholog of S. cerevisiae Rpa12p; expression reduced after exposure to farnesol	null	6.31846	0.000217	0.001215
AN11253	Has domain(s) with predicted transferase activity, transferring phosphorus-containing groups activity	null	6.37435	0.000217	0.001215
AN11979	Ortholog(s) have IgE binding activity and fungal-type cell wall localization	null	6.37435	0.000217	0.001215
AN11987	null	null	6.37435	0.000217	0.001215
AN12156	Ortholog of A. fumigatus Af293 : Afu6g11520, A. fumigatus A1163 : AFUB_077530 and Aspergillus aculeatus ATCC16872 : Aacu16872_046590	null	6.37435	0.000217	0.001215
AN12339	Ortholog of A. fumigatus Af293 : Afu8g01800, A. niger CBS 513.88 : An03g05910, A. oryzae RIB40 : AO090010000636, A. niger ATCC 1015 : 126296-mRNA and Aspergillus versicolor : Aspve1_0046675	null	6.37435	0.000217	0.001215
AN1311	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	6.31846	0.000217	0.001215
AN1619	Putative 2-methylcitrate dehydratase	mcdA	-4.4144	0.000217	0.001215

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AN1792	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	-6.4683	0.000217	0.001215
AN2187	null	null	-6.4683	0.000217	0.001215
AN2534	Putative arabinan endo-1,5-alpha-L-arabinosidase with a predicted role in arabinose polymer metabolism	abnA	-6.4683	0.000217	0.001215
AN3567	Ortholog of Aspergillus versicolor : Aspve1_0195944 and Aspergillus sydowii : Aspsy1_0057674	null	-4.4144	0.000217	0.001215
AN4389	Putative CMP glycosylase with a predicted role in nucleotide salvage pathways	null	-6.4683	0.000217	0.001215
AN7739	Has domain(s) with predicted DNA binding activity	null	6.31846	0.000217	0.001215
AN8610	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane localization	null	-6.4683	0.000217	0.001215
AN8928	Putative plasma membrane ATP-binding cassette (ABC) transporter with a predicted role in multidrug resistance; transcript induced by the fungicide imazalil	atrA	6.31846	0.000217	0.001215
AN4927	Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism	null	2.56884	0.000218	0.00122
AN3456	Putative cystathionine gamma-synthase with a predicted role in methionine metabolism	null	2.69311	0.000219	0.001225
AN3626	Putative phosphoribosylamino-imidazole-carboxylase with a predicted role in purine metabolism	null	3.02272	0.00022	0.001229
AN9123	Ortholog of Aspergillus brasiliensis : Aspbr1_0040215, Aspbr1_0678615, Aspergillus versicolor : Aspve1_0140141, Aspergillus niger ATCC 1015 : 183284-mRNA and Aspergillus sydowii : Aspsy1_0158152	null	3.75974	0.000221	0.001232
AN1137	Putative quinate 5-dehydrogenase with a predicted role in aromatic amino acid biosynthesis	qutB	4.39923	0.000224	0.001247
AN2207	Has domain(s) with predicted O-methyltransferase activity	null	4.39923	0.000224	0.001247
AN5412	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	null	-3.776	0.000224	0.001247
AN5445	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	null	4.39923	0.000224	0.001247
AN10828	Ortholog(s) have protein channel activity, role in protein import into mitochondrial matrix, protein import into mitochondrial outer membrane and endoplasmic reticulum, mitochondrial outer membrane translocase complex localization	null	2.4741	0.000225	0.001252
AN9408	Fatty acid synthase, beta subunit; multifunctional enzyme with a predicted role in cytosolic fatty acid formation	fasB	2.41683	0.000226	0.001256
AN10849	Protein with similarity to Saccharomyces cerevisiae Vam6p/Vps39p; plays a role in vacuolar morphogenesis	avaB	-2.5503	0.000227	0.001256
AN1543	Putative succinate dehydrogenase	null	-2.5689	0.00023	0.001273

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AN2623	Isopenicillin-N N-acyltransferase; null produces reduced levels of penicillin; partially redundant with aatB	aatA	-2.775	0.000231	0.00128
AN6089	Putative 60 kilodalton heat shock protein	null	2.47017	0.000231	0.00128
AN2020	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	null	-3.0315	0.000235	0.001294
AN2465	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.2163	0.000235	0.001294
AN7356	Ortholog of A. fumigatus Af293 : Afu2g16350, A. niger CBS 513.88 : An15g06720, A. oryzae RIB40 : AO090102000229, A. niger ATCC 1015 : 182373-mRNA and Aspergillus versicolor : Aspve1_0038652	null	-3.2163	0.000235	0.001294
AN8223	Protein with a putative role in carbon-starvation response; two ABM motifs; induced by carbon starvation-induced autophagy	null	-3.2163	0.000235	0.001294
AN8741	Has domain(s) with predicted DNA binding, zinc ion binding activity and intracellular localization	null	-3.2163	0.000235	0.001294
AN4973	Ortholog of A. fumigatus Af293 : Afu3g10150, A. niger CBS 513.88 : An16g03980, A. oryzae RIB40 : AO090003000550, A. niger ATCC 1015 : 53611-mRNA and Aspergillus versicolor : Aspve1_0039831	null	-2.9887	0.000236	0.001299
AN5111	Ortholog(s) have role in conjugation with cellular fusion, regulation of conjugation with cellular fusion and cytosol, nucleolus localization	null	3.14037	0.000236	0.001299
AN4424	Has domain(s) with predicted FMN binding, heme binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.7067	0.000237	0.001305
AN11120	Ortholog(s) have endoplasmic reticulum localization	null	-2.558	0.000242	0.001329
AN6858	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	null	-2.5419	0.000243	0.001332
AN2894	Ortholog of A. fumigatus Af293 : Afu3g11550, A. niger CBS 513.88 : An02g07350, A. oryzae RIB40 : AO090003000710, A. niger ATCC 1015 : 52301-mRNA and Aspergillus versicolor : Aspve1_0081788	null	-2.7108	0.000243	0.001332
AN1923	Putative alanine transaminase with a predicted role in alanine and aspartate metabolism; intracellular, menadione stress-induced protein	null	2.44656	0.000246	0.00135
AN5947	Ortholog of A. niger CBS 513.88 : An11g05770, Aspergillus brasiliensis : Aspbr1_0050758, N. fischeri NRRL 181 : NFIA_007650 and Aspergillus versicolor : Aspve1_0047552	null	-2.4768	0.000248	0.001361
AN1536	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	null	-3.2314	0.00025	0.001367
AN3803	Ortholog(s) have cytosol, nucleus localization	null	2.57419	0.00025	0.00137

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AN7554	Ortholog(s) have poly(A) RNA binding activity	null	2.66606	0.000253	0.001381
AN5919	Ortholog(s) have role in ascospore formation, cellular response to nitrogen starvation, multivesicular body membrane disassembly, piecemeal microautophagy of nucleus, vacuolar protein processing	null	-2.6173	0.000253	0.001381
AN10091	Ortholog(s) have cytosol, mitochondrion, nucleus localization	null	2.63314	0.000255	0.001395
AN5736	Ortholog(s) have endoplasmic reticulum localization	null	3.12035	0.000258	0.00141
AN3153	Ortholog of A. fumigatus Af293 : Afu3g13850, A. niger CBS 513.88 : An02g09560, Aspergillus versicolor : Aspve1_0039248, Aspergillus sydowii : Aspsy1_0147325 and Aspergillus terreus NIH2624 : ATET_04044	null	-2.6936	0.00026	0.001418
AN0374	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.5214	0.00026	0.001418
AN6368	Putative arginyl-tRNA synthetase with a predicted role in tRNA charging for translation	null	2.56302	0.000262	0.001424
AN3897	Has domain(s) with predicted ammonia-lyase activity, role in L-phenylalanine catabolic process, biosynthetic process and cytoplasm localization	null	2.68762	0.000262	0.001426
AN4600	Ortholog of A. fumigatus Af293 : Afu2g02210, A. niger CBS 513.88 : An07g06630, A. niger ATCC 1015 : 180337-mRNA, Aspergillus versicolor : Aspve1_0134605 and Aspergillus sydowii : Aspsy1_0180963	null	3.12206	0.000266	0.001446
AN3140	Ortholog of A. niger CBS 513.88 : An02g08990, A. oryzae RIB40 : AO090012000820, A. niger ATCC 1015 : 173033-mRNA, Aspergillus versicolor : Aspve1_0060750 and Aspergillus sydowii : Aspsy1_1171750	null	-2.4548	0.000269	0.00146
AN1412	Ortholog of A. fumigatus Af293 : Afu8g04030, A. niger CBS 513.88 : An16g09150, A. oryzae RIB40 : AO090103000016, A. niger ATCC 1015 : 55047-mRNA and Aspergillus versicolor : Aspve1_0037155	null	-2.9942	0.000271	0.001469
AN2144	Ortholog(s) have cytosol, nucleus localization	null	-2.9942	0.000271	0.001469
AN8454	Has domain(s) with predicted copper ion binding, primary amine oxidase activity, quinone binding activity and role in amine metabolic process, oxidation-reduction process	null	-3.179	0.000271	0.001469
AN11125	Ortholog(s) have glycine-tRNA ligase activity, role in DNA-dependent transcription, termination, mitochondrial glycyl-tRNA aminoacylation and cytosol, mitochondrion localization	null	2.47812	0.000272	0.001474
AN7492	Ortholog(s) have enzyme activator activity, m7G(5')pppN diphosphatase activity	null	2.89054	0.000274	0.001485
AN11899	Ortholog of A. clavatus NRRL 1 : ACLA_007370	null	-3.7199	0.000276	0.00149
AN1833	Ortholog(s) have role in zinc ion homeostasis, zinc ion transmembrane transport	null	4.33103	0.000276	0.00149
AN4336	Putative L-arabinitol 4-dehydrogenase with a predicted role in L-arabinose/arabitol and D-xylose/D,L-xylulose/xylitol metabolism	ladB	4.33103	0.000276	0.00149
AN6172	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	null	-3.7199	0.000276	0.00149

AN6949	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.7199	0.000276	0.00149
AN4525	Putative cytochrome c oxidase subunit with a predicted role in energy metabolism	null	2.58618	0.000277	0.001491
AN6621	Ortholog of A. nidulans FGSC A4 : AN7403, A. fumigatus Af293 : Afu8g01810, A. niger CBS 513.88 : An05g02280, A. oryzae RIB40 : AO090026000198 and A. niger ATCC 1015 : 135939-mRNA	null	2.41321	0.000282	0.001518
AN10832	Ortholog(s) have role in protein urmylation, regulation of transcription from RNA polymerase II promoter, tRNA wobble uridine modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	2.65098	0.000285	0.001531
AN0437	Ortholog of A. fumigatus Af293 : Afu1g04570, A. niger CBS 513.88 : An01g03540, Aspergillus versicolor : Aspve1_0243211, Aspergillus sydowii : Aspsy1_0642698 and Aspergillus terreus NIH2624 : ATET_03749	null	-2.9742	0.000288	0.001544
AN8389	Has domain(s) with predicted acid phosphatase activity	null	-2.9742	0.000288	0.001544
AN12461	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	null	-2.396	0.000288	0.001544
AN0197	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	null	-6.3762	0.000297	0.001579
AN0737	Possible pseudogene, similar to Zn(II)2Cys6 transcription factor	null	-6.3762	0.000297	0.001579
AN10465	Ortholog(s) have COPI-coated vesicle, Golgi apparatus localization	null	6.26032	0.000297	0.001579
AN10913	Ortholog(s) have mitochondrion localization	null	6.26032	0.000297	0.001579
AN1320	Has domain(s) with predicted serine-type peptidase activity and role in proteolysis	null	-6.3762	0.000297	0.001579
AN2346	null	null	-6.3762	0.000297	0.001579
AN2604	Ortholog of Aspergillus sydowii : Aspsy1_0439518	null	-6.3762	0.000297	0.001579
AN2821	Ortholog of A. fumigatus Af293 : Afu2g00180, Afu2g17480, A. niger CBS 513.88 : An03g05360, An04g09420, A. oryzae RIB40 : AO090102000063, AO090009000716 and A. niger ATCC 1015 : 191223-mRNA	null	-6.3762	0.000297	0.001579
AN3199	MFS sugar transporter; induced by lactose and galactose	lacpA	-4.3223	0.000297	0.001579
AN3318	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding, zinc ion binding activity and role in lipid metabolic process	null	-6.3762	0.000297	0.001579
AN3398	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-4.3223	0.000297	0.001579

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AN5733	Ortholog of A. fumigatus Af293 : Afu6g06970, A. oryzae RIB40 : AO090003000079, N. fischeri NRRL 181 : NFIA_052620, Aspergillus flavus NRRL 3357 : AFL2T_02868 and A. clavatus NRRL 1 : ACLA_088750	null	-6.3762	0.000297	0.001579
AN6770	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-6.3762	0.000297	0.001579
AN7952	Has domain(s) with predicted hydrolase activity	null	-6.3762	0.000297	0.001579
AN9457	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-6.3762	0.000297	0.001579
AN0904	Ortholog of A. fumigatus Af293 : Afu1g15700, A. niger CBS 513.88 : An01g14040, A. oryzae RIB40 : AO090005001136, A. niger ATCC 1015 : 46275-mRNA and Aspergillus versicolor : Aspve1_0024083	null	-2.6585	0.000299	0.001587
AN4601	Ortholog(s) have sterol 3-beta-glucosyltransferase activity, role in ascospore-type prospore membrane assembly, sterol metabolic process and cytoplasm localization	null	-2.5056	0.0003	0.001589
AN6346	Putative dihydroxy-acid dehydratase with a predicted role in valine, leucine, and isoleucine metabolism; intracellular, menadione stress-induced protein	null	2.50026	0.0003	0.001589
AN5049	Has domain(s) with predicted cation transmembrane transporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	3.10352	0.0003	0.00159
AN1873	Ortholog(s) have cytosol, nucleus localization	null	2.41166	0.000302	0.001599
AN9506	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	2.78082	0.000302	0.001599
AN1378	Ortholog of A. niger CBS 513.88 : An08g00540, A. oryzae RIB40 : AO090005001622, A. niger ATCC 1015 : 38647-mRNA, Aspergillus versicolor : Aspve1_0049649 and Aspergillus sydowii : Aspsy1_0138364	null	-2.3502	0.000303	0.001599
AN0672	Has domain(s) with predicted coenzyme binding, nucleotide binding, phosphogluconate dehydrogenase (decarboxylating) activity and role in pentose-phosphate shunt	null	2.68514	0.000308	0.001627
AN2165	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	null	-2.3717	0.000308	0.001627
AN3555	Small heat-shock protein; Hsp30p ortholog/paralog; expression upregulated after exposure to farnesol; palA-dependent expression independent of pH	null	2.52872	0.000313	0.00165
AN1782	Has domain(s) with predicted NAD+ binding, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, zinc ion binding activity and role in chromatin silencing, protein deacetylation	null	-3.2518	0.000318	0.001672
AN20000	Mitochondrially encoded subunit 4L of NADH dehydrogenase	ndhDL	3.67283	0.000318	0.001672
AN4403	Has domain(s) with predicted heat shock protein binding, unfolded protein binding activity and role in protein folding	null	3.67283	0.000318	0.001672

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AN8644	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	null	-2.6517	0.000318	0.001672
AN2867	Putative phosphoglucomutase with a predicted role in carbohydrate metabolism; intracellular; protein abundance decreased by menadione stress; transcript levels increase during asexual development	pgmB	2.40445	0.000324	0.001701
AN2614	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.7933	0.000325	0.001704
AN0857	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	null	2.56022	0.000326	0.001713
AN10122	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.9395	0.000328	0.001722
AN5522	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.51842	0.00033	0.001731
AN0142	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	2.65833	0.000333	0.001741
AN10078	Ortholog(s) have ATPase activity, coupled to transmembrane movement of substances activity, role in fatty acid transport and integral to peroxisomal membrane localization	null	-2.4733	0.000334	0.001745
AN2952	Ortholog of A. fumigatus Af293 : Afu3g07900, Afu8g00900, A. niger CBS 513.88 : An02g11330, An03g05560, A. oryzae RIB40 : AO090120000471 and A. niger ATCC 1015 : 213572-mRNA, 47124-mRNA	null	2.6444	0.000336	0.001756
AN1059	Carnitine acetyltransferase, required for utilization of acetate as carbon source; transcriptional induction by acetate is mediated by FacB; carbon catabolite repression is mediated by CreA; predicted role in the carnitine shuttle	facC	-2.4608	0.000336	0.001757
AN0473	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	3.08474	0.000339	0.001771
AN10229	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity and role in oxidation-reduction process	null	3.06571	0.000339	0.001771
AN4118	Ortholog(s) have sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity	null	4.29568	0.000341	0.001779
AN7378	Ortholog of A. fumigatus Af293 : Afu4g14205, A. niger CBS 513.88 : An15g07560, A. oryzae RIB40 : AO090103000092, A. niger ATCC 1015 : 40862-mRNA and Aspergillus versicolor : Aspve1_0187655	null	4.29568	0.000341	0.001779
AN5138	Putative dihydroxy acid dehydratase with a predicted role in branched-chain amino acid biosynthesis	null	-3.1885	0.000345	0.001797

AN4361	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	metR	2.4827	0.000346	0.001798
AN11187	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-3.9181	0.000351	0.001825
AN0490	Putative CTP synthase with a predicted role in pyrimidine metabolism	null	2.39307	0.000354	0.00184
AN20015	Has domain(s) with predicted DNA binding, cytochrome-c oxidase activity, electron carrier activity, endonuclease activity, heme binding, iron ion binding activity and role in aerobic respiration, intron homing	null	2.59619	0.000355	0.001841
AN20014	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	oxiA	2.33163	0.000361	0.001875
AN6244	Ortholog(s) have role in exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), nuclear polyadenylation-dependent tRNA catabolic process, rRNA catabolic process	null	2.85506	0.000366	0.0019
AN10170	Ortholog(s) have ATPase activity and cytosol, nucleus localization	null	2.3657	0.000367	0.0019
AN4456	Ortholog(s) have nucleolus localization	null	2.77911	0.000368	0.001905
AN7734	Basic-region helix-loop-helix (bHLH) transcription factor; represses expression of the penicillin biosynthesis gene aatA	anbH1	-2.6139	0.000369	0.00191
AN7630	Ortholog(s) have role in ribosomal large subunit assembly and cytosolic ribosome, nucleus localization	null	2.64822	0.000371	0.00192
AN6141	Ortholog(s) have role in negative regulation of apoptotic process, pyridoxine metabolic process and cytoplasm localization	null	3.21297	0.000376	0.001941
AN1089	Ortholog(s) have ubiquitin protein ligase binding activity and role in positive regulation of ubiquitin-dependent endocytosis, regulation of intracellular transport	null	-2.3559	0.000377	0.001947
AN3167	Putative ribosome biogenesis protein; ortholog of S. cerevisiae Nop58p; expression reduced after exposure to farnesol	nop58	2.38143	0.000378	0.001949
AN7451	Putative NAD-glutamate dehydrogenase with a predicted role in glutamate and glutamine metabolism	null	-2.3168	0.000378	0.001951
AN11961	Ortholog(s) have role in nucleotide-excision repair, phosphorylation of RNA polymerase II C-terminal domain, transcription from RNA polymerase II promoter and core TFIIH complex, cytosol, holo TFIIH complex localization	null	3.61184	0.000383	0.00197
AN7786	Ortholog of A. fumigatus Af293 : Afu6g00600, A. oryzae RIB40 : AO090663000003, AO090113000133, A. niger ATCC 1015 : 171597-mRNA and Aspergillus versicolor : Aspve1_0068932, Aspve1_0150790	null	-3.2015	0.000383	0.00197

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AN8762	Ortholog(s) have pyruvate transmembrane transporter activity, role in mitochondrial pyruvate transport and mitochondrial membrane localization	null	2.60737	0.000391	0.00201
AN10018	Ortholog of A. fumigatus Af293 : Afu5g11850, A. niger CBS 513.88 : An18g02850, A. oryzae RIB40 : AO090120000304 and Aspergillus terreus NIH2624 : ATET_02087	null	2.4574	0.000391	0.00201
AN6167	Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process	null	3.02447	0.000393	0.002021
AN5673	Possible pseudogene	null	-2.6129	0.000397	0.002038
AN1968	Ortholog(s) have endoplasmic reticulum localization	null	2.8425	0.000398	0.002039
AN2432	Ortholog(s) have chaperone binding, unfolded protein binding activity, role in protein refolding and mitochondrial matrix localization	null	2.82982	0.000398	0.002039
AN7682	Ortholog(s) have clathrin binding activity, role in Golgi to vacuole transport, endosomal transport and AP-1 adaptor complex, cytosol, endosome, nucleus localization	null	2.8425	0.000398	0.002039
AN8164	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	null	-2.6704	0.000398	0.002039
AN0689	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	facB	-2.3564	0.000406	0.002075
AN10532	Has domain(s) with predicted hydrolase activity	null	-3.1444	0.000407	0.002082
AN11136	Ortholog(s) have protein transporter activity, role in protein import into mitochondrial inner membrane and cytosol, mitochondrial intermembrane space protein transporter complex localization	null	2.54414	0.000408	0.002086
AN0829	Low-affinity cAMP phosphodiesterase	pdeA	-4.224	0.000411	0.002093
AN7274	Ortholog(s) have role in secondary metabolic process	null	6.19973	0.000411	0.002093
AN7651	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	null	-4.224	0.000411	0.002093
AN7891	Putative beta-1,4-endoglucanase	null	6.19973	0.000411	0.002093
AN2147	Putative ribosomal RNA processing protein; ortholog of S. cerevisiae Rrp5p; expression reduced after exposure to farnesol	rrp5	2.44848	0.000413	0.002101
AN3813	Ortholog(s) have copper uptake transmembrane transporter activity, role in copper ion import and integral to plasma membrane localization	null	2.43046	0.000415	0.002111
AN1215	Putative GTPase; S. cerevisiae ortholog Nug1p has role in rRNA processing; expression reduced after exposure to farnesol	null	2.512	0.000416	0.002114

AN0785	Putative manganese superoxide dismutase	sodM	4.25945	0.000424	0.002152
AN10131	Dihydroorotase, catalyzes the third step in pyrimidine biosynthesis	pyrD	4.22228	0.000424	0.002152
AN6234	Ortholog(s) have role in ergosterol biosynthetic process, siderophore biosynthetic process and cytosol, nucleus localization	null	2.42671	0.000426	0.002161
AN1427	Ortholog(s) have cytoplasm localization	null	-2.3241	0.00044	0.002232
AN1999	Ortholog(s) have hexaprenyldihydroxybenzoate methyltransferase activity, role in ubiquinone biosynthetic process and extrinsic to membrane, mitochondrial inner membrane localization	null	2.5166	0.000461	0.002336
AN9065	Ortholog(s) have translation regulator activity and role in mitochondrial respiratory chain complex IV biogenesis, positive regulation of mitochondrial translation	null	2.34497	0.000462	0.002336
AN10915	Ortholog of A. niger CBS 513.88 : An04g09630, An03g01920, A. niger ATCC 1015 : 195107-mRNA, 45712-mRNA, Aspergillus versicolor : Aspve1_0513563 and Aspergillus terreus NIH2624 : ATET_08921	null	3.58036	0.000462	0.002336
AN11043	Has domain(s) with predicted N-acetyltransferase activity and role in metabolic process	null	3.58036	0.000462	0.002336
AN8167	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	null	-3.1494	0.000462	0.002336
AN5852	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-2.6443	0.000463	0.00234
AN8815	Putative isoflavone reductase family protein; intracellular, menadione stress-induced protein	null	2.30694	0.000477	0.002407
AN7151	Putative alpha-L-rhamnosidase; induced by L-rhamnose and repressed by D-glucose; more closely related to bacterial rhamnosidases than other alpha-L-rhamnosidases of fungal origin	rhaE	-3.0989	0.000482	0.00243
AN5482	Putative Ran GTPase, GTP binding protein; protein abundance decreased by menadione stress; palA-dependent expression independent of pH	ran	2.41253	0.000488	0.002456
AN4750	null	null	2.99104	0.000488	0.002456
AN7010	Ortholog(s) have role in chromatin silencing by small RNA and cytosol, nucleus localization	null	2.97403	0.000488	0.002456
AN0753	Ortholog(s) have cytosol localization	null	2.30249	0.00049	0.002462
AN6412	Ortholog(s) have endoplasmic reticulum localization	null	3.4001	0.000491	0.002467
AN5402	Has domain(s) with predicted role in lipid metabolic process	null	-2.8677	0.000494	0.002479
AN6568	Ortholog(s) have protein-lysine N-methyltransferase activity, role in peptidyl-lysine monomethylation, regulation of translation in response to stress and nucleus localization	null	3.16946	0.000494	0.002479
AN1256	Ortholog(s) have cytosol localization	null	2.66755	0.0005	0.00251
AN5909	Dihydroorotate dehydrogenase, catalyzes the fourth step in pyrimidine biosynthesis	pyrE	2.45582	0.000503	0.002521
AN1709	Bifunctional protein with mitochondrial tyrosyl-tRNA synthetase and group I intron splicing activities; splices the group I intron of the mitochondrial large (23S) rRNA precursor	null	2.71839	0.000507	0.002538

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AN5525	Putative aconitate hydratase with a predicted role in the TCA cycle; intracellular; protein abundance decreased by menadione stress; protein expressed at increased levels in a hapX mutant versus wild-type	acoA	-2.2846	0.000508	0.002545
AN1763	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.4012	0.00051	0.002549
AN10348	Ortholog(s) have 3'-5'-exoribonuclease activity	null	2.77798	0.000513	0.002566
AN10841	Ortholog(s) have dodecenoyl-CoA delta-isomerase activity, role in fatty acid beta-oxidation and peroxisome localization	null	-2.4326	0.000514	0.002569
AN4309	Ortholog(s) have role in N-terminal peptidyl-methionine acetylation and mitochondrion localization	null	2.62674	0.000517	0.002582
AN9308	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	2.3209	0.000518	0.002582
AN10648	Ortholog(s) have delta24(24-1) sterol reductase activity	null	2.66726	0.000524	0.002615
AN1150	Putative transaminase with a predicted role in arginine metabolism	null	2.85692	0.000536	0.002671
AN3236	Has domain(s) with predicted O-methyltransferase activity	null	2.52217	0.000546	0.002719
AN10906	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	2.6165	0.000554	0.002754
AN11009	Putative mitochondrial pyruvate carboxylase	null	-3.45	0.00056	0.002782
AN8018	Transcript induced by light in in developmentally competent mycelia	null	3.54816	0.00056	0.002782
AN11728	Ortholog of A. fumigatus Af293 : Afu6g12620, A. niger CBS 513.88 : An06g01820, A. niger ATCC 1015 : 207677-mRNA, Aspergillus versicolor : Aspve1_0683151 and Aspergillus sydowii : Aspsy1_0044100	null	2.96661	0.000561	0.002785
AN12472	Has domain(s) with predicted hydrolase activity, acting on acid halide bonds, in C-halide compounds activity and role in metabolic process	null	3.1472	0.000568	0.002817
AN4716	Ortholog(s) have alpha-1,6-mannosyltransferase activity, role in N-glycan processing, cell wall mannoprotein biosynthetic process and alpha-1,6-mannosyltransferase complex, cytosol, nucleus localization	null	3.37514	0.000572	0.002822
AN0126	Ortholog(s) have ATP binding, ATPase activity, dinucleotide insertion or deletion binding, loop DNA binding, single-stranded DNA binding activity	null	6.1365	0.000573	0.002822
AN12227	Ortholog of Aspergillus brasiliensis : Aspbr1_0047122, A. niger ATCC 1015 : 127671-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_08325 and Aspergillus acidus : Aspfo1_0167284	null	6.1365	0.000573	0.002822
AN12484	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-6.2779	0.000573	0.002822
AN3956	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	null	6.1365	0.000573	0.002822

AN6417	Ortholog(s) have cell cortex localization	null	-6.2779	0.000573	0.002822
AN6696	Ortholog(s) have chromatin binding activity, role in response to DNA damage stimulus and Rpd3L-Expanded complex, mitochondrion localization	null	6.1365	0.000573	0.002822
AN6884	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	null	-6.2779	0.000573	0.002822
AN7074	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-6.2779	0.000573	0.002822
AN8371	null	null	-6.2779	0.000573	0.002822
AN8484	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-6.2779	0.000573	0.002822
AN8507	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.1365	0.000573	0.002822
AN7193	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	null	2.7466	0.000582	0.00286
AN8604	Putative GNAT-type acetyltransferase	ngn23	2.7466	0.000582	0.00286
AN6227	Ortholog(s) have cytosol, nucleus localization	null	-2.2851	0.000586	0.002879
AN0926	Non-essential nuclear transport receptor importin-beta2 subunit; karyopherin superfamily; expression reduced after exposure to farnesol	kapC	2.36856	0.000587	0.002881
AN1084	Putative elongation factor EF-Tu; intracellular, menadione stress-induced protein	null	2.37315	0.000588	0.002886
AN3255	Ortholog(s) have glutathione peroxidase activity, glutathione transferase activity, phosphoprotein binding, protein heterodimerization activity, protein homodimerization activity, transcription corepressor activity	null	-3.7676	0.000592	0.002901
AN6114	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	null	-3.7676	0.000592	0.002901
AN4405	Ortholog(s) have sphingolipid delta-4 desaturase activity, role in oxidation-reduction process, sphingosine biosynthetic process and endoplasmic reticulum localization	null	2.84086	0.000594	0.00291
AN7539	Putative hydrophobin; transcript is induced by nitrate	null	2.35664	0.000599	0.00293
AN3147	Ortholog(s) have intracellular localization	null	2.29866	0.000602	0.002942
AN2513	Putative serine/threonine protein kinase, interacts with PtkA, cyclin-dependent kinase, in metulae, phialides and conidia; essential; involved in hyphal growth and asexual development	pipA	2.47175	0.000602	0.002943
AN2056	Ortholog(s) have endoplasmic reticulum localization	null	2.25873	0.000603	0.002944

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AN7683	Protein associated with the nonclassical protein export pathway; ortholog of S. cerevisiae Nce102p	null	2.32563	0.000608	0.002966
AN7629	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity and mitochondrion localization	null	2.34833	0.000616	0.003004
AN8498	Has domain(s) with predicted peptidase activity	null	-2.446	0.000622	0.003033
AN3608	Putative ATP-binding cassette (ABC) transporter; atrC mRNA levels increase in response to cyclohexamide treatment	atrC	-2.7927	0.000623	0.003033
AN7141	Putative NAD-dependent aldehyde dehydrogenase; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.58532	0.000634	0.003087
AN1854	Putative inositol pentakisphosphate 2-kinase; locus contains the conserved upstream open reading frame (uORF) AN1854-uORF	null	-2.3154	0.000635	0.00309
AN8689	Putative glucokinase; 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	glkA	2.2295	0.000638	0.0031
AN1393	Ortholog(s) have mitochondrion localization	null	2.66791	0.000648	0.003146
AN1021	Ortholog of A. fumigatus Af293 : Afu1g12980, A. oryzae RIB40 : AO090012000595, A. niger ATCC 1015 : 208023-mRNA, Aspergillus versicolor : Aspve1_0280973 and Aspergillus sydowii : Aspsy1_0053349	null	3.10163	0.000654	0.003171
AN8066	Ortholog(s) have tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and nucleus, tRNA (m1A) methyltransferase complex localization	null	3.10163	0.000654	0.003171
AN0956	Ortholog(s) have tRNA dihydrouridine synthase activity, role in tRNA modification and mitochondrion, nucleus localization	null	2.80818	0.00066	0.003197
AN6954	null	null	4.14494	0.000661	0.0032
AN8309	Putative cytochrome P450	CYP682B1	-3.5369	0.000661	0.0032
AN12255	Ortholog(s) have hydrolase activity, acting on ester bonds activity, role in iron assimilation and cytoplasm localization	null	2.27016	0.000662	0.003203
AN2049	Ortholog(s) have cytosol, nucleus localization	null	2.53143	0.000663	0.003206
AN2933	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	null	2.32271	0.000667	0.003222
AN2801	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.4421	0.00067	0.003234
AN5732	Ortholog(s) have cytoplasm localization	null	2.55924	0.000675	0.003255
AN2133	Putative uracil phosphoribosyltransferase	null	-2.6507	0.00068	0.00327
AN0372	Ortholog(s) have endoplasmic reticulum localization	null	-3.0953	0.000681	0.00327
AN10699	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-3.0953	0.000681	0.00327

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AN2115	Ortholog of A. fumigatus Af293 : Afu2g00940, A. niger CBS 513.88 : An14g02830, A. niger ATCC 1015 : 49276-mRNA, N. fischeri NRRL 181 : NFIA_007880, NFIA_033250 and A. clavatus NRRL 1 : ACLA_076860	null	-3.0953	0.000681	0.00327
AN7884	Putative nonribosomal peptide synthase (NRPS) similar to ferrichrome peptide synthetases involved in siderophore biosynthesis	null	3.48154	0.000681	0.00327
AN7898	Major facilitator superfamily (MFS) transporter with a role in secondary metabolism; member of the dba gene cluster	dbaD	-3.3959	0.000681	0.00327
AN8025	Ortholog of A. fumigatus Af293 : Afu1g01450, A. niger CBS 513.88 : An11g08050, An05g01890, An11g03950, A. oryzae RIB40 : AO090010000064, AO090701000602 and A. niger ATCC 1015 : 195287-mRNA, 39295-mRNA	null	-3.3959	0.000681	0.00327
AN4189	Putative mitogen-activated protein kinase kinase (MAPKK)	mkkA	-2.5632	0.000684	0.003281
AN0381	Ortholog(s) have unfolded protein binding activity, role in protein folding and chaperonin-containing T-complex, nucleus localization	null	2.23815	0.000692	0.003318
AN6199	Ortholog(s) have RNA cap binding activity, role in deadenylation-dependent decapping of nuclear-transcribed mRNA and cytoplasmic mRNA processing body, cytosol, mRNA cap binding complex, nucleus localization	null	2.61253	0.000697	0.003344
AN1780	Ortholog(s) have aminopeptidase activity, role in protein processing, protein stabilization and extrinsic to mitochondrial inner membrane, nucleus localization	null	2.37252	0.000707	0.003385
AN6551	Has domain(s) with predicted ATP binding activity	null	-2.3062	0.000707	0.003385
AN8565	Putative serine O-acetyltransferase with a predicted role in cysteine metabolism	cysA	2.41315	0.00071	0.003399
AN3586	Ortholog(s) have mitochondrion localization	null	2.35667	0.000714	0.003416
AN5429	Ortholog of A. nidulans FGSC A4 : AN8498, AN8310, AN11121, A. fumigatus Af293 : Afu3g01350 and A. niger CBS 513.88 : An12g08560, An09g02370, An13g02790, An13g02620	null	2.43082	0.000715	0.003417
AN0299	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin hydrolysis	null	-2.2337	0.000718	0.003428
AN2846	Putative glutathione peroxidase with a predicted role in glutathione biosynthesis; protein induced by farnesol	gpxA	2.28797	0.000718	0.003429
AN3348	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	null	2.90371	0.000727	0.003467
AN2988	Ortholog(s) have cytosol, nucleus localization	null	2.55345	0.000728	0.00347
AN1882	Ortholog(s) have cytosol, nucleus localization	null	-2.3037	0.00073	0.003476
AN2887	Has domain(s) with predicted role in autophagy	null	-2.2389	0.000733	0.003489

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AN8050	Ortholog(s) have role in meiotic chromosome segregation and cytosol, nucleus localization	null	2.36244	0.000743	0.003528
AN5897	Ortholog(s) have mitochondrion localization	null	2.49482	0.000743	0.003528
AN2939	Ortholog(s) have mitochondrion localization	null	2.31758	0.000743	0.003528
AN10598	Has domain(s) with predicted calcium ion binding, calcium-dependent phospholipid binding activity	null	-2.2777	0.000747	0.003545
AN4902	Ortholog of A. niger CBS 513.88 : An02g06740, A. oryzae RIB40 : AO090003001585, N. fischeri NRRL 181 : NFIA_066360, Aspergillus flavus NRRL 3357 : AFL2T_02363 and A. clavatus NRRL 1 : ACLA_038800	null	3.07829	0.000754	0.003577
AN0310	Ortholog(s) have cytosol, nucleolus localization	null	2.33132	0.000759	0.003599
AN3157	Ortholog(s) have endoplasmic reticulum, fungal-type vacuole membrane localization	null	2.45317	0.000767	0.003635
AN8540	Siderophore iron transporter	mirB	2.17978	0.000778	0.003687
AN6569	Ortholog(s) have chromatin DNA binding activity and role in positive regulation of transcription from RNA polymerase II promoter, telomere maintenance, threonylcarbamoyladenosine metabolic process	null	3.3239	0.000782	0.003698
AN7301	Putative glucosyltransferase; ortholog of S. cerevisiae Alg8p; expression reduced after exposure to farnesol	alg8	3.29758	0.000782	0.003698
AN8660	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.2492	0.000784	0.003708
AN1960	Ortholog of A. fumigatus Af293 : Afu4g10850, A. oryzae RIB40 : AO090003001126, A. niger ATCC 1015 : 45375-mRNA, Aspergillus versicolor : Aspve1_0463675 and Aspergillus sydowii : Aspsy1_0026393	null	-2.7274	0.000793	0.003745
AN4833	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	2.26856	0.000803	0.003765
AN11738	Ortholog of Aspergillus versicolor : Aspve1_0035989, Aspergillus sydowii : Aspsy1_0129331 and Aspergillus terreus NIH2624 : ATET_05766	null	-4.1185	0.000808	0.003765
AN11959	Putative acylglycerone-phosphate reductase with a predicted role in phospholipid metabolism	null	-4.1185	0.000808	0.003765
AN11990	null	null	6.00104	0.000808	0.003765
AN12330	Has domain(s) with predicted catalytic activity and role in biosynthetic process	null	6.00104	0.000808	0.003765
AN1419	null	null	-6.1725	0.000808	0.003765
AN2252	Ortholog of A. fumigatus Af293 : Afu5g06653, A. niger CBS 513.88 : An17g01010, A. oryzae RIB40 : AO090701000198, Aspergillus versicolor : Aspve1_0496720 and Aspergillus sydowii : Aspsy1_0357115	null	6.07036	0.000808	0.003765
AN2325	Ortholog of A. nidulans FGSC A4 : AN3054, A. fumigatus Af293 : Afu5g10520, A. niger CBS 513.88 : An14g04240, An16g02910, A. oryzae RIB40 : AO090010000486 and A. niger ATCC 1015 : 41807-mRNA, 49061-mRNA	null	-6.1725	0.000808	0.003765
AN2685	Ortholog of A. niger ATCC 1015 : 184563-mRNA, Aspergillus versicolor : Aspve1_0134218, Aspergillus sydowii : Aspsy1_0155644 and Aspergillus terreus NIH2624 : ATET_06110	null	-4.1185	0.000808	0.003765
AN2720	Has domain(s) with predicted catalytic activity	null	6.00104	0.000808	0.003765

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AN3048	Predicted mariner transposon-related ORF	null	6.00104	0.000808	0.003765
AN3304	Putative GABA transporter; transcript repressed by light in developmentally competent mycelia	null	-6.1725	0.000808	0.003765
AN3588	Ortholog(s) have alpha-1,6-mannosyltransferase activity, role in dolichol-linked oligosaccharide biosynthetic process, protein glycosylation and endoplasmic reticulum localization	null	6.00104	0.000808	0.003765
AN3601	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-6.1725	0.000808	0.003765
AN4776	Ortholog(s) have cell division site, cell tip, cytosol, nucleus localization	null	6.00104	0.000808	0.003765
AN5540	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.07036	0.000808	0.003765
AN6431	Putative polyketide synthase	null	-6.1725	0.000808	0.003765
AN6762	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	null	-6.1725	0.000808	0.003765
AN7263	Ortholog of A. oryzae RIB40 : AO090012000392, AO090009000463, Aspergillus flavus NRRL 3357 : AFL2T_03298, Aspergillus acidus : Aspfo1_0050741 and Aspergillus versicolor : Aspve1_0077651	null	-6.1725	0.000808	0.003765
AN8322	Has domain(s) with predicted ADP binding, ATP binding, identical protein binding, microtubule motor activity, role in apoptotic process and kinesin complex localization	null	-6.1725	0.000808	0.003765
AN8340	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.07036	0.000808	0.003765
AN8917	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-4.1185	0.000808	0.003765
AN8020	Putative protein of unknown function; expression upregulated after exposure to farnesol	null	-3.0032	0.000809	0.003766
AN10584	Ortholog(s) have enzyme activator activity, role in iron-sulfur cluster assembly and cytosol, extrinsic to mitochondrial inner membrane, mitochondrial matrix, nucleus localization	null	2.4903	0.000809	0.003766
AN1718	Ortholog of A. nidulans FGSC A4 : AN1714, A. fumigatus Af293 : Afu4g08380, Afu4g08420, A. niger CBS 513.88 : An04g03190, An04g03210 and A. oryzae RIB40 : AO090023000718	null	-2.3389	0.000812	0.003777
AN5965	Ortholog of A. fumigatus Af293 : Afu2g10540, A. niger CBS 513.88 : An02g06010, A. oryzae RIB40 : AO090011000586, A. niger ATCC 1015 : 52252-mRNA and Aspergillus versicolor : Aspve1_0082739	null	-2.2655	0.000815	0.003789
AN0597	Ortholog of A. fumigatus Af293 : Afu6g10970, A. niger ATCC 1015 : 176254-mRNA, Aspergillus versicolor : Aspve1_0023684, Aspergillus sydowii : Aspsy1_0656004 and Aspergillus terreus NIH2624 : ATET_05066	null	2.34269	0.000828	0.003839
AN2040	Putative cytochrome P450	CYP552A2	-3.0392	0.00083	0.003839
AN5877	Putative fatty acyl-CoA synthetase	fatB	-3.3397	0.00083	0.003839
AN7352	Ortholog of A. fumigatus Af293 : Afu2g16390, A. niger CBS 513.88 : An15g06770, A. oryzae RIB40 : AO090102000224, A. niger ATCC 1015 : 182008-mRNA and Aspergillus versicolor : Aspve1_0506157	null	-3.0392	0.00083	0.003839

AN0366	Has domain(s) with predicted membrane localization	null	4.10466	0.000831	0.003839
AN0658	Has domain(s) with predicted DNA binding, copper ion binding, sequence-specific DNA binding transcription factor activity, role in regulation of transcription, DNA-dependent and nucleus localization	null	4.10466	0.000831	0.003839
AN3195	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.4703	0.000831	0.003839
AN4120	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	4.10466	0.000831	0.003839
AN5918	Putative catalase with a predicted role in gluconic acid and gluconate metabolism	catC	-3.4703	0.000831	0.003839
AN5634	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	acuD	-2.2025	0.000833	0.003845
AN1389	Ortholog of A. niger CBS 513.88 : An08g00380, A. oryzae RIB40 : AO090005001637, A. niger ATCC 1015 : 129776-mRNA, Aspergillus versicolor : Aspve1_0059354 and Aspergillus sydowii : Aspsy1_1153720	null	-2.3453	0.000833	0.003846
AN0232	Nickel-binding protein involved in utilization of urea as a nitrogen source	ureD	2.20956	0.000841	0.003877
AN10299	Has domain(s) with predicted carboxy-lyase activity, pyridoxal phosphate binding activity and role in cellular amino acid metabolic process	null	2.33927	0.000841	0.003877
AN11083	Ortholog of A. fumigatus Af293 : Afu3g00660, A. niger CBS 513.88 : An03g00720, A. niger ATCC 1015 : 194178-mRNA, Aspergillus versicolor : Aspve1_0142724 and Aspergillus sydowii : Aspsy1_0049802	null	2.2259	0.000843	0.003883
AN10178	Ortholog(s) have copper ion binding activity, role in metal ion transport, mitochondrial respiratory chain complex IV assembly and cytosol, mitochondrial intermembrane space, nucleus localization	null	2.3791	0.00085	0.003912
AN5768	Ortholog(s) have role in actin cytoskeleton organization, inositol lipid-mediated signaling, vacuole organization and plasma membrane localization	null	2.3791	0.00085	0.003912
AN7190	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	null	-2.3554	0.000858	0.003943
AN8811	Ortholog of A. fumigatus Af293 : Afu5g09500, A. niger CBS 513.88 : An07g03450, A. oryzae RIB40 : AO090020000576, A. niger ATCC 1015 : 40043-mRNA and Aspergillus versicolor : Aspve1_0141760	null	2.4573	0.000858	0.003943
AN0948	Has domain(s) with predicted ATP binding, ATPase activity	null	2.66887	0.000863	0.003957
AN3745	Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more	null	2.66887	0.000863	0.003957
AN5575	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	null	-2.5913	0.000863	0.003957

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AN0797	Putative phosphoribosyl-AMP cyclohydrolase; multifunctional enzyme with a predicted role in histidine metabolism; protein induced by farnesol	null	2.5024	0.000863	0.003957
AN2120	Putative karyopherin (importin) beta 3; expression reduced after exposure to farnesol	kapJ	2.27485	0.000864	0.003958
AN8553	Putative catalase with a predicted role in gluconic acid and gluconate metabolism	null	-2.7528	0.000871	0.003986
AN5008	Ortholog(s) have cytoplasm, nucleus localization	null	2.60221	0.000906	0.004144
AN6812	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in nitrogen compound metabolic process	null	-2.5792	0.000908	0.004147
AN11137	Ortholog of Aspergillus brasiliensis : Aspbr1_0132849, A. niger ATCC 1015 : 204582-mRNA, N. fischeri NRRL 181 : NFIA_037530, Aspergillus acidus : Aspfo1_0144659 and Aspergillus versicolor : Aspve1_0344287	null	2.19215	0.000908	0.004147
AN0844	Protein required for actin cytoskeleton organization and cell cycle progression; ortholog of S. cerevisiae Sda1p;	null	3.27078	0.000917	0.004184
AN12101	Ortholog(s) have NADPH dehydrogenase activity, role in apoptotic process, ergot alkaloid biosynthetic process and cytosol, nucleus localization	null	3.27078	0.000917	0.004184
AN4654	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	null	2.29775	0.000923	0.004211
AN5580	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	null	2.30565	0.000934	0.00426
AN2870	Putative GNAT-type acetyltransferase	ngn15	-2.4874	0.000949	0.004321
AN6038	Ortholog of A. fumigatus Af293 : Afu2g09780, A. niger CBS 513.88 : An16g05430, A. oryzae RIB40 : AO090011000660, A. niger ATCC 1015 : 184220-mRNA and Aspergillus versicolor : Aspve1_0627568	null	2.63656	0.000954	0.004344
AN4729	Ortholog of A. fumigatus Af293 : Afu5g09280, A. niger CBS 513.88 : An07g03730, An14g07330, A. oryzae RIB40 : AO090023000535, AO090020000531 and A. niger ATCC 1015 : 180084-mRNA	null	-2.3224	0.000957	0.004352
AN8076	Predicted DNA binding protein; locus contains the conserved upstream open reading frame (uORF) AN8076-uORF	null	-2.2871	0.000957	0.004352
AN6536	Imidazole glycerol-phosphate dehydratase, catalyzes the seventh enzymatic step in histidine biosynthesis; expression is under the cross-pathway control regulatory system; mutation blocks sexual development	hisB	2.49872	0.000963	0.004378
AN3293	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.9529	0.000967	0.004389
AN1003	Putative isocitrate dehydrogenase (NAD+) with a predicted role in the TCA cycle; intracellular, menadione stress-induced protein	null	2.2614	0.000967	0.004389

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AN5983	Ortholog of A. fumigatus Af293 : Afu2g10260, A. niger CBS 513.88 : An16g04730, A. oryzae RIB40 : AO090011000610, A. niger ATCC 1015 : 184314-mRNA and Aspergillus versicolor : Aspve1_0027901	null	-2.2019	0.000974	0.00442
AN9304	Glutathione S-transferase; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.14043	0.001004	0.004552
AN12279	Putative chitinase; glycoside hydrolase family 18 (GH18) protein with a predicted role in chitin hydrolysis	null	3.03045	0.001007	0.004564
AN11803	Ortholog(s) have cytosol, nucleus localization	null	2.72311	0.001009	0.004566
AN2794	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	2.42361	0.001011	0.004573
AN5576	Ortholog of A. fumigatus Af293 : Afu4g11590, A. niger CBS 513.88 : An04g04860, A. oryzae RIB40 : AO090003001061, A. niger ATCC 1015 : 45439-mRNA and Aspergillus versicolor : Aspve1_0042237	null	3.41169	0.001016	0.004592
AN11177	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-3.686	0.001024	0.00462
AN12013	null	null	-3.686	0.001024	0.00462
AN1503	Protein expressed at increased levels during osmoadaptation; contains dihydrodipicolinate synthase family DHDPS-like conserved domain	null	-3.686	0.001024	0.00462
AN8574	null	null	-3.686	0.001024	0.00462
AN1319	Ortholog(s) have RNA binding activity and role in mRNA splicing, via spliceosome, maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	null	2.39917	0.001026	0.004623
AN3459	Ortholog(s) have metallodipeptidase activity, omega peptidase activity, role in glutathione catabolic process and cytosol, mitochondrion, nucleus, ribosome localization	null	-2.1275	0.001027	0.004625
AN5447	Putative glutamate decarboxylase with a predicted role in 4-aminobutyrate (GABA) shunt	null	2.2041	0.001028	0.004628
AN3824	Ortholog(s) have phenylalanine-tRNA ligase activity and cytosol, phenylalanine-tRNA ligase complex localization	null	2.23248	0.001034	0.004652
AN7572	Putative response regulator of a two-component phosphorelay system	srrB	-2.1995	0.001042	0.004684
AN3159	Has domain(s) with predicted guanyl-nucleotide exchange factor activity, role in regulation of small GTPase mediated signal transduction, small GTPase mediated signal transduction and intracellular localization	null	4.06322	0.001049	0.004715
AN10336	Ortholog(s) have acetyltransferase activity, chromatin binding activity	null	-2.3296	0.00105	0.004717
AN0610	Ortholog(s) have cytosol, nucleus localization	null	-2.5639	0.001056	0.00474
AN0941	Protein with alpha-glucosidase activity, predicted role in maltose metabolism; transcriptionally induced by isomaltose in an amyR-dependent manner	agdE	2.43718	0.001062	0.004762

AN8457	Has domain(s) with predicted microtubule motor activity, role in nucleoside metabolic process and kinesin complex localization	null	-2.5579	0.001073	0.00481
AN5349	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	null	3.24346	0.001077	0.004825
AN6437	Ortholog of Aspergillus versicolor : Aspve1_0052718 and Aspergillus sydowii : Aspsy1_0031878	null	3.24346	0.001077	0.004825
AN6058	DUF833 domain-containing protein; intracellular, menadione stress-induced protein	null	2.13262	0.001088	0.004868
AN0481	null	null	-2.2313	0.001089	0.00487
AN1080	Has domain(s) with predicted translation initiation factor activity, role in translational initiation and cytoplasm localization	null	-2.4675	0.001099	0.004911
AN9375	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	2.4937	0.001108	0.004952
AN6104	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	null	-2.1353	0.001111	0.004961
AN11892	Ortholog(s) have 3'-tRNA processing endoribonuclease activity, role in tRNA 3'-trailer cleavage, endonucleolytic and mitochondrion, nucleus localization	null	2.31569	0.001119	0.004993
AN1270	Putative translation initiation factor 3, subunit h (eIF-3h); expression reduced after exposure to farnesol	null	2.29658	0.001124	0.005011
AN12181	null	null	2.42632	0.001137	0.005049
AN7686	Ortholog of A. fumigatus Af293 : Afu2g01670, A. niger CBS 513.88 : An03g04770, A. oryzae RIB40 : AO090701000780, Aspergillus versicolor : Aspve1_0085624 and Aspergillus sydowii : Aspsy1_0152669	null	-2.151	0.001138	0.005049
AN4906	Ortholog(s) have endoplasmic reticulum localization	null	-2.1399	0.00114	0.005049
AN0365	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	null	2.23655	0.001151	0.005049
AN0018	Possible pseudogene	null	-6.0587	0.001152	0.005049
AN0577	null	null	-6.0587	0.001152	0.005049
AN1067	Has domain(s) with predicted oxidoreductase activity, role in antibiotic biosynthetic process and cytoplasm localization	null	-6.0587	0.001152	0.005049
AN11015	Has domain(s) with predicted S-(hydroxymethyl)glutathione synthase activity, zinc ion binding activity and role in formaldehyde catabolic process	null	-6.0587	0.001152	0.005049
AN11772	Ortholog of A. fumigatus Af293 : Afu3g10060, A. niger CBS 513.88 : An16g03810, A. oryzae RIB40 : AO090003000539, A. niger ATCC 1015 : 183471-mRNA and Aspergillus versicolor : Aspve1_0081939	null	5.92823	0.001152	0.005049
AN12061	null	null	-4.0047	0.001152	0.005049

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AN12388	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	null	-4.0047	0.001152	0.005049
AN1477	Putative beta-1,4-xylosidase	null	-6.0587	0.001152	0.005049
AN1877	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-6.0587	0.001152	0.005049
AN1925	null	null	-6.0587	0.001152	0.005049
AN3380	Putative fatty-acyl-CoA synthase with a predicted role in cytosolic fatty acid formation; involved in secondary metabolite production	pkiB	-6.0587	0.001152	0.005049
AN3987	Tetratricopeptide repeat domain-containing protein; intracellular, menadione stress-induced protein	null	5.92823	0.001152	0.005049
AN4524	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	-6.0587	0.001152	0.005049
AN5017	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-4.0047	0.001152	0.005049
AN5305	Has domain(s) with predicted catalytic activity	null	-6.0587	0.001152	0.005049
AN5691	Ortholog(s) have cytosol, nucleus localization	null	-6.0587	0.001152	0.005049
AN5837	Putative cytochrome P450	CYP630B2	-6.0587	0.001152	0.005049
AN6128	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity, role in carbohydrate metabolic process and membrane localization	null	5.92823	0.001152	0.005049
AN7061	Putative transcription factor; predicted role in secondary metabolite production	null	-6.0587	0.001152	0.005049
AN7186	Ortholog of A. fumigatus Af293 : Afu5g14180, A. niger CBS 513.88 : An14g05580, A. oryzae RIB40 : AO090001000217, A. niger ATCC 1015 : 185461-mRNA and Aspergillus versicolor : Aspve1_0186358	null	-6.0587	0.001152	0.005049
AN7275	Putative beta-1,4-xylosidase	null	-6.0587	0.001152	0.005049
AN7744	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	null	-6.0587	0.001152	0.005049
AN7819	Ortholog(s) have role in aflatoxin biosynthetic process, regulation of aflatoxin biosynthetic process	null	-6.0587	0.001152	0.005049
AN8566	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	null	-4.0047	0.001152	0.005049
AN9274	Ortholog of A. fumigatus Af293 : Afu3g14810, A. niger CBS 513.88 : An02g03200, An04g09720, An04g08110, A. oryzae RIB40 : AO090103000427 and A. niger ATCC 1015 : 55177-mRNA	null	-4.0047	0.001152	0.005049
AN7375	Has domain(s) with predicted role in lipid biosynthetic process	null	2.17265	0.001158	0.00507

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AN0783	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	null	-2.9008	0.001158	0.00507
AN4178	UPF0160 domain-containing protein; intracellular; protein abundance decreased by menadione stress	myg1	2.50846	0.001168	0.005106
AN2583	Putative glyceraldehyde-3-phosphate dehydrogenase with a predicted role in gluconeogenesis and glycolysis	gpdC	-2.8346	0.001168	0.005106
AN3216	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-2.536	0.00117	0.005111
AN0270	Ortholog(s) have role in cellular bud site selection, pyridoxal phosphate biosynthetic process and cytosol, nucleus localization	null	2.45339	0.001194	0.005208
AN1601	Putative cytochrome P450; O-methylsterigmatocystin oxidoreductase with a predicted role in sterigmatocystin/aflatoxin biosynthesis	CYP620E1	-2.4046	0.001194	0.005208
AN4473	Ortholog of A. nidulans FGSC A4 : AN5608, A. fumigatus Af293 : Afu4g07720, A. niger CBS 513.88 : An14g07030, An04g02100 and A. oryzae RIB40 : AO090023000800, AO090009000070	null	-2.3464	0.001194	0.005208
AN3649	Ortholog(s) have role in fatty acid metabolic process	null	2.14541	0.001198	0.005224
AN2741	Has domain(s) with predicted selenium binding activity and role in cell redox homeostasis	null	2.7919	0.001206	0.00525
AN6223	Ortholog(s) have RNA polymerase II repressing transcription factor binding, RNA polymerase II transcription coactivator activity, RNA polymerase II transcription corepressor activity	null	2.7919	0.001206	0.00525
AN9444	Ortholog of A. nidulans FGSC A4 : AN7400, Aspergillus flavus NRRL 3357 : AFL2T_02908, Aspergillus acidus : Aspfo1_0034827, Aspergillus versicolor : Aspve1_0037710 and Aspergillus sydowii : Aspsy1_0038876	null	-2.5269	0.00121	0.005266
AN1056	Ortholog(s) have cytosol, nucleus localization	null	2.32799	0.001213	0.005276
AN7231	Has domain(s) with predicted serine-type peptidase activity and role in proteolysis	null	-2.1409	0.001214	0.005276
AN4846	Ortholog of A. nidulans FGSC A4 : AN3529, AN4144, AN8311, A. fumigatus Af293 : Afu1g17260, Afu4g07950, Afu4g09380, Afu6g00560, Afu6g12140, Afu8g01900 and A. niger CBS 513.88 : An16g06170, An06g00470, An11g07840	null	-2.645	0.001242	0.005397
AN2999	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	idpA	-2.2793	0.001244	0.005398
AN5713	Putative chaperonin complex component, TCP-1 eta subunit; ortholog of S. cerevisiae Cct7p; expression reduced after exposure to farnesol	cct7	2.09607	0.001244	0.005398
AN2079	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, nucleus localization	null	2.66955	0.001254	0.005436

AN2427	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.66955	0.001254	0.005436
AN0428	Putative lysyl-tRNA synthetase with a predicted role in tRNA aminoacylation	null	2.34133	0.001259	0.005451
AN3021	Ortholog of A. fumigatus Af293 : Afu3g08920, A. niger CBS 513.88 : An16g02420, A. oryzae RIB40 : AO090005001345, A. niger ATCC 1015 : 41197-mRNA and Aspergillus versicolor : Aspve1_0051328	null	-2.3852	0.001259	0.005451
AN1439	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	null	3.21562	0.001269	0.005487
AN2845	Ortholog of A. fumigatus Af293 : Afu3g12260, A. oryzae RIB40 : AO090003000791, A. niger ATCC 1015 : 37158-mRNA, Aspergillus versicolor : Aspve1_0081846 and Aspergillus sydowii : Aspsy1_0087513	null	3.18723	0.001269	0.005487
AN12119	Has domain(s) with predicted N-methyltransferase activity, protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity and role in C-terminal protein methylation, phospholipid metabolic process	null	2.34638	0.001278	0.005522
AN5849	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	null	-2.1155	0.001279	0.005524
AN1710	Ortholog(s) have aspartate-tRNA ligase activity, role in mitochondrial aspartyl-tRNA aminoacylation and mitochondrion localization	null	2.3811	0.001282	0.005533
AN4210	Has domain(s) with predicted RNA polymerase II transcription cofactor activity, zinc ion binding activity, role in regulation of transcription from RNA polymerase II promoter and mediator complex localization	null	-2.1248	0.001301	0.005613
AN11897	Has domain(s) with predicted RNA binding, ribonuclease T2 activity	null	-2.3289	0.001306	0.005631
AN8770	Putative bifunctional enzyme with a predicted role in arginine metabolism; putative acetylglutamate kinase	null	2.20386	0.001307	0.005632
AN6347	Has domain(s) with predicted ATP binding, protein serine/threonine kinase activity, protein tyrosine kinase activity and role in protein phosphorylation	null	-2.363	0.001308	0.005632
AN1328	Putative GNAT-type acetyltransferase	nnaA	2.1706	0.001327	0.005709
AN2483	Protein of unknown function; transcript repressed by nitrate	null	-3.4005	0.001331	0.005724
AN7138	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.17237	0.001335	0.005738
AN6048	Putative aspartate transaminase with a predicted role in amino acid metabolism; palA-dependent expression independent of pH; induced by carbon starvation-induced autophagy	null	2.07621	0.00135	0.005802
AN6014	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	faaA	-2.0793	0.001355	0.005818

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AN3725	Developmentally regulated protein with similarity to Candida albicans Wh11p; transcription is repressed by StuA; expression upregulated after exposure to farnesol	awh11	-2.6052	0.001357	0.005818
AN4843	Putative alpha-glucosidase with a predicted role in maltose metabolism	agdG	-2.4926	0.001357	0.005818
AN0159	Ortholog of Aspergillus versicolor : Aspve1_0023174 and Aspergillus sydowii : Aspsy1_0054986	null	-3.5995	0.00136	0.005824
AN11222	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	null	-3.5995	0.00136	0.005824
AN7227	Ortholog of Aspergillus versicolor : Aspve1_0123469 and Aspergillus sydowii : Aspsy1_0140327	null	-3.5995	0.00136	0.005824
AN10794	Has domain(s) with predicted ATP binding, DNA binding, helicase activity, zinc ion binding activity	null	-2.2035	0.001367	0.005849
AN10873	Ortholog(s) have mitochondrion localization	null	2.11417	0.001377	0.005888
AN10282	Ortholog(s) have cytosol, nucleus localization	null	2.33351	0.001381	0.005901
AN7146	Putative S-adenosyl-methionine delta-24-sterol-C-methyltransferase with a predicted role in sterol metabolism	null	2.22149	0.001386	0.00592
AN1102	Putative serine C-palmitoyltransferase with a predicted role in sphingoglycolipid metabolism	null	2.13086	0.001397	0.005963
AN3831	Ortholog of A. fumigatus Af293 : Afu4g08130, A. niger CBS 513.88 : An04g02570, A. oryzae RIB40 : AO090023000757, A. niger ATCC 1015 : 203569-mRNA and Aspergillus versicolor : Aspve1_0041892	null	2.15763	0.001401	0.00597
AN10036	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.65125	0.001401	0.00597
AN6588	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	null	-2.4851	0.001401	0.00597
AN4081	Has domain(s) with predicted cysteine dioxygenase activity, iron ion binding activity and role in L-cysteine metabolic process, oxidation-reduction process	null	-2.1372	0.001407	0.005993
AN1437	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-2.4093	0.001422	0.006049
AN5638	Ortholog(s) have ubiquitin-specific protease activity, role in protein deubiquitination and cytosol, ribosome localization	null	2.45356	0.001422	0.006049
AN5991	Putative peroxisomal protein (peroxin) with a role in fatty acid utilization; required for growth on long chain fatty acids	pexA	-2.1249	0.001434	0.006097
AN2008	Ortholog(s) have phosphatidylglycerophosphatase activity, role in cardiolipin biosynthetic process, phosphorylated carbohydrate dephosphorylation and mitochondrial matrix localization	null	2.392	0.001436	0.006103
AN4633	Ortholog(s) have role in protein import into mitochondrial matrix and mitochondrial inner membrane presequence translocase complex localization	null	2.09313	0.001443	0.006128
AN4865	Has domain(s) with predicted nucleic acid binding, nucleotide binding activity	null	2.07385	0.001462	0.006207

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AN3684	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	null	-2.3435	0.001466	0.006218
AN8496	Has domain(s) with predicted metal ion binding activity	null	-2.2726	0.001467	0.006218
AN8229	Ortholog(s) have membrane insertase activity, mitochondrial ribosome binding activity	null	2.11532	0.001485	0.00629
AN1900	Has domain(s) with predicted zinc ion binding activity	null	2.40659	0.001485	0.00629
AN4347	Ortholog(s) have nucleus localization	null	3.15827	0.001498	0.00634
AN8859	Putative aspartate kinase with a predicted role in glycine, serine, and threonine metabolism	null	2.56505	0.0015	0.006344
AN8273	Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism; hapX-repressed; protein levels decrease in response to farnesol	null	2.07796	0.001524	0.006444
AN1450	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	null	-2.0513	0.001527	0.006449
AN0049	Ortholog(s) have endoplasmic reticulum localization	null	2.73245	0.001528	0.006449
AN10838	Has domain(s) with predicted cation binding, chitin binding, chitinase activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, chitin catabolic process	null	2.73245	0.001528	0.006449
AN9080	Ortholog(s) have cytosol, nucleus localization	null	2.30208	0.001536	0.00647
AN10767	Purine-cytosine transporter; localized to the plasma membrane; abundantly expressed in ascogenous hyphae, hulle cells and young asci	fcyB	3.33829	0.001537	0.00647
AN2326	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity, role in GPI anchor metabolic process, intracellular protein transport and intrinsic to endoplasmic reticulum membrane localization	null	-2.9198	0.001537	0.00647
AN6477	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane localization	null	3.30014	0.001537	0.00647
AN5115	Has domain(s) with predicted DNA binding activity	null	2.42616	0.001547	0.006505
AN6072	Ortholog(s) have protein-arginine N5-methyltransferase activity, role in peptidyl-arginine methylation and cytosol, nucleus localization	null	2.42616	0.001547	0.006505
AN9124	Ortholog(s) have ATPase inhibitor activity, Hsp70 protein binding, Hsp90 protein binding, mRNA binding activity, role in protein folding and cytosol, nucleus localization	null	2.13587	0.001563	0.006569
AN1673	Has domain(s) with predicted 3-deoxy-7-phosphoheptulonate synthase activity and role in aromatic amino acid family biosynthetic process	null	-2.2106	0.00157	0.006594
AN2639	Has domain(s) with predicted hydrolase activity	null	2.90341	0.001578	0.006625
AN1037	Oleate delta-12 desaturase; transcriptionally regulated by low temperature and by light	odeA	2.29432	0.00159	0.006672

AN2397	Ortholog of A. fumigatus Af293 : Afu8g06960, N. fischeri NRRL 181 : NFIA_099650, Aspergillus flavus NRRL 3357 : AFL2T_05473 and Aspergillus versicolor : Aspve1_0026050	null	-2.4785	0.001598	0.006701
AN8812	Has domain(s) with predicted ATP binding, ATPase activity, phosphatidylinositol phospholipase C activity and role in intracellular signal transduction, lipid metabolic process	null	-2.2869	0.001599	0.006701
AN3134	Ortholog(s) have chaperonin-containing T-complex, nucleus localization	null	2.0915	0.001601	0.006707
AN2283	Ortholog(s) have nucleolus localization	null	2.3479	0.001613	0.006748
AN7225	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.35937	0.001613	0.006748
AN10404	Ortholog of A. fumigatus Af293 : Afu7g01410, A. niger CBS 513.88 : An12g01490, A. oryzae RIB40 : AO090010000217, N. fischeri NRRL 181 : NFIA_114100 and A. clavatus NRRL 1 : ACLA_066160	null	-2.2151	0.001615	0.006755
AN0430	Ortholog of S. cerevisiae : STB6, A. fumigatus Af293 : Afu1g04480, A. niger CBS 513.88 : An01g03630, A. oryzae RIB40 : AO090003000868 and A. niger ATCC 1015 : 170355-mRNA	null	-2.1938	0.001636	0.006839
AN7361	Ortholog(s) have role in mitochondrial translation and mitochondrion localization	null	2.7453	0.001639	0.006842
AN10672	Has domain(s) with predicted catalytic activity	null	-3.8812	0.001662	0.006842
AN11798	Has domain(s) with predicted hydrolase activity	null	-5.9351	0.001662	0.006842
AN12199	Ortholog of Aspergillus brasiliensis : Aspbr1_0078801, A. clavatus NRRL 1 : ACLA_074610, Aspergillus acidus : Aspfo1_0207590 and Aspergillus versicolor : Aspve1_0080732	null	-3.8812	0.001662	0.006842
AN2444	null	null	-5.9351	0.001662	0.006842
AN2541	Putative alpha-N-arabinofuranosidase with a predicted role in arabinose polymer metabolism; the feature AN9520 has been merged into AN2541	abfA	-5.9351	0.001662	0.006842
AN2679	Ortholog of Aspergillus versicolor : Aspve1_0133833 and Aspergillus sydowii : Aspsy1_1181333	null	-5.9351	0.001662	0.006842
AN2723	Putative multifunctional enzyme with a predicted role in histidine metabolism	null	-5.9351	0.001662	0.006842
AN3077	null	null	-5.9351	0.001662	0.006842
AN3230	Putative polyketide synthase	pkfA	-5.9351	0.001662	0.006842
AN3249	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.9351	0.001662	0.006842
AN3564	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.9351	0.001662	0.006842
AN3903	Putative beta-glucosidase with a predicted role in polysaccharide degradation	bglH	-3.8812	0.001662	0.006842
AN4304	Ortholog(s) have disulfide oxidoreductase activity, role in cellular response to oxidative stress, response to osmotic stress and mitochondrial matrix localization	null	5.85154	0.001662	0.006842
AN4649	Ortholog(s) have Golgi apparatus, endoplasmic reticulum localization	null	5.85154	0.001662	0.006842

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AN5400	Ortholog of A. nidulans FGSC A4 : AN9282, AN0025, AN7063, AN7804/stcW, AN8757, A. fumigatus Af293 : Afu6g03020, Afu6g13790 and A. niger CBS 513.88 : An08g09190, An03g06480, An11g08030, An13g01810, An12g07380	null	-5.9351	0.001662	0.006842
AN5672	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.9351	0.001662	0.006842
AN6198	Ortholog of A. fumigatus Af293 : Afu2g11790, A. niger CBS 513.88 : An02g03840, A. oryzae RIB40 : AO090026000463, A. niger ATCC 1015 : 175169-mRNA and Aspergillus versicolor : Aspve1_0130915	null	-3.8812	0.001662	0.006842
AN6283	Ortholog(s) have role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and cytosol, nucleus localization	null	5.85154	0.001662	0.006842
AN6395	Protein with rhamnogalacturonan lyase activity, involved in degradation of pectin	rglB	-5.9351	0.001662	0.006842
AN6776	Has domain(s) with predicted hydrolase activity	null	-5.9351	0.001662	0.006842
AN7383	Ortholog of A. oryzae RIB40 : AO090010000377, Aspergillus flavus NRRL 3357 : AFL2T_11553, Aspergillus versicolor : Aspve1_0137812 and Aspergillus sydowii : Aspsy1_0092249	null	-5.9351	0.001662	0.006842
AN8149	Protein with alpha-fucosidase activity, involved in degradation of xyloglucans	afcA	-3.8812	0.001662	0.006842
AN8727	Ortholog of A. nidulans FGSC A4 : AN3303, AN3348, AN2044, A. fumigatus Af293 : Afu4g10080, Afu7g00420, Afu4g01242 and A. niger CBS 513.88 : An02g09530, An03g00420, An16g01900, An16g06080, An04g06980, An03g00215	null	5.85154	0.001662	0.006842
AN8733	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	5.85154	0.001662	0.006842
AN8998	Putative dioxygenase	null	-5.9351	0.001662	0.006842
AN9002	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.8812	0.001662	0.006842
AN6982	Putative phosphotyrosine-specific protein phosphatase of the HOG signaling pathway that regulates osmotic stress response	ptpA	-2.0988	0.001674	0.00689
AN5509	Putative F-box protein	null	-2.8467	0.001676	0.006892
AN7794	Has domain(s) with predicted chitin binding activity	null	-2.1472	0.001681	0.006909
AN2577	Has domain(s) with predicted oxidoreductase activity and role in metabolic process	null	-2.3859	0.001683	0.006911
AN5589	Putative glycerol kinase with a predicted role in glycerol metabolism; required for growth on glycerol; transcript upregulated by growth in glycerol	null	-2.1093	0.001683	0.006911
AN3681	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	null	-2.1964	0.001693	0.006946
AN0908	Ortholog(s) have DNA binding, bending and RNA polymerase III type 1 promoter sequence-specific DNA binding, more	null	3.93124	0.001697	0.006946

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AN12343	Ortholog of Aspergillus brasiliensis : Aspbr1_0032227, A. niger ATCC 1015 : 188904-mRNA, A. clavatus NRRL 1 : ACLA_001690, Aspergillus acidus : Aspfo1_0051036 and Aspergillus versicolor : Aspve1_0057213	null	3.93124	0.001697	0.006946
AN6757	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-3.3272	0.001697	0.006946
AN8391	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	null	-3.3272	0.001697	0.006946
AN4050	Putative salicylaldehyde dehydrogenase with a predicted role in naphthalene degradation	null	-2.3195	0.001698	0.006947
AN6083	Ortholog(s) have role in ribosomal large subunit assembly, translational termination and cytosol localization	null	2.10252	0.001701	0.006956
AN0591	Ortholog(s) have cytosol, nucleus localization	null	2.42198	0.001711	0.006991
AN7525	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding activity	null	2.33634	0.001731	0.007073
AN7497	Has domain(s) with predicted oxidoreductase activity, acting on NADH or NADPH activity, role in electron transport chain and mitochondrial inner membrane localization	null	2.05774	0.001737	0.007094
AN1715	Putative mannose-6-phosphate isomerase with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism	null	-2.2289	0.001748	0.007132
AN10642	Ortholog(s) have ubiquinone binding activity, role in cellular respiration and mitochondrial inner membrane localization	null	2.5949	0.001753	0.007147
AN6236	Putative nonribosomal peptide synthetase	null	2.03335	0.001762	0.007181
AN3013	Ortholog(s) have cytoplasm localization	null	-2.0854	0.001763	0.007181
AN6023	Has domain(s) with predicted FMN binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.7912	0.001772	0.007215
AN1862	Ortholog of A. fumigatus Af293 : Afu4g09790, A. niger CBS 513.88 : An04g07280, A. niger ATCC 1015 : 45270-mRNA, Aspergillus versicolor : Aspve1_0117695 and Aspergillus sydowii : Aspsy1_0138374	null	-2.1052	0.001775	0.007223
AN7007	Ortholog(s) have protein heterodimerization activity	null	-2.1351	0.001818	0.007394
AN6645	Putative 8-amino-7-oxononanoate synthase with a predicted role in Coenzyme A and pantothenate biosynthesis	bioF	2.15157	0.001819	0.007394
AN6139	Putative 1-acylglycerol-3-phosphate acyltransferase with a predicted role in phospholipid metabolism	null	2.44619	0.001823	0.007401
AN7040	Ortholog of A. nidulans FGSC A4 : AN11062, A. fumigatus Af293 : Afu5g03780, A. niger CBS 513.88 : An14g00780, An09g06380, A. oryzae RIB40 : AO090206000110 and A. niger ATCC 1015 : 185495-mRNA, 50029-mRNA	null	2.44619	0.001823	0.007401

AN5865	Putative GTP-binding protein; S. cerevisiae ortholog Nog1p has role in ribosomal subunit export from nucleus, ribosomal large subunit biogenesis and rRNA processing; expression reduced after exposure to farnesol	null	2.08088	0.001834	0.007444
AN4216	Ortholog(s) have mitochondrion localization	null	2.03949	0.001838	0.007448
AN10099	Has domain(s) with predicted FMN binding, pyridoxamine-phosphate oxidase activity and role in oxidation-reduction process	null	-2.7476	0.001839	0.007448
AN4552	Ortholog of Ku80; 80 kDa subunit of Ku70/Ku80 complex involved in non-homologous double-stranded break repair	nkuB	2.8766	0.001839	0.007448
AN8668	Ortholog(s) have role in rRNA processing, ribosomal large subunit assembly and nucleoplasm, spindle pole body localization	null	2.8766	0.001839	0.007448
AN10495	Has domain(s) with predicted CoA-transferase activity and role in ketone body catabolic process	null	-2.2458	0.001855	0.007503
AN5939	Putative 5'-nucleotidase with a predicted role in nucleotide salvage pathways; predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.028	0.001855	0.007503
AN10115	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.2511	0.00186	0.007518
AN1151	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	null	-2.5653	0.001887	0.007625
AN3312	Putative L-xylulose reductase	null	-3.1567	0.0019	0.00767
AN8173	Ortholog(s) have actin monomer binding, protein kinase inhibitor activity, ribosome binding activity, role in negative regulation of protein phosphorylation and cytoplasm, nucleus, polysome, ribosome localization	null	3.26095	0.0019	0.00767
AN1455	Ortholog(s) have dolichyl-diphosphooligosaccharide-protein glycotransferase activity, role in protein N-linked glycosylation and oligosaccharyltransferase complex localization	null	2.06433	0.001924	0.007761
AN10070	Ortholog of A. fumigatus Af293 : Afu1g01790, A. niger CBS 513.88 : An01g06420, A. oryzae RIB40 : AO090005000908, A. niger ATCC 1015 : 170638-mRNA and Aspergillus versicolor : Aspve1_0035815	null	2.69142	0.001946	0.007835
AN1730	Protein of the prn gene cluster; predicted to be involved in proline metabolism	prnX	2.69142	0.001946	0.007835
AN2043	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-2.5368	0.001946	0.007835
AN8851	Predicted pseudouridylate synthase, involved in establishment of cell polarity; mutants show defects in anisotropic growth, endocytosis, nuclear distribution and compartmentation; transcript upregulated in response to camptothecin	swoC	2.08219	0.00195	0.00785
AN5210	Putative pyruvate kinase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein	pkiA	2.05409	0.001961	0.007888

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AN4890	Ortholog(s) have role in Golgi to plasma membrane transport, exocytosis and cell division site, cell tip, plasma membrane localization	null	-2.1508	0.001963	0.007892
AN4746	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	null	2.4815	0.001976	0.00794
AN8497	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	2.12228	0.001985	0.007974
AN2293	Putative phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase with a predicted role in histidine metabolism	null	2.43114	0.001995	0.008008
AN6701	Ortholog of A. fumigatus Af293 : Afu7g05650, A. niger CBS 513.88 : An07g02600, A. oryzae RIB40 : AO090005000427, Aspergillus versicolor : Aspve1_0056558 and Aspergillus sydowii : Aspsy1_0034940	null	-2.2686	0.001998	0.008012
AN5557	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	2.3011	0.001998	0.008012
AN3672	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	null	-2.2786	0.001999	0.008012
AN3334	Has domain(s) with predicted nucleotide binding activity	null	-2.7905	0.002025	0.008102
AN3683	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	null	-2.7905	0.002025	0.008102
AN6704	null	null	-2.7905	0.002025	0.008102
AN11095	Ortholog of A. niger CBS 513.88 : An03g02610, A. niger ATCC 1015 : 45669-mRNA, A. clavatus NRRL 1 : ACLA_008440 and Aspergillus sydowii : Aspsy1_1049915	null	2.17123	0.002042	0.008167
AN5216	Ortholog(s) have role in nucleotide-excision repair and nucleus localization	null	-2.1362	0.002073	0.008287
AN1970	Ortholog(s) have cytoplasm localization	null	2.19475	0.002089	0.008346
AN7248	Ortholog of A. fumigatus Af293 : Afu2g17200, A. niger CBS 513.88 : An04g09270, A. oryzae RIB40 : AO090102000099, A. niger ATCC 1015 : 194752-mRNA and Aspergillus versicolor : Aspve1_0125338	null	3.06772	0.002101	0.00839
AN1713	Ortholog(s) have calcium-independent phospholipase A2 activity, lysophosphatidic acid acyltransferase activity, sterol esterase activity, triglyceride lipase activity	null	-2.0621	0.002127	0.008477
AN2854	Ortholog(s) have RNA polymerase II core promoter proximal region sequence-specific DNA binding, more	null	-2.1986	0.002127	0.008477
AN1948	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	null	-2.0401	0.002127	0.008477
AN0745	Putative nucleolar protein; ortholog of S. cerevisiae Nop1p; related to mammalian fibrillarin; expression reduced after exposure to farnesol	null	2.03582	0.00213	0.008487

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AN1176	Putative long chain base kinase with a predicted role in sphingoglycolipid metabolism	null	2.84928	0.002148	0.008535
AN11982	null	null	-2.5382	0.002148	0.008535
AN2554	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	null	-2.702	0.002148	0.008535
AN3797	Ortholog(s) have role in cellular response to UV, postreplication repair, recombinational repair and nucleus, spindle pole body localization	null	2.84928	0.002148	0.008535
AN7183	Protein of unknown function; transcript upregulated by nitrate limitation	null	-2.5382	0.002148	0.008535
AN6699	Ortholog(s) have mitochondrion localization	null	-1.9917	0.002152	0.008547
AN8057	Cysteine synthase; plays a role in amino acid metabolism	cysB	2.05188	0.002161	0.008575
AN2553	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	null	-3.25	0.002174	0.008615
AN3799	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	null	3.88442	0.002174	0.008615
AN7943	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-3.25	0.002174	0.008615
AN0246	Ortholog of A. fumigatus Af293 : Afu1g05300, A. niger CBS 513.88 : An01g04570, A. oryzae RIB40 : AO090003000826, A. niger ATCC 1015 : 119367-mRNA and Aspergillus versicolor : Aspve1_0122336	null	2.6717	0.002176	0.008618
AN10422	null	null	2.47022	0.002191	0.008673
AN4009	Has domain(s) with predicted transferase activity, transferring acyl groups other than amino-acyl groups activity and role in metabolic process	null	-2.3014	0.002196	0.008685
AN5933	Ortholog of A. fumigatus Af293 : Afu2g10720, A. niger CBS 513.88 : An02g02500, A. niger ATCC 1015 : 173949-mRNA, Aspergillus versicolor : Aspve1_0052165 and Aspergillus sydowii : Aspsy1_0044922	null	-2.3872	0.002196	0.008685
AN10235	Ortholog of A. fumigatus Af293 : Afu2g04400, A. oryzae RIB40 : AO090003001565, A. niger ATCC 1015 : 179194-mRNA and Aspergillus terreus NIH2624 : ATET_06071	null	-2.3877	0.0022	0.008695
AN10164	Ortholog(s) have mRNA binding, poly(U) RNA binding activity and role in nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, regulation of mRNA stability, stress granule assembly	null	-2.3882	0.002202	0.008696
AN8206	Ortholog(s) have mitochondrion localization	null	2.1775	0.002203	0.008697
AN0404	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	null	2.01881	0.002212	0.008729
AN9140	Putative MFS-type amino acid transporter; transcript repressed by nitrogen limitation	null	-2.1937	0.002245	0.008852
AN1950	Ortholog(s) have FAD transmembrane transporter activity, calcium channel activity	null	-2.0587	0.002255	0.00889

AN1959	Nuclear protein involved in spore formation and trehalose accumulation; potential transcription-activating domain; mutants have low spore viability; two overlapping transcripts; VosA-VelB form a dimeric complex in hyphae grown in the dark	vosA	-2.1354	0.002264	0.008917
AN5646	Putative enzyme with a predicted role in fatty acid degradation	null	-2.0602	0.002278	0.008967
AN5712	Putative metacaspase	casA	-2.0785	0.002289	0.009006
AN3070	Ortholog(s) have chaperonin-containing T-complex, nucleus localization	null	2.00975	0.002294	0.009022
AN2899	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	null	-2.2172	0.002296	0.009024
AN3687	Ortholog(s) have cytosol, nucleus localization	null	2.19519	0.002298	0.009028
AN11938	null	null	-1.9804	0.002304	0.009048
AN3634	Putative anthranilate phosphoribosyltransferase with a predicted role in aromatic amino acid biosynthesis	null	2.14479	0.00231	0.009065
AN4102	Putative beta-glucosidase; induced by carbon starvation-induced autophagy	bglA	-2.0042	0.002315	0.009082
AN8765	Protein with a predicted role in the regulation of chitin synthase activity	null	-2.2563	0.002341	0.00918
AN11152	Putative 1,3-beta-transglycosidase with a predicted role in glucan processing; predicted glycosylphosphatidylinositol (GPI)-anchored protein	gelD	3.22067	0.002359	0.009235
AN1579	Ortholog of A. nidulans FGSC A4 : AN12486, A. oryzae RIB40 : AO090003001382, N. fischeri NRRL 181 : NFIA_081910 and A. clavatus NRRL 1 : ACLA_089450	null	-2.7896	0.002359	0.009235
AN7247	null	null	-3.0902	0.002359	0.009235
AN2703	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	null	2.09739	0.002386	0.009328
AN6564	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	2.09739	0.002386	0.009328
AN1205	Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and nucleus, prefoldin complex localization	null	2.385	0.002394	0.009357
AN7687	Ortholog(s) have mitochondrion localization	null	1.973	0.002404	0.00939
AN6217	Putative F-box protein	null	-2.0726	0.002409	0.009404
AN10220	Putatice cytochrome c peroxidase; intracellular; protein abundance decreased by menadione stress	ccp1	-2.0668	0.002421	0.009443
AN1216	Putative glycerol 3-phosphate phosphatase with a predicted role in glycerol metabolism	gppA	2.24686	0.002421	0.009443
AN1847	null	null	-1.9941	0.002429	0.009468
AN3164	Ortholog of A. fumigatus Af293 : Afu3g13430, A. niger CBS 513.88 : An02g09300, A. oryzae RIB40 : AO090012000788, A. niger ATCC 1015 : 172938-mRNA and Aspergillus versicolor : Aspve1_0051191	null	2.28374	0.002441	0.009511
AN1380	Ortholog(s) have cytosol localization	null	2.04466	0.002444	0.009514

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AN10756	Ortholog(s) have role in regulation of conjugation with cellular fusion and TORC2 complex, cell division site, cytosol, nucleus localization	null	-2.041	0.002445	0.009514
AN0132	Ortholog of A. fumigatus Af293 : Afu5g11630, A. niger CBS 513.88 : An18g03110, A. oryzae RIB40 : AO090026000663, A. niger ATCC 1015 : 42787-mRNA and Aspergillus versicolor : Aspve1_0035450	null	2.44466	0.002452	0.009515
AN6876	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.7321	0.002454	0.009515
AN11110	Has domain(s) with predicted ATP binding, ligase activity, forming aminoacyl-tRNA and related compounds activity, role in tRNA aminoacylation, translation and cytoplasm localization	null	-3.4091	0.002454	0.009515
AN4078	null	null	-3.4091	0.002454	0.009515
AN5808	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	null	-3.4091	0.002454	0.009515
AN7597	Ortholog(s) have oligopeptide transmembrane transporter activity, role in conjugation with cellular fusion, transmembrane transport and endoplasmic reticulum localization	null	-3.4091	0.002454	0.009515
AN9324	Has domain(s) with predicted carbon-nitrogen ligase activity, with glutamine as amido-N-donor activity	null	-3.4091	0.002454	0.009515
AN4316	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.0511	0.002469	0.009562
AN0631	Ortholog of A. fumigatus Af293 : Afu1g17000, A. niger CBS 513.88 : An01g09850, A. oryzae RIB40 : AO090005000975, A. niger ATCC 1015 : 171415-mRNA and Aspergillus versicolor : Aspve1_0117449	null	2.18524	0.00247	0.009562
AN5816	Ortholog(s) have role in mitochondrial proton-transporting ATP synthase complex assembly, protein processing and mitochondrial inner membrane, mitochondrial intermembrane space localization	null	2.17615	0.00247	0.009562
AN3894	Putative aconitate hydratase with a predicted role in the TCA cycle	null	2.51617	0.002471	0.009562
AN2951	Putative UDP-glucose 4-epimerase with a predicted role in galactose and galactitol metabolism	null	2.03502	0.002482	0.009599
AN10117	Ortholog of A. fumigatus Af293 : Afu1g14050/fbpA, A. oryzae RIB40 : AO090012000463, A. niger ATCC 1015 : 205573-mRNA, Aspergillus versicolor : Aspve1_0048993 and Aspergillus sydowii : Aspsy1_0086500	null	-2.1094	0.002485	0.009603
AN8202	Ortholog of A. fumigatus Af293 : Afu5g03340, A. niger CBS 513.88 : An09g05655, A. oryzae RIB40 : AO090102000539, A. niger ATCC 1015 : 212456-mRNA and Aspergillus versicolor : Aspve1_0089228	null	2.06881	0.002486	0.009603
AN5177	Ortholog(s) have role in ribosomal large subunit biogenesis and nucleolus localization	null	2.62759	0.002489	0.009611
AN12033	Has domain(s) with predicted catalytic activity	null	-2.6888	0.002498	0.00964

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AN6115	Ortholog(s) have nickel cation transmembrane transporter activity, role in nickel cation transmembrane transport, regulation of urea catabolic process and endoplasmic reticulum localization	null	2.12682	0.002503	0.009654
AN3603	Has domain(s) with predicted tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and tRNA (m1A) methyltransferase complex localization	null	2.64631	0.002514	0.009686
AN4708	Ortholog(s) have mitochondrion localization	null	2.79305	0.002514	0.009686
AN0359	Putative eIF3b subunit of translation initiation factor 3 (eIF3); required for conidial germination	sgdA	1.96047	0.002534	0.009756
AN8670	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	null	-2.2336	0.002536	0.009756
AN2875	Putative fructose-bisphosphate aldolase with a predicted role in gluconeogenesis and glycolysis; intracellular, menadione stress-induced protein; palA-dependent expression independent of pH	fbaA	1.9595	0.002536	0.009756
AN1461	Ortholog of A. fumigatus Af293 : Afu8g04530, A. niger CBS 513.88 : An16g08470, A. oryzae RIB40 : AO090023000334, A. niger ATCC 1015 : 45507-mRNA and Aspergillus versicolor : Aspve1_0125562	null	-2.2267	0.002564	0.009858
AN8283	Putative sterol 14-demethylase with a predicted role in sterol metabolism; putative cytochrome P450	cyp51B	2.05866	0.002565	0.009858
AN6992	Ortholog of Aspergillus versicolor : Aspve1_0154813, Aspergillus sydowii : Aspsy1_0158352, Aspergillus terreus NIH2624 : ATET_02748 and Aspergillus carbonarius ITEM 5010 : Acar5010_009668	null	2.32595	0.002594	0.009962
AN10480	Ortholog of A. fumigatus Af293 : Afu4g07990, A. niger CBS 513.88 : An04g02410, A. oryzae RIB40 : AO090023000772, A. niger ATCC 1015 : 190965-mRNA and Aspergillus versicolor : Aspve1_0132267	null	2.10777	0.002596	0.009965
AN10468	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-2.1393	0.002611	0.01002
AN11981	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.089	0.002626	0.010073
AN6276	Has domain(s) with predicted 4-alpha-hydroxytetrahydrobiopterin dehydratase activity and role in tetrahydrobiopterin biosynthetic process	null	2.07514	0.002645	0.010138
AN5764	Transcript induced by light in in developmentally competent mycelia	null	-2.0088	0.00265	0.010151
AN5563	Putative dehydrogenase with a predicted role in carbohydrate metabolism; NADP+-dependent glycerol dehydrogenase; required for osmotolerance; transcript downregulated by growth in glycerol; expression upregulated after exposure to farnesol	gldB	1.95785	0.002654	0.010157
AN6246	Cytochrome C	cycA	1.97597	0.002654	0.010157
AN0388	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	null	-2.0733	0.002675	0.010234

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AN3121	Ortholog of A. fumigatus Af293 : Afu3g12790, A. niger CBS 513.88 : An02g08810, A. niger ATCC 1015 : 52344-mRNA, Aspergillus sydowii : Aspsy1_0087203 and Aspergillus terreus NIH2624 : ATET_04117	null	-2.0163	0.002677	0.010236
AN2284	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	hemA	2.07885	0.002682	0.010247
AN9419	Ortholog(s) have alanine-tRNA ligase activity, role in alanyl-tRNA aminoacylation and cytosol, mitochondrion localization	null	1.98959	0.002688	0.010264
AN2748	Ortholog(s) have cytosol, nucleus localization	null	-2.3576	0.002697	0.010289
AN8051	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	null	-2.2718	0.002697	0.010289
AN8532	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-1.9683	0.002703	0.010301
AN10652	Ortholog(s) have mitochondrion localization	null	2.12999	0.002704	0.010301
AN5407	Has domain(s) with predicted Rab GTPase activator activity, role in regulation of Rab GTPase activity and intracellular localization	null	2.12999	0.002704	0.010301
AN10914	null	null	2.28248	0.00271	0.010318
AN5753	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	null	2.19246	0.002726	0.010376
AN6735	Ortholog(s) have role in mRNA splicing, via spliceosome and U1 snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snRNP, cytosol localization	null	2.05986	0.002751	0.010463
AN0579	Putative isopentenyl-diphosphate delta-isomerase with a predicted role in sterol metabolism	null	1.95343	0.00276	0.010491
AN4932	Putative G-protein coupled receptor; haemolysin III-related protein	gprO	2.4958	0.002777	0.010552
AN3455	Ortholog(s) have role in rRNA processing and CURI complex, UTP-C complex, small-subunit processome localization	null	2.12337	0.002785	0.010577
AN1976	Ortholog(s) have histone acetyltransferase activity	null	-2.0112	0.002796	0.010603
AN7184	Ortholog(s) have cytosol, spliceosomal complex localization	null	-2.1348	0.002798	0.010603
AN10158	Ortholog of A. nidulans FGSC A4 : AN7874, A. fumigatus Af293 : Afu1g12200, Afu3g00570, Afu8g02315 and A. niger CBS 513.88 : An08g04520, An06g00280	null	3.78597	0.002801	0.010603
AN3305	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.1684	0.002801	0.010603
AN6043	null	null	-3.1684	0.002801	0.010603
AN9037	Has domain(s) with predicted molybdenum ion binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.1684	0.002801	0.010603

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AN10498	Ortholog of A. fumigatus Af293 : Afu1g03930, A. niger CBS 513.88 : An01g02790, A. oryzae RIB40 : AO090003000957, Aspergillus sydowii : Aspsy1_0044555 and Aspergillus terreus NIH2624 : ATET_03817	null	2.00869	0.002808	0.010625
AN0468	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	null	1.92251	0.002815	0.010646
AN5597	Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism	null	1.93032	0.002819	0.010657
AN6769	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-2.465	0.00282	0.010657
AN0836	Ortholog(s) have D-arabinono-1,4-lactone oxidase activity, role in cellular response to oxidative stress, dehydro-D-arabinono-1,4-lactone biosynthetic process and integral to mitochondrial outer membrane localization	null	1.99778	0.002832	0.010695
AN7771	Ortholog of A. fumigatus Af293 : Afu5g07480, A. niger CBS 513.88 : An15g02850, A. oryzae RIB40 : AO090701000657, A. niger ATCC 1015 : 48718-mRNA and Aspergillus versicolor : Aspve1_0072039	null	2.00822	0.002844	0.010735
AN5163	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	null	-2.4723	0.002865	0.010799
AN8885	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	null	-2.4723	0.002865	0.010799
AN12198	Ortholog of A. fumigatus Af293 : Afu2g15810, A. niger CBS 513.88 : An15g06100, A. niger ATCC 1015 : 40747-mRNA, Aspergillus versicolor : Aspve1_0080747 and Aspergillus sydowii : Aspsy1_0026968	null	-2.098	0.002866	0.010799
AN2903	Aspartic protease; protein expressed at decreased levels in a hapX mutant versus wild-type	pepE	-1.9322	0.002908	0.010952
AN0773	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	null	2.14855	0.00292	0.010992
AN1200	Ortholog(s) have role in ribosomal large subunit assembly and Noc1p-Noc2p complex, nucleolus localization	null	2.01614	0.002931	0.011028
AN12232	null	null	3.13656	0.00294	0.011048
AN5076	Has domain(s) with predicted role in cell wall macromolecule catabolic process	null	3.13656	0.00294	0.011048
AN5257	Ortholog(s) have mitochondrion localization	null	3.13656	0.00294	0.011048
AN1793	Has domain(s) with predicted magnesium ion binding, terpene synthase activity	null	3.00404	0.002976	0.011177
AN1330	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	1.96496	0.002982	0.011191
AN8269	90 kilodalton heat shock protein; physically associates with importin-alpha, KapA; palA-dependent expression independent of pH	hsp90	1.90512	0.002986	0.011202

AN10197	Has domain(s) with predicted catalytic activity and role in coenzyme M biosynthetic process	null	-2.1152	0.002996	0.011235
AN9357	Ortholog(s) have cytosol, nucleus localization	null	2.19313	0.003002	0.011251
AN10442	Predicted guanine nucleotide exchange factor	null	-1.9476	0.003026	0.011336
AN4066	Has domain(s) with predicted phospholipid binding activity	null	-1.9652	0.00305	0.01142
AN6849	Ortholog(s) have role in cellular response to heat, cellular response to hydrogen peroxide	null	-2.3238	0.003055	0.011432
AN5372	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	2.08881	0.003067	0.011471
AN8557	Protein of unknown function; transcript is induced by nitrate	null	2.10682	0.003078	0.011505
AN0252	Putative F1F0-ATPase complex gamma subunit with a predicted role in energy metabolism; expression reduced after exposure to farnesol	null	2.08348	0.003092	0.011552
AN5781	Putative 30 kilodalton heat shock protein; transcript levels increase during the unfolded-protein response (UPR); palA-dependent expression independent of pH	null	1.9647	0.003096	0.011556
AN4580	Has domain(s) with predicted 7S RNA binding, endoplasmic reticulum signal peptide binding activity and role in SRP-dependent cotranslational protein targeting to membrane, negative regulation of translational elongation	null	2.28077	0.003096	0.011556
AN4544	Has domain(s) with predicted protein tyrosine phosphatase activity, protein tyrosine/serine/threonine phosphatase activity and role in protein dephosphorylation	null	-2.0326	0.003105	0.011585
AN7676	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	null	-2.0442	0.00312	0.011635
AN2386	Ortholog of A. nidulans FGSC A4 : AN6413, AN8328, AN3395, AN3241, AN10369, AN1930, AN1738, AN9266, AN10886, AN7232, AN7406, AN7774, AN12202	null	2.47513	0.003124	0.011644
AN1432	Ortholog(s) have cytoplasm, nucleus localization	null	-2.1375	0.003164	0.01178
AN6691	Ortholog of N. fischeri NRRL 181 : NFIA_005070, Aspergillus versicolor : Aspve1_0043949 and Aspergillus sydowii : Aspsy1_1018177	null	2.24307	0.003164	0.01178
AN7367	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity and role in nitrogen compound metabolic process	null	-1.9087	0.003168	0.011791
AN2920	Possible pseudogene	null	-1.9843	0.003192	0.011873
AN3974	Ortholog of Aspergillus versicolor : Aspve1_0135108, Aspergillus sydowii : Aspsy1_0057545 and Aspergillus terreus NIH2624 : ATET_08256	null	-1.9549	0.0032	0.011892
AN4900	Putative bZIP DNA-binding protein involved in regulating nitrogen metabolite repression	meaB	-2.0154	0.003201	0.011892
AN3843	Ortholog(s) have role in cristae formation, protein import into mitochondrial intermembrane space and integral to mitochondrial inner membrane, mitochondrial crista, mitochondrial crista junction localization	null	1.91404	0.003204	0.011898

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AN4367	Putative chitin synthase III with a predicted role in chitin biosynthesis; transcript is induced by nitrate	chsF	2.38614	0.003239	0.012022
AN8822	Ortholog(s) have cytosol, nucleus localization	null	1.99285	0.003251	0.012051
AN10459	Ortholog(s) have cytosol localization	null	1.93671	0.003251	0.012051
AN1721	Ortholog of A. fumigatus Af293 : Afu4g08350, A. niger CBS 513.88 : An04g03130, A. oryzae RIB40 : AO090023000724, A. niger ATCC 1015 : 190566-mRNA and Aspergillus versicolor : Aspve1_0049965	null	1.93671	0.003251	0.012051
AN9199	Putative G-protein coupled receptor	gprE	-1.969	0.003264	0.012091
AN4378	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.1361	0.003274	0.012123
AN0984	Ortholog(s) have nucleus localization	null	2.11096	0.003286	0.012154
AN4537	Has domain(s) with predicted Rab GTPase activator activity, role in regulation of Rab GTPase activity and intracellular localization	null	-2.0294	0.003286	0.012154
AN10172	Ortholog(s) have dicarboxylic acid transmembrane transporter activity, role in mitochondrial transport and mitochondrial inner membrane localization	null	1.91101	0.003298	0.012193
AN11908	Has domain(s) with predicted hydrolase activity, acting on ester bonds, zinc ion binding activity and nucleus localization	null	-1.9967	0.003302	0.012201
AN8017	Ortholog(s) have cytosol, nucleus, spindle pole body localization	null	-1.9652	0.003304	0.012202
AN6443	Ortholog(s) have plasma membrane localization	null	-1.9157	0.003327	0.012281
AN10936	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	null	2.20269	0.003344	0.012339
AN3704	Has domain(s) with predicted 1-aminocyclopropane-1-carboxylate synthase activity, pyridoxal phosphate binding, transferase activity, transferring nitrogenous groups activity	null	-2.4367	0.003371	0.01243
AN10960	Ortholog of Aspergillus versicolor : Aspve1_0135933	null	-1.9823	0.003381	0.012462
AN0332	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.2654	0.003386	0.012462
AN1295	Ortholog(s) have cytosol, nucleus localization	null	2.2654	0.003386	0.012462
AN6817	Predicted NAD-dependent oxidoreductase; expression upregulated after exposure to farnesol	null	-2.1677	0.003386	0.012462
AN4046	Ortholog(s) have Golgi apparatus, endoplasmic reticulum localization	null	2.08804	0.003396	0.012494
AN0714	Ortholog(s) have role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex localization	null	-2.2908	0.003415	0.012543
AN3114	Ortholog of A. fumigatus Af293 : Afu3g12710, A. niger CBS 513.88 : An02g08680, A. oryzae RIB40 : AO090012000852, A. niger ATCC 1015 : 52342-mRNA and Aspergillus versicolor : Aspve1_0026716	null	-2.2908	0.003415	0.012543

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AN4052	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	exgC	2.36802	0.003415	0.012543
AN7229	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-2.0752	0.003441	0.012633
AN0641	Protein expressed at increased levels during osmoadaptation; contains a TCTP (translationally controlled tumor protein) domain	null	1.9856	0.003445	0.012641
AN2782	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	null	-2.1065	0.003452	0.012661
AN11929	Ortholog(s) have role in rRNA processing, ribosomal small subunit assembly and CURI complex, UTP-C complex, cytosol localization	null	2.73454	0.003463	0.01269
AN7834	null	null	-2.4426	0.003463	0.01269
AN5619	Ortholog(s) have metallopeptidase activity, role in ascospore wall assembly and ascospore wall, endoplasmic reticulum membrane localization	null	-1.9422	0.003471	0.012711
AN8431	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	null	2.30467	0.003476	0.012726
AN11135	Prephenate dehydratase involved in phenylalanine biosynthesis	phenA	2.45417	0.003518	0.012873
AN9148	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	galF	1.92632	0.003532	0.012916
AN10483	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	null	2.97111	0.003555	0.012955
AN1275	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	null	2.97111	0.003555	0.012955
AN2088	Ortholog of A. fumigatus Af293 : Afu2g04950, A. niger CBS 513.88 : An11g04660, A. oryzae RIB40 : AO090003000298, A. niger ATCC 1015 : 178612-mRNA and Aspergillus versicolor : Aspve1_0038117	null	2.97111	0.003555	0.012955
AN9292	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	null	-2.6347	0.003555	0.012955
AN8121	Putative 5'-phosphoribosylformyl glycinamidine synthetase with a predicted role in purine metabolism	null	2.36872	0.003578	0.012955
AN0389	Ortholog of A. fumigatus Af293 : Afu1g01570, A. niger CBS 513.88 : An04g08610, Aspergillus versicolor : Aspve1_0119805 and Aspergillus sydowii : Aspsy1_0086024	null	-3.746	0.003595	0.012955
AN0529	Ortholog of A. nidulans FGSC A4 : AN7899/dbaE, AN9159, AN2031, AN1032/afoC, A. fumigatus Af293 : Afu8g00910 and A. niger CBS 513.88 : An03g01180, An09g01790, An03g01810	null	-5.7999	0.003595	0.012955

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AN0718	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	null	-3.746	0.003595	0.012955
AN11753	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	null	-5.7999	0.003595	0.012955
AN11781	null	null	-3.746	0.003595	0.012955
AN11876	Has domain(s) with predicted transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.7999	0.003595	0.012955
AN12116	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.7999	0.003595	0.012955
AN12374	null	null	-5.7999	0.003595	0.012955
AN1840	Has domain(s) with predicted 3-oxoacyl-[acyl-carrier-protein] synthase activity and role in fatty acid biosynthetic process	null	-5.7999	0.003595	0.012955
AN2060	Putative exo-arabinanase	abxA	-5.7999	0.003595	0.012955
AN2469	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.7999	0.003595	0.012955
AN2672	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	null	-5.7999	0.003595	0.012955
AN2716	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.7999	0.003595	0.012955
AN3291	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-5.7999	0.003595	0.012955
AN3379	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	null	-5.7999	0.003595	0.012955
AN5401	Ortholog of A. fumigatus Af293 : Afu6g13860, A. niger CBS 513.88 : An08g08500, A. oryzae RIB40 : AO090103000362, A. niger ATCC 1015 : 38052-mRNA and Aspergillus versicolor : Aspve1_0045294	null	-5.7999	0.003595	0.012955
AN5864	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.7999	0.003595	0.012955
AN6015	Has domain(s) with predicted DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-5.7999	0.003595	0.012955
AN6278	Ortholog of A. fumigatus Af293 : Afu2g12540, Aspergillus versicolor : Aspve1_0041153, Aspergillus sydowii : Aspsy1_0058158 and Aspergillus terreus NIH2624 : ATET_01222	null	-3.746	0.003595	0.012955
AN7529	Putative metal-dependent amidase	null	-5.7999	0.003595	0.012955

AN8116	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	null	-5.7999	0.003595	0.012955
AN8468	Ortholog of A. niger CBS 513.88 : An11g07530, Aspergillus brasiliensis : Aspbr1_0424327, A. niger ATCC 1015 : 129126-mRNA and Aspergillus versicolor : Aspve1_0088511	null	-5.7999	0.003595	0.012955
AN8469	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	null	-5.7999	0.003595	0.012955
AN8490	Ortholog of Aspergillus versicolor : Aspve1_0369297 and Aspergillus sydowii : Aspsy1_0471403	null	-3.746	0.003595	0.012955
AN9315	Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.7999	0.003595	0.012955
AN11631	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.15258	0.003597	0.012955
AN4751	Has domain(s) with predicted ATP binding, ATP-dependent helicase activity, nucleic acid binding activity	null	3.7341	0.003627	0.013058
AN11374	null	null	-2.3894	0.003635	0.013071
AN10011	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	null	-2.6712	0.003636	0.013071
AN6678	Ortholog(s) have nucleus localization	null	-2.6712	0.003636	0.013071
AN10664	Ortholog of A. fumigatus Af293 : Afu6g14120, A. oryzae RIB40 : AO090103000398, A. niger ATCC 1015 : 37809-mRNA, Aspergillus versicolor : Aspve1_0044715 and Aspergillus sydowii : Aspsy1_0035748	null	-1.9109	0.003647	0.013102
AN2918	Putative chaperonin complex component, TCP-1 delta subunit; ortholog of S. cerevisiae Cct4p; expression reduced after exposure to farnesol	cct4	1.95872	0.003651	0.01311
AN4209	Has domain(s) with predicted sugar:hydrogen symporter activity, role in carbohydrate transport and Golgi membrane, integral to membrane localization	null	-1.9884	0.00367	0.013151
AN4988	Ortholog(s) have intracellular localization	null	-2.0018	0.003679	0.013151
AN0355	null	null	-3.0204	0.00368	0.013151
AN12378	null	null	3.0926	0.00368	0.013151
AN1734	Ortholog of A. fumigatus Af293 : Afu6g08740, A. niger CBS 513.88 : An11g06130, A. oryzae RIB40 : AO090001000548, A. niger ATCC 1015 : 39163-mRNA and Aspergillus versicolor : Aspve1_0124562	null	-2.7198	0.00368	0.013151
AN2335	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	null	-2.7198	0.00368	0.013151
AN3162	Putative GNAT-type acetyltransferase	ngn4	-3.0204	0.00368	0.013151

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AN4519	Has domain(s) with predicted DNA binding activity, role in DNA recombination, double-strand break repair and nucleus localization	null	-3.0204	0.00368	0.013151
AN7434	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-3.0204	0.00368	0.013151
AN8635	Has domain(s) with predicted hydrolase activity	null	-3.0204	0.00368	0.013151
AN3829	Putative succinate-semialdehyde dehydrogenase [NAD(P)+] with a predicted role in 4-aminobutyrate (GABA) shunt	null	-1.9286	0.003693	0.013191
AN3708	Ortholog(s) have hydrolase activity, role in nucleotide metabolic process and cytoplasm, nucleus localization	null	1.91397	0.003724	0.013289
AN6285	Ortholog of A. fumigatus Af293 : Afu2g12420, A. niger CBS 513.88 : An02g04555, A. niger ATCC 1015 : 52210-mRNA, Aspergillus versicolor : Aspve1_0083083 and Aspergillus sydowii : Aspsy1_0089680	null	1.95157	0.003724	0.013289
AN4956	Large subunit of acetolactate synthase involved in branched-chain amino acid biosynthesis under hypoxic conditions	null	1.92792	0.003729	0.013303
AN2002	Protein predicted to have a role in pheromone precursor processing	null	-1.9196	0.003748	0.013361
AN2949	Ortholog of A. fumigatus Af293 : Afu3g07920, A. niger CBS 513.88 : An02g11300, A. niger ATCC 1015 : 37382-mRNA, Aspergillus versicolor : Aspve1_0127154 and Aspergillus sydowii : Aspsy1_0056305	null	2.12752	0.003761	0.013402
AN0742	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	null	-1.9675	0.003783	0.013475
AN0752	Ortholog(s) have DNA-directed RNA polymerase activity, RNA-directed RNA polymerase activity	null	2.06009	0.003793	0.013504
AN4014	Putative vacuolar sorting protein; ortholog of S. cerevisiae Vps52p; expression reduced after exposure to farnesol	vps52	2.32812	0.00382	0.013591
AN1103	Has domain(s) with predicted acetoacetate-CoA ligase activity and role in lipid metabolic process	null	2.28805	0.003823	0.013591
AN1682	Ortholog of A. fumigatus Af293 : Afu4g08680, A. niger CBS 513.88 : An04g03500, A. oryzae RIB40 : AO090023000689, A. niger ATCC 1015 : 190697-mRNA and Aspergillus versicolor : Aspve1_0025027	null	2.04111	0.003823	0.013591
AN11543	Ortholog of A. niger CBS 513.88 : An14g00820, Aspergillus brasiliensis : Aspbr1_0190176, A. clavatus NRRL 1 : ACLA_054360, Aspergillus versicolor : Aspve1_0046161 and Aspergillus sydowii : Aspsy1_0092848	null	1.87446	0.003852	0.013688
AN10737	Ortholog of A. fumigatus Af293 : Afu2g07490, A. niger CBS 513.88 : An05g00040, A. niger ATCC 1015 : 186597-mRNA, Aspergillus versicolor : Aspve1_0605101 and Aspergillus sydowii : Aspsy1_0044731	null	2.02915	0.003885	0.013786
AN3429	Protein of unknown function; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.02915	0.003885	0.013786

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AN8129	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	sfgA	-2.0051	0.003885	0.013786
AN1534	Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism	null	1.96465	0.003907	0.013855
AN5565	Ortholog(s) have lipase activity	null	-2.3912	0.003913	0.013868
AN8823	Ortholog of A. fumigatus Af293 : Afu5g06020, A. niger CBS 513.88 : An17g01805, A. oryzae RIB40 : AO090009000658, A. niger ATCC 1015 : 51067-mRNA and Aspergillus versicolor : Aspve1_0088214	null	-2.07	0.003914	0.013868
AN8750	Has domain(s) with predicted oxidoreductase activity, role in oxidation-reduction process and mitochondrion localization	null	1.94819	0.003927	0.013907
AN5416	Ortholog of Aspergillus brasiliensis : Aspbr1_0037182, Aspergillus versicolor : Aspve1_0199240, Aspergillus sydowii : Aspsy1_0046516 and Aspergillus carbonarius ITEM 5010 : Acar5010_010444	null	-1.951	0.003939	0.013944
AN7631	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-2.1049	0.003957	0.014001
AN10429	Ortholog(s) have cytosol, nucleus localization	null	2.4113	0.003967	0.014028
AN3865	Ortholog(s) have mitochondrion localization	null	1.94865	0.004003	0.014149
AN10995	null	null	-2.1837	0.004057	0.014333
AN10280	Ortholog(s) have rDNA binding activity	null	2.1214	0.004063	0.014348
AN2445	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	2.67355	0.004077	0.014392
AN12358	Ortholog(s) have mitochondrion localization	null	1.86216	0.004084	0.01441
AN8224	Ortholog(s) have cytosol, nucleus localization	null	1.93865	0.004125	0.014545
AN12478	IMP dehydrogenase/GMP reductase; expression reduced after exposure to farnesol	null	1.88631	0.004133	0.014565
AN6107	Putative voltage-gated anion channel protein with a role in copper homeostasis	clcA	-1.8438	0.004171	0.014692
AN7949	Ortholog of A. fumigatus Af293 : Afu7g05200, A. oryzae RIB40 : AO090011000198, AO090003000528, Aspergillus versicolor : Aspve1_0087362 and Aspergillus sydowii : Aspsy1_0033753	null	2.03864	0.004172	0.014692
AN2426	Histone H4.2, core histone protein; nearly identical to histone H4.1	H4.2	-1.9257	0.00422	0.014853
AN1541	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	null	2.01218	0.004225	0.014858
AN8867	Ortholog(s) have cytosol localization	null	1.85253	0.004226	0.014858
AN11920	Has domain(s) with predicted oxidoreductase activity and role in metabolic process	null	2.03158	0.00424	0.014903
AN5978	Ortholog of A. fumigatus Af293 : Afu2g10290, A. niger CBS 513.88 : An16g04700, A. niger ATCC 1015 : 200967-mRNA, Aspergillus versicolor : Aspve1_0040780 and Aspergillus sydowii : Aspsy1_0044998	null	2.16668	0.004246	0.014916
AN1020	Ortholog of A. nidulans FGSC A4 : AN2784, AN9281, A. fumigatus Af293 : Afu1g12970, A. niger CBS 513.88 : An15g05320, A. oryzae RIB40 : AO090012000596 and A. niger ATCC 1015 : 47491-mRNA	null	-2.5785	0.004258	0.01495
AN5110	Ortholog(s) have cytosol, nucleus localization	null	-2.257	0.004278	0.015008

AN5206	Putative homoisocitrate dehydrogenase with a predicted role in lysine metabolism	lysB	2.30775	0.004278	0.015008
AN2260	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity, electron carrier activity and membrane localization	null	1.96517	0.004299	0.015072
AN7772	Putative cytochrome P450; transcript repressed by nitrate	CYP5080B1	-2.1266	0.004337	0.015192
AN9295	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.0685	0.004337	0.015192
AN11900	Ortholog(s) have Golgi apparatus localization	null	1.8873	0.004361	0.015268
AN10733	Ortholog of A. fumigatus Af293 : Afu2g07650, N. fischeri NRRL 181 : NFIA_083380, Aspergillus versicolor : Aspve1_0040554 and A. fumigatus A1163 : AFUB_023690	null	2.31516	0.004376	0.015308
AN3056	Ortholog(s) have role in maturation of SSU-rRNA and cytosol, nucleolus localization	null	2.33324	0.004376	0.015308
AN0328	Ortholog(s) have nucleus localization	null	-1.98	0.004393	0.015357
AN7205	Ortholog(s) have role in ribosome biogenesis and cytosol, nucleolus localization	null	2.11078	0.004416	0.015431
AN0734	Histone H4.1, core histone protein; nearly identical to histone H4.2	H4.1	1.8267	0.004421	0.015441
AN2525	Putative L-serine dehydratase with a predicted role in glycine, serine, and threonine metabolism	null	2.05694	0.004443	0.015504
AN9342	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	null	-2.087	0.004445	0.015504
AN1958	null	null	-2.6075	0.004447	0.015504
AN7123	Transcript repressed by exposure of A. nidulans to bafilomycin	breB	-2.6075	0.004447	0.015504
AN5144	Putative 6-phosphofructo-2-kinase with a predicted role in mannose/mannitol, fructose, and sorbose/sorbitol metabolism	pfkZ	1.83726	0.004515	0.015733
AN2389	Ortholog(s) have cell division site, cell tip, cytoplasm localization	null	2.51218	0.004551	0.015844
AN3264	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.48379	0.004551	0.015844
AN1797	Ortholog(s) have role in detection of glucose, fructose transport, glucose transport, mannose transport, negative regulation of meiosis and plasma membrane localization	null	2.14209	0.004558	0.015861
AN10971	Ortholog of A. niger CBS 513.88 : An09g02810, A. oryzae RIB40 : AO090001000746, A. niger ATCC 1015 : 43379-mRNA, Aspergillus sydowii : Aspsy1_0045732 and Aspergillus terreus NIH2624 : ATET_05619	null	-3.3037	0.004567	0.015878
AN11840	null	null	-3.3037	0.004567	0.015878
AN0337	Ortholog of A. fumigatus Af293 : Afu1g07195, A. niger CBS 513.88 : An07g09780, A. oryzae RIB40 : AO090012000973, A. niger ATCC 1015 : 39611-mRNA and Aspergillus versicolor : Aspve1_0045681	null	2.08255	0.004579	0.015911
AN10378	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	null	1.86711	0.004581	0.015912

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AN6260	Ortholog of A. fumigatus Af293 : Afu2g12960, A. oryzae RIB40 : AO090026000339, A. niger ATCC 1015 : 174067-mRNA, Aspergillus versicolor : Aspve1_0642947 and Aspergillus sydowii : Aspsy1_0988268	null	-1.8868	0.004593	0.015945
AN2497	Has domain(s) with predicted palmitoyl-(protein) hydrolase activity and role in cellular protein modification process	null	-1.8871	0.0046	0.015963
AN3616	Has domain(s) with predicted oxidoreductase activity, role in antibiotic biosynthetic process and cytoplasm localization	null	2.04258	0.004608	0.015981
AN5662	Ortholog(s) have cytosol localization	null	1.85245	0.004612	0.01599
AN1443	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	null	-2.6465	0.004624	0.016014
AN5173	Has domain(s) with predicted hydrolase activity	null	-2.9471	0.004624	0.016014
AN2145	Has domain(s) with predicted phosphoric diester hydrolase activity and role in lipid metabolic process	null	-2.1437	0.004632	0.016034
AN4862	Putative Ran GTPase activating protein (GAP) with homology to Saccharomyces cerevisiae Rna1p; endogenously tagged RanGAP is excluded from nuclei during interphase and disperses throughout the cell at mitosis	ranGAP	1.92194	0.004654	0.016105
AN0163	Ortholog(s) have Rho GDP-dissociation inhibitor activity and role in actin filament organization, regulation of vacuole fusion, non-autophagic, small GTPase mediated signal transduction	null	1.88854	0.004699	0.01625
AN0285	Putative 6-phosphogluconolactonase with a predicted role in gluconic acid and gluconate metabolism; expression upregulated after exposure to farnesol	null	1.88953	0.004701	0.016253
AN2249	Ortholog of A. niger CBS 513.88 : An17g00940, A. oryzae RIB40 : AO090701000204, Aspergillus versicolor : Aspve1_0050588, Aspergillus sydowii : Aspsy1_0026878 and Aspergillus terreus NIH2624 : ATET_09356	null	-2.3501	0.004709	0.016262
AN3345	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	2.49077	0.004709	0.016262
AN11060	Ortholog(s) have 4 iron, 4 sulfur cluster binding activity, role in iron-sulfur cluster assembly, tRNA wobble uridine modification and cytoplasm localization	null	3.68029	0.004724	0.016301
AN6801	Ortholog of A. oryzae RIB40 : AO090001000089, Aspergillus flavus NRRL 3357 : AFL2T_07326, Aspergillus versicolor : Aspve1_0046605, Aspve1_0656082 and Aspergillus sydowii : Aspsy1_0046335	null	-3.0819	0.004724	0.016301
AN2438	Ortholog(s) have role in establishment of mitotic sister chromatid cohesion and cytosol, nucleus localization	null	2.09884	0.004729	0.016309
AN2888	Ortholog of A. fumigatus Af293 : Afu3g11580, A. niger CBS 513.88 : An03g03490, A. oryzae RIB40 : AO090003000717, A. niger ATCC 1015 : 213417-mRNA and Aspergillus versicolor : Aspve1_0556144	null	1.94981	0.004733	0.016315
AN1561	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	2.0348	0.004737	0.016321

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AN1995	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	null	-1.8944	0.004789	0.016494
AN11164	Ortholog of A. fumigatus Af293 : Afu7g02110, A. oryzae RIB40 : AO090038000589, N. fischeri NRRL 181 : NFIA_114840, Aspergillus flavus NRRL 3357 : AFL2T_07915 and A. clavatus NRRL 1 : ACLA_065410	null	-1.8919	0.004798	0.016516
AN1631	Ortholog(s) have L-methionine secondary active transmembrane transporter activity and role in cysteine transport, methionine transport	null	2.64206	0.004811	0.016546
AN7488	Ortholog(s) have endoplasmic reticulum, fungal-type vacuole localization	null	-2.504	0.004811	0.016546
AN8500	Ortholog of A. niger CBS 513.88 : An13g02820, A. oryzae RIB40 : AO090009000060, Aspergillus brasiliensis : Aspbr1_0056184, A. niger ATCC 1015 : 192087-mRNA and Aspergillus flavus NRRL 3357 : AFL2T_10590	null	-1.8407	0.004833	0.016613
AN6897	Ortholog(s) have GTPase activity, protein homodimerization activity, role in mitochondrial fusion and integral to mitochondrial outer membrane, mitochondrial inner membrane localization	null	1.89901	0.004838	0.016624
AN1381	Ortholog of A. fumigatus Af293 : Afu1g09000, A. oryzae RIB40 : AO090005001625, A. niger ATCC 1015 : 47752-mRNA, Aspergillus versicolor : Aspve1_0121963 and Aspergillus sydowii : Aspsy1_0140811	null	2.18748	0.004887	0.016767
AN7662	Putative metalloreductase with a predicted role in iron homeostasis; regulated by iron independently of SreA	freA	2.20238	0.004887	0.016767
AN9163	Ortholog of A. fumigatus Af293 : Afu8g07190, A. oryzae RIB40 : AO090138000059, Aspergillus versicolor : Aspve1_0402803, Aspergillus sydowii : Aspsy1_0061494 and Aspergillus terreus NIH2624 : ATET_09159	null	-2.0897	0.004887	0.016767
AN6819	Has domain(s) with predicted hydrolase activity, hydrolyzing O-glycosyl compounds activity and role in carbohydrate metabolic process	null	-1.9834	0.004889	0.016767
AN5215	Ortholog(s) have role in endocytic recycling and cytosol, endosome, nucleus localization	null	2.05952	0.004893	0.016768
AN7362	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-2.036	0.004894	0.016768
AN11003	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	null	-1.917	0.004944	0.016935
AN7468	Putative binuclear zinc-cluster type transcriptional activator of gluconeogenesis	acuK	-1.9075	0.004988	0.017075
AN10445	Ortholog(s) have mitochondrion localization	null	2.04416	0.005035	0.017231
AN6376	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.0236	0.005051	0.017274
AN3779	Ortholog(s) have exopolyphosphatase activity, role in polyphosphate catabolic process and cytosol, nucleus localization	null	2.36712	0.005059	0.017288

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AN7505	Protein with alpha-xylosidase activity, involved in degradation of xyloglucans	agdD	2.36712	0.005059	0.017288
AN3417	Putative malonyl CoA synthetase; required for conidial germination	sgdD	1.89111	0.005071	0.017321
AN8137	Has domain(s) with predicted alcohol O-acetyltransferase activity and role in alcohol metabolic process	null	1.97229	0.005091	0.017382
AN1068	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity, role in GPI anchor metabolic process, intracellular protein transport and intrinsic to endoplasmic reticulum membrane localization	null	-2.0751	0.005101	0.017408
AN10421	Ortholog of A. nidulans FGSC A4 : AN3523, A. fumigatus Af293 : Afu6g13470, A. niger CBS 513.88 : An08g03030, A. oryzae RIB40 : AO090020000658 and A. niger ATCC 1015 : 38455-mRNA	null	-2.5201	0.005112	0.017412
AN11109	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	null	-2.5201	0.005112	0.017412
AN3658	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.5201	0.005112	0.017412
AN3663	Ortholog(s) have mitochondrion localization	null	2.86757	0.005112	0.017412
AN11018	Ortholog of A. fumigatus Af293 : Afu5g07902, A. niger CBS 513.88 : An03g03930, A. oryzae RIB40 : AO090701000702, Aspergillus versicolor : Aspve1_0131793 and Aspergillus sydowii : Aspsy1_0058760	null	-1.8508	0.005131	0.017454
AN1795	Ortholog(s) have cobalt ion transmembrane transporter activity, zinc ion transmembrane transporter activity	null	1.99433	0.005131	0.017454
AN5698	Putative transferase with a predicted role in fatty acid metabolism; predicted N-terminal mitochondrial targeting sequence	null	-1.9688	0.005131	0.017454
AN8044	Ortholog(s) have metalloendopeptidase activity, role in peptide pheromone maturation and cytosol, extrinsic to membrane localization	null	1.82502	0.005143	0.017486
AN4820	Putative succinate-semialdehyde dehydrogenase [NAD(P)+] with a predicted role in 4-aminobutyrate (GABA) shunt	null	-1.8188	0.005156	0.01752
AN4000	Protein with similarity to poly(A)-binding proteins; overexpression results in increased brlA expression and asexual development; expression reduced after exposure to farnesol	fabM	1.96761	0.005177	0.017585
AN6200	Putative ortholog of S. cerevisiae Rrp12p; expression reduced after exposure to farnesol	null	1.95022	0.0052	0.017651
AN9103	Putative apoptosis-inducing factor (AIF)-like mitochondrial oxidoreductase; mutants display decreased survival in the presence of farnesol or menadione, decreased electron transport; expression upregulated after exposure to farnesol	aifA	-1.8668	0.005201	0.017651
AN4308	Ortholog(s) have mitochondrion localization	null	1.88149	0.00523	0.017724
AN4887	Putative mitogen-activated protein kinase kinase kinase (MAPKKK)	bckA	-1.8698	0.00523	0.017724

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AN5660	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	wscA	-1.8147	0.00523	0.017724
AN7571	Ortholog(s) have endoplasmic reticulum localization	null	2.11707	0.005258	0.017806
AN2238	Ortholog(s) have cytosol, nucleus localization	null	1.80134	0.005259	0.017806
AN5276	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	2.45483	0.005302	0.017944
AN11841	Putative GNAT-type acetyltransferase	ngn18	-2.197	0.005369	0.018008
AN4822	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	-2.3097	0.005369	0.018008
AN6565	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	null	-2.197	0.005369	0.018008
AN6737	Ortholog(s) have mitochondrion localization	null	2.44213	0.005369	0.018008
AN8649	Ortholog of A. oryzae RIB40 : AO090009000519, A. niger ATCC 1015 : 186804-mRNA, Aspergillus versicolor : Aspve1_0044547, Aspergillus sydowii : Aspsy1_0048337 and Aspergillus terreus NIH2624 : ATET_07276	null	2.44213	0.005369	0.018008
AN5211	Ortholog(s) have 1-phosphatidylinositol-3-phosphate 5-kinase activity, phosphatidylinositol-3-phosphate binding activity	null	-1.8141	0.005373	0.018008
AN3073	Putative asparaginyl-tRNA synthetase with a predicted role in tRNA charging for translation	null	1.91668	0.005374	0.018008
AN6175	Ortholog(s) have cytosol, nucleus localization	null	2.26612	0.005382	0.018008
AN1015	Putative phosphorylase with a predicted role in glycogen degradation	null	-1.7873	0.005388	0.018008
AN0058	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.6508	0.005402	0.018008
AN0567	Putative alcohol oxidase with a predicted role in glycerol metabolism	null	-5.6508	0.005402	0.018008
AN10039	Putative histidine acid phosphatase	null	-5.6508	0.005402	0.018008
AN1088	Ortholog of A. fumigatus Af293 : Afu4g14470, Afu8g00430, A. niger CBS 513.88 : An07g00070, An07g00010, An02g08300, An11g06450 and A. oryzae RIB40 : AO090001000323	null	-5.6508	0.005402	0.018008
AN11810	Putative GNAT-type acetyltransferase	ngn14	-5.6508	0.005402	0.018008
AN1301	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	null	-5.6508	0.005402	0.018008
AN2528	Protein with rhamnogalacturonan acetylesterase activity, involved in degradation of pectin	null	-5.6508	0.005402	0.018008
AN2652	Ortholog of A. niger CBS 513.88 : An08g10210, A. niger ATCC 1015 : 37921-mRNA, Aspergillus acidus : Aspfo1_0205882, Aspfo1_0218903 and Aspergillus versicolor : Aspve1_0084525, Aspve1_0160293	null	-5.6508	0.005402	0.018008
AN3041	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.6508	0.005402	0.018008
AN3316	null	null	-5.6508	0.005402	0.018008

AN3402	Putative alpha-amylase with a predicted role in starch metabolism; transcriptionally induced by isomaltose in an amyR-dependent manner	amyB	-5.6508	0.005402	0.018008
AN3575	Has domain(s) with predicted protein serine/threonine kinase activity and role in protein phosphorylation	null	-5.6508	0.005402	0.018008
AN5182	Ortholog(s) have RNA polymerase II core promoter proximal region sequence-specific DNA binding, more	null	-5.6508	0.005402	0.018008
AN5411	Has domain(s) with predicted metal ion binding, phosphoric diester hydrolase activity	null	-5.6508	0.005402	0.018008
AN7067	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.6508	0.005402	0.018008
AN7669	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines, metal ion binding activity	null	-3.5969	0.005402	0.018008
AN8355	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	null	-5.6508	0.005402	0.018008
AN8373	Putative GNAT-type acetyltransferase	ngn11	-5.6508	0.005402	0.018008
AN8585	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.6508	0.005402	0.018008
AN8697	Has domain(s) with predicted nucleic acid binding activity	null	-5.6508	0.005402	0.018008
AN8779	Has domain(s) with predicted hydrolase activity	null	-5.6508	0.005402	0.018008
AN9011	Putative aryl-alcohol oxidase-related protein	null	-5.6508	0.005402	0.018008
AN9128	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.6508	0.005402	0.018008
AN9205	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	null	-5.6508	0.005402	0.018008
AN2992	Ortholog(s) have cytosol, eukaryotic translation initiation factor 2 complex, multi-eIF complex localization	null	1.79969	0.005404	0.018009
AN3744	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	1.8268	0.005454	0.01816
AN10392	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.541	0.005457	0.01816
AN4720	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-2.541	0.005457	0.01816

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AN4863	Ortholog(s) have copper chaperone activity, role in intracellular copper ion transport, mitochondrial respiratory chain complex IV assembly and cytosol, mitochondrial intermembrane space, nucleus localization	null	1.97069	0.005484	0.018242
AN12127	Ortholog of A. fumigatus Af293 : Afu3g07310, A. niger CBS 513.88 : An02g13400, A. oryzae RIB40 : AO090020000191 and A. niger ATCC 1015 : 173674-mRNA	null	1.93153	0.005492	0.018261
AN4753	Ortholog(s) have unfolded protein binding activity, role in aerobic respiration, mitochondrial respiratory chain complex IV assembly and integral to membrane, mitochondrial inner membrane localization	null	1.86051	0.005501	0.018281
AN7298	Protein of unknown function; induced by carbon starvation-induced autophagy	null	-1.9088	0.00551	0.018303
AN7143	Ortholog(s) have cytosol localization	null	1.93755	0.005566	0.018477
AN4070	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	null	1.86236	0.005568	0.018477
AN4453	Ortholog(s) have role in N-terminal peptidyl-methionine acetylation, regulation of cytokinesis, actomyosin contractile ring assembly and cytosol localization	null	1.82908	0.00557	0.018477
AN10142	null	null	1.83051	0.005585	0.018519
AN10189	Ortholog(s) have protein-arginine omega-N monomethyltransferase activity and role in peptidyl-arginine methylation	null	1.97281	0.005626	0.018639
AN6303	Protein with similarity to DNA replication factor C; mutations cause hypersensitivity to UV; transcript upregulated in response to camptothecin	uvsF	-1.931	0.005626	0.018639
AN5534	Ortholog(s) have glyoxylate reductase activity, role in glyoxylate catabolic process and cytosol, mitochondrion, nucleus localization	null	2.60987	0.005688	0.018835
AN10064	Has domain(s) with predicted catalytic activity	null	-1.8158	0.00569	0.018835
AN8062	Has domain(s) with predicted outer membrane localization	null	-2.3032	0.00574	0.018991
AN0059	Ortholog(s) have nucleolus, spliceosomal complex localization	null	2.95204	0.005834	0.019243
AN0200	Ortholog(s) have cytosol, nucleus localization	null	-2.5693	0.005834	0.019243
AN1920	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	-2.8699	0.005834	0.019243
AN2814	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.5693	0.005834	0.019243
AN4256	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	null	-2.8699	0.005834	0.019243

AN5227	Has domain(s) with predicted DNA binding activity and role in DNA integration	null	-2.5693	0.005834	0.019243
AN8241	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	chiA	3.00043	0.005834	0.019243
AN6596	Ortholog of A. fumigatus Af293 : Afu6g04060, A. niger CBS 513.88 : An15g01300, A. oryzae RIB40 : AO090701000130, A. niger ATCC 1015 : 53410-mRNA and Aspergillus versicolor : Aspve1_0197466	null	1.80325	0.005857	0.019308
AN1178	Ortholog(s) have cytosol, nucleus localization	null	1.88725	0.005866	0.01933
AN7338	Has domain(s) with predicted acid-amino acid ligase activity and role in post-translational protein modification	null	-2.1	0.005869	0.019331
AN8847	Phosducin-like protein	phnC	1.91274	0.005886	0.019378
AN10200	Protein required for biogenesis of the ribosomal 60S subunit; ortholog of S. cerevisiae Rpf2p; expression reduced after exposure to farnesol	null	2.24051	0.005955	0.019598
AN10196	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	null	2.01234	0.005981	0.019664
AN11859	Ortholog(s) have 1-acylglycerophosphocholine O-acyltransferase activity	null	2.01234	0.005981	0.019664
AN2069	Ortholog(s) have electron carrier activity, role in sterol biosynthetic process and endoplasmic reticulum membrane, mitochondrion localization	null	1.77595	0.006053	0.019892
AN3693	Ortholog(s) have Rpd3L-Expanded complex, Set3 complex, cytosol localization	null	-1.9482	0.006075	0.019948
AN6567	Ortholog(s) have role in histone acetylation and NuA4 histone acetyltransferase complex localization	null	-1.9983	0.006075	0.019948
AN4689	Ortholog of A. fumigatus Af293 : Afu5g08920, A. niger CBS 513.88 : An07g04290, A. oryzae RIB40 : AO090020000494, A. niger ATCC 1015 : 39991-mRNA and Aspergillus versicolor : Aspve1_0084711	null	-2.2681	0.006131	0.020123
AN0174	Has domain(s) with predicted D-amino-acid oxidase activity, nucleotide binding activity and role in oxidation-reduction process	null	2.83134	0.006154	0.020171
AN1457	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.83134	0.006154	0.020171
AN6086	Putative F-box protein; ortholog(s) have role in SCF-dependent proteasomal ubiquitin-dependent protein catabolism, cellular response to methylmercury and SCF ubiquitin ligase complex localization; NeddH-associated protein	fbx1	2.83134	0.006154	0.020171
AN1954	Ortholog of A. fumigatus Af293 : Afu4g13410, A. niger CBS 513.88 : An01g09120, A. niger ATCC 1015 : 142364-mRNA, Aspergillus versicolor : Aspve1_0185950 and Aspergillus sydowii : Aspsy1_0053894	null	1.98131	0.006178	0.020242
AN11161	Has domain(s) with predicted phosphatidylserine decarboxylase activity and role in phospholipid biosynthetic process	null	-2.9899	0.006189	0.020249

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AN6604	Ortholog(s) have ATPase activity, tRNA binding activity, role in tRNA modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	3.6244	0.006189	0.020249
AN7870	Ortholog of A. fumigatus Af293 : Afu3g01650, Afu6g11970, N. fischeri NRRL 181 : NFIA_002730, NFIA_057640, Aspergillus versicolor : Aspve1_0204208 and Aspergillus sydowii : Aspsy1_0160874	null	3.6244	0.006189	0.020249
AN4512	Ortholog of A. fumigatus Af293 : Afu2g03155, A. niger CBS 513.88 : An07g07580, A. oryzae RIB40 : AO090120000271, A. niger ATCC 1015 : 199982-mRNA and Aspergillus versicolor : Aspve1_0171018	null	2.16603	0.00621	0.020305
AN11145	Functional ortholog of S. cerevisiae CGR1; nucleolar protein with a predicted role in ribosome biogenesis and rRNA processing	cgrA	1.97459	0.006211	0.020305
AN2862	Predicted CAP-Gly domain protein with similarity to Saccharomyces cerevisiae Bim1p	null	1.77989	0.00624	0.02039
AN2907	Ortholog(s) have role in ascospore formation, cellular response to caffeine, eukaryotic translation initiation factor 3 complex assembly and mitotic sister chromatid segregation, more	null	1.85512	0.006247	0.020405
AN8200	Ortholog of A. fumigatus Af293 : Afu5g03310, A. niger CBS 513.88 : An09g05630, A. oryzae RIB40 : AO090102000535, A. niger ATCC 1015 : 143961-mRNA and Aspergillus versicolor : Aspve1_0155723	null	1.77119	0.006282	0.020508
AN5906	Has domain(s) with predicted ubiquitin-protein ligase activity, role in protein ubiquitination and ubiquitin ligase complex localization	null	1.80058	0.006294	0.020541
AN0944	Putative ATP-dependent RNA helicase; transcript repressed by nitrogen limitation	null	2.14183	0.006305	0.020559
AN7719	Ortholog(s) have cytosol, nucleus localization	null	1.9425	0.00631	0.020559
AN2628	Predicted mariner transposon-related ORF	null	-3.1898	0.006311	0.020559
AN5002	null	null	-3.1898	0.006311	0.020559
AN7299	Ortholog(s) have DNA binding activity and cytosol, nucleus localization	null	1.76307	0.006321	0.020582
AN0815	Ortholog of A. fumigatus Af293 : Afu4g14380, A. niger CBS 513.88 : An06g00370, A. oryzae RIB40 : AO090005001119, A. niger ATCC 1015 : 207580-mRNA and Aspergillus versicolor : Aspve1_0049082	null	1.848	0.006328	0.020597
AN11953	Ortholog(s) have nucleus localization	null	-2.0799	0.00634	0.020626
AN10572	Ortholog of A. fumigatus Af293 : Afu2g02450, A. niger CBS 513.88 : An07g06200, A. oryzae RIB40 : AO090026000558, A. niger ATCC 1015 : 200072-mRNA and Aspergillus versicolor : Aspve1_0134225	null	1.9452	0.006346	0.020638
AN2011	Ortholog(s) have phospholipid-translocating ATPase activity, role in intracellular protein transport, phospholipid translocation and trans-Golgi network transport vesicle localization	null	-1.7884	0.006393	0.02078
AN5884	Orotate phosphoribosyltransferase (OPRTase) that catalyzes the fifth step in pyrimidine biosynthesis	pyrF	2.0003	0.006399	0.02079
AN3030	Alcohol dehydrogenase, class V; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	2.10187	0.006447	0.020917
AN5228	Putative NADH:flavin oxidoreductase/NADH oxidase; intracellular, menadione stress-induced protein	null	2.11908	0.006447	0.020917

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AN7640	Ortholog of A. nidulans FGSC A4 : AN5292, A. fumigatus Af293 : Afu5g12490, Afu5g13780, A. niger CBS 513.88 : An14g06730 and A. oryzae RIB40 : AO090120000374, AO090020000661	null	2.10187	0.006447	0.020917
AN7480	Ortholog(s) have role in negative regulation of conjugation with cellular fusion and cytosol localization	null	1.92291	0.006453	0.020928
AN10844	Putative fructose-2,6-bisphosphate 2-phosphatase	fbpZ	-1.7558	0.006465	0.020959
AN10317	Ortholog of A. fumigatus Af293 : Afu3g14445, A. niger CBS 513.88 : An09g03980, A. oryzae RIB40 : AO090701000586, N. fischeri NRRL 181 : NFIA_062810 and Aspergillus flavus NRRL 3357 : AFL2T_06202	null	2.29821	0.006482	0.020986
AN4372	Protein with polygalacturonase activity, involved in degradation of pectin	pgaB	2.29821	0.006482	0.020986
AN6740	null	null	2.29821	0.006482	0.020986
AN4954	Ortholog of A. fumigatus Af293 : Afu3g10330, A. oryzae RIB40 : AO090003000582, A. niger ATCC 1015 : 56429-mRNA, Aspergillus versicolor : Aspve1_0061102 and Aspergillus sydowii : Aspsy1_0130681	null	2.07367	0.006503	0.021046
AN5025	Ortholog(s) have polyamine oxidase activity, role in pantothenate biosynthetic process, polyamine catabolic process and cytoplasm localization	null	-1.9548	0.006549	0.021176
AN6625	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	null	-1.9109	0.006549	0.021176
AN4701	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	null	-1.9381	0.006556	0.021181
AN6367	Has domain(s) with predicted phosphatidylinositol phosphate kinase activity and role in phosphatidylinositol metabolic process	null	-1.9381	0.006556	0.021181
AN1230	Ortholog(s) have unfolded protein binding activity, role in mitochondrial proton-transporting ATP synthase complex assembly and integral to mitochondrial membrane, mitochondrial inner membrane localization	null	2.22122	0.00661	0.021344
AN3783	null	null	-2.4712	0.006718	0.021647
AN3822	Has domain(s) with predicted hydrolase activity	null	-2.4712	0.006718	0.021647
AN3952	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of substances activity, role in transport and integral to membrane localization	null	-2.4712	0.006718	0.021647
AN5505	Ortholog of Aspergillus versicolor : Aspve1_0052822 and Aspergillus sydowii : Aspsy1_0046382	null	-2.4712	0.006718	0.021647
AN6392	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	null	-2.4712	0.006718	0.021647
AN0377	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.4499	0.00674	0.021679
AN10980	null	null	-2.4499	0.00674	0.021679
AN2112	Ortholog(s) have cytosol, nucleus localization	null	-2.2861	0.00674	0.021679

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AN6312	Ortholog(s) have cytosol, nucleus localization	null	-2.2861	0.00674	0.021679
AN3012	Ortholog(s) have importin-alpha export receptor activity, role in protein export from nucleus, tRNA re-export from nucleus and cytosol, nuclear envelope localization	kapL	1.7935	0.00677	0.021765
AN1913	Putative lysyl-tRNA synthetase with a predicted role in lysine metabolism	null	2.20133	0.006798	0.021837
AN6783	Has domain(s) with predicted nucleobase transmembrane transporter activity, role in nucleobase transport and membrane localization	null	-2.1505	0.006798	0.021837
AN4526	Putative nucleoside transporter	pttA	1.88682	0.006844	0.021975
AN4382	Ortholog(s) have cytosol, nucleus localization	null	1.98815	0.006849	0.021977
AN6838	Beta-tubulin, highly conserved component of microtubules; A. nidulans has two beta-tubulin genes, tubC and benA; expression of tubC increases during conidiation	tubC	1.72622	0.006854	0.021977
AN2572	Putative dipeptidyl-peptidase; transcript upregulated by nitrate limitation	null	-1.8188	0.006856	0.021977
AN6195	Transcriptional regulator that mediates carbon catabolite repression; mutants display increased extracellular protease activity	creA	-1.8004	0.006856	0.021977
AN5717	Non-essential karyopherin family protein; required for normal hyphal growth and conidial development; predicted to contain five HEAT (huntingtin-elongation-A subunit-TOR) motifs	kapI	1.74749	0.00687	0.022006
AN8630	Ortholog(s) have cytosol, nucleus localization	null	-2.0119	0.006871	0.022006
AN2166	Ortholog of A. fumigatus Af293 : Afu2g15850, A. niger CBS 513.88 : An15g06150, A. oryzae RIB40 : AO090012000227, A. niger ATCC 1015 : 48827-mRNA and Aspergillus versicolor : Aspve1_0125759	null	-1.8247	0.006878	0.022019
AN0347	Putative GTPase with a predicted role in intra-Golgi transport; transcript levels increase during the unfolded-protein response (UPR)	srgE	-1.92	0.00696	0.02226
AN3184	Putative aldose 1-epimerase with a predicted role in glucose metabolism; transcriptionally induced by growth on xylose	null	-1.92	0.00696	0.02226
AN1191	Small ubiquitin-like modifier (SUMO) protein; mutant is viable, slow growing with pleiotropic phenotypes; punctate nucleoplasmic localization at interphase; deletion causes dramatic increase in asperthecin; camptothecin induced transcript	sumO	1.79355	0.006994	0.022361
AN10055	Ortholog(s) have cell division site, cytosol, nucleolus localization	null	1.8495	0.007031	0.022468
AN8743	Has domain(s) with predicted triglyceride lipase activity and role in lipid metabolic process	null	-1.7851	0.007037	0.022477
AN11112	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	null	-1.9455	0.007062	0.02254
AN11173	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_11268	null	-1.9455	0.007062	0.02254
AN9517	Has domain(s) with predicted DNA binding activity	null	-2.1311	0.007083	0.022591

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AN6201	Ortholog of A. fumigatus Af293 : Afu2g11830, A. oryzae RIB40 : AO090026000461, Aspergillus versicolor : Aspve1_0052426, Aspergillus sydowii : Aspsy1_0151758 and Aspergillus terreus NIH2624 : ATET_01122	null	-1.8787	0.007084	0.022591
AN7158	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	1.82583	0.007095	0.022614
AN5677	Ortholog(s) have role in establishment or maintenance of actin cytoskeleton polarity and cell cortex of cell tip, medial cortex localization	null	-1.8007	0.0071	0.02262
AN1711	Ortholog(s) have ribosomal large subunit binding activity, role in ribosomal large subunit export from nucleus and cytosol, cytosolic large ribosomal subunit, nucleus localization	null	1.8129	0.007141	0.022741
AN3160	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	1.87299	0.007144	0.022741
AN7044	Putative histidinol-phosphatase with a predicted role in histidine metabolism	null	1.77751	0.007181	0.02285
AN0858	Putative chaperone	hsp104	1.71357	0.007215	0.022947
AN11111	Ortholog(s) have 3-phytase activity, acid phosphatase activity, protein tyrosine phosphatase activity and role in dephosphorylation, thiamine-containing compound metabolic process	null	2.3951	0.007236	0.022996
AN9498	Ortholog of A. fumigatus Af293 : Afu6g10770, A. niger CBS 513.88 : An11g00650, A. oryzae RIB40 : AO090023000195, A. niger ATCC 1015 : 38742-mRNA and Aspergillus versicolor : Aspve1_0083263	null	2.3951	0.007236	0.022996
AN0868	Acyl-CoA thioesterase; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	-1.9401	0.007241	0.023002
AN1149	Protein of unknown function; upregulated in A. oryzae and A. nidulans under hypoxic growth conditions	null	1.8104	0.007356	0.023355
AN4251	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	1.93898	0.00739	0.023447
AN0661	Has domain(s) with predicted RNA binding, RNA-directed DNA polymerase activity and role in RNA-dependent DNA replication	null	2.90198	0.007394	0.023447
AN5207	Ortholog(s) have cytosol, nucleus localization	null	-2.7883	0.007394	0.023447
AN10037	null	null	1.87352	0.007404	0.02346
AN5602	Ortholog(s) have ATPase activator activity, chaperone binding activity, role in protein folding, response to stress and cytosol localization	null	1.7511	0.007405	0.02346
AN4894	Ortholog(s) have structural molecule activity, role in conjugation with cellular fusion, histone acetylation, protein complex assembly and SAGA complex, SLIK (SAGA-like) complex, mitochondrion localization	null	-1.9588	0.007409	0.023463
AN1095	Ortholog(s) have nucleolus localization	null	1.91098	0.007427	0.023493

AN2006	Ortholog of A. fumigatus Af293 : Afu4g10260, A. niger CBS 513.88 : An04g06660, A. oryzae RIB40 : AO090003001196, A. niger ATCC 1015 : 45320-mRNA and Aspergillus versicolor : Aspve1_0124983	null	2.75602	0.007428	0.023493
AN5842	Putative L-lactate dehydrogenase with a predicted role in the methylglyoxal bypass	ldhA	2.79417	0.007428	0.023493
AN6248	Ortholog(s) have adenyl-nucleotide exchange factor activity, role in protein import into mitochondrial matrix, protein refolding and mitochondrial matrix, presequence translocase-associated import motor localization	null	1.87838	0.007532	0.023814
AN6497	Ortholog of A. fumigatus Af293 : Afu6g05250, A. niger ATCC 1015 : 200411-mRNA, Aspergillus versicolor : Aspve1_0085986, Aspergillus sydowii : Aspsy1_0037098 and Aspergillus terreus NIH2624 : ATET_05650	null	2.12919	0.007578	0.023949
AN1684	Ortholog of A. fumigatus Af293 : Afu4g08650, A. niger CBS 513.88 : An04g03490, A. oryzae RIB40 : AO090023000691, A. niger ATCC 1015 : 44071-mRNA and Aspergillus versicolor : Aspve1_0445671	null	-2.1132	0.007651	0.024159
AN8284	Ortholog of A. fumigatus Af293 : Afu7g03730, A. niger CBS 513.88 : An13g00080, A. oryzae RIB40 : AO090026000843, A. niger ATCC 1015 : 44662-mRNA and Aspergillus versicolor : Aspve1_0044842	null	2.17907	0.007651	0.024159
AN5621	Ortholog of A. fumigatus Af293 : Afu4g11130, A. niger CBS 513.88 : An04g05550, A. niger ATCC 1015 : 214353-mRNA, Aspergillus versicolor : Aspve1_0053400 and Aspergillus sydowii : Aspsy1_0088403	null	-2.2107	0.00766	0.024178
AN3431	Ortholog(s) have nicotinate-nucleotide diphosphorylase (carboxylating) activity, role in de novo NAD biosynthetic process from tryptophan and cytoplasm, nucleus localization	null	1.79521	0.007771	0.024515
AN5957	Putative branched chain amino acid aminotransferase with a predicted role in valine, leucine, and isoleucine metabolism	null	1.79557	0.007783	0.024544
AN0768	Ortholog of A. fumigatus Af293 : Afu1g14300, A. oryzae RIB40 : AO090011000381, A. niger ATCC 1015 : 171293-mRNA, Aspergillus versicolor : Aspve1_0067752 and Aspergillus sydowii : Aspsy1_0672839	null	-2.0413	0.007794	0.024568
AN3689	Ortholog(s) have role in meiosis and cytosol, nucleus localization	null	-1.8302	0.007808	0.0246
AN10217	Ortholog(s) have oxidoreductase activity, acting on CH-OH group of donors activity, role in oxidation-reduction process and cytosol, nucleus localization	null	-1.7712	0.007835	0.024675
AN8730	Ortholog of Aspergillus versicolor : Aspve1_0038959, Aspergillus sydowii : Aspsy1_0040193 and Aspergillus terreus NIH2624 : ATET_07838	null	-1.8831	0.007848	0.024707
AN1794	Putative cytochrome P450; expression reduced after exposure to farnesol	CYP682D1	1.9511	0.007853	0.024712
AN4583	Putative peptidyl-prolyl cis-trans isomerase D (PPIase); cyclophilin family member; protein abundance decreased by menadione stress; transcript levels increase during the unfolded-protein response (UPR) and in response to camptothecin	cyp7	1.71796	0.007907	0.024871
AN11679	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-2.2299	0.008004	0.025132
AN11893	Ortholog of A. fumigatus Af293 : Afu1g16553, A. niger CBS 513.88 : An01g10690, A. oryzae RIB40 : AO090005001056, Aspergillus versicolor : Aspve1_0036569 and Aspergillus sydowii : Aspsy1_0025816	null	2.54324	0.008004	0.025132

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AN12167	Has domain(s) with predicted zinc ion binding activity	null	2.50874	0.008004	0.025132
AN1806	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	-2.2299	0.008004	0.025132
AN0936	Ortholog(s) have mitochondrion localization	null	1.83941	0.008008	0.025136
AN2500	Putative nicotinamide N-methyltransferase	null	2.36593	0.008026	0.025181
AN6721	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity	null	-1.7907	0.008041	0.025216
AN0061	Ortholog of S. cerevisiae : YLR326W, A. fumigatus Af293 : Afu5g12410, A. oryzae RIB40 : AO090120000361, A. niger ATCC 1015 : 56633-mRNA and Aspergillus versicolor : Aspve1_0023052	null	-1.8591	0.00807	0.025296
AN4942	Ortholog(s) have Ran GTPase binding activity, role in protein import into nucleus and cytosol, nuclear envelope localization	ntfA	1.72334	0.008114	0.025425
AN7679	Ortholog(s) have role in ER to Golgi vesicle-mediated transport and ER to Golgi transport vesicle, integral to Golgi membrane, integral to endoplasmic reticulum membrane localization	null	2.0124	0.008147	0.025484
AN12112	Ortholog(s) have role in establishment or maintenance of cytoskeleton polarity, regulation of microtubule polymerization or depolymerization and cytosol, nucleus localization	null	3.50568	0.008156	0.025484
AN1809	Has domain(s) with predicted fumarylacetoacetase activity and role in aromatic amino acid family metabolic process	null	-2.8916	0.008156	0.025484
AN2587	Ortholog of A. nidulans FGSC A4 : AN5639, AN7395, A. fumigatus Af293 : Afu5g00840, A. oryzae RIB40 : AO090102000018 and A. niger ATCC 1015 : 134885-mRNA, 194124-mRNA	null	-2.8916	0.008156	0.025484
AN6379	null	null	-2.8916	0.008156	0.025484
AN6780	Ortholog of A. nidulans FGSC A4 : AN10401, A. fumigatus Af293 : Afu7g01210, A. niger ATCC 1015 : 194249-mRNA and Aspergillus versicolor : Aspve1_0039423, Aspve1_0128644	null	3.50568	0.008156	0.025484
AN10647	Putative cytochrome P450 protein; involved in hyphal branching; mutant branches excessively	ahbB	1.84779	0.00816	0.025484
AN7050	Putative transcription factor containing a Zn2-Cys6 binuclear cluster domain; required for transcriptional activation of genes involved in fatty acid utilization; highly conserved in filamentous ascomycetes	farA	-1.8167	0.00816	0.025484
AN5675	Ortholog(s) have ubiquitin binding activity, role in proteasomal ubiquitin-dependent protein catabolic process and cytoplasm, nucleus localization	null	-1.8576	0.008172	0.025501
AN5984	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	2.07863	0.008174	0.025501
AN5491	Ortholog(s) have role in CVT pathway, autophagic vacuole assembly, mitochondrion degradation, peroxisome degradation, piecemeal microautophagy of nucleus and extrinsic to membrane, pre-autophagosomal structure localization	null	-1.6971	0.008179	0.025501

AN11317	Ortholog of A. niger CBS 513.88 : An04g07180, Aspergillus brasiliensis : Aspbr1_0196407, A. niger ATCC 1015 : 204621-mRNA, N. fischeri NRRL 181 : NFIA_106180 and Aspergillus flavus NRRL 3357 : AFL2T_01814	null	1.74448	0.00818	0.025501
AN4148	Sugar transporter; transcriptionally induced by growth on xylose	null	-1.79	0.008186	0.02551
AN0918	Putative ceramide hydroxylase with a predicted role in sphingoglycolipid metabolism	null	1.69872	0.008217	0.025594
AN8407	Ortholog of Aspergillus brasiliensis : Aspbr1_0177798, Aspergillus versicolor : Aspve1_0046756, Aspergillus sydowii : Aspsy1_0210366 and A. fumigatus A1163 : AFUB_071580	null	1.93507	0.008226	0.025614
AN9359	Ortholog(s) have DNA translocase activity	null	1.75859	0.008331	0.02593
AN1445	Ortholog(s) have protein-histidine N-methyltransferase activity, role in peptidyl-histidine methylation, to form tele-methylhistidine and cytosol, nucleus localization	null	2.22584	0.008343	0.025945
AN4415	Ortholog(s) have holocytochrome-c synthase activity, role in cytochrome c-heme linkage and cytosol, mitochondrial intermembrane space, nucleus localization	null	2.25037	0.008343	0.025945
AN5904	Putative beta-ketoacyl-[acyl-carrier-protein] synthase with a predicted role in cytosolic fatty acid formation	null	1.72258	0.008402	0.026118
AN11862	Ortholog(s) have TRC complex, nucleus localization	null	1.85798	0.008455	0.026271
AN3581	Thioredoxin reductase with a predicted role in pyrimidine metabolism; putative flavoprotein; intracellular, menadione stress-induced protein; transcripts of two different sizes have been detected	trxR	2.33279	0.008477	0.026317
AN9102	Has domain(s) with predicted DNA-directed RNA polymerase activity and role in transcription, DNA-dependent	null	2.33279	0.008477	0.026317
AN6060	Has domain(s) with predicted DNA binding, RNA binding activity and role in RNA metabolic process	null	1.77999	0.008535	0.026486
AN2451	Ortholog(s) have cytosol localization	null	2.04896	0.008578	0.026598
AN6690	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	null	2.03089	0.008578	0.026598
AN12480	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	null	-1.7018	0.008599	0.026651
AN10301	Has domain(s) with predicted nucleotide binding activity	null	2.15647	0.008621	0.026685
AN4161	Ortholog(s) have cytoplasm, nucleus, ribosome localization	null	-2.0749	0.008621	0.026685
AN4812	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.0749	0.008621	0.026685
AN6775	Protein involved in penicillin biosynthesis, null produces reduced levels of penicillin; partially redundant with aatA	aatB	-1.9108	0.008641	0.026737

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AN0379	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	null	-1.7481	0.008676	0.026834
AN8040	Ortholog(s) have role in phosphate ion transport and endoplasmic reticulum, membrane, mitochondrion localization	null	1.68921	0.008741	0.027022
AN1667	Ortholog of A. fumigatus Af293 : Afu4g08940, A. niger CBS 513.88 : An04g03800, A. oryzae RIB40 : AO090023000640, A. niger ATCC 1015 : 190740-mRNA and Aspergillus versicolor : Aspve1_0037538	null	1.99876	0.008776	0.027119
AN0386	Ortholog of A. nidulans FGSC A4 : AN5371, A. fumigatus Af293 : Afu1g01610, Afu4g01060, A. niger CBS 513.88 : An04g08650 and A. oryzae RIB40 : AO090113000157, AO090020000683	null	-3.0663	0.008799	0.027134
AN0801	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-3.0663	0.008799	0.027134
AN10697	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	null	-3.0663	0.008799	0.027134
AN1586	Has domain(s) with predicted copper ion binding, primary amine oxidase activity, quinone binding activity and role in amine metabolic process, oxidation-reduction process	null	-3.0663	0.008799	0.027134
AN4949	Ortholog(s) have chromatin insulator sequence binding, core RNA polymerase III binding transcription factor activity, tDNA binding activity and role in transcription initiation from RNA polymerase III promoter	null	-3.0663	0.008799	0.027134
AN0085	Ortholog of A. fumigatus Af293 : Afu5g12170, A. niger CBS 513.88 : An18g02150, A. oryzae RIB40 : AO090120000334, A. niger ATCC 1015 : 54106-mRNA and Aspergillus versicolor : Aspve1_0215604	null	-1.6866	0.008859	0.027299
AN3313	Putative methyltransferase with a predicted role in histidine metabolism; ribosomal RNA adenine dimethylase; expression reduced after exposure to farnesol	null	1.89536	0.00886	0.027299
AN1770	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit, nucleus localization	null	1.86921	0.008956	0.027585
AN6510	Translocase of outer mitochondrial membrane complex; ortholog of S. cerevisiae Tom40p has role in protein import into mitochondrial matrix; expression reduced after exposure to farnesol	null	1.85684	0.008978	0.027631
AN3207	Ortholog of A. nidulans FGSC A4 : AN1505, A. fumigatus Af293 : Afu2g15470, Afu8g00720, Afu8g05070 and A. niger CBS 513.88 : An07g04980, An16g07680, An14g02720, An14g07130, An15g05540	null	-1.7533	0.008979	0.027631
AN10726	null	null	2.71683	0.00899	0.027653
AN6037	Putative glucose-6-phosphate isomerase with a predicted role in gluconeogenesis and glycolysis; mutant defective in hyphal polarity and conidiation	swoM	1.75095	0.009015	0.027719
AN8339	Transcript induced by light in in developmentally competent mycelia	null	-1.6971	0.009019	0.027719
AN3656	Putative nitrilase with a predicted role in nitrogen or cyanoamino acid metabolism	null	2.01248	0.009073	0.027862

AN8832	Ortholog(s) have aminoacyl-tRNA hydrolase activity, role in mitochondrial translation and mitochondrion localization	null	2.01248	0.009073	0.027862
AN0560	Ortholog(s) have role in Golgi to plasma membrane transport, exocyst assembly, exocyst localization, spliceosomal complex assembly	null	-1.9989	0.009082	0.027879
AN1632	Ortholog(s) have protein serine/threonine kinase activity	null	-1.7463	0.009112	0.027958
AN0917	Ortholog(s) have nucleus localization	null	-1.8036	0.009126	0.027971
AN0066	Ortholog(s) have isopropylmalate transmembrane transporter activity, oxaloacetate secondary active transmembrane transporter activity, secondary active sulfate transmembrane transporter activity	null	1.88195	0.009127	0.027971
AN11395	Possible pseudogene	null	1.88195	0.009127	0.027971
AN6272	Ortholog(s) have NADP binding, NADPH-adrenodoxin reductase activity, ferredoxin-NADP+ reductase activity, flavin adenine dinucleotide binding activity, role in oxidation-reduction process and mitochondrion localization	null	1.88613	0.009134	0.027982
AN0227	Ortholog of A. niger CBS 513.88 : An14g03700, A. oryzae RIB40 : AO090010000440, Aspergillus brasiliensis : Aspbr1_0190452 and Aspergillus flavus NRRL 3357 : AFL2T_11608	null	-2.1811	0.009201	0.028141
AN4889	Ortholog(s) have RNA binding activity, role in tRNA modification and cytoplasm, nucleus localization	null	2.31281	0.009201	0.028141
AN5234	Has domain(s) with predicted metal ion binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.1811	0.009201	0.028141
AN5622	Ortholog of A. oryzae RIB40 : AO090102000090, Aspergillus flavus NRRL 3357 : AFL2T_09542, Aspergillus versicolor : Aspve1_0131828 and Aspergillus sydowii : Aspsy1_0149081	null	-2.0685	0.009201	0.028141
AN8638	Transcript enriched in dormant conidia; induced by light in in developmentally competent mycelia	cetJ	-1.9891	0.009275	0.028354
AN1762	Ortholog of A. fumigatus Af293 : Afu6g09150, A. niger CBS 513.88 : An11g06890, A. niger ATCC 1015 : 48037-mRNA, Aspergillus versicolor : Aspve1_0037651 and Aspergillus sydowii : Aspsy1_0139038	null	1.90067	0.009326	0.028498
AN2349	Putative ATP-binding cassette (ABC) transporter of the P-glycoprotein cluster	null	-1.7625	0.009386	0.028663
AN0367	Putative integral membrane protein; transcript repressed by light in developmentally competent mycelia	null	-1.6855	0.009388	0.028663
AN12437	Ortholog(s) have cytosol, nucleus localization	null	2.85011	0.009413	0.028716
AN9179	Ortholog(s) have cytoplasm localization	null	2.85011	0.009413	0.028716
AN6080	Ortholog(s) have role in retrograde vesicle-mediated transport, Golgi to ER and COPI vesicle coat, cytosol, nucleus localization	null	1.8477	0.009441	0.02879
AN6287	Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism	null	2.47339	0.009526	0.029036

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AN0256	Predicted calpain-like cysteine protease involved in a signaling pathway that activates PacC transcription factor in response to alkaline ambient pH	palB	-1.7771	0.009556	0.029118
AN8267	Ortholog of A. fumigatus Af293 : Afu5g04155, A. oryzae RIB40 : AO090102000618, A. niger ATCC 1015 : 128442-mRNA, Aspergillus versicolor : Aspve1_0057271 and Aspergillus sydowii : Aspsy1_0061914	null	1.71429	0.009598	0.029233
AN9074	Ortholog of A. fumigatus Af293 : Afu7g02440, A. oryzae RIB40 : AO090038000622, A. niger ATCC 1015 : 54440-mRNA, Aspergillus versicolor : Aspve1_0089922 and Aspergillus sydowii : Aspsy1_0093793	null	-1.7529	0.009609	0.029253
AN9118	Ortholog of A. fumigatus Af293 : Afu7g01900, A. niger CBS 513.88 : An12g00740, A. niger ATCC 1015 : 212826-mRNA, Aspergillus versicolor : Aspve1_0047801 and Aspergillus sydowii : Aspsy1_0093842	null	1.90017	0.009668	0.029421
AN2171	Ortholog(s) have cytosol, nucleus localization	null	-1.743	0.009708	0.029531
AN12319	Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localization	null	2.11016	0.009723	0.029566
AN10562	Putative methionine sulfoxide reductase with a predicted role in the reduction of methionine sulfoxide to methionine	msrA	2.02934	0.009745	0.029606
AN10816	Ortholog of A. fumigatus Af293 : Afu8g05030, A. oryzae RIB40 : AO090003001446, AO090009000107, A. niger ATCC 1015 : 188511-mRNA and Aspergillus versicolor : Aspve1_0130291	null	2.02934	0.009745	0.029606
AN8065	Ortholog(s) have role in Arp2/3 complex-mediated actin nucleation, establishment of mitochondrion localization and Arp2/3 protein complex, actin cortical patch, cell division site, cell tip, cytosol, mitochondrion, nucleus localization	null	1.86949	0.009763	0.029645
AN2484	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	null	1.66492	0.009765	0.029645
AN10407	Has domain(s) with predicted zinc ion binding activity	null	-1.6547	0.009793	0.029718
AN6560	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	null	-1.7568	0.009844	0.02986
AN3743	Ortholog of A. nidulans FGSC A4 : AN5603, A. fumigatus Af293 : Afu4g11320, Afu7g04400, A. niger CBS 513.88 : An13g00980, An04g05280 and A. oryzae RIB40 : AO090005000127	null	-1.703	0.009858	0.02989
AN8894	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	null	-1.8044	0.009867	0.029905
AN10163	Ortholog of A. fumigatus Af293 : Afu1g12110, A. niger CBS 513.88 : An08g04410, A. niger ATCC 1015 : 176207-mRNA, Aspergillus versicolor : Aspve1_0036720 and Aspergillus sydowii : Aspsy1_0038225	null	1.68652	0.009929	0.030075
AN0590	Ortholog(s) have nucleus localization	null	1.88902	0.009934	0.030075
AN3827	Ortholog(s) have nucleolus localization	null	1.74749	0.009936	0.030075

AN10354	Putative signal sequence processing protein with a predicted role in targeting proteins to the endoplasmic reticulum	null	1.72456	0.00994	0.030075
AN1262	Ortholog of A. fumigatus Af293 : Afu1g10170, A. oryzae RIB40 : AO090038000416, A. niger ATCC 1015 : 38529-mRNA, Aspergillus versicolor : Aspve1_0121257 and Aspergillus sydowii : Aspsy1_0025487	null	2.3006	0.009949	0.030078
AN2172	Ortholog(s) have cyclin-dependent protein kinase regulator activity	null	2.3006	0.009949	0.030078
AN1949	Ortholog(s) have ATP-dependent RNA helicase activity, RNA binding activity, role in rRNA processing and 90S preribosome, nuclear envelope, nucleolus, preribosome, large subunit precursor localization	null	1.75986	0.009968	0.030123
AN10834	Protein with an acyl-CoA dehydrogenase domain	acdB	1.68023	0.009975	0.030133
AN0111	Ortholog(s) have cytosol, spindle pole body, spliceosomal complex localization	null	-1.6878	0.010032	0.030292
AN6902	Protein with a predicted role in mRNA turnover; ortholog of S. cerevisiae Mrt4p; expression reduced after exposure to farnesol	null	1.80025	0.010045	0.03032
AN0932	Putative glutathione oxidoreductase with a predicted role in glutathione biosynthesis	glrA	1.79104	0.010092	0.03045
AN4483	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	null	-1.6827	0.010157	0.030634
AN12084	Ortholog of Aspergillus brasiliensis : Aspbr1_0198574, Aspergillus acidus : Aspfo1_0207812, Aspergillus versicolor : Aspve1_0052887 and Aspergillus sydowii : Aspsy1_1045764	null	1.67457	0.010194	0.030731
AN4430	Small subunit of acetolactate synthase involved in branched-chain amino acid biosynthesis under hypoxic conditions	null	1.74652	0.010214	0.030779
AN5692	Ortholog(s) have role in peroxisome organization and integral to peroxisomal membrane localization	null	-1.6804	0.010222	0.030792
AN5971	Putative NADH-ubiquinone oxidoreductase	null	1.66918	0.010252	0.030868
AN0248	Putative protein disulfide isomerase; pdiB mRNA levels increase in the presence of farnesol	pdiB	-1.8318	0.010285	0.030943
AN5704	Putative Type II fatty acid synthase with a predicted role in mitochondrial fatty acid formation	null	1.92037	0.010285	0.030943
AN6986	Ortholog(s) have calcium:hydrogen antiporter activity, potassium:hydrogen antiporter activity, sodium:hydrogen antiporter activity and role in hydrogen transport, potassium ion transport, sodium ion transport	null	-1.6477	0.010302	0.030982
AN6904	Ortholog(s) have structural constituent of ribosome activity, role in aerobic respiration and mitochondrial large ribosomal subunit localization	null	1.73877	0.010333	0.031052
AN5611	Putative carbonic anhydrase	canA	1.79119	0.010336	0.031052
AN2292	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytoplasm, nucleolus localization	null	1.8114	0.010338	0.031052

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AN8182	Septin, involved in development; prevents formation of inappropriate germ tubes and branches; required for formation of normal conidiophores	aspC	1.65121	0.010344	0.031058
AN0833	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	null	1.62807	0.010428	0.031298
AN4250	Ortholog(s) have organic acid transmembrane transporter activity, role in mitochondrial transport and mitochondrion localization	null	1.80066	0.010495	0.031484
AN2210	Probable ABC-transporter; transcript upregulated in response to camptothecin	null	1.68446	0.010511	0.03152
AN0250	Sugar transporter; transcriptionally induced by growth on xylose	null	-2.1355	0.010563	0.031626
AN12164	null	null	2.28549	0.010563	0.031626
AN1368	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	null	-2.0229	0.010563	0.031626
AN7332	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	null	2.28549	0.010563	0.031626
AN0680	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding RNA polymerase II transcription factor activity, zinc ion binding activity and role in regulation of transcription, DNA-dependent	null	-1.8066	0.010585	0.031671
AN3628	Putative peptide alpha-N-acetyltransferase with a predicted role in protein, peptide, and amino acid metabolism	null	1.65899	0.010588	0.031671
AN6087	Ortholog(s) have metallochaperone activity, role in manganese ion transport and mitochondrion localization	null	1.69112	0.010591	0.031671
AN3943	Has domain(s) with predicted role in proteolysis	null	-1.6887	0.01061	0.031713
AN7659	Ortholog(s) have RNA helicase activity, RNA-dependent ATPase activity, inositol hexakisphosphate binding activity and role in mRNA export from nucleus, translational termination	null	1.80831	0.010629	0.031759
AN1405	Ortholog of A. fumigatus Af293 : Afu8g03950, A. niger CBS 513.88 : An16g09240, A. oryzae RIB40 : AO090103000008, A. niger ATCC 1015 : 194066-mRNA and Aspergillus versicolor : Aspve1_0024658	null	1.72427	0.010665	0.031854
AN0184	Ortholog(s) have Arp2/3 complex binding activity, role in actin cortical patch assembly, actin filament debranching, negative regulation of Arp2/3 complex-mediated actin nucleation and actin cortical patch, cytosol, nucleus localization	null	1.79131	0.01067	0.031855
AN1143	Has domain(s) with predicted zinc ion binding activity	null	1.82559	0.010706	0.031949
AN3422	MAP kinase kinase (MAPKK), component of a signaling module SteD-SteC-MkkB-MpkB that controls coordination of development and secondary metabolism	ste7	-1.8389	0.010749	0.032064

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AN2052	Ortholog(s) have oligopeptide-transporting ATPase activity, role in oligopeptide export from mitochondrion and mitochondrial inner membrane localization	null	1.71003	0.010777	0.032136
AN2658	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	null	-2.0082	0.01079	0.032161
AN11288	null	null	3.44244	0.010816	0.032212
AN7345	Protein with glucosidase activity, involved in degradation of glucans; predicted role in maltose metabolism	agdC	3.44244	0.010816	0.032212
AN2489	Ortholog(s) have RNA polymerase II carboxy-terminal domain kinase activity, cyclin-dependent protein kinase activity	null	-1.7276	0.010849	0.032297
AN8010	Putative glycogen (starch) synthase with a predicted role in glycogen biosynthesis	null	-1.661	0.010906	0.03244
AN2359	Beta-xylosidase, involved in degradation of xylans; transcriptionally induced by growth on xylose	xlnD	-2.329	0.01091	0.03244
AN6373	Ortholog of Aspergillus sydowii : Aspsy1_0999397	null	-2.329	0.01091	0.03244
AN2985	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-1.7212	0.010967	0.032597
AN5986	Putative reductase with a predicted role in carbohydrate metabolism	null	-1.7576	0.011028	0.032754
AN8609	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-1.6414	0.011029	0.032754
AN4698	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	null	-1.647	0.01105	0.032805
AN7042	Has domain(s) with predicted carbonate dehydratase activity, zinc ion binding activity and role in carbon utilization	null	-1.663	0.011086	0.032898
AN10433	Ortholog(s) have role in ER-associated protein catabolic process and cytoplasm, nucleolus localization	null	1.7235	0.011092	0.032902
AN2289	Ortholog(s) have alpha-glucoside transmembrane transporter activity, role in carbohydrate transmembrane transport and Golgi apparatus, fungal-type vacuole membrane localization	null	-1.6887	0.011107	0.032934
AN1859	Ortholog(s) have role in DNA repair, chromatin silencing at telomere, histone exchange and NuA4 histone acetyltransferase complex, Swr1 complex, cytosol localization	null	1.79137	0.011132	0.032994
AN2955	Has domain(s) with predicted role in biosynthetic process	null	1.64607	0.011157	0.033057
AN7458	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	null	1.77571	0.011248	0.033313
AN2190	Has domain(s) with predicted methyltransferase activity	null	1.85349	0.011281	0.033397
AN1391	Ortholog of A. fumigatus Af293 : Afu1g08870, A. niger CBS 513.88 : An08g00360, A. oryzae RIB40 : AO090005001639, A. niger ATCC 1015 : 176655-mRNA and Aspergillus versicolor : Aspve1_0079394	null	-1.8063	0.011326	0.033516

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AN1465	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	null	-1.6259	0.011339	0.03354
AN0400	Ortholog of A. fumigatus Af293 : Afu4g09610, A. niger CBS 513.88 : An04g07500, A. oryzae RIB40 : AO090003001281 and Aspergillus terreus NIH2624 : ATET_00785	null	2.43716	0.011363	0.033598
AN3307	Putative catalytic subunit of the alpha-1,3 glucan synthase complex	agsB	1.64254	0.011407	0.033715
AN4433	Ortholog of A. fumigatus Af293 : Afu4g07240, A. niger CBS 513.88 : An04g01640, A. oryzae RIB40 : AO090023000851, A. niger ATCC 1015 : 215028-mRNA and Aspergillus versicolor : Aspve1_0043170	null	1.73965	0.011446	0.033818
AN6557	Ortholog of A. niger CBS 513.88 : An15g00690, Aspergillus brasiliensis : Aspbr1_0046471, A. niger ATCC 1015 : 40355-mRNA, N. fischeri NRRL 181 : NFIA_051150 and Aspergillus flavus NRRL 3357 : AFL2T_05733	null	1.71723	0.011481	0.033887
AN10218	null	null	-1.9485	0.011484	0.033887
AN5399	Ortholog of A. fumigatus Af293 : Afu2g15280, A. niger CBS 513.88 : An18g02600, A. oryzae RIB40 : AO090003001548, A. niger ATCC 1015 : 42737-mRNA and Aspergillus versicolor : Aspve1_0045700	null	-1.8792	0.011484	0.033887
AN3913	Adenylate cyclase involved in cAMP-dependent signaling during conidial germination	cyaA	-1.6266	0.011544	0.034052
AN3543	null	null	-1.8756	0.011569	0.034098
AN5871	Ortholog(s) have methyltransferase activity, role in rRNA processing and nucleolus localization	null	1.90732	0.011569	0.034098
AN10415	Ortholog(s) have protein heterodimerization activity, role in DNA repair and Smc5-Smc6 complex, nucleus localization	null	-1.7419	0.01159	0.034134
AN5883	Putative methylenetetrahydrofolate reductase (NADPH) with predicted role in one-carbon metabolism; mutation causes methionine auxotrophy and decreased mycelial pigment production; expression induced by homocysteine and decreased by farnesol	metF	1.78232	0.01159	0.034134
AN10134	Ortholog(s) have protein-lysine N-methyltransferase activity, role in negative regulation of G2/M transition of mitotic cell cycle, peptidyl-lysine methylation and cytosol, nucleus localization	null	1.9783	0.011643	0.034261
AN1722	Ortholog(s) have role in heme a biosynthetic process and mitochondrion localization	null	1.9783	0.011643	0.034261
AN3461	Ortholog(s) have mitochondrion localization	null	1.64836	0.011647	0.034261
AN6525	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	aciA	-1.6435	0.011664	0.034295
AN8755	Methylisocitrate lyase; predicted role in the glyoxylate shunt; mitochondrial localization signal predicted	mclA	-1.6062	0.011767	0.034585
AN3206	Putative aryl-alcohol oxidase-related protein; protein expressed at decreased levels in a hapX mutant versus wild-type; transcript is induced by nitrate	null	-1.6182	0.01183	0.034756

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AN0097	Ortholog(s) have role in DNA recombination, double-strand break repair via nonhomologous end joining	null	-1.7843	0.011862	0.034837
AN6005	Ortholog of A. fumigatus Af293 : Afu2g10020, A. niger CBS 513.88 : An16g05030, Aspergillus versicolor : Aspve1_0040814 and Aspergillus sydowii : Aspsy1_0089381	null	-1.6857	0.011885	0.034892
AN6978	Putative nucleotide exchange factor involved in nucleocytoplasmic trafficking of macromolecules	rcc1	1.66159	0.011912	0.034956
AN0265	Ortholog of A. fumigatus Af293 : Afu1g03380, A. niger CBS 513.88 : An01g04760, A. oryzae RIB40 : AO090005000763, A. niger ATCC 1015 : 172247-mRNA and Aspergillus versicolor : Aspve1_0078045	null	-1.6447	0.011943	0.035033
AN2070	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	null	-1.8077	0.011971	0.035087
AN7700	Ortholog(s) have role in regulation of barrier septum assembly, regulation of fungal-type cell wall biogenesis and cytoplasm localization	null	-1.8077	0.011971	0.035087
AN2659	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-1.7862	0.012027	0.035184
AN3294	Protein with acetylxylan esterase activity, involved in degradation of xylans	null	1.64148	0.012033	0.035184
AN12261	null	null	-2.7018	0.012037	0.035184
AN1998	Has domain(s) with predicted hydrolase activity and role in metabolic process	null	-2.7018	0.012037	0.035184
AN2792	Ortholog of A. fumigatus Af293 : Afu8g02480, A. niger CBS 513.88 : An12g05730, A. niger ATCC 1015 : 211525-mRNA and Aspergillus versicolor : Aspve1_0038333	null	-2.7018	0.012037	0.035184
AN3558	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-2.7018	0.012037	0.035184
AN6692	null	null	2.7963	0.012037	0.035184
AN2053	Putative nucleoside transporter	pnpA	-1.7865	0.012051	0.035211
AN9093	Ortholog(s) have mRNA binding, single-stranded DNA binding, translation regulator activity, role in positive regulation of translation and polysomal ribosome localization	null	1.79178	0.012128	0.035422
AN12316	Ortholog(s) have cytosine deaminase activity, role in cytidine metabolic process, cytosine metabolic process, pyrimidine-containing compound salvage and cytoplasm, nucleus localization	null	2.25765	0.012144	0.03544
AN3947	Ortholog(s) have 3'-tyrosyl-DNA phosphodiesterase activity, DNA-(apurinic or apyrimidinic site) lyase activity, double-stranded DNA specific 3'-5' exodeoxyribonuclease activity and role in base-excision repair	null	-1.9759	0.012144	0.03544
AN8695	Ortholog of A. fumigatus Af293 : Afu6g02340, Aspergillus versicolor : Aspve1_0055004, Aspergillus sydowii : Aspsy1_0092193 and Aspergillus terreus NIH2624 : ATET_07216	null	-1.755	0.012158	0.035467
AN3087	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	null	1.74658	0.012195	0.03556
AN6266	Ortholog(s) have nucleus localization	null	1.73157	0.012293	0.035825

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AN6073	Putative prohibitin with a predicted role in mitochondrial maintenance; transcript upregulated in response to camptothecin	phbA	1.61576	0.012295	0.035825
AN0757	Ortholog(s) have tRNA (cytosine-5-)-methyltransferase activity, role in tRNA methylation and nucleus localization	null	1.67991	0.01235	0.03597
AN0194	Putative beta-galactosidase	lacC	-2.9311	0.012384	0.035999
AN0318	Putative plasma membrane ATPase with a predicted role in energy metabolism	null	-2.9311	0.012384	0.035999
AN12435	Ortholog of A. fumigatus Af293 : Afu5g09390, A. niger CBS 513.88 : An07g03590, A. oryzae RIB40 : AO090020000556, A. niger ATCC 1015 : 180772-mRNA and Aspergillus versicolor : Aspve1_0201346	null	-2.9311	0.012384	0.035999
AN6850	Has domain(s) with predicted role in signal transduction and intracellular localization	null	-2.9311	0.012384	0.035999
AN7270	Ortholog of A. oryzae RIB40 : AO090001000616	null	-2.9311	0.012384	0.035999
AN1145	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-1.9952	0.012408	0.036013
AN11582	null	null	2.03779	0.012408	0.036013
AN3043	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-1.9952	0.012408	0.036013
AN3367	Ortholog(s) have cytosol, nucleus localization	null	2.03779	0.012408	0.036013
AN1686	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-1.9837	0.012499	0.036262
AN10700	Ortholog of S. cerevisiae : YER010C, A. fumigatus Af293 : Afu4g10940, A. niger CBS 513.88 : An04g05730, A. oryzae RIB40 : AO090003001122 and A. niger ATCC 1015 : 51189-mRNA	null	-1.8925	0.012571	0.036442
AN5533	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	null	2.0785	0.012571	0.036442
AN5141	Ortholog of A. fumigatus Af293 : Afu1g07280, A. niger CBS 513.88 : An07g09830, A. oryzae RIB40 : AO090012000982, A. niger ATCC 1015 : 56120-mRNA and Aspergillus versicolor : Aspve1_0045774	null	1.65781	0.012624	0.036561
AN10268	null	null	1.99228	0.012628	0.036561
AN3637	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	null	1.99228	0.012628	0.036561
AN4388	Putative ubiquinol-cytochrome-c reductase subunit with a predicted role in energy metabolism	null	1.65564	0.012632	0.036561
AN3934	Has domain(s) with predicted GTP binding activity, role in small GTPase mediated signal transduction and intracellular localization	null	-1.6493	0.012649	0.036596

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AN1142	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-1.8469	0.012673	0.036637
AN12150	null	null	-1.8469	0.012673	0.036637
AN3925	Has domain(s) with predicted catalytic activity, cation binding activity and role in carbohydrate metabolic process	null	-1.6798	0.012729	0.036781
AN1841	Has domain(s) with predicted nucleotide binding activity	null	1.96088	0.012738	0.036781
AN8253	Ortholog(s) have cytosol, nucleus localization	null	1.96088	0.012738	0.036781
AN8225	Putative ribosomal protein L1; ortholog of S. cerevisiae Mrpl1p	null	1.71334	0.012747	0.036794
AN3596	Has domain(s) with predicted FMN binding, riboflavin reductase (NADPH) activity and role in oxidation-reduction process	null	1.91552	0.01276	0.036807
AN11978	Ortholog(s) have endoplasmic reticulum localization	null	1.71683	0.012775	0.036807
AN0518	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	null	-2.3207	0.012796	0.036807
AN0556	Putative DNA repair protein; plays a role in the mitotic checkpoint in response to DNA damaging agents; transcript induced in response to DNA damaging agents; required for normal meiosis and ascospore viability	mreA	2.45631	0.012796	0.036807
AN10617	Putative cytochrome P450	CYP539B2	-2.3207	0.012796	0.036807
AN12074	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.3207	0.012796	0.036807
AN1765	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	null	-2.3207	0.012796	0.036807
AN4079	Has domain(s) with predicted DNA binding activity	null	-2.3207	0.012796	0.036807
AN4438	Ortholog of Aspergillus versicolor : Aspve1_0744861 and Aspergillus sydowii : Aspsy1_0095004	null	2.45631	0.012796	0.036807
AN4283	Ortholog(s) have cytosol, nucleus localization	null	-1.7288	0.012802	0.036809
AN1750	Ortholog(s) have nucleolus localization	null	1.78203	0.012812	0.03681
AN6866	Putative chorismate mutase with a predicted role in aromatic amino acid biosynthesis	aroC	1.78203	0.012812	0.03681
AN7795	Putative heterotrimeric G-protein coupled receptor component; contains both a 7-transmembrane domain and an RGS signaling domain	gprK	-1.6094	0.013161	0.037798
AN1846	Ortholog of A. fumigatus Af293 : Afu4g09670, A. oryzae RIB40 : AO090003001272, Aspergillus versicolor : Aspve1_0050076, Aspergillus sydowii : Aspsy1_0026263 and Aspergillus terreus NIH2624 : ATET_00776	null	-1.6674	0.013169	0.037804

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AN4026	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	null	1.68926	0.013203	0.037888
AN8491	Ortholog(s) have role in ribosomal large subunit biogenesis and cytosol, nucleolus, preribosome, large subunit precursor localization	null	1.71387	0.013268	0.038013
AN1438	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-2.2592	0.013277	0.038013
AN1519	Putative Argonaute protein involved in inverted repeat transgene (IRT)-induced RNA silencing	rsdA	-2.2592	0.013277	0.038013
AN6809	Ortholog of A. fumigatus Af293 : Afu5g00680, A. niger CBS 513.88 : An16g00250, A. oryzae RIB40 : AO090010000081, A. niger ATCC 1015 : 210803-mRNA and Aspergillus terreus NIH2624 : ATET_09248	null	2.63511	0.013277	0.038013
AN7690	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	null	-2.2592	0.013277	0.038013
AN8643	Ortholog(s) have role in cellular response to heat, cellular response to hydrogen peroxide	null	-2.2592	0.013277	0.038013
AN10741	Pcl-like cyclin, interacts with PtkA, cyclin-dependent kinase, in metulae, phialides and conidia	pclB	1.7178	0.013376	0.03825
AN4910	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-1.7054	0.013376	0.03825
AN9402	Ortholog(s) have endoplasmic reticulum localization	null	-1.7054	0.013376	0.03825
AN4683	Putative oligosaccharyltransferase beta subunit; ortholog of S. cerevisiae Wbp1p	null	1.73252	0.013393	0.038271
AN6576	Ortholog(s) have oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen activity and role in L-methionine salvage from methylthioadenosine	null	1.73252	0.013393	0.038271
AN8036	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-1.6845	0.01343	0.038361
AN10214	Ortholog(s) have cytosol localization	null	-1.6474	0.013485	0.038504
AN0105	Ortholog(s) have cytosol, nucleus localization	null	2.39999	0.013585	0.038639
AN10052	Ortholog(s) have nucleolus localization	null	2.39999	0.013585	0.038639
AN10319	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-2.2743	0.013585	0.038639
AN1052	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	veA	-2.2743	0.013585	0.038639
AN1054	Ortholog of A. fumigatus Af293 : Afu1g12400, A. niger CBS 513.88 : An08g05070, A. oryzae RIB40 : AO090001000239, A. niger ATCC 1015 : 177406-mRNA and Aspergillus versicolor : Aspve1_0283265	null	-2.2743	0.013585	0.038639
AN10608	Ortholog of A. fumigatus Af293 : Afu3g07630, A. niger ATCC 1015 : 175467-mRNA and A. fumigatus A1163 : AFUB_041470	null	2.36184	0.013585	0.038639

AN10764	Ortholog(s) have role in N',N'',N'''-triacetylfusarinine C biosynthetic process, cellular response to hydrogen peroxide, cellular response to iron ion starvation, ergosterol biosynthetic process, pathogenesis	null	-2.2743	0.013585	0.038639
AN1906	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	2.36184	0.013585	0.038639
AN4010	Ortholog of Aspergillus sydowii : Aspsy1_0165051	null	-2.2743	0.013585	0.038639
AN5492	Has domain(s) with predicted deaminase activity and role in purine ribonucleoside monophosphate biosynthetic process	null	-2.2743	0.013585	0.038639
AN10057	Has domain(s) with predicted extracellular region localization	null	-1.729	0.013628	0.038734
AN3632	Ortholog(s) have iron-sulfur cluster binding activity, role in iron-sulfur cluster assembly and cytosol, membrane, nucleus localization	null	1.75759	0.013628	0.038734
AN1281	Ortholog(s) have chaperone binding, protein binding, bridging activity, role in protein import into mitochondrial matrix and presequence translocase-associated import motor localization	null	1.65389	0.013657	0.038801
AN7636	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	null	1.69328	0.013702	0.038912
AN3145	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	null	-1.7854	0.013736	0.038995
AN0458	Ortholog of A. fumigatus Af293 : Afu1g04410, A. niger CBS 513.88 : An01g03270, A. oryzae RIB40 : AO090003000909, A. niger ATCC 1015 : 206228-mRNA and Aspergillus versicolor : Aspve1_0121756	null	2.19948	0.013781	0.039048
AN2374	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in metabolic process	null	2.23398	0.013781	0.039048
AN2859	Has domain(s) with predicted lyase activity and role in metabolic process	null	-2.0829	0.013781	0.039048
AN3641	Ortholog(s) have gluconokinase activity, role in D-gluconate metabolic process and cytosol, nucleus localization	gukA	-2.0829	0.013781	0.039048
AN3820	null	null	-2.0829	0.013781	0.039048
AN11058	Ortholog(s) have intracellular localization	null	1.85088	0.013794	0.039054
AN5209	Putative F-box protein	null	1.83657	0.013794	0.039054
AN10707	Ortholog(s) have nucleus localization	null	-1.7593	0.013824	0.039123
AN1761	Ortholog(s) have ubiquitin-protein ligase activity	null	-1.5984	0.013856	0.0392
AN10230	Ortholog(s) have S-methyl-5-thioadenosine phosphorylase activity, mRNA binding activity, role in L-methionine salvage from methylthioadenosine, glutamate biosynthetic process and cytosol, nucleus localization	null	1.89871	0.013914	0.039347

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AN3747	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	null	1.60796	0.013929	0.039377
AN8523	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	null	2.2003	0.01398	0.039504
AN0784	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-1.8832	0.013995	0.039517
AN4469	Ortholog(s) have role in chromosome organization, ribosomal large subunit biogenesis and PeBoW complex, preribosome, large subunit precursor localization	null	1.9174	0.013995	0.039517
AN0775	Has domain(s) with predicted NAD binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	1.97161	0.014017	0.039563
AN0123	Ortholog(s) have mitochondrion localization	null	2.03499	0.014033	0.039594
AN8633	null	null	2.01284	0.014039	0.039596
AN1356	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	null	-1.5703	0.014044	0.039596
AN1416	Has domain(s) with predicted N-acetyltransferase activity, hydrolase activity, hydrolyzing O-glycosyl compounds activity and role in carbohydrate metabolic process	null	-1.6036	0.014059	0.039623
AN0408	Ortholog(s) have cytoplasm localization	null	1.62439	0.014175	0.039934
AN5670	Has domain(s) with predicted protein transporter activity, role in protein transport and mitochondrial inner membrane localization	null	1.56352	0.014304	0.040283
AN6040	Ortholog(s) have phosphoprotein phosphatase activity, thiosulfate sulfurtransferase activity, role in DNA-dependent DNA replication, protein dephosphorylation, regulation of DNA-dependent DNA replication and cytosol, nucleus localization	null	1.74975	0.014336	0.040356
AN1493	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-1.6436	0.014345	0.040368
AN0562	Has domain(s) with predicted catalytic activity and role in metabolic process	null	3.30699	0.014434	0.040524
AN4993	Putative GNAT-type acetyltransferase	nnaC	3.37631	0.014434	0.040524
AN5701	Putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with a predicted role in aromatic amino acid biosynthesis; feedback-inhibited by tyrosine	aroF	3.37631	0.014434	0.040524
AN7392	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	3.37631	0.014434	0.040524
AN7955	Protein with homology to the Saccharomyces cerevisiae uracil transporter Fur4p; mutant is unaffected in uracil transport in A. nidulans	furG	-2.7861	0.014434	0.040524
AN9173	Sugar transporter; transcriptionally induced by growth on xylose	null	3.30699	0.014434	0.040524

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AN4602	Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and nucleus, polysome, prefoldin complex localization	null	1.63424	0.014441	0.040528
AN1019	Putative Scf complex protein; NeddH-associated protein; transcript upregulated in response to camptothecin	culA	-1.5809	0.014449	0.040537
AN10175	Ortholog(s) have role in ribosome biogenesis and cytoplasm, ribosome localization	null	1.63602	0.014683	0.041176
AN0897	Ortholog(s) have cytosol, nucleus localization	null	1.72154	0.014734	0.041303
AN10661	Has domain(s) with predicted hydrolase activity and role in nucleotide catabolic process	null	1.65175	0.014752	0.04134
AN5693	Ortholog(s) have protein domain specific binding activity, role in protein import into mitochondrial matrix and presequence translocase-associated import motor localization	null	1.63716	0.01476	0.041347
AN8548	Ortholog of A. nidulans FGSC A4 : AN5943, AN8661, AN4642, A. fumigatus Af293 : Afu3g00850, Afu4g08850 and A. niger CBS 513.88 : An02g13470, An11g00090, An03g01430, An12g09260	null	1.55623	0.014818	0.041494
AN1092	Ortholog(s) have gamma-glutamyltransferase activity, omega peptidase activity, role in glutathione catabolic process and cytoplasm localization	null	-1.7359	0.014858	0.041574
AN2022	Putative heterokaryon incompatibility protein	null	-1.7359	0.014858	0.041574
AN2946	Protein predicted to have a role in pheromone precursor processing	ste13	-1.5627	0.014877	0.041612
AN8702	Ortholog(s) have protein homodimerization activity, ubiquitin-protein ligase activity and role in cellular response to ionizing radiation, free ubiquitin chain polymerization, postreplication repair, protein K63-linked ubiquitination	null	1.65987	0.014905	0.041674
AN1799	Has domain(s) with predicted triglyceride lipase activity and role in lipid catabolic process	null	-1.7338	0.014932	0.041734
AN0876	Has domain(s) with predicted FMN binding, riboflavin reductase (NADPH) activity and role in oxidation-reduction process	null	-1.6745	0.014962	0.041801
AN3169	Putative ribose-phosphate pyrophosphokinase with a predicted role in histidine metabolism; interacts with prs1 and prs2	prs3	1.80869	0.01501	0.04192
AN1420	Ortholog of A. fumigatus Af293 : Afu8g04180, A. niger CBS 513.88 : An16g08910/srpB, A. oryzae RIB40 : AO090103000033, A. niger ATCC 1015 : 55055-mRNA and Aspergillus versicolor : Aspve1_0024681	null	-1.5896	0.01503	0.041959
AN10540	Ortholog(s) have dipeptidyl-peptidase activity and cytoplasm, nucleus localization	null	-1.6464	0.015126	0.042212
AN1192	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	null	-1.6504	0.015176	0.042327
AN1024	Ortholog(s) have role in mitotic recombination	null	-1.7535	0.015179	0.042327
AN9448	Ortholog of A. fumigatus Af293 : Afu1g03030, A. oryzae RIB40 : AO090005000796, A. niger ATCC 1015 : 51952-mRNA, Aspergillus versicolor : Aspve1_0048537 and Aspergillus sydowii : Aspsy1_0628822	null	-1.5579	0.015285	0.042608
AN5123	Has domain(s) with predicted nucleotide binding, oxidoreductase activity	null	-1.5834	0.015327	0.042708

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AN11730	Ortholog of A. fumigatus Af293 : Afu6g12430, A. niger CBS 513.88 : An06g01590, A. oryzae RIB40 : AO090009000169, A. niger ATCC 1015 : 37850-mRNA and Aspergillus carbonarius ITEM 5010 : Acar5010_502743	null	1.69782	0.015376	0.042829
AN0827	Ortholog(s) have glucosaminyl-phosphotidylinositol O-acyltransferase activity and role in GPI anchor biosynthetic process, cellular response to drug	null	1.64844	0.01539	0.042852
AN4764	Has domain(s) with predicted histone-lysine N-methyltransferase activity and nucleus localization	null	-1.6361	0.015449	0.0429
AN4744	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	null	1.61495	0.015453	0.0429
AN0450	Ortholog(s) have tRNA binding activity and role in protein urmylation, regulation of cell shape, regulation of translational fidelity, tRNA wobble position uridine thiolation	null	2.74042	0.015464	0.0429
AN11722	Ortholog(s) have structural molecule activity	null	2.74042	0.015464	0.0429
AN2108	Ortholog of Aspergillus brasiliensis : Aspbr1_0037101, A. niger ATCC 1015 : 178726-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_02657 and Aspergillus acidus : Aspfo1_0439200	null	-2.3092	0.015464	0.0429
AN2602	Putative lipase/esterase domain family protein; transcript is induced by nitrate	null	-2.6097	0.015464	0.0429
AN4586	Has domain(s) with predicted nucleic acid binding, zinc ion binding activity and intracellular localization	null	-2.3092	0.015464	0.0429
AN6430	Putative transcription factor; predicted role in secondary metabolite production	null	2.74042	0.015464	0.0429
AN7656	Putative diamine transaminase with a predicted role in aromatic amino acid biosynthesis	null	2.74042	0.015464	0.0429
AN3447	Ortholog(s) have cytosol localization	null	1.89759	0.015465	0.0429
AN2473	Ortholog of A. fumigatus Af293 : Afu4g03090, A. niger CBS 513.88 : An16g01740, An14g02280, A. oryzae RIB40 : AO090102000258, AO090003001331 and A. niger ATCC 1015 : 56560-mRNA	null	1.68159	0.015574	0.043185
AN7578	Ortholog of A. fumigatus Af293 : Afu2g15060, A. niger CBS 513.88 : An15g03030, A. oryzae RIB40 : AO090012000426, A. niger ATCC 1015 : 210168-mRNA and Aspergillus versicolor : Aspve1_0136088	null	1.69084	0.015596	0.04323
AN2889	Ortholog of A. fumigatus Af293 : Afu3g11570, A. niger CBS 513.88 : An02g07370, A. oryzae RIB40 : AO090003000716, A. niger ATCC 1015 : 37091-mRNA and Aspergillus sydowii : Aspsy1_0029412	null	1.9201	0.015789	0.043748
AN2775	Ortholog(s) have cytosol localization	null	1.57801	0.015862	0.043934
AN3173	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	1.61645	0.015892	0.043993
AN2188	Ortholog of A. fumigatus Af293 : Afu7g03930, A. niger CBS 513.88 : An13g00390, A. oryzae RIB40 : AO090026000821, A. niger ATCC 1015 : 192237-mRNA and Aspergillus versicolor : Aspve1_0025939	null	-1.9107	0.015901	0.043993
AN8162	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-1.9107	0.015901	0.043993

AN4989	Ortholog of A. fumigatus Af293 : Afu3g09980, A. niger CBS 513.88 : An16g03710, A. niger ATCC 1015 : 128352-mRNA, Aspergillus versicolor : Aspve1_0039797 and Aspergillus sydowii : Aspsy1_0042878	null	-1.606	0.01594	0.044085
AN7428	Ortholog(s) have role in autophagy, cellular response to nitrogen starvation and cytosol, nucleus localization	null	-1.556	0.015946	0.044085
AN1691	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.2391	0.015974	0.044095
AN2393	Ortholog(s) have cytosol localization	null	-2.2391	0.015974	0.044095
AN3125	Has domain(s) with predicted role in response to stress and integral to membrane localization	null	2.35785	0.015974	0.044095
AN8014	Has domain(s) with predicted ATP binding, DNA binding, DNA ligase (ATP) activity and role in DNA recombination, DNA repair	null	-2.2391	0.015974	0.044095
AN7262	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	null	-1.5457	0.015988	0.044119
AN5790	Putative isocitrate dehydrogenase (NAD+) with a predicted role in the TCA cycle	null	1.59524	0.016053	0.044282
AN10347	Ortholog of A. fumigatus Af293 : Afu3g12050, A. niger ATCC 1015 : 37126-mRNA, N. fischeri NRRL 181 : NFIA_065260, Aspergillus flavus NRRL 3357 : AFL2T_02246 and A. clavatus NRRL 1 : ACLA_039920	null	-1.9273	0.016115	0.044419
AN12016	null	null	-1.9273	0.016115	0.044419
AN1947	Has domain(s) with predicted hydrolase activity	null	-1.7079	0.016136	0.04446
AN1523	Putative F1F0-ATPase complex subunit with a predicted role in energy metabolism	null	1.537	0.016153	0.044491
AN8119	Has domain(s) with predicted GDP-Man:Man3GlcNAc2-PP-Dol alpha-1,2-mannosyltransferase activity, role in protein glycosylation and membrane localization	null	1.70355	0.016196	0.044591
AN9221	Putative transcription factor; predicted role in secondary metabolite production	null	2.54848	0.016204	0.044596
AN3665	Ortholog(s) have Golgi apparatus, endoplasmic reticulum, fungal-type vacuole membrane localization	null	1.67399	0.016211	0.0446
AN8298	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	null	-2.0244	0.016266	0.044702
AN4813	Has domain(s) with predicted DNA binding activity and role in regulation of transcription, DNA-dependent	null	1.7771	0.01627	0.044702
AN10058	Ortholog(s) have role in ribosomal large subunit assembly and nucleolus, ribosome localization	null	2.32265	0.016279	0.044702
AN1658	Has domain(s) with predicted zinc ion binding activity	null	-2.2107	0.016279	0.044702
AN2410	Has domain(s) with predicted hydrolase activity and role in cellular metabolic process	null	-1.5908	0.016285	0.044702
AN3674	Has domain(s) with predicted phospholipid binding activity	null	-1.5779	0.016285	0.044702

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AN5403	Ortholog of A. fumigatus Af293 : Afu6g13660, A. niger CBS 513.88 : An08g08590, A. oryzae RIB40 : AO090103000319, A. niger ATCC 1015 : 38046-mRNA and Aspergillus versicolor : Aspve1_0199259	null	1.61609	0.016319	0.044781
AN0647	Ortholog(s) have rRNA primary transcript binding, single-stranded telomeric DNA binding, snoRNA binding activity and Mpp10 complex, small-subunit processome localization	null	1.71041	0.016376	0.044912
AN9023	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	null	1.65454	0.016379	0.044912
AN2715	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in metabolic process	null	-1.6634	0.016391	0.044927
AN10417	Ortholog(s) have RNA helicase activity	null	-1.59	0.016443	0.045038
AN2001	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	null	-1.5312	0.016443	0.045038
AN3566	Putative alpha-mannosidase with a predicted role in mannose polymer metabolism	mns1C	1.6665	0.016469	0.045074
AN7996	Ortholog of A. fumigatus Af293 : Afu5g02540, A. niger CBS 513.88 : An02g10230, A. oryzae RIB40 : AO090102000369, A. niger ATCC 1015 : 37312-mRNA and Aspergillus versicolor : Aspve1_0087382	null	-1.6436	0.016469	0.045074
AN8827	Ca2+/calmodulin-dependent protein kinase, involved in nuclear division; required for normal timing of NimX activation at G1/S transition	cmkC	-1.629	0.016518	0.045193
AN2530	Heat shock protein 30; expression and protein levels upregulated after exposure to farnesol	hsp30	1.61962	0.016551	0.045266
AN12062	Ortholog(s) have cytosol, nucleus localization	null	1.71323	0.016607	0.045384
AN2749	Has domain(s) with predicted phospholipid binding activity	null	-1.6402	0.016607	0.045384
AN0896	Putative succinate dehydrogenase	null	-1.6688	0.016723	0.045687
AN2938	Ortholog(s) have pyrophosphatase activity and peroxisome localization	null	-1.7814	0.016733	0.045696
AN6330	Putative elongation factor 2; intracellular; protein abundance decreased by menadione stress	null	1.53147	0.016798	0.045856
AN11787	null	null	-1.5121	0.016849	0.045979
AN3922	Ortholog(s) have mitochondrion localization	null	1.57635	0.01686	0.045992
AN0167	Ortholog(s) have enzyme regulator activity, guanyl-nucleotide exchange factor activity, translation initiation factor activity and role in regulation of translational initiation	null	1.65867	0.016876	0.046018
AN6845	Has domain(s) with predicted iron ion transmembrane transporter activity, role in iron ion transmembrane transport and integral to membrane localization	null	1.81338	0.016911	0.046096
AN3408	Ortholog(s) have dipeptide transporter activity, tripeptide transporter activity, role in dipeptide transport, tripeptide transport and fungal-type vacuole, plasma membrane localization	null	1.72486	0.016925	0.0461

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AN7472	Ortholog(s) have dolichyl-diphosphooligosaccharide-protein glycotransferase activity, role in protein N-linked glycosylation via asparagine and oligosaccharyltransferase complex localization	null	1.73863	0.016925	0.0461
AN4998	Putative Ras GTPase-activating protein; required for normal cell polarity and conidiophore development	gapA	-1.5864	0.017047	0.046411
AN8824	Ortholog(s) have ribosomal large subunit binding activity	null	1.6384	0.017051	0.046411
AN3117	Has domain(s) with predicted ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, metal ion binding activity and role in ATP biosynthetic process, metal ion transport	null	1.55252	0.017066	0.046434
AN0864	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	null	1.64656	0.017079	0.046451
AN11064	Putative alpha-1,3-glucanase	agnD	1.8775	0.017102	0.04648
AN6572	Ortholog(s) have antioxidant activity, role in aerobic respiration, cellular sulfide ion homeostasis, sulfide oxidation, ubiquinone biosynthetic process and extrinsic to mitochondrial inner membrane, mitochondrial matrix localization	null	1.8775	0.017102	0.04648
AN10527	Ortholog(s) have mitochondrion localization	null	1.55733	0.01717	0.046647
AN8709	Putative aspartate transaminase with a predicted role in alanine and aspartate metabolism	null	-1.5356	0.01718	0.046659
AN4096	Ortholog(s) have cytoplasm, nucleus localization	null	-1.647	0.017229	0.046773
AN7173	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-1.5766	0.017236	0.046777
AN4320	Has domain(s) with predicted role in chromatin remodeling and nuclear chromosome localization	null	1.79277	0.017258	0.046819
AN0384	Ortholog of A. fumigatus Af293 : Afu1g01700, A. niger CBS 513.88 : An01g06520, A. oryzae RIB40 : AO090005000935, A. niger ATCC 1015 : 46605-mRNA and Aspergillus versicolor : Aspve1_0023441	null	1.92937	0.017308	0.046886
AN1291	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-1.8158	0.017308	0.046886
AN4445	Ortholog(s) have role in histone exchange and NuA4 histone acetyltransferase complex, Swr1 complex localization	null	-1.8158	0.017308	0.046886
AN8055	Ortholog(s) have nucleolus localization	null	1.92937	0.017308	0.046886
AN5741	Ortholog of A. fumigatus Af293 : Afu6g06890, A. niger CBS 513.88 : An18g06010, A. oryzae RIB40 : AO090003000070, A. niger ATCC 1015 : 56837-mRNA and Aspergillus versicolor : Aspve1_0042452	null	1.70313	0.0175	0.047371
AN8188	Putative GTP cyclohydrolase I with a predicted role in folate biosynthesis	null	1.69296	0.0175	0.047371
AN1049	Putative zinc metalloproteinase; PalA-dependent expression independent of pH	null	1.59185	0.017509	0.047378
AN5685	Ortholog(s) have nucleolus localization	null	1.96716	0.017531	0.047402

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AN8251	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	hapX	1.96716	0.017531	0.047402
AN10215	Putative peroxisomal targeting signal 1 (PTS1) receptor protein; required for growth on long chain fatty acids	pexE	-1.5224	0.017546	0.047426
AN0055	Transmembrane protein involved in regulation of conidium development; required for expression of brlA; predicted oxidoreductase with FAD-binding and haem-binding domains	tmpA	1.87145	0.017771	0.047963
AN4049	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-1.8181	0.017771	0.047963
AN5010	null	null	1.87145	0.017771	0.047963
AN9004	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	null	1.89598	0.017771	0.047963
AN6235	Ortholog(s) have role in N',N'',N'''-triacetylfusarinine C biosynthetic process, cellular response to hydrogen peroxide, cellular response to iron ion starvation, ergosterol biosynthetic process, pathogenesis	null	1.57248	0.017799	0.048021
AN0183	Putative molybdopterin binding domain protein	null	1.67612	0.017814	0.048021
AN2464	Ceramide synthase with a role in sphingoglycolipid biosynthesis; mutant makes fewer conidia and more Hulle cells; cleistothecia maturation is decreased	lagA	1.67612	0.017814	0.048021
AN9078	Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity and mitochondrion localization	null	1.56119	0.017818	0.048021
AN11444	Ortholog(s) have hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism activity	null	1.79323	0.017859	0.048115
AN11232	Ortholog(s) have endoplasmic reticulum localization	null	1.93528	0.018029	0.048537
AN7005	Ortholog of A. fumigatus Af293 : Afu4g04440, A. niger CBS 513.88 : An14g00390, A. oryzae RIB40 : AO090206000049, A. niger ATCC 1015 : 49207-mRNA and Aspergillus versicolor : Aspve1_0339952	null	1.93528	0.018029	0.048537
AN2262	Ortholog(s) have role in cellular response to oxidative stress, response to osmotic stress, ribosomal small subunit biogenesis, ribosomal small subunit export from nucleus	null	1.60808	0.018232	0.049064
AN6520	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	2.04136	0.018307	0.049231
AN6682	Ortholog(s) have oxidized purine nucleobase lesion DNA N-glycosylase activity, role in base-excision repair, AP site formation and mitochondrion localization	null	2.04136	0.018307	0.049231
AN5725	Protein with a predicted role in asparagine-linked glycosylation; S. cerevisiae ortholog Alg11p has alpha-1,2-mannosyltransferase activity	null	1.56211	0.018344	0.049313
AN7048	Has domain(s) with predicted DNA binding activity	null	1.73561	0.018375	0.049377

AN7649	Ortholog(s) have protein transporter activity, unfolded protein binding activity and role in protein import into mitochondrial inner membrane	null	1.68271	0.018445	0.049549
AN1435	Ortholog(s) have DNA replication origin binding, chromatin binding activity and role in DNA replication initiation, chromatin silencing at silent mating-type cassette, pre-replicative complex assembly	null	-1.6479	0.018532	0.049764
AN0441	Has domain(s) with predicted zinc ion binding activity	null	-1.877	0.018603	0.04993
AN6118	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	agtA	-1.6855	0.01861	0.04993
AN5321	Putative triacylglycerol lipase with a predicted role in glycerolipid metabolism	null	1.59764	0.018614	0.04993
AN10645	Ortholog of A. fumigatus Af293 : Afu1g07310, A. niger CBS 513.88 : An07g09850, A. oryzae RIB40 : AO090012000984, A. niger ATCC 1015 : 209271-mRNA and Aspergillus versicolor : Aspve1_0045803	null	-1.7478	0.018622	0.049934

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Supplementary Table 3d

Effect of glucose under nitrogen repressing conditions (ammonium as a nitrogen source) in the wild type strain

Differentially expressed genes (FNH_4 vs. GNH_4) are shown.

Gene expression was regarded as significantly changed if the FDR was <0.05 and the fold change |FC| >2

1073 differentially regulated genes were identified under these conditions: 387 upregulated and 686 downregulated

gene	Description	Name	log_2FC	PValue	FDR
AN2831	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-11.211	5.71E-28	4.00E-24
AN8781	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	null	-8.5195	1.33E-21	3.93E-18
AN2583	Putative glyceraldehyde-3-phosphate dehydrogenase with a predicted role in gluconeogenesis and glycolysis	gpdC	-8.77	1.68E-21	3.93E-18
AN4003	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	-8.1752	3.55E-20	6.22E-17
AN5030	Has domain(s) with predicted NAD binding, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity and role in oxidation-reduction process	null	-11.867	7.41E-19	1.04E-15
AN12088	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-7.283	7.49E-17	8.75E-14
AN8539	Ortholog of A. fumigatus sidG; GNAT family acetyltransferase; transcript induced by light in in developmentally competent mycelia	ngn26	-7.577	1.33E-16	1.34E-13
AN5031	Putative malate dehydrogenase with a predicted role in the methylglyoxal bypass or the TCA cycle	mdhB	-11.069	3.13E-16	2.50E-13
AN8611	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	-7.6382	3.21E-16	2.50E-13
AN9184	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-6.3114	2.90E-15	1.90E-12
AN7388	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	cpeA	-7.7156	2.98E-15	1.90E-12
AN1428	Has domain(s) with predicted N-acetylglucosamine-6-phosphate deacetylase activity and role in N-acetylglucosamine metabolic process	null	-7.307	3.88E-15	2.15E-12
AN5444	Putative tryptophan synthase with a predicted role in aromatic amino acid biosynthesis	null	-6.5191	4.06E-15	2.15E-12
AN1659	Putative amino acid transporter; transcript is induced by nitrate	null	-7.2877	4.43E-15	2.15E-12
AN8175	Has domain(s) with predicted viral capsid localization	null	-6.9637	4.60E-15	2.15E-12
AN8445	Putative aminopeptidase Y; transcript is induced by nitrate	null	-7.0879	5.27E-15	2.31E-12
AN2388	Putative beta-1,4-endoglucanase	null	-7.1667	1.10E-14	4.55E-12

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AN1897	Homogentisate 1,2-dioxygenase, enzyme in phenylalanine catabolism; required for growth on phenylalanine or phenylacetate as the sole carbon source; mutation in human ortholog results in alkaptonuria	hmgA	-7.0217	4.13E-14	1.61E-11
AN8910	Putative polyketide synthase (PKS)	null	-10.411	4.47E-14	1.65E-11
AN1899	Putative 4-hydroxyphenylpyruvate dioxygenase with a predicted role in aromatic amino acid biosynthesis; expression induced by phenylalanine and repressed by glucose; mutants unable to use phenylalanine as a sole carbon source	hpdA	-7.7347	1.11E-13	3.88E-11
AN3130	Ortholog of A. fumigatus Af293 : Afu3g12990, A. niger CBS 513.88 : An02g08890, A. niger ATCC 1015 : 207115-mRNA, Aspergillus versicolor : Aspve1_0026699 and Aspergillus sydowii : Aspsy1_0029142	null	-6.8371	1.27E-13	4.23E-11
AN7287	Putative mitochondrial succinate/fumarate antiporter	acuL	-5.9936	1.64E-13	5.23E-11
AN10588	Ortholog of A. fumigatus Af293 : Afu5g08870, A. niger CBS 513.88 : An07g04510, A. oryzae RIB40 : AO090020000457 and Aspergillus carbonarius ITEM 5010 : Acar5010_507640	null	-7.0981	2.97E-13	9.05E-11
AN1731	Putative proline dehydrogenase with a predicted role in proline metabolism; expression is regulated by carbon and nitrogen repression; negatively regulated by CreA	prnD	-7.5843	3.44E-13	1.01E-10
AN9121	Protein with a glycogen binding domain involved in sexual development; regulated by VeA and FlbA	esdC	-5.8497	4.83E-13	1.35E-10
AN1792	Has domain(s) with predicted hydrolase activity, acting on ester bonds activity and role in lipid metabolic process	null	-5.6707	6.87E-13	1.85E-10
AN5860	Low affinity glucose transporter of the major facilitator superfamily (MFS); transcriptionally repressed by growth on xylose	mstE	5.6691	8.79E-13	2.28E-10
AN2466	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.5625	1.07E-12	2.69E-10
AN9183	Putative beta-glucosidase with a predicted role in polysaccharide degradation	bglR	-9.9522	1.36E-12	3.30E-10
AN4691	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-5.3832	1.47E-12	3.44E-10
AN12477	Has domain(s) with predicted GTP binding, GTPase activity	null	-8.1398	1.71E-12	3.88E-10
AN1677	Short-chain dehydrogenase; transcriptionally induced by growth on xylose	null	-5.518	1.79E-12	3.92E-10
AN1553	Has domain(s) with predicted role in fruiting body development, hemolysis by symbiont of host erythrocytes	null	-9.9023	1.92E-12	4.09E-10
AN2157	Putative aspartic endopeptidase	pepAa	-5.6723	3.80E-12	7.84E-10
AN6404	Has domain(s) with predicted zinc ion binding activity	null	-7.9617	6.16E-12	1.23E-09
AN5060	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_03090, Aspergillus versicolor : Aspve1_0144439, Aspergillus sydowii : Aspsy1_0061440 and Aspergillus terreus NIH2624 : ATET_06090	null	-6.0532	8.62E-12	1.68E-09

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AN10891	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-9.6829	9.77E-12	1.85E-09
AN11874	Ortholog of Aspergillus versicolor : Aspve1_0141900 and Aspergillus sydowii : Aspsy1_0035361	null	-5.4876	1.14E-11	2.09E-09
AN11965	null	null	-6.0208	1.41E-11	2.53E-09
AN1848	Zinc(II)2Cys6 putative transcription factor involved in the regulation of sexual development; mutant produces immature cleistothecia and reduced numbers of ascospores	nosA	-5.5986	2.05E-11	3.60E-09
AN4692	null	null	-6.5066	2.26E-11	3.86E-09
AN2366	Putative trypsin-like protease with a role in the proteolytic cleavage of NmrA	null	-5.0994	2.41E-11	3.87E-09
AN2993	Ortholog of A. fumigatus Af293 : Afu3g08610, A. niger CBS 513.88 : An02g12330, A. oryzae RIB40 : AO090005001411, A. niger ATCC 1015 : 173126-mRNA and Aspergillus versicolor : Aspve1_0081680	null	-9.5594	2.43E-11	3.87E-09
AN3557	Ortholog of Aspergillus versicolor : Aspve1_0145302 and Aspergillus aculeatus ATCC16872 : Aacu16872_053773	null	-9.5594	2.43E-11	3.87E-09
AN2572	Putative dipeptidyl-peptidase; transcript upregulated by nitrate limitation	null	-5.2009	3.44E-11	5.36E-09
AN1825	Putative sulfide:quinone oxidoreductase; transcript repressed by nitrogen limitation	null	-5.8337	4.26E-11	6.50E-09
AN4339	null	null	-9.4476	5.17E-11	7.72E-09
AN0483	Ortholog of Aspergillus versicolor : Aspve1_0158177, Aspergillus sydowii : Aspsy1_0144898, Aspergillus terreus NIH2624 : ATET_04939 and Aspergillus brasiliensis : Aspbr1_0204336	null	-5.6762	6.06E-11	8.85E-09
AN0301	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	null	-5.9525	8.35E-11	1.20E-08
AN10949	Ortholog(s) have xenobiotic-transporting ATPase activity, role in response to drug and mitochondrion, plasma membrane localization	null	-5.1022	1.12E-10	1.58E-08
AN1628	Putative membrane ATPase with a predicted role in energy metabolism	enaB	-5.1947	1.18E-10	1.63E-08
AN11233	Has domain(s) with predicted cation binding, chitin binding, chitinase activity and role in carbohydrate metabolic process, chitin catabolic process	null	-4.779	1.25E-10	1.68E-08
AN6642	Putative potassium-transporting ATPase with a predicted role in energy metabolism; locus contains the conserved upstream open reading frames (uORFs) AN6642-uORF and AN6642-uORF.2	enaA	-6.6964	1.95E-10	2.58E-08
AN6761	Putative acyl-coA dehydrogenase	null	-9.2486	2.33E-10	2.98E-08
AN3866	Putative dehydratase with a predicted role in glycine, serine, and threonine metabolism	null	-4.9327	2.34E-10	2.98E-08
AN8400	Sugar transporter; transcriptionally induced by growth on xylose	null	-7.4424	2.79E-10	3.49E-08
AN9007	Putative cytochrome P450	CYP548D1	-4.8616	2.96E-10	3.64E-08
AN4008	Has domain(s) with predicted O-methyltransferase activity	null	-9.1943	3.35E-10	4.05E-08
AN2533	Putative alpha-L-arabinofuranosidase	null	-6.085	4.44E-10	5.07E-08
AN7509	null	null	-5.7141	4.44E-10	5.07E-08

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AN8559	Putative branched chain alpha-keto acid dehydrogenase E1, beta subunit	null	-5.7141	4.44E-10	5.07E-08
AN8540	Siderophore iron transporter	mirB	-4.472	4.48E-10	5.07E-08
AN7532	Ortholog of A. niger CBS 513.88 : An11g07940, A. oryzae RIB40 : AO090001000606, Aspergillus brasiliensis : Aspbr1_0050895, N. fischeri NRRL 181 : NFIA_054950 and A. clavatus NRRL 1 : ACLA_083130	null	-4.9921	4.93E-10	5.49E-08
AN9130	Has domain(s) with predicted cholinesterase activity	null	-6.0559	5.38E-10	5.89E-08
AN3342	Has domain(s) with predicted zinc ion binding activity	null	-6.0262	6.54E-10	7.05E-08
AN5032	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-9.079	7.21E-10	7.66E-08
AN0964	Ortholog of A. fumigatus Af293 : Afu1g16640, A. niger CBS 513.88 : An01g10620, A. oryzae RIB40 : AO090005001050, A. niger ATCC 1015 : 136898-mRNA and Aspergillus versicolor : Aspve1_0036577	null	-5.2881	7.35E-10	7.69E-08
AN2549	Putative acyl-CoA ligase; required for emericellamide biosynthesis	easD	-5.0525	1.02E-09	1.05E-07
AN4702	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-7.2384	1.20E-09	1.22E-07
AN5168	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding activity	null	-4.6771	1.24E-09	1.24E-07
AN8007	Protein with arabinan endo-1,5-alpha-L-arabinosidase activity, involved in degradation of pectin	abnC	-6.4339	1.33E-09	1.31E-07
AN5603	Ortholog of A. nidulans FGSC A4 : AN3743, A. fumigatus Af293 : Afu4g11320, Afu7g04400, A. niger CBS 513.88 : An13g00980, An04g05280 and A. oryzae RIB40 : AO090005000127	null	-6.3684	2.04E-09	1.96E-07
AN6804	Predicted transporter of the major facilitator superfamily (MFS); expression upregulated after exposure to farnesol	null	-4.4476	2.04E-09	1.96E-07
AN6438	Ortholog(s) have dipeptidyl-peptidase activity and role in proteolysis involved in cellular protein catabolic process	null	-4.4375	2.11E-09	2.00E-07
AN5669	Putative succinyl-CoA:3-ketoacid-coenzyme A transferase	null	-4.6476	2.79E-09	2.61E-07
AN7892	Small heat-shock protein; molecular chaperone; expression upregulated after exposure to farnesol	null	-4.2986	3.47E-09	3.20E-07
AN5303	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	null	-4.7435	3.97E-09	3.59E-07
AN0740	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	null	-6.2643	4.00E-09	3.59E-07
AN7508	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	null	-5.4193	4.49E-09	3.94E-07
AN4822	Putative tartrate dehydrogenase with a predicted role in tartrate (four-carbon) metabolism	null	-4.1165	4.49E-09	3.94E-07
AN8903	Putative peptide transporter; transcript upregulated by nitrate limitation	null	-4.3806	4.93E-09	4.21E-07
AN5408	Has domain(s) with predicted RNA binding, ribonuclease III activity and role in RNA processing	null	-8.8165	5.05E-09	4.21E-07

AN7990	Ortholog of A. niger CBS 513.88 : An11g06780, A. niger ATCC 1015 : 208909-mRNA, Aspergillus versicolor : Aspve1_0045473, Aspergillus sydowii : Aspsy1_0047960 and Aspergillus terreus NIH2624 : ATET_06661	null	-5.3564	5.05E-09	4.21E-07
AN8046	Putative triacylglycerol lipase with a predicted role in glycerolipid metabolism	null	-5.3564	5.05E-09	4.21E-07
AN0841	null	null	-4.6515	5.53E-09	4.56E-07
AN4264	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	null	-4.4608	5.73E-09	4.67E-07
AN0593	Putative dehydrogenase; expression reduced after exposure to farnesol	null	-4.3759	1.02E-08	8.25E-07
AN8093	Ortholog of A. nidulans FGSC A4 : AN12197, A. fumigatus Af293 : Afu4g13910, Afu5g12760, A. niger CBS 513.88 : An15g06460, An13g02370, A. oryzae RIB40 : AO090012000187 and A. niger ATCC 1015 : 40780-mRNA	null	-8.6243	1.76E-08	1.40E-06
AN4277	Ortholog(s) have glucose transmembrane transporter activity and plasma membrane localization	null	-4.8593	1.82E-08	1.43E-06
AN3265	Arrestin domains and PY motif-containing protein with homology to Saccharomyces cerevisiae Rod1p and Rog3p proteins	apyA	5.99204	2.09E-08	1.63E-06
AN1131	Putative cytosolic Cu/Zn superoxide dismutase; transcript repressed by light in developmentally competent mycelia	null	-4.8347	2.13E-08	1.64E-06
AN8737	Putative sugar transporter	mstA	-6.8033	2.30E-08	1.75E-06
AN20017	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	atp9	-3.8924	2.33E-08	1.76E-06
AN2860	Ortholog(s) have alcohol dehydrogenase (NADP+) activity, hydroxymethylfurfural reductase (NADH) activity, hydroxymethylfurfural reductase (NADPH) activity and role in alcohol metabolic process, furaldehyde metabolic process	null	-4.6758	3.26E-08	2.43E-06
AN10506	Ortholog of A. fumigatus Af293 : Afu5g14780, A. niger CBS 513.88 : An18g01640, A. oryzae RIB40 : AO090103000417, A. niger ATCC 1015 : 42671-mRNA and Aspergillus versicolor : Aspve1_0173600	null	-5.9432	3.48E-08	2.57E-06
AN2585	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.8736	3.55E-08	2.59E-06
AN5421	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-6.716	4.01E-08	2.90E-06
AN1866	null	null	-4.3185	4.30E-08	3.08E-06
AN1895	Maleyl-acetoacetate isomerase, enzyme involved in phenylalanine catabolism	maiA	-8.4954	4.63E-08	3.28E-06
AN10982	Putative P-type ATPase sodium pump	enaC	-4.1036	4.75E-08	3.33E-06
AN2828	Putative beta-glucosidase with a predicted role in polysaccharide degradation	bglL	-4.9789	6.20E-08	4.26E-06

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AN8174	Ortholog of A. oryzae RIB40 : AO090102000187, AO090102000186, Aspergillus flavus NRRL 3357 : AFL2T_09624, Aspergillus versicolor : Aspve1_0089187 and Aspergillus sydowii : Aspsy1_0064970, Aspsy1_0505144	null	-5.3498	6.20E-08	4.26E-06
AN5170	Putative Zn(II)2Cys6 transcription factor; negative regulator of sexual development	rosA	-5.8503	7.19E-08	4.90E-06
AN9138	Putative amidase/acetamidase	null	-3.9093	7.36E-08	4.96E-06
AN10090	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	null	-4.9301	8.37E-08	5.53E-06
AN9274	Ortholog of A. fumigatus Af293 : Afu3g14810, A. niger CBS 513.88 : An02g03200, An04g09720, An04g08110, A. oryzae RIB40 : AO090103000427 and A. niger ATCC 1015 : 55177-mRNA	null	-6.6232	8.37E-08	5.53E-06
AN8390	GPR1/FUN34/YaaH family member; ethanol- and ethylacetate-induced gene	null	-4.2826	9.38E-08	6.14E-06
AN3961	Ortholog of Aspergillus versicolor : Aspve1_0054191	null	-3.7645	9.75E-08	6.33E-06
AN7108	Ortholog(s) have ATP binding activity and cytosol, nucleus localization	null	-3.7074	1.01E-07	6.47E-06
AN4821	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-3.9965	1.05E-07	6.67E-06
AN8969	Has domain(s) with predicted cation binding, lysozyme activity and role in carbohydrate metabolic process, cell wall macromolecule catabolic process, peptidoglycan catabolic process	null	-4.2192	1.06E-07	6.67E-06
AN8308	Ortholog of A. oryzae RIB40 : AO090001000393 and Aspergillus flavus NRRL 3357 : AFL2T_09046	null	-5.2505	1.33E-07	8.35E-06
AN8972	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-6.524	1.56E-07	9.71E-06
AN7271	null	null	-3.9727	1.76E-07	1.08E-05
AN11124	Has domain(s) with predicted hydrolase activity and role in dUTP metabolic process	null	-4.6443	2.04E-07	1.23E-05
AN5939	Putative 5'-nucleotidase with a predicted role in nucleotide salvage pathways; predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-3.7281	2.04E-07	1.23E-05
AN5029	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-8.251	2.17E-07	1.29E-05
AN11938	null	null	-3.5998	2.17E-07	1.29E-05
AN4609	Has domain(s) with predicted nucleoside-triphosphatase activity, nucleotide binding activity	null	-4.5766	2.45E-07	1.44E-05
AN4590	Sugar transporter; transcriptionally induced by growth on xylose	null	-4.4368	3.02E-07	1.77E-05
AN0800	null	null	-4.7769	3.21E-07	1.84E-05
AN5373	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-4.7769	3.21E-07	1.84E-05
AN7463	Major ammonium transporter of A. nidulans; transcript upregulated by nitrate limitation	meaA	4.28429	3.34E-07	1.91E-05

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AN0323	Ortholog of A. nidulans FGSC A4 : AN2370, AN10160, A. fumigatus Af293 : Afu1g02440, Afu4g02760, A. niger CBS 513.88 : An01g05750, An12g09350, An13g03290 and A. oryzae RIB40 : AO090020000719, AO090005000852	null	-5.0876	3.61E-07	2.04E-05
AN7814	Putative polyketide synthase/fatty acid synthase beta; required for sterigmatocystin biosynthesis; member of the sterigmatocystin biosynthesis gene cluster	stcK	-4.258	3.70E-07	2.07E-05
AN2847	Ortholog(s) have RNA binding, single-stranded telomeric DNA binding activity and cytosol, nucleus localization	null	5.52257	3.89E-07	2.15E-05
AN9303	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	null	-3.7038	3.90E-07	2.15E-05
AN3328	Has domain(s) with predicted GTP binding, nucleoside-triphosphatase activity	null	-3.7595	4.55E-07	2.47E-05
AN6535	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-3.7743	4.55E-07	2.47E-05
AN1756	Ortholog of A. fumigatus Af293 : Afu6g08950, A. niger ATCC 1015 : 48025-mRNA, Aspergillus versicolor : Aspve1_0025102, Aspergillus sydowii : Aspsy1_0138552 and Aspergillus brasiliensis : Aspbr1_0254359	null	-5.0289	5.13E-07	2.77E-05
AN1826	Has domain(s) with predicted hydrolase activity	null	-8.0817	6.15E-07	3.24E-05
AN2395	Putative beta-glucuronidase with a predicted role in polysaccharide degradation	null	-6.3023	6.15E-07	3.24E-05
AN5267	Protein with ferulic acid esterase activity, involved in degradation of xylans	faeC	-6.3023	6.15E-07	3.24E-05
AN4246	Ortholog of A. fumigatus Af293 : Afu1g06480, A. niger CBS 513.88 : An18g05510, A. oryzae RIB40 : AO090001000450, A. niger ATCC 1015 : 54213-mRNA and Aspergillus versicolor : Aspve1_0845556	null	-4.2695	6.55E-07	3.43E-05
AN4197	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	null	-3.7289	6.95E-07	3.61E-05
AN1726	Putative 3-methyl-2-oxobutanoate dehydrogenase	null	-3.7701	8.33E-07	4.29E-05
AN1427	Ortholog(s) have cytoplasm localization	null	-3.3909	8.74E-07	4.47E-05
AN3141	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-6.2412	8.91E-07	4.53E-05
AN6046	Putative p67phox regulatory subunit homolog with a predicted role in regulating hyphal reactive oxygen species (ROS) production; required for normal sexual and asexual development	null	-3.4746	9.34E-07	4.71E-05
AN7583	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-4.1175	9.61E-07	4.81E-05
AN5558	Broad specificity thermostable alkaline protease; extracellular; regulated by nitrogen, carbon and sulfur metabolite repression; transcript repressed by light in developmentally competent mycelia	prtA	-3.4447	9.79E-07	4.87E-05
AN10356	Ortholog of A. oryzae RIB40 : AO090012000821, Aspergillus flavus NRRL 3357 : AFL2T_03687, A. clavatus NRRL 1 : ACLA_040800, Aspergillus versicolor : Aspve1_0164205 and Aspergillus sydowii : Aspsy1_0087183	null	-3.3347	1.01E-06	4.99E-05

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AN1579	Ortholog of A. nidulans FGSC A4 : AN12486, A. oryzae RIB40 : AO090003001382, N. fischeri NRRL 181 : NFIA_081910 and A. clavatus NRRL 1 : ACLA_089450	null	-8.0205	1.08E-06	5.24E-05
AN6762	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	null	-8.0205	1.08E-06	5.24E-05
AN3359	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-3.3141	1.16E-06	5.61E-05
AN5169	Has domain(s) with predicted phospholipid binding activity	null	-6.1773	1.31E-06	6.28E-05
AN10197	Has domain(s) with predicted catalytic activity and role in coenzyme M biosynthetic process	null	-3.5916	1.44E-06	6.85E-05
AN3627	Ortholog(s) have intracellular localization	null	-3.3474	1.47E-06	6.95E-05
AN10996	Ortholog(s) have cytosol, nucleus localization	null	-3.747	1.48E-06	6.98E-05
AN10217	Ortholog(s) have oxidoreductase activity, acting on CH-OH group of donors activity, role in oxidation-reduction process and cytosol, nucleus localization	null	-3.3378	1.56E-06	7.20E-05
AN0453	Putative G1/S cyclin; physically interacts with nimX; expression is transcriptionally regulated by BrlA and AbaA; mutants produce abnormal conidiophores with extra layers of phialides	pclA	-5.3376	1.59E-06	7.20E-05
AN3312	Putative L-xylulose reductase	null	-5.3376	1.59E-06	7.20E-05
AN4922	Ortholog of A. fumigatus Af293 : Afu3g10670, A. niger CBS 513.88 : An02g06330, A. oryzae RIB40 : AO090003000612, A. niger ATCC 1015 : 120930-mRNA and Aspergillus versicolor : Aspve1_0129208	null	-5.3376	1.59E-06	7.20E-05
AN6650	Methylcitrate synthase with a predicted role in the methylcitrate pathway or the TCA cycle; transcript upregulated by exposure to ethanol	mcsA	-7.9566	1.59E-06	7.20E-05
AN9288	Ortholog(s) have cytoplasm, nucleus localization	null	-7.9566	1.59E-06	7.20E-05
AN10771	Ortholog(s) have cytosol, nucleus localization	null	8.32045	1.61E-06	7.21E-05
AN3027	Ortholog(s) have flavin-linked sulfhydryl oxidase activity and role in cellular iron ion homeostasis, cellular response to oxidative stress, protein import into mitochondrial intermembrane space	null	-3.8861	1.71E-06	7.58E-05
AN9273	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_00195, Aspergillus versicolor : Aspve1_0083996, Aspergillus sydowii : Aspsy1_0900274 and Aspergillus terreus NIH2624 : ATET_04373	null	-3.7893	1.71E-06	7.58E-05
AN12052	null	null	-4.148	1.90E-06	8.40E-05
AN2835	Has domain(s) with predicted D-arabinono-1,4-lactone oxidase activity, UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity, role in oxidation-reduction process and membrane localization	null	-4.2775	2.10E-06	9.15E-05
AN3901	Putative lactic acid dehydrogenase with a predicted role in energy metabolism	null	-4.0949	2.10E-06	9.15E-05
AN0759	Ortholog of A. fumigatus Af293 : Afu1g14190, A. niger CBS 513.88 : An01g12200, A. niger ATCC 1015 : 172849-mRNA, Aspergillus versicolor : Aspve1_0078668 and Aspergillus sydowii : Aspsy1_0041575	null	-3.4585	2.31E-06	0.0001

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AN2601	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-5.2675	2.38E-06	0.000102
AN6876	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-4.7669	2.38E-06	0.000102
AN9285	Ortholog of A. fumigatus grg1; homologous to ccg-1 from N. crassa; transcript induced by light in developmentally competent mycelia	null	-3.5633	2.44E-06	0.000104
AN4255	Non-catalytic atypical hexokinase involved in regulation of extracellular proteases in response to carbon starvation; associates with mitochondria	hxkC	-3.2199	2.48E-06	0.000105
AN2621	Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase, nonribosomal peptide synthase, the first enzyme of the penicillin biosynthesis pathway	acvA	-3.7253	2.49E-06	0.000105
AN2530	Heat shock protein 30; expression and protein levels upregulated after exposure to farnesol	hsp30	-3.2201	2.55E-06	0.000106
AN4025	Has domain(s) with predicted hydrolase activity, tubulin-tyrosine ligase activity and role in cellular protein modification process	null	3.30628	2.63E-06	0.000109
AN7727	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	null	-3.6237	2.75E-06	0.000113
AN2043	Has domain(s) with predicted amino acid transmembrane transporter activity, role in amino acid transmembrane transport and membrane localization	null	-4.0477	2.77E-06	0.000113
AN8467	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.2303	2.77E-06	0.000113
AN7026	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	null	-3.3524	2.78E-06	0.000113
AN6127	Has domain(s) with predicted hydrogen ion transmembrane transporter activity, role in ATP hydrolysis coupled proton transport and proton-transporting V-type ATPase, V0 domain localization	null	-3.4739	2.93E-06	0.000118
AN3310	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	3.41083	3.00E-06	0.00012
AN4688	Putative acyl-coA dehydrogenase	ivdA	-3.4736	3.06E-06	0.000122
AN1733	Putative delta-1-pyrroline-5-carboxylate dehydrogenase with a predicted role in glutamate and glutamine metabolism; expression is negatively regulated by CreA	prnC	-4.0657	3.08E-06	0.000122
AN1716	Ortholog of Aspergillus versicolor : Aspve1_0037607, Aspergillus sydowii : Aspsy1_0084105 and Aspergillus terreus NIH2624 : ATET_05357	null	-3.7296	3.09E-06	0.000122
AN3555	Small heat-shock protein; Hsp30p ortholog/paralog; expression upregulated after exposure to farnesol; palA-dependent expression independent of pH	null	-3.1661	3.19E-06	0.000125

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AN0787	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	mns1B	-3.3075	3.32E-06	0.000129
AN1918	Putative phosphoenolpyruvate carboxykinase with a predicted role in gluconeogenesis and glycolysis; transcriptionally induced by acetate and after exposure to farnesol	acuF	-3.1783	3.32E-06	0.000129
AN7874	Ortholog(s) have endoplasmic reticulum localization	null	-6.0404	3.63E-06	0.000139
AN8146	Ortholog of A. nidulans FGSC A4 : AN6727, A. fumigatus Af293 : Afu6g03180, Afu7g05880, A. niger CBS 513.88 : An07g02000, An01g14710 and Aspergillus versicolor : Aspve1_0079826	null	-7.8197	3.63E-06	0.000139
AN10993	Ortholog of A. fumigatus Af293 : Afu2g01310, A. niger CBS 513.88 : An03g05110, A. oryzae RIB40 : AO090701000405, A. niger ATCC 1015 : 50726-mRNA and Aspergillus versicolor : Aspve1_0043704	null	-4.1816	3.68E-06	0.000139
AN7305	Ortholog(s) have ATPase activator activity, RNA binding activity	null	8.1823	3.68E-06	0.000139
AN1882	Ortholog(s) have cytosol, nucleus localization	null	-3.3038	4.06E-06	0.000153
AN1611	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-3.3731	4.25E-06	0.000159
AN7528	Ortholog of Aspergillus brasiliensis : Aspbr1_0191334, Aspergillus versicolor : Aspve1_0789753, Aspergillus sydowii : Aspsy1_1018139 and Aspergillus terreus NIH2624 : ATET_06707	null	-4.1186	4.36E-06	0.000163
AN7286	Has domain(s) with predicted bile acid:sodium symporter activity, role in sodium ion transport and membrane localization	null	-5.1938	4.50E-06	0.000166
AN7269	Ortholog(s) have role in secondary metabolic process	null	-3.8242	4.50E-06	0.000166
AN5709	null	null	-3.9094	4.53E-06	0.000166
AN4603	Putative allantoinase with a predicted role in purine metabolism	null	-3.6849	5.52E-06	0.000201
AN9375	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	5.08113	5.52E-06	0.000201
AN2629	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-7.746	5.61E-06	0.000201
AN3530	Ortholog of A. nidulans FGSC A4 : AN2658, A. fumigatus Af293 : Afu1g13760, Afu4g00490, Afu4g14350, A. niger CBS 513.88 : An09g01580, A. oryzae RIB40 : AO090166000071 and A. niger ATCC 1015 : 188861-mRNA	null	-7.746	5.61E-06	0.000201
AN5413	Ortholog of Aspergillus acidus : Aspfo1_0061846	null	-5.9667	5.61E-06	0.000201
AN3194	Ortholog(s) have cytosol, nucleus localization	null	-3.7488	5.69E-06	0.000201
AN10915	Ortholog of A. niger CBS 513.88 : An04g09630, An03g01920, A. niger ATCC 1015 : 195107-mRNA, 45712-mRNA, Aspergillus versicolor : Aspve1_0513563 and Aspergillus terreus NIH2624 : ATET_08921	null	8.09515	5.71E-06	0.000201
AN2364	Ortholog of A. fumigatus Af293 : Afu4g14020, Afu8g06990, N. fischeri NRRL 181 : NFIA_099740, Aspergillus versicolor : Aspve1_0043947 and Aspergillus sydowii : Aspsy1_1155373	null	8.10793	5.71E-06	0.000201

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AN8147	Ortholog of A. nidulans FGSC A4 : AN1625, A. fumigatus Af293 : Afu3g01080, Afu3g12760, A. niger CBS 513.88 : An02g08740 and A. oryzae RIB40 : AO090012000846, AO090023000643	null	-4.3021	6.20E-06	0.000217
AN6158	Ortholog of A. fumigatus Af293 : Afu2g08370, A. niger CBS 513.88 : An12g03580, A. niger ATCC 1015 : 128428-mRNA, Aspergillus versicolor : Aspve1_0634305 and Aspergillus sydowii : Aspsy1_0089574	null	3.69043	6.32E-06	0.000221
AN3818	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	null	-4.0788	6.64E-06	0.00023
AN2999	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	idpA	-3.2126	7.40E-06	0.000254
AN3639	Putative dihydrolipoamide transacylase; alpha keto acid dehydrogenase E2 subunit	null	-3.1848	7.40E-06	0.000254
AN4690	Alpha subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccA	-3.48	7.55E-06	0.000258
AN5569	Ortholog(s) have phosphatidylinositol-3-phosphate binding, phosphatidylinositol-5-phosphate binding activity	null	4.13796	7.62E-06	0.000259
AN7402	Putative glucoamylase with a predicted role in starch metabolism	glaB	-3.504	8.08E-06	0.000272
AN7552	Ortholog of A. fumigatus Af293 : Afu2g14790, A. oryzae RIB40 : AO090026000798, A. niger ATCC 1015 : 119038-mRNA, Aspergillus versicolor : Aspve1_0085801 and Aspergillus sydowii : Aspsy1_0058559	null	-3.435	8.08E-06	0.000272
AN0051	Putative dioxygenase	null	-5.8891	8.83E-06	0.000289
AN12307	Ortholog of A. nidulans FGSC A4 : AN4261, A. fumigatus Af293 : Afu5g13200, Afu7g03960, A. oryzae RIB40 : AO090020000704, AO090026000818 and A. niger ATCC 1015 : 44684-mRNA	null	-5.8891	8.83E-06	0.000289
AN4338	Ortholog of A. niger ATCC 1015 : 203785-mRNA, N. fischeri NRRL 181 : NFIA_109840, A. clavatus NRRL 1 : ACLA_045620, Aspergillus versicolor : Aspve1_0755913 and Aspergillus sydowii : Aspsy1_0540484	null	-7.6684	8.83E-06	0.000289
AN5614	Ortholog(s) have role in plasma membrane fusion involved in cytogamy, response to pheromone and cytoplasm, mating projection tip localization	null	-5.8891	8.83E-06	0.000289
AN7944	Putative GNAT-type acetyltransferase; expression upregulated after exposure to farnesol	ngn3	-5.8891	8.83E-06	0.000289
AN8347	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-7.6684	8.83E-06	0.000289
AN12013	null	null	-4.533	8.90E-06	0.00029
AN10548	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	null	-4.0245	9.02E-06	0.00029
AN4990	Ortholog(s) have ferrous iron transmembrane transporter activity, manganese ion transmembrane transporter activity	null	-4.0245	9.02E-06	0.00029
AN8533	null	null	-3.8419	9.02E-06	0.00029

AN3925	Has domain(s) with predicted catalytic activity, cation binding activity and role in carbohydrate metabolic process	null	-3.2843	9.32E-06	0.000297
AN0485	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	null	-3.5142	9.36E-06	0.000297
AN3221	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.5142	9.36E-06	0.000297
AN10177	null	null	-3.8856	9.85E-06	0.000311
AN5257	Ortholog(s) have mitochondrion localization	null	7.98864	1.05E-05	0.000332
AN7204	Putative oleoyl-delta12 desaturase	an2	3.50453	1.08E-05	0.000339
AN1256	Ortholog(s) have cytosol localization	null	3.96761	1.11E-05	0.000346
AN10147	Putative pectin lyase with a predicted role in the degradation of pectin	pelC	-5.0342	1.12E-05	0.000346
AN1338	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-3.0383	1.18E-05	0.000366
AN6424	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	null	-3.0018	1.19E-05	0.000367
AN9162	Putative acyl-coA dehydrogenase	null	-3.9681	1.24E-05	0.000378
AN4845	null	null	-3.0664	1.38E-05	0.000422
AN5173	Has domain(s) with predicted hydrolase activity	null	-4.4466	1.42E-05	0.000428
AN5780	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	null	-5.807	1.42E-05	0.000428
AN0875	Has domain(s) with predicted O-acetyltransferase activity and cytoplasm localization	null	-3.4364	1.45E-05	0.000437
AN0859	null	null	-3.0855	1.47E-05	0.000437
AN10060	Putative alpha-amylase; glycogen debranching enzyme	null	-3.0855	1.47E-05	0.000437
AN9295	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.7005	1.48E-05	0.000441
AN6426	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	null	3.13598	1.53E-05	0.000451
AN5604	Putative fructose-bisphosphatase with a predicted role in gluconeogenesis and glycolysis; intracellular; protein abundance decreased by menadione stress; expression upregulated after exposure to farnesol	acuG	-3.0368	1.54E-05	0.000454
AN5748	Putative mannosyl-oligosaccharide 1,2-alpha-mannosidase with a predicted role in mannose polymer metabolism	null	3.90829	1.66E-05	0.000486

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AN10789	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	null	-3.7269	1.71E-05	0.000497
AN11090	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.7269	1.71E-05	0.000497
AN3591	Protein with similarity to bacterial propionyl-CoA-yielding methylmalonate semialdehyde dehydrogenase; may be involved in isoleucine and valine catabolism	null	-3.1002	1.81E-05	0.000526
AN3203	Putative F-box protein	null	-2.87	1.89E-05	0.000542
AN0620	Ortholog of Aspergillus versicolor : Aspve1_0023747 and Aspergillus sydowii : Aspsy1_0086329	null	-3.3523	1.90E-05	0.000542
AN0770	Ortholog(s) have endoplasmic reticulum localization	null	3.00075	1.90E-05	0.000542
AN2937	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	null	-4.1013	1.91E-05	0.000542
AN5457	Putative oxidoreductase with a predicted role in energy metabolism; NADPH oxidase; involved in the generation of reactive oxygen species (ROS); mutation blocks cleistothecia formation; homology to p91phox	noxA	-4.396	1.91E-05	0.000542
AN6669	Putative sugar transporter	null	-3.1552	1.92E-05	0.000543
AN7521	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	null	3.01871	1.96E-05	0.000551
AN0191	Ortholog(s) have ATPase activity, tRNA binding activity, role in regulation of transcription from RNA polymerase II promoter, tRNA wobble uridine modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	4.1912	2.01E-05	0.000559
AN12386	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	null	7.85859	2.02E-05	0.000559
AN5684	Ortholog(s) have endoplasmic reticulum, fungal-type vacuole membrane localization	null	7.85859	2.02E-05	0.000559
AN5888	Ortholog(s) have UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase activity, role in aerobic respiration, protein N-linked glycosylation and UDP-N-acetylglucosamine transferase complex localization	null	7.85859	2.02E-05	0.000559
AN11926	null	null	-2.8482	2.04E-05	0.000563
AN3456	Putative cystathionine gamma-synthase with a predicted role in methionine metabolism	null	3.59055	2.11E-05	0.000581
AN4659	Putative acyl-CoA synthetase/AMP-binding domain protein; has a predicted mitochondrial localization signal	null	-3.5884	2.30E-05	0.000627
AN9192	Ortholog of A. fumigatus Af293 : Afu3g03910, A. niger CBS 513.88 : An13g01790, A. oryzae RIB40 : AO090038000138, N. fischeri NRRL 181 : NFIA_006190 and A. clavatus NRRL 1 : ACLA_060900	null	-3.5547	2.30E-05	0.000627
AN2602	Putative lipase/esterase domain family protein; transcript is induced by nitrate	null	-4.354	2.32E-05	0.000627

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AN3776	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-7.4993	2.32E-05	0.000627
AN4877	Predicted DDE1 transposon-related ORF	null	-7.4993	2.32E-05	0.000627
AN7860	Ortholog of A. nidulans FGSC A4 : AN9318, A. fumigatus Af293 : Afu8g01270 and A. oryzae RIB40 : AO090010000599, AO090005000383, AO090011000082, AO090020000631	null	-3.2743	2.34E-05	0.000627
AN1418	Has domain(s) with predicted glucosamine-6-phosphate deaminase activity and role in N-acetylglucosamine metabolic process, carbohydrate metabolic process	null	-2.8573	2.38E-05	0.000637
AN6525	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	aciA	2.91712	2.40E-05	0.00064
AN5781	Putative 30 kilodalton heat shock protein; transcript levels increase during the unfolded-protein response (UPR); palA-dependent expression independent of pH	null	-2.8089	2.45E-05	0.000651
AN7081	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	4.80177	2.59E-05	0.000684
AN10495	Has domain(s) with predicted CoA-transferase activity and role in ketone body catabolic process	null	-3.0689	2.70E-05	0.000713
AN6556	Ortholog(s) have mRNA binding activity	null	3.81805	2.73E-05	0.000717
AN11391	null	null	-3.8483	2.83E-05	0.00073
AN4474	Ortholog of A. niger CBS 513.88 : An04g02110, A. oryzae RIB40 : AO090023000799, A. niger ATCC 1015 : 203625-mRNA, Aspergillus versicolor : Aspve1_0133959 and Aspergillus sydowii : Aspsy1_0095044	null	-3.8483	2.83E-05	0.00073
AN7144	Ortholog(s) have role in mitochondrial respiratory chain complex III assembly and mitochondrial matrix localization	null	7.79681	2.83E-05	0.00073
AN9289	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.8483	2.83E-05	0.00073
AN2894	Ortholog of A. fumigatus Af293 : Afu3g11550, A. niger CBS 513.88 : An02g07350, A. oryzae RIB40 : AO090003000710, A. niger ATCC 1015 : 52301-mRNA and Aspergillus versicolor : Aspve1_0081788	null	-4.3224	2.85E-05	0.00073
AN6118	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	agtA	-4.3224	2.85E-05	0.00073
AN6785	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	null	-4.0276	2.85E-05	0.00073
AN2018	Putative alpha-amylase with a predicted role in starch metabolism	amyA	-3.2491	2.97E-05	0.000758

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AN3641	Ortholog(s) have gluconokinase activity, role in D-gluconate metabolic process and cytosol, nucleus localization	gukA	-3.5342	3.09E-05	0.000786
AN5698	Putative transferase with a predicted role in fatty acid metabolism; predicted N-terminal mitochondrial targeting sequence	null	-2.9169	3.13E-05	0.000793
AN7679	Ortholog(s) have role in ER to Golgi vesicle-mediated transport and ER to Golgi transport vesicle, integral to Golgi membrane, integral to endoplasmic reticulum membrane localization	null	3.78179	3.24E-05	0.000818
AN3349	Putative cytochrome P450	CYP659A1	-3.2187	3.29E-05	0.000826
AN2004	null	null	-3.2604	3.30E-05	0.000826
AN5732	Ortholog(s) have cytoplasm localization	null	3.76702	3.54E-05	0.000882
AN11892	Ortholog(s) have 3'-tRNA processing endoribonuclease activity, role in tRNA 3'-trailer cleavage, endonucleolytic and mitochondrion, nucleus localization	null	3.28937	3.88E-05	0.000946
AN0058	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-7.4068	3.90E-05	0.000946
AN2781	Ortholog(s) have endoplasmic reticulum localization	null	-7.4068	3.90E-05	0.000946
AN3079	Secreted thaumatin-like protein; role in early conidial germination; localized to the cell wall of germinating conidia but not to germ tubes; cetA transcript is repressed by glucose	cetA	-4.2551	3.90E-05	0.000946
AN3360	Has domain(s) with predicted hydrolase activity, hydrolyzing O-glycosyl compounds activity and role in carbohydrate metabolic process	null	-4.2551	3.90E-05	0.000946
AN4345	Has domain(s) with predicted magnesium ion binding, thiamine pyrophosphate binding, transferase activity	null	-5.6275	3.90E-05	0.000946
AN8912	Ortholog(s) have role in ascospore formation, conjugation with cellular fusion and Golgi apparatus, fungal-type vacuole membrane localization	null	-7.4068	3.90E-05	0.000946
AN9193	Ortholog of A. nidulans FGSC A4 : AN3975, AN2891 and A. fumigatus Af293 : Afu1g10150, Afu2g04380, Afu3g15150, Afu3g15280, Afu6g03300	null	-7.4068	3.90E-05	0.000946
AN10091	Ortholog(s) have cytosol, mitochondrion, nucleus localization	null	3.22399	3.92E-05	0.000949
AN4732	Ortholog of A. fumigatus Af293 : Afu5g10730, A. niger CBS 513.88 : An14g03950, A. oryzae RIB40 : AO090010000468, A. niger ATCC 1015 : 184967-mRNA and Aspergillus versicolor : Aspve1_0718613	null	7.73225	4.02E-05	0.000967
AN8609	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.8514	4.09E-05	0.000982
AN11981	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-3.3052	4.12E-05	0.000985
AN4010	Ortholog of Aspergillus sydowii : Aspsy1_0165051	null	-4.2447	4.33E-05	0.001031
AN5786	Ortholog(s) have role in cellular ion homeostasis, mitochondrion inheritance, regulation of cardiolipin metabolic process and mitochondrial inner membrane, nucleus localization	null	2.78686	4.34E-05	0.001031

AN0404	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	null	-2.752	4.44E-05	0.001051
AN10166	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	null	-3.5084	4.85E-05	0.001146
AN6072	Ortholog(s) have protein-arginine N5-methyltransferase activity, role in peptidyl-arginine methylation and cytosol, nucleus localization	null	4.02679	4.96E-05	0.001166
AN0394	Ortholog(s) have role in positive regulation of apoptotic process, response to singlet oxygen and mitochondrion, nucleus localization	null	-4.7557	5.10E-05	0.001184
AN1109	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-4.7557	5.10E-05	0.001184
AN11869	null	null	-4.7557	5.10E-05	0.001184
AN1600	Has domain(s) with predicted nucleotide binding activity	null	-4.7557	5.10E-05	0.001184
AN6095	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.7589	5.26E-05	0.001214
AN12192	Ortholog of A. nidulans FGSC A4 : AN3979, Aspergillus flavus NRRL 3357 : AFL2T_09411, Aspergillus versicolor : Aspve1_0043435 and Aspergillus sydowii : Aspsy1_0051867	null	-3.0678	5.26E-05	0.001214
AN2584	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-2.7133	5.36E-05	0.001231
AN9003	Has domain(s) with predicted aspartic-type endopeptidase activity, zinc ion binding activity and role in proteolysis	null	-3.0193	5.40E-05	0.001238
AN5467	Ortholog of Aspergillus terreus NIH2624 : ATET_07601	null	2.93794	5.46E-05	0.001247
AN0713	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	-3.1519	5.51E-05	0.001254
AN2161	Putative GNAT-type acetyltransferase	ngn1	-2.7699	5.73E-05	0.0013
AN10193	Ortholog(s) have role in vacuolar protein processing and Golgi apparatus, endoplasmic reticulum, fungal-type vacuole membrane localization	null	7.66468	5.76E-05	0.001302
AN6470	Protein with lysozyme activity, involved in carbohydrate catabolism	null	-2.8722	5.89E-05	0.001328
AN4480	null	null	-2.7819	6.00E-05	0.001349
AN11143	Putative glucoamylase with a predicted role in starch metabolism	glaA	-3.3747	6.10E-05	0.001366
AN4446	Ortholog(s) have role in ER to Golgi vesicle-mediated transport and ER to Golgi transport vesicle, Golgi apparatus, endoplasmic reticulum, mitochondrion localization	null	2.82661	6.36E-05	0.00142

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AN7042	Has domain(s) with predicted carbonate dehydratase activity, zinc ion binding activity and role in carbon utilization	null	-2.7107	6.55E-05	0.001458
AN6778	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.8679	6.67E-05	0.001476
AN8483	Ortholog of A. niger CBS 513.88 : An13g02730, Aspergillus brasiliensis : Aspbr1_0180212, N. fischeri NRRL 181 : NFIA_001870, Aspergillus flavus NRRL 3357 : AFL2T_10566 and A. clavatus NRRL 1 : ACLA_063590	null	-4.1627	6.67E-05	0.001476
AN10812	Protein of unknown function; transcript repressed by nitrate	null	-7.3078	6.72E-05	0.001476
AN3959	Has domain(s) with predicted metalloendopeptidase activity and role in proteolysis	null	-5.5285	6.72E-05	0.001476
AN3589	Dynactin complex p50 subunit; p50 mutant cells exhibit a nud phenotype and lowered dynein plus-end accumulation	null	4.62723	6.93E-05	0.001518
AN10444	Ortholog(s) have gamma-glutamyltransferase activity, role in cellular response to nitrogen starvation and endoplasmic reticulum localization	null	-2.8586	7.00E-05	0.001529
AN7836	Ortholog of A. fumigatus Af293 : Afu7g01060, A. oryzae RIB40 : AO090003000833, Aspergillus brasiliensis : Aspbr1_0035748, N. fischeri NRRL 181 : NFIA_113770 and Aspergillus flavus NRRL 3357 : AFL2T_02186	null	-3.0038	7.41E-05	0.001613
AN0457	null	null	-2.8742	7.50E-05	0.001628
AN0791	null	null	-2.6724	7.57E-05	0.001636
AN2733	Ortholog(s) have uroporphyrinogen decarboxylase activity, role in heme biosynthetic process and cytosol, nucleus localization	null	3.94185	7.58E-05	0.001636
AN3021	Ortholog of A. fumigatus Af293 : Afu3g08920, A. niger CBS 513.88 : An16g02420, A. oryzae RIB40 : AO090005001345, A. niger ATCC 1015 : 41197-mRNA and Aspergillus versicolor : Aspve1_0051328	null	-3.3579	7.93E-05	0.00169
AN3764	Has domain(s) with predicted catalytic activity	null	-3.3579	7.93E-05	0.00169
AN7131	Putative cytochrome P450	CYP52H1	-3.3579	7.93E-05	0.00169
AN8127	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.5036	7.93E-05	0.00169
AN0367	Putative integral membrane protein; transcript repressed by light in developmentally competent mycelia	null	-2.6952	8.06E-05	0.001713
AN4353	Has domain(s) with predicted 3-oxoacyl-[acyl-carrier-protein] synthase activity and role in fatty acid biosynthetic process	null	-2.7316	8.23E-05	0.001743
AN4067	Ortholog of A. fumigatus Af293 : Afu1g05430, A. niger ATCC 1015 : 137492-mRNA, Aspergillus versicolor : Aspve1_0085507, Aspergillus sydowii : Aspsy1_0149851 and Aspergillus terreus NIH2624 : ATET_03084	null	7.59378	8.36E-05	0.001754

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AN7091	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	-3.6475	8.36E-05	0.001754
AN8561	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.4649	8.36E-05	0.001754
AN0353	Putative F-box protein	null	-2.6775	8.45E-05	0.001767
AN10491	Putative transcription factor; predicted role in secondary metabolite production	null	-2.7933	8.52E-05	0.001778
AN11563	Ortholog of A. clavatus NRRL 1 : ACLA_068330, A. fumigatus A1163 : AFUB_023040 and Aspergillus aculeatus ATCC16872 : Aacu16872_043662	null	-3.0286	8.82E-05	0.001825
AN0484	Has domain(s) with predicted glycerophosphodiester phosphodiesterase activity and role in glycerol metabolic process, lipid metabolic process	null	-5.4223	8.90E-05	0.001825
AN2060	Putative exo-arabinanase	abxA	-4.6494	8.90E-05	0.001825
AN3992	Ortholog of A. nidulans FGSC A4 : AN8424, AN7089, A. fumigatus Af293 : Afu7g05085, A. oryzae RIB40 : AO090005000321 and N. fischeri NRRL 181 : NFIA_026200	null	-5.4223	8.90E-05	0.001825
AN4687	Beta subunit of 3-methylcrotonyl-CoA carboxylase, involved in leucine degradation	mccB	-5.4223	8.90E-05	0.001825
AN4801	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-4.6494	8.90E-05	0.001825
AN10507	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	null	-2.6907	9.39E-05	0.001919
AN10664	Ortholog of A. fumigatus Af293 : Afu6g14120, A. oryzae RIB40 : AO090103000398, A. niger ATCC 1015 : 37809-mRNA, Aspergillus versicolor : Aspve1_0044715 and Aspergillus sydowii : Aspsy1_0035748	null	-2.7499	9.57E-05	0.00195
AN8366	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.8613	9.62E-05	0.001956
AN4376	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	gdhA	2.58464	9.88E-05	0.002002
AN1422	Ortholog of Aspergillus brasiliensis : Aspbr1_0125634, Aspergillus acidus : Aspfo1_0134032, Aspergillus versicolor : Aspve1_0037180 and Aspergillus sydowii : Aspsy1_0041970	null	7.53822	0.000101	0.002026
AN4117	Putative cytochrome P450	CYP660A1	7.53822	0.000101	0.002026
AN4830	Ortholog(s) have role in coenzyme A biosynthetic process and cytosol, nucleus localization	null	7.53822	0.000101	0.002026
AN8292	Ortholog of A. oryzae RIB40 : AO090124000092, Aspergillus brasiliensis : Aspbr1_0118961, N. fischeri NRRL 181 : NFIA_006570, Aspergillus acidus : Aspfo1_0178460 and Aspergillus versicolor : Aspve1_0086706	null	7.55698	0.000101	0.002026
AN0728	Has domain(s) with predicted snoRNA binding activity and role in ribosome biogenesis, snRNA pseudouridine synthesis	null	4.53134	0.000103	0.00205

AN8899	Ortholog(s) have cytosol, nucleus localization	null	-3.0976	0.000105	0.002099
AN3147	Ortholog(s) have intracellular localization	null	2.69015	0.000108	0.002138
AN9433	Ortholog of A. fumigatus Af293 : Afu4g07600, A. niger CBS 513.88 : An04g01960, A. niger ATCC 1015 : 190605-mRNA, Aspergillus versicolor : Aspve1_0743999 and Aspergillus sydowii : Aspsy1_0062370	null	3.03922	0.000108	0.002148
AN7264	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	-3.294	0.00011	0.002182
AN3706	S. cerevisiae ortholog RPS10A has role in rRNA export from nucleus; palA-dependent expression independent of pH	null	2.58935	0.000112	0.002201
AN11510	Has domain(s) with predicted role in defense response	null	-7.2016	0.000119	0.002311
AN12015	null	null	-7.2016	0.000119	0.002311
AN7847	Has domain(s) with predicted role in cell wall macromolecule catabolic process	null	-4.0342	0.000119	0.002311
AN8149	Protein with alpha-fucosidase activity, involved in degradation of xyloglucans	afcA	-7.2016	0.000119	0.002311
AN10761	Predicted PIN domain-containing RNA-binding protein; expression upregulated after exposure to farnesol	null	-2.562	0.000119	0.002311
AN9025	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	null	-2.7482	0.000121	0.002335
AN1166	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation, ribosomal large subunit assembly and cytosolic large ribosomal subunit, nucleolus localization	null	2.54019	0.000123	0.002358
AN3779	Ortholog(s) have exopolyphosphatase activity, role in polyphosphate catabolic process and cytosol, nucleus localization	null	7.51921	0.000123	0.002358
AN3988	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-3.5738	0.000123	0.002358
AN3313	Putative methyltransferase with a predicted role in histidine metabolism; ribosomal RNA adenine dimethylase; expression reduced after exposure to farnesol	null	3.15887	0.000124	0.00237
AN10964	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	-2.7221	0.000124	0.00237
AN6253	Putative phenylalanine tRNA synthetase alpha subunit	podG	2.73829	0.000125	0.002385
AN4424	Has domain(s) with predicted FMN binding, heme binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.853	0.00013	0.002475
AN1445	Ortholog(s) have protein-histidine N-methyltransferase activity, role in peptidyl-histidine methylation, to form tele-methylhistidine and cytosol, nucleus localization	null	3.2538	0.000138	0.002607
AN10863	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	null	-2.6574	0.00014	0.002643

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AN4201	Putative acyl-CoA synthetase/AMP-binding domain protein	null	-2.9215	0.000145	0.002724
AN2844	Ortholog of A. fumigatus Af293 : Afu3g12255, A. niger CBS 513.88 : An02g08130, A. oryzae RIB40 : AO090003000790, A. niger ATCC 1015 : 37157-mRNA and Aspergillus versicolor : Aspve1_0080524	null	2.97079	0.000153	0.002882
AN5324	Dehydrin-like protein; protein induced by farnesol	dlpA	-3.3729	0.000155	0.002893
AN5503	null	null	-3.3729	0.000155	0.002893
AN0589	Putative ATP-dependent RNA helicase with a predicted role in rRNA processing; ortholog of S. cerevisiae Hca4p; expression reduced after exposure to farnesol	null	3.48066	0.000156	0.002893
AN2686	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	null	4.28901	0.000156	0.002893
AN8265	null	null	4.27427	0.000156	0.002893
AN10165	Has domain(s) with predicted outer membrane localization	null	-5.3077	0.00016	0.002945
AN4521	Forkhead domain protein with a possible role in sexual development	fhpA	-5.3077	0.00016	0.002945
AN6767	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-5.3077	0.00016	0.002945
AN11697	Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and membrane localization	null	3.78813	0.000166	0.00303
AN3656	Putative nitrilase with a predicted role in nitrogen or cyanoamino acid metabolism	null	3.78813	0.000166	0.00303
AN2123	Ortholog(s) have RNA polymerase II transcription cofactor activity and role in negative regulation of transcription from RNA polymerase II promoter, positive regulation of transcription from RNA polymerase II promoter	null	7.12577	0.000167	0.00303
AN6024	Protein with glutathione S-transferase and glutathione peroxidase activities; intracellular, menadione stress-induced protein	gstB	-3.9831	0.000167	0.00303
AN6399	Putative bleomycin hydrolase	null	-3.9831	0.000167	0.00303
AN8784	Ortholog of A. fumigatus Af293 : Afu5g09700, A. niger CBS 513.88 : An07g03080, A. oryzae RIB40 : AO090005000275, A. niger ATCC 1015 : 127717-mRNA and Aspergillus versicolor : Aspve1_0046376	null	7.12577	0.000167	0.00303
AN7430	Putative glutamine amidotransferase with a predicted role in histidine metabolism	hisHF	2.51813	0.00017	0.003071
AN5423	Ortholog of A. oryzae RIB40 : AO090003001412, Aspergillus flavus NRRL 3357 : AFL2T_01664, Aspergillus versicolor : Aspve1_0083396 and Aspergillus carbonarius ITEM 5010 : Acar5010_169601	null	-2.5728	0.000172	0.003098
AN0590	Ortholog(s) have nucleus localization	null	2.95218	0.000174	0.003123
AN2270	C2H2 zinc-finger transcription factor involved in regulation of structural genes for acetamidase (amdS), formate dehydrogenase (aciA), and alcohol dehydrogenase II (alcB)	amdA	4.42863	0.000177	0.003174
AN3681	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	null	2.9398	0.000178	0.003191

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AN4599	Ortholog(s) have polynucleotide 5'-hydroxyl-kinase activity, role in rRNA processing, termination of RNA polymerase I transcription and nucleolar chromatin localization	null	4.25939	0.000182	0.003237
AN3259	Ortholog of A. oryzae RIB40 : AO090011000035, Aspergillus flavus NRRL 3357 : AFL2T_04841, Aspergillus versicolor : Aspve1_0040331 and Aspergillus sydowii : Aspsy1_0029969	null	-3.3136	0.000183	0.003237
AN3845	null	null	7.42024	0.000183	0.003237
AN3855	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-3.3136	0.000183	0.003237
AN10762	Ortholog(s) have cytosol localization	null	2.75081	0.000184	0.003242
AN5222	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	2.45101	0.000195	0.003428
AN0784	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.0651	0.000204	0.003562
AN6763	Ortholog of A. fumigatus Af293 : Afu3g11800, N. fischeri NRRL 181 : NFIA_065520, A. clavatus NRRL 1 : ACLA_039690 and A. fumigatus A1163 : AFUB_037380	null	-3.1689	0.000204	0.003562
AN9241	Has domain(s) with predicted zinc ion binding activity and role in lipid metabolic process	null	-3.0651	0.000204	0.003562
AN6565	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	null	-2.8884	0.00021	0.003655
AN1519	Putative Argonaute protein involved in inverted repeat transgene (IRT)-induced RNA silencing	rsdA	-3.1044	0.000213	0.00367
AN5000	Ortholog(s) have enoyl-CoA hydratase activity, role in sphingolipid biosynthetic process, vacuolar transport and fungal-type vacuole membrane, integral to endoplasmic reticulum membrane localization	null	7.10041	0.000213	0.00367
AN8711	Ortholog of A. fumigatus Af293 : Afu6g02515, A. niger CBS 513.88 : An12g07890, A. niger ATCC 1015 : 42149-mRNA, Aspergillus versicolor : Aspve1_0044454 and Aspergillus sydowii : Aspsy1_0048236	null	7.07461	0.000213	0.00367
AN11046	Protein of unknown function; transcript is induced by nitrate	null	-7.087	0.000217	0.00367
AN12126	null	null	-3.9097	0.000217	0.00367
AN1419	null	null	-7.087	0.000217	0.00367
AN1503	Protein expressed at increased levels during osmoadaptation; contains dihydrodipicolinate synthase family DHDPS-like conserved domain	null	-3.9097	0.000217	0.00367
AN2402	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-7.087	0.000217	0.00367
AN7074	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.9097	0.000217	0.00367

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AN7896	Zn(II)2Cys6 transcription factor with a role in secondary metabolite biosynthesis; member of the dba gene cluster; overexpression upregulates dba gene cluster expression	dbaA	-7.087	0.000217	0.00367
AN7961	Ortholog of A. fumigatus Af293 : Afu4g13760, A. oryzae RIB40 : AO090010000492, Aspergillus versicolor : Aspve1_0045462, Aspergillus sydowii : Aspsy1_1151790 and Aspergillus terreus NIH2624 : ATET_04942	null	-4.4102	0.000217	0.00367
AN8298	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	null	-7.087	0.000217	0.00367
AN9523	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	null	-7.087	0.000217	0.00367
AN11419	Ortholog(s) have cytosol localization	null	2.43086	0.000222	0.00374
AN8026	Ortholog of A. fumigatus Af293 : Afu3g00120, A. niger CBS 513.88 : An12g05610, A. oryzae RIB40 : AO090010000524, AO090166000107 and A. niger ATCC 1015 : 186000-mRNA, 50976-mRNA	null	7.3996	0.000224	0.003772
AN1425	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	farB	-2.5008	0.00024	0.00402
AN0554	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	aldA	-2.4369	0.000245	0.004103
AN6286	Ortholog(s) have cytoplasm localization	null	-2.5359	0.000247	0.004122
AN10134	Ortholog(s) have protein-lysine N-methyltransferase activity, role in negative regulation of G2/M transition of mitotic cell cycle, peptidyl-lysine methylation and cytosol, nucleus localization	null	2.95093	0.000252	0.004198
AN4015	Ortholog(s) have ribosome binding, translation elongation factor activity, translation initiation factor activity	null	2.38592	0.00026	0.00431
AN0601	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.8754	0.00026	0.00431
AN6345	Ortholog(s) have lysophosphatidic acid acyltransferase activity, role in cellular triglyceride homeostasis, lipid particle organization, protein targeting to vacuole and Golgi apparatus, endoplasmic reticulum, lipid particle localization	null	3.71038	0.000266	0.004352
AN5960	Ortholog(s) have mRNA binding activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit assembly	null	2.38587	0.000267	0.004352
AN5415	Has domain(s) with predicted O-methyltransferase activity	null	-2.6614	0.00027	0.004352

AN10283	Has domain(s) with predicted FMN binding, iron ion binding, oxidoreductase activity and role in oxidation-reduction process	null	2.68344	0.00027	0.004352
AN8376	null	null	-3.1125	0.000271	0.004352
AN0498	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	7.02158	0.000273	0.004352
AN10959	Has domain(s) with predicted catalytic activity	null	-3.5894	0.000273	0.004352
AN12087	null	null	-3.8842	0.000273	0.004352
AN3199	MFS sugar transporter; induced by lactose and galactose	lacpA	-3.8842	0.000273	0.004352
AN3479	Ortholog of A. nidulans FGSC A4 : AN8495, A. fumigatus Af293 : Afu3g01440, Afu4g03340, Afu5g07620, A. niger CBS 513.88 : An13g02880, A. oryzae RIB40 : AO090009000050 and A. niger ATCC 1015 : 129924-mRNA	null	7.02158	0.000273	0.004352
AN3895	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-3.8842	0.000273	0.004352
AN4198	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-3.8842	0.000273	0.004352
AN4953	Putative Rho-like GTPase	null	7.04834	0.000273	0.004352
AN7137	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.5894	0.000273	0.004352
AN7181	Ortholog of A. fumigatus Af293 : Afu4g03200, A. oryzae RIB40 : AO090011000112, N. fischeri NRRL 181 : NFIA_030260, Aspergillus flavus NRRL 3357 : AFL2T_04908 and A. clavatus NRRL 1 : ACLA_055410	null	-3.8842	0.000273	0.004352
AN12449	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	null	-2.8109	0.000274	0.004352
AN10486	Putative nonribosomal peptide synthetase (NRPS)-like enzyme	null	-3.4141	0.000276	0.004352
AN1452	Ortholog(s) have nucleolus localization	null	7.31397	0.000276	0.004352
AN4682	Ortholog of A. fumigatus Af293 : Afu5g08980, A. niger CBS 513.88 : An07g04180, A. niger ATCC 1015 : 209689-mRNA, Aspergillus versicolor : Aspve1_0084718 and Aspergillus sydowii : Aspsy1_0155159	null	7.35742	0.000276	0.004352
AN4708	Ortholog(s) have mitochondrion localization	null	7.35742	0.000276	0.004352
AN5112	Ortholog of A. fumigatus Af293 : Afu1g07620, A. niger CBS 513.88 : An07g10250, A. oryzae RIB40 : AO090012001014, A. niger ATCC 1015 : 39574-mRNA and Aspergillus versicolor : Aspve1_0045822	null	7.33586	0.000276	0.004352
AN6684	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	null	7.35742	0.000276	0.004352

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AN0689	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	facB	-2.4286	0.000285	0.004473
AN0647	Ortholog(s) have rRNA primary transcript binding, single-stranded telomeric DNA binding, snoRNA binding activity and Mpp10 complex, small-subunit processome localization	null	2.92218	0.000286	0.004492
AN1893	Light response regulator	silA	-2.4673	0.00029	0.004543
AN8257	Ortholog(s) have mitochondrion localization	null	4.15064	0.000293	0.004578
AN5302	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-2.4988	0.000294	0.004588
AN10715	Ortholog of A. fumigatus Af293 : Afu6g06560, A. niger CBS 513.88 : An03g03300, A. oryzae RIB40 : AO090003000028, A. niger ATCC 1015 : 57126-mRNA and Aspergillus versicolor : Aspve1_0133004	null	-5.1831	0.000297	0.004623
AN1982	Ortholog of A. fumigatus Af293 : Afu4g10570, A. niger CBS 513.88 : An04g06100, A. oryzae RIB40 : AO090003001154, A. niger ATCC 1015 : 193413-mRNA and Aspergillus versicolor : Aspve1_0465099	null	-2.6465	0.000305	0.004737
AN5564	Putative phosphatidyl synthase; intracellular, menadione stress-induced protein; transcript and protein upregulated after exposure to farnesol	null	2.70892	0.00031	0.004805
AN6629	Putative ribosomal protein L14; ortholog of S. cerevisiae Rpl14Ap; expression reduced after exposure to farnesol	null	2.38778	0.000321	0.004951
AN3690	Ortholog(s) have iron ion transmembrane transporter activity, role in RNA splicing, mitochondrial iron ion transport and mitochondrion localization	null	3.14669	0.00033	0.00508
AN6706	Has domain(s) with predicted DNA binding activity	null	7.26917	0.000341	0.00525
AN11978	Ortholog(s) have endoplasmic reticulum localization	null	2.81638	0.00035	0.005351
AN2913	Ortholog of A. nidulans FGSC A4 : AN4375, A. fumigatus Af293 : Afu3g07740, Afu4g06610, A. niger CBS 513.88 : An04g00930 and A. oryzae RIB40 : AO090023000927, AO090020000420	null	-2.5815	0.00035	0.005351
AN1382	Ortholog(s) have role in cellular zinc ion homeostasis, endoplasmic reticulum inheritance, protein targeting to nuclear inner membrane, septin ring assembly	null	6.96652	0.000351	0.005351
AN6555	Ortholog(s) have role in medium-chain fatty acid biosynthetic process	null	6.99431	0.000351	0.005351
AN8406	Putative alcohol dehydrogenase; intracellular, menadione stress-induced protein; protein expressed at decreased levels in a hapX mutant versus wild-type	null	-2.4162	0.000378	0.005755
AN8930	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	null	-3.2291	0.000383	0.005807
AN1163	Putative chaperone; ortholog of S. cerevisiae Hsp78p; expression upregulated after exposure to farnesol	null	-2.3146	0.000384	0.00582
AN1662	Ortholog(s) have cytosol, nucleus, ribosome localization	null	2.51566	0.000385	0.00582

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AN2262	Ortholog(s) have role in cellular response to oxidative stress, response to osmotic stress, ribosomal small subunit biogenesis, ribosomal small subunit export from nucleus	null	2.70127	0.000389	0.005843
AN0628	Putative D-lactate dehydrogenase with a role in pyruvate-acetyl-coA metabolism; transcript is induced by nitrate	null	-2.3582	0.000389	0.005843
AN5587	Ortholog of A. fumigatus Af293 : Afu4g11520, A. niger CBS 513.88 : An04g04980, A. niger ATCC 1015 : 214408-mRNA, Aspergillus versicolor : Aspve1_0084227 and Aspergillus sydowii : Aspsy1_0030385	null	-2.7469	0.00039	0.005843
AN6653	Malate synthase, required for utilization of acetate as carbon source; transcription induction by acetate mediated by FacB; carbon catabolite repression mediated by CreA; transcription induction by long-chain fatty acids mediated by FarA	acuE	-2.4837	0.00039	0.005843
AN6985	Putative ribulokinase with a predicted role in ribulose metabolism	null	-2.5573	0.000395	0.005903
AN3797	Ortholog(s) have role in cellular response to UV, postreplication repair, recombinational repair and nucleus, spindle pole body localization	null	-2.62	0.000398	0.005916
AN0278	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	2.38218	0.000398	0.005916
AN1723	Ortholog(s) have cell septum, hyphal tip localization	null	-2.5987	0.000398	0.005916
AN5162	Putative pyruvate dehydrogenase (lipoamide) with a predicted role in pyruvate metabolism	pdhB	2.30518	0.000401	0.005916
AN1979	Ortholog of A. fumigatus Af293 : Afu4g10610, A. niger CBS 513.88 : An04g06070, A. niger ATCC 1015 : 214295-mRNA, Aspergillus versicolor : Aspve1_0080153 and Aspergillus sydowii : Aspsy1_0053917	null	-3.0949	0.000407	0.005916
AN6379	null	null	-3.0949	0.000407	0.005916
AN5880	Ortholog(s) have cytosol, nucleus localization	null	2.69693	0.000408	0.005916
AN0736	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	null	-6.9624	0.000411	0.005916
AN10368	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-6.9624	0.000411	0.005916
AN1088	Ortholog of A. fumigatus Af293 : Afu4g14470, Afu8g00430, A. niger CBS 513.88 : An07g00070, An07g00010, An02g08300, An11g06450 and A. oryzae RIB40 : AO090001000323	null	-6.9624	0.000411	0.005916
AN1482	Has domain(s) with predicted acetoacetate-CoA ligase activity and role in lipid metabolic process	null	-6.9624	0.000411	0.005916
AN2753	null	null	-6.9624	0.000411	0.005916
AN3290	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	null	-4.2739	0.000411	0.005916
AN4582	Ortholog of A. fumigatus Af293 : Afu2g01970, A. niger CBS 513.88 : An07g05780, A. oryzae RIB40 : AO090011000467, A. niger ATCC 1015 : 133628-mRNA and Aspergillus versicolor : Aspve1_0053889	null	-3.7733	0.000411	0.005916

AN6727	Ortholog of A. nidulans FGSC A4 : AN8146, A. fumigatus Af293 : Afu6g03180, Afu7g05880, A. niger CBS 513.88 : An07g02000, An01g14710 and Aspergillus versicolor : Aspve1_0079826	null	-3.7733	0.000411	0.005916
AN7385	Putative phosphatidylserine decarboxylase with a predicted role in phospholipid metabolism	null	-6.9624	0.000411	0.005916
AN8513	Putative single-module nonribosomal peptide synthetase (NRPS); member of the tdi (terrequinone A biosynthesis) gene cluster; transcriptionally regulated by LaeA	tdiA	-6.9624	0.000411	0.005916
AN9468	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, cytosol localization	null	2.32878	0.000411	0.005916
AN11979	Ortholog(s) have IgE binding activity and fungal-type cell wall localization	null	7.22294	0.000424	0.006064
AN4685	Predicted Ras GTPase	null	7.22294	0.000424	0.006064
AN5574	Ortholog(s) have role in DNA replication initiation, DNA replication preinitiation complex assembly, GINS complex assembly, double-strand break repair via break-induced replication	null	7.22294	0.000424	0.006064
AN9032	Ortholog of A. nidulans FGSC A4 : AN10883, A. fumigatus Af293 : Afu7g06950, Afu8g02470, A. niger CBS 513.88 : An03g06330, An03g00350, An05g02580 and A. oryzae RIB40 : AO090010000660	null	2.45655	0.000429	0.006121
AN7231	Has domain(s) with predicted serine-type peptidase activity and role in proteolysis	null	-2.38	0.00043	0.006122
AN2108	Ortholog of Aspergillus brasiliensis : Aspbr1_0037101, A. niger ATCC 1015 : 178726-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_02657 and Aspergillus acidus : Aspfo1_0439200	null	-2.8776	0.00043	0.006122
AN10700	Ortholog of S. cerevisiae : YER010C, A. fumigatus Af293 : Afu4g10940, A. niger CBS 513.88 : An04g05730, A. oryzae RIB40 : AO090003001122 and A. niger ATCC 1015 : 51189-mRNA	null	-2.8988	0.000435	0.006176
AN5601	Putative saccharopine dehydrogenase (NADP+, L-glutamate-forming) with a predicted role in lysine metabolism	null	2.41762	0.000448	0.006352
AN6176	Ortholog(s) have beta-tubulin binding activity, role in tubulin complex assembly and cytoplasm localization	null	2.83232	0.000452	0.006387
AN5490	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	null	-3.778	0.000455	0.006387
AN6718	Has domain(s) with predicted ATP binding, nucleoside-triphosphatase activity	null	-3.4832	0.000455	0.006387
AN7543	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	null	6.90927	0.000455	0.006387
AN0441	Has domain(s) with predicted zinc ion binding activity	null	-3.0058	0.000462	0.006481
AN3916	Putative glycerol kinase with a predicted role in glycerol metabolism	null	-2.4367	0.000472	0.006601
AN10189	Ortholog(s) have protein-arginine omega-N monomethyltransferase activity and role in peptidyl-arginine methylation	null	2.75484	0.000474	0.006625

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AN10533	Putative trehalose-6-phosphate synthase; ortholog of S. cerevisiae Tps3p; expression upregulated after exposure to farnesol	null	-2.2852	0.000484	0.006751
AN5315	Ortholog of A. niger CBS 513.88 : An01g01450, A. oryzae RIB40 : AO090001000269, Aspergillus brasiliensis : Aspbr1_0053207, A. niger ATCC 1015 : 36402-mRNA and N. fischeri NRRL 181 : NFIA_044920	null	-2.9926	0.000491	0.006823
AN1719	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	null	-2.7687	0.000491	0.006823
AN7301	Putative glucosyltransferase; ortholog of S. cerevisiae Alg8p; expression reduced after exposure to farnesol	alg8	3.59148	0.000494	0.00684
AN8074	Has domain(s) with predicted ubiquitin thiolesterase activity, zinc ion binding activity and role in ubiquitin-dependent protein catabolic process	null	-2.3937	0.00051	0.007046
AN1267	Has domain(s) with predicted DNA binding activity	null	2.68071	0.000523	0.007216
AN7365	Ortholog of Aspergillus versicolor : Aspve1_0124183 and Aspergillus sydowii : Aspsy1_1157656	null	-2.5186	0.000524	0.007224
AN4699	Ortholog of A. niger CBS 513.88 : An07g04660, A. oryzae RIB40 : AO090020000435, Aspergillus brasiliensis : Aspbr1_0122889, A. niger ATCC 1015 : 209660-mRNA and Aspergillus flavus NRRL 3357 : AFL2T_10883	null	-2.4045	0.000539	0.007404
AN4576	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-2.4513	0.000572	0.007789
AN1852	Putative chitin deacetylase	null	-5.0467	0.000573	0.007789
AN3997	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-5.0467	0.000573	0.007789
AN4104	Ortholog of A. fumigatus Af293 : Afu1g05860, A. niger CBS 513.88 : An18g03590, A. oryzae RIB40 : AO090009000354, A. niger ATCC 1015 : 124341-mRNA and Aspergillus versicolor : Aspve1_0054294	null	-5.0467	0.000573	0.007789
AN6723	Putative 2,3-dihydroxybenzoate carboxylyase	dhbD	-5.0467	0.000573	0.007789
AN8163	Putative short-chain dehydrogenase/reductase	null	-5.0467	0.000573	0.007789
AN4268	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-2.3493	0.000575	0.007794
AN0867	Ortholog of A. nidulans FGSC A4 : AN4122, AN2881, AN10123, A. fumigatus Af293 : Afu1g13860, Afu1g15180, Afu3g11650 and A. niger CBS 513.88 : An08g07010, An02g07440, An01g13480	null	-2.2762	0.000588	0.007952
AN3190	Ortholog of A. fumigatus Af293 : Afu4g02920, A. niger CBS 513.88 : An14g02990, A. oryzae RIB40 : AO090001000192, A. niger ATCC 1015 : 201534-mRNA and Aspergillus versicolor : Aspve1_0140942	null	6.84966	0.000592	0.007979
AN6254	Putative mitochondrial dicarboxylate:inorganic phosphate antiporter	dicA	6.84966	0.000592	0.007979
AN4794	Putative ribosomal protein; expression increased in salt-adapted strains	null	2.23771	0.000593	0.007979
AN6249	Putative calcineurin binding protein, calcipressin	rcnA	-2.42	0.000602	0.00809

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AN3894	Putative aconitate hydratase with a predicted role in the TCA cycle	null	2.70837	0.000609	0.008158
AN1682	Ortholog of A. fumigatus Af293 : Afu4g08680, A. niger CBS 513.88 : An04g03500, A. oryzae RIB40 : AO090023000689, A. niger ATCC 1015 : 190697-mRNA and Aspergillus versicolor : Aspve1_0025027	null	2.50765	0.000657	0.008791
AN10626	Has domain(s) with predicted ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism activity	null	-3.2346	0.000661	0.008793
AN2798	Has domain(s) with predicted role in response to stress and integral to membrane localization	null	-3.2346	0.000661	0.008793
AN5402	Has domain(s) with predicted role in lipid metabolic process	null	-3.2346	0.000661	0.008793
AN8216	Putative nucleoside diphosphate kinase with a predicted role in phospholipid metabolism; required for normal hyphal growth and conidiation; mutants display increased hyphal cell lysis; transcript upregulated in response to camptothecin	swoH	2.27268	0.000673	0.00894
AN4594	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosolic small ribosomal subunit localization	null	2.21002	0.000678	0.008981
AN2010	Has domain(s) with predicted transferase activity, transferring hexosyl groups activity and role in metabolic process	null	2.74308	0.000679	0.008987
AN9042	Putative alpha-1,3-glucanase	agnC	-2.9238	0.000681	0.008987
AN11574	null	null	-2.3313	0.000715	0.009421
AN2272	Putative kinase with a predicted role in ribose metabolism or nucleotide salvage pathways	null	2.30356	0.000717	0.009437
AN6708	Putative dihydrolipoamide S-acetyltransferase with a predicted role in pyruvate metabolism	pdhA	2.20823	0.000724	0.009508
AN6487	Putative aspartyl protease; ortholog of S. cerevisiae BAR1; expression reduced after exposure to farnesol	null	3.48877	0.000727	0.009508
AN9173	Sugar transporter; transcriptionally induced by growth on xylose	null	-2.7923	0.000727	0.009508
AN8206	Ortholog(s) have mitochondrion localization	null	2.67252	0.000736	0.009611
AN2939	Ortholog(s) have mitochondrion localization	null	2.30209	0.000756	0.009858
AN4401	Putative asparagine synthase with a predicted role in asparagine metabolism	null	2.24806	0.000758	0.009859
AN9001	null	null	-2.2314	0.000761	0.009884
AN6071	Has domain(s) with predicted membrane localization	null	-2.3917	0.000763	0.009884
AN7772	Putative cytochrome P450; transcript repressed by nitrate	CYP5080B1	-2.5073	0.000765	0.009896
AN9297	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	null	-2.1764	0.00077	0.00993
AN3724	Ortholog of A. fumigatus Af293 : Afu6g12460, A. niger CBS 513.88 : An06g01620, A. oryzae RIB40 : AO090009000166, A. niger ATCC 1015 : 177709-mRNA and Aspergillus versicolor : Aspve1_0131430	null	6.81891	0.000776	0.00993
AN4351	Protein involved in a signaling pathway that activates PacC transcription factor in response to alkaline ambient pH	palA	6.81891	0.000776	0.00993

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AN5391	Has domain(s) with predicted zinc ion binding activity and role in intracellular signal transduction	null	6.81891	0.000776	0.00993
AN6062	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	null	6.81891	0.000776	0.00993
AN8503	Ortholog of A. niger CBS 513.88 : An13g03080, Aspergillus brasiliensis : Aspbr1_0044529, Aspergillus flavus NRRL 3357 : AFL2T_10601 and Aspergillus acidus : Aspfo1_0328979	null	-3.6633	0.000776	0.00993
AN7331	Has domain(s) with predicted DNA binding, cyanate hydratase activity, hydro-lyase activity and role in cyanate metabolic process	null	2.47216	0.000778	0.009939
AN1122	Ortholog(s) have cytosol localization	null	2.20707	0.000807	0.009987
AN10691	Has domain(s) with predicted GTP binding, GTPase activity	null	-6.8261	0.000808	0.009987
AN10698	null	null	-6.8261	0.000808	0.009987
AN11190	Has domain(s) with predicted NAD+ binding, hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides, zinc ion binding activity and role in chromatin silencing, protein deacetylation	null	-4.8962	0.000808	0.009987
AN11703	null	null	-4.8962	0.000808	0.009987
AN12116	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.8261	0.000808	0.009987
AN1869	Ortholog of A. oryzae RIB40 : AO090003000242, Aspergillus flavus NRRL 3357 : AFL2T_02736 and Aspergillus sydowii : Aspsy1_0167761	null	-6.8261	0.000808	0.009987
AN1898	Ortholog(s) have role in melanin biosynthetic process from tyrosine, tyrosine catabolic process and cytoplasm localization	null	-4.8962	0.000808	0.009987
AN3741	Alcohol dehydrogenase II, has a predicted role in two-carbon compound metabolism	alcB	-4.1233	0.000808	0.009987
AN4394	Ortholog(s) have role in asexual sporulation resulting in formation of a cellular spore, positive regulation of asexual sporulation resulting in formation of a cellular spore, regulation of transcription, DNA-dependent	null	-6.8261	0.000808	0.009987
AN6849	Ortholog(s) have role in cellular response to heat, cellular response to hydrogen peroxide	null	-4.1233	0.000808	0.009987
AN7215	null	null	-4.8962	0.000808	0.009987
AN7962	Extracellular deuterolysin-type metallo-proteinase	pepJ	-6.8261	0.000808	0.009987
AN8518	Similar to NADPH-dependent quinone reductases; member of the tdi (terrequinone A biosynthesis) gene cluster; transcriptionally regulated by LaeA	tdiC	-6.8261	0.000808	0.009987
AN8529	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	null	-6.8261	0.000808	0.009987

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AN9010	Ortholog(s) have nicotinamide mononucleotide transmembrane transporter activity, role in nicotinamide mononucleotide transport and mitochondrion localization	null	-6.8261	0.000808	0.009987
AN9365	Protein with endo-1,4-beta-xylanase activity, involved in degradation of xylans	xlnB	-6.8261	0.000808	0.009987
AN2744	Ortholog of A. fumigatus Af293 : Afu1g05190, A. niger CBS 513.88 : An01g04420, A. oryzae RIB40 : AO090003000815, A. niger ATCC 1015 : 55430-mRNA and Aspergillus versicolor : Aspve1_0072930	null	3.92397	0.000809	0.009987
AN7481	Ortholog of A. fumigatus Af293 : Afu2g05680, A. niger CBS 513.88 : An02g14110, A. oryzae RIB40 : AO090001000682, A. niger ATCC 1015 : 174251-mRNA and Aspergillus versicolor : Aspve1_0074033	null	3.94273	0.000809	0.009987
AN5634	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	acuD	-2.2217	0.000814	0.010026
AN4453	Ortholog(s) have role in N-terminal peptidyl-methionine acetylation, regulation of cytokinesis, actomyosin contractile ring assembly and cytosol localization	null	2.26116	0.000828	0.01018
AN1304	null	null	-2.5709	0.000852	0.010445
AN4779	Ortholog of A. fumigatus Af293 : Afu3g06660, A. niger CBS 513.88 : An11g09650, A. oryzae RIB40 : AO090020000332, A. niger ATCC 1015 : 209032-mRNA and Aspergillus versicolor : Aspve1_0051759	null	-2.5709	0.000852	0.010445
AN8079	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	null	-2.5234	0.000863	0.010553
AN4547	Ortholog(s) have cytosol localization	null	2.30882	0.000864	0.010553
AN5777	Has domain(s) with predicted triglyceride lipase activity and role in lipid metabolic process	null	-2.4109	0.000866	0.010556
AN3826	Ortholog(s) have GPI-anchor transamidase complex localization	null	2.5752	0.000888	0.010814
AN1490	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.2066	0.000898	0.010906
AN0978	Ortholog(s) have guanyl-nucleotide exchange factor activity, translation initiation factor activity and role in regulation of translational initiation	null	2.54127	0.0009	0.010918
AN1079	Ortholog of N. fischeri NRRL 181 : NFIA_013390	null	2.88185	0.000906	0.010967
AN5213	Ortholog(s) have Golgi apparatus, cell division site, cell tip localization	null	-2.504	0.000908	0.01097
AN2994	Ortholog of A. niger CBS 513.88 : An02g12350, A. niger ATCC 1015 : 52433-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_01318 and Aspergillus terreus NIH2624 : ATET_01608	null	-2.8619	0.000917	0.011064
AN4802	60S ribosomal protein L21; ortholog of S. cerevisiae Rpl21Ap; expression reduced after exposure to farnesol	null	2.1572	0.000932	0.011215
AN6630	Putative nascent polypeptide-associated complex subunit alpha; induced by rapamycin-induced autophagy	null	2.22052	0.000933	0.011215
AN0678	Ortholog(s) have nucleus localization	null	3.44828	0.000948	0.011375

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AN6276	Has domain(s) with predicted 4-alpha-hydroxytetrahydrobiopterin dehydratase activity and role in tetrahydrobiopterin biosynthetic process	null	2.42127	0.000963	0.011538
AN12281	null	null	3.90496	0.000967	0.011566
AN1543	Putative succinate dehydrogenase	null	-2.1915	0.000987	0.011782
AN0262	Ortholog(s) have role in ribosomal large subunit assembly and cytosol, nucleolus localization	null	2.16502	0.000988	0.011782
AN0860	Ortholog of A. fumigatus Af293 : Afu1g15260, A. niger CBS 513.88 : An01g13370, A. oryzae RIB40 : AO090103000449, AO090005001207 and A. niger ATCC 1015 : 205440-mRNA	null	-2.4153	0.000991	0.011801
AN6858	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	null	-2.3345	0.001003	0.011915
AN1115	Putative purine nucleosidase with a predicted role in nucleotide salvage pathways	null	2.28752	0.001007	0.011927
AN1087	Putative cytochrome P450	CYP578B1	-2.7921	0.001007	0.011927
AN6632	Putative 40S ribosomal protein S28; ortholog of S. cerevisiae Rps28Bp; expression reduced after exposure to farnesol	null	2.1692	0.001009	0.011927
AN8705	Ortholog(s) have cytoplasmic stress granule, cytosol, nucleus localization	null	2.12206	0.001017	0.011987
AN0226	Ortholog(s) have protein homodimerization activity, ubiquitin-protein ligase activity	null	-2.2767	0.001024	0.011987
AN10465	Ortholog(s) have COPI-coated vesicle, Golgi apparatus localization	null	6.7225	0.001024	0.011987
AN10913	Ortholog(s) have mitochondrion localization	null	6.68888	0.001024	0.011987
AN2204	Protein expressed at increased levels during osmoadaptation	null	6.75536	0.001024	0.011987
AN2370	Ortholog of A. nidulans FGSC A4 : AN10160, AN0323, A. fumigatus Af293 : Afu1g02440, Afu4g02760, A. niger CBS 513.88 : An01g05750, An12g09350, An13g03290 and A. oryzae RIB40 : AO090020000719, AO090005000852	null	6.7225	0.001024	0.011987
AN9286	Alpha-glucuronidase, involved in degradation of xylans; transcriptionally induced by growth on xylose	aguA	-2.2605	0.001037	0.012112
AN10740	Ortholog(s) have cytosol localization	null	2.14472	0.001038	0.012112
AN3028	Ortholog of A. fumigatus Af293 : Afu3g08860, A. niger CBS 513.88 : An16g02480, A. oryzae RIB40 : AO090005001356, A. niger ATCC 1015 : 49077-mRNA and Aspergillus versicolor : Aspve1_0070326	null	-2.2323	0.001065	0.012398
AN12398	Ortholog of A. nidulans FGSC A4 : AN6460, A. oryzae RIB40 : AO090023000067, AO090010000683, Aspergillus flavus NRRL 3357 : AFL2T_03967, AFL2T_11823 and Aspergillus versicolor : Aspve1_0086685	null	3.42065	0.001084	0.012585
AN3232	Ortholog(s) have pantothenate transmembrane transporter activity, role in fatty acid biosynthetic process, pantothenate transmembrane transport, regulation of mitotic cell cycle and Golgi apparatus localization	null	3.40663	0.001084	0.012585

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AN1450	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	null	-2.1276	0.001102	0.012774
AN8859	Putative aspartate kinase with a predicted role in glycine, serine, and threonine metabolism	null	2.65497	0.001111	0.012855
AN6205	Ortholog of A. fumigatus Af293 : Afu6g11420, A. niger CBS 513.88 : An05g02520, An02g13310, An08g07320, A. oryzae RIB40 : AO090010000327, AO090103000241, AO090023000470 and A. niger ATCC 1015 : 37520-mRNA	null	-2.2833	0.001119	0.012925
AN9159	Ortholog of A. nidulans FGSC A4 : AN7899/dbaE, AN2031, AN0529, AN1032/afoC, A. fumigatus Af293 : Afu8g00910 and A. niger CBS 513.88 : An03g01180, An09g01790, An03g01810	null	2.75133	0.001137	0.013112
AN4464	Putative bifunctional enzyme with a predicted role in purine metabolism; protein expressed at increased levels in a hapX mutant versus wild-type	purH	2.16712	0.001159	0.01334
AN2964	Putative pyruvate dehydrogenase complex component	pdhX	2.57229	0.001161	0.013346
AN10784	Ortholog of A. fumigatus Af293 : Afu2g12010, A. niger CBS 513.88 : An02g04070, A. oryzae RIB40 : AO090026000446, A. niger ATCC 1015 : 120659-mRNA and Aspergillus versicolor : Aspve1_0129630	null	2.62673	0.001194	0.013701
AN0954	Has domain(s) with predicted heme binding activity	null	2.29107	0.001204	0.01379
AN1381	Ortholog of A. fumigatus Af293 : Afu1g09000, A. oryzae RIB40 : AO090005001625, A. niger ATCC 1015 : 47752-mRNA, Aspergillus versicolor : Aspve1_0121963 and Aspergillus sydowii : Aspsy1_0140811	null	3.06385	0.001206	0.01379
AN8639	Putative alpha,alpha-trehalose-phosphate synthase (UDP-forming) with a predicted role in trehalose biosynthesis	null	-2.2402	0.001215	0.013868
AN3745	Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more	null	2.70391	0.001233	0.014052
AN8644	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	null	-2.9825	0.001247	0.014192
AN9097	Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, mitochondrion, nucleolus localization	null	2.10329	0.001252	0.014223
AN7975	null	null	-2.7918	0.001269	0.014396
AN5688	Has domain(s) with predicted role in lipid biosynthetic process	null	2.26218	0.001272	0.014407
AN12443	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	null	-2.3632	0.001284	0.014468
AN2545	Putative nonribosomal peptide synthetase; emericellamide synthetase; required for emericellamide biosynthesis; present in an emericellamide gene cluster	easA	-2.3632	0.001284	0.014468
AN4792	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.3288	0.001284	0.014468

AN5833	Putative acetyl-CoA synthase with a predicted role in two-carbon metabolism or the methylcitrate pathway; transcript induced by heptadecanoic acid	pcsA	-2.4362	0.001297	0.014586
AN0742	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	null	-2.2794	0.0013	0.014586
AN10604	Ortholog of A. fumigatus Af293 : Afu2g17760, A. niger CBS 513.88 : An03g02870, Aspergillus versicolor : Aspve1_0070749 and Aspergillus sydowii : Aspsy1_0148182	null	-2.3067	0.0013	0.014586
AN8683	Ortholog(s) have ferric-chelate reductase activity, role in copper ion import, iron ion transport and plasma membrane localization	null	-2.5629	0.001304	0.014604
AN1050	Putative 3-ketoacyl-CoA thiolase with a predicted role in fatty acid metabolism; protein is mislocalized in a pexG mutant	null	-2.3565	0.001306	0.014604
AN5014	Ortholog(s) have cytosol, nucleolus localization	null	2.09996	0.001321	0.014745
AN5187	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	3.05171	0.001357	0.01488
AN7822	Ortholog of A. fumigatus Af293 : Afu5g00770, Aspergillus brasiliensis : Aspbr1_0058805, N. fischeri NRRL 181 : NFIA_041410, Aspergillus flavus NRRL 3357 : AFL2T_07218 and A. clavatus NRRL 1 : ACLA_004530	null	-2.5346	0.001357	0.01488
AN1502	Extracellular N-acetyl-beta-glucosaminidase with a predicted role in chitin hydrolysis	nagA	-2.2033	0.001357	0.01488
AN1000	Ortholog of A. fumigatus Af293 : Afu1g12780, A. niger CBS 513.88 : An08g05560, A. niger ATCC 1015 : 38264-mRNA, Aspergillus versicolor : Aspve1_0036614 and Aspergillus sydowii : Aspsy1_0142138	null	6.61919	0.00136	0.01488
AN10333	Has domain(s) with predicted hydrolase activity, pyridoxal phosphate binding activity and role in metabolic process	null	-3.5388	0.00136	0.01488
AN11432	null	null	6.61919	0.00136	0.01488
AN11691	Ortholog of A. fumigatus Af293 : Afu3g08080, A. niger CBS 513.88 : An02g11570, A. niger ATCC 1015 : 174264-mRNA, Aspergillus versicolor : Aspve1_0039584 and Aspergillus sydowii : Aspsy1_0770695	null	6.65445	0.00136	0.01488
AN3940	Ortholog(s) have role in DNA-dependent DNA replication, cellular protein localization, double-strand break repair via break-induced replication and GINS complex, cytosol, replication fork protection complex localization	null	6.61919	0.00136	0.01488
AN6380	Ortholog of A. fumigatus Af293 : Afu2g13930, A. niger CBS 513.88 : An02g05120, A. oryzae RIB40 : AO090026000179, A. niger ATCC 1015 : 197269-mRNA and Aspergillus versicolor : Aspve1_0052622	null	-3.5388	0.00136	0.01488
AN6549	Ortholog(s) have RNA polymerase II transcription coactivator activity involved in preinitiation complex assembly activity	null	6.65445	0.00136	0.01488

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AN8128	Ortholog of A. fumigatus Af293 : Afu3g13590, N. fischeri NRRL 181 : NFIA_063770 and A. fumigatus A1163 : AFUB_035600	null	6.65445	0.00136	0.01488
AN8638	Transcript enriched in dormant conidia; induced by light in in developmentally competent mycelia	cetJ	-3.5388	0.00136	0.01488
AN9324	Has domain(s) with predicted carbon-nitrogen ligase activity, with glutamine as amido-N-donor activity	null	-3.244	0.00136	0.01488
AN6659	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.4558	0.001367	0.014925
AN0495	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	null	2.4167	0.00139	0.015146
AN0360	Ortholog(s) have cytoplasm, nucleolus localization	null	3.80599	0.001391	0.015146
AN9393	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	2.43609	0.001396	0.015178
AN3713	null	null	-2.4526	0.001401	0.015203
AN4613	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	2.38197	0.001413	0.015317
AN4916	Ortholog(s) have role in ribosome biogenesis and cytosol, nucleolus, small-subunit processome localization	null	2.06738	0.001417	0.015334
AN7724	Ortholog of A. fumigatus Af293 : Afu5g08100, A. niger CBS 513.88 : An03g04310, A. oryzae RIB40 : AO090701000727, A. niger ATCC 1015 : 191368-mRNA and Aspergillus versicolor : Aspve1_0052931	null	2.84064	0.001439	0.015542
AN1393	Ortholog(s) have mitochondrion localization	null	2.58332	0.001485	0.016014
AN1013	Putative 60S ribosomal protein L5; ortholog of S. cerevisiae Rpl5p which is an RNA binding protein with a role in ribosomal large subunit assembly	null	2.0724	0.00149	0.016014
AN12335	Protein with an acyl-CoA dehydrogenase domain	acdA	-2.2024	0.001491	0.016014
AN4920	Putative calcium-transporting mitochondrial ATPase involved in calcium homeostasis	pmcB	-2.0998	0.001492	0.016014
AN0570	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	2.06345	0.001521	0.016295
AN2271	Ortholog of A. fumigatus Af293 : Afu5g06400, A. niger CBS 513.88 : An17g01320, A. niger ATCC 1015 : 214021-mRNA, Aspergillus versicolor : Aspve1_0050563 and Aspergillus sydowii : Aspsy1_0054275	null	2.77839	0.001525	0.016295
AN5807	Ortholog of A. fumigatus Af293 : Afu2g07470, A. niger CBS 513.88 : An05g00010, A. oryzae RIB40 : AO090011000945, A. niger ATCC 1015 : 186864-mRNA and Aspergillus versicolor : Aspve1_0130354	null	2.76943	0.001525	0.016295
AN7299	Ortholog(s) have DNA binding activity and cytosol, nucleus localization	null	2.08171	0.001537	0.016398
AN3823	Ortholog(s) have structural constituent of ribosome activity	null	2.03766	0.001583	0.016865

AN6236	Putative nonribosomal peptide synthetase	null	-2.0381	0.001614	0.01706
AN10731	Has domain(s) with predicted ATP binding, protein kinase activity and role in protein phosphorylation	null	3.30448	0.001639	0.01706
AN11243	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	2.21285	0.001657	0.01706
AN10311	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	mnpA	-6.6755	0.001662	0.01706
AN10371	Ortholog of A. fumigatus Af293 : Afu3g07945, A. oryzae RIB40 : AO090005001494, Aspergillus versicolor : Aspve1_0127963 and Aspergillus sydowii : Aspsy1_0029335	null	-3.9551	0.001662	0.01706
AN10672	Has domain(s) with predicted catalytic activity	null	-3.9551	0.001662	0.01706
AN10909	Has domain(s) with predicted trans-aconitate 2-methyltransferase activity and role in metabolic process	null	-3.9551	0.001662	0.01706
AN11622	null	null	-3.9551	0.001662	0.01706
AN1840	Has domain(s) with predicted 3-oxoacyl-[acyl-carrier-protein] synthase activity and role in fatty acid biosynthetic process	null	-6.6755	0.001662	0.01706
AN1917	Putative mitochondrial dicarboxylate-tricarboxylate carrier	dicB	-6.6755	0.001662	0.01706
AN2604	Ortholog of Aspergillus sydowii : Aspsy1_0439518	null	-6.6755	0.001662	0.01706
AN2609	Has domain(s) with predicted O-methyltransferase activity, RNA binding activity	null	-6.6755	0.001662	0.01706
AN2672	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	null	-6.6755	0.001662	0.01706
AN2924	Putative nonribosomal peptide synthetase (NRPS)-like enzyme	null	-4.728	0.001662	0.01706
AN3346	null	null	-6.6755	0.001662	0.01706
AN3528	Ortholog of A. niger CBS 513.88 : An04g09610, A. oryzae RIB40 : AO090113000188, Aspergillus brasiliensis : Aspbr1_0162074, A. niger ATCC 1015 : 46056-mRNA and Aspergillus flavus NRRL 3357 : AFL2T_08660	null	-6.6755	0.001662	0.01706
AN4451	null	null	-6.6755	0.001662	0.01706
AN5117	null	null	-3.9551	0.001662	0.01706
AN5505	Ortholog of Aspergillus versicolor : Aspve1_0052822 and Aspergillus sydowii : Aspsy1_0046382	null	-6.6755	0.001662	0.01706
AN6441	null	null	-6.6755	0.001662	0.01706
AN7624	Putative alpha-galactosidase with a predicted role in galactose and galactitol metabolism and in degradation of mannans	aglB	-3.9551	0.001662	0.01706

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AN7744	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	null	-4.728	0.001662	0.01706
AN8351	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-4.728	0.001662	0.01706
AN8502	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-6.6755	0.001662	0.01706
AN9028	Has domain(s) with predicted catalytic activity, coenzyme binding, nucleotide binding activity and role in cellular metabolic process	null	-4.728	0.001662	0.01706
AN0311	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	null	-2.1365	0.001673	0.017129
AN6729	Has domain(s) with predicted catalytic activity, molybdenum ion binding, pyridoxal phosphate binding activity	null	3.76442	0.001676	0.017129
AN8496	Has domain(s) with predicted metal ion binding activity	null	-2.6703	0.001676	0.017129
AN1356	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	null	-2.0431	0.001681	0.017152
AN1919	null	null	-2.5065	0.001686	0.017159
AN8662	Ortholog of A. nidulans FGSC A4 : AN11201, A. niger CBS 513.88 : An12g09180, A. oryzae RIB40 : AO090023000027, A. niger ATCC 1015 : 42065-mRNA and Aspergillus versicolor : Aspve1_0031400, Aspve1_0153960	null	-2.5065	0.001686	0.017159
AN10152	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-3.2386	0.001697	0.017213
AN2590	Has domain(s) with predicted FMN binding, heme binding, oxidoreductase activity and role in oxidation-reduction process	null	-3.2386	0.001697	0.017213
AN5155	Ortholog(s) have cytosol, nucleus localization	null	2.36753	0.001699	0.017213
AN6721	Has domain(s) with predicted hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds activity	null	-2.1686	0.001737	0.017554
AN5884	Orotate phosphoribosyltransferase (OPRTase) that catalyzes the fifth step in pyrimidine biosynthesis	pyrF	2.49228	0.00174	0.017554
AN6031	Has domain(s) with predicted nitronate monooxygenase activity and role in oxidation-reduction process	null	-2.2601	0.00174	0.017554
AN10014	null	null	-2.6144	0.001772	0.017851
AN11787	null	null	-2.0073	0.001777	0.017854
AN6558	Ortholog(s) have DNA-directed RNA polymerase activity and role in tRNA transcription from RNA polymerase III promoter, transcription from RNA polymerase I promoter	null	2.18227	0.001778	0.017854

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AN8188	Putative GTP cyclohydrolase I with a predicted role in folate biosynthesis	null	2.39377	0.00178	0.017855
AN1952	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	null	-2.1789	0.001784	0.017868
AN6540	Ortholog(s) have role in RNA processing, anaerobic respiration, positive regulation of mitochondrial RNA catabolic process, regulation of mRNA stability and mitochondrial envelope localization	null	2.6475	0.00181	0.018102
AN11968	Ortholog(s) have 5-amino-6-(5-phosphoribosylamino)uracil reductase activity, role in riboflavin biosynthetic process and cytosol, nucleus localization	null	6.58304	0.00182	0.018102
AN12121	Ortholog(s) have protein tag activity and role in cell budding, cellular response to oxidative stress, invasive growth in response to glucose limitation, protein urmylation, tRNA wobble position uridine thiolation	null	6.54596	0.00182	0.018102
AN4219	Ortholog(s) have DNA-directed RNA polymerase activity and role in tRNA 3'-trailer cleavage, tRNA transcription from RNA polymerase III promoter, termination of RNA polymerase III transcription	null	6.58304	0.00182	0.018102
AN5901	Ortholog(s) have role in DNA-dependent DNA replication, double-strand break repair via break-induced replication and GINS complex, replication fork protection complex localization	null	6.54596	0.00182	0.018102
AN9180	Putative transketolase; intracellular; protein abundance decreased by menadione stress	null	-2.0848	0.001828	0.018153
AN10539	Ortholog(s) have cytoplasm localization	null	2.53856	0.001855	0.018393
AN0490	Putative CTP synthase with a predicted role in pyrimidine metabolism	null	2.06791	0.001859	0.018409
AN6266	Ortholog(s) have nucleus localization	null	2.22793	0.001882	0.018567
AN1474	Ortholog(s) have endoplasmic reticulum localization	null	2.26982	0.001883	0.018567
AN8966	Has domain(s) with predicted neurotransmitter:sodium symporter activity, role in neurotransmitter transport and integral to membrane localization	null	-2.148	0.001883	0.018567
AN7038	Ortholog of A. fumigatus Af293 : Afu4g04090, A. niger CBS 513.88 : An14g00760, A. oryzae RIB40 : AO090206000113, A. niger ATCC 1015 : 41518-mRNA and Aspergillus versicolor : Aspve1_0140874	null	-2.0354	0.00191	0.018809
AN8461	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	null	-1.9958	0.001965	0.019312
AN8049	Ortholog of A. fumigatus Af293 : Afu5g02080, A. oryzae RIB40 : AO090003001313, A. niger ATCC 1015 : 207272-mRNA, Aspergillus versicolor : Aspve1_0139773 and Aspergillus sydowii : Aspsy1_0156853	null	2.26552	0.001967	0.019312
AN9373	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	null	-2.3969	0.001976	0.019374
AN2019	Ortholog of A. oryzae RIB40 : AO090011000511, A. niger ATCC 1015 : 37117-mRNA, Aspergillus flavus NRRL 3357 : AFL2T_05272 and Aspergillus sydowii : Aspsy1_0046222	null	-2.3845	0.001985	0.019407
AN3605	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.3845	0.001985	0.019407

AN1278	Has domain(s) with predicted serine-type endopeptidase inhibitor activity and role in response to wounding	null	-2.3639	0.001995	0.01948
AN7107	Ortholog(s) have nucleolus localization	null	1.99907	0.002005	0.019554
AN6679	Ortholog(s) have SSU rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	null	2.01634	0.002083	0.020279
AN3481	Ortholog of A. fumigatus Af293 : Afu1g02290, A. niger CBS 513.88 : An01g05960, A. oryzae RIB40 : AO090026000175, A. niger ATCC 1015 : 51930-mRNA and Aspergillus versicolor : Aspve1_0039102	null	1.99128	0.002105	0.02047
AN8602	Ortholog of A. fumigatus Af293 : Afu2g00500, A. oryzae RIB40 : AO090023000371, Aspergillus versicolor : Aspve1_0031494 and Aspergillus sydowii : Aspsy1_0060228	null	-2.0761	0.002122	0.020604
AN6639	Putative 2-methylcitrate dehydratase with a predicted role in lysine metabolism	mcdB	-2.1033	0.002161	0.020957
AN3644	Ortholog(s) have protein homodimerization activity, ubiquitin-protein ligase activity and role in cellular response to ionizing radiation, free ubiquitin chain polymerization, postreplication repair, protein K63-linked ubiquitination	null	3.2427	0.002176	0.021003
AN4540	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	3.2427	0.002176	0.021003
AN8682	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	null	3.2427	0.002176	0.021003
AN6250	Ortholog(s) have cytosol, nucleus localization	null	-2.2756	0.002178	0.021003
AN10524	Ortholog(s) have RSC complex, SWI/SNF complex, cytosol localization	null	2.92442	0.002199	0.021144
AN5679	Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex, U6 snRNP, nucleolus, small nucleolar ribonucleoprotein complex localization	null	2.93767	0.002199	0.021144
AN1310	Ortholog(s) have role in secondary metabolic process	null	-2.3534	0.002202	0.021144
AN4581	Ortholog(s) have nucleolus localization	null	2.34161	0.002245	0.021529
AN10526	Arginine methyltransferase	rmtA	2.25734	0.002264	0.021682
AN6139	Putative 1-acylglycerol-3-phosphate acyltransferase with a predicted role in phospholipid metabolism	null	2.38454	0.002269	0.021701
AN6543	Ortholog(s) have adenyl-nucleotide exchange factor activity, role in cytoplasmic translation and cytosolic ribosome, nucleus localization	null	-2.0826	0.002394	0.022637
AN2613	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.2795	0.002394	0.022637
AN8774	Transcript induced in response to calcium dichloride in a CrzA-dependent manner	null	-2.2795	0.002394	0.022637
AN6181	Ortholog(s) have cytosol localization	null	1.97361	0.002401	0.022637
AN0752	Ortholog(s) have DNA-directed RNA polymerase activity, RNA-directed RNA polymerase activity	null	2.26779	0.002401	0.022637

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AN7003	Ortholog(s) have cytosol localization	null	1.98375	0.00244	0.022637
AN5567	Ortholog of A. fumigatus Af293 : Afu1g01530, A. oryzae RIB40 : AO090011000484, Aspergillus brasiliensis : Aspbr1_0038067, N. fischeri NRRL 181 : NFIA_023130 and Aspergillus versicolor : Aspve1_0084207	null	-2.2946	0.002452	0.022637
AN0181	Ortholog of Aspergillus versicolor : Aspve1_0035530	null	-2.7045	0.002454	0.022637
AN0298	Ortholog(s) have RNA binding activity, role in mRNA cleavage, mRNA polyadenylation and mRNA cleavage and polyadenylation specificity factor complex localization	null	-2.5833	0.002454	0.022637
AN10288	null	null	-2.7045	0.002454	0.022637
AN12316	Ortholog(s) have cytosine deaminase activity, role in cytidine metabolic process, cytosine metabolic process, pyrimidine-containing compound salvage and cytoplasm, nucleus localization	null	3.69972	0.002454	0.022637
AN1569	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	null	-2.5833	0.002454	0.022637
AN2276	Has domain(s) with predicted methyltransferase activity, sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity, zinc ion binding activity and role in regulation of transcription, DNA-dependent	null	-2.7045	0.002454	0.022637
AN3113	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	ugtA	3.6775	0.002454	0.022637
AN5110	Ortholog(s) have cytosol, nucleus localization	null	-2.5833	0.002454	0.022637
AN5422	Putative beta-lactamase family protein; intracellular; protein abundance decreased by menadione stress	null	-2.8368	0.002454	0.022637
AN5458	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	null	-2.5833	0.002454	0.022637
AN8223	Protein with a putative role in carbon-starvation response; two ABM motifs; induced by carbon starvation-induced autophagy	null	3.6775	0.002454	0.022637
AN0319	Ortholog of A. fumigatus Af293 : Afu1g02490, A. niger CBS 513.88 : An01g05680, A. oryzae RIB40 : AO090005000843, A. niger ATCC 1015 : 122243-mRNA and Aspergillus versicolor : Aspve1_0067268	null	-3.4024	0.002454	0.022637
AN12353	null	null	-3.1076	0.002454	0.022637
AN2622	Isopenicillin-N synthase with a role in penicillin biosynthesis; expression is negatively regulated by glucose and acidic pH	ipnA	-3.4024	0.002454	0.022637
AN4909	null	null	-3.1076	0.002454	0.022637

AN5633	Ortholog(s) have inorganic cation transmembrane transporter activity, solute:hydrogen symporter activity	null	6.5079	0.002454	0.022637
AN6805	Has domain(s) with predicted substrate-specific transmembrane transporter activity, role in transmembrane transport and integral to membrane localization	null	6.46881	0.002454	0.022637
AN8005	Putative GNAT-type acetyltransferase	ngn9	6.46881	0.002454	0.022637
AN9026	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	null	6.46881	0.002454	0.022637
AN9294	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.46881	0.002454	0.022637
AN8215	Putative methylenetetrahydrofolate reductase (NADPH) with a predicted role in one-carbon metabolism; metA expression is induced by homocysteine; mutation causes methionine auxotrophy	metA	2.91105	0.002489	0.022931
AN11095	Ortholog of A. niger CBS 513.88 : An03g02610, A. niger ATCC 1015 : 45669-mRNA, A. clavatus NRRL 1 : ACLA_008440 and Aspergillus sydowii : Aspsy1_1049915	null	2.47664	0.00251	0.023039
AN5488	null	null	-2.5522	0.002514	0.023039
AN2659	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-2.5006	0.002514	0.023039
AN5342	Protein expressed at increased levels during osmoadaptation	null	-2.5006	0.002514	0.023039
AN9465	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleus localization	null	1.9727	0.002521	0.023071
AN4729	Ortholog of A. fumigatus Af293 : Afu5g09280, A. niger CBS 513.88 : An07g03730, An14g07330, A. oryzae RIB40 : AO090023000535, AO090020000531 and A. niger ATCC 1015 : 180084-mRNA	null	-2.1973	0.002536	0.023179
AN3573	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	null	2.55488	0.002564	0.023355
AN4178	UPF0160 domain-containing protein; intracellular; protein abundance decreased by menadione stress	myg1	2.27988	0.002564	0.023355
AN3635	Ortholog of A. fumigatus Af293 : Afu4g11990, A. niger CBS 513.88 : An01g07270, A. oryzae RIB40 : AO090003001010, A. niger ATCC 1015 : 35965-mRNA and Aspergillus versicolor : Aspve1_0045171	null	2.10881	0.002565	0.023355
AN5737	Has domain(s) with predicted nucleotide binding, oxidoreductase activity and role in oxidation-reduction process	null	-2.1981	0.002675	0.024326
AN2748	Ortholog(s) have cytosol, nucleus localization	null	2.69503	0.002736	0.024813
AN8176	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.69503	0.002736	0.024813

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AN5838	Has domain(s) with predicted FMN binding, NADPH-hemoprotein reductase activity, iron ion binding activity and role in oxidation-reduction process	null	-2.3011	0.002777	0.025123
AN6049	Has domain(s) with predicted zinc ion binding activity	null	-2.3011	0.002777	0.025123
AN4063	Ortholog of A. fumigatus Af293 : Afu1g05380, A. niger ATCC 1015 : 42868-mRNA, Aspergillus versicolor : Aspve1_0054332, Aspergillus sydowii : Aspsy1_0057615 and Aspergillus terreus NIH2624 : ATET_03088	null	-2.9148	0.002801	0.025192
AN6383	Ortholog of A. fumigatus Af293 : Afu1g03300, Afu5g00450, Afu6g10780, A. niger CBS 513.88 : An03g05860, A. oryzae RIB40 : AO090003001528, AO090023001010 and A. niger ATCC 1015 : 47798-mRNA	null	-3.1239	0.002801	0.025192
AN7247	null	null	-2.9148	0.002801	0.025192
AN6940	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-2.0325	0.002803	0.025192
AN0779	Putative glucan 1,3-beta-glucosidase with a predicted role in glucan metabolism	null	-2.0491	0.002803	0.025192
AN10520	Putative alpha/beta hydrolase	null	-2.3087	0.00282	0.025254
AN11133	Has domain(s) with predicted peptidase activity, role in signal peptide processing and integral to membrane, signal peptidase complex localization	null	2.87018	0.00282	0.025254
AN1437	Has domain(s) with predicted zinc ion binding activity and intracellular localization	null	-2.3717	0.00282	0.025254
AN7722	Putative N-acetyltransferase with a predicted role in arginine metabolism	null	1.92822	0.00288	0.025732
AN6658	Has domain(s) with predicted oxidoreductase activity and role in oxidation-reduction process	null	-2.2817	0.002881	0.025732
AN4727	UDP-glucose 4-epimerase, involved in galactose metabolism; converts UDP-galactose to UDP-glucose; intracellular; protein abundance decreased by menadione stress	ugeA	1.97679	0.002888	0.02576
AN4824	Has domain(s) with predicted transferase activity, transferring glycosyl groups activity and membrane localization	null	3.19455	0.002908	0.025906
AN1191	Small ubiquitin-like modifier (SUMO) protein; mutant is viable, slow growing with pleiotropic phenotypes; punctate nucleoplasmic localization at interphase; deletion causes dramatic increase in asperthecin; camptothecin induced transcript	sumO	2.03623	0.002912	0.025906
AN1750	Ortholog(s) have nucleolus localization	null	2.22763	0.002927	0.025932
AN5461	Ortholog of A. fumigatus Af293 : Afu5g00130, A. niger CBS 513.88 : An01g00570, A. niger ATCC 1015 : 170427-mRNA, Aspergillus versicolor : Aspve1_0039792 and Aspergillus sydowii : Aspsy1_0050989	null	-2.2863	0.002934	0.025932
AN10297	Protein with similarity to nonribosomal peptide synthases (NRPS-like); putative acyl CoA synthetase with an NAD-binding domain	null	-2.953	0.00294	0.025932
AN2822	Has domain(s) with predicted transporter activity, role in transmembrane transport, water transport and integral to membrane localization	null	-2.953	0.00294	0.025932

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AN5598	Ortholog(s) have cytosol, nucleus localization	null	-2.953	0.00294	0.025932
AN7684	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-2.791	0.00294	0.025932
AN8793	Putative succinate dehydrogenase (ubiquinone) with a predicted role in the TCA cycle; palA-dependent expression independent of pH	carC	-2.791	0.00294	0.025932
AN5441	Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), rRNA export from nucleus	null	1.93351	0.002963	0.026099
AN3154	Ortholog(s) have RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription, sequence-specific DNA binding activity	null	-2.2916	0.002992	0.026279
AN4456	Ortholog(s) have nucleolus localization	null	2.14691	0.002997	0.026279
AN10214	Ortholog(s) have cytosol localization	null	-2.0401	0.003	0.026279
AN0776	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit localization	null	1.96439	0.003002	0.026279
AN5068	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	null	1.95467	0.003002	0.026279
AN5056	Homologous to ccg-1 from N. crassa; transcript induced by light in in developmentally competent mycelia	null	-2.1583	0.003035	0.026528
AN10614	Ortholog(s) have telomeric DNA binding, triplex DNA binding activity	null	1.93145	0.003151	0.027513
AN0445	Ortholog(s) have RNA binding, structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	1.91071	0.003164	0.027593
AN4475	Ortholog(s) have role in ribosomal large subunit assembly and cytosol localization	null	1.92174	0.003168	0.027595
AN4170	Arrestin domains and PY motif-containing protein with homology to Saccharomyces cerevisiae Rod1p and Rog3p proteins; expression reduced after exposure to farnesol	creD	1.97986	0.003262	0.02837
AN6521	Homoaconitate hydratase, enzyme of the lysine biosynthesis pathway; negatively regulated by the CCAAT-binding complex AnCF (HapB/C/E)	lysF	1.99715	0.003296	0.028601
AN10363	Ortholog of A. fumigatus Af293 : Afu3g08340, A. niger CBS 513.88 : An02g11950, A. oryzae RIB40 : AO090005001445, A. niger ATCC 1015 : 207326-mRNA and Aspergillus versicolor : Aspve1_0127651	null	-2.0185	0.0033	0.028601
AN3452	Ortholog(s) have endoplasmic reticulum localization	null	2.4925	0.003304	0.028601
AN4489	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	null	2.50158	0.003304	0.028601

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AN11281	Ortholog of A. fumigatus Af293 : Afu3g01196, Aspergillus sydowii : Aspsy1_0281282, Aspergillus terreus NIH2624 : ATET_06475 and Aspergillus carbonarius ITEM 5010 : Acar5010_212232	null	6.42864	0.003334	0.028681
AN1747	Ortholog(s) have mitochondrion localization	null	6.42864	0.003334	0.028681
AN3710	Ortholog(s) have role in attachment of spindle microtubules to mitotic chromosome, cellular response to osmotic stress, mitotic cell cycle spindle assembly checkpoint, regulation of mitotic anaphase	null	6.38731	0.003334	0.028681
AN5874	Has domain(s) with predicted methyltransferase activity and role in metabolic process	null	6.38731	0.003334	0.028681
AN6513	Ortholog(s) have tRNA dimethylallyltransferase activity, role in tRNA modification and cytosol, mitochondrion, nucleolus localization	null	6.38731	0.003334	0.028681
AN8545	Has domain(s) with predicted ADP binding, ATP binding, GTP binding, identical protein binding, nucleoside-triphosphatase activity	null	-2.1642	0.003344	0.028733
AN8254	Putative snoRNP complex protein; ortholog of S. cerevisiae Nop10p; expression reduced after exposure to farnesol	nop10	2.28942	0.003369	0.028913
AN3060	Ortholog(s) have tubulin binding activity, role in protein folding, tubulin complex assembly and nucleus, prefoldin complex localization	null	2.63486	0.003415	0.029267
AN2209	Ortholog of A. fumigatus Af293 : Afu5g07010, A. niger CBS 513.88 : An17g00230, A. oryzae RIB40 : AO090701000283, A. niger ATCC 1015 : 45070-mRNA and Aspergillus versicolor : Aspve1_0125550	null	-2.1276	0.003421	0.029286
AN10717	Ortholog(s) have role in mitochondrial respiratory chain complex II assembly and mitochondrion localization	null	-2.0768	0.003441	0.029419
AN11174	Ortholog of A. fumigatus Af293 : Afu7g02120, A. niger CBS 513.88 : An12g00530, A. oryzae RIB40 : AO090038000590, N. fischeri NRRL 181 : NFIA_114850 and Aspergillus flavus NRRL 3357 : AFL2T_07916	null	2.98411	0.003463	0.029503
AN3139	Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.4269	0.003463	0.029503
AN6678	Ortholog(s) have nucleus localization	null	-2.4269	0.003463	0.029503
AN6105	Has domain(s) with predicted carbon-sulfur lyase activity and role in metabolic process	null	-2.1949	0.003476	0.029548
AN2879	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	null	-2.4547	0.003555	0.029548
AN6683	Ortholog of A. nidulans FGSC A4 : AN8537, AN5260, A. fumigatus Af293 : Afu4g06200 and A. niger CBS 513.88 : An12g04370, An11g06510, An14g01260	null	-2.4547	0.003555	0.029548
AN7322	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	null	-2.5585	0.003555	0.029548
AN4397	Ortholog of S. cerevisiae Pcs60p	fatD	-2.2406	0.003578	0.029548

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AN5943	Ortholog of A. nidulans FGSC A4 : AN8548, AN8661, AN4642, A. fumigatus Af293 : Afu3g00850, Afu4g08850 and A. niger CBS 513.88 : An02g13470, An11g00090, An03g01430, An12g09260	null	-2.194	0.003578	0.029548
AN10182	Putative translation initiation factor 3, subunit f (eIF-3f); expression reduced after exposure to farnesol	null	1.94033	0.003591	0.029548
AN10238	Putative GNAT-type acetyltransferase	ngn21	-4.5376	0.003595	0.029548
AN10530	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	null	-6.5073	0.003595	0.029548
AN10836	Has domain(s) with predicted 2 iron, 2 sulfur cluster binding, iron ion binding, oxidoreductase activity, acting on paired donors and with incorporation or reduction of molecular oxygen, more	null	-3.7647	0.003595	0.029548
AN10897	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	null	-6.5073	0.003595	0.029548
AN10898	null	null	-6.5073	0.003595	0.029548
AN11641	Ortholog of Aspergillus versicolor : Aspve1_0117193	null	-6.5073	0.003595	0.029548
AN12487	null	null	-6.5073	0.003595	0.029548
AN1619	Putative 2-methylcitrate dehydratase	mcdA	-3.7647	0.003595	0.029548
AN2023	Ortholog of A. niger CBS 513.88 : An11g07220, An18g00750, An16g04060, A. oryzae RIB40 : AO090001000252, AO090701000624 and A. niger ATCC 1015 : 179170-mRNA, 187809-mRNA, 210569-mRNA	null	-3.7647	0.003595	0.029548
AN2521	ESCRT I complex required for trafficking from the membrane to the vacuoles targeting to vacuole; essential for pH signaling; mutants exhibit fragmented vacuoles	vps23	-6.5073	0.003595	0.029548
AN2605	null	null	-6.5073	0.003595	0.029548
AN3077	null	null	-6.5073	0.003595	0.029548
AN3606	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	null	-6.5073	0.003595	0.029548
AN4009	Has domain(s) with predicted transferase activity, transferring acyl groups other than amino-acyl groups activity and role in metabolic process	null	-4.5376	0.003595	0.029548
AN5172	Ortholog of A. fumigatus Af293 : Afu4g09700, Afu6g07000, A. niger CBS 513.88 : An04g07430, A. oryzae RIB40 : AO090012000946, AO090003001270 and A. niger ATCC 1015 : 53150-mRNA, 57315-mRNA	null	-4.5376	0.003595	0.029548
AN6116	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	null	-6.5073	0.003595	0.029548

AN6242	null	null	-4.5376	0.003595	0.029548
AN6476	null	null	-6.5073	0.003595	0.029548
AN6649	Putative fatty acyl-CoA synthetase	fatC	-6.5073	0.003595	0.029548
AN7046	Putative triacylglycerol lipase with a predicted role in glycerolipid metabolism; mutation confers resistance to undecanoic acid, a fungitoxic medium-chain fatty acid	lipA	-3.7647	0.003595	0.029548
AN8092	Ortholog of Aspergillus versicolor : Aspve1_0034535, Aspergillus sydowii : Aspsy1_0038908, Aspsy1_0527520 and Aspergillus terreus NIH2624 : ATET_08397	null	-6.5073	0.003595	0.029548
AN8956	Has domain(s) with predicted inorganic phosphate transmembrane transporter activity, role in phosphate ion transport and membrane localization	null	-6.5073	0.003595	0.029548
AN9131	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-6.5073	0.003595	0.029548
AN6206	Ortholog of A. fumigatus Af293 : Afu2g11880, A. oryzae RIB40 : AO090026000453, Aspergillus brasiliensis : Aspbr1_0203997, N. fischeri NRRL 181 : NFIA_087110 and A. clavatus NRRL 1 : ACLA_070820	null	-2.1189	0.0036	0.029555
AN0753	Ortholog(s) have cytosol localization	null	1.89367	0.003612	0.02962
AN1157	Putative nuclear pore complex protein	gle1	2.81383	0.003635	0.029676
AN8138	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	aglC	-2.3789	0.003635	0.029676
AN5924	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	null	3.585	0.003636	0.029676
AN8888	Ortholog of A. fumigatus Af293 : Afu8g02680, A. niger ATCC 1015 : 50777-mRNA, Aspergillus versicolor : Aspve1_0034587 and Aspergillus sydowii : Aspsy1_0094518	null	3.56092	0.003636	0.029676
AN3497	Putative cytochrome P450	CYP623B2	-2.0521	0.00366	0.029842
AN8676	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	mcmA	-2.6848	0.00368	0.029963
AN7111	Peroxisomal multifunctional enzyme involved in fatty acid beta-oxidation; required for growth on very long-chain fatty acids; transcription is induced by fatty acids	foxA	-2.2429	0.003692	0.030026
AN10816	Ortholog of A. fumigatus Af293 : Afu8g05030, A. oryzae RIB40 : AO090003001446, AO090009000107, A. niger ATCC 1015 : 188511-mRNA and Aspergillus versicolor : Aspve1_0130291	null	2.38691	0.003701	0.030065
AN4905	theta class glutathione S-transferase; involved in resistance to a variety of xenobiotics and metals; confers susceptibility to the systemic fungicide carboxin	gstA	-1.9228	0.003707	0.030085

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AN1290	Has domain(s) with predicted solute:hydrogen antiporter activity, role in cation transport, transmembrane transport and integral to membrane localization	null	-2.0465	0.003738	0.030263
AN8374	Ortholog(s) have oligopeptide transporter activity and role in oligopeptide transport, vacuole fusion, non-autophagic	null	-2.071	0.003738	0.030263
AN0858	Putative chaperone	hsp104	-1.853	0.003748	0.030308
AN8847	Phosducin-like protein	phnC	2.02826	0.003763	0.030348
AN3876	Ortholog(s) have carnitine transmembrane transporter activity, polyamine transmembrane transporter activity	null	-2.3953	0.003766	0.030348
AN8670	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	null	-2.3228	0.003766	0.030348
AN4297	Has domain(s) with predicted 4 iron, 4 sulfur cluster binding, NADH dehydrogenase (ubiquinone) activity, quinone binding activity and role in oxidation-reduction process	null	1.8653	0.003783	0.030448
AN10983	Ortholog(s) have cytosol, mitochondrion, nucleus localization	null	-1.9761	0.003858	0.031017
AN0246	Ortholog of A. fumigatus Af293 : Afu1g05300, A. niger CBS 513.88 : An01g04570, A. oryzae RIB40 : AO090003000826, A. niger ATCC 1015 : 119367-mRNA and Aspergillus versicolor : Aspve1_0122336	null	3.11057	0.003913	0.031326
AN10790	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	3.12776	0.003913	0.031326
AN11444	Ortholog(s) have hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism activity	null	3.11057	0.003913	0.031326
AN7611	Has domain(s) with predicted catalytic activity, iron-sulfur cluster binding activity	null	2.22074	0.003914	0.031326
AN6865	Ortholog(s) have endoplasmic reticulum, nuclear envelope localization	null	2.18656	0.003923	0.031338
AN6068	Ortholog(s) have role in chromatin remodeling and ASTRA complex, mitochondrion localization	null	2.4556	0.003924	0.031338
AN1345	Ortholog(s) have structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), regulation of translational fidelity	null	1.84481	0.003936	0.031394
AN10477	Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome localization	null	2.47072	0.003955	0.031506
AN10552	Ortholog of A. fumigatus Af293 : Afu4g07060, A. niger CBS 513.88 : An04g01460, A. oryzae RIB40 : AO090023000870, A. niger ATCC 1015 : 44254-mRNA and Aspergillus versicolor : Aspve1_0085132	null	-1.9721	0.003959	0.031506
AN3068	Ortholog of A. fumigatus Af293 : Afu3g09570, A. niger CBS 513.88 : An16g03070, A. niger ATCC 1015 : 49047-mRNA, Aspergillus versicolor : Aspve1_0128162 and Aspergillus sydowii : Aspsy1_0029214	null	1.85275	0.003987	0.031691
AN0708	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	aromA	2.13156	0.004001	0.031768

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AN0890	Ortholog(s) have fungal-type vacuole membrane localization	null	-1.9534	0.004046	0.032086
AN8491	Ortholog(s) have role in ribosomal large subunit biogenesis and cytosol, nucleolus, preribosome, large subunit precursor localization	null	2.01381	0.004125	0.032678
AN0910	Putative phosphatidylserine decarboxylase with a predicted role in phospholipid metabolism; expression reduced after exposure to farnesol	null	1.88934	0.004166	0.032968
AN6202	Putative ribosomal protein L3	rpl3	1.83506	0.004209	0.033269
AN8421	Putative endo-mannanase GH76 family protein	dfgB	2.09205	0.004225	0.033356
AN8095	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-1.9752	0.004247	0.033492
AN10647	Putative cytochrome P450 protein; involved in hyphal branching; mutant branches excessively	ahbB	2.05553	0.004267	0.033557
AN1154	Ortholog(s) have role in ER to Golgi vesicle-mediated transport, protein retention in ER lumen, vesicle organization and ER to Golgi transport vesicle, endoplasmic reticulum localization	null	1.95417	0.004271	0.033557
AN0137	Ortholog(s) have glycerophosphocholine phosphodiesterase activity, role in glycerophospholipid catabolic process and cytosol, ribosome localization	null	-2.2454	0.004278	0.033557
AN8024	Ortholog(s) have cytosol, nucleus localization	null	2.58485	0.004278	0.033557
AN10230	Ortholog(s) have S-methyl-5-thioadenosine phosphorylase activity, mRNA binding activity, role in L-methionine salvage from methylthioadenosine, glutamate biosynthetic process and cytosol, nucleus localization	null	2.4273	0.004281	0.033557
AN1228	Ortholog(s) have role in maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and cytosol, nucleolus, preribosome, large subunit precursor localization	null	1.8629	0.004284	0.033557
AN1270	Putative translation initiation factor 3, subunit h (eIF-3h); expression reduced after exposure to farnesol	null	1.95356	0.00429	0.033569
AN2171	Ortholog(s) have cytosol, nucleus localization	null	-1.9801	0.004393	0.034333
AN11920	Has domain(s) with predicted oxidoreductase activity and role in metabolic process	null	2.35901	0.004445	0.034643
AN6311	Has domain(s) with predicted voltage-gated chloride channel activity, role in chloride transport, transmembrane transport and membrane localization	null	2.34898	0.004445	0.034643
AN5350	Has domain(s) with predicted role in response to stress and integral to membrane localization	null	3.51152	0.004447	0.034643
AN6645	Putative 8-amino-7-oxononanoate synthase with a predicted role in Coenzyme A and pantothenate biosynthesis	bioF	1.94719	0.004534	0.0349
AN8361	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	null	-2.4152	0.004551	0.0349
AN0255	Ortholog of A. fumigatus Af293 : Afu1g03460, A. niger CBS 513.88 : An01g04670, A. oryzae RIB40 : AO090005000754, A. niger ATCC 1015 : 46681-mRNA and Aspergillus versicolor : Aspve1_0078037	null	6.34476	0.004567	0.0349

AN0450	Ortholog(s) have tRNA binding activity and role in protein urmylation, regulation of cell shape, regulation of translational fidelity, tRNA wobble position uridine thiolation	null	6.30092	0.004567	0.0349
AN0562	Has domain(s) with predicted catalytic activity and role in metabolic process	null	6.30092	0.004567	0.0349
AN10487	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	-2.957	0.004567	0.0349
AN10627	Has domain(s) with predicted GTP binding, GTPase activity, structural molecule activity, role in GTP catabolic process, microtubule-based movement, protein polymerization and microtubule localization	null	6.34476	0.004567	0.0349
AN10703	Has domain(s) with predicted nucleotide binding, oxidoreductase activity, zinc ion binding activity and role in oxidation-reduction process	null	-3.2518	0.004567	0.0349
AN12059	Ortholog(s) have tRNA-specific adenosine deaminase activity, role in tRNA modification and cytoplasm, nucleus localization	null	6.30092	0.004567	0.0349
AN12392	Ortholog of A. fumigatus Af293 : Afu8g01920, Aspergillus brasiliensis : Aspbr1_0134398, N. fischeri NRRL 181 : NFIA_095530, A. clavatus NRRL 1 : ACLA_043940 and Aspergillus versicolor : Aspve1_0034524	null	-2.957	0.004567	0.0349
AN1285	Endo-beta-1,4-glucanase A; cellulase involved in degradation of glucans; expression induced by carboxymethylcellulose and cellobiose	eglA	6.30092	0.004567	0.0349
AN3143	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	null	-3.2518	0.004567	0.0349
AN4419	Ortholog(s) have protein tyrosine phosphatase activity and role in ascospore wall assembly, cAMP-mediated signaling, meiosis, protein dephosphorylation, ribosomal large subunit assembly	null	6.30092	0.004567	0.0349
AN8003	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	null	6.34476	0.004567	0.0349
AN8136	Ortholog of Aspergillus versicolor : Aspve1_0202914 and Aspergillus sydowii : Aspsy1_0072548	null	-2.957	0.004567	0.0349
AN8828	Ortholog(s) have Rab guanyl-nucleotide exchange factor activity, role in ER to Golgi vesicle-mediated transport and TRAPP complex, cytosol, nucleus localization	null	6.34476	0.004567	0.0349
AN9481	Ortholog of A. fumigatus Af293 : Afu5g09380, A. oryzae RIB40 : AO090020000555, A. niger ATCC 1015 : 40034-mRNA, Aspergillus versicolor : Aspve1_0141435 and Aspergillus sydowii : Aspsy1_0093275	null	6.34476	0.004567	0.0349
AN10525	Ortholog of A. fumigatus Af293 : Afu1g05820, A. niger ATCC 1015 : 143807-mRNA, Aspergillus versicolor : Aspve1_0138953 and Aspergillus sydowii : Aspsy1_0046943	null	1.8601	0.00457	0.0349
AN0465	Ortholog of S. cerevisiae RPS8A and RPS8B; palA-dependent expression independent of pH	null	1.81734	0.00461	0.035158
AN11085	Putative D-arabinitol 4-dehydrogenaset	null	-2.8468	0.004624	0.035158

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AN11149	Has domain(s) with predicted arylsulfatase activity and role in phenol-containing compound metabolic process	null	-2.8468	0.004624	0.035158
AN6579	Ortholog of A. fumigatus Af293 : Afu6g04470, A. niger CBS 513.88 : An15g01120, A. oryzae RIB40 : AO090701000109, A. niger ATCC 1015 : 40387-mRNA and Aspergillus versicolor : Aspve1_0197429	null	-2.8468	0.004624	0.035158
AN8870	Expression increased in salt-adapted strains	null	1.80979	0.004641	0.035255
AN10681	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation, regulation of translational fidelity and cytosolic large ribosomal subunit localization	null	1.82184	0.004665	0.035396
AN3309	Putative alpha-amylase with a predicted role in starch metabolism	amyG	2.32675	0.004698	0.035575
AN0807	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	laeA	-2.2518	0.004709	0.035575
AN6682	Ortholog(s) have oxidized purine nucleobase lesion DNA N-glycosylase activity, role in base-excision repair, AP site formation and mitochondrion localization	null	2.75518	0.004709	0.035575
AN10392	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	-2.7902	0.004724	0.035575
AN11038	Has domain(s) with predicted carbohydrate binding, carbon-oxygen lyase activity and role in amino sugar catabolic process, carbohydrate metabolic process	null	-2.9993	0.004724	0.035575
AN6797	null	null	-2.7902	0.004724	0.035575
AN7776	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	null	-2.9993	0.004724	0.035575
AN10878	Ortholog(s) have role in ER to Golgi vesicle-mediated transport, vesicle fusion with Golgi apparatus and ER to Golgi transport vesicle, endoplasmic reticulum membrane, integral to Golgi membrane localization	null	2.04629	0.004741	0.035662
AN3075	Zinc finger protein of unknown function; overexpression confers the "fluffy" phenotype	oefC	-1.9836	0.004747	0.035668
AN4787	Putative ribosomal protein L37; palA-dependent expression independent of pH	rpl37	1.80983	0.004759	0.035721
AN3799	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	null	2.57208	0.004796	0.035964
AN2081	Ortholog(s) have GTPase regulator activity and cytosol, nucleus localization	null	2.92632	0.004811	0.035995
AN2129	Subunit 5 of the COP9 signalosome (CSN) responsible for cleaving the ubiquitin-like protein Nedd8 from cullin-RING E3 ubiquitin ligases; required for normal cleistothecia development; mutants impaired in secondary metabolism	csnE	2.92632	0.004811	0.035995

AN8857	Ortholog(s) have role in cellular bud site selection, mRNA splicing, via spliceosome and U2 snRNP, spliceosomal complex localization	null	2.43714	0.004846	0.036219
AN2387	Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, flavin adenine dinucleotide binding activity and role in oxidation-reduction process	null	1.8555	0.004896	0.036553
AN1455	Ortholog(s) have dolichyl-diphosphooligosaccharide-protein glycotransferase activity, role in protein N-linked glycosylation and oligosaccharyltransferase complex localization	null	1.85112	0.004935	0.036809
AN0843	Ortholog(s) have structural constituent of ribosome activity, role in rRNA export from nucleus and 90S preribosome, cytosolic small ribosomal subunit, nucleolus localization	null	1.80694	0.004948	0.036868
AN4223	Has domain(s) with predicted sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity and role in regulation of transcription, DNA-dependent	null	-1.865	0.004954	0.036874
AN2547	Putative polyketide synthase; required for emericellamide biosynthesis	easB	-2.256	0.00498	0.036987
AN4715	null	null	-2.256	0.00498	0.036987
AN7937	Protein responsive to Concanamycin A	cipC	1.84065	0.004987	0.037001
AN4580	Has domain(s) with predicted 7S RNA binding, endoplasmic reticulum signal peptide binding activity and role in SRP-dependent cotranslational protein targeting to membrane, negative regulation of translational elongation	null	2.12367	0.005035	0.037319
AN11721	Ortholog(s) have 5'-flap endonuclease activity, ATP-dependent DNA helicase activity, single-stranded DNA specific endodeoxyribonuclease activity, telomeric DNA binding activity	null	-2.0366	0.005101	0.037768
AN5782	Has domain(s) with predicted catalytic activity and role in metabolic process	null	-1.8864	0.005152	0.038104
AN8812	Has domain(s) with predicted ATP binding, ATPase activity, phosphatidylinositol phospholipase C activity and role in intracellular signal transduction, lipid metabolic process	null	-1.995	0.005177	0.038248
AN5648	Has domain(s) with predicted Rho GTPase binding, actin binding activity and role in actin cytoskeleton organization	null	3.05772	0.005302	0.038643
AN4202	Predicted ribosomal protein of the large (60S) ribosomal subunit; differentially expressed during sexual development	rpl16a	1.78366	0.005313	0.038643
AN6191	Ortholog(s) have cytoplasm localization	null	2.01675	0.005346	0.038643
AN7795	Putative heterotrimeric G-protein coupled receptor component; contains both a 7-transmembrane domain and an RGS signaling domain	gprK	-1.8399	0.005364	0.038643
AN0349	Ortholog(s) have role in protein refolding and mitochondrial matrix localization	null	2.72494	0.005369	0.038643
AN0561	Ortholog(s) have mitochondrion localization	null	2.059	0.00537	0.038643
AN6823	Ortholog of A. fumigatus Af293 : Afu5g12860, A. niger CBS 513.88 : An14g06360, A. oryzae RIB40 : AO090120000406, A. niger ATCC 1015 : 201762-mRNA and Aspergillus versicolor : Aspve1_0122523	null	-2.1911	0.005382	0.038643
AN0649	Putative long-chain-fatty-acid-CoA ligase with a predicted role in fatty acid metabolism	null	-6.3169	0.005402	0.038643

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AN10346	Putative cutinase with a predicted role in the hydrolysis of cutin	null	-6.3169	0.005402	0.038643
AN10447	Has domain(s) with predicted transferase activity, transferring acyl groups activity	null	-6.3169	0.005402	0.038643
AN11188	Ortholog(s) have role in endocrocin biosynthetic process and cytosol, nucleus localization	null	-6.3169	0.005402	0.038643
AN11850	null	null	-6.3169	0.005402	0.038643
AN11896	Ortholog of A. fumigatus Af293 : Afu1g16564, N. fischeri NRRL 181 : NFIA_008860, A. clavatus NRRL 1 : ACLA_019010, Aspergillus versicolor : Aspve1_0275963 and A. fumigatus A1163 : AFUB_015920	null	-6.3169	0.005402	0.038643
AN13001	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	null	-6.3169	0.005402	0.038643
AN2121	Has domain(s) with predicted proline racemase activity	null	-6.3169	0.005402	0.038643
AN2542	Putative pectate lyase with a predicted role in the degradation of pectin	plyD	-6.3169	0.005402	0.038643
AN2956	Ortholog of Aspergillus versicolor : Aspve1_0081721 and Aspergillus sydowii : Aspsy1_0087389	null	-6.3169	0.005402	0.038643
AN3849	Has domain(s) with predicted protein disulfide oxidoreductase activity and outer membrane-bounded periplasmic space localization	null	-6.3169	0.005402	0.038643
AN4256	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	null	-6.3169	0.005402	0.038643
AN4812	Predicted glycosylphosphatidylinositol (GPI)-anchored protein	null	-6.3169	0.005402	0.038643
AN4829	Putative reductase with a predicted role in carbohydrate metabolism	null	-6.3169	0.005402	0.038643
AN5432	Has domain(s) with predicted serine-type peptidase activity and role in proteolysis	null	-6.3169	0.005402	0.038643
AN5489	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	null	-6.3169	0.005402	0.038643
AN5765	Ortholog of A. fumigatus Af293 : Afu2g09480, A. oryzae RIB40 : AO090011000718, N. fischeri NRRL 181 : NFIA_084970, Aspergillus flavus NRRL 3357 : AFL2T_05450 and Aspergillus versicolor : Aspve1_0072730	null	-6.3169	0.005402	0.038643
AN6135	Has domain(s) with predicted coenzyme binding, nucleotide binding, phosphogluconate dehydrogenase (decarboxylating) activity and role in pentose-phosphate shunt	null	-6.3169	0.005402	0.038643
AN7452	null	null	-6.3169	0.005402	0.038643
AN7775	Has domain(s) with predicted role in response to stress and integral to membrane localization	null	-6.3169	0.005402	0.038643
AN7895	Putative oxidoreductase; contains Zn-dependent alcohol dehydrogenase domain; protein expressed at increased levels during osmoadaptation	cipB	-6.3169	0.005402	0.038643
AN8457	Has domain(s) with predicted microtubule motor activity, role in nucleoside metabolic process and kinesin complex localization	null	-6.3169	0.005402	0.038643

AN8460	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	null	-6.3169	0.005402	0.038643
AN9038	Has domain(s) with predicted role in Mo-molybdopterin cofactor biosynthetic process	null	-6.3169	0.005402	0.038643
AN10924	Ortholog(s) have tRNA adenylyltransferase activity, role in tRNA 3'-terminal CCA addition and mitochondrial matrix localization	null	2.18758	0.005428	0.038796
AN11253	Has domain(s) with predicted transferase activity, transferring phosphorus-containing groups activity	null	3.46036	0.005457	0.038841
AN1566	Ortholog(s) have cytosol, nucleus localization	null	3.48616	0.005457	0.038841
AN4769	ATP sulfurylase involved in sulfate assimilation; mutants are resistant to selenate	sC	3.48616	0.005457	0.038841
AN6078	Adenine deaminase with a role in nucleotide salvage pathways; induced by ammonium, uric acid and adenosine; nadA mRNA levels regulated by UaY and AreA; ortholog of Saccharomyces cerevisiae Aah1p and Schizosaccharomyces pombe dea2	nadA	-2.513	0.005457	0.038841
AN6082	Ortholog(s) have pre-mRNA 5'-splice site binding, structural constituent of ribosome activity, role in negative regulation of mRNA splicing, via spliceosome, rRNA processing and cytosol localization	null	1.8127	0.005463	0.038846
AN8253	Ortholog(s) have cytosol, nucleus localization	null	2.30019	0.005522	0.039226
AN11053	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	null	-2.0902	0.00568	0.040306
AN3413	Protein with homology to ribosomal protein S2 and S5; ortholog of S. cerevisiae Rps2p; expression reduced after exposure to farnesol	null	1.78132	0.005735	0.040654
AN4602	Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and nucleus, polysome, prefoldin complex localization	null	1.93793	0.005764	0.040769
AN8755	Methylisocitrate lyase; predicted role in the glyoxylate shunt; mitochondrial localization signal predicted	mclA	-1.7735	0.005767	0.040769
AN6891	Ortholog of A. fumigatus Af293 : Afu5g13330, A. niger CBS 513.88 : An14g04740, A. oryzae RIB40 : AO090120000478, A. niger ATCC 1015 : 211185-mRNA and Aspergillus versicolor : Aspve1_0120830	null	1.80945	0.005768	0.040769
AN2035	Putative polyketide synthase; involved in secondary metabolite production	pkhB	-2.5701	0.005834	0.04111
AN5509	Putative F-box protein	null	-2.5701	0.005834	0.04111
AN5796	Ortholog of A. fumigatus Af293 : Afu6g06328, A. niger ATCC 1015 : 188103-mRNA, Aspergillus versicolor : Aspve1_0042541, Aspergillus sydowii : Aspsy1_0056900 and Aspergillus terreus NIH2624 : ATET_07402	null	-2.5701	0.005834	0.04111

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AN4803	Ortholog(s) have rRNA binding, structural constituent of ribosome activity and role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), positive regulation of translational fidelity	null	1.78325	0.005844	0.041139
AN0369	Has domain(s) with predicted aminopeptidase activity, metalloexopeptidase activity and role in cellular process, proteolysis	null	-1.7629	0.005894	0.041447
AN5192	Putative fatty acyl-CoA synthetase with a predicted role in very long-chain fatty acid metabolism	fatA	-1.958	0.006041	0.042351
AN9103	Putative apoptosis-inducing factor (AIF)-like mitochondrial oxidoreductase; mutants display decreased survival in the presence of farnesol or menadione, decreased electron transport; expression upregulated after exposure to farnesol	aifA	2.08439	0.006041	0.042351
AN9460	Ortholog(s) have peptidase activity, role in protein targeting to ER, signal peptide processing and signal peptidase complex localization	null	2.07774	0.006041	0.042351
AN6564	Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit localization	null	1.89733	0.006074	0.042543
AN1421	Ortholog of A. fumigatus Af293 : Afu8g04170, A. niger CBS 513.88 : An16g08920, A. oryzae RIB40 : AO090103000032, A. niger ATCC 1015 : 194006-mRNA and Aspergillus versicolor : Aspve1_0037181	null	2.69405	0.006131	0.04288
AN6866	Putative chorismate mutase with a predicted role in aromatic amino acid biosynthesis	aroC	2.11046	0.006134	0.04288
AN5996	Ortholog(s) have cytosol localization	null	1.75426	0.006144	0.042904
AN4912	Ortholog(s) have Golgi apparatus, cell division site, cell tip localization	null	3.02138	0.006189	0.043129
AN8505	Ortholog of Aspergillus brasiliensis : Aspbr1_0111846, A. fumigatus A1163 : AFUB_075260, A. niger ATCC 1015 : 199457-mRNA and Aspergillus aculeatus ATCC16872 : Aacu16872_050877	null	-2.261	0.006189	0.043129
AN10468	Has domain(s) with predicted metal ion transmembrane transporter activity, role in metal ion transport, transmembrane transport and membrane localization	null	-1.9176	0.006211	0.043244
AN1198	Putative aminomethyltransferase with a predicted role in glycine, serine, and threonine metabolism	null	-1.7752	0.006306	0.043507
AN0203	Ortholog(s) have role in chromatin remodeling and ASTRA complex, cytosol localization	null	6.20903	0.006311	0.043507
AN0908	Ortholog(s) have DNA binding, bending and RNA polymerase III type 1 promoter sequence-specific DNA binding, more	null	6.25571	0.006311	0.043507
AN10332	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.25571	0.006311	0.043507
AN10401	Ortholog of A. nidulans FGSC A4 : AN6780, A. fumigatus Af293 : Afu7g01210, A. niger ATCC 1015 : 194249-mRNA and Aspergillus versicolor : Aspve1_0039423, Aspve1_0128644	null	6.20903	0.006311	0.043507
AN11823	Has domain(s) with predicted role in transmembrane transport and integral to membrane localization	null	6.20903	0.006311	0.043507

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AN6604	Ortholog(s) have ATPase activity, tRNA binding activity, role in tRNA modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	6.20903	0.006311	0.043507
AN6910	null	null	6.25571	0.006311	0.043507
AN7832	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	null	6.25571	0.006311	0.043507
AN8754	Putative asparagine synthase with a predicted role in asparagine metabolism	null	6.20903	0.006311	0.043507
AN11411	Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit, nucleus localization	null	1.81965	0.006322	0.043538
AN1814	null	null	-1.8904	0.006358	0.043745
AN1732	Proline transporter; localized to plasma membrane, mislocalized in shrA null mutant; expression is regulated by carbon and nitrogen repression; negatively regulated by CreA	prnB	2.25548	0.006447	0.044267
AN4512	Ortholog of A. fumigatus Af293 : Afu2g03155, A. niger CBS 513.88 : An07g07580, A. oryzae RIB40 : AO090120000271, A. niger ATCC 1015 : 199982-mRNA and Aspergillus versicolor : Aspve1_0171018	null	2.26617	0.006447	0.044267
AN4148	Sugar transporter; transcriptionally induced by growth on xylose	null	-1.8271	0.006455	0.044282
AN1718	Ortholog of A. nidulans FGSC A4 : AN1714, A. fumigatus Af293 : Afu4g08380, Afu4g08420, A. niger CBS 513.88 : An04g03190, An04g03210 and A. oryzae RIB40 : AO090023000718	null	-1.8304	0.006519	0.044675
AN8943	Ortholog of A. fumigatus Af293 : Afu2g00900, Afu6g11560, A. niger CBS 513.88 : An01g11690, An05g02420, An03g01300 and A. oryzae RIB40 : AO090113000175, AO090023000422	null	1.86416	0.006567	0.044963
AN6576	Ortholog(s) have oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen activity and role in L-methionine salvage from methylthioadenosine	null	1.94023	0.006623	0.045277
AN0953	Ortholog(s) have cytosol, nucleus localization	null	-2.1859	0.006626	0.045277
AN6625	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	null	-1.9483	0.006693	0.045523
AN4087	Putative 40S ribosomal protein subunit; ortholog of S. cerevisiae Rps3p; expression reduced after exposure to farnesol	null	1.8112	0.006693	0.045523
AN1802	Ortholog(s) have role in mRNA splicing, via spliceosome and U1 snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snRNP localization	null	2.14163	0.006695	0.045523
AN10875	Ortholog(s) have Golgi apparatus, endoplasmic reticulum, fungal-type vacuole membrane localization	null	3.40733	0.006718	0.045523
AN1275	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	null	3.40733	0.006718	0.045523

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AN1832	N-glycosylated membrane protein, immunodominant antigen in sera from aspergilloma patients; repressed by bafilomycin; production increases under zinc-limiting conditions	aspnd1	3.43409	0.006718	0.045523
AN3921	Ortholog of A. fumigatus Af293 : Afu6g08430, A. niger CBS 513.88 : An11g01600, A. niger ATCC 1015 : 199092-mRNA, Aspergillus versicolor : Aspve1_0117555 and Aspergillus sydowii : Aspsy1_0122151	null	3.43409	0.006718	0.045523
AN12027	Ortholog(s) have cytosol, nucleus localization	null	-2.3579	0.00674	0.045523
AN1444	Ortholog of A. fumigatus Af293 : Afu8g04320, A. niger CBS 513.88 : An16g08740, A. niger ATCC 1015 : 214477-mRNA, Aspergillus versicolor : Aspve1_0037193 and Aspergillus sydowii : Aspsy1_0055850	null	2.84549	0.00674	0.045523
AN2760	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	null	2.82456	0.00674	0.045523
AN4048	Ortholog(s) have role in regulation of mitotic metaphase/anaphase transition and cytosol, nucleus localization	null	2.82456	0.00674	0.045523
AN7363	Has domain(s) with predicted catalytic activity and role in nucleoside metabolic process	null	-2.2672	0.00674	0.045523
AN10443	Has domain(s) with predicted catalytic activity and role in base-excision repair	null	2.46557	0.006798	0.04587
AN0138	Ortholog(s) have cytosol, nucleus localization	null	2.05082	0.006829	0.046038
AN4864	Putative glucosyltransferase; locus contains the conserved upstream open reading frame (uORF) AN4864-uORF	alg6	1.83914	0.006966	0.046858
AN6621	Ortholog of A. nidulans FGSC A4 : AN7403, A. fumigatus Af293 : Afu8g01810, A. niger CBS 513.88 : An05g02280, A. oryzae RIB40 : AO090026000198 and A. niger ATCC 1015 : 135939-mRNA	null	1.76672	0.006968	0.046858
AN12246	Ortholog(s) have cytosol localization	null	1.7428	0.006971	0.046858
AN11123	Putative transmenbrane-containing nuclear pore complex protein with homology to Schizosaccharomyces pombe Pom34	pom34	2.07419	0.006994	0.046925
AN9406	Putative 2,N2-dimethylguanosine tRNA methyltransferase; mutants are self-sterile	trm1	2.07419	0.006994	0.046925
AN10324	Putative neddylation machinery protein; constitutively expressed during all stages of the fungal life cycle	ubcL	1.92433	0.007021	0.047061
AN2980	Ortholog(s) have structural constituent of ribosome activity, role in cytoplasmic translation and cytosolic large ribosomal subunit, nucleolus localization	null	1.7491	0.007072	0.047355
AN4758	Ortholog(s) have role in apoptotic process and cytoplasm, nucleus localization	null	1.86187	0.007089	0.047428
AN5800	Ortholog(s) have cytosol localization	null	1.72828	0.007123	0.047605
AN4300	NADH-ubiquinone oxidoreductase 21.3 kDa subunit; protein levels decrease in response to farnesol	null	1.74114	0.007132	0.04762
AN10832	Ortholog(s) have role in protein urmylation, regulation of transcription from RNA polymerase II promoter, tRNA wobble uridine modification and Elongator holoenzyme complex, cytosol, nucleus localization	null	1.9413	0.00715	0.047696

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AN0381	Ortholog(s) have unfolded protein binding activity, role in protein folding and chaperonin-containing T-complex, nucleus localization	null	1.74931	0.007207	0.048032
AN1124	Ortholog of A. fumigatus Af293 : Afu1g11720, A. niger CBS 513.88 : An08g03680, A. oryzae RIB40 : AO090038000251, A. niger ATCC 1015 : 208202-mRNA and Aspergillus versicolor : Aspve1_0288823	null	-1.9489	0.007241	0.048167
AN8756	Has domain(s) with predicted monooxygenase activity and role in oxidation-reduction process	null	-1.9818	0.007241	0.048167
AN3748	Putative ATP phosphoribosyltransferase with a predicted role in histidine metabolism	null	1.93486	0.007268	0.048298
AN0314	Putative aspartyl-tRNA synthetase with a predicted role in tRNA aminoacylation; expression upregulated after exposure to farnesol	null	-1.7398	0.007316	0.048573
AN11977	null	null	-1.9263	0.007333	0.048609
AN0123	Ortholog(s) have mitochondrion localization	null	2.33146	0.007342	0.048609
AN0623	Has domain(s) with predicted flavin adenine dinucleotide binding, long-chain-alcohol oxidase activity and role in oxidation-reduction process	null	-2.0706	0.00735	0.048609
AN7434	Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-dependent and nucleus localization	null	-2.1285	0.00735	0.048609
AN11778	Putative exoinulinase	null	-1.7562	0.007356	0.048609
AN12482	Ortholog of Aspergillus flavus NRRL 3357 : AFL2T_05996	null	-2.4907	0.007428	0.048897
AN1772	Type B feruloyl esterase	null	-2.3789	0.007428	0.048897
AN3104	Putative allantoicase with a predicted role in purine metabolism	null	-2.2752	0.007428	0.048897
AN8531	Ortholog(s) have trans-aconitate 3-methyltransferase activity and cytosol localization	null	-2.4907	0.007428	0.048897
AN3813	Ortholog(s) have copper uptake transmembrane transporter activity, role in copper ion import and integral to plasma membrane localization	null	1.82164	0.007474	0.049157
AN12452	Has domain(s) with predicted phosphotransferase activity, for other substituted phosphate groups activity, role in phospholipid biosynthetic process and membrane localization	null	1.99263	0.007509	0.049342
AN10416	Putative 60s ribosomal protein similar to subunits L15 and L27; ortholog of S. cerevisiae RPL28; expression reduced after exposure to farnesol; palA-dependent expression independent of pH	null	1.74317	0.007544	0.049523
AN0046	Putative histidyl-tRNA synthetase with a predicted role in tRNA aminoacylation; intracellular, menadione stress-induced protein; expression reduced after exposure to farnesol	null	1.72742	0.007571	0.049655
AN6923	Putative high-affinity hexose transporter with a predicted role in hexose transport; induced upon starvation and during sexual development	hxtA	-2.009	0.007578	0.049655
AN11137	Ortholog of Aspergillus brasiliensis : Aspbr1_0132849, A. niger ATCC 1015 : 204582-mRNA, N. fischeri NRRL 181 : NFIA_037530, Aspergillus acidus : Aspfo1_0144659 and Aspergillus versicolor : Aspve1_0344287	null	1.75466	0.007598	0.04974

AN0933	Putative transglycosidase with a predicted role in glucan processing; predicted glycosyl phosphatidylinositol (GPI)-anchor	crhC	-1.7828	0.007626	0.049878
AN0074	Ortholog(s) have role in nuclear division, rRNA processing and nuclear periphery, nucleolus, preribosome, large subunit precursor, spindle pole body localization	null	2.45168	0.007651	0.049993

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Supplementary Table 4.

Groups of genes regulated by nitrogen and/or carbon source in the wild type strain.
Expressions decreased (↓), increased (↑) or not changed (-) in the presence of ammonium or glucose, respectively.

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Number of genes in the group	**587**	**574**	**532**	**406**	**275**	**153**	**141**	**141**	**134**	**125**	**119**	**93**	**63**	**61**
"Expression profile codes" for groups of genes (compare Fig. 1B)	- - ↑ -	- - ↓ -	- ↑ ↑ -	- ↓ ↓ -	- - ↓ ↓	- - - ↓	- ↓ - -	- ↑ - -	- - ↑ ↑	- ↓ ↓ ↓	- - - ↑	- ↑ - ↓	- ↑ ↑ ↑	- ↓ - ↑
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AN8251
AN8256
AN8267
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AN8340
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AN9315
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19	**15**	**8**	**7**	**5**	**4**	**4**	**3**	**3**	**3**	**3**	**2**	**2**	**2**
↓ – ↑ –	– ↑ ↑ ↓	↓ – – ↓	↓ – ↓ ↓	– ↓ ↓ ↑	↓ ↓ – –	↓ – – –	↑ – – ↑	↑ – ↓ –	↓ ↑ ↑ –	↑ ↑ – ↓	– ↑ ↓ ↓	↑ – – –	↓ ↑ ↑ ↓
AN0300	AN0858	AN0319	AN0483	AN11174	AN3400	AN0960	AN3479	AN10638	AN0402	AN11233	AN2583	AN3531	AN0404
AN0374	AN10507	AN10626	AN1628	AN2748	AN5941	AN1515	AN6729	AN4949	AN0403	AN3961	AN7287	AN8011	AN8540
AN0418	AN11574	AN3079	AN3627	AN3681	AN6881	AN4870	AN7937	AN8490	AN7800	AN7108			
AN0609	AN2530	AN5056	AN4339	AN8223	AN7324	AN6274							
AN0701	AN2613	AN5489	AN5939	AN9103									
AN11064	AN3555	AN7990	AN6118										
AN11121	AN3797	AN8539	AN9288										
AN1181	AN4480	AN9285											
AN1831	AN5781												
AN2390	AN6236												
AN3159	AN6543												
AN3160	AN8374												
AN3357	AN8602												
AN7323	AN9173												
AN7801	AN9297												
AN7922													
AN8647													
AN8652													
AN8913													

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2	**1**	**1**	**1**	**1**	**1**
↑↑↓↓	↑↓ ↓↑	↓ – ↑ ↑	↓ – ↑ ↓	↓ ↓ ↑ –	↓ ↓ ↓ –
AN1792 AN4822	AN6525	AN1832	AN7322	AN7539	AN6005

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Supplementary Table 5a.

Functional enrichment analysis for genes regulated by ammonium under carbon repressing conditions (glucose as a carbon source) in the wild type strain

Only clusters comprising at lest 5 genes and corrected P - value <0.05 are shown

GOID	GO term	Cluster frequency	Background frequency	Corrected P-value	Genes annotated to the term
6875	cellular metal ion homeostasis	5 out of 65 genes, 7.7%	85 out of 10988 background genes, 0.8%	0.01891	sidI:enaB:aspnd1:AN7801:mirB
55065	metal ion homeostasis	5 out of 65 genes, 7.7%	89 out of 10988 background genes, 0.8%	0.02350	sidI:enaB:aspnd1:AN7801:mirB
30003	cellular cation homeostasis	5 out of 65 genes, 7.7%	97 out of 10988 background genes, 0.9%	0.03519	sidI:enaB:aspnd1:AN7801:mirB
55080	cation homeostasis	5 out of 65 genes, 7.7%	102 out of 10988 background genes, 0.9%	0.04446	sidI:enaB:aspnd1:AN7801:mirB
98771	inorganic ion homeostasis	5 out of 65 genes, 7.7%	102 out of 10988 background genes, 0.9%	0.04446	sidI:enaB:aspnd1:AN7801:mirB
6873	cellular ion homeostasis	5 out of 65 genes, 7.7%	104 out of 10988 background genes, 0.9%	0.04864	sidI:enaB:aspnd1:AN7801:mirB

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Supplementary Table 5b.

Functional enrichment analysis for genes regulated by ammonium under carbon derepressing conditions (fructose as a carbon source) in the wild type strain

Only clusters comprising at lest 5 genes and corrected P - value <0.05 are shown

GOID	GO term	Cluster frequency	Background frequency	Corrected P-value	Genes annotated to the term
44281	small molecule metabolic process	280 out of 1601 genes, 17.5%	967 out of 10988 background genes, 8.8%	8.48e-31	AN0034:pdiB:antA:AN0270:aroG:xyrA:AN0451:AN0551:aldA:pyrABCN:AN0593:basA:AN0649:spdA:AN0688:AN0705:AN0720:mns1B:scdA:AN0840:uaY:adB:AN0912:AN0918:ladA:atp20:AN0949:AN1003:niiA:ureB:pyrD:AN10287:AN10290:AN10298:afoE:odeA:AN10475:AN1050:mthA:AN10619:AN10648:AN10663:AN1071:AN10710:AN10762:AN10863:AN10903:bzuA:AN11008:AN11015:AN11045:AN11110:AN11303:AN11347:qutG:qutB:AN12152:AN12201:sasA:AN12331:pgkA:AN1274:xprG:AN1524:abfB:AN1593:oliC:hxB:AN1673:AN1685:AN1715:prnC:artC:otaA:AN1857:AN1858:AN1860:AN1868:AN1883:fahA:AN1898:hpdA:pdmA:AN1923:AN1990:AN1993:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:pkhB:AN2144:AN2208:gatA:alcC:AN2316:aclA:aclB:AN2440:AN2509:AN2526:gpdC:acvA:pgmB:fbaA:agaA:AN2914:AN2951:gsdA:AN3031:suAprgA1:AN3058:ugmA:AN3222:pfkA:AN3276:pkiB:micA:AN3431:AN3586:AN3626:AN3639:mns1A:alcB:AN3829:ileA:AN3840:AN3865:AN3866:AN3881:AN3954:gmdA:CYP61A1:AN4055:AN4094:AN4126:sdeB:glnA:AN4258:AN4323:ladB:palA:metR:AN4401:metH

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19752	carboxylic acid metabolic process	170 out of 1601 genes, 10.6%	547 out of 10988 background genes, 5.0%	6.56e-21	antA:aroG:aldA:pyrABCN:AN0593:basA:AN0649:spdA:AN0705:AN0720:scdA:AN0840:adB:AN0912:AN0918:AN0949:AN1003:AN10287:AN10298:odeA:AN10475:AN1050:mthA:AN10619:AN10863:bzuA:AN11045:AN11110:qutB:sasA:AN12331:pgkA:xprG:AN1524:AN1673:prnC:artC:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1923:AN1990:AN1993:pkhB:AN2208:gatA:alcC:aclA:aclB:AN2509:AN2526:gpdC:acvA:fbaA:agaA:AN2914:AN3031:suAprgA1:AN3058:pfkA:AN3276:pkiB:AN3431:alcB:AN3829:ileA:AN3840:AN3865:AN3866:AN3954:gmdA:AN4055:AN4126:sdeB:glnA:AN4323:palA:metR:AN4401:metH:fmdS:mccB:mccA:AN4739:sA:gtaA:AN4830:pdcA:AN4901:AN5000:mdhB:gltA:pdhB:lysB:pkiA:AN5447:AN5601:AN5610:AN5731:acuN:pcsA:ldhA:pdkA:echA:AN5990:faaA:swoM:AN6048:accA:maeA:AN6209:AN6227:trpB:ppoB:AN6346:AN6399:AN6506:aciA:AN6526:AN6555:biA:acuE:sdeA:tpiA:AN6973:hadA:metG:foxA:AN7278:acuL:cpeA:hisHF:hxkA:AN7479:AN7600:AN7722:pyroA:AN7770:stcK:stcA:gpdA:phacA:AN8099:citA:cy

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43436	oxoacid metabolic process	172 out of 1601 genes, 10.7%	564 out of 10988 background genes, 5.1%	3.57e-20	antA:aroG:aldA:pyrABCN:AN0593:basA:AN0649:spdA:AN0705:AN0720:scdA:AN0840:adB:AN0912:AN0918:AN0949:AN1003:niiA:AN10287:AN10298:odeA:AN10475:AN1050:mthA:AN10619:AN10863:bzuA:AN11045:AN11110:qutB:sasA:AN12331:pgkA:xprG:AN1524:AN1673:prnC:artC:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1923:AN1990:AN1993:pkhB:AN2208:gatA:alcC:aclA:aclB:AN2509:AN2526:gpdC:acvA:fbaA:agaA:AN2914:AN3031:suAprgA1:AN3058:pfkA:AN3276:pkiB:AN3431:alcB:AN3829:ileA:AN3840:AN3865:AN3866:AN3954:gmdA:AN4055:AN4126:sdeB:glnA:AN4323:palA:metR:AN4401:metH:fmdS:mccB:mccA:AN4739:sA:gtaA:AN4830:pdcA:AN4901:AN5000:mdhB:gltA:pdhB:lysB:pkiA:AN5447:AN5601:AN5610:AN5731:acuN:sidA:pcsA:ldhA:pdkA:echA:AN5990:faaA:swoM:AN6048:accA:maeA:AN6209:AN6227:trpB:ppoB:AN6346:AN6399:AN6506:aciA:AN6526:AN6555:biA:acuE:sdeA:tpiA:AN6973:hadA:metG:foxA:AN7278:acuL:cpeA:hisHF:hxkA:AN7479:AN7600:AN7722:pyroA:AN7770:stcK:stcA:gpdA:phacA:AN8

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6082 organic acid metabolic process	173 out of 1601 genes, 10.8%	569 out of 10988 background genes, 5.2%	3.81e-20	antA:aroG:aldA:pyrABCN:AN0593:basA:AN0649:spdA:AN0705:AN0720:scdA:AN0840:adB:AN0912:AN0918:AN0949:AN1003:niiA:AN10287:AN10298:odeA:AN10475:AN1050:mthA:AN10619:AN10863:bzuA:AN11045:AN11110:qutB:sasA:AN12331:pgkA:xprG:AN1524:AN1673:prnC:artC:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1923:AN1990:AN1993:pkhB:AN2208:gatA:alcC:aclA:aclB:AN2509:AN2526:gpdC:acvA:fbaA:agaA:AN2914:AN3031:suAprgA1:AN3058:pfkA:AN3276:pkiB:AN3431:alcB:AN3829:ileA:AN3840:AN3865:AN3866:AN3954:gmdA:AN4055:AN4126:sdeB:glnA:AN4323:palA:metR:AN4401:metH:fmdS:mccB:mccA:AN4739:sA:gtaA:AN4830:pdcA:AN4901:AN5000:mdhB:gltA:pdhB:lysB:pkiA:AN5447:AN5601:AN5610:AN5731:acuN:sidA:pcsA:ldhA:pdkA:echA:AN5990:faaA:swoM:AN6048:accA:maeA:AN6209:AN6227:trpB:ppoB:AN6346:AN6399:AN6506:aciA:AN6526:AN6555:biA:acuE:sdeA:tpiA:AN6973:hadA:metG:foxA:AN7278:acuL:AN7331:cpeA:hisHF:hxkA:AN7479:AN7600:AN7722:pyroA:AN7770:stcK:stcA:gpdA:ph

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44283	small molecule biosynthetic process	130 out of 1601 genes, 8.1%	410 out of 10988 background genes, 3.7%	3.36e-16	AN0270:aroG:AN0451:aldA:AN0593:basA:spdA:AN0840:AN0912:AN0918:AN0949:AN10290:AN10298:afoE:odeA:AN10648:AN10663:AN10710:AN10762:AN11008:qutB:AN12152:AN12201:AN12331:pgkA:AN1524:AN1673:prnC:artC:AN1857:AN1858:AN1860:AN1883:fahA:hpdA:pdmA:AN1923:AN1990:AN1993:pkhB:alcC:AN2509:AN2526:gpdC:acvA:fbaA:AN2914:AN3031:suAprgA1:AN3058:AN3222:pfkA:AN3276:pkiB:AN3586:ileA:AN3840:AN3954:gmdA:CYP61A1:AN4094:AN4126:sdeB:glnA:AN4323:palA:AN4401:metH:AN4569:fmdS:mccA:AN4757:sA:pdcA:AN5000:gltA:pdhB:lysB:pkiA:AN5497:AN5566:AN5601:AN5610:AN5731:acuN:sidA:ldhA:swoM:AN6048:accA:AN6141:pyrG:AN6227:trpB:sidF:sidD:ppoB:AN6346:AN6506:AN6555:biA:sdeA:tpiA:AN6973:metG:AN7146:hisHF:hxkA:AN7469:AN7600:AN7625:AN7722:pyroA:stcK:stcA:AN8012:
72521	purine-containing compound metabolic process	64 out of 1601 genes, 4.0%	144 out of 10988 background genes, 1.3%	6.05e-15	AN0593:uaY:adB:atp20:AN10298:AN10903:AN11303:AN11347:pgkA:AN1524:AN1593:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:AN3222:pfkA:AN3626:AN3639:AN3954:metH:purH:AN4525:AN4603:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:AN81
9259	ribonucleotide metabolic process	59 out of 1601 genes, 3.7%	128 out of 10988 background genes, 1.2%	1.48e-14	AN0593:adB:atp20:AN11303:AN11347:pgkA:AN1593:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpd

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9150	purine ribonucleotide metabolic process	57 out of 1601 genes, 3.6%	123 out of 10988 background genes, 1.1%	3.93e-14	AN0593:adB:atp20:AN11303:AN11347:pgkA:AN1593:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:AN8118:citA
6163	purine nucleotide metabolic process	57 out of 1601 genes, 3.6%	125 out of 10988 background genes, 1.1%	9.90e-14	AN0593:adB:atp20:AN11303:AN11347:pgkA:AN1593:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:AN8118:citA
19693	ribose phosphate metabolic process	63 out of 1601 genes, 3.9%	147 out of 10988 background genes, 1.3%	1.01e-13	AN0593:AN0688:adB:atp20:AN11303:AN11347:pgkA:AN1593:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:gpdC:fbaA:gsdA:pfkA:AN3626:AN3639:AN3954:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpdA:AN8118:citA:AN8551:alc

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46394	carboxylic acid biosynthetic process	94 out of 1601 genes, 5.9%	273 out of 10988 background genes, 2.5%	1.13e-13	aroG:aldA:basA:spdA:AN0840:AN0912:AN0918:AN0949:AN10298:odeA:qutB:AN12331:pgkA:AN1524:AN1673:prnC:AN1857:AN1858:AN1883:fahA:hpdA:AN1923:AN1990:AN1993:pkhB:AN2509:AN2526:gpdC:acvA:fbaA:AN2914:AN3031:suAprgA1:AN3058:pfkA:AN3276:pkiB:ileA:AN3840:AN3954:gmdA:AN4126:sdeB:glnA:AN4323:palA:AN4401:metH:fmdS:mccA:sA:pdcA:AN5000:gltA:pdhB:lysB:pkiA:AN5601:AN5610:AN5731:acuN:ldhA:swoM:AN6048:accA:AN6227:trpB:ppoB:AN6346:AN6506:AN6555:biA:sdeA:tpiA:AN6973:metG:hisHF:hxkA:AN7600:AN7722:pyroA:stcK:stcA:gpdA:phacA:cysD:
16053	organic acid biosynthetic process	94 out of 1601 genes, 5.9%	274 out of 10988 background genes, 2.5%	1.48e-13	aroG:aldA:basA:spdA:AN0840:AN0912:AN0918:AN0949:AN10298:odeA:qutB:AN12331:pgkA:AN1524:AN1673:prnC:AN1857:AN1858:AN1883:fahA:hpdA:AN1923:AN1990:AN1993:pkhB:AN2509:AN2526:gpdC:acvA:fbaA:AN2914:AN3031:suAprgA1:AN3058:pfkA:AN3276:pkiB:ileA:AN3840:AN3954:gmdA:AN4126:sdeB:glnA:AN4323:palA:AN4401:metH:fmdS:mccA:sA:pdcA:AN5000:gltA:pdhB:lysB:pkiA:AN5601:AN5610:AN5731:acuN:ldhA:swoM:AN6048:accA:AN6227:trpB:ppoB:AN6346:AN6506:AN6555:biA:sdeA:tpiA:AN6973:metG:hisHF:hxkA:AN7600:AN7722:pyroA:stcK:stcA:gpdA:phacA:cysD:
9161	ribonucleoside monophosphate metabolic process	49 out of 1601 genes, 3.1%	100 out of 10988 background genes, 0.9%	4.09e-13	adB:atp20:AN11303:AN11347:pgkA:oliC:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3954:purH:AN4525:mccA:AN4739:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gp

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55114	oxidation-reduction process	209 out of 1601 genes, 13.1%	850 out of 10988 background genes, 7.7%	9.41e-13	antA:AN0330:AN0403:xyrA:AN0443:aldA:AN0593:AN0628:basA:AN0740:AN0774:scdA:AN0836:lccD:AN0895:AN0912:AN0918:ladA:AN0949:AN10026:AN1003:niiA:AN10108:AN10223:AN10229:CYP532A4:AN10290:AN10296:AN10358:odeA:mthA:AN10585:AN10648:AN10703:acdB:AN10863:CYP578B1:bzuA:AN11008:AN11045:AN11090:AN11094:AN11177:AN11347:qutB:AN11861:acdA:AN1274:AN1310:phacB:codA:AN1510:AN1524:AN1593:CYP620E1:AN1699:CYP5128A1:prnC:artC:AN1752:AN1868:hpdA:pdmA:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:pkhB:CYP552A2:AN2042:AN2197:AN2208:alcC:AN2316:AN2387:aclA:aclB:AN2526:gpdC:AN2704:AN2801:AN2835:gpxA:AN2866:pgmB:gsdA:AN3027:AN3030:suAprgA1:AN3043:AN3068:AN3139:AN3205:AN3239:CYP567E1:AN3399:AN3573:AN3586:AN3591:alcB:AN3829:CYP539D1:AN3920:AN3954:AN3973:AN4003:CYP61A1:AN4064:CYP660A1:AN4126:sdeB:AN4268:ladB:AN4525:AN4569:ivdA:sA:AN4822:pdcA:AN4975:AN5030:mdhB:AN5130:gltA:pdhB:lysB:pkiA:AN5228:AN5338:AN5435:AN5497:AN5601:AN5610:CYP531D2:AN5690:AN5838:ldhA:AN5846
9123	nucleoside monophosphate metabolic process	49 out of 1601 genes, 3.1%	102 out of 10988 background genes, 0.9%	1.13e-12	adB:atp20:AN11303:AN11347:pgkA:oliC:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3954:purH:AN4525:mccA:AN4739:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gp

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1901566	organonitrogen compound biosynthetic process	227 out of 1601 genes, 14.2%	951 out of 10988 background genes, 8.7%	1.60e-12	AN0116:AN0128:AN0142:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0465:AN0470:aldA:pyrABCN:AN0570:basA:spdA:AN0705:AN0776:mns1B:AN0840:AN0843:adB:AN0907:AN0912:atp20:AN1013:pyrD:AN10290:AN10298:AN10416:AN10475:AN10681:AN10762:AN1084:AN11080:AN1122:AN11303:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN12201:AN12246:AN1228:pgkA:AN1345:AN1524:AN1565:oliC:hxB:AN1673:prnC:AN1798:AN1857:AN1858:AN1883:fahA:hpdA:AN1915:AN1923:AN1964:AN1990:AN1993:URFA3:atp8:oliA:AN20013:atp9:AN2057:hemA:AN2301:AN2509:AN2526:gpdC:acvA:AN2734:gpxA:fbaA:AN2914:AN2932:AN2980:AN2997:AN3031:suAprgA1:AN3058:AN3172:AN3222:pfkA:AN3413:AN3431:AN3595:AN3626:AN3639:AN3823:ileA:AN3832:AN3840:AN3865:AN3920:AN3954:gmdA:rps16:AN4073:AN4087:AN4126:glnA:rpl16a:AN4218:AN4222:pcmA:AN4258:AN4323:barA:palA:chsF:AN4401:metH:AN4452:purH:AN4475:AN4494:AN4522:fmdS:AN4594:ssz1:mccA:ugeA:AN4739:sA:AN4777:AN4794:AN4802:AN4803:AN4830:cnxH:ubi1:pdcA:AN4916:AN5000:AN5014:AN5122:hsp70:AN5130:gltA:pdh
9126	purine nucleoside monophosphate metabolic process	47 out of 1601 genes, 2.9%	96 out of 10988 background genes, 0.9%	1.74e-12	adB:atp20:AN11303:AN11347:pgkA:oliC:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3954:purH:AN4525:mccA:AN4739:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:AN8118:al

9167	purine ribonucleoside monophosphate metabolic process	47 out of 1601 genes, 2.9%	96 out of 10988 background genes, 0.9%	1.74e-12	adB:atp20:AN11303:AN11347:pgkA:oliC:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3626:AN3954:purH:AN4525:mccA:AN4739:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:AN8118:al
17144	drug metabolic process	107 out of 1601 genes, 6.7%	344 out of 10988 background genes, 3.1%	2.71e-12	AN0270:aldA:uaY:adB:atp20:AN1003:AN10290:afoE:AN10762:AN10838:bzuA:AN11015:AN11233:AN11303:AN11347:sasA:AN12279:AN12331:pgkA:abfB:oliC:AN1685:fahA:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:pkhB:gatA:alcC:AN2316:aclA:aclB:gpdC:acvA:gpxA:fbaA:suAprgA1:AN3058:pfkA:pmeA:AN3829:AN3840:AN3954:AN4126:pcmA:palA:chsF:metH:AN4525:AN4603:mccA:chiB:pdcA:mdhB:gltA:pdhB:pkiA:AN5447:AN5497:AN5669:acuN:pcsA:ldhA:swoM:AN6141:AN6209:ppoB:aciA:biA:acuE:tpiA:metG:rglA:AN7278:acuL:hxkA:AN7469:AN7600:AN7661:pyroA:abnC:gpdA:phacA:AN8118:citA:cysD

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8152	metabolic process	790 out of 1601 genes, 49.3%	4435 out of 10988 background genes, 40.4%	3.55e-12	AN0034:rabS:AN0094:AN0116:AN0126:AN0128:AN0142:AN0179:AN0191:AN0224:ivoB:pdiB:antA:AN0262:AN0270:AN0278:AN0330:aroG:AN0403:xyrA:AN0433:AN0443:AN0445:AN0451:AN0465:AN0470:engA:AN0507:AN0551:aldA:pyrABCN:AN0570:AN0574:AN0591:AN0593:AN0628:basA:AN0649:AN0661:AN0666:spdA:AN0688:AN0695:AN0705:AN0714:AN0716:AN0720:AN0740:AN0770:AN0774:AN0776:mns1B:AN0804:swd1:scdA:AN0836:AN0840:AN0843:hsp104:lccD:uaY:adB:AN0895:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN10005:AN10024:AN10026:AN1003:niiA:ureB:AN10108:AN10122:AN1013:pyrD:AN10164:culA:env7:AN10213:AN10223:AN10229:AN10258:CYP532A4:AN10287:AN10290:AN10296:AN10297:AN10298:AN10331:afoE:AN10351:AN10358:odeA:AN10416:ggtA:AN1045:AN10475:bglF:AN10491:AN1050:mthA:AN10517:AN10523:AN10585:AN10618:AN10619:AN10648:AN10663:AN10681:AN10703:AN1071:AN10710:AN10712:AN10762:AN10805:ffkB:acdB:AN10838:AN1084:AN10863:CYP578B1:AN10875:AN10880:AN10903:AN10906:AN10910:AN10921:bzuA:AN10952:AN10957:AN10964:AN1099
9117	nucleotide metabolic process	71 out of 1601 genes, 4.4%	194 out of 10988 background genes, 1.8%	2.27e-11	AN0593:AN0688:adB:atp20:pyrD:AN10663:AN11303:AN11347:pgkA:AN1593:oliC:hxB:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:fbaA:gsdA:AN3222:pfkA:AN3431:AN3626:AN3639:AN3954:AN4258:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpdA:AN8118:ndxC:ci

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46034	ATP metabolic process	39 out of 1601 genes, 2.4%	75 out of 10988 background genes, 0.7%	3.76e-11	atp20:AN11303:AN11347:pgkA:oliC:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3954:AN4525:mccA:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:AN8118:alcA
9199	ribonucleoside triphosphate metabolic process	41 out of 1601 genes, 2.6%	82 out of 10988 background genes, 0.7%	4.69e-11	atp20:AN11303:AN11347:pgkA:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3954:AN4525:mccA:cnxH:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:AN8118:alcA
9205	purine ribonucleoside triphosphate metabolic process	41 out of 1601 genes, 2.6%	82 out of 10988 background genes, 0.7%	4.69e-11	atp20:AN11303:AN11347:pgkA:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3954:AN4525:mccA:cnxH:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:AN8118:alcA
6753	nucleoside phosphate metabolic process	71 out of 1601 genes, 4.4%	199 out of 10988 background genes, 1.8%	1.00e-10	AN0593:AN0688:adB:atp20:pyrD:AN10663:AN11303:AN11347:pgkA:AN1593:oliC:hxB:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:fbaA:gsdA:AN3222:pfkA:AN3431:AN3626:AN3639:AN3954:AN4258:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpdA:AN8118:ndxC:ci
9144	purine nucleoside triphosphate metabolic process	41 out of 1601 genes, 2.6%	84 out of 10988 background genes, 0.8%	1.34e-10	atp20:AN11303:AN11347:pgkA:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3954:AN4525:mccA:cnxH:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:AN8118:alcA

44249	cellular biosynthetic process	340 out of 1601 genes, 21.2%	1640 out of 10988 background genes, 14.9%	1.82e-10	AN0094:AN0116:AN0142:ivoB:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0451:AN0465:AN0470:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0661:spdA:AN0705:AN0716:AN0720:AN0776:mns1B:AN0836:AN0840:AN0843:uaY:adB:AN0907:AN0912:AN0913:AN0918:atp20:AN0949:AN1013:pyrD:AN10213:AN10290:AN10298:AN10331:afoE:odeA:AN10416:AN10475:AN10491:AN10517:AN10648:AN10663:AN10681:AN10710:AN10762:AN1084:AN10906:AN10910:AN10957:AN11003:AN11008:AN11080:AN11093:AN11112:AN11161:AN11212:AN1122:AN11303:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11961:AN12152:AN12201:sasA:AN12246:AN1228:AN12331:AN12419:pgkA:AN1345:AN1524:AN1565:AN1593:oliC:hxB:AN1673:AN1715:prnC:artC:AN1798:nosA:AN1857:AN1858:AN1860:AN1883:fahA:AN1898:hpdA:pdmA:AN1915:AN1923:vosA:AN1964:AN1976:AN1990:AN1993:URFA3:atp8:oliA:AN20013:atp9:pkhB:AN2057:bipA:AN2235:amdA:AN2283:hemA:alcC:AN2301:H4.2:AN2509:AN2526:gpdC:acvA:AN2677:AN2734:AN2780:gpxA:pgmB:fbaA:AN2914:AN2932:AN2980:AN2997:AN3031:suAprgA1:AN3058:

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1901576	organic substance biosynthetic process	343 out of 1601 genes, 21.4%	1668 out of 10988 background genes, 15.2%	4.46e-10	AN0094:AN0116:AN0128:AN0142:ivoB:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0451:AN0465:AN0470:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0661:spdA:AN0705:AN0716:AN0776:mns1B:AN0836:AN0840:AN0843:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1013:pyrD:AN10213:AN10290:AN10298:AN10331:afoE:odeA:AN10416:AN10475:AN10491:AN10517:AN10648:AN10663:AN10681:AN10710:AN10762:AN1084:AN10906:AN10910:AN10957:AN11003:AN11008:AN11080:AN11093:AN11112:AN11161:AN11212:AN1122:AN11303:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11961:AN12152:AN12201:sasA:AN12246:AN1228:AN12331:AN12419:pgkA:AN1345:AN1524:AN1565:AN1593:oliC:hxB:AN1673:AN1715:prnC:artC:AN1798:nosA:AN1857:AN1858:AN1860:AN1883:fahA:AN1898:hpdA:pdmA:AN1915:AN1923:vosA:AN1964:AN1976:AN1990:AN1993:URFA3:atp8:oliA:AN20013:atp9:pkhB:AN2057:bipA:AN2235:amdA:AN2283:hemA:alcC:AN2301:H4.2:AN2509:AN2526:gpdC:acvA:AN2677:AN2734:AN2780:gpxA:pgmB:fbaA:AN2914:AN2932:AN2980:AN2997:AN3031:suAprgA1:

For Peer Review

For Peer Review

9058	biosynthetic process	355 out of 1601 genes, 22.2%	1742 out of 10988 background genes, 15.9%	5.51e-10	AN0094:AN0116:AN0128:AN0142:ivoB:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0451:AN0465:AN0470:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0661:spdA:AN0705:AN0716:AN0720:AN0776:mns1B:AN0836:AN0840:AN0843:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1013:pyrD:AN10213:AN10290:AN10298:AN10331:afoE:odeA:AN10416:AN10475:AN10491:AN10517:AN10648:AN10663:AN10681:AN10710:AN10762:AN1084:AN10906:AN10910:AN10957:AN11003:AN11008:AN1102:AN11080:AN11093:AN11112:AN11161:AN11212:AN1122:AN11303:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11961:AN12152:AN12201:sasA:AN12246:AN1228:AN12331:AN12419:pgkA:AN1345:AN1524:AN1565:AN1593:oliC:hxB:AN1673:AN1715:prnC:artC:AN1798:nosA:AN1857:AN1858:AN1860:AN1883:fahA:AN1898:hpdA:pdmA:AN1915:AN1923:vosA:AN1964:AN1976:AN1990:AN1993:URFA3:atp8:oliA:AN20013:atp9:pkhB:AN2057:bipA:AN2235:amdA:AN2283:hemA:alcC:AN2301:H4.2:AN2509:AN2526:gpdC:acvA:AN2677:AN2734:AN2780:gpxA:pgmB:fbaA:AN2914:AN2932:AN2980:AN2997:AN

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55086	nucleobase-containing small molecule metabolic process	85 out of 1601 genes, 5.3%	267 out of 10988 background genes, 2.4%	5.71e-10	pyrABCN:AN0593:AN0688:uaY:adB:atp20:pyrD:AN10298:AN10663:AN1071:AN10710:AN10903:AN11303:AN11347:pgkA:AN1524:AN1593:oliC:hxB:AN1715:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:pgmB:fbaA:gsdA:AN3222:pfkA:AN3431:AN3626:AN3639:AN3881:AN3954:AN4258:metH:purH:AN4525:AN4603:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:faaA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:AN8019:gpdA:AN811
32787	monocarboxylic acid metabolic process	81 out of 1601 genes, 5.1%	250 out of 10988 background genes, 2.3%	7.27e-10	antA:aldA:basA:AN0649:spdA:scdA:AN0912:AN0918:AN0949:AN10287:odeA:AN1050:mthA:bzuA:AN11045:qutB:pgkA:xprG:AN1990:AN2208:gatA:alcC:gpdC:acvA:fbaA:suAprgA1:pfkA:AN3276:pkiB:AN3829:AN3954:AN4055:AN4126:sdeB:palA:AN4401:mccA:AN4830:pdcA:AN5000:pdhB:pkiA:AN5447:acuN:pcsA:ldhA:pdkA:echA:AN5990:faaA:swoM:accA:ppoB:AN6506:aciA:AN6555:biA:acuE:sdeA:tpiA:AN6973:hadA:foxA:acuL:cpeA:hxkA:AN7770:stcK:stcA:gpdA:phacA:faaB:pdcB:AN8907:alcP:alcA

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71704	organic substance metabolic process	622 out of 1601 genes, 38.9%	3414 out of 10988 background genes, 31.1%	7.68e-10	AN0034:AN0094:AN0116:AN0126:AN0128:AN0142:AN0191:AN0224:ivoB:pdiB:antA:AN0262:AN0270:AN0278:aroG:xyrA:AN0433:AN0445:AN0451:AN0465:AN0470:engA:AN0507:AN0551:aldA:pyrABCN:AN0570:AN0593:basA:AN0649:AN0661:spdA:AN0688:AN0695:AN0705:AN0714:AN0716:AN0720:AN0770:AN0776:mns1B:AN0804:swd1:scdA:AN0836:AN0840:AN0843:hsp104:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1003:niiA:ureB:AN1013:pyrD:AN10164:culA:env7:AN10213:AN10258:AN10287:AN10290:AN10298:AN10331:afoE:AN10351:odeA:AN10416:ggtA:AN1045:AN10475:bglF:AN10491:AN1050:mthA:AN10517:AN10523:AN10618:AN10619:AN10648:AN10663:AN10681:AN1071:AN10710:AN10712:AN10762:ffkB:AN10838:AN1084:AN10863:AN10880:AN10903:AN10906:AN10910:AN10921:bzuA:AN10957:AN10994:AN11003:AN11008:AN11015:AN1102:AN11045:AN11060:AN11080:AN11093:AN11110:AN11112:AN11133:AN11161:AN11212:AN1122:AN11233:AN11303:AN11347:qutG:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11903:AN11959:AN11961:AN1197:AN12121:AN1215:AN1215
9141	nucleoside triphosphate metabolic process	41 out of 1601 genes, 2.6%	88 out of 10988 background genes, 0.8%	9.65e-10	atp20:AN11303:AN11347:pgkA:oliC:hxB:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pfkA:AN3954:AN4525:mccA:cnxH:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:AN8118:alcA

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1901605	alpha-amino acid metabolic process	65 out of 1601 genes, 4.1%	183 out of 10988 background genes, 1.7%	1.48e-09	aldA:pyrABCN:AN0593:spdA:AN0720:AN0840:AN0912:AN10298:AN10863:sasA:prnC:artC:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1923:AN1990:AN1993:gatA:AN2509:agaA:AN2914:AN3031:AN3058:AN3431:AN3829:ileA:gmdA:glnA:AN4323:AN4401:metH:mccB:mccA:sA:gtaA:AN4901:gltA:lysB:AN5447:AN5601:AN5610:echA:AN6048:trpB:AN6399:metG:AN7278:hisHF:AN7722:pyroA:cysD:cysA:AN8709:AN8770:amdS:AN8866:alcR
1901564	organonitrogen compound metabolic process	362 out of 1601 genes, 22.6%	1818 out of 10988 background genes, 16.5%	8.67e-09	AN0116:AN0128:AN0142:AN0224:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0465:AN0470:aldA:pyrABCN:AN0570:AN0593:basA:spdA:AN0688:AN0705:AN0720:AN0770:AN0776:mns1B:swd1:AN0840:AN0843:hsp104:uaY:adB:AN0907:AN0912:AN0918:atp20:ureB:AN1013:pyrD:culA:env7:AN10258:AN10290:AN10298:AN10351:AN10416:ggtA:AN10475:AN10681:AN1071:AN10762:ffkB:AN10838:AN1084:AN10863:AN10880:AN10903:AN10994:AN1102:AN11080:AN11110:AN11133:AN1122:AN11233:AN11303:AN11347:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11903:AN11961:AN12121:AN12201:sasA:AN12246:AN12279:AN1228:pgkA:AN1320:AN1345:AN1426:codA:AN1524:csnD:AN1565:AN1593:oliC:hxB:AN1673:prnC:artC:AN1780:AN1798:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1915:AN1923:AN1964:AN1976:AN1982:AN1990:AN1993:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:AN20013:oxiA:atp9:ndhC:oxiB:AN2057:bipA:csnE:AN2144:cct1:gatA:hemA:alcC:AN2301:AN2316:H4.2:AN2440:AN2509:AN2526:AN2555:gpdC:acvA:AN2731:AN2734:gpxA:fbaA:agaA:AN2914:AN29

19637	organophosphate metabolic process	96 out of 1601 genes, 6.0%	332 out of 10988 background genes, 3.0%	1.01e-08	AN0270:pyrABCN:AN0593:basA:AN0688:AN0716:adB:AN0913:AN0918:ladA:atp20:pyrD:AN10213:AN10663:AN10921:AN11161:AN11303:AN11347:qutG:AN11959:pgkA:AN1593:oliC:hxB:AN1685:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:pgmB:fbaA:gsdA:AN3222:pfkA:AN3276:AN3431:AN3626:AN3639:AN3954:AN4258:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:AN5888:AN5919:faaA:swoM:AN6141:pyrG:AN6209:AN6541:AN6610:tpiA:AN7385:hxkA:AN7469:AN7
6520	cellular amino acid metabolic process	85 out of 1601 genes, 5.3%	280 out of 10988 background genes, 2.5%	1.02e-08	aroG:aldA:pyrABCN:AN0593:spdA:AN0705:AN0720:AN0840:AN0912:AN10298:AN10475:AN10863:AN11110:qutB:sasA:AN1673:prnC:artC:otaA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1923:AN1990:AN1993:gatA:AN2509:AN2526:agaA:AN2914:AN3031:AN3058:AN3431:AN3829:ileA:AN3865:AN3866:gmdA:AN4126:glnA:AN4323:metR:AN4401:metH:fmdS:mccB:mccA:sA:gtaA:AN4901:gltA:lysB:AN5447:AN5601:AN5610:AN5731:echA:AN6048:AN6227:trpB:AN6346:AN6399:AN6526:metG:AN7278:hisHF:AN7479:AN7600:AN7722:pyroA:cy
6091	generation of precursor metabolites and energy	56 out of 1601 genes, 3.5%	152 out of 10988 background genes, 1.4%	1.04e-08	AN1003:AN10585:AN11347:pgkA:oliC:artC:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:aclA:aclB:gpdC:pgmB:fbaA:ippA:suAprgA1:AN3068:pfkA:AN3954:AN4064:AN4525:mccA:pdcA:mdhB:AN5088:pdhB:pkiA:AN5497:AN5669:acuN:ldhA:AN5888:swoM:cycA:AN6255:AN6297:tpiA:hxkA:gpdA:AN8118:AN8273:

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44238	primary metabolic process	560 out of 1601 genes, 35.0%	3085 out of 10988 background genes, 28.1%	6.21e-08	AN0034:AN0094:AN0116:AN0126:AN0128:AN0142:AN0191:AN0224:antA:AN0262:AN0278:aroG:xyrA:AN0433:AN0445:AN0451:AN0465:AN0470:engA:AN0507:AN0551:aldA:pyrABCN:AN0570:AN0593:basA:AN0649:AN0661:spdA:AN0688:AN0695:AN0705:AN0714:AN0716:AN0720:AN0770:AN0776:mns1B:AN0804:swd1:scdA:AN0840:AN0843:hsp104:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1003:AN1013:pyrD:AN10164:culA:env7:AN10213:AN10258:AN10287:AN10298:AN10331:AN10351:odeA:AN10416:AN1045:AN10475:bglF:AN10491:AN1050:mthA:AN10517:AN10523:AN10618:AN10648:AN10663:AN10681:AN1071:AN10710:AN10712:ffkB:AN10838:AN1084:AN10863:AN10880:AN10903:AN10906:AN10910:AN10921:AN10957:AN10994:AN11003:AN11008:AN1102:AN11060:AN11080:AN11093:AN11110:AN11112:AN11133:AN11161:AN11212:AN1122:AN11233:AN11303:AN11347:qutG:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11903:AN11959:AN11961:AN1197:AN12121:AN1215:sasA:AN12246:AN12279:AN1228:AN12419:AN12429:pgkA:AN1274:AN1320:AN1345:xprG:AN1426:AN1477:A
72522	purine-containing compound biosynthetic process	37 out of 1601 genes, 2.3%	85 out of 10988 background genes, 0.8%	1.55e-07	adB:atp20:AN10298:AN11303:pgkA:AN1524:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:AN3222:pfkA:AN3626:AN3639:AN3954:metH:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA:pdhC:panK
9260	ribonucleotide biosynthetic process	35 out of 1601 genes, 2.2%	78 out of 10988 background genes, 0.7%	1.77e-07	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpdA:pdhC:panK

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5975	carbohydrate metabolic process	120 out of 1601 genes, 7.5%	472 out of 10988 background genes, 4.3%	2.73e-07	AN0034:xyrA:engA:AN0551:AN0688:mns1B:AN0912:ladA:bglF:AN10710:AN10838:AN11233:qutG:AN11802:AN1197:AN12279:pgkA:AN1274:xprG:AN1477:xgcA:abfB:AN1685:AN1715:AN1772:AN1868:AN1870:vosA:bipA:AN2208:alcC:AN2325:AN2395:AN2424:aclB:AN2533:gpdC:bglK:pgmB:fbaA:AN2951:gsdA:AN3013:ugmA:ugtA:AN3200:pfkA:AN3360:pmeA:mns1A:alcB:AN3764:agnB:AN3954:AN4003:exgC:AN4055:pcmA:hxkC:ladB:mccA:ugeA:AN4822:AN4825:chiB:pdcA:mdhB:pdhB:pkiA:AN5414:acuN:AN5748:ldhA:agsA:AN5917:bglG:swoM:AN6128:amyE:AN6405:AN6518:acuE:tpiA:AN6985:foxA:rglA:AN7275:mutA:cpeA:bglM:glaB:hxkA:agdD:AN7590:AN7625:AN7708:bxlD:bglJ:eglC:abnC:gpdA:AN8068:aglC:citA:AN8347:aglE:plyH:AN8481:
44282	small molecule catabolic process	55 out of 1601 genes, 3.4%	160 out of 10988 background genes, 1.5%	3.54e-07	AN0034:antA:xyrA:aldA:pyrABCN:scdA:ladA:ureB:mthA:bzuA:AN11015:AN11045:qutG:qutB:AN1274:AN1685:prnC:otaA:AN1857:AN1858:fahA:AN1898:hpdA:AN1923:gatA:AN2509:pgmB:agaA:AN3829:ileA:AN3954:AN4323:ladB:mccB:mccA:pdhB:pkiA:AN5447:AN5669:echA:AN6399:aciA:acuE:tpiA:hadA:foxA:AN7278:acuL:AN7708:AN7770:phacA:
46390	ribose phosphate biosynthetic process	35 out of 1601 genes, 2.2%	80 out of 10988 background genes, 0.7%	4.20e-07	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpdA:pdhC:panK
45333	cellular respiration	31 out of 1601 genes, 1.9%	66 out of 10988 background genes, 0.6%	4.98e-07	AN1003:AN10585:AN11347:artC:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:aclA:aclB:suAprgA1:AN3068:AN4064:AN4525:mdhB:AN5497:AN5888:cycA:AN6297:AN

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6732	coenzyme metabolic process	54 out of 1601 genes, 3.4%	158 out of 10988 background genes, 1.4%	6.59e-07	AN0270:AN0593:spdA:AN0688:AN12152:AN12201:sasA:pgkA:AN1524:AN1593:hxB:artC:AN1857:AN1860:alcC:AN2440:AN2509:AN2526:gpdC:fbaA:gsdA:AN3058:pfkA:AN3431:AN3586:AN3639:AN3840:AN3954:AN4569:mccA:AN4757:AN4830:cnxH:pdcA:pdhB:pkiA:acuN:ldhA:faaA:swoM:AN6141:biA:tpiA:hxkA:AN7469:pyroA:gpdA:ndxC:citA:tdiB:A
1901135	carbohydrate derivative metabolic process	98 out of 1601 genes, 6.1%	366 out of 10988 background genes, 3.3%	7.11e-07	AN0128:AN0593:basA:AN0688:mns1B:adB:AN0918:ladA:atp20:AN1071:AN10710:AN10838:AN10921:AN1102:AN11233:AN11303:AN11347:AN11802:AN12279:pgkA:AN1593:oliC:hxB:AN1715:AN1798:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:gpdC:pgmB:fbaA:gsdA:AN3013:AN3222:pfkA:AN3499:AN3626:AN3639:AN3881:AN3954:pcmA:barA:chsF:purH:AN4525:mccA:ugeA:AN4739:AN4830:cnxH:chiB:pdcA:AN5122:pdhB:pkiA:AN5566:acuN:AN5748:ldhA:AN5888:faaA:swoM:pyrG:AN6209:AN6405:AN6541:AN6610:AN6736:tpiA:pdiA:hxkA:AN7469:AN8019:gpdA:AN8118:citA:AN84
9152	purine ribonucleotide biosynthetic process	33 out of 1601 genes, 2.1%	75 out of 10988 background genes, 0.7%	1.13e-06	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:
8652	cellular amino acid biosynthetic process	48 out of 1601 genes, 3.0%	135 out of 10988 background genes, 1.2%	1.36e-06	aroG:AN0840:AN0912:AN10298:qutB:AN1673:prnC:AN1857:AN1858:AN1883:fahA:hpdA:AN1923:AN1990:AN1993:AN2509:AN2526:AN2914:AN3031:AN3058:ileA:gmdA:glnA:AN4323:AN4401:metH:fmdS:sA:gltA:lysB:AN5601:AN5610:AN5731:AN6048:AN6227:trpB:AN6346:metG:hisHF:AN7600:AN7722:pyroA:cysD:cysA:AN8770:amdS:AN8866:AN8

6164	purine nucleotide biosynthetic process	33 out of 1601 genes, 2.1%	76 out of 10988 background genes, 0.7%	1.72e-06	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3639:AN3954:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:
15980	energy derivation by oxidation of organic compounds	35 out of 1601 genes, 2.2%	84 out of 10988 background genes, 0.8%	2.10e-06	AN1003:AN10585:AN11347:artC:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:aclA:aclB:pgmB:suAprgA1:AN3068:AN4064:AN4525:pdcA:mdhB:AN5497:AN5888:cycA:AN6297:AN8118:citA:carC:alcA
51188	cofactor biosynthetic process	51 out of 1601 genes, 3.2%	151 out of 10988 background genes, 1.4%	3.22e-06	AN0270:spdA:AN0836:AN10290:AN12152:AN12201:sasA:pgkA:AN1524:hxB:artC:AN1857:AN1860:AN1915:hemA:AN2509:AN2526:gpdC:gpxA:fbaA:pfkA:AN3431:AN3586:AN3639:AN3840:AN3920:AN3954:AN4569:mccA:AN4757:AN4830:cnxH:AN5130:pdhB:pkiA:acuN:sidA:ldhA:swoM:AN6141:sidF:biA:tpiA:hxkA:AN7469:pyroA:gpdA:AN8346:tdiB

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44237	cellular metabolic process	566 out of 1601 genes, 35.4%	3205 out of 10988 background genes, 29.2%	6.09e-06	AN0034:rabS:AN0094:AN0116:AN0126:AN0128:AN0142:AN0191:ivoB:antA:AN0262:AN0270:AN0278:aroG:xyrA:AN0433:AN0445:AN0451:AN0465:AN0470:engA:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0649:AN0661:spdA:AN0688:AN0695:AN0705:AN0714:AN0716:AN0720:AN0770:AN0776:mns1B:AN0804:swd1:scdA:AN0836:AN0840:AN0843:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1003:niiA:ureB:AN1013:pyrD:AN10164:culA:env7:AN10213:AN10258:AN10287:AN10290:AN10298:AN10331:afoE:odeA:AN10416:ggtA:AN1045:AN10475:AN10491:AN1050:mthA:AN10517:AN10523:AN10585:AN10618:AN10619:AN10648:AN10663:AN10681:AN1071:AN10710:AN10712:AN10762:ffkB:AN10838:AN1084:AN10863:AN10880:AN10903:AN10906:AN10910:AN10921:bzuA:AN10957:AN10994:AN11003:AN11008:AN11015:AN1102:AN11045:AN11060:AN11080:AN11093:AN11110:AN11112:AN11133:AN11161:AN11212:AN1122:AN11233:AN11303:AN11347:qutG:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11959:AN11961:AN12121:AN1215:AN12152:AN12201:sasA:AN12246:AN12279:AN1228:AN
5996	monosaccharide metabolic process	37 out of 1601 genes, 2.3%	95 out of 10988 background genes, 0.9%	6.76e-06	xyrA:AN0551:AN0688:mns1B:AN10710:pgkA:AN1274:abfB:AN1715:alcC:gpdC:pgmB:fbaA:AN2951:gsdA:ugmA:pfkA:mns1A:ladB:mccA:ugeA:pdcA:pkiA:acuN:AN5748:swoM:tpiA:AN6985:hxkA:AN7590:AN7708:abnC:gpdA:aglC:AN8551:alcA:xlnB

51186	cofactor metabolic process	68 out of 1601 genes, 4.2%	232 out of 10988 background genes, 2.1%	6.90e-06	AN0270:AN0593:spdA:AN0688:AN0836:AN10290:ggtA:AN11060:AN12152:AN12201:sasA:pgkA:AN1524:AN1593:hxB:artC:AN1857:AN1860:AN1915:hemA:alcC:AN2440:AN2509:AN2526:gpdC:gpxA:fbaA:gsdA:AN3058:pfkA:AN3431:AN3586:AN3639:AN3840:AN3920:AN3954:AN4569:mccA:AN4757:AN4830:cnxH:pdcA:AN5130:pdhB:pkiA:acuN:sidA:ldhA:faaA:swoM:AN6141:sidF:AN6239:biA:tpiA:hxkA:AN7469:pyroA:gpdA:ndxC:citA:AN8346:tdiB:A
9156	ribonucleoside monophosphate biosynthetic process	31 out of 1601 genes, 1.9%	72 out of 10988 background genes, 0.7%	7.08e-06	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3954:purH:mccA:AN4739:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpd
42773	ATP synthesis coupled electron transport	15 out of 1601 genes, 0.9%	21 out of 10988 background genes, 0.2%	9.61e-06	AN11347:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN4525:AN8118
42775	mitochondrial ATP synthesis coupled electron transport	15 out of 1601 genes, 0.9%	21 out of 10988 background genes, 0.2%	9.61e-06	AN11347:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN4525:AN8118
9124	nucleoside monophosphate biosynthetic process	31 out of 1601 genes, 1.9%	73 out of 10988 background genes, 0.7%	1.06e-05	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3954:purH:mccA:AN4739:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7469:gpd
22904	respiratory electron transport chain	16 out of 1601 genes, 1.0%	24 out of 10988 background genes, 0.2%	1.40e-05	AN11347:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN4525:AN8118

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72524	pyridine-containing compound metabolic process	31 out of 1601 genes, 1.9%	74 out of 10988 background genes, 0.7%	1.57e-05	AN0270:AN0593:AN0688:AN10290:pgkA:AN1857:alcC:AN2440:AN2509:gpdC:fbaA:gsdA:AN3222:pfkA:AN3431:AN3954:mccA:pdcA:pdhB:pkiA:acuN:ldhA:swoM:AN6141:tpiA:hxkA:pyroA:gpdA:ndxC:AN8551:alcA
19318	hexose metabolic process	28 out of 1601 genes, 1.7%	63 out of 10988 background genes, 0.6%	1.68e-05	xyrA:AN0551:mns1B:AN10710:pgkA:AN1715:alcC:gpdC:pgmB:fbaA:AN2951:gsdA:ugmA:pfkA:mns1A:ladB:mccA:ugeA:pdcA:pkiA:acuN:AN5748:swoM:tpiA:hxkA:gpdA:aglC:alcA
46031	ADP metabolic process	18 out of 1601 genes, 1.1%	30 out of 10988 background genes, 0.3%	1.90e-05	pgkA:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
6733	oxidoreduction coenzyme metabolic process	33 out of 1601 genes, 2.1%	83 out of 10988 background genes, 0.8%	2.53e-05	AN0593:AN0688:AN12152:AN12201:pgkA:artC:AN1857:AN1860:alcC:AN2440:AN2509:gpdC:fbaA:gsdA:pfkA:AN3431:AN3586:AN3954:AN4569:mccA:AN4757:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hx
6119	oxidative phosphorylation	15 out of 1601 genes, 0.9%	22 out of 10988 background genes, 0.2%	2.61e-05	AN11347:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN4525:AN8118
9127	purine nucleoside monophosphate biosynthetic process	29 out of 1601 genes, 1.8%	68 out of 10988 background genes, 0.6%	2.89e-05	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3954:purH:mccA:AN4739:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA
9168	purine ribonucleoside monophosphate biosynthetic process	29 out of 1601 genes, 1.8%	68 out of 10988 background genes, 0.6%	2.89e-05	adB:atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3626:AN3954:purH:mccA:AN4739:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:AN6209:AN6541:tpiA:hxkA:gpdA
9108	coenzyme biosynthetic process	40 out of 1601 genes, 2.5%	112 out of 10988 background genes, 1.0%	2.98e-05	AN0270:spdA:AN12152:AN12201:sasA:pgkA:AN1524:artC:AN1857:AN1860:AN2509:AN2526:gpdC:fbaA:pfkA:AN3431:AN3586:AN3639:AN3840:AN3954:AN4569:mccA:AN4757:AN4830:cnxH:pdhB:pkiA:acuN:ldhA:swoM:AN6141:biA:tpiA:hxkA:AN746

6090	pyruvate metabolic process	21 out of 1601 genes, 1.3%	40 out of 10988 background genes, 0.4%	3.04e-05	pgkA:AN1990:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:pdhB:pkiA:acuN:ldhA:pdkA:swoM:tpiA:hxkA:gpdA:pdcB:alcA:pdhC
9135	purine nucleoside diphosphate metabolic process	18 out of 1601 genes, 1.1%	31 out of 10988 background genes, 0.3%	3.91e-05	pgkA:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:alcA
9179	purine ribonucleoside diphosphate metabolic process	18 out of 1601 genes, 1.1%	31 out of 10988 background genes, 0.3%	3.91e-05	pgkA:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:alcA
97064	ncRNA export from nucleus	12 out of 1601 genes, 0.7%	15 out of 10988 background genes, 0.1%	4.14e-05	AN0843:AN3172:AN3413:AN3455:AN3706:rps16:AN4087:AN4218:AN5441:AN5715:AN5997:AN663
9165	nucleotide biosynthetic process	40 out of 1601 genes, 2.5%	114 out of 10988 background genes, 1.0%	5.27e-05	adB:atp20:pyrD:AN11303:pgkA:oliC:AN1857:URFA3:atp8:oliA:atp9:AN2509:gpdC:fbaA:pfkA:AN3431:AN3626:AN3639:AN3954:AN4258:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7
51029	rRNA transport	10 out of 1601 genes, 0.6%	11 out of 10988 background genes, 0.1%	6.36e-05	AN0843:AN3172:AN3413:AN3706:rps16:AN4087:AN5441:AN5715:AN5997:AN6632
6407	rRNA export from nucleus	10 out of 1601 genes, 0.6%	11 out of 10988 background genes, 0.1%	6.36e-05	AN0843:AN3172:AN3413:AN3706:rps16:AN4087:AN5441:AN5715:AN5997:AN6632

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44271	cellular nitrogen compound biosynthetic process	225 out of 1601 genes, 14.1%	1114 out of 10988 background genes, 10.1%	6.76e-05	AN0094:AN0116:AN0142:AN0262:AN0270:AN0278:AN0433:AN0445:AN0465:AN0470:AN0507:aldA:pyrABCN:AN0570:AN0593:AN0661:spdA:AN0705:AN0776:AN0843:uaY:adB:AN0907:atp20:AN1013:pyrD:AN10290:AN10298:AN10331:AN10416:AN10475:AN10491:AN10517:AN10663:AN10681:AN10710:AN10762:AN1084:AN10906:AN10910:AN10957:AN11003:AN11080:AN11093:AN11112:AN11212:AN1122:AN11303:AN11419:AN1162:AN1166:AN11776:AN11961:AN12201:AN12246:AN1228:AN12419:pgkA:AN1345:AN1524:oliC:AN1715:nosA:AN1857:AN1915:AN1964:AN1976:URFA3:atp8:oliA:AN20013:atp9:AN2057:AN2235:amdA:AN2283:hemA:AN2301:H4.2:AN2509:gpdC:acvA:AN2677:AN2734:AN2780:gpxA:fbaA:AN2932:AN2980:AN2997:suAprgA1:AN3172:AN3222:pfkA:AN3290:AN3413:AN3431:AN3595:AN3626:AN3639:AN3823:AN3832:AN3840:AN3863:AN3865:AN3920:AN3954:AN4013:rps16:AN4073:AN4087:AN4126:rpl16a:AN4218:AN4222:AN4258:barA:palA:metR:AN4401:metH:AN4452:purH:AN4475:AN4494:AN4522:AN4594:AN4600:ssz1:mccA:AN4739:AN4777:AN4794:AN4802:AN4803:AN4821:AN4830:AN4837:ubi1:
72525	pyridine-containing compound biosynthetic process	22 out of 1601 genes, 1.4%	45 out of 10988 background genes, 0.4%	7.59e-05	AN0270:AN10290:pgkA:AN1857:AN2509:gpdC:fbaA:AN3222:pfkA:AN3431:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:AN6141:tpiA:hxkA:pyroA:gpdA
72330	monocarboxylic acid biosynthetic process	43 out of 1601 genes, 2.7%	129 out of 10988 background genes, 1.2%	9.08e-05	aldA:basA:spdA:AN0918:AN0949:odeA:pgkA:gpdC:acvA:fbaA:suAprgA1:pfkA:AN3276:pkiB:AN3954:AN4126:sdeB:palA:AN4401:mccA:pdcA:AN5000:pdhB:pkiA:acuN:ldhA:swoM:accA:ppoB:AN6506:AN6555:biA:sdeA:tpiA:AN6973:hxkA:stcK:stcA:gpdA:

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16054	organic acid catabolic process	40 out of 1601 genes, 2.5%	116 out of 10988 background genes, 1.1%	9.15e-05	antA:aldA:pyrABCN:scdA:mthA:bzuA:AN11045:qutB:prnC:otaA:AN1857:AN1858:fahA:AN1898:hpdA:AN1923:gatA:AN2509:agaA:AN3829:ileA:AN3954:AN4323:mccB:mccA:pdhB:AN5447:echA:AN6399:aciA:acuE:hadA:foxA:AN7278:acuL:AN7770:phacA
1901293	nucleoside phosphate biosynthetic process	40 out of 1601 genes, 2.5%	116 out of 10988 background genes, 1.1%	9.15e-05	adB:atp20:pyrD:AN11303:pgkA:oliC:AN1857:URFA3:atp8:oliA:atp9:AN2509:gpdC:fbaA:pfkA:AN3431:AN3626:AN3639:AN3954:AN4258:purH:mccA:AN4739:AN4830:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:AN6209:AN6541:tpiA:hxkA:AN7
46395	carboxylic acid catabolic process	40 out of 1601 genes, 2.5%	116 out of 10988 background genes, 1.1%	9.15e-05	antA:aldA:pyrABCN:scdA:mthA:bzuA:AN11045:qutB:prnC:otaA:AN1857:AN1858:fahA:AN1898:hpdA:AN1923:gatA:AN2509:agaA:AN3829:ileA:AN3954:AN4323:mccB:mccA:pdhB:AN5447:echA:AN6399:aciA:acuE:hadA:foxA:AN7278:acuL:AN7770:phacA
9185	ribonucleoside diphosphate metabolic process	18 out of 1601 genes, 1.1%	33 out of 10988 background genes, 0.3%	0.00014	pgkA:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:alcA
22900	electron transport chain	16 out of 1601 genes, 1.0%	27 out of 10988 background genes, 0.2%	0.00016	AN11347:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN4525:A

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43603	cellular amide metabolic process	129 out of 1601 genes, 8.1%	573 out of 10988 background genes, 5.2%	0.00018	AN0116:AN0142:AN0262:AN0278:AN0433:AN0445:AN0465:AN0470:aldA:AN0570:AN0593:spdA:AN0705:AN0776:AN0843:uaY:AN0907:ureB:AN1013:AN10416:ggtA:AN10475:AN10681:AN1084:bzuA:AN11133:AN1122:AN11419:AN1162:AN1166:AN11776:AN12246:AN1228:AN1345:AN1524:AN1964:AN20013:AN2057:AN2144:gatA:AN2301:acvA:AN2734:gpxA:AN2932:AN2980:AN2997:suAprgA1:AN3058:AN3172:AN3413:AN3595:AN3639:AN3823:AN3832:AN3840:AN3865:gmdA:rps16:AN4073:AN4087:AN4126:rpl16a:AN4218:AN4222:barA:palA:AN4401:AN4452:AN4475:AN4494:AN4522:AN4594:AN4603:ssz1:AN4777:AN4794:AN4802:AN4803:AN4830:ubi1:pdcA:AN4916:AN5014:hsp70:pdhB:AN5222:AN5441:AN5715:AN5719:sidA:AN5960:AN5979:AN5996:AN5997:faaA:AN6039:AN6146:AN6181:rpl3:sidF:ppoB:AN6500:AN6526:AN6629:AN6632:biA:acuE:AN6679:AN6843:AN7354:AN747
6631	fatty acid metabolic process	36 out of 1601 genes, 2.2%	102 out of 10988 background genes, 0.9%	0.00021	antA:basA:AN0649:scdA:AN0918:AN0949:AN10287:odeA:AN1050:mthA:AN3276:pkiB:sdeB:mccA:AN5000:pcsA:echA:AN5990:faaA:accA:ppoB:AN6506:AN6555:acuE:sdeA:AN6973:hadA:foxA:acuL:AN7770:stcK:faaB:AN8907:AN9297:fasA:fasB
9060	aerobic respiration	23 out of 1601 genes, 1.4%	51 out of 10988 background genes, 0.5%	0.00024	AN1003:AN10585:AN11347:artC:cobA:oxiC:oxiA:oxiB:AN2316:aclA:aclB:suAprgA1:AN3068:AN4064:AN4525:mdhB:AN5497:AN5888:cycA:AN6297:AN
9132	nucleoside diphosphate metabolic process	18 out of 1601 genes, 1.1%	35 out of 10988 background genes, 0.3%	0.00048	pgkA:alcC:gpdC:fbaA:pfkA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:alcA

90407	organophosphate biosynthetic process	56 out of 1601 genes, 3.5%	201 out of 10988 background genes, 1.8%	0.00101	AN0270:pyrABCN:AN0716:adB:AN0913:ladA:atp20:pyrD:AN10213:AN11161:AN11303:pgkA:oliC:hxB:AN1857:URFA3:atp8:oliA:atp9:AN2509:gpdC:fbaA:pfkA:AN3276:AN3431:AN3626:AN3639:AN3954:AN4258:purH:mccA:AN4739:AN4830:cnxH:AN5122:pdhB:pkiA:AN5566:acuN:ldhA:AN5888:swoM:AN6141:pyrG:AN6209:AN6541:tpiA:AN7385:hxk
46939	nucleotide phosphorylation	16 out of 1601 genes, 1.0%	30 out of 10988 background genes, 0.3%	0.00115	pgkA:gpdC:fbaA:pfkA:AN3954:AN4258:mccA:AN5122:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
43648	dicarboxylic acid metabolic process	22 out of 1601 genes, 1.4%	51 out of 10988 background genes, 0.5%	0.00119	adB:prnC:AN1923:AN1993:gatA:alcC:alcB:AN3829:AN3840:glnA:AN4739:mdhB:gltA:AN5447:AN6048:maeA:AN6209:aciA:AN7278:AN8099:AN8709:al

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1901362	organic cyclic compound biosynthetic process	167 out of 1601 genes, 10.4%	811 out of 10988 background genes, 7.4%	0.00133	AN0094:ivoB:AN0270:aroG:AN0451:AN0507:aldA:pyrABCN:AN0593:AN0661:AN0836:uaY:adB:atp20:pyrD:AN10290:AN10298:AN10331:afoE:AN10491:AN10517:AN10648:AN10663:AN10710:AN10762:AN10906:AN10910:AN10957:AN11003:AN11008:AN11080:AN11093:AN11112:AN11212:AN11303:qutB:AN11961:AN12201:AN12331:AN12419:pgkA:AN1524:oliC:hxB:AN1673:AN1715:prnC:nosA:AN1857:AN1858:fahA:AN1898:hpdA:pdmA:AN1915:AN1976:AN1993:URFA3:atp8:oliA:atp9:pkhB:AN2235:amdA:AN2283:hemA:H4.2:AN2509:gpdC:acvA:AN2677:AN2780:fbaA:suAprgA1:AN3222:pfkA:AN3290:micA:AN3400:AN3431:AN3626:AN3639:AN3840:AN3863:AN3920:AN3954:gmdA:AN4013:CYP61A1:AN4094:AN4126:AN4258:palA:metR:metH:purH:AN4465:fmdS:AN4600:mccA:AN4739:AN4821:AN4830:AN4837:cnxH:pdcA:AN5122:AN5130:pdhB:pkiA:AN5274:AN5497:AN5566:AN5569:AN5731:acuN:sidA:ldhA:swoM:AN6048:AN6091:AN6114:AN6141:pyrG:AN6209:trpB:sidF:sidD:AN6396:AN6506:AN6541:AN6549:biA:AN6747:tpiA:AN6973:AN7146:fhbA:hisHF:hxkA:AN7469:pyroA:stcK:st
1901606	alpha-amino acid catabolic process	24 out of 1601 genes, 1.5%	59 out of 10988 background genes, 0.5%	0.00139	aldA:pyrABCN:prnC:otaA:AN1857:AN1858:fahA:AN1898:hpdA:AN1923:gatA:AN2509:agaA:AN3829:ileA:mccB:mccA:AN5447:echA:AN6399:AN7278:al
9064	glutamine family amino acid metabolic process	21 out of 1601 genes, 1.3%	48 out of 10988 background genes, 0.4%	0.00160	pyrABCN:spdA:prnC:otaA:AN1883:gatA:agaA:AN2914:AN3829:gmdA:glnA:gtaA:AN4901:gltA:AN5447:AN7278:AN7722:AN8770:amdS:rrmA:AN9400

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43604	amide biosynthetic process	114 out of 1601 genes, 7.1%	511 out of 10988 background genes, 4.7%	0.00165	AN0116:AN0142:AN0262:AN0278:AN0433:AN0445:AN0465:AN0470:aldA:AN0570:spdA:AN0705:AN0776:AN0843:AN0907:AN1013:AN10416:AN10475:AN10681:AN1084:AN1122:AN11419:AN1162:AN1166:AN11776:AN12246:AN1228:AN1345:AN1524:AN1964:AN20013:AN2057:AN2301:acvA:AN2734:gpxA:AN2932:AN2980:AN2997:suAprgA1:AN3172:AN3413:AN3595:AN3639:AN3823:AN3832:AN3840:AN3865:rps16:AN4073:AN4087:AN4126:rpl16a:AN4218:AN4222:barA:palA:AN4401:AN4452:AN4475:AN4494:AN4522:AN4594:ssz1:AN4777:AN4794:AN4802:AN4803:AN4830:ubi1:pdcA:AN4916:AN5014:hsp70:pdhB:AN5222:AN5441:AN5715:AN5719:sidA:AN5960:AN5979:AN5996:AN5997:AN6039:AN6146:AN6181:rpl3:sidF:AN6500:AN6526:AN6629:AN6632:biA:AN6679:AN6843:AN7354:
6120	mitochondrial electron transport, NADH to ubiquinone	7 out of 1601 genes, 0.4%	7 out of 10988 background genes, 0.1%	0.00218	ndhDL:ndhE:ndhB:ndhA:ndhD:ndhF:ndhC
6123	mitochondrial electron transport, cytochrome c to oxygen	7 out of 1601 genes, 0.4%	7 out of 10988 background genes, 0.1%	0.00218	AN11347:oxiC:oxiA:oxiB:AN2316:AN4525:AN8118
6754	ATP biosynthetic process	21 out of 1601 genes, 1.3%	49 out of 10988 background genes, 0.4%	0.00241	atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
42866	pyruvate biosynthetic process	14 out of 1601 genes, 0.9%	25 out of 10988 background genes, 0.2%	0.00266	pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA

6096	glycolytic process	14 out of 1601 genes, 0.9%	25 out of 10988 background genes, 0.2%	0.00266	pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
6757	ATP generation from ADP	14 out of 1601 genes, 0.9%	25 out of 10988 background genes, 0.2%	0.00266	pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
19362	pyridine nucleotide metabolic process	26 out of 1601 genes, 1.6%	69 out of 10988 background genes, 0.6%	0.00282	AN0593:AN0688:pgkA:AN1857:alcC:AN2440:AN2509:gpdC:fbaA:gsdA:pfkA:AN3431:AN3954:mccA:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:ndxC:AN8551:alcA
46496	nicotinamide nucleotide metabolic process	26 out of 1601 genes, 1.6%	69 out of 10988 background genes, 0.6%	0.00282	AN0593:AN0688:pgkA:AN1857:alcC:AN2440:AN2509:gpdC:fbaA:gsdA:pfkA:AN3431:AN3954:mccA:pdcA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:ndxC:AN8551:alcA
9063	cellular amino acid catabolic process	25 out of 1601 genes, 1.6%	65 out of 10988 background genes, 0.6%	0.00286	aldA:pyrABCN:prnC:otaA:AN1857:AN1858:fahA:AN1898:hpdA:AN1923:gatA:AN2509:agaA:AN3829:ileA:AN4323:mccB:mccA:AN5447:echA:AN6399:A

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9987	cellular process	674 out of 1601 genes, 42.1%	4056 out of 10988 background genes, 36.9%	0.00345	AN0034:rabS:AN0094:AN0116:AN0126:AN0128:AN0142:AN0179:AN0191:ivoB:pdiB:antA:AN0262:AN0270:AN0278:tubA:AN0349:aroG:xyrA:AN0433:AN0445:AN0451:AN0465:AN0470:engA:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0649:AN0661:spdA:AN0688:AN0695:AN0705:AN0714:AN0716:AN0720:AN0770:AN0776:mns1B:AN0804:swd1:scdA:AN0836:AN0840:AN0843:hsp104:uaY:adB:AN0907:AN0912:AN0913:AN0918:ladA:atp20:AN0949:AN1003:niiA:ureB:AN1013:pyrD:AN10164:culA:env7:AN10213:AN10223:AN10229:AN10258:AN10287:AN10290:AN10296:AN10298:AN10331:afoE:AN10351:odeA:AN10416:ggtA:AN1045:AN10475:AN10491:AN1050:hsp20:mthA:AN10517:AN10518:AN10523:AN10585:AN1061:AN10618:AN10619:AN10627:AN10648:AN10663:AN10681:AN1071:AN10710:AN10712:AN10762:ffkB:AN10838:AN1084:AN10863:AN10873:AN10880:AN10903:AN10906:AN10910:AN10921:bzuA:AN10957:AN10994:AN11003:AN11008:AN11015:AN1102:AN11045:AN11060:AN11080:AN11093:AN11110:AN11112:AN11133:AN11161:AN11212:AN1122:AN11233:AN11278:AN11303:AN11347:qutG:qutB:AN11419:
9145	purine nucleoside triphosphate biosynthetic process	21 out of 1601 genes, 1.3%	50 out of 10988 background genes, 0.5%	0.00360	atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
9201	ribonucleoside triphosphate biosynthetic process	21 out of 1601 genes, 1.3%	50 out of 10988 background genes, 0.5%	0.00360	atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA

9206	purine ribonucleoside triphosphate biosynthetic process	21 out of 1601 genes, 1.3%	50 out of 10988 background genes, 0.5%	0.00360	atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
6006	glucose metabolic process	15 out of 1601 genes, 0.9%	29 out of 10988 background genes, 0.3%	0.00431	pgkA:alcC:gpdC:fbaA:gsdA:pfkA:mccA:pdcA:pkiA:acuN:swoM:tpiA:hxkA:gpdA:alcA
6081	cellular aldehyde metabolic process	20 out of 1601 genes, 1.2%	47 out of 10988 background genes, 0.4%	0.00490	AN0270:xyrA:aldA:AN0593:AN0688:AN0912:AN11015:AN2440:gsdA:AN3954:AN4126:mdhB:ldhA:AN6141:acuE:foxA:pyroA:AN8551:alcR:alcA
9066	aspartate family amino acid metabolic process	21 out of 1601 genes, 1.3%	51 out of 10988 background genes, 0.5%	0.00528	aldA:AN0720:sasA:AN1923:AN1990:AN1993:AN3031:ileA:AN4401:metH:sA:lysB:AN5601:AN5610:AN6048:metG:cysD:cysA:AN8709:alcR:alcA
6525	arginine metabolic process	12 out of 1601 genes, 0.7%	20 out of 10988 background genes, 0.2%	0.00561	pyrABCN:spdA:otaA:AN1883:agaA:AN2914:gmdA:AN7722:AN8770:amdS:rrmA:AN9400
9166	nucleotide catabolic process	17 out of 1601 genes, 1.1%	37 out of 10988 background genes, 0.3%	0.00760	AN0593:AN10663:pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:citA
9142	nucleoside triphosphate biosynthetic process	21 out of 1601 genes, 1.3%	52 out of 10988 background genes, 0.5%	0.00766	atp20:AN11303:pgkA:oliC:URFA3:atp8:oliA:atp9:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA

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6796	phosphate-containing compound metabolic process	113 out of 1601 genes, 7.1%	521 out of 10988 background genes, 4.7%	0.00767	AN0270:pyrABCN:AN0593:basA:AN0688:AN0716:adB:AN0913:AN0918:ladA:atp20:pyrD:env7:AN10213:AN10663:ffkB:AN10921:AN11161:AN11303:AN11347:qutG:AN11959:AN11961:pgkA:AN1593:oliC:hxB:AN1685:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:pgmB:fbaA:ippA:gsdA:AN3181:hk-8-5:AN3222:pfkA:AN3276:ste7:AN3431:AN3626:AN3639:AN3954:mkkA:AN4258:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:psk1:AN5122:pdhB:pkiA:AN5566:AN5569:mst1:acuN:stk19:ldhA:pdkA:AN5888:AN5919:pkcB:faaA:swoM:AN6141:pyrG:AN6209:AN6541:AN6610:tpiA:AN6985:AN7385:hxkA:AN7469:AN7604:AN7625:pyroA:ffkA:AN8012:g
6165	nucleoside diphosphate phosphorylation	14 out of 1601 genes, 0.9%	27 out of 10988 background genes, 0.2%	0.00899	pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
19319	hexose biosynthetic process	12 out of 1601 genes, 0.7%	21 out of 10988 background genes, 0.2%	0.01136	AN10710:pgkA:gpdC:fbaA:pfkA:mccA:pkiA:acuN:swoM:tpiA:hxkA:gpdA
46364	monosaccharide biosynthetic process	12 out of 1601 genes, 0.7%	21 out of 10988 background genes, 0.2%	0.01136	AN10710:pgkA:gpdC:fbaA:pfkA:mccA:pkiA:acuN:swoM:tpiA:hxkA:gpdA
6633	fatty acid biosynthetic process	19 out of 1601 genes, 1.2%	46 out of 10988 background genes, 0.4%	0.01462	basA:AN0918:AN0949:odeA:AN3276:pkiB:sdeB:mccA:AN5000:accA:ppoB:AN6506:AN6555:sdeA:AN6973:stcK:AN8907:fasA:fasB
19646	aerobic electron transport chain	7 out of 1601 genes, 0.4%	8 out of 10988 background genes, 0.1%	0.01524	AN11347:oxiC:oxiA:oxiB:AN2316:AN4525:AN8118

33993	response to lipid	20 out of 1601 genes, 1.2%	50 out of 10988 background genes, 0.5%	0.01527	AN0179:spdA:odeA:AN10518:aclA:hsp30:gpxA:pkfC:glnA:cpcB:ssz1:hsp70:acuN:trpB:tpiA:AN7208:AN7590:hsp90:AN8273:alcA
71396	cellular response to lipid	20 out of 1601 genes, 1.2%	50 out of 10988 background genes, 0.5%	0.01527	AN0179:spdA:odeA:AN10518:aclA:hsp30:gpxA:pkfC:glnA:cpcB:ssz1:hsp70:acuN:trpB:tpiA:AN7208:AN7590:hsp90:AN8273:alcA
1901607	alpha-amino acid biosynthetic process	30 out of 1601 genes, 1.9%	93 out of 10988 background genes, 0.8%	0.01881	AN0840:AN0912:AN10298:prnC:AN1883:AN1923:AN1990:AN2914:AN3031:AN3058:ileA:glnA:AN4323:AN4401:metH:sA:gltA:lysB:AN5601:AN5610:AN6048:trpB:metG:hisHF:AN7722:pyroA:cysD:cysA:
46434	organophosphate catabolic process	20 out of 1601 genes, 1.2%	51 out of 10988 background genes, 0.5%	0.02171	AN0593:AN10663:qutG:pgkA:AN1685:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:AN5919:swoM:tpiA:hxkA:gpdA:citA
6793	phosphorus metabolic process	113 out of 1601 genes, 7.1%	533 out of 10988 background genes, 4.9%	0.02293	AN0270:pyrABCN:AN0593:basA:AN0688:AN0716:adB:AN0913:AN0918:ladA:atp20:pyrD:env7:AN10213:AN10663:ffkB:AN10921:AN11161:AN11303:AN11347:qutG:AN11959:AN11961:pgkA:AN1593:oliC:hxB:AN1685:AN1857:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:alcC:AN2316:AN2440:AN2509:gpdC:pgmB:fbaA:ippA:gsdA:AN3181:hk-8-5:AN3222:pfkA:AN3276:ste7:AN3431:AN3626:AN3639:AN3954:mkkA:AN4258:purH:AN4525:mccA:AN4739:AN4830:cnxH:pdcA:psk1:AN5122:pdhB:pkiA:AN5566:AN5569:mst1:acuN:stk19:ldhA:pdkA:AN5888:AN5919:pkcB:faaA:swoM:AN6141:pyrG:AN6209:AN6541:AN6610:tpiA:AN6985:AN7385:hxkA:AN7469:AN7604:AN7625:pyroA:ffkA:AN8012:g

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42254	ribosome biogenesis	49 out of 1601 genes, 3.1%	185 out of 10988 background genes, 1.7%	0.02293	AN0262:AN0465:AN0695:AN0776:AN0843:AN1013:AN10618:AN10712:AN1166:AN1215:AN1228:AN1345:AN1964:AN2734:AN3172:AN3413:AN3455:AN3706:AN3823:rps16:AN4087:AN4475:AN4594:ssz1:AN4777:AN4803:ubi1:AN4916:AN5177:AN5222:AN5441:AN5520:AN5715:AN5785:AN5960:AN5979:AN5997:AN6082:rpl3:AN6632:AN6679:AN7107:AN7305:AN8668:AN8805:AN8856:AN8870:A
6094	gluconeogenesis	11 out of 1601 genes, 0.7%	19 out of 10988 background genes, 0.2%	0.02345	pgkA:gpdC:fbaA:pfkA:mccA:pkiA:acuN:swoM:tpiA:hxkA:gpdA
1901292	nucleoside phosphate catabolic process	17 out of 1601 genes, 1.1%	40 out of 10988 background genes, 0.4%	0.02745	AN0593:AN10663:pgkA:gpdC:fbaA:pfkA:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA:citA
19359	nicotinamide nucleotide biosynthetic process	17 out of 1601 genes, 1.1%	40 out of 10988 background genes, 0.4%	0.02745	pgkA:AN1857:AN2509:gpdC:fbaA:pfkA:AN3431:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
19363	pyridine nucleotide biosynthetic process	17 out of 1601 genes, 1.1%	40 out of 10988 background genes, 0.4%	0.02745	pgkA:AN1857:AN2509:gpdC:fbaA:pfkA:AN3431:AN3954:mccA:pdhB:pkiA:acuN:ldhA:swoM:tpiA:hxkA:gpdA
34404	nucleobase-containing small molecule biosynthetic process	20 out of 1601 genes, 1.2%	52 out of 10988 background genes, 0.5%	0.03049	AN0593:AN10663:pgkA:gpdC:fbaA:AN3222:pfkA:AN3954:mccA:pdhB:pkiA:AN5566:acuN:ldhA:swoM:pyrG:tpiA:hxkA:gpdA:citA
28	ribosomal small subunit assembly	8 out of 1601 genes, 0.5%	11 out of 10988 background genes, 0.1%	0.03457	AN3172:AN4777:ubi1:AN5222:AN5960:AN5979:AN6632:AN7305
16125	sterol metabolic process	20 out of 1601 genes, 1.2%	53 out of 10988 background genes, 0.5%	0.04232	AN0451:AN10648:AN11008:AN1593:AN1798:pdmA:CYP61A1:AN4094:AN4465:sidA:sidF:sidD:AN6506:AN6973:AN7146:AN7211:AN7661:AN8012:AN8

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6807	nitrogen compound metabolic process	452 out of 1601 genes, 28.2%	2654 out of 10988 background genes, 24.2%	0.04263	AN0094:AN0116:AN0126:AN0128:AN0142:AN0191:AN0224:AN0262:AN0270:AN0278:aroG:AN0433:AN0445:AN0465:AN0470:AN0507:aldA:pyrABCN:AN0570:AN0593:basA:AN0661:spdA:AN0688:AN0695:AN0705:AN0714:AN0720:AN0770:AN0776:mns1B:AN0804:swd1:AN0840:AN0843:hsp104:uaY:adB:AN0907:AN0912:AN0918:atp20:niiA:ureB:AN1013:pyrD:AN10164:culA:env7:AN10258:AN10290:AN10298:AN10331:AN10351:AN10416:ggtA:AN1045:AN10475:AN10491:AN10517:AN10523:AN10618:AN10663:AN10681:AN1071:AN10710:AN10712:AN10762:ffkB:AN10838:AN1084:AN10863:AN10880:AN10903:AN10906:AN10910:bzuA:AN10957:AN10994:AN11003:AN1102:AN11060:AN11080:AN11093:AN11110:AN11112:AN11133:AN11212:AN1122:AN11233:AN11303:AN11347:qutB:AN11419:AN1162:AN1166:AN11776:AN11802:AN11903:AN11961:AN12121:AN1215:AN12201:sasA:AN12246:AN12279:AN1228:AN12419:pgkA:AN1320:AN1345:AN1426:codA:AN1524:csnD:AN1565:AN1593:oliC:hxB:AN1673:AN1715:prnC:artC:AN1751:AN1780:AN1798:otaA:nosA:AN1857:AN1858:AN1883:fahA:AN1898:hpdA:AN1915:AN1923:AN19

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6629	lipid metabolic process	87 out of 1601 genes, 5.4%	393 out of 10988 background genes, 3.6%	0.04329	antA:AN0451:basA:AN0649:AN0716:scdA:AN0913:AN0918:AN0949:AN10213:AN10287:odeA:AN1050:mthA:AN10648:AN10921:AN11008:AN1102:AN11161:qutG:AN11802:AN11959:AN12429:AN1593:CYP5128A1:AN1792:AN1798:AN1855:pdmA:AN3013:AN3276:AN3318:pkiB:CYP61A1:AN4094:sdeB:AN4154:AN4258:barA:AN4465:mccA:AN5000:AN5228:sidA:pcsA:AN5888:echA:AN5919:AN5990:faaA:accA:sidF:sidD:ppoB:AN6382:AN6506:AN6555:AN6610:acuE:sdeA:AN6973:hadA:foxA:AN7146:AN7158:AN7211:acuL:AN7385:AN7604:AN7625:AN7661:AN7770:stcK:stcA:AN8012:AN8046:AN8
42274	ribosomal small subunit biogenesis	24 out of 1601 genes, 1.5%	70 out of 10988 background genes, 0.6%	0.04478	AN0465:AN10618:AN1345:AN1964:AN3172:AN3823:rps16:AN4594:AN4777:AN4803:ubi1:AN5222:AN5441:AN5785:AN5960:AN5979:AN6632:AN6679:AN7107:AN7305:AN8805:AN8870:AN9097:AN9

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1901360	organic cyclic compound metabolic process	287 out of 1601 genes, 17.9%	1599 out of 10988 background genes, 14.6%	0.04759	AN0094:AN0126:AN0128:AN0191:ivoB:AN0270:aroG:AN0451:AN0465:AN0507:aldA:pyrABCN:AN0593:AN0661:AN0688:AN0695:AN0705:AN0714:AN0776:AN0804:AN0836:uaY:adB:atp20:pyrD:AN10164:AN10290:AN10298:AN10331:afoE:AN1045:AN10475:AN10491:AN10517:AN10523:AN10618:AN10648:AN10663:AN1071:AN10710:AN10712:AN10762:AN10903:AN10906:AN10910:bzuA:AN10957:AN11003:AN11008:AN11060:AN11080:AN11093:AN11110:AN11112:AN11212:AN11303:AN11347:qutB:AN11961:AN12121:AN1215:AN12201:AN1228:AN12331:AN12419:pgkA:AN1345:AN1524:AN1593:oliC:hxB:AN1673:CYP5128A1:AN1715:prnC:artC:AN1751:AN1798:otaA:nosA:AN1857:AN1858:fahA:AN1898:hpdA:pdmA:AN1915:AN1964:AN1976:AN1993:ndhDL:ndhE:ndhB:AN20003:URFA3:cobA:I-AniI:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:atp9:ndhC:oxiB:pkhB:AN2139:rrp5:AN2235:amdA:AN2283:hemA:alcC:AN2316:H4.2:AN2440:AN2509:gpdC:acvA:AN2677:AN2780:AN2847:pgmB:fbaA:agaA:gsdA:AN3013:suAprgA1:AN3058:AN3172:AN3222:pfkA:AN3290:micA:AN3400:AN3431:AN3455:AN3

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Supplementary Table 5c.

Functional enrichment analysis for genes regulated by glucose under nitrogen derepressing conditions (urea as a nitrogen source) in the wild type strain

Only clusters comprising at lest 5 genes and corrected P - value <0.05 are shown

GOID	GO term	Cluster frequency	Background frequency	Corrected P-value	Genes annotated to the term
44281	small molecule metabolic process	476 out of 2759 genes, 17.3%	967 out of 10988 background genes, 8.8%	1.57e-61	AN0034:AN0046:AN0057:AN0137:AN0174:ureD:pppA:pdiB:AN0252:palB:AN0270:AN0285:AN0300:AN0318:aroG:araR:AN0428:AN0451:AN0490:AN0495:aldA:pyrABCN:AN0567:AN0593:AN0608:sidI:basA:AN0649:AN0672:spdA:AN0688:facB:AN0705:aromA:AN0720:mns1B:AN0797:laeA:scdA:pdeA:AN0840:AN0868:adB:AN0912:AN0918:AN0936:ladA:atp20:AN1003:niaD:niiA:pyrD:AN10197:pexE:AN10230:AN10287:AN10290:AN10298:AN10299:sgdB:odeA:AN10475:AN10495:AN1050:mthA:veA:AN10525:AN1054:msrA:facC:AN10599:AN10619:AN10642:AN10648:AN10661:AN10700:AN1071:AN10710:AN10764:AN10841:fbpZ:AN10901:AN10903:AN10936:bzuA:AN10981:AN10996:AN11008:AN11015:AN11045:AN11110:AN11111:AN11125:phenA:AN11252:AN11303:AN11347:qutG:qutB:AN11444:AN1150:AN11859:sumO:sD:AN1198:AN12152:gppA:AN12201:AN12213:sasA:AN12256:AN12316:AN12331:pgkA:AN12478:AN1263:AN1274:AN1380:AN1409:xprG:farB:AN1523:AN1524:AN1534:AN1593:mcdA:oliC:hxB:AN1673:AN1709:AN1710:AN1715:prnD:prnC:artC:AN1806:AN1809:otaA:AN1840:AN1857:AN1858:AN1860:AN1868:AN1883:maiA:fahA:hmgA:AN1898:hpdA:pdmA:AN1913:acuF:AN1923:AN1968:AN1990:AN1993:AN1999:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2069:AN2133:AN2144:AN2208:gatA:AN2272:alcC:AN2293:AN2316:AN2335:xlnD:AN2389:aclA:aclB:AN2440:AN2525:AN2526:a

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19752	carboxylic acid metabolic process	289 out of 2759 genes, 10.5%	547 out of 10988 background genes, 5.0%	7.27e-43	AN0046:AN0057:AN0174:palB:AN0285:AN0300:aroG:AN0428:aldA:pyrABCN:AN0593:basA:AN0649:spdA:facB:AN0705:aromA:AN0720:AN0797:laeA:scdA:AN0840:AN0868:adB:AN0912:AN0918:AN0936:AN1003:pexE:AN10230:AN10287:AN10298:AN10299:sgdB:odeA:AN10475:AN1050:mthA:veA:AN1054:msrA:facC:AN10599:AN10619:AN10700:AN10841:AN10901:bzuA:AN10996:AN11045:AN11110:AN11125:phenA:AN11252:qutB:AN1150:sD:AN1198:sasA:AN12331:pgkA:AN1263:AN1380:AN1409:xprG:farB:AN1524:mcdA:AN1673:AN1709:AN1710:prnD:prnC:artC:AN1809:otaA:AN1840:AN1857:AN1858:AN1883:maiA:fahA:hmgA:AN1898:hpdA:AN1913:acuF:AN1923:AN1968:AN1990:AN1993:AN2208:gatA:alcC:AN2293:AN2389:aclA:aclB:AN2525:AN2526:easB:gpdC:aatA:AN2723:lysA:fbaA:agaA:AN2914:pdhX:idpA:AN3031:suAprgA1:AN3058:pgmA:AN3073:prs3:pfkA:AN3276:AN3313:pkiB:AN3431:AN3456:AN3593:AN3634:AN3638:gukA:AN3656:AN3695:alcB:AN3748:AN3824:AN3829:ileA:AN3840:AN3865:AN3866:AN3894:AN3897:AN3901:AN3954:gmdA:AN4055:AN4081:AN4086:sdeB:glnA:AN4290:AN4323:AN4353:metR:pgaB:gdhA:AN4401:AN4405:AN4430:metH:fmdS:mccB:mccA:AN4739:sC:sA:AN4774:AN4793:gtaA:AN4820:pdcA:AN4901:AN4956:AN5025:ppoC:AN5060:AN5138:pdhB:fatA:AN5200:lysB:pkiA:AN5300:AN5444:AN5447:acoA:AN5534:AN5601:acuG:AN5610:facA:acuD:AN5646:AN5662:AN5698:aroF:AN5704:acuN:AN

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43436	oxoacid metabolic process	295 out of 2759 genes, 10.7%	564 out of 10988 background genes, 5.1%	1.12e-42	AN0046:AN0057:AN0174:palB:AN0285:AN0300:aroG:AN0428:aldA:pyrABCN:AN0593:sidI:basA:AN0649:spdA:facB:AN0705:aromA:AN0720:AN0797:laeA:scdA:AN0840:AN0868:adB:AN0912:AN0918:AN0936:AN1003:niaD:niiA:pexE:AN10230:AN10287:AN10298:AN10299:sgdB:odeA:AN10475:AN1050:mthA:veA:AN1054:msrA:facC:AN10599:AN10619:AN10700:AN10841:AN10901:bzuA:AN10996:AN11045:AN11110:AN11125:phenA:AN11252:qutB:AN1150:sD:AN1198:sasA:AN12331:pgkA:AN1263:AN1380:AN1409:xprG:farB:AN1524:mcdA:AN1673:AN1709:AN1710:prnD:prnC:artC:AN1809:otaA:AN1840:AN1857:AN1858:AN1883:maiA:fahA:hmgA:AN1898:hpdA:AN1913:acuF:AN1923:AN1968:AN1990:AN1993:AN2208:gatA:alcC:AN2293:AN2389:aclA:aclB:AN2525:AN2526:easB:gpdC:aatA:AN2723:lysA:fbaA:agaA:AN2914:pdhX:idpA:AN3031:suAprgA1:AN3058:pgmA:AN3073:prs3:pfkA:AN3276:AN3313:pkiB:AN3431:AN3456:AN3593:AN3634:AN3638:gukA:AN3656:AN3695:alcB:AN3748:AN3779:AN3824:AN3829:ileA:AN3840:AN3865:AN3866:AN3894:AN3897:AN3901:AN3954:gmdA:AN4055:AN4081:AN4086:sdeB:glnA:AN4290:AN4323:AN4353:metR:pgaB:gdhA:AN4401:AN4405:AN4430:metH:fmdS:mccB:mccA:AN4739:sC:sA:AN4774:AN4793:gtaA:AN4820:pdcA:AN4901:AN4956:AN5025:ppoC:AN5060:AN5138:pdhB:fatA:AN5200:lysB:pkiA:AN5300:AN5444:AN5447:acoA:AN5534:AN5601:acuG:AN5610:facA:acuD:AN5646:AN5662:AN5698:ar

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6082	organic acid metabolic process	296 out of 2759 genes, 10.7%	569 out of 10988 background genes, 5.2%	3.30e-42	AN0046:AN0057:AN0174:palB:AN0285:AN0300:aroG:AN0428:aldA:pyrABCN:AN0593:sidI:basA:AN0649:spdA:facB:AN0705:aromA:AN0720:AN0797:laeA:scdA:AN0840:AN0868:adB:AN0912:AN0918:AN0936:AN1003:niaD:niiA:AN10197:pexE:AN10230:AN10287:AN10298:AN10299:sgdB:odeA:AN10475:AN1050:mthA:veA:AN1054:msrA:facC:AN10599:AN10619:AN10700:AN10841:AN10901:bzuA:AN10996:AN11045:AN11110:AN11125:phenA:AN11252:qutB:AN1150:sD:AN1198:sasA:AN12331:pgkA:AN1263:AN1380:AN1409:xprG:farB:AN1524:mcdA:AN1673:AN1709:AN1710:prnD:prnC:artC:AN1809:otaA:AN1840:AN1857:AN1858:AN1883:maiA:fahA:hmgA:AN1898:hpdA:AN1913:acuF:AN1923:AN1968:AN1990:AN1993:AN2208:gatA:alcC:AN2293:AN2389:aclA:aclB:AN2525:AN2526:easB:gpdC:aatA:AN2723:lysA:fbaA:agaA:AN2914:pdhX:idpA:AN3031:suAprgA1:AN3058:pgmA:AN3073:prs3:pfkA:AN3276:AN3313:pkiB:AN3431:AN3456:AN3593:AN3634:AN3638:gukA:AN3656:AN3695:alcB:AN3748:AN3779:AN3824:AN3829:ileA:AN3840:AN3865:AN3866:AN3894:AN3897:AN3901:AN3954:gmdA:AN4055:AN4081:AN4086:sdeB:glnA:AN4290:AN4323:AN4353:metR:pgaB:gdhA:AN4401:AN4405:AN4430:metH:fmdS:mccB:mccA:AN4739:sC:sA:AN4774:AN4793:gtaA:AN4820:pdcA:AN4901:AN4956:AN5025:ppoC:AN5060:AN5138:pdhB:fatA:AN5200:lysB:pkiA:AN5300:AN5444:AN5447:acoA:AN5534:AN5601:acuG:AN5610:facA:acuD:AN5646:AN56

For Peer Review

6520	cellular amino acid metabolic process	163 out of 2759 genes, 5.9%	280 out of 10988 background genes, 2.5%	2.07e-29	AN0046:AN0057:AN0174:AN0300:aroG:AN0428:aldA:pyrABCN:AN0593:spdA:AN0705:aromA:AN0720:AN0797:AN0840:AN0912:AN0936:AN10230:AN10298:AN10299:sgdB:AN10475:AN1054:msrA:AN10599:AN10901:AN10996:AN11110:AN11125:phenA:AN11252:qutB:AN1150:sD:AN1198:sasA:AN1263:AN1380:AN1673:AN1709:AN1710:prnD:prnC:artC:AN1809:otaA:AN1857:AN1858:AN1883:maiA:fahA:hmgA:AN1898:hpdA:AN1913:AN1923:AN1990:AN1993:gatA:AN2293:AN2525:AN2526:AN2723:lysA:agaA:AN2914:idpA:AN3031:AN3058:AN3073:prs3:AN3313:AN3431:AN3456:AN3593:AN3634:AN3656:AN3695:AN3748:AN3824:AN3829:ileA:AN3865:AN3866:AN3897:gmdA:AN4081:AN4086:glnA:AN4290:AN4323:metR:gdhA:AN4401:AN4430:metH:fmdS:mccB:mccA:sC:sA:AN4774:AN4793:gtaA:AN4820:AN4901:AN4956:AN5060:AN5138:AN5200:lysB:AN5444:AN5447:AN5601:AN5610:AN5662:aroF:AN5867:metF:echA:AN5957:AN5999:AN6048:AN6227:trpB:podG:AN6338:AN6346:AN6368:AN6399:AN6526:hisB:AN6576:aroC:AN6889:AN7044:metG:AN7278:AN7361:hisHF:AN7451:AN7479:AN7600:AN7656:AN7722:pyroA:cysB:metA:AN8224:cysD:cysA:AN8654:AN8709:AN8770:amdS:AN8815:AN8859:AN8866:AN8867:alcR:alcA:AN9157:AN9419

For Peer Review

44283	small molecule biosynthetic process	207 out of 2759 genes, 7.5%	410 out of 10988 background genes, 3.7%	3.86e-26	palB:AN0270:aroG:AN0451:aldA:AN0593:AN0608:sidI:basA:spdA:aromA:AN0797:laeA:pdeA:AN0840:AN0912:AN0918:AN10197:pexE:AN10230:AN10290:AN10298:odeA:veA:msrA:AN10642:AN10648:AN10661:AN10710:AN10764:AN10936:AN10981:AN10996:AN11008:AN11111:phenA:qutB:AN1150:AN12152:gppA:AN12201:AN12331:pgkA:AN1409:AN1524:AN1673:prnD:prnC:artC:AN1840:AN1857:AN1858:AN1860:AN1883:maiA:fahA:hmgA:hpdA:pdmA:acuF:AN1923:AN1990:AN1993:AN1999:AN2069:AN2272:alcC:AN2293:AN2389:AN2526:easB:gpdC:aatA:AN2723:AN2814:lysA:fbaA:AN2914:idpA:AN3031:suAprgA1:AN3058:pgmA:AN3222:pfkA:AN3276:pkiB:AN3586:AN3593:AN3634:AN3638:gukA:AN3695:AN3748:ileA:AN3840:AN3954:gmdA:CYP61A1:AN4094:AN4118:sdeB:glnA:AN4290:AN4323:AN4353:gdhA:AN4401:AN4405:AN4430:metH:AN4569:fmdS:mccA:AN4757:sA:AN4774:AN4793:pdcA:AN4923:AN4956:AN5025:ppoC:AN5138:pdhB:AN5200:lysB:pkiA:AN5415:AN5444:AN5497:AN5566:AN5601:acuG:AN5610:aroF:AN5704:acuN:sidA:ldhA:AN5862:AN5867:metF:pyrF:AN5904:pyrE:catC:AN5939:AN5957:swoM:AN6048:accA:AN6141:pyrG:AN6227:trpB:sidF:sidH:sidD:AN6276:AN6338:AN6346:AN6506:hisB:AN6572:AN6576:biA:bioF:sdeA:aatB:aroC:tpiA:AN6973:AN7044:metG:AN7146:an2:hisHF:hxkA:AN7600:AN7625:AN7656:AN7722:pyroA:AN7856:AN8012:gpdA:cysB:phacA:AN8188:metA:swoH:citA:cysD:cyp51B:AN8553:cysA:g

For Peer Review

1901566	organonitrogen compound biosynthetic process	386 out of 2759 genes, 14.0%	951 out of 10988 background genes, 8.7%	6.29e-25	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0128:AN0142:AN0167:AN0183:AN0252:palB:AN0262:AN0270:AN0278:AN0318:aroG:AN0428:AN0433:AN0445:AN0465:AN0470:AN0490:AN0495:aldA:pyrABCN:AN0570:AN0608:sidI:basA:spdA:AN0705:aromA:AN0776:mns1B:AN0797:laeA:AN0827:AN0840:AN0843:adB:AN0907:AN0912:glrA:AN0936:atp20:brlA:AN1013:pyrD:AN10182:pexE:AN10230:AN10290:AN10298:sgdB:AN10416:AN10459:AN10475:veA:AN10527:msrA:AN10614:AN10681:AN10740:AN10764:AN1080:AN1084:AN10913:AN10914:AN10936:AN1095:AN10981:AN10996:AN11111:AN11125:phenA:AN1122:AN11232:AN11252:AN11303:qutB:AN11411:AN11419:AN11444:AN1150:AN1162:AN11631:AN1166:AN12101:AN12201:AN12246:AN1228:AN12316:AN12319:pgkA:hscA:AN12478:AN1263:AN1345:AN1380:AN1393:AN1455:AN1523:AN1524:AN1534:oliC:hxB:AN1673:AN1709:AN1710:AN1722:prnD:prnC:AN1770:AN1857:AN1858:AN1883:maiA:fahA:hmgA:hpdA:AN1913:AN1915:acuF:AN1923:AN1950:AN1964:AN1970:AN1990:AN1993:URFA3:atp8:oliA:AN20013:AN2057:AN2272:AN2275:hemA:AN2293:AN2301:AN2389:lagA:AN2526:easA:easB:easD:gpdC:aatA:AN2723:AN2733:AN2734:gpxA:lysA:fbaA:AN2914:AN2932:pdhX:AN2980:AN2992:AN2997:idpA:AN3031:suAprgA1:AN3058:pgmA:AN3073:AN3172:AN3173:AN3222:pfkA:AN3413:AN3431:AN3588:AN3593:AN3595:AN3626:AN3634:AN3639:gukA:AN3649:A

For Peer Review

For Peer Review

1901605	alpha-amino acid metabolic process	113 out of 2759 genes, 4.1%	183 out of 10988 background genes, 1.7%	9.93e-23	AN0174:AN0300:aldA:pyrABCN:AN0593:spdA:AN0720:AN0797:AN0840:AN0912:AN10230:AN10298:AN1054:msrA:AN10901:AN10996:phenA:AN11252:AN1150:sD:AN1198:sasA:AN1263:prnD:prnC:artC:otaA:AN1857:AN1858:AN1883:maiA:fahA:hmgA:AN1898:hpdA:AN1923:AN1990:AN1993:gatA:AN2293:AN2525:AN2723:lysA:agaA:AN2914:idpA:AN3031:AN3058:prs3:AN3313:AN3431:AN3456:AN3593:AN3634:AN3695:AN3748:AN3829:ileA:AN3897:gmdA:AN4081:glnA:AN4290:AN4323:gdhA:AN4401:metH:mccB:mccA:sC:sA:AN4774:AN4793:gtaA:AN4820:AN4901:AN4956:AN5060:AN5200:lysB:AN5447:AN5601:AN5610:AN5867:metF:echA:AN5999:AN6048:trpB:AN6338:AN6399:hisB:AN6576:aroC:AN7044:metG:AN7278:hisHF:AN7451:AN7722:pyroA:cysB:metA:cysD:cysA:AN8654:AN8709:AN8770:amdS:AN8859:AN8866:alcR:alcA

16053	organic acid biosynthetic process	145 out of 2759 genes, 5.3%	274 out of 10988 background genes, 2.5%	3.90e-20	palB:aroG:aldA:basA:spdA:aromA:AN0797:AN0840:AN0912:AN0918:AN10197:pexE:AN10230:AN10298:odeA:veA:msrA:AN10996:phenA:qutB:AN1150:AN12331:pgkA:AN1524:AN1673:prnD:prnC:AN1840:AN1857:AN1858:AN1883:maiA:fahA:hmgA:hpdA:acuF:AN1923:AN1990:AN1993:AN2293:AN2389:AN2526:easB:gpdC:aatA:AN2723:lysA:fbaA:AN2914:idpA:AN3031:suAprgA1:AN3058:pgmA:pfkA:AN3276:pkiB:AN3593:AN3634:AN3638:gukA:AN3695:AN3748:ileA:AN3840:AN3954:gmdA:sdeB:glnA:AN4290:AN4323:AN4353:gdhA:AN4401:AN4405:AN4430:metH:fmdS:mccA:sA:AN4774:AN4793:pdcA:AN4956:AN5025:ppoC:AN5138:pdhB:AN5200:lysB:pkiA:AN5444:AN5601:acuG:AN5610:aroF:AN5704:acuN:ldhA:AN5867:metF:AN5904:AN5957:swoM:AN6048:accA:AN6227:trpB:AN6338:AN6346:AN6506:hisB:AN6576:biA:bioF:sdeA:aatB:aroC:tpiA:AN6973:AN7044:metG:an2:hisHF:hxkA:AN7600:AN7656:AN7722:pyroA:AN7856:gpdA:cysB:phacA:AN8188:metA:cysD:cysA:glkA:AN8770:amdS:AN8859:AN8866:AN8907:fasA:fasB

For Peer Review

46394	carboxylic acid biosynthetic process	144 out of 2759 genes, 5.2%	273 out of 10988 background genes, 2.5%	8.50e-20	palB:aroG:aldA:basA:spdA:aromA:AN0797:AN0840:AN0912:AN0918:pexE:AN10230:AN10298:odeA:veA:msrA:AN10996:phenA:qutB:AN1150:AN12331:pgkA:AN1524:AN1673:prnD:prnC:AN1840:AN1857:AN1858:AN1883:maiA:fahA:hmgA:hpdA:acuF:AN1923:AN1990:AN1993:AN2293:AN2389:AN2526:easB:gpdC:aatA:AN2723:lysA:fbaA:AN2914:idpA:AN3031:suAprgA1:AN3058:pgmA:pfkA:AN3276:pkiB:AN3593:AN3634:AN3638:gukA:AN3695:AN3748:ileA:AN3840:AN3954:gmdA:sdeB:glnA:AN4290:AN4323:AN4353:gdhA:AN4401:AN4405:AN4430:metH:fmdS:mccA:sA:AN4774:AN4793:pdcA:AN4956:AN5025:ppoC:AN5138:pdhB:AN5200:lysB:pkiA:AN5444:AN5601:acuG:AN5610:aroF:AN5704:acuN:ldhA:AN5867:metF:AN5904:AN5957:swoM:AN6048:accA:AN6227:trpB:AN6338:AN6346:AN6506:hisB:AN6576:biA:bioF:sdeA:aatB:aroC:tpiA:AN6973:AN7044:metG:an2:hisHF:hxkA:AN7600:AN7656:AN7722:pyroA:AN7856:gpdA:cysB:phacA:AN8188:metA:cysD:cysA:glkA:AN8770:amdS:AN8859:AN8866:AN8907:fasA:fasB

For Peer Review

19693	ribose phosphate metabolic process	93 out of 2759 genes, 3.4%	147 out of 10988 background genes, 1.3%	2.02e-19	pppA:AN0252:AN0285:AN0318:AN0495:AN0593:AN0672:AN0688:pdeA:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:AN1593:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:AN2335:AN2440:gpdC:fbaA:pdhX:gsdA:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:faaA:swoM:pyrG:creA:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:ndxB:gpdA:AN8118:AN8121:swoH:AN8219:citA:AN8551:glkA:alcA:pdhC:panK

For Peer Review

55086	nucleobase-containing small molecule metabolic process	141 out of 2759 genes, 5.1%	267 out of 10988 background genes, 2.4%	2.11e-19	pppA:AN0252:AN0285:AN0318:AN0490:AN0495:pyrABCN:AN0593:AN0672:AN0688:pdeA:adB:atp20:pyrD:AN10230:AN10298:AN10525:AN10661:AN1071:AN10710:AN10903:AN11252:AN11303:AN11347:AN11444:AN11859:AN12213:AN12256:AN12316:pgkA:AN12478:AN1263:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1715:AN1806:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2133:AN2272:alcC:AN2316:AN2335:AN2440:gpdC:pgmB:fbaA:pdhX:gsdA:pgmA:AN3077:prs3:AN3222:pfkA:AN3431:AN3557:AN3626:AN3639:gukA:AN3708:AN3881:cyaA:AN3922:AN3954:AN4258:AN4388:mag1:metH:purH:AN4525:AN4603:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:AN5200:pkiA:AN5492:AN5566:acuG:hxA:facA:acuN:ldhA:pyrF:pyrE:AN5939:faaA:swoM:pyrG:creA:AN6209:AN6287:AN6325:AN6541:pdhA:tpiA:hxkA:AN8019:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:citA:AN8457:AN8533:AN8551:AN8611:glkA:alcA:AN9116:galF:AN9315:AN9402:pdhC:AN9426:panK

For Peer Review

For Peer Review

8152	metabolic process	1332 out of 2759 genes, 48.3%	4435 out of 10988 background genes, 40.4%	2.25e-19	AN0016:AN0034:AN0046:AN0051:AN0057:AN0058:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0137:AN0142:AN0160:AN0167:AN0174:AN0183:lacC:AN0224:ivoB:ureD:pppA:pdiB:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0367:AN0370:AN0377:AN0381:araR:AN0403:AN0408:AN0428:AN0433:AN0443:AN0445:AN0450:AN0451:AN0465:AN0470:engA:AN0490:AN0495:AN0507:aldA:mreA:AN0560:AN0562:pyrABCN:AN0567:AN0570:AN0574:AN0579:AN0591:AN0593:AN0608:sidI:basA:AN0647:AN0649:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0701:AN0705:aromA:bglB:AN0714:AN0718:AN0720:H4.1:AN0740:AN0742:AN0745:AN0752:AN0757:AN0773:AN0775:AN0776:AN0779:AN0784:sodM:mns1B:AN0797:AN0801:laeA:scdA:AN0827:pdeA:AN0836:AN0840:AN0843:hsp104:AN0868:AN0876:adB:AN0907:AN0908:AN0912:AN0913:AN0917:AN0918:glrA:AN0936:agdE:ladA:atp20:AN0956:AN0963:brlA:AN0984:AN10005:AN10011:oca2:AN10024:AN10026:AN1003:niaD:AN10060:niiA:AN10099:AN10108:AN10122:AN1013:pyrD:AN10134:AN1015:ganB:AN10164:AN10182:AN10189:culA:AN10197:pexE:ccp1:AN10223:AN10229:AN10230:AN1024:CYP532A4:AN10280:AN10287:AN10290:AN10296:AN10297:AN10298:AN10299:AN10335:AN10336:AN10348:sgdB:AN10354:AN10358:AN10368:odeA:AN10392:AN10399:AN10415:AN10416:AN10417:agdF:AN10429:AN10433:ggtA:A

For Peer Review

9117	nucleotide metabolic process	112 out of 2759 genes, 4.1%	194 out of 10988 background genes, 1.8%	4.55e-19	pppA:AN0252:AN0285:AN0318:AN0490:AN0495:AN0593:AN0672:AN0688:pdeA:adB:atp20:pyrD:AN10525:AN10661:AN11252:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN12478:AN1523:AN1534:AN1593:oliC:hxB:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2272:alcC:AN2316:AN2335:AN2440:gpdC:fbaA:pdhX:gsdA:pgmA:prs3:AN3222:pfkA:AN3431:AN3626:AN3639:gukA:AN3708:cyaA:AN3922:AN3954:AN4258:AN4388:mag1:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:AN5200:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:AN5939:faaA:swoM:pyrG:creA:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:citA:AN8551:glkA:alcA:AN9116:AN9315:AN9402:pdhC:panK
72521	purine-containing compound metabolic process	91 out of 2759 genes, 3.3%	144 out of 10988 background genes, 1.3%	6.58e-19	AN0252:AN0318:AN0495:AN0593:pdeA:adB:atp20:AN10298:AN10903:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN12478:AN1263:AN1523:AN1524:AN1534:AN1593:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2272:alcC:AN2316:gpdC:fbaA:pdhX:pgmA:AN3222:pfkA:AN3626:AN3639:gukA:cyaA:AN3922:AN3954:AN4388:metH:purH:AN4525:AN4603:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:hxA:facA:acuN:ldhA:faaA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:swoH:AN8219:citA:glkA:alcA:pdhC:panK

For Peer Review

6753	nucleoside phosphate metabolic process	113 out of 2759 genes, 4.1%	199 out of 10988 background genes, 1.8%	1.89e-18	pppA:AN0252:AN0285:AN0318:AN0490:AN0495:AN0593:AN0672:AN0688:pdeA:adB:atp20:pyrD:AN10525:AN10661:AN11252:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN12478:AN1523:AN1534:AN1593:oliC:hxB:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2272:alcC:AN2316:AN2335:AN2440:gpdC:fbaA:pdhX:gsdA:pgmA:prs3:AN3222:pfkA:AN3431:AN3626:AN3639:gukA:AN3708:cyaA:AN3922:AN3954:AN4258:AN4388:mag1:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:AN5200:pkiA:AN5492:AN5566:acuG:facA:acuN:ldhA:pyrE:AN5939:faaA:swoM:pyrG:creA:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:citA:AN8551:glkA:alcA:AN9116:AN9315:AN9402:pdhC:panK
6163	purine nucleotide metabolic process	82 out of 2759 genes, 3.0%	125 out of 10988 background genes, 1.1%	2.23e-18	AN0252:AN0318:AN0495:AN0593:pdeA:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN12478:AN1523:AN1534:AN1593:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:faaA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:swoH:AN8219:citA:glkA:alcA:pdhC:panK

9150	purine ribonucleotide metabolic process	81 out of 2759 genes, 2.9%	123 out of 10988 background genes, 1.1%	2.72e-18	AN0252:AN0318:AN0495:AN0593:pdeA:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:AN1593:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:faaA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:swoH:AN8219:citA:glkA:alcA:pdhC:panK
9259	ribonucleotide metabolic process	83 out of 2759 genes, 3.0%	128 out of 10988 background genes, 1.2%	3.91e-18	AN0252:AN0318:AN0495:AN0593:pdeA:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:AN1593:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:faaA:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8118:AN8121:swoH:AN8219:citA:glkA:alcA:pdhC:panK

For Peer Review

1901564	organonitrogen compound metabolic process	620 out of 2759 genes, 22.5%	1818 out of 10988 background genes, 16.5%	5.43e-18	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0128:AN0142:AN0167:AN0174:AN0183:AN0224:ureD:pppA:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0381:AN0428:AN0433:AN0445:AN0450:AN0465:AN0470:AN0490:AN0495:aldA:pyrABCN:AN0570:AN0593:AN0608:sidI:basA:AN0672:spdA:AN0688:AN0705:aromA:AN0720:AN0745:AN0776:mns1B:AN0797:laeA:AN0827:pdeA:AN0840:AN0843:hsp104:adB:AN0907:AN0912:AN0918:glrA:AN0936:atp20:brlA:oca2:AN1013:pyrD:AN10134:AN10182:AN10189:culA:pexE:AN10230:AN10290:AN10298:AN10299:AN10336:sgdB:AN10354:AN10416:AN10433:ggtA:AN10459:AN10475:FKBP5:veA:AN10525:AN10527:AN1054:AN10540:msrA:ltpA:facC:AN10599:AN10614:AN10681:AN1071:AN10740:AN10764:AN1080:ffkB:AN10832:AN10838:AN1084:AN10901:AN10903:AN10913:AN10914:AN1092:AN10936:AN1095:AN10981:AN10996:AN1102:AN11110:AN11111:AN11125:phenA:AN1122:AN11232:AN11252:AN11303:AN11347:qutB:AN11411:AN11419:AN11444:AN1150:AN1162:AN11631:AN1166:AN11722:AN1176:AN1179:AN11859:AN11903:sumO:sD:AN11961:AN1198:AN12101:AN12201:AN12213:sasA:AN12246:AN12256:AN12279:AN1228:AN12316:AN12319:AN12437:pgkA:hscA:AN12478:AN1263:AN1320:nnaA:AN1345:AN1380:AN1393:AN1426:codA:AN1445:AN1455:nagA:AN1523:AN1524:AN1534:csnD:AN1573:AN1586:AN1593:oliC:atg1:hxB:AN1

For Peer Review

6091	generation of precursor metabolites and energy	93 out of 2759 genes, 3.4%	152 out of 10988 background genes, 1.4%	6.36e-18	AN0252:AN0318:AN1003:AN10060:AN1015:AN10495:AN10585:facC:AN10642:AN11347:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:enaB:artC:AN1915:acuF:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:aclA:aclB:gpdC:pgmB:fbaA:ippA:idpA:suAprgA1:pgmA:AN3068:pfkA:gukA:AN3813:AN3894:AN3901:AN3922:AN3954:AN4064:AN4388:AN4525:mccA:AN4863:pdcA:AN4927:AN5088:pdhB:pkiA:AN5300:noxA:AN5497:acoA:AN5597:acuG:AN5669:acuN:AN5790:ldhA:AN5971:swoM:cycA:AN6255:AN6287:AN6297:AN6564:enaA:mcsA:tpiA:hxkA:AN7497:AN7629:AN8010:gpdA:AN8118:AN8219:AN8273:citA:AN8399:glkA:alcA:galF
8652	cellular amino acid biosynthetic process	84 out of 2759 genes, 3.0%	135 out of 10988 background genes, 1.2%	1.16e-16	aroG:aromA:AN0797:AN0840:AN0912:AN10230:AN10298:msrA:AN10996:phenA:qutB:AN1150:AN1673:prnD:prnC:AN1857:AN1858:AN1883:maiA:fahA:hmgA:hpdA:AN1923:AN1990:AN1993:AN2293:AN2526:AN2723:lysA:AN2914:idpA:AN3031:AN3058:AN3593:AN3634:AN3695:AN3748:ileA:gmdA:glnA:AN4290:AN4323:gdhA:AN4401:AN4430:metH:fmdS:sA:AN4774:AN4793:AN4956:AN5138:AN5200:lysB:AN5444:AN5601:AN5610:aroF:AN5867:metF:AN5957:AN6048:AN6227:trpB:AN6338:AN6346:hisB:AN6576:aroC:AN7044:metG:hisHF:AN7600:AN7656:AN7722:pyroA:cysB:metA:cysD:cysA:AN8770:amdS:AN8859:AN8866

For Peer Review

55114	oxidation-reduction process	328 out of 2759 genes, 11.9%	850 out of 10988 background genes, 7.7%	2.24e-16	AN0051:AN0174:AN0377:AN0403:AN0443:aldA:AN0567:AN0593:basA:AN0672:AN0701:AN0740:AN0773:AN0775:sodM:AN0797:scdA:AN0836:AN0868:AN0876:AN0912:AN0918:glrA:ladA:AN0956:AN10011:AN10026:AN1003:niaD:AN10060:niiA:AN10099:AN10108:AN1015:pexE:ccp1:AN10223:AN10229:CYP532A4:AN10290:AN10296:AN10358:odeA:AN10392:mthA:AN10525:AN10527:msrA:AN10585:facC:CYP539B2:AN10642:ahbB:AN10648:AN10703:acdB:AN10841:CYP578B1:AN10901:bzuA:AN11008:AN11045:AN11094:AN11177:AN11243:AN11252:AN1131:AN11347:qutB:AN1142:AN11859:AN11861:sD:AN11981:AN12101:AN12213:acdA:AN12449:AN12478:AN1274:AN1301:phacB:codA:AN1510:AN1524:AN1541:AN1543:AN1586:AN1593:CYP620E1:AN1699:prnD:prnC:artC:AN1752:CYP682D1:AN1868:AN1882:hmgA:hpdA:pdmA:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:CYP552A2:AN2042:AN2208:alcC:AN2316:AN2335:AN2387:AN2389:AN2390:aclA:aclB:AN2526:easB:gpdC:AN2682:AN2704:AN2723:AN2801:AN2835:gpxA:AN2860:AN2866:pgmB:gsdA:idpA:AN3030:suAprgA1:AN3043:AN3068:AN3205:AN3206:AN3208:AN3239:AN3291:AN3296:CYP659A1:AN3399:trxR:AN3586:AN3591:AN3596:AN3605:AN3638:AN3672:alcB:AN3813:AN3829:AN3855:AN3894:AN3901:AN3902:CYP539D1:AN3920:AN3922:AN3954:AN3973:CYP61A1:AN4050:AN4064:AN4070:AN4081:AN4120:sdeB:AN4212:ladB:gdhA:AN438

For Peer Review

For Peer Review

9161	ribonucleoside monophosphate metabolic process	68 out of 2759 genes, 2.5%	100 out of 10988 background genes, 0.9%	3.47e-16	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:pdcA:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8118:AN8121:AN8219:glkA:alcA
9126	purine nucleoside monophosphate metabolic process	66 out of 2759 genes, 2.4%	96 out of 10988 background genes, 0.9%	4.78e-16	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:pdcA:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:swoM:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8118:AN8121:AN8219:glkA:alcA
9167	purine ribonucleoside monophosphate metabolic process	66 out of 2759 genes, 2.4%	96 out of 10988 background genes, 0.9%	4.78e-16	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:pdcA:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:swoM:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8118:AN8121:AN8219:glkA:alcA

71704	organic substance metabolic process	1047 out of 2759 genes, 37.9%	3414 out of 10988 background genes, 31.1%	5.53e-16	AN0016:AN0034:AN0046:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0137:AN0142:AN0160:AN0167:AN0174:AN0183:lacC:AN0224:ivoB:ureD:pppA:pdiB:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0367:AN0381:araR:AN0408:AN0428:AN0433:AN0445:AN0450:AN0451:AN0465:AN0470:engA:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0567:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0647:AN0649:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:aromA:bglB:AN0714:AN0718:AN0720:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0779:mns1B:AN0797:laeA:scdA:AN0827:pdeA:AN0836:AN0840:AN0843:hsp104:AN0868:adB:AN0907:AN0908:AN0912:AN0913:AN0917:AN0918:glrA:AN0936:agdE:ladA:atp20:AN0956:AN0963:brlA:AN0984:oca2:AN1003:niaD:AN10060:niiA:AN1013:pyrD:AN10134:AN1015:ganB:AN10164:AN10182:AN10189:culA:AN10197:pexE:AN10230:AN1024:AN10280:AN10287:AN10290:AN10298:AN10299:AN10336:AN10348:sgdB:AN10354:odeA:AN10415:AN10416:AN10417:agdF:AN10433:ggtA:AN1045:AN10459:AN10475:bglF:FKBP5:AN10495:AN1050:mthA:veA:AN10525:AN10527:AN1054:AN10540:AN10548:msrA:ltpA:facC:AN10599:AN10600:AN10614:AN10618:AN10619:AN10638:AN10642:AN10648:AN10661:AN10672:AN1068:AN10681:AN10697:AN10700:AN1071:AN10710:AN10712:AN10740:AN10764:AN10789:AN

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9123	nucleoside monophosphate metabolic process	68 out of 2759 genes, 2.5%	102 out of 10988 background genes, 0.9%	1.82e-15	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3922:AN3954:AN4388:purH:AN4525:mccA:AN4739:pdcA:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8118:AN8121:AN8219:glkA:alcA
46034	ATP metabolic process	55 out of 2759 genes, 2.0%	75 out of 10988 background genes, 0.7%	4.35e-15	AN0252:AN0318:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:gukA:AN3922:AN3954:AN4388:AN4525:mccA:pdcA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8118:AN8219:glkA:alcA
9199	ribonucleoside triphosphate metabolic process	58 out of 2759 genes, 2.1%	82 out of 10988 background genes, 0.7%	8.76e-15	AN0252:AN0318:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:gukA:AN3922:AN3954:AN4388:AN4525:mccA:cnxH:pdcA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8118:swoH:AN8219:glkA:alcA

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9205	purine ribonucleoside triphosphate metabolic process	58 out of 2759 genes, 2.1%	82 out of 10988 background genes, 0.7%	8.76e-15	AN0252:AN0318:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:gukA:AN3922:AN3954:AN4388:AN4525:mccA:cnxH:pdcA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8118:swoH:AN8219:glkA:alcA
17144	drug metabolic process	159 out of 2759 genes, 5.8%	344 out of 10988 background genes, 3.1%	1.17e-14	AN0252:palB:AN0270:AN0299:AN0318:aldA:facB:laeA:adB:atp20:AN1003:pexE:AN10230:AN10290:AN10495:veA:msrA:facC:AN10700:AN10838:AN10901:AN10936:bzuA:AN10981:AN11015:AN11111:phenA:AN11303:AN11347:AN11444:AN11859:AN1198:AN12213:sasA:AN12279:AN12331:pgkA:nagA:AN1523:AN1534:mcdA:oliC:maiA:fahA:hmgA:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:gatA:alcC:AN2316:aclA:aclB:AN2525:AN2528:easB:gpdC:aatA:AN2814:gpxA:fbaA:idpA:suAprgA1:AN3058:pgmA:pfkA:plyE:pmeA:AN3593:gukA:AN3829:AN3840:AN3894:AN3897:AN3922:AN3954:pcmA:AN4290:chsF:pgaB:AN4388:metH:AN4525:AN4603:mccA:AN4820:chiB:pdcA:AN4927:AN5025:pdhB:pkiA:AN5300:AN5415:AN5447:AN5497:acoA:acuG:facA:acuD:AN5669:acuN:AN5790:pcsA:ldhA:catC:swoM:AN6141:AN6209:AN6276:AN6287:AN6338:rglB:aciA:AN6576:biA:bioF:mcsA:acuE:aatB:aroC:tpiA:metG:rglA:AN7278:acuL:hxkA:AN7600:AN7661:pyroA:abnC:gpdA:phacA:AN8118:AN8188:AN8219:chiA:citA:cysD:AN8390:plyH:AN8654:glkA:mclA:alcR:alcA:AN8999

For Peer Review

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44249	cellular biosynthetic process	554 out of 2759 genes, 20.1%	1640 out of 10988 background genes, 14.9%	1.59e-14	AN0016:AN0046:AN0057:AN0097:AN0105:AN0116:AN0123:AN0142:AN0167:AN0183:ivoB:AN0252:palB:AN0262:AN0270:AN0278:AN0318:aroG:araR:AN0428:AN0433:AN0445:AN0451:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:pyrABCN:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0661:spdA:facB:AN0705:aromA:AN0718:AN0720:H4.1:AN0742:AN0752:AN0776:mns1B:AN0797:laeA:AN0827:pdeA:AN0836:AN0840:AN0843:adB:AN0907:AN0908:AN0912:AN0913:AN0918:glrA:AN0936:atp20:brlA:AN10060:AN1013:pyrD:AN10182:AN10197:pexE:AN10230:AN10290:AN10298:AN10336:sgdB:odeA:AN10416:AN10459:AN10475:veA:AN10527:AN10548:msrA:AN10600:AN10614:AN10638:AN10642:AN10648:AN10661:AN10681:AN10697:AN10710:AN10740:AN10764:AN10789:AN1080:AN1084:AN10906:AN10910:AN10913:AN10914:AN10936:AN1095:AN10970:AN10981:AN10996:AN11003:AN11008:AN11093:AN11111:AN11112:AN11125:phenA:AN11161:AN11197:AN11212:AN1122:AN11232:AN11252:AN11303:qutB:AN11411:AN11419:AN11444:AN1150:AN1162:AN11631:AN1166:AN11859:sumO:AN11961:AN12101:AN12152:gppA:AN12201:sasA:AN12246:AN1228:AN12316:AN12319:AN12331:pgkA:hscA:AN12478:AN12489:AN1263:AN1345:AN1380:AN1393:AN1409:farB:AN1435:AN1455:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1673:AN1709:AN1710:AN1715:AN1722:prnD:prnC:artC:AN1770:AN1840:nosA:AN1857:AN1858

For Peer Review

9144	purine nucleoside triphosphate metabolic process	58 out of 2759 genes, 2.1%	84 out of 10988 background genes, 0.8%	5.39e-14	AN0252:AN0318:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:gukA:AN3922:AN3954:AN4388:AN4525:mccA:cnxH:pdcA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8118:swoH:AN8219:glkA:alcA
32787	monocarboxylic acid metabolic process	124 out of 2759 genes, 4.5%	250 out of 10988 background genes, 2.3%	6.58e-14	palB:AN0285:AN0300:aldA:basA:AN0649:spdA:facB:laeA:scdA:AN0868:AN0912:AN0918:pexE:AN10287:odeA:AN1050:mthA:veA:facC:AN10700:AN10841:bzuA:AN11045:qutB:pgkA:AN1409:xprG:farB:mcdA:AN1840:acuF:AN1968:AN1990:AN2208:gatA:alcC:AN2389:easB:gpdC:aatA:fbaA:pdhX:suAprgA1:pgmA:pfkA:AN3276:pkiB:AN3638:gukA:AN3829:AN3901:AN3954:AN4055:AN4081:sdeB:AN4353:pgaB:AN4401:AN4405:mccA:pdcA:AN5025:ppoC:AN5138:pdhB:fatA:pkiA:AN5447:AN5534:acuG:facA:acuD:AN5646:AN5698:AN5704:acuN:pcsA:ldhA:pdkA:AN5904:echA:catC:AN5977:AN5990:pexA:faaA:swoM:accA:AN6506:aciA:biA:bioF:mcsA:acuE:pdhA:sdeA:aatB:tpiA:AN6973:hadA:farA:foxA:an2:acuL:cpeA:hxkA:AN7770:AN7856:gpdA:phacA:faaB:pdcB:AN8553:catA:glkA:mclA:AN8907:alcP:alcA:AN9297:pdhC:fasA:fasB

44238	primary metabolic process	947 out of 2759 genes, 34.3%	3085 out of 10988 background genes, 28.1%	9.55e-14	AN0034:AN0046:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0137:AN0142:AN0160:AN0167:AN0174:AN0183:lacC:AN0224:pppA:AN0252:palB:AN0262:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0367:AN0381:araR:AN0408:AN0428:AN0433:AN0445:AN0450:AN0451:AN0465:AN0470:engA:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0567:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0647:AN0649:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:aromA:bglB:AN0714:AN0718:AN0720:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0779:mns1B:AN0797:scdA:AN0827:pdeA:AN0840:AN0843:hsp104:AN0868:adB:AN0907:AN0908:AN0912:AN0913:AN0917:AN0918:glrA:AN0936:agdE:ladA:atp20:AN0956:AN0963:AN0984:oca2:AN1003:AN10060:AN1013:pyrD:AN10134:AN1015:ganB:AN10164:AN10182:AN10189:culA:pexE:AN10230:AN1024:AN10280:AN10287:AN10298:AN10299:AN10336:AN10348:sgdB:AN10354:odeA:AN10415:AN10416:AN10417:agdF:AN10433:AN1045:AN10459:AN10475:bglF:FKBP5:AN1050:mthA:AN10525:AN1054:AN10540:AN10548:msrA:ltpA:AN10599:AN10600:AN10614:AN10618:AN10638:AN10648:AN10661:AN10672:AN1068:AN10681:AN10697:AN1071:AN10710:AN10712:AN10740:AN10764:AN10789:AN1080:ffkB:AN10832:AN10838:AN1084:AN10841:fbpZ:AN10901:AN10903:AN10906:AN10910:AN10921:AN10936:AN1095:AN10970:AN10996:A

For Peer Review

1901135	carbohydrate derivative metabolic process	164 out of 2759 genes, 5.9%	366 out of 10988 background genes, 3.3%	1.36e-13	AN0128:pppA:AN0252:AN0285:AN0299:AN0318:AN0495:AN0593:basA:AN0672:AN0688:mns1B:AN0827:pdeA:adB:AN0918:ladA:atp20:AN10230:AN1068:AN1071:AN10710:AN10838:fbpZ:AN10921:AN1102:AN11232:AN11303:AN11347:AN11444:AN1176:AN11859:AN12213:AN12256:AN12279:AN12316:pgkA:AN1263:AN1428:AN1455:nagA:AN1523:AN1534:AN1593:oliC:hxB:AN1715:AN1806:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2133:AN2272:alcC:AN2316:AN2326:AN2335:AN2440:lagA:gpdC:pgmB:fbaA:pdhX:gsdA:AN3013:pgmA:AN3077:prs3:AN3222:pfkA:AN3499:AN3557:AN3588:AN3626:AN3639:gukA:AN3881:cyaA:AN3916:AN3922:AN3954:pcmA:chsF:AN4388:purH:AN4525:AN4683:mccA:AN4691:AN4716:ugeA:AN4739:cnxH:alg6:chiB:pdcA:AN4923:AN4927:AN5122:pfkZ:pdhB:pkiA:prtA:AN5566:AN5589:acuG:facA:AN5688:AN5725:AN5736:acuN:ldhA:pyrF:pyrE:faaA:swoM:pyrG:creA:AN6209:AN6287:AN6405:AN6470:AN6541:pdhA:AN6736:tpiA:AN6992:breB:hxkA:AN7472:ndxB:AN8019:gpdA:AN8118:AN8119:AN8121:swoH:AN8219:chiA:citA:AN8457:AN8533:AN8551:AN8611:glkA:AN8969:alcA:AN8999:galF:pdhC:AN9426:panK

For Peer Review

For Peer Review

1901576	organic substance biosynthetic process	557 out of 2759 genes, 20.2%	1668 out of 10988 background genes, 15.2%	1.88e-13	AN0016:AN0046:AN0057:AN0097:AN0105:AN0116:AN0123:AN0128:AN0142:AN0167:AN0183:ivoB:AN0252:palB:AN0262:AN0270:AN0278:AN0318:aroG:araR:AN0428:AN0433:AN0445:AN0451:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:pyrABCN:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0661:spdA:facB:AN0705:aromA:AN0718:H4.1:AN0742:AN0752:AN0776:mns1B:AN0797:laeA:AN0827:pdeA:AN0836:AN0840:AN0843:adB:AN0907:AN0908:AN0912:AN0913:AN0918:glrA:AN0936:ladA:atp20:brlA:AN10060:AN1013:pyrD:AN10182:AN10197:pexE:AN10230:AN10290:AN10298:AN10336:sgdB:odeA:AN10416:AN10459:AN10475:veA:AN10527:AN10548:msrA:AN10600:AN10614:AN10638:AN10642:AN10648:AN10661:AN10681:AN10697:AN10710:AN10740:AN10764:AN10789:AN1080:AN1084:AN10906:AN10910:AN10913:AN10914:AN10936:AN1095:AN10970:AN10981:AN10996:AN11003:AN11008:AN11093:AN11111:AN11112:AN11125:phenA:AN11161:AN11197:AN11212:AN1122:AN11232:AN11252:AN11303:qutB:AN11411:AN11419:AN11444:AN1150:AN1162:AN11631:AN1166:AN11859:sumO:AN11961:AN12101:AN12152:gppA:AN12201:sasA:AN12246:AN1228:AN12316:AN12319:AN12331:pgkA:hscA:AN12478:AN12489:AN1263:AN1345:AN1380:AN1393:AN1409:farB:AN1435:AN1455:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1673:AN1709:AN1710:AN1715:AN1722:prnD:prnC:artC:AN1770:AN1840:nosA:AN1857:

44282	small molecule catabolic process	89 out of 2759 genes, 3.2%	160 out of 10988 background genes, 1.5%	2.56e-13	AN0034:ureD:AN0300:araR:aldA:pyrABCN:facB:scdA:AN0868:ladA:pexE:AN10495:mthA:AN1054:facC:AN10599:AN10700:AN10841:AN10901:bzuA:AN10996:AN11015:AN11045:qutG:qutB:AN1198:AN1263:AN1274:farB:mcdA:prnD:prnC:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1923:gatA:pgmB:agaA:pgmA:gukA:AN3829:ileA:AN3897:AN3954:AN4081:AN4323:ladB:mccB:mccA:AN4691:AN4820:AN5060:pdhB:pkiA:AN5447:AN5534:facA:acuD:AN5646:AN5669:echA:AN6338:AN6399:aciA:mcsA:acuE:pdhA:AN6889:tpiA:hadA:farA:foxA:larA:AN7278:acuL:AN7708:AN7770:phacA:AN8390:AN8654:mclA:alcR:alcA

For Peer Review

9058	biosynthetic process	577 out of 2759 genes, 20.9%	1742 out of 10988 background genes, 15.9%	2.91e-13	AN0016:AN0046:AN0057:AN0097:AN0105:AN0116:AN0123:AN0128:AN0142:AN0167:AN0183:ivoB:AN0252:palB:AN0262:AN0270:AN0278:AN0318:aroG:araR:AN0428:AN0433:AN0445:AN0451:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:pyrABCN:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0661:spdA:facB:AN0705:aromA:AN0718:AN0720:H4.1:AN0742:AN0752:AN0776:mns1B:AN0797:laeA:AN0827:pdeA:AN0836:AN0840:AN0843:adB:AN0907:AN0908:AN0912:AN0913:AN0918:glrA:AN0936:ladA:atp20:brlA:AN10060:AN1013:pyrD:AN10182:AN10197:pexE:AN10230:AN10290:AN10298:AN10336:sgdB:odeA:AN10416:AN10459:AN10475:veA:AN10527:AN10548:msrA:AN10600:AN10614:AN10638:AN10642:AN10648:AN10661:AN10681:AN10697:AN10710:AN10740:AN10764:AN10789:AN1080:AN1084:AN10906:AN10910:AN10913:AN10914:AN10936:AN1095:AN10970:AN10981:AN10996:AN11003:AN11008:AN1102:AN11093:AN11111:AN11112:AN11125:phenA:AN11161:AN11197:AN11212:AN1122:AN11232:AN11252:AN11303:qutB:AN11411:AN11419:AN11444:AN1150:AN1162:AN11631:AN1166:AN11859:sumO:AN11961:AN12101:AN12152:gppA:AN12201:sasA:AN12246:AN1228:AN12316:AN12319:AN12331:pgkA:hscA:AN12478:AN12489:AN1263:AN1345:AN1380:AN1393:AN1409:farB:AN1435:AN1455:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1673:AN1709:AN1710:AN1715:AN1722:prnD:prnC:artC:AN1770:AN184

For Peer Review

16054	organic acid catabolic process	71 out of 2759 genes, 2.6%	116 out of 10988 background genes, 1.1%	3.25e-13	AN0300:aldA:pyrABCN:facB:scdA:AN0868:pexE:mthA:AN1054:facC:AN10599:AN10700:AN10841:AN10901:bzuA:AN10996:AN11045:qutB:AN1198:AN1263:farB:mcdA:prnD:prnC:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1923:gatA:agaA:gukA:AN3829:ileA:AN3897:AN3954:AN4081:AN4323:mccB:mccA:AN4820:AN5060:pdhB:AN5447:AN5534:facA:acuD:AN5646:echA:AN6338:AN6399:aciA:mcsA:acuE:pdhA:AN6889:hadA:farA:foxA:AN7278:acuL:AN7770:phacA:AN8654:mclA:alcR:alcA
46395	carboxylic acid catabolic process	71 out of 2759 genes, 2.6%	116 out of 10988 background genes, 1.1%	3.25e-13	AN0300:aldA:pyrABCN:facB:scdA:AN0868:pexE:mthA:AN1054:facC:AN10599:AN10700:AN10841:AN10901:bzuA:AN10996:AN11045:qutB:AN1198:AN1263:farB:mcdA:prnD:prnC:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1923:gatA:agaA:gukA:AN3829:ileA:AN3897:AN3954:AN4081:AN4323:mccB:mccA:AN4820:AN5060:pdhB:AN5447:AN5534:facA:acuD:AN5646:echA:AN6338:AN6399:aciA:mcsA:acuE:pdhA:AN6889:hadA:farA:foxA:AN7278:acuL:AN7770:phacA:AN8654:mclA:alcR:alcA

For Peer Review

19637	organophosphate metabolic process	151 out of 2759 genes, 5.5%	332 out of 10988 background genes, 3.0%	4.92e-13	AN0137:AN0183:pppA:AN0252:AN0270:AN0285:AN0318:AN0490:AN0495:pyrABCN:AN0579:AN0593:basA:AN0672:AN0688:AN0827:pdeA:adB:AN0913:AN0918:ladA:atp20:pyrD:AN10525:AN10661:AN1068:fbpZ:AN10921:AN11161:AN11232:AN11252:AN11303:AN11347:qutG:AN11444:AN11859:AN11959:AN12213:pgkA:AN12478:AN1263:AN1523:AN1534:AN1593:oliC:hxB:AN1713:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2008:AN2272:alcC:AN2316:AN2326:AN2335:AN2440:gpdC:pgmB:fbaA:pdhX:gsdA:pgmA:prs3:AN3222:pfkA:AN3276:AN3431:AN3588:AN3626:AN3639:gukA:AN3708:cyaA:AN3916:AN3922:AN3954:AN4258:AN4388:mag1:purH:AN4525:mccA:AN4691:AN4739:cnxH:pdcA:AN4923:AN4927:AN5122:pfkZ:pdhB:AN5200:pkiA:AN5211:AN5492:AN5566:AN5589:acuG:facA:acuN:ldhA:pyrE:AN5919:AN5939:faaA:swoM:AN6139:AN6141:pyrG:creA:AN6209:AN6287:AN6367:AN6541:pdhA:tpiA:hxkA:AN7625:ndxB:pyroA:AN8012:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:AN8233:citA:AN8551:glkA:alcA:AN9116:AN9315:AN9402:pdhC:panK

For Peer Review

44237	cellular metabolic process	974 out of 2759 genes, 35.3%	3205 out of 10988 background genes, 29.2%	6.73e-13	AN0016:AN0034:AN0046:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0137:AN0142:AN0167:AN0174:AN0183:ivoB:ureD:pppA:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0381:araR:AN0408:AN0428:AN0433:AN0445:AN0450:AN0451:AN0465:AN0470:engA:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0567:AN0570:AN0579:AN0593:AN0608:sidI:basA:AN0647:AN0649:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:aromA:AN0714:AN0718:AN0720:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:sodM:mns1B:AN0797:laeA:scdA:AN0827:pdeA:AN0836:AN0840:AN0843:AN0868:adB:AN0907:AN0908:AN0912:AN0913:AN0917:AN0918:glrA:AN0936:agdE:ladA:atp20:AN0956:brlA:AN0984:oca2:AN1003:niaD:AN10060:niiA:AN1013:pyrD:AN10134:AN1015:ganB:AN10164:AN10182:AN10189:culA:AN10197:pexE:AN10230:AN1024:AN10280:AN10287:AN10290:AN10298:AN10299:AN10336:AN10348:sgdB:AN10354:odeA:AN10415:AN10416:AN10417:agdF:AN10433:ggtA:AN1045:AN10459:AN10475:FKBP5:AN10495:AN1050:mthA:veA:AN10525:AN10527:AN1054:AN10548:msrA:ltpA:AN10584:AN10585:facC:AN10599:AN10600:AN10614:AN10618:AN10619:AN10638:AN10642:AN10648:AN10661:AN1068:AN10681:AN10697:AN10700:AN1071:AN10710:AN10712:AN10740:AN10764:AN10789:AN1080:ffkB:AN10832:AN10838:AN1084:AN10841:fbpZ:AN10901

For Peer Review

72522	purine-containing compound biosynthetic process	57 out of 2759 genes, 2.1%	85 out of 10988 background genes, 0.8%	8.16e-13	AN0252:AN0318:AN0495:adB:atp20:AN10298:AN11303:AN11444:pgkA:AN12478:AN1523:AN1524:AN1534:oliC:acuF:URFA3:atp8:oliA:AN2272:gpdC:fbaA:pdhX:pgmA:AN3222:pfkA:AN3626:AN3639:gukA:cyaA:AN3954:metH:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:pdhC:panK
9141	nucleoside triphosphate metabolic process	58 out of 2759 genes, 2.1%	88 out of 10988 background genes, 0.8%	1.50e-12	AN0252:AN0318:atp20:AN11303:AN11347:AN11444:AN11859:AN12213:pgkA:AN1523:AN1534:oliC:hxB:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:gpdC:fbaA:pgmA:pfkA:gukA:AN3922:AN3954:AN4388:AN4525:mccA:cnxH:pdcA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8118:swoH:AN8219:glkA:alcA
9260	ribonucleotide biosynthetic process	53 out of 2759 genes, 1.9%	78 out of 10988 background genes, 0.7%	3.78e-12	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:pdhC:panK
6164	purine nucleotide biosynthetic process	52 out of 2759 genes, 1.9%	76 out of 10988 background genes, 0.7%	4.45e-12	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN12478:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:pdhC:panK

For Peer Review

For Peer Review

1901607	alpha-amino acid biosynthetic process	59 out of 2759 genes, 2.1%	93 out of 10988 background genes, 0.8%	1.16e-11	AN0797:AN0840:AN0912:AN10230:AN10298:msrA:AN10996:phenA:AN1150:prnD:prnC:AN1883:AN1923:AN1990:AN2293:AN2723:lysA:AN2914:idpA:AN3031:AN3058:AN3593:AN3634:AN3695:AN3748:ileA:glnA:AN4290:AN4323:gdhA:AN4401:metH:sA:AN4774:AN4793:AN4956:lysB:AN5601:AN5610:AN5867:metF:AN6048:trpB:AN6338:hisB:AN6576:aroC:AN7044:metG:hisHF:AN7722:pyroA:cysB:metA:cysD:cysA:AN8770:AN8859:AN8866
9152	purine ribonucleotide biosynthetic process	51 out of 2759 genes, 1.8%	75 out of 10988 background genes, 0.7%	1.23e-11	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:swoM:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:pdhC:panK
46390	ribose phosphate biosynthetic process	53 out of 2759 genes, 1.9%	80 out of 10988 background genes, 0.7%	1.95e-11	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pdhX:pgmA:pfkA:AN3626:AN3639:gukA:cyaA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:pdhC:panK

1901293	nucleoside phosphate biosynthetic process	67 out of 2759 genes, 2.4%	116 out of 10988 background genes, 1.1%	1.33e-10	AN0252:AN0318:AN0490:AN0495:adB:atp20:pyrD:AN11252:AN11303:AN11444:pgkA:AN12478:AN1523:AN1534:oliC:AN1857:acuF:URFA3:atp8:oliA:AN2272:gpdC:fbaA:pdhX:pgmA:prs3:pfkA:AN3431:AN3626:AN3639:gukA:cyaA:AN3954:AN4258:mag1:purH:mccA:AN4739:AN4927:AN5122:pdhB:AN5200:pkiA:AN5492:AN5566:acuG:facA:acuN:ldhA:pyrE:AN5939:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:AN9116:pdhC:panK
9165	nucleotide biosynthetic process	66 out of 2759 genes, 2.4%	114 out of 10988 background genes, 1.0%	1.75e-10	AN0252:AN0318:AN0490:AN0495:adB:atp20:pyrD:AN11252:AN11303:AN11444:pgkA:AN12478:AN1523:AN1534:oliC:AN1857:acuF:URFA3:atp8:oliA:AN2272:gpdC:fbaA:pdhX:pgmA:prs3:pfkA:AN3431:AN3626:AN3639:gukA:cyaA:AN3954:AN4258:mag1:purH:mccA:AN4739:AN4927:AN5122:pdhB:AN5200:pkiA:AN5566:acuG:facA:acuN:ldhA:pyrE:AN5939:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:gpdA:AN8121:swoH:AN8219:glkA:AN9116:pdhC:panK

For Peer Review

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51186	cofactor metabolic process	110 out of 2759 genes, 4.0%	232 out of 10988 background genes, 2.1%	2.12e-10	AN0183:pppA:AN0270:AN0285:AN0593:AN0608:sidI:AN0672:spdA:AN0688:AN0836:glrA:AN10197:AN10290:ggtA:AN10525:AN10584:AN10642:AN1092:AN11060:AN11252:sumO:AN12152:AN12201:sasA:pgkA:AN1263:AN1524:AN1593:hxB:AN1722:artC:AN1857:AN1860:AN1915:acuF:AN1999:hemA:alcC:AN2335:AN2389:AN2440:AN2526:gpdC:AN2733:gpxA:fbaA:pdhX:gsdA:AN2988:AN3058:pgmA:pfkA:AN3431:AN3459:AN3586:AN3632:AN3639:gukA:AN3663:AN3840:AN3920:AN3954:AN4250:AN4304:AN4569:mccA:AN4757:AN4774:cnxH:pdcA:AN4923:AN5025:AN5130:pdhB:AN5200:pkiA:acuG:facA:acuN:sidA:ldhA:catC:faaA:swoM:AN6141:creA:sidF:AN6239:AN6276:AN6572:biA:bioF:pdhA:tpiA:hxkA:pyroA:gpdA:AN8188:ndxC:hapX:citA:AN8346:AN8551:glkA:alcA:AN9116:AN9315:pdhC:panK
15980	energy derivation by oxidation of organic compounds	53 out of 2759 genes, 1.9%	84 out of 10988 background genes, 0.8%	3.94e-10	AN1003:AN10060:AN1015:AN10585:facC:AN10642:AN11347:AN11859:AN12213:artC:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:alcC:AN2316:aclA:aclB:pgmB:idpA:suAprgA1:AN3068:AN3813:AN3894:AN3922:AN4064:AN4388:AN4525:AN4863:pdcA:AN5300:AN5497:acoA:AN5790:AN5971:cycA:AN6297:AN6564:mcsA:AN8010:AN8118:citA:glkA:alcA:galF
45333	cellular respiration	44 out of 2759 genes, 1.6%	66 out of 10988 background genes, 0.6%	2.67e-09	AN1003:AN10585:facC:AN10642:AN11347:AN11859:AN12213:artC:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:aclA:aclB:idpA:suAprgA1:AN3068:AN3813:AN3894:AN3922:AN4064:AN4388:AN4525:AN4863:AN5300:AN5497:acoA:AN5790:AN5971:cycA:AN6297:AN6564:mcsA:AN8118:citA

For Peer Review

9156	ribonucleoside monophosphate biosynthetic process	46 out of 2759 genes, 1.7%	72 out of 10988 background genes, 0.7%	8.19e-09	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8121:AN8219:glkA
51188	cofactor biosynthetic process	77 out of 2759 genes, 2.8%	151 out of 10988 background genes, 1.4%	1.22e-08	AN0183:AN0270:AN0608:sidI:spdA:AN0836:glrA:AN10197:AN10290:AN10642:AN11252:AN12152:AN12201:sasA:pgkA:AN1524:hxB:AN1722:artC:AN1857:AN1860:AN1915:acuF:AN1999:hemA:AN2389:AN2526:gpdC:AN2733:gpxA:fbaA:pdhX:pgmA:pfkA:AN3431:AN3586:AN3639:gukA:AN3663:AN3840:AN3920:AN3954:AN4250:AN4569:mccA:AN4757:AN4774:cnxH:AN5025:AN5130:pdhB:AN5200:pkiA:acuG:facA:acuN:sidA:ldhA:swoM:AN6141:sidF:AN6276:AN6572:biA:bioF:pdhA:tpiA:hxkA:pyroA:gpdA:AN8188:hapX:AN8346:glkA:AN9116:pdhC:panK
9127	purine nucleoside monophosphate biosynthetic process	44 out of 2759 genes, 1.6%	68 out of 10988 background genes, 0.6%	1.26e-08	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:swoM:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8121:AN8219:glkA
9168	purine ribonucleoside monophosphate biosynthetic process	44 out of 2759 genes, 1.6%	68 out of 10988 background genes, 0.6%	1.26e-08	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:swoM:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8121:AN8219:glkA

9124	nucleoside monophosphate biosynthetic process	46 out of 2759 genes, 1.7%	73 out of 10988 background genes, 0.7%	1.67e-08	AN0252:AN0318:AN0495:adB:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:AN3626:gukA:AN3954:purH:mccA:AN4739:AN4927:AN5122:pdhB:pkiA:AN5492:AN5566:acuG:acuN:ldhA:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:tpiA:hxkA:gpdA:AN8121:AN8219:glkA
44271	cellular nitrogen compound biosynthetic process	375 out of 2759 genes, 13.6%	1114 out of 10988 background genes, 10.1%	1.92e-08	AN0016:AN0046:AN0057:AN0097:AN0105:AN0116:AN0123:AN0142:AN0167:AN0252:palB:AN0262:AN0270:AN0278:AN0318:araR:AN0428:AN0433:AN0445:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:pyrABCN:AN0570:AN0593:AN0608:sidI:AN0661:spdA:facB:AN0705:AN0718:H4.1:AN0742:AN0752:AN0776:laeA:pdeA:AN0843:adB:AN0907:AN0908:glrA:AN0936:atp20:brlA:AN1013:pyrD:AN10182:pexE:AN10290:AN10298:sgdB:AN10416:AN10459:AN10475:veA:AN10527:AN10548:AN10600:AN10614:AN10638:AN10661:AN10681:AN10697:AN10710:AN10740:AN10789:AN1080:AN1084:AN10906:AN10910:AN10913:AN10914:AN10936:AN1095:AN10970:AN10981:AN10996:AN11003:AN11093:AN11111:AN11112:AN11125:AN11197:AN11212:AN1122:AN11252:AN11303:AN11411:AN11419:AN11444:AN1162:AN11631:AN1166:AN11961:AN12101:AN12201:AN12246:AN1228:AN12316:AN12319:pgkA:hscA:AN12478:AN12489:AN1345:AN1380:AN1393:farB:AN1523:AN1524:AN1534:oliC:AN1709:AN1710:AN1715:AN1722:AN1770:nosA:AN1857:AN1913:AN1915:acuF:AN1964:AN1970:AN1976:URFA3:atp8:oliA:AN20013:AN2057:AN2235:AN2272:AN2275:AN2283:hemA:AN2301:AN2389:H4.2:lagA:easA:easB:easD:AN2553:gpdC:aatA:AN2672:AN2677:AN2733:AN2734:AN2780:gpxA:AN2854:fbaA:AN2932:pdhX:AN2980:AN2992:AN2997:suAprgA1:pgmA:AN3073:prs3:AN3172:AN3173:AN3222:pfkA:clrB:AN3413:AN3431:AN3595:AN362

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9066	aspartate family amino acid metabolic process	36 out of 2759 genes, 1.3%	51 out of 10988 background genes, 0.5%	2.29e-08	AN0300:aldA:AN0720:AN10230:msrA:sasA:AN1263:AN1923:AN1990:AN1993:lysA:AN3031:AN3456:AN3593:ileA:AN4290:AN4401:metH:sA:AN4774:AN4793:lysB:AN5601:AN5610:metF:AN6048:AN6338:AN6576:metG:metA:cysD:cysA:AN8709:AN8859:alcR:alcA
6732	coenzyme metabolic process	79 out of 2759 genes, 2.9%	158 out of 10988 background genes, 1.4%	2.37e-08	AN0183:pppA:AN0270:AN0285:AN0593:AN0672:spdA:AN0688:AN10197:AN10525:AN10642:AN11252:AN12152:AN12201:sasA:pgkA:AN1524:AN1593:hxB:artC:AN1857:AN1860:acuF:AN1999:alcC:AN2335:AN2389:AN2440:AN2526:gpdC:fbaA:pdhX:gsdA:AN3058:pgmA:pfkA:AN3431:AN3586:AN3639:gukA:AN3840:AN3954:AN4569:mccA:AN4757:cnxH:pdcA:AN4923:AN5025:pdhB:AN5200:pkiA:acuG:facA:acuN:ldhA:faaA:swoM:AN6141:creA:AN6276:AN6572:biA:bioF:pdhA:tpiA:hxkA:pyroA:gpdA:AN8188:ndxC:citA:AN8551:glkA:alcA:AN9116:AN9315:pdhC:panK
6733	oxidoreduction coenzyme metabolic process	50 out of 2759 genes, 1.8%	83 out of 10988 background genes, 0.8%	2.37e-08	pppA:AN0285:AN0593:AN0672:AN0688:AN10525:AN10642:AN11252:AN12152:AN12201:pgkA:artC:AN1857:AN1860:acuF:AN1999:alcC:AN2335:AN2440:gpdC:fbaA:gsdA:pgmA:pfkA:AN3431:AN3586:gukA:AN3954:AN4569:mccA:AN4757:pdcA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:creA:AN6572:tpiA:hxkA:gpdA:ndxC:AN8551:glkA:alcA:AN9116:AN9315

For Peer Review

For Peer Review

5975	carbohydrate metabolic process	183 out of 2759 genes, 6.6%	472 out of 10988 background genes, 4.3%	3.28e-08	AN0034:AN0137:AN0160:lacC:pppA:AN0285:AN0299:AN0367:araR:engA:AN0567:AN0688:bglB:AN0779:mns1B:AN0912:agdE:ladA:AN10060:AN1015:ganB:agdF:bglF:AN10599:AN10672:AN10710:AN10838:fbpZ:glaA:gelD:qutG:AN11778:AN1197:AN11979:gppA:AN12279:pgkA:AN1274:xprG:AN1416:AN1477:nagA:xgcA:AN1715:AN1772:AN1852:AN1868:AN1870:acuF:vosA:AN2008:AN2208:AN2272:alcC:AN2325:xlnD:AN2395:AN2424:aclB:lacF:AN2528:abnA:abfA:gpdC:bglK:AN2690:bglL:pgmB:fbaA:AN2936:AN2951:gsdA:AN3013:pgmA:ugmA:AN3184:AN3200:pfkA:AN3294:agsB:plyE:clrB:pmeA:amyB:mns1C:gukA:mns1A:alcB:AN3764:agnB:bglH:cyaA:AN3916:AN3925:AN3954:exgC:AN4055:bglA:pcmA:ladB:pgaB:AN4601:mccA:AN4691:ugeA:AN4822:AN4825:agdG:chiB:pdcA:AN5138:pfkZ:pdhB:pkiA:faeC:gldB:AN5589:acuG:acuD:AN5672:acuN:clrA:ldhA:agsA:AN5917:catC:bglG:AN5986:swoM:AN6113:AN6128:amyE:rglB:AN6405:AN6470:AN6518:mcsA:acuE:AN6819:tpiA:AN6985:foxA:breB:rglA:larA:AN7275:agdC:mutA:cpeA:bglM:hxkA:agdD:AN7590:AN7625:AN7708:bxlD:bglJ:eglC:abnC:AN8010:gpdA:AN8068:aglC:afcA:chiA:citA:AN8347:aglE:plyH:AN8551:AN8553:catA:glkA:mclA:AN8890:pgxB:agdB:AN8969:alcP:alcA:AN8999:galF:AN9380

9987	cellular process	1165 out of 2759 genes, 42.2%	4056 out of 10988 background genes, 36.9%	3.47e-08	AN0016:AN0034:AN0046:tmpA:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0137:AN0142:AN0163:AN0167:AN0174:AN0183:AN0184:ivoB:ureD:pppA:pdiB:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:tubA:AN0318:rabE:aroG:AN0381:araR:AN0408:AN0428:AN0433:AN0445:AN0450:AN0451:AN0465:AN0470:engA:AN0490:AN0495:AN0507:aldA:mreA:AN0559:AN0560:pyrABCN:AN0567:AN0570:AN0579:AN0593:AN0608:sidI:basA:tcpA:AN0647:AN0649:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:aromA:AN0714:AN0718:AN0720:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:sodM:mns1B:AN0797:laeA:scdA:AN0827:pdeA:AN0836:AN0840:AN0843:hsp104:AN0868:adB:AN0907:AN0908:AN0912:AN0913:AN0917:AN0918:glrA:AN0936:agdE:ladA:atp20:AN0956:brlA:AN0984:oca2:AN1003:AN10058:niaD:AN10060:AN10064:niiA:AN1013:pyrD:AN10134:AN1015:ganB:AN10164:AN10178:AN10182:AN10189:culA:AN10197:rpf2:pexE:ccp1:AN10223:AN10229:AN10230:AN1024:AN1026:AN10280:AN10287:AN10290:AN10296:AN10298:AN10299:mnpA:AN10336:AN10348:sgdB:AN10354:odeA:AN10415:AN10416:AN10417:agdF:AN10433:AN10442:ggtA:AN1045:AN10459:AN10475:FKBP5:AN10495:AN1050:hsp20:mthA:AN10518:veA:AN10525:AN10527:AN1054:AN10548:msrA:ltpA:AN10584:AN10585:facC:AN10599:AN10600:AN10614:AN10618:AN10619:AN10638:AN10642:AN10648:
6090	pyruvate metabolic process	30 out of 2759 genes, 1.1%	40 out of 10988 background genes, 0.4%	1.03e-07	pgkA:acuF:AN1990:alcC:gpdC:fbaA:pdhX:pgmA:pfkA:gukA:AN3954:AN4081:mccA:pdcA:pdhB:pkiA:acuG:acuN:ldhA:pdkA:AN5977:swoM:pdhA:tpiA:hxkA:gpdA:pdcB:glkA:alcA:pdhC

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72524	pyridine-containing compound metabolic process	45 out of 2759 genes, 1.6%	74 out of 10988 background genes, 0.7%	1.63e-07	pppA:AN0270:AN0285:AN0593:AN0672:AN0688:AN10290:AN10525:AN11252:pgkA:AN1857:acuF:alcC:AN2335:AN2440:gpdC:fbaA:gsdA:pgmA:AN3222:pfkA:AN3431:gukA:AN3954:mccA:pdcA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:AN6141:creA:tpiA:hxkA:pyroA:gpdA:ndxC:AN8551:glkA:alcA:AN9116:AN9315
22900	electron transport chain	23 out of 2759 genes, 0.8%	27 out of 10988 background genes, 0.2%	1.89e-07	AN11347:AN11859:AN12213:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN3922:AN4388:AN4525:AN5971:AN7497:AN7629:AN8118

For Peer Review

6807	nitrogen compound metabolic process	791 out of 2759 genes, 28.7%	2654 out of 10988 background genes, 24.2%	3.01e-07	AN0016:AN0046:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0142:AN0167:AN0174:AN0183:AN0224:ureD:pppA:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0299:AN0300:AN0318:aroG:AN0381:araR:AN0428:AN0433:AN0445:AN0450:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0570:AN0593:AN0608:sidI:basA:AN0647:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:aromA:AN0714:AN0718:AN0720:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:mns1B:AN0797:laeA:AN0827:pdeA:AN0840:AN0843:hsp104:adB:AN0907:AN0908:AN0912:AN0917:AN0918:glrA:AN0936:atp20:AN0956:brlA:AN0984:oca2:niaD:niiA:AN1013:pyrD:AN10134:AN10164:AN10182:AN10189:culA:pexE:AN10230:AN1024:AN10280:AN10290:AN10298:AN10299:AN10336:AN10348:sgdB:AN10354:AN10415:AN10416:AN10417:AN10433:ggtA:AN1045:AN10459:AN10475:FKBP5:veA:AN10525:AN10527:AN1054:AN10540:AN10548:msrA:ltpA:facC:AN10599:AN10600:AN10614:AN10618:AN10638:AN10661:AN10681:AN10697:AN1071:AN10710:AN10712:AN10740:AN10764:AN10789:AN1080:ffkB:AN10832:AN10838:AN1084:AN10901:AN10903:AN10906:AN10910:AN10913:AN10914:AN1092:AN10936:AN1095:bzuA:AN10970:AN10981:AN10996:AN11003:AN1102:AN11060:AN11093:AN11110:AN11111:AN11112:AN11125:phenA:cgrA:AN11197:AN11212:AN1122:AN11232:AN11252:AN11303:AN11

For Peer Review

1901360	organic cyclic compound metabolic process	505 out of 2759 genes, 18.3%	1599 out of 10988 background genes, 14.6%	3.15e-07	AN0016:AN0046:AN0057:AN0097:AN0111:AN0126:AN0128:AN0183:ivoB:pppA:AN0252:palB:AN0270:AN0285:AN0318:aroG:araR:AN0428:AN0450:AN0451:AN0465:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0579:AN0593:AN0608:sidI:AN0647:AN0661:AN0672:AN0688:facB:AN0695:AN0705:aromA:AN0714:AN0718:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0797:laeA:pdeA:AN0836:adB:AN0908:AN0917:AN0936:atp20:AN0956:brlA:AN0984:pyrD:AN10164:pexE:AN10230:AN1024:AN10280:AN10290:AN10298:AN10336:AN10348:sgdB:AN10415:AN10417:AN1045:AN10459:AN10475:veA:AN10525:AN1054:AN10548:AN10600:AN10614:AN10618:AN10638:AN10648:AN10661:AN10697:AN10700:AN1071:AN10710:AN10712:AN10764:AN10789:AN10832:AN10903:AN10906:AN10910:AN10913:AN10914:AN10936:bzuA:AN10970:AN10981:AN10996:AN11003:AN11008:AN11060:AN11093:AN11110:AN11111:AN11112:AN11125:phenA:cgrA:AN11197:AN11212:AN11252:AN11303:AN11347:qutB:AN11444:AN11859:AN11892:AN11893:sumO:AN11929:AN11961:AN12101:AN1215:AN12201:AN12213:AN12256:AN1228:AN12316:AN12331:pgkA:hscA:AN12478:AN12489:AN1263:AN1319:AN1345:AN1380:AN1409:farB:AN1435:rsdA:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1673:AN1709:AN1710:AN1715:AN1722:prnD:prnC:artC:CYP682D1:AN1806:AN1809:otaA:nosA:AN1857:AN1858:AN1859:maiA:fahA:hmgA:AN18
72329	monocarboxylic acid catabolic process	35 out of 2759 genes, 1.3%	52 out of 10988 background genes, 0.5%	3.66e-07	AN0300:facB:scdA:AN0868:pexE:mthA:facC:AN10700:AN10841:bzuA:AN11045:qutB:farB:mcdA:gatA:gukA:AN3829:AN3954:pdhB:AN5534:facA:acuD:AN5646:echA:aciA:mcsA:acuE:pdhA:hadA:farA:foxA:acuL:AN7770:phacA:mclA

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42254	ribosome biogenesis	86 out of 2759 genes, 3.1%	185 out of 10988 background genes, 1.7%	3.88e-07	AN0262:AN0465:AN0647:AN0695:AN0745:AN0776:AN0843:AN10058:AN1013:AN10175:rpf2:AN10348:AN10618:AN10712:cgrA:AN1166:AN11929:AN1200:AN1215:AN1228:hscA:AN1319:AN1345:AN1445:AN1711:AN1949:AN1964:AN2079:AN2210:AN2262:AN2292:AN2734:AN3056:nop58:AN3172:AN3313:AN3413:AN3455:AN3706:rrs1:AN3823:AN3827:rps16:AN4087:AN4469:AN4475:AN4594:ssz1:AN4777:AN4803:ubi1:AN4916:AN5177:AN5222:AN5441:AN5520:AN5715:AN5865:AN5871:AN5960:AN5979:AN5997:AN6082:AN6083:rpl3:AN6244:AN6266:AN6556:AN6563:AN6632:AN6679:AN6902:rcc1:AN7107:AN7205:AN7526:AN7630:AN8491:AN8668:AN8805:AN8824:swoC:AN8856:AN8870:AN9097:AN9468
9145	purine nucleoside triphosphate biosynthetic process	34 out of 2759 genes, 1.2%	50 out of 10988 background genes, 0.5%	4.37e-07	AN0252:AN0318:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:swoH:AN8219:glkA
9201	ribonucleoside triphosphate biosynthetic process	34 out of 2759 genes, 1.2%	50 out of 10988 background genes, 0.5%	4.37e-07	AN0252:AN0318:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:swoH:AN8219:glkA
9206	purine ribonucleoside triphosphate biosynthetic process	34 out of 2759 genes, 1.2%	50 out of 10988 background genes, 0.5%	4.37e-07	AN0252:AN0318:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:swoH:AN8219:glkA

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22904	respiratory electron transport chain	21 out of 2759 genes, 0.8%	24 out of 10988 background genes, 0.2%	4.62e-07	AN11347:AN11859:AN12213:AN1915:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN3922:AN4388:AN4525:AN5971:AN8118
9073	aromatic amino acid family biosynthetic process	32 out of 2759 genes, 1.2%	46 out of 10988 background genes, 0.4%	6.01e-07	aroG:aromA:AN0797:phenA:qutB:AN1673:AN1857:AN1858:maiA:fahA:hmgA:hpdA:AN1993:AN2293:AN2723:AN3634:AN3695:AN3748:gmdA:fmdS:AN5200:AN5444:aroF:AN6048:trpB:AN6338:hisB:aroC:AN7044:hisHF:AN7656:amdS
9072	aromatic amino acid family metabolic process	44 out of 2759 genes, 1.6%	74 out of 10988 background genes, 0.7%	7.52e-07	aroG:aromA:AN0797:AN1054:AN10996:phenA:AN11252:qutB:AN1673:artC:AN1809:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1993:AN2293:AN2723:prs3:AN3313:AN3431:AN3634:AN3695:AN3748:AN3897:gmdA:fmdS:AN5060:AN5200:AN5444:aroF:AN6048:trpB:AN6338:hisB:aroC:AN6889:AN7044:hisHF:AN7656:amdS
6631	fatty acid metabolic process	55 out of 2759 genes, 2.0%	102 out of 10988 background genes, 0.9%	8.79e-07	basA:AN0649:scdA:AN0868:AN0918:pexE:AN10287:odeA:AN1050:mthA:AN10841:AN1409:farB:mcdA:AN1840:AN1968:AN3276:pkiB:AN3638:sdeB:AN4353:AN4405:mccA:ppoC:fatA:facA:acuD:AN5646:AN5698:AN5704:pcsA:AN5904:echA:AN5990:pexA:faaA:accA:AN6506:mcsA:acuE:sdeA:AN6973:hadA:farA:foxA:an2:acuL:AN7770:AN7856:faaB:mclA:AN8907:AN9297:fasA:fasB
42773	ATP synthesis coupled electron transport	19 out of 2759 genes, 0.7%	21 out of 10988 background genes, 0.2%	1.01e-06	AN11347:AN11859:AN12213:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN3922:AN4388:AN4525:AN8118
42775	mitochondrial ATP synthesis coupled electron transport	19 out of 2759 genes, 0.7%	21 out of 10988 background genes, 0.2%	1.01e-06	AN11347:AN11859:AN12213:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN3922:AN4388:AN4525:AN8118

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9063	cellular amino acid catabolic process	40 out of 2759 genes, 1.4%	65 out of 10988 background genes, 0.6%	1.11e-06	AN0300:aldA:pyrABCN:AN1054:AN10599:AN10901:AN10996:AN1198:AN1263:prnD:prnC:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1923:gatA:agaA:AN3829:ileA:AN3897:AN4081:AN4323:mccB:mccA:AN4820:AN5060:AN5447:echA:AN6338:AN6399:AN6889:AN7278:AN8654:alcR:alcA
6754	ATP biosynthetic process	33 out of 2759 genes, 1.2%	49 out of 10988 background genes, 0.4%	1.20e-06	AN0252:AN0318:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:AN8219:glkA
5996	monosaccharide metabolic process	52 out of 2759 genes, 1.9%	95 out of 10988 background genes, 0.9%	1.28e-06	araR:AN0688:mns1B:AN10710:fbpZ:pgkA:AN1274:AN1715:acuF:AN2272:alcC:xlnD:abnA:abfA:gpdC:pgmB:fbaA:AN2936:AN2951:gsdA:pgmA:ugmA:AN3184:pfkA:mns1C:mns1A:ladB:pgaB:mccA:AN4691:ugeA:pdcA:pfkZ:pkiA:gldB:acuG:acuN:AN5986:swoM:tpiA:AN6985:larA:hxkA:AN7590:AN7708:abnC:gpdA:aglC:AN8551:glkA:alcA:galF
90407	organophosphate biosynthetic process	90 out of 2759 genes, 3.3%	201 out of 10988 background genes, 1.8%	1.66e-06	AN0183:AN0252:AN0270:AN0318:AN0490:AN0495:pyrABCN:AN0579:AN0827:adB:AN0913:ladA:atp20:pyrD:AN11161:AN11232:AN11252:AN11303:AN11444:AN11859:pgkA:AN12478:AN1263:AN1523:AN1534:oliC:hxB:AN1857:acuF:URFA3:atp8:oliA:AN2008:AN2272:gpdC:fbaA:pdhX:pgmA:prs3:pfkA:AN3276:AN3431:AN3588:AN3626:AN3639:gukA:cyaA:AN3954:AN4258:mag1:purH:mccA:AN4691:AN4739:cnxH:AN4923:AN4927:AN5122:pdhB:AN5200:pkiA:AN5492:AN5566:acuG:facA:acuN:ldhA:pyrE:AN5939:swoM:AN6139:AN6141:pyrG:AN6209:AN6287:AN6541:pdhA:tpiA:hxkA:AN7625:pyroA:AN8012:gpdA:AN8121:swoH:AN8219:glkA:AN9116:pdhC:panK

97064	ncRNA export from nucleus	15 out of 2759 genes, 0.5%	15 out of 10988 background genes, 0.1%	2.12e-06	AN0285:AN0843:kapL:AN3172:AN3413:AN3455:AN3706:rps16:AN4087:AN4218:AN5441:AN5715:AN5997:AN6632:rcc1
9142	nucleoside triphosphate biosynthetic process	34 out of 2759 genes, 1.2%	52 out of 10988 background genes, 0.5%	2.18e-06	AN0252:AN0318:atp20:AN11303:AN11444:pgkA:AN1523:AN1534:oliC:acuF:URFA3:atp8:oliA:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:AN4927:pdhB:pkiA:acuG:acuN:ldhA:swoM:AN6287:tpiA:hxkA:gpdA:swoH:AN8219:glkA
1901606	alpha-amino acid catabolic process	37 out of 2759 genes, 1.3%	59 out of 10988 background genes, 0.5%	2.31e-06	AN0300:aldA:pyrABCN:AN1054:AN10901:AN10996:AN1198:AN1263:prnD:prnC:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1923:gatA:agaA:AN3829:ileA:AN3897:AN4081:mccB:mccA:AN4820:AN5060:AN5447:echA:AN6338:AN6399:AN7278:AN8654:alcR:alcA
6418	tRNA aminoacylation for protein translation	26 out of 2759 genes, 0.9%	35 out of 10988 background genes, 0.3%	2.98e-06	AN0046:AN0057:AN0428:AN0705:AN0936:sgdB:AN10475:AN11125:AN1380:AN1709:AN1710:AN1913:AN3073:AN3824:AN3865:AN4086:AN5662:podG:AN6368:AN6526:AN7361:AN7479:AN8224:AN8867:AN9157:AN9419

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43604	amide biosynthetic process	187 out of 2759 genes, 6.8%	511 out of 10988 background genes, 4.7%	5.17e-06	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0142:AN0167:palB:AN0262:AN0278:AN0428:AN0433:AN0445:AN0465:AN0470:aldA:AN0570:AN0608:sidI:spdA:AN0705:AN0776:laeA:AN0843:AN0907:glrA:AN0936:AN1013:AN10182:pexE:sgdB:AN10416:AN10459:AN10475:veA:AN10614:AN10681:AN10740:AN1080:AN1084:AN1095:AN11125:AN1122:AN11411:AN11419:AN1162:AN11631:AN1166:AN12246:AN1228:AN12319:hscA:AN1345:AN1380:AN1393:AN1524:AN1709:AN1710:AN1770:AN1913:AN1964:AN1970:AN20013:AN2057:AN2275:AN2301:AN2389:lagA:easA:easB:easD:aatA:AN2734:gpxA:AN2932:pdhX:AN2980:AN2992:AN2997:suAprgA1:AN3073:AN3172:AN3173:AN3413:AN3595:AN3639:AN3649:AN3823:AN3824:AN3832:AN3840:AN3865:AN3894:AN4015:rps16:AN4073:AN4086:AN4087:rpl16a:AN4218:AN4222:AN4251:AN4259:AN4308:AN4401:AN4452:AN4475:AN4494:AN4522:AN4594:ssz1:AN4652:AN4777:AN4794:AN4802:AN4803:ubi1:pdcA:AN4916:AN5014:AN5025:pdhB:AN5222:AN5441:AN5522:facA:AN5662:AN5688:AN5715:AN5719:sidA:AN5897:AN5960:AN5979:AN5996:AN5997:AN6039:AN6083:AN6146:AN6181:rpl3:sidF:podG:AN6330:AN6368:AN6500:AN6526:AN6563:AN6564:AN6629:AN6632:biA:bioF:AN6679:pdhA:aatB:AN6843:AN6864:AN7003:AN7354:AN7361:AN7479:AN7554:AN7659:AN7701:AN7884:AN8066:phacA:AN8188:AN8224:AN8225:hapX:AN8256:AN8346:apdA:AN8705:AN8832:AN8
6119	oxidative phosphorylation	19 out of 2759 genes, 0.7%	22 out of 10988 background genes, 0.2%	5.66e-06	AN11347:AN11859:AN12213:ndhDL:ndhE:ndhB:cobA:ndhA:ndhD:ndhF:oxiC:oxiA:ndhC:oxiB:AN2316:AN3922:AN4388:AN4525:AN8118

43038	amino acid activation	27 out of 2759 genes, 1.0%	38 out of 10988 background genes, 0.3%	7.31e-06	AN0046:AN0057:AN0428:AN0705:AN0936:sgdB:AN10475:AN11110:AN11125:AN1380:AN1709:AN1710:AN1913:AN3073:AN3824:AN3865:AN4086:AN5662:podG:AN6368:AN6526:AN7361:AN7479:AN8224:AN8867:AN9157:AN9419
43039	tRNA aminoacylation	27 out of 2759 genes, 1.0%	38 out of 10988 background genes, 0.3%	7.31e-06	AN0046:AN0057:AN0428:AN0705:AN0936:sgdB:AN10475:AN11110:AN11125:AN1380:AN1709:AN1710:AN1913:AN3073:AN3824:AN3865:AN4086:AN5662:podG:AN6368:AN6526:AN7361:AN7479:AN8224:AN8867:AN9157:AN9419

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43603	cellular amide metabolic process	205 out of 2759 genes, 7.4%	573 out of 10988 background genes, 5.2%	7.54e-06	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0142:AN0167:ureD:palB:AN0262:AN0278:AN0300:AN0428:AN0433:AN0445:AN0465:AN0470:aldA:AN0570:AN0593:AN0608:sidI:spdA:AN0705:AN0776:laeA:AN0843:AN0907:glrA:AN0936:AN1013:AN10182:pexE:sgdB:AN10354:AN10416:ggtA:AN10459:AN10475:veA:AN10614:AN10681:AN10740:AN1080:AN1084:AN1092:AN1095:bzuA:AN11125:AN1122:AN11411:AN11419:AN1162:AN11631:AN1166:AN12246:AN1228:AN12319:hscA:AN1345:AN1380:AN1393:AN1524:AN1709:AN1710:AN1770:AN1913:AN1964:AN1970:AN20013:AN2057:AN2144:gatA:AN2275:AN2301:AN2389:lagA:easA:easB:easD:aatA:AN2734:gpxA:AN2932:pdhX:AN2980:AN2988:AN2992:AN2997:suAprgA1:AN3058:AN3073:AN3172:AN3173:AN3413:AN3459:AN3595:AN3639:AN3649:AN3823:AN3824:AN3832:AN3840:AN3865:AN3894:gmdA:AN4015:rps16:AN4073:AN4086:AN4087:rpl16a:AN4218:AN4222:AN4251:AN4259:AN4308:AN4401:AN4452:AN4475:AN4494:AN4522:AN4594:AN4603:ssz1:AN4652:AN4777:AN4794:AN4802:AN4803:ubi1:pdcA:AN4916:AN4923:AN5014:AN5025:pdhB:AN5222:AN5441:AN5522:facA:AN5662:AN5688:AN5715:AN5719:sidA:AN5897:AN5960:AN5979:AN5996:AN5997:faaA:AN6039:AN6083:AN6146:AN6181:rpl3:sidF:podG:AN6330:AN6368:AN6500:AN6526:AN6563:AN6564:AN6629:AN6632:biA:bioF:acuE:AN6679:pdhA:aatB:AN6843:AN6864:AN7003:AN7354:AN7361:AN7479:

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9108	coenzyme biosynthetic process	57 out of 2759 genes, 2.1%	112 out of 10988 background genes, 1.0%	7.61e-06	AN0183:AN0270:spdA:AN10197:AN10642:AN11252:AN12152:AN12201:sasA:pgkA:AN1524:artC:AN1857:AN1860:acuF:AN1999:AN2389:AN2526:gpdC:fbaA:pdhX:pgmA:pfkA:AN3431:AN3586:AN3639:gukA:AN3840:AN3954:AN4569:mccA:AN4757:cnxH:AN5025:pdhB:AN5200:pkiA:acuG:facA:acuN:ldhA:swoM:AN6141:AN6276:AN6572:biA:bioF:pdhA:tpiA:hxkA:pyroA:gpdA:AN8188:glkA:AN9116:pdhC:panK
16129	phytosteroid biosynthetic process	22 out of 2759 genes, 0.8%	28 out of 10988 background genes, 0.3%	9.47e-06	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
44108	cellular alcohol biosynthetic process	22 out of 2759 genes, 0.8%	28 out of 10988 background genes, 0.3%	9.47e-06	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
6696	ergosterol biosynthetic process	22 out of 2759 genes, 0.8%	28 out of 10988 background genes, 0.3%	9.47e-06	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
97384	cellular lipid biosynthetic process	22 out of 2759 genes, 0.8%	28 out of 10988 background genes, 0.3%	9.47e-06	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
46031	ADP metabolic process	23 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	9.69e-06	pgkA:acuF:alcC:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:alcA

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22613	ribonucleoprotein complex biogenesis	91 out of 2759 genes, 3.3%	210 out of 10988 background genes, 1.9%	1.02e-05	AN0262:AN0465:AN0560:AN0647:AN0695:AN0745:AN0776:AN0843:AN10058:AN1013:AN10164:AN10175:rpf2:AN10348:AN10417:AN10618:AN10712:cgrA:AN1166:AN11929:AN1200:AN1215:AN1228:hscA:AN1319:AN1345:AN1445:AN1711:AN1949:AN1964:AN2079:AN2210:AN2262:AN2292:AN2734:AN2992:AN3056:nop58:AN3172:AN3313:AN3413:AN3455:AN3706:rrs1:AN3823:AN3827:rps16:AN4087:AN4469:AN4475:AN4594:ssz1:AN4777:AN4803:ubi1:AN4916:AN5177:AN5222:AN5441:AN5520:AN5715:AN5865:AN5871:AN5960:AN5979:AN5997:AN6082:AN6083:rpl3:AN6244:AN6266:AN6556:AN6563:AN6632:AN6679:AN6902:rcc1:AN7107:AN7205:AN7526:AN7630:hsp90:AN8491:AN8668:AN8805:AN8824:swoC:AN8856:AN8870:AN9097:AN9468
96	sulfur amino acid metabolic process	29 out of 2759 genes, 1.1%	43 out of 10988 background genes, 0.4%	1.28e-05	AN0720:AN10230:msrA:AN10996:sD:sasA:AN1263:AN3456:AN3593:AN4081:AN4290:metR:metH:sC:sA:AN4774:AN4793:metF:AN6227:AN6399:AN6576:metG:AN7600:pyroA:cysB:metA:cysD:cysA:AN8859
19362	pyridine nucleotide metabolic process	40 out of 2759 genes, 1.4%	69 out of 10988 background genes, 0.6%	1.34e-05	pppA:AN0285:AN0593:AN0672:AN0688:AN10525:AN11252:pgkA:AN1857:acuF:alcC:AN2335:AN2440:gpdC:fbaA:gsdA:pgmA:pfkA:AN3431:gukA:AN3954:mccA:pdcA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:creA:tpiA:hxkA:gpdA:ndxC:AN8551:glkA:alcA:AN9116:AN9315
46496	nicotinamide nucleotide metabolic process	40 out of 2759 genes, 1.4%	69 out of 10988 background genes, 0.6%	1.34e-05	pppA:AN0285:AN0593:AN0672:AN0688:AN10525:AN11252:pgkA:AN1857:acuF:alcC:AN2335:AN2440:gpdC:fbaA:gsdA:pgmA:pfkA:AN3431:gukA:AN3954:mccA:pdcA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:creA:tpiA:hxkA:gpdA:ndxC:AN8551:glkA:alcA:AN9116:AN9315

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9135	purine nucleoside diphosphate metabolic process	23 out of 2759 genes, 0.8%	31 out of 10988 background genes, 0.3%	2.86e-05	pgkA:acuF:alcC:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:alcA
9179	purine ribonucleoside diphosphate metabolic process	23 out of 2759 genes, 0.8%	31 out of 10988 background genes, 0.3%	2.86e-05	pgkA:acuF:alcC:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:alcA

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1901362	organic cyclic compound biosynthetic process	272 out of 2759 genes, 9.9%	811 out of 10988 background genes, 7.4%	3.02e-05	AN0016:AN0097:AN0183:ivoB:AN0252:palB:AN0270:AN0318:aroG:araR:AN0451:AN0490:AN0495:AN0507:aldA:pyrABCN:AN0593:AN0608:sidI:AN0661:facB:aromA:AN0718:H4.1:AN0742:AN0752:AN0797:laeA:pdeA:AN0836:adB:AN0908:atp20:brlA:pyrD:pexE:AN10290:AN10298:veA:AN10548:AN10600:AN10638:AN10648:AN10661:AN10697:AN10710:AN10764:AN10789:AN10906:AN10910:AN10913:AN10914:AN10936:AN10970:AN10981:AN11003:AN11008:AN11093:AN11111:AN11112:AN11125:phenA:AN11197:AN11212:AN11252:AN11303:qutB:AN11444:sumO:AN11961:AN12201:AN12316:AN12331:pgkA:AN12478:AN12489:AN1409:farB:AN1523:AN1524:AN1534:oliC:hxB:AN1673:AN1715:AN1722:prnC:nosA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:pdmA:AN1915:acuF:AN1976:AN1993:URFA3:atp8:oliA:AN2069:AN2235:AN2272:AN2283:hemA:AN2293:H4.2:easA:easB:easD:AN2553:gpdC:aatA:AN2672:AN2677:AN2723:AN2733:AN2780:AN2854:fbaA:pdhX:suAprgA1:pgmA:prs3:AN3222:pfkA:clrB:micA:AN3431:AN3626:AN3634:AN3637:AN3639:gukA:AN3663:AN3683:AN3684:AN3695:AN3748:AN3840:cyaA:AN3920:AN3954:gmdA:AN4013:CYP61A1:AN4094:AN4096:AN4118:AN4250:AN4258:AN4283:metR:mag1:metH:purH:fmdS:AN4600:mccA:AN4739:AN4744:AN4774:AN4837:cnxH:pdcA:AN4923:AN4927:AN4949:AN5122:AN5130:pdhB:AN5200:pkiA:AN5274:AN5415:AN5444:AN5492:AN5497:AN5566:acuG:facA:aroF:a
19318	hexose metabolic process	37 out of 2759 genes, 1.3%	63 out of 10988 background genes, 0.6%	3.06e-05	mns1B:AN10710:fbpZ:pgkA:AN1715:acuF:alcC:gpdC:pgmB:fbaA:AN2936:AN2951:gsdA:pgmA:ugmA:AN3184:pfkA:mns1C:mns1A:ladB:mccA:ugeA:pdcA:pfkZ:pkiA:acuG:acuN:AN5986:swoM:tpiA:larA:hxkA:gpdA:aglC:glkA:alcA:galF

34641	cellular nitrogen compound metabolic process	553 out of 2759 genes, 20.0%	1825 out of 10988 background genes, 16.6%	4.34e-05	AN0016:AN0046:AN0057:AN0097:AN0105:AN0111:AN0116:AN0123:AN0126:AN0128:AN0142:AN0167:ureD:ppA:AN0252:palB:AN0262:AN0270:AN0278:AN0285:AN0300:AN0318:araR:AN0428:AN0433:AN0445:AN0450:AN0465:AN0470:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0570:AN0593:AN0608:sidI:AN0647:AN0661:AN0672:spdA:AN0688:facB:AN0695:AN0705:AN0714:AN0718:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0797:laeA:pdeA:AN0843:adB:AN0907:AN0908:AN0917:glrA:AN0936:atp20:AN0956:brlA:AN0984:AN1013:pyrD:AN10164:AN10182:pexE:AN10230:AN1024:AN10280:AN10290:AN10298:AN10336:AN10348:sgdB:AN10354:AN10415:AN10416:AN10417:ggtA:AN1045:AN10459:AN10475:veA:AN10525:AN10527:AN1054:AN10548:facC:AN10600:AN10614:AN10618:AN10638:AN10661:AN10681:AN10697:AN1071:AN10710:AN10712:AN10740:AN10789:AN1080:AN10832:AN1084:AN10903:AN10906:AN10910:AN10913:AN10914:AN1092:AN10936:AN1095:bzuA:AN10970:AN10981:AN10996:AN11003:AN11060:AN11093:AN11110:AN11111:AN11112:AN11125:cgrA:AN11197:AN11212:AN1122:AN11252:AN11303:AN11347:AN11411:AN11419:AN11444:AN1162:AN11631:AN1166:AN11859:AN11892:AN11893:sumO:AN11929:AN11961:AN12101:AN1215:AN12201:AN12213:AN12246:AN12256:AN1228:AN12316:AN12319:pgkA:hscA:AN12478:AN12489:AN1263:AN1319:AN1345:AN1380:AN1393:f
34404	nucleobase-containing small molecule biosynthetic process	32 out of 2759 genes, 1.2%	52 out of 10988 background genes, 0.5%	6.07e-05	AN0593:pdeA:AN10661:pgkA:acuF:AN2272:gpdC:fbaA:pgmA:AN3222:pfkA:gukA:AN3954:mccA:pdhB:pkiA:AN5566:acuG:acuN:ldhA:pyrF:pyrE:AN5939:swoM:pyrG:tpiA:hxkA:gpdA:swoH:citA:glkA:AN9402

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72525	pyridine-containing compound biosynthetic process	29 out of 2759 genes, 1.1%	45 out of 10988 background genes, 0.4%	6.15e-05	AN0270:AN10290:AN11252:pgkA:AN1857:acuF:gpdC:fbaA:pgmA:AN3222:pfkA:AN3431:gukA:AN3954:mccA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:AN6141:tpiA:hxkA:pyroA:gpdA:glkA:AN9116
16128	phytosteroid metabolic process	22 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	8.55e-05	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
44107	cellular alcohol metabolic process	22 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	8.55e-05	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
46939	nucleotide phosphorylation	22 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	8.55e-05	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:AN4258:mccA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:swoH:glkA
71428	rRNA-containing ribonucleoprotein complex export from nucleus	22 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	8.55e-05	AN0843:AN10618:AN1215:hscA:AN1711:AN2210:AN2262:AN3172:AN3413:AN3706:rrs1:rps16:AN4087:AN5441:AN5715:AN5865:AN5997:AN6556:AN6632:rcc1:AN8805:AN8824
8204	ergosterol metabolic process	22 out of 2759 genes, 0.8%	30 out of 10988 background genes, 0.3%	8.55e-05	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
9166	nucleotide catabolic process	25 out of 2759 genes, 0.9%	37 out of 10988 background genes, 0.3%	0.00013	AN0593:pdeA:AN10661:pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:AN5939:swoM:tpiA:hxkA:gpdA:citA:glkA:AN9402

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9060	aerobic respiration	31 out of 2759 genes, 1.1%	51 out of 10988 background genes, 0.5%	0.00015	AN1003:AN10585:AN11347:AN12213:artC:cobA:oxiC:oxiA:oxiB:AN2316:aclA:aclB:idpA:suAprgA1:AN3068:AN3813:AN3894:AN4064:AN4388:AN4525:AN4863:AN5300:AN5497:acoA:AN5790:cycA:AN6297:AN6564:mcsA:AN8118:citA
9067	aspartate family amino acid biosynthetic process	24 out of 2759 genes, 0.9%	35 out of 10988 background genes, 0.3%	0.00016	AN10230:msrA:AN1990:lysA:AN3031:AN3593:AN4290:AN4401:metH:sA:AN4774:AN4793:lysB:AN5601:AN5610:metF:AN6048:AN6338:AN6576:metG:metA:cysD:cysA:AN8859
9132	nucleoside diphosphate metabolic process	24 out of 2759 genes, 0.9%	35 out of 10988 background genes, 0.3%	0.00016	pgkA:acuF:alcC:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:swoH:glkA:alcA
9185	ribonucleoside diphosphate metabolic process	23 out of 2759 genes, 0.8%	33 out of 10988 background genes, 0.3%	0.00019	pgkA:acuF:alcC:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdcA:AN5122:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:alcA
16126	sterol biosynthetic process	22 out of 2759 genes, 0.8%	31 out of 10988 background genes, 0.3%	0.00022	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
6006	glucose metabolic process	21 out of 2759 genes, 0.8%	29 out of 10988 background genes, 0.3%	0.00025	fbpZ:pgkA:acuF:alcC:gpdC:fbaA:gsdA:pgmA:AN3184:pfkA:mccA:pdcA:pkiA:acuG:acuN:swoM:tpiA:hxkA:gpdA:glkA:alcA
6165	nucleoside diphosphate phosphorylation	20 out of 2759 genes, 0.7%	27 out of 10988 background genes, 0.2%	0.00027	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:swoH:glkA
97	sulfur amino acid biosynthetic process	20 out of 2759 genes, 0.7%	27 out of 10988 background genes, 0.2%	0.00027	AN10230:msrA:AN10996:AN3593:AN4290:metH:sA:AN4774:AN4793:metF:AN6227:AN6576:metG:AN7600:pyroA:cysB:metA:cysD:cysA:AN8859

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6725	cellular aromatic compound metabolic process	446 out of 2759 genes, 16.2%	1453 out of 10988 background genes, 13.2%	0.00028	AN0016:AN0046:AN0057:AN0097:AN0111:AN0126:AN0128:ivoB:pppA:AN0252:AN0270:AN0285:AN0318:aroG:araR:AN0428:AN0450:AN0465:AN0490:AN0495:AN0507:mreA:AN0560:pyrABCN:AN0593:AN0647:AN0661:AN0672:AN0688:facB:AN0695:AN0705:aromA:AN0714:AN0718:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0797:laeA:pdeA:adB:AN0908:AN0917:AN0936:atp20:AN0956:brlA:AN0984:pyrD:AN10164:AN10230:AN1024:AN10280:AN10290:AN10298:AN10336:AN10348:sgdB:AN10415:AN10417:AN1045:AN10459:AN10475:veA:AN10525:AN1054:AN10548:AN10600:AN10614:AN10618:AN10638:AN10661:AN10697:AN10700:AN1071:AN10710:AN10712:AN10789:AN10832:AN10903:AN10906:AN10910:AN10913:AN10914:AN10936:bzuA:AN10970:AN10996:AN11003:AN11060:AN11093:AN11110:AN11111:AN11112:AN11125:phenA:cgrA:AN11197:AN11212:AN11252:AN11303:AN11347:qutB:AN11444:AN11859:AN11892:AN11893:sumO:AN11929:AN11961:AN1215:AN12201:AN12213:AN12256:AN1228:AN12316:pgkA:hscA:AN12478:AN12489:AN1263:AN1301:AN1319:AN1345:AN1380:farB:AN1435:rsdA:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1673:AN1709:AN1710:AN1715:AN1722:artC:AN1806:AN1809:nosA:AN1857:AN1858:AN1859:maiA:fahA:hmgA:AN1898:hpdA:AN1913:AN1915:acuF:SPA10:AN1949:AN1964:AN1976:AN1993:ndhDL:ndhE:ndhB:AN20003:URFA3:cobA:I-
42866	pyruvate biosynthetic process	19 out of 2759 genes, 0.7%	25 out of 10988 background genes, 0.2%	0.00028	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA
6096	glycolytic process	19 out of 2759 genes, 0.7%	25 out of 10988 background genes, 0.2%	0.00028	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA

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6555	methionine metabolic process	19 out of 2759 genes, 0.7%	25 out of 10988 background genes, 0.2%	0.00028	AN0720:AN10230:msrA:sasA:AN1263:AN3456:AN3593:AN4290:metH:sA:AN4774:AN4793:metF:AN6576:metG:metA:cysD:cysA:AN8859
6757	ATP generation from ADP	19 out of 2759 genes, 0.7%	25 out of 10988 background genes, 0.2%	0.00028	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA
16052	carbohydrate catabolic process	72 out of 2759 genes, 2.6%	165 out of 10988 background genes, 1.5%	0.00029	AN0034:araR:engA:bglB:mns1B:agdE:ladA:AN10060:AN1015:ganB:agdF:AN10599:glaA:AN11778:pgkA:AN1274:AN1772:acuF:xlnD:AN2528:abnA:abfA:gpdC:bglK:pgmB:fbaA:pgmA:pfkA:AN3294:plyE:clrB:pmeA:amyB:mns1C:gukA:cyaA:AN3954:bglA:ladB:pgaB:mccA:AN4691:agdG:pdhB:pkiA:faeC:acuG:AN5672:acuN:clrA:ldhA:AN5917:swoM:amyE:rglB:AN6470:tpiA:rglA:larA:agdC:mutA:hxkA:AN7708:eglC:abnC:gpdA:aglC:AN8347:plyH:glkA:AN8890:pgxB

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43043	peptide biosynthetic process	160 out of 2759 genes, 5.8%	447 out of 10988 background genes, 4.1%	0.00040	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0142:AN0167:AN0262:AN0278:AN0428:AN0433:AN0445:AN0465:AN0470:AN0570:AN0608:sidI:AN0705:AN0776:laeA:AN0843:AN0907:glrA:AN0936:AN1013:AN10182:sgdB:AN10416:AN10459:AN10475:AN10614:AN10681:AN10740:AN1080:AN1084:AN1095:AN11125:AN1122:AN11411:AN11419:AN1162:AN11631:AN1166:AN12246:AN1228:AN12319:hscA:AN1345:AN1380:AN1393:AN1709:AN1710:AN1770:AN1913:AN1964:AN1970:AN20013:AN2057:AN2275:AN2301:easA:easB:easD:AN2734:gpxA:AN2932:AN2980:AN2992:AN2997:AN3073:AN3172:AN3173:AN3413:AN3595:AN3649:AN3823:AN3824:AN3832:AN3865:AN3894:AN4015:rps16:AN4073:AN4086:AN4087:rpl16a:AN4218:AN4222:AN4251:AN4259:AN4308:AN4452:AN4475:AN4494:AN4522:AN4594:ssz1:AN4652:AN4777:AN4794:AN4802:AN4803:ubi1:AN4916:AN5014:AN5222:AN5441:AN5522:AN5662:AN5715:AN5719:sidA:AN5897:AN5960:AN5979:AN5996:AN5997:AN6039:AN6083:AN6146:AN6181:rpl3:sidF:podG:AN6330:AN6368:AN6500:AN6526:AN6563:AN6564:AN6629:AN6632:AN6679:AN6843:AN6864:AN7003:AN7354:AN7361:AN7479:AN7554:AN7659:AN7701:AN7884:AN8066:AN8224:AN8225:hapX:AN8256:AN8346:AN8705:AN8832:AN8856:AN8867:AN8870:AN9097:AN9157:AN9419:AN9465:AN9468
51029	rRNA transport	11 out of 2759 genes, 0.4%	11 out of 10988 background genes, 0.1%	0.00054	AN0843:AN3172:AN3413:AN3706:rps16:AN4087:AN5441:AN5715:AN5997:AN6632:rcc1
6407	rRNA export from nucleus	11 out of 2759 genes, 0.4%	11 out of 10988 background genes, 0.1%	0.00054	AN0843:AN3172:AN3413:AN3706:rps16:AN4087:AN5441:AN5715:AN5997:AN6632:rcc1

6796	phosphate-containing compound metabolic process	181 out of 2759 genes, 6.6%	521 out of 10988 background genes, 4.7%	0.00068	AN0137:AN0183:pppA:AN0252:AN0270:AN0285:AN0318:AN0490:AN0495:pyrABCN:AN0579:AN0593:basA:AN0672:AN0688:AN0827:pdeA:adB:AN0908:AN0913:AN0918:ladA:atp20:oca2:pyrD:AN10525:ltpA:AN10661:AN1068:ffkB:fbpZ:AN10921:AN11111:AN11161:AN11232:AN11252:AN11303:AN11347:qutG:AN11444:AN11859:AN11959:AN11961:AN12213:pgkA:AN12478:AN1263:AN1523:AN1534:AN1593:oliC:atg1:hxB:AN1713:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2008:AN2272:alcC:AN2316:AN2326:AN2335:AN2440:ssn3:pipA:gpdC:pgmB:fbaA:pdhX:ippA:gsdA:pgmA:prs3:AN3222:pfkA:AN3276:ste7:AN3431:AN3588:AN3626:AN3639:gukA:AN3708:ppzA:cyaA:AN3916:AN3922:AN3954:mkkA:ffkF:AN4258:AN4388:mag1:purH:cmkD:AN4525:msgA:mccA:AN4691:AN4739:cnxH:bckA:pdcA:AN4923:AN4927:psk1:AN5122:pfkZ:pdhB:AN5200:pkiA:AN5211:AN5492:AN5566:AN5589:acuG:facA:mst1:acuN:ldhA:pdkA:pyrE:AN5919:AN5939:faaA:swoM:AN6040:AN6139:AN6141:pyrG:creA:AN6209:AN6287:AN6312:stk26:AN6367:AN6541:AN6572:pdhA:ffkI:tpiA:ptpA:AN6985:hxkA:srrB:AN7625:ndxB:pyroA:ffkA:AN8012:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:AN8233:citA:AN8551:glkA:cmkC:alcA:AN9116:AN9315:AN9402:pdhC:panK

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6518	peptide metabolic process	165 out of 2759 genes, 6.0%	468 out of 10988 background genes, 4.3%	0.00080	AN0016:AN0046:AN0057:AN0105:AN0116:AN0123:AN0142:AN0167:AN0262:AN0278:AN0428:AN0433:AN0445:AN0465:AN0470:AN0570:AN0608:sidI:AN0705:AN0776:laeA:AN0843:AN0907:glrA:AN0936:AN1013:AN10182:sgdB:AN10354:AN10416:ggtA:AN10459:AN10475:AN10614:AN10681:AN10740:AN1080:AN1084:AN1092:AN1095:AN11125:AN1122:AN11411:AN11419:AN1162:AN11631:AN1166:AN12246:AN1228:AN12319:hscA:AN1345:AN1380:AN1393:AN1709:AN1710:AN1770:AN1913:AN1964:AN1970:AN20013:AN2057:AN2275:AN2301:easA:easB:easD:AN2734:gpxA:AN2932:AN2980:AN2988:AN2992:AN2997:AN3073:AN3172:AN3173:AN3413:AN3459:AN3595:AN3649:AN3823:AN3824:AN3832:AN3865:AN3894:AN4015:rps16:AN4073:AN4086:AN4087:rpl16a:AN4218:AN4222:AN4251:AN4259:AN4308:AN4452:AN4475:AN4494:AN4522:AN4594:ssz1:AN4652:AN4777:AN4794:AN4802:AN4803:ubi1:AN4916:AN5014:AN5222:AN5441:AN5522:AN5662:AN5715:AN5719:sidA:AN5897:AN5960:AN5979:AN5996:AN5997:AN6039:AN6083:AN6146:AN6181:rpl3:sidF:podG:AN6330:AN6368:AN6500:AN6526:AN6563:AN6564:AN6629:AN6632:AN6679:AN6843:AN6864:AN7003:AN7354:AN7361:AN7479:AN7554:AN7659:AN7701:AN7884:AN8066:AN8224:AN8225:hapX:AN8256:AN8346:AN8705:AN8832:AN8856:AN8867:AN8870:AN9097:AN9157:AN9419:AN9465:AN9468
42255	ribosome assembly	26 out of 2759 genes, 0.9%	42 out of 10988 background genes, 0.4%	0.00104	AN0262:AN10058:AN1013:rpf2:AN1166:AN11929:AN1200:AN1445:AN2734:AN3172:rrs1:AN4475:AN4777:ubi1:AN5222:AN5715:AN5960:AN5979:AN6083:rpl3:AN6632:AN6902:AN7630:AN8668:AN8824:AN8856

1901137	carbohydrate derivative biosynthetic process	81 out of 2759 genes, 2.9%	197 out of 10988 background genes, 1.8%	0.00107	AN0128:AN0252:AN0318:AN0495:mns1B:AN0827:adB:ladA:atp20:AN10710:AN11232:AN11303:AN11444:pgkA:AN1455:AN1523:AN1534:oliC:AN1715:acuF:URFA3:atp8:oliA:AN2272:gpdC:fbaA:pdhX:pgmA:AN3222:pfkA:AN3588:AN3626:AN3639:gukA:cyaA:AN3954:pcmA:chsF:purH:AN4683:mccA:AN4691:AN4716:ugeA:AN4739:alg6:AN4927:AN5122:pdhB:pkiA:AN5566:acuG:facA:AN5688:AN5725:AN5736:acuN:ldhA:pyrF:pyrE:swoM:pyrG:AN6209:AN6287:AN6541:pdhA:AN6736:tpiA:AN6992:breB:hxkA:AN7472:gpdA:AN8119:AN8121:swoH:AN8219:glkA:galF:pdhC:panK
6790	sulfur compound metabolic process	66 out of 2759 genes, 2.4%	152 out of 10988 background genes, 1.4%	0.00120	palB:aldA:AN0593:AN0720:laeA:glrA:AN10197:pexE:AN10230:ggtA:veA:msrA:AN10584:AN1092:AN10996:AN11060:AN11111:sD:AN12201:sasA:AN1263:AN1752:aatA:gpxA:pdhX:AN2988:suAprgA1:AN3456:AN3459:AN3593:AN3632:AN3639:AN4081:AN4290:AN4304:metR:metH:sC:sA:AN4774:AN4793:pdcA:AN4923:pdhB:facA:metF:faaA:AN6227:AN6399:AN6576:biA:bioF:pdhA:aatB:metG:AN7600:pyroA:cysB:phacA:metA:citA:cysD:AN8346:cysA:AN8859:pdhC
44272	sulfur compound biosynthetic process	44 out of 2759 genes, 1.6%	89 out of 10988 background genes, 0.8%	0.00132	palB:aldA:laeA:glrA:AN10197:pexE:AN10230:veA:msrA:AN10996:AN11111:sasA:aatA:gpxA:pdhX:suAprgA1:AN3593:AN3639:AN4290:metH:sA:AN4774:AN4793:pdcA:pdhB:facA:metF:AN6227:AN6576:biA:bioF:pdhA:aatB:metG:AN7600:pyroA:cysB:phacA:metA:cysD:AN8346:cysA:AN8859:pdhC
1901292	nucleoside phosphate catabolic process	25 out of 2759 genes, 0.9%	40 out of 10988 background genes, 0.4%	0.00133	AN0593:pdeA:AN10661:pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:AN5939:swoM:tpiA:hxkA:gpdA:citA:glkA:AN9402

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6066	alcohol metabolic process	56 out of 2759 genes, 2.0%	123 out of 10988 background genes, 1.1%	0.00135	AN0034:AN0137:AN0451:aldA:AN0567:AN0608:sidI:laeA:ladA:facC:AN10648:AN10764:AN11008:qutG:gppA:AN1409:AN1868:pdmA:AN2069:alcC:AN2814:AN2860:alcB:AN3916:CYP61A1:AN4094:AN4118:ladB:AN4405:AN4691:pdcA:AN4923:AN5415:gldB:AN5589:sidA:AN5862:catC:AN5946:sidF:sidH:sidD:AN6276:AN6506:AN6973:AN7146:larA:AN7590:AN7625:AN8012:AN8137:cyp51B:AN8390:AN8553:alcR:alcA

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6793	phosphorus metabolic process	183 out of 2759 genes, 6.6%	533 out of 10988 background genes, 4.9%	0.00146	AN0137:AN0183:pppA:AN0252:AN0270:AN0285:AN0318:AN0490:AN0495:pyrABCN:AN0579:AN0593:basA:AN0672:AN0688:AN0827:pdeA:adB:AN0908:AN0913:AN0918:ladA:atp20:oca2:pyrD:AN10525:ltpA:AN10661:AN1068:ffkB:fbpZ:AN10921:AN11111:AN11161:AN11232:AN11252:AN11303:AN11347:qutG:AN11444:AN11859:AN11959:AN11961:AN12213:pgkA:AN12478:AN1263:AN1523:AN1534:AN1593:oliC:atg1:hxB:AN1713:AN1857:acuF:ndhDL:ndhE:ndhB:URFA3:cobA:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:ndhC:oxiB:AN2008:AN2272:alcC:AN2316:AN2326:AN2335:AN2440:ssn3:pipA:gpdC:pgmB:fbaA:pdhX:ippA:gsdA:pgmA:prs3:AN3222:pfkA:AN3276:ste7:AN3431:AN3588:AN3626:AN3639:gukA:AN3708:AN3779:ppzA:cyaA:AN3916:AN3922:AN3954:mkkA:ffkF:AN4258:AN4388:mag1:purH:cmkD:AN4525:msgA:mccA:AN4691:AN4739:cnxH:bckA:pdcA:AN4923:AN4927:psk1:AN5122:pfkZ:pdhB:AN5200:pkiA:AN5211:AN5492:AN5566:AN5589:acuG:facA:mst1:acuN:ldhA:pdkA:pyrE:AN5919:AN5939:faaA:swoM:AN6040:AN6139:AN6141:pyrG:creA:AN6209:AN6287:AN6312:stk26:AN6367:AN6541:AN6572:pdhA:ffkI:tpiA:ptpA:AN6985:hxkA:srrB:AN7625:ndxB:pyroA:ffkA:AN8012:gpdA:AN8118:AN8121:ndxC:swoH:AN8219:AN8233:citA:AN8551:glkA:cmkC:alcA:AN9116:galF:AN9315:AN9402:pdhC:panK

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44262	cellular carbohydrate metabolic process	83 out of 2759 genes, 3.0%	205 out of 10988 background genes, 1.9%	0.00167	AN0034:AN0137:AN0285:engA:AN0567:mns1B:AN0912:agdE:ladA:AN10060:AN1015:ganB:agdF:AN10599:qutG:AN11778:gppA:xprG:xgcA:AN1868:vosA:AN2008:AN2208:alcC:aclB:lacF:pgmB:ugmA:agsB:clrB:amyB:mns1C:gukA:alcB:agnB:cyaA:AN3916:AN3954:exgC:AN4055:bglA:pcmA:ladB:AN4691:agdG:AN5138:pfkZ:gldB:AN5589:acuD:AN5672:clrA:ldhA:agsA:AN5917:catC:AN6470:mcsA:acuE:AN6985:foxA:breB:larA:agdC:mutA:cpeA:hxkA:agdD:AN7590:AN7625:AN8010:aglC:afcA:citA:AN8347:AN8553:catA:glkA:mclA:agdB:alcP:alcA:galF
6694	steroid biosynthetic process	22 out of 2759 genes, 0.8%	34 out of 10988 background genes, 0.3%	0.00271	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B

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6412	translation	146 out of 2759 genes, 5.3%	412 out of 10988 background genes, 3.7%	0.00275	AN0046:AN0057:AN0105:AN0116:AN0123:AN0142:AN0167:AN0262:AN0278:AN0428:AN0433:AN0445:AN0465:AN0470:AN0570:AN0705:AN0776:AN0843:AN0907:AN0936:AN1013:AN10182:sgdB:AN10416:AN10459:AN10475:AN10614:AN10681:AN10740:AN1080:AN1084:AN1095:AN11125:AN1122:AN11411:AN11419:AN1162:AN11631:AN1166:AN12246:AN1228:AN12319:hscA:AN1345:AN1380:AN1393:AN1709:AN1710:AN1770:AN1913:AN1964:AN1970:AN20013:AN2057:AN2275:AN2301:AN2734:AN2932:AN2980:AN2992:AN2997:AN3073:AN3172:AN3173:AN3413:AN3595:AN3649:AN3823:AN3824:AN3832:AN3865:AN3894:AN4015:rps16:AN4073:AN4086:AN4087:rpl16a:AN4218:AN4222:AN4251:AN4259:AN4308:AN4452:AN4475:AN4494:AN4522:AN4594:ssz1:AN4652:AN4777:AN4794:AN4802:AN4803:ubi1:AN4916:AN5014:AN5222:AN5441:AN5522:AN5662:AN5715:AN5719:AN5897:AN5960:AN5979:AN5996:AN5997:AN6039:AN6083:AN6146:AN6181:rpl3:podG:AN6330:AN6368:AN6500:AN6526:AN6563:AN6564:AN6629:AN6632:AN6679:AN6843:AN6864:AN7003:AN7354:AN7361:AN7479:AN7554:AN7659:AN7701:AN8066:AN8224:AN8225:AN8256:AN8705:AN8832:AN8856:AN8867:AN8870:AN9097:AN9157:AN9419:AN9465:AN9468
72330	monocarboxylic acid biosynthetic process	57 out of 2759 genes, 2.1%	129 out of 10988 background genes, 1.2%	0.00357	palB:aldA:basA:spdA:AN0918:pexE:odeA:veA:pgkA:AN1840:acuF:AN2389:easB:gpdC:aatA:fbaA:suAprgA1:pgmA:pfkA:AN3276:pkiB:AN3638:gukA:AN3954:sdeB:AN4353:AN4401:AN4405:mccA:pdcA:AN5025:ppoC:pdhB:pkiA:acuG:AN5704:acuN:ldhA:AN5904:swoM:accA:AN6506:biA:bioF:sdeA:aatB:tpiA:AN6973:an2:hxkA:AN7856:gpdA:phacA:glkA:AN8907:fasA:fasB

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46483	heterocycle metabolic process	440 out of 2759 genes, 15.9%	1461 out of 10988 background genes, 13.3%	0.00382	AN0016:AN0046:AN0057:AN0097:AN0111:AN0126:AN0128:AN0183:pppA:AN0252:palB:AN0270:AN0285:AN0318:araR:AN0428:AN0450:AN0465:AN0490:AN0495:AN0507:aldA:mreA:AN0560:pyrABCN:AN0593:AN0647:AN0661:AN0672:AN0688:facB:AN0695:AN0705:AN0714:AN0718:H4.1:AN0742:AN0745:AN0752:AN0757:AN0776:AN0797:laeA:pdeA:AN0836:adB:AN0908:AN0917:AN0936:atp20:AN0956:brlA:AN0984:pyrD:AN10164:pexE:AN10230:AN1024:AN10280:AN10290:AN10298:AN10336:AN10348:sgdB:AN10415:AN10417:AN1045:AN10459:AN10475:veA:AN10525:AN1054:AN10548:AN10600:AN10614:AN10618:AN10638:AN10661:AN10697:AN1071:AN10710:AN10712:AN10789:AN10832:AN10903:AN10906:AN10910:AN10913:AN10914:AN10936:AN10970:AN10981:AN10996:AN11003:AN11060:AN11093:AN11110:AN11111:AN11112:AN11125:cgrA:AN11197:AN11212:AN11252:AN11303:AN11347:AN11444:AN11859:AN11892:AN11893:sumO:AN11929:AN11961:AN1215:AN12201:AN12213:AN12256:AN1228:AN12316:AN12331:pgkA:hscA:AN12478:AN12489:AN1263:AN1319:AN1345:AN1380:farB:AN1435:rsdA:AN1523:AN1524:AN1534:AN1593:oliC:hxB:AN1709:AN1710:AN1715:AN1722:prnD:prnC:artC:AN1806:otaA:nosA:AN1857:AN1858:AN1859:AN1913:AN1915:acuF:SPA10:AN1949:AN1964:AN1976:ndhDL:ndhE:ndhB:AN20003:URFA3:cobA:I-AniI:ndhA:ndhD:atp8:oliA:ndhF:oxiC:oxiA:AN20015:ndh
1901700	response to oxygen-containing compound	49 out of 2759 genes, 1.8%	106 out of 10988 background genes, 1.0%	0.00390	pppA:sidI:spdA:AN0757:AN0797:glrA:ganB:ccp1:odeA:AN10518:veA:AN10764:AN10996:AN11015:AN11094:AN1131:AN1416:AN1428:AN1797:vosA:aclA:hsp30:gpxA:gsdA:pkfC:trxR:cyaA:glnA:cpcB:AN4259:gdhA:ssz1:AN5564:acuN:catC:AN5999:creA:trpB:sidH:AN6849:tpiA:hxtA:AN7208:cpeA:AN7590:AN8273:catA:AN8643:alcA

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6081	cellular aldehyde metabolic process	27 out of 2759 genes, 1.0%	47 out of 10988 background genes, 0.4%	0.00508	pppA:AN0270:AN0285:aldA:AN0593:AN0672:AN0688:AN0912:AN11015:AN2335:AN2440:AN2860:gsdA:AN3954:AN5534:acuD:ldhA:AN5977:AN6141:creA:acuE:foxA:pyroA:AN8551:mclA:alcR:alcA
1902653	secondary alcohol biosynthetic process	22 out of 2759 genes, 0.8%	35 out of 10988 background genes, 0.3%	0.00556	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
1901701	cellular response to oxygen-containing compound	44 out of 2759 genes, 1.6%	93 out of 10988 background genes, 0.8%	0.00604	pppA:sidI:spdA:AN0757:AN0797:glrA:ganB:ccp1:odeA:AN10518:veA:AN10764:AN11015:AN1131:AN1416:AN1428:AN1797:vosA:aclA:hsp30:gpxA:pkfC:trxR:cyaA:glnA:cpcB:AN4259:gdhA:ssz1:AN5564:acuN:catC:AN5999:trpB:sidH:AN6849:tpiA:hxtA:AN7208:AN7590:AN8273:catA:AN8643:alcA
19359	nicotinamide nucleotide biosynthetic process	24 out of 2759 genes, 0.9%	40 out of 10988 background genes, 0.4%	0.00643	AN11252:pgkA:AN1857:acuF:gpdC:fbaA:pgmA:pfkA:AN3431:gukA:AN3954:mccA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:AN9116
19363	pyridine nucleotide biosynthetic process	24 out of 2759 genes, 0.9%	40 out of 10988 background genes, 0.4%	0.00643	AN11252:pgkA:AN1857:acuF:gpdC:fbaA:pgmA:pfkA:AN3431:gukA:AN3954:mccA:pdhB:AN5200:pkiA:acuG:acuN:ldhA:swoM:tpiA:hxkA:gpdA:glkA:AN9116
16125	sterol metabolic process	29 out of 2759 genes, 1.1%	53 out of 10988 background genes, 0.5%	0.00832	AN0451:AN0579:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:AN1593:pdmA:AN2069:AN3638:CYP61A1:AN4094:AN4601:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN7211:AN7661:AN8012:cyp51B:AN8907
46165	alcohol biosynthetic process	35 out of 2759 genes, 1.3%	69 out of 10988 background genes, 0.6%	0.00875	AN0451:AN0608:sidI:laeA:AN10648:AN10764:AN11008:gppA:AN1409:pdmA:AN2069:alcC:AN2814:CYP61A1:AN4094:AN4118:AN4405:pdcA:AN4923:AN5415:sidA:AN5862:catC:sidF:sidH:sidD:AN6276:AN6506:AN6973:AN7146:AN7625:AN8012:cyp51B:AN8553:alcA

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9064	glutamine family amino acid metabolic process	27 out of 2759 genes, 1.0%	48 out of 10988 background genes, 0.4%	0.00886	AN0300:pyrABCN:spdA:AN10230:AN1150:prnD:prnC:otaA:AN1883:gatA:agaA:AN2914:idpA:AN3829:gmdA:glnA:gdhA:gtaA:AN4820:AN4901:AN5447:AN5999:AN7278:AN7451:AN7722:AN8770:amdS
6629	lipid metabolic process	138 out of 2759 genes, 5.0%	393 out of 10988 background genes, 3.6%	0.00940	AN0137:AN0408:AN0451:AN0579:AN0608:sidI:basA:AN0649:scdA:AN0827:AN0868:AN0913:AN0918:AN0963:pexE:AN10287:odeA:AN1050:mthA:AN10648:AN1068:AN10764:AN10841:AN10921:AN11008:AN1102:AN1103:AN11161:AN11232:qutG:AN1176:AN11859:AN11959:AN12101:AN1263:AN1330:AN1409:farB:AN1593:mcdA:AN1713:AN1792:CYP682D1:AN1799:AN1840:AN1855:pdmA:AN1950:AN1968:AN2008:AN2069:AN2326:lagA:AN2528:easA:easB:easD:AN3013:AN3276:AN3318:pkiB:AN3588:AN3638:CYP61A1:AN4094:sdeB:AN4258:AN4353:AN4405:AN4601:mccA:alg6:AN4923:ppoC:fatA:AN5211:AN5228:AN5321:AN5402:facA:acuD:AN5646:AN5688:AN5698:AN5704:AN5725:AN5736:AN5777:sidA:pcsA:AN5862:AN5904:echA:AN5919:AN5990:pexA:faaA:accA:AN6139:sidF:sidH:sidD:AN6367:AN6382:AN6506:mcsA:acuE:sdeA:AN6973:AN6992:hadA:farA:foxA:breB:AN7146:AN7158:an2:AN7211:acuL:AN7375:AN7625:AN7661:AN7770:AN7856:AN8012:AN8046:swoH:AN8233:faaB:cyp51B:CYP682B1:AN8743:mclA:CYP537B1:AN8907:AN9297:fasA:fasB

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1901575	organic substance catabolic process	200 out of 2759 genes, 7.2%	606 out of 10988 background genes, 5.5%	0.00961	AN0034:AN0137:ureD:AN0299:AN0300:araR:engA:aldA:pyrABCN:AN0593:facB:bglB:mns1B:scdA:pdeA:AN0868:agdE:ladA:AN10060:AN1015:ganB:AN10164:culA:pexE:AN10417:agdF:AN10433:ggtA:AN10495:mthA:AN1054:facC:AN10599:AN10661:AN10700:AN10838:AN10841:AN10901:AN10903:AN1092:bzuA:AN10996:AN11015:AN11045:glaA:qutG:qutB:AN11722:AN11778:AN1179:AN1198:AN12279:pgkA:AN1263:AN1274:farB:AN1428:codA:nagA:mcdA:hxB:AN1713:prnD:prnC:AN1761:AN1772:AN1799:otaA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:acuF:AN1923:gatA:xlnD:ssn3:AN2528:abnA:abfA:gpdC:bglK:pgmB:fbaA:agaA:pepE:AN2988:AN3013:pgmA:pfkA:AN3276:AN3294:plyE:clrB:pmeA:amyB:AN3459:mns1C:gukA:AN3779:AN3829:ileA:AN3897:cyaA:AN3954:AN4081:bglA:AN4323:ladB:pgaB:AN4532:AN4603:mccB:mccA:AN4691:AN4820:agdG:chiB:AN5025:AN5060:pdhB:pkiA:faeC:AN5447:AN5534:prtA:acuG:hxA:facA:acuD:AN5646:AN5669:AN5672:AN5675:casA:acuN:clrA:ldhA:echA:AN5917:AN5919:AN5939:swoM:fbx1:AN6199:AN6244:amyE:AN6338:rglB:AN6399:AN6405:AN6438:AN6470:aciA:AN6543:mcsA:acuE:pdhA:AN6889:tpiA:AN6902:hadA:farA:foxA:rglA:larA:AN7278:acuL:agdC:mutA:hxkA:AN7492:AN7554:AN7708:AN7770:eglC:abnC:gpdA:AN8046:AN8074:phacA:aglC:chiA:citA:AN8347:AN8390:plyH:AN8654:glkA:mclA:AN8890:pgxB:AN8969:alcR:alcA:AN8999:AN9402
46434	organophosphate catabolic process	28 out of 2759 genes, 1.0%	51 out of 10988 background genes, 0.5%	0.01119	AN0137:AN0593:pdeA:AN10661:qutG:pgkA:acuF:gpdC:fbaA:pgmA:pfkA:gukA:AN3954:mccA:pdhB:pkiA:acuG:acuN:ldhA:AN5919:AN5939:swoM:tpiA:hxkA:gpdA:citA:glkA:AN9402

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55085	transmembrane transport	235 out of 2759 genes, 8.5%	731 out of 10988 background genes, 6.7%	0.01206	AN0015:xtrD:AN0252:AN0318:AN0332:AN0374:AN0404:ureA:AN0473:AN0498:AN0528:AN0559:AN0601:AN0870:AN0890:atp20:AN10036:AN10075:AN10115:AN10172:pexE:AN10221:AN10267:AN10319:AN10332:AN10445:AN10468:AN10487:AN10568:facC:fcyB:AN10828:AN10845:AN10891:AN10949:AN1109:AN1110:AN11120:AN11136:AN11303:AN11444:AN1145:AN1174:mepA:AN11876:AN12074:AN12116:AN12449:AN1276:AN1281:AN1290:AN1427:AN1457:AN1523:AN1534:oliC:enaB:AN1631:AN1659:AN1681:AN1691:AN1724:AN1795:AN1797:AN1833:dicB:AN1920:AN1950:URFA3:atp8:oliA:AN2043:AN2052:pnpA:AN2289:AN2349:AN2432:AN2465:AN2466:AN2544:AN2601:AN2613:AN2614:AN2663:AN2675:AN2794:AN2814:fbaA:AN2958:AN2985:AN3041:AN3160:AN3195:lacpA:AN3220:AN3221:xtrB:AN3304:AN3345:AN3347:AN3357:AN3398:AN3408:atrC:AN3658:AN3663:AN3763:AN3799:AN3813:AN3843:AN3876:AN3952:AN3988:AN3990:AN4019:AN4064:AN4119:AN4131:xtrE:AN4150:AN4209:AN4250:AN4277:AN4316:AN4378:pttA:AN4590:AN4633:AN4649:AN4927:AN5049:AN5088:AN5104:AN5132:AN5540:AN5596:AN5693:AN5734:AN5742:AN5763:mstE:AN5864:AN5917:AN5935:pexA:AN6088:AN6089:jenA:clcA:AN6115:agtA:AN6237:AN6248:AN6287:AN6306:xtrA:AN6417:AN6418:cicA:AN6477:AN6510:enaA:AN6690:AN6757:AN6769:AN6770:AN6778:AN6783:AN6804:AN6831:AN6834:AN6845:hxtA:AN6934:AN6949:

1901615	organic hydroxy compound metabolic process	83 out of 2759 genes, 3.0%	214 out of 10988 background genes, 1.9%	0.01269	AN0034:AN0137:ivoB:AN0270:AN0451:aldA:AN0567:AN0579:AN0608:sidI:laeA:ladA:brlA:AN10290:facC:AN10648:AN10700:AN10764:AN11008:AN11045:qutG:qutB:sumO:gppA:AN1409:AN1593:AN1868:AN1898:hpdA:pdmA:AN2069:alcC:easB:AN2814:AN2860:agsB:AN3638:alcB:AN3901:AN3916:CYP61A1:AN4094:AN4118:ladB:AN4405:AN4532:AN4601:AN4691:pdcA:AN4923:AN5415:gldB:AN5589:sidA:AN5862:agsA:catC:AN5946:AN6141:sidF:sidH:sidD:AN6276:AN6506:AN6973:AN7146:larA:AN7211:AN7590:AN7625:AN7661:pyroA:AN8012:AN8137:cyp51B:AN8390:AN8553:AN8566:AN8907:alcR:alcA:AN8998:AN9363
42274	ribosomal small subunit biogenesis	35 out of 2759 genes, 1.3%	70 out of 10988 background genes, 0.6%	0.01331	AN0465:AN0647:AN10618:AN11929:AN1319:AN1345:AN1949:AN1964:AN2079:AN2262:AN2292:AN3056:nop58:AN3172:AN3313:rrs1:AN3823:rps16:AN4594:AN4777:AN4803:ubi1:AN5222:AN5441:AN5960:AN5979:AN6556:AN6632:AN6679:AN7107:AN7526:AN8805:AN8870:AN9097:AN9468
9062	fatty acid catabolic process	18 out of 2759 genes, 0.7%	27 out of 10988 background genes, 0.2%	0.01380	scdA:AN0868:pexE:mthA:AN10841:farB:mcdA:acuD:AN5646:echA:mcsA:acuE:hadA:farA:foxA:acuL:AN7770:mclA

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34660	ncRNA metabolic process	99 out of 2759 genes, 3.6%	266 out of 10988 background genes, 2.4%	0.01393	AN0046:AN0057:AN0128:AN0428:AN0450:AN0465:AN0647:AN0695:AN0705:AN0745:AN0752:AN0757:AN0776:AN0908:AN0936:AN0956:AN10348:sgdB:AN10475:AN10618:AN10712:AN10832:AN10936:AN10970:AN11060:AN11110:AN11125:cgrA:AN11892:AN11929:AN1215:AN1228:hscA:AN1319:AN1345:AN1380:AN1709:AN1710:AN1913:AN1949:AN1964:AN2079:AN2292:AN2451:AN3056:AN3073:nop58:AN3172:AN3313:AN3455:AN3603:rrs1:AN3823:AN3824:AN3865:AN4086:AN4594:ssz1:AN4777:AN4803:ubi1:AN4889:AN5155:AN5222:AN5441:AN5520:AN5662:AN5865:AN5871:AN5960:AN6082:rpl3:AN6244:podG:AN6368:AN6526:AN6556:AN6558:kaeA:AN6604:AN6632:AN6679:AN6902:AN7107:AN7361:AN7479:AN7526:AN8066:AN8224:AN8491:AN8668:AN8824:swoC:AN8867:AN8870:AN9097:AN9157:AN9419:AN9468

19438	aromatic compound biosynthetic process	221 out of 2759 genes, 8.0%	685 out of 10988 background genes, 6.2%	0.01776	AN0016:AN0097:ivoB:AN0252:AN0270:AN0318:aroG:araR:AN0490:AN0495:AN0507:AN0593:AN0661:facB:aromA:AN0718:H4.1:AN0742:AN0752:AN0797:pdeA:adB:AN0908:atp20:brlA:pyrD:AN10290:AN10298:veA:AN10548:AN10600:AN10638:AN10661:AN10697:AN10710:AN10789:AN10906:AN10910:AN10913:AN10914:AN10970:AN11003:AN11093:AN11111:AN11112:AN11125:phenA:AN11197:AN11212:AN11252:AN11303:qutB:AN11444:sumO:AN11961:AN12201:AN12316:pgkA:AN12478:AN12489:farB:AN1523:AN1524:AN1534:oliC:AN1673:AN1715:AN1722:nosA:AN1857:AN1858:maiA:fahA:hmgA:AN1898:hpdA:AN1915:acuF:AN1976:AN1993:URFA3:atp8:oliA:AN2235:AN2272:AN2283:hemA:AN2293:H4.2:easA:easB:AN2553:gpdC:AN2672:AN2677:AN2723:AN2733:AN2780:AN2854:fbaA:pdhX:pgmA:prs3:AN3222:pfkA:clrB:AN3431:AN3626:AN3634:AN3637:AN3639:gukA:AN3663:AN3683:AN3684:AN3695:AN3748:AN3840:cyaA:AN3920:AN3954:gmdA:AN4013:AN4096:AN4118:AN4250:AN4258:AN4283:metR:mag1:metH:purH:fmdS:AN4600:mccA:AN4739:AN4744:AN4774:AN4837:AN4927:AN4949:AN5122:AN5130:pdhB:AN5200:pkiA:AN5274:AN5415:AN5444:AN5492:AN5566:acuG:facA:aroF:acuN:ldhA:pyrF:pyrE:AN5939:swoM:AN6048:AN6114:AN6141:pyrG:AN6209:trpB:AN6276:AN6287:AN6338:AN6430:hisB:AN6541:AN6558:mcsA:AN6667:AN6682:pdhA:AN6747:AN6762:aroC:tpiA:AN7044:farA:AN7061:fhbA:AN7332:hisHF:

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70887	cellular response to chemical stimulus	157 out of 2759 genes, 5.7%	462 out of 10988 background genes, 4.2%	0.01779	AN0016:AN0137:pppA:tubA:rabE:AN0408:AN0451:aldA:mreA:sidI:spdA:AN0757:AN0776:AN0797:AN0827:AN0836:hsp104:adB:glrA:AN10058:ganB:ccp1:AN10223:AN10296:odeA:hsp20:AN10518:veA:msrA:AN10764:fcyB:AN10949:AN11008:AN11015:AN1131:AN11722:AN1200:AN12478:AN1274:AN1345:AN1416:AN1428:AN1435:atg1:artC:AN1795:AN1797:otaA:pdmA:AN1923:vosA:dnfC:AN2172:AN2210:AN2262:AN2272:aclA:ssn3:hsp30:easA:gpxA:AN2854:AN2997:AN3134:pkfC:agsB:ste7:trxR:awh11:rrs1:ppzA:cypA:AN3829:cyaA:AN3954:AN3973:AN4066:AN4086:glnA:cpcB:mkkA:AN4259:AN4277:AN4304:AN4309:gdhA:AN4456:cmkD:ssz1:sA:AN4774:bckA:AN4894:gstA:AN4923:AN5182:AN5211:AN5447:AN5564:wscA:acuN:sidA:AN5865:agsA:catC:AN5971:pexA:AN5999:gstB:fbx1:agtA:creA:trpB:sidH:cycA:AN6330:AN6506:AN6543:AN6849:tpiA:AN6902:hxtA:ptpA:AN7146:fhbA:AN7170:AN7208:acuK:AN7554:srrB:AN7590:AN7597:AN7661:AN7668:AN7708:AN7884:gpdA:AN8065:phacA:AN8122:hapX:hsp90:AN8273:cyp51B:AN8346:AN8454:AN8502:catA:AN8643:prxA:AN8805:phnC:atrA:alcA:AN9093:aifA:fasB
1902652	secondary alcohol metabolic process	22 out of 2759 genes, 0.8%	37 out of 10988 background genes, 0.3%	0.02057	AN0451:AN0608:sidI:AN10648:AN10764:AN11008:AN1409:pdmA:AN2069:CYP61A1:AN4094:AN4923:sidA:AN5862:sidF:sidH:sidD:AN6506:AN6973:AN7146:AN8012:cyp51B
19319	hexose biosynthetic process	15 out of 2759 genes, 0.5%	21 out of 10988 background genes, 0.2%	0.02334	AN10710:pgkA:acuF:gpdC:fbaA:pgmA:pfkA:mccA:pkiA:acuG:acuN:swoM:tpiA:hxkA:gpdA
46364	monosaccharide biosynthetic process	15 out of 2759 genes, 0.5%	21 out of 10988 background genes, 0.2%	0.02334	AN10710:pgkA:acuF:gpdC:fbaA:pgmA:pfkA:mccA:pkiA:acuG:acuN:swoM:tpiA:hxkA:gpdA

9086	methionine biosynthetic process	15 out of 2759 genes, 0.5%	21 out of 10988 background genes, 0.2%	0.02334	AN10230:msrA:AN3593:AN4290:metH:sA:AN4774:AN4793:metF:AN6576:metG:metA:cysD:cysA:AN8859
6094	gluconeogenesis	14 out of 2759 genes, 0.5%	19 out of 10988 background genes, 0.2%	0.02625	pgkA:acuF:gpdC:fbaA:pgmA:pfkA:mccA:pkiA:acuG:acuN:swoM:tpiA:hxkA:gpdA
44255	cellular lipid metabolic process	113 out of 2759 genes, 4.1%	318 out of 10988 background genes, 2.9%	0.03778	AN0137:AN0408:AN0451:AN0579:AN0608:sidI:basA:AN0649:scdA:AN0827:AN0868:AN0913:AN0918:pexE:AN10287:odeA:AN1050:mthA:AN10648:AN1068:AN10764:AN10841:AN10921:AN11008:AN1102:AN11161:AN11232:qutG:AN1176:AN11859:AN11959:AN1263:AN1409:farB:AN1593:mcdA:AN1713:AN1840:pdmA:AN1950:AN1968:AN2008:AN2069:AN2326:lagA:AN3276:pkiB:AN3588:AN3638:CYP61A1:AN4094:sdeB:AN4258:AN4353:AN4405:AN4601:mccA:alg6:AN4923:ppoC:fatA:AN5211:AN5321:facA:acuD:AN5646:AN5688:AN5698:AN5704:AN5725:AN5736:sidA:pcsA:AN5862:AN5904:echA:AN5919:AN5990:pexA:faaA:accA:AN6139:sidF:sidH:sidD:AN6367:AN6506:mcsA:acuE:sdeA:AN6973:AN6992:hadA:farA:foxA:breB:AN7146:an2:acuL:AN7625:AN7770:AN7856:AN8012:AN8046:swoH:AN8233:faaB:cyp51B:mclA:AN8907:AN9297:fasA:fasB
43648	dicarboxylic acid metabolic process	27 out of 2759 genes, 1.0%	51 out of 10988 background genes, 0.5%	0.04033	aromA:adB:AN10230:prnD:prnC:AN1923:AN1993:gatA:alcC:idpA:alcB:AN3829:AN3840:glnA:gdhA:AN4739:AN4793:AN4820:AN5447:AN6048:AN6209:aciA:aroC:AN7278:AN8188:AN8709:alcA
8643	carbohydrate transport	16 out of 2759 genes, 0.6%	24 out of 10988 background genes, 0.2%	0.04611	xtrD:AN10891:AN1797:AN2289:AN2814:AN4209:AN4277:mstE:AN5917:hxtA:hxkA:AN8122:AN8347:glkA:mstA:AN9168

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Supplementary Table 5d.

Functional enrichment analysis for genes regulated by glucose under nitrogen repressing conditions (ammonium as a nitrogen source) in the wild type strain

Only clusters comprising at lest 5 genes and corrected P - value <0.05 are shown

GOID	GO term	Cluster frequency	Background frequency	Corrected P-value	Genes annotated to the term
16054	organic acid catabolic process	31 out of 1073 genes, 2.9%	116 out of 10988 background genes, 1.1%	0.00014	aldA:facB:AN10700:AN10996:AN11053:AN1198:farB:mcdA:prnD:prnC:maiA:hmgA:AN1898:hpdA:gukA:mccB:mccA:AN5060:AN5068:pdhB:acuD:AN6399:aciA:mcdB:mcsA:acuE:pdhA:lipA:foxA:acuL:mclA
46395	carboxylic acid catabolic process	31 out of 1073 genes, 2.9%	116 out of 10988 background genes, 1.1%	0.00014	aldA:facB:AN10700:AN10996:AN11053:AN1198:farB:mcdA:prnD:prnC:maiA:hmgA:AN1898:hpdA:gukA:mccB:mccA:AN5060:AN5068:pdhB:acuD:AN6399:aciA:mcdB:mcsA:acuE:pdhA:lipA:foxA:acuL:mclA
42254	ribosome biogenesis	42 out of 1073 genes, 3.9%	185 out of 10988 background genes, 1.7%	0.00015	AN0074:AN0262:AN0465:AN0647:AN0728:AN0776:AN0843:AN1013:AN1166:AN1228:AN1345:AN1445:AN1474:AN2262:AN3313:AN3413:AN3706:rrs1:AN3823:AN4087:AN4419:AN4475:AN4594:AN4599:AN4803:AN4916:AN5222:AN5441:AN5960:AN6082:rpl3:AN6266:AN6556:AN6632:AN6679:AN7107:AN7305:nop10:AN8491:AN8870:AN9097:AN9468

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44281	small molecule metabolic process	142 out of 1073 genes, 13.2%	967 out of 10988 background genes, 8.8%	0.00023	AN0046:AN0137:AN0314:AN0484:AN0490:AN0495:aldA:AN0593:AN0649:facB:aromA:mns1B:laeA:AN10197:AN10230:AN10495:AN1050:AN10525:AN10626:AN10700:AN10762:AN10863:AN10996:AN11053:AN11124:AN1115:AN11188:AN11444:sumO:AN11968:AN1198:AN12316:farB:mcdA:prnD:prnC:AN1840:maiA:hmgA:AN1898:hpdA:acuF:atp9:pkhB:AN2272:easB:gpdC:acvA:ipnA:AN2860:pdhX:idpA:AN3077:AN3313:AN3456:AN3557:AN3639:gukA:AN3656:alcB:AN3748:AN3779:AN3866:AN3894:AN3901:AN3916:palA:AN4353:gdhA:AN4401:purH:AN4603:mccB:mccA:AN4691:ugeA:sC:AN4829:AN4830:AN5000:mdhB:AN5060:AN5068:pdhB:fatA:AN5415:AN5444:AN5601:acuG:acuD:AN5669:AN5698:AN5748:pcsA:pyrF:AN5939:nadA:AN6135:sidD:podG:AN6276:AN6399:lysF:aciA:AN6555:AN6576:mcdB:bioF:mcsA:acuE:pdhA:aroC:AN6985:lipA:foxA:an2:acuL:AN7331:AN7363:cpeA:hisHF:aglB:AN7722:stcK:abnC:aglC:AN8188:metA:swoH:AN8390:AN8457:tdiA:AN8533:AN8545:AN8611:AN8754:mclA:carC:AN8859:AN9038:AN9297:xlnB

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6082	organic acid metabolic process	92 out of 1073 genes, 8.6%	569 out of 10988 background genes, 5.2%	0.00067	AN0046:AN0314:aldA:AN0593:AN0649:facB:aromA:laeA:AN10197:AN10230:AN1050:AN10700:AN10863:AN10996:AN11053:AN11188:AN1198:farB:mcdA:prnD:prnC:AN1840:maiA:hmgA:AN1898:hpdA:acuF:pkhB:easB:gpdC:acvA:ipnA:pdhX:idpA:AN3313:AN3456:gukA:AN3656:alcB:AN3748:AN3779:AN3866:AN3894:AN3901:palA:AN4353:gdhA:AN4401:mccB:mccA:sC:AN4830:AN5000:mdhB:AN5060:AN5068:pdhB:fatA:AN5444:AN5601:acuG:acuD:AN5698:pcsA:podG:AN6399:lysF:aciA:AN6555:AN6576:mcdB:bioF:mcsA:acuE:pdhA:aroC:lipA:foxA:an2:acuL:AN7331:cpeA:hisHF:AN7722:stcK:AN8188:metA:AN8754:mclA:carC:AN8859:AN9297
19752	carboxylic acid metabolic process	89 out of 1073 genes, 8.3%	547 out of 10988 background genes, 5.0%	0.00079	AN0046:AN0314:aldA:AN0593:AN0649:facB:aromA:laeA:AN10230:AN1050:AN10700:AN10863:AN10996:AN11053:AN11188:AN1198:farB:mcdA:prnD:prnC:AN1840:maiA:hmgA:AN1898:hpdA:acuF:pkhB:easB:gpdC:acvA:ipnA:pdhX:idpA:AN3313:AN3456:gukA:AN3656:alcB:AN3748:AN3866:AN3894:AN3901:palA:AN4353:gdhA:AN4401:mccB:mccA:sC:AN4830:AN5000:mdhB:AN5060:AN5068:pdhB:fatA:AN5444:AN5601:acuG:acuD:AN5698:pcsA:podG:AN6399:lysF:aciA:AN6555:AN6576:mcdB:bioF:mcsA:acuE:pdhA:aroC:lipA:foxA:an2:acuL:cpeA:hisHF:AN7722:stcK:AN8188:metA:AN8754:mclA:carC:AN8859:AN9297

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43436	oxoacid metabolic process	90 out of 1073 genes, 8.4%	564 out of 10988 background genes, 5.1%	0.00161	AN0046:AN0314:aldA:AN0593:AN0649:facB:aromA:laeA:AN10230:AN1050:AN10700:AN10863:AN10996:AN11053:AN11188:AN1198:farB:mcdA:prnD:prnC:AN1840:maiA:hmgA:AN1898:hpdA:acuF:pkhB:easB:gpdC:acvA:ipnA:pdhX:idpA:AN3313:AN3456:gukA:AN3656:alcB:AN3748:AN3779:AN3866:AN3894:AN3901:palA:AN4353:gdhA:AN4401:mccB:mccA:sC:AN4830:AN5000:mdhB:AN5060:AN5068:pdhB:fatA:AN5444:AN5601:acuG:acuD:AN5698:pcsA:podG:AN6399:lysF:aciA:AN6555:AN6576:mcdB:bioF:mcsA:acuE:pdhA:aroC:lipA:foxA:an2:acuL:cpeA:hisHF:AN7722:stcK:AN8188:metA:AN8754:mclA:carC:AN8859:AN9297
44282	small molecule catabolic process	35 out of 1073 genes, 3.3%	160 out of 10988 background genes, 1.5%	0.00415	aldA:facB:AN10495:AN10700:AN10996:AN11053:AN1198:farB:mcdA:prnD:prnC:maiA:hmgA:AN1898:hpdA:gukA:mccB:mccA:AN4691:AN5060:AN5068:pdhB:acuD:AN5669:AN6399:aciA:mcdB:mcsA:acuE:pdhA:lipA:foxA:acuL:AN8390:mclA
22613	ribonucleoprotein complex biogenesis	42 out of 1073 genes, 3.9%	210 out of 10988 background genes, 1.9%	0.00535	AN0074:AN0262:AN0465:AN0647:AN0728:AN0776:AN0843:AN1013:AN1166:AN1228:AN1345:AN1445:AN1474:AN2262:AN3313:AN3413:AN3706:rrs1:AN3823:AN4087:AN4419:AN4475:AN4594:AN4599:AN4803:AN4916:AN5222:AN5441:AN5960:AN6082:rpl3:AN6266:AN6556:AN6632:AN6679:AN7107:AN7305:nop10:AN8491:AN8870:AN9097:AN9468
34470	ncRNA processing	41 out of 1073 genes, 3.8%	203 out of 10988 background genes, 1.8%	0.00537	AN0074:AN0191:AN0450:AN0465:AN0647:AN0776:AN10832:AN10924:AN11892:AN12059:AN12121:AN1228:AN1345:AN2847:AN3313:rrs1:AN3823:AN4219:AN4594:AN4599:AN4803:AN5155:AN5222:AN5441:AN5960:AN6082:rpl3:podG:AN6513:AN6556:AN6604:AN6632:AN6679:AN7107:AN7305:nop10:AN8491:AN8870:AN9097:trm1:AN9468

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462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	17 out of 1073 genes, 1.6%	52 out of 10988 background genes, 0.5%	0.00544	AN0465:AN1345:AN3313:rrs1:AN3823:AN4594:AN4803:AN5222:AN5441:AN5960:AN6556:AN6679:AN7107:AN7305:AN8870:AN9097:AN9468
42274	ribosomal small subunit biogenesis	20 out of 1073 genes, 1.9%	70 out of 10988 background genes, 0.6%	0.00834	AN0465:AN0647:AN1345:AN2262:AN3313:rrs1:AN3823:AN4594:AN4803:AN5222:AN5441:AN5960:AN6556:AN6632:AN6679:AN7107:AN7305:AN8870:AN9097:AN9468
30490	maturation of SSU-rRNA	18 out of 1073 genes, 1.7%	60 out of 10988 background genes, 0.5%	0.01127	AN0465:AN1345:AN3313:rrs1:AN3823:AN4594:AN4803:AN5222:AN5441:AN5960:AN6556:AN6632:AN6679:AN7107:AN7305:AN8870:AN9097:AN9468

1901566	organonitrogen compound biosynthetic process	132 out of 1073 genes, 12.3%	951 out of 10988 background genes, 8.7%	0.01376	AN0046:AN0123:AN0262:AN0278:AN0314:AN0445:AN0465:AN0490:AN0495:aldA:AN0570:aromA:AN0713:AN0776:mns1B:laeA:AN0843:AN0910:AN0978:AN1013:AN10182:AN10230:AN10416:AN10477:AN10614:AN10626:AN10681:AN10740:AN10762:AN10913:AN10996:AN1122:AN11411:AN11419:AN11444:AN1166:AN11968:AN12246:AN1228:AN12316:AN1345:AN1393:AN1455:prnD:prnC:maiA:hmgA:hpdA:acuF:atp9:AN2272:easA:easB:easD:gpdC:acvA:ipnA:AN2733:pdhX:AN2980:idpA:AN3413:AN3639:gukA:AN3748:AN3823:AN3826:AN3894:AN4015:AN4087:rpl16a:palA:gdhA:AN4401:purH:AN4475:AN4594:AN4613:mccA:ugeA:AN4794:AN4802:AN4803:AN4830:alg6:AN4916:AN5000:AN5014:pdhB:AN5222:AN5415:AN5441:AN5444:AN5601:acuG:AN5688:pyrF:AN5888:AN5960:AN5996:nadA:AN6181:rpl3:sidD:podG:AN6276:lysF:AN6564:AN6576:AN6629:AN6632:bioF:AN6679:pdhA:aroC:AN7003:AN7269:hisHF:AN7722:AN8176:AN8188:metA:swoH:tdiA:AN8705:AN8754:AN8859:AN8870:AN9038:AN9097:AN9465:AN9468
32787	monocarboxylic acid metabolic process	46 out of 1073 genes, 4.3%	250 out of 10988 background genes, 2.3%	0.01931	aldA:AN0649:facB:laeA:AN1050:AN10700:AN11188:farB:mcdA:AN1840:acuF:easB:gpdC:acvA:ipnA:pdhX:gukA:AN3901:palA:AN4353:AN4401:mccA:AN4830:AN5000:pdhB:fatA:acuG:acuD:AN5698:pcsA:aciA:AN6555:mcdB:bioF:mcsA:acuE:pdhA:lipA:foxA:an2:acuL:cpeA:stcK:AN8754:mclA:AN9297
72329	monocarboxylic acid catabolic process	16 out of 1073 genes, 1.5%	52 out of 10988 background genes, 0.5%	0.02460	facB:AN10700:farB:mcdA:gukA:pdhB:acuD:aciA:mcdB:mcsA:acuE:pdhA:lipA:foxA:acuL:mclA

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34660	ncRNA metabolic process	47 out of 1073 genes, 4.4%	266 out of 10988 background genes, 2.4%	0.04600	AN0046:AN0074:AN0191:AN0314:AN0450:AN0465:AN0647:AN0728:AN0752:AN0776:AN0908:AN10832:AN10924:AN11892:AN12059:AN12121:AN1228:AN1345:AN2847:AN3313:rrs1:AN3823:AN4219:AN4594:AN4599:AN4803:AN5155:AN5222:AN5441:AN5960:AN6082:rpl3:podG:AN6513:AN6556:AN6558:AN6604:AN6632:AN6679:AN7107:AN7305:nop10:AN8491:AN8870:AN9097:trm1:AN9468

For Peer Review