SCIENCE CHINA
Life Sciences

• RESEARCH PAPER •

May 2013 Vol.56 No.5: 467–475
doi: 10.1007/s11427-013-4480-6

pyrG is required for maintaining stable cellular uracil level and normal sporulation pattern under excess uracil stress in *Aspergillus nidulans*

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Received February 25, 2013; accepted March 28, 2013

Tight control of the intracellular uracil level is believed to be important to reduce the occurrence of uracil incorporation into DNA. The *pyrG* gene of *Aspergillus nidulans* encodes orotidine 5′-phosphate decarboxylase, which catalyzes the conversion of orotidine monophosphate (OMP) to uridine monophosphate (UMP). In this study, we found that *pyrG* is critical for maintaining uracil at a low concentration in *A. nidulans* cells in the presence of exogenous uracil. Excess uracil and its derivatives had a stronger inhibitory effect on the growth of the *pyrG89* mutant with defective OMP decarboxylase activity than on the growth of wild type, and induced sexual development in the *pyrG89* mutant but not in wild type. Analysis of transcriptomic responses to excess uracil by digital gene expression profiling (DGE) revealed that genes related to sexual development were transcriptionally activated in the *pyrG89* mutant but not in wild type. Quantitative analysis by HPLC showed that the cellular uracil level was 6.5 times higher in the *pyrG89* mutant than in wild type in the presence of exogenous uracil. This study not only provides new information on uracil recycling and adaptation to excess uracil but also reveals the potential effects of OMP decarboxylase on fungal growth and development.

orotidine 5′-phosphate decarboxylase, stress, uracil, sexual development

Citation: Sun X Y, Zhu J F, Bao L, et al. *pyrG* is required for maintaining stable cellular uracil level and normal sporulation pattern under excess uracil stress in *Aspergillus nidulans*. Sci China Life Sci, 2013, 56: 467–475, doi: 10.1007/s11427-013-4480-6

Orotidine 5′-phosphate decarboxylase (OMP decarboxylase; EC 4.1.1.23) is essential for the *de novo* biosynthesis of pyrimidine. It catalyzes the conversion of orotidine monophosphate (OMP) to uridine monophosphate (UMP) by decarboxylation. OMP decarboxylase is encoded by *URA3* in *Saccharomyces cerevisiae* [1], *pyrG* in *Aspergillus nidulans* [2], and *pyr-4* in *Neurospora crassa* [3]. Auxotrophic mutants with impaired OMP decarboxylase can grow normally if exogenous uridine and uracil are added to the growth medium, and their deficiency is easily complemented by genes encoding functional OMP decarboxylases. Therefore, genetic transformation systems based upon complementation of OMP decarboxylase mutants are widely used for many fungal species, such as *S. cerevisiae* [4], *A. nidulans* [5], *Penicillium chrysogenum* [6], *Aspergillus niger* [7], *Trichoderma reesei* [8] and *Aspergillus fumigatus* [9]. In filamentous fungi, the *N. crassa pyr-4* gene is a widely used selectable marker to complement OMP decarboxylase mutants [5–11].

When the phenotype of a newly generated mutant is characterized, the corresponding OMP decarboxylase-deficient parent strain is often used as a control. In this case,

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*Corresponding author (email: shaojieli@gmail.com) uracil must be added to the medium to allow the parent strain to grow. However, it is not known whether the exogenous uracil has different effects on the growth or development between *pyrG* mutants and wild type. Several lines of evidence suggest that the cellular uracil level is tightly controlled to prevent the accumulation of excess cellular uracil in fungi. In response to exogenous uracil, the transcriptional level of *FUR4*, which encodes a uracil permease for uracil transport in *S. cerevisiae* [12], is downregulated [13,14]. Similarly, exogenous uracil triggers the transcriptional down-regulation of *A. nidulans furD*, a gene encoding Fur4p-like uracil permease [15]. At the posttranslational level, the presence of exogenous uracil accelerates the degradation of Fur4p by enhancing its ubiquitylation [14]. Tight control of the cellular uracil level is believed to be important to maintain a low ratio of uracil/thymine to prevent the incorporation of uracil into DNA [15]. Replacement of thymine with uracil in regulatory regions of genomic DNA can disrupt the specificity of protein-DNA interactions [16].

In this study, we found that the loss of OMP decarboxylase in *A. nidulans* increased its sensitivity to excess uracil and its derivatives. Excess uracil and its derivatives induced sexual development in OMP decarboxylase mutants but not wild type. Transcriptomic profiling of uracil responses by DGE also revealed that genes involved in sexual development were activated by excess uracil in the OMP decarboxylase mutant.

1 Materials and methods

1.1 Strains and media

In this study, the *A. nidulans* strain FGSC A773 (*pyrG89*; *wA3*; *pyroA4*; *veA1*) was used as the parental strain. A PCR fragment containing the *N. crassa pyr-4* sequence was transformed into FGSC A773, yielding strain AHC01 (*pyrG89*; *wA3*; *pyroA4*; *pyr-4*; *veA1*). Fungal transformation was conducted as described by Miller et al. [17] and Calvo et al. [18]. ALS05 (*wA3*; *pyroA4*; *veA1*) was generated by crossing FGSC A773 (*pyrG89*; *wA3*; *pyroA4*; *veA1*) with FGSC A4 (*veA*+).

MMV medium (1% glucose, nitrate salts, trace elements, and vitamins, pH 6.5) was used for growing *A. nidulans*. The composition of trace elements, vitamins, and nitrate salts in the medium were as described by Käfer [19]. Uridine (5 mmol L^{-1} as 1×) and uracil (10 mmol L^{-1} as 1×) were added as needed. Media were solidified with 1.5% agar.

1.2 Analysis of cellular uracil and other intermediates

The spores of *A. nidulans* A773 or ALS05 were inoculated into a 300-mL flask containing 150 mL medium (MMV+1×uridine+4×uracil) and incubated at 28°C with constant agitation at 180 r $\min^{-1}$ for 30 h. Subsequently, metabolites were extracted following the method described by Ruijiter and Visser [20]. The extracted mycelia were collected and lyophilized to determine dry weight.

The extracts were filtered through 0.45-μm filters and intermediary metabolites were identified and quantified by high performance liquid chromatography (HPLC) using a COSMOSIL C18 column (4.6 I.D.×250 mm) with 5% acetonitrile and 0.04% trifluoroacetate solution as the eluent.

1.3 Studies on sexual development

To compare sexual development of the *pyrG89* mutant with that of wild type, the production of Hülle cells was evaluated. Four plugs (0.5 cm in diameter) of fungi growing on the surface of the agar medium (MMV+1×uridine+4×uracil) were harvested with a borer and homogenized in 2 mL distilled water. Hülle cells were counted with a hemacytometer under a light microscope. The average number of Hülle cells per square millimeter from three replicates was calculated.

1.4 Analysis of transcriptomic responses to excess uracil by digital gene expression profiling analysis

To compare the differences in transcriptomic responses to excess uracil between wild type and the *pyrG89* mutant, we examined genome-wide transcriptional responses to excess uracil by digital gene expression (DGE) profiling [21]. Briefly, the spores of *A. nidulans* wild type or the *pyrG89* mutant were inoculated into 150-ml flasks containing 75 mL liquid medium (MMV+1×uridine+4×uracil and MMV+1× uridine+1×uracil) and incubated at 28°C with shaking at 180 r $\min^{-1}$ for 30 h. Then RNA was extracted from three replicate samples for the DGE profiling assay. Isolation of mRNA from total RNA samples and preparation of sequencing tags were conducted using the DGE Tag Profile Kit (Illumina, San Diego, CA, USA) according to the manufacturer's instructions. Details of the method were described by Sun et al. [22].

After treatment of raw data, all clean tags were mapped to the reference sequences (http://www.broadinsti tute.org/annotation/genome/aspergillus_group/Blast.html). To monitor mapping events on both strands, both sense and complementary antisense sequences were included in the mapping process. The clean tag numbers corresponding to each gene were counted.

1.5 Identification of differentially transcribed genes

To identify genes differentially transcribed between two samples, the number of raw clean tags in each sample was normalized to tags per million (TPM). Detection of differentially transcribed genes or tags across samples was performed according to the method previously reported, i.e., transcriptional ratios between two samples of greater than 2 and less than 0.5 were the thresholds to define differentially transcribed genes [23]. Correlations between count numbers in two parallel libraries were assessed statistically by calculating Pearson correlation coefficients. In addition to the *P*-value, the false discovery rate (FDR) was manipulated to determine differentially transcribed genes [24]. In this study, $P \leqslant 0.01$, FDR⩽0.1, and the absolute value of log2 ratio⩾1 were used as the thresholds to assess the significance of differences in gene transcription.

1.6 Biological function annotation and enrichment analysis

To reveal the biological functions of differentially transcribed genes in response to excess uracil, annotation of the important subsets of genes was performed using BLAST (ver. 2.2.23+) software against the FunCat database (http://mips.helmholtz-muenchen.de/proj/funcatDB/), with an *E*-value cut-off of 1×10^{-10}. To further highlight significant biological changes, gene set enrichment analysis was conducted with R statistical software (http://www.r-projects.org/), and the hypergeometric test algorithm was applied with the threshold values of $P \leqslant 0.01$ and FDR⩽0.1.

1.7 Quantitative real-time PCR analysis

cDNA was synthesized from total cellular RNA using a cDNA Synthesis Kit (Fermentas, Burlington, Canada). PCR was performed in using a iQ5 Multicolor Real-Time PCR Detection System (Bio-Rad, Hercules, CA, USA) with SYBR-Green detection (SYBR PrimeScript RT-PCR Kit, TaKaRa Biotechnology Co., Ltd., Dalian, Liaoning, China), according to the manufacturer's instructions. Each cDNA sample was analyzed in triplicate, and the average threshold cycle was calculated. Relative expression levels were calculated using the $2^{-\Delta\Delta C_t}$ method [25]. The results were normalized to level of β-tubulin transcripts. The primer pairs used for qRT-PCRs are shown in Table 1.

Table 1 Gene-specific primer pairs used for quantitative real-time PCR

Gene	Sequences of primers (5′→3′)
nsdD	QnsdDF: GGCGGAACCATCACGTTCAAGTTT QnsdDR: TAACAGTGCTTGCACTTTGCGTCG
nosA	QnosAF: ACCCATACGTTCTTCCTCCGTTCA QnosAR1: TTTCGATCGGTAGGTGTGGGCAAA
noxA	QnoxAF: ACCGAACTGAAGAGCAGGACCAAT QnoxAR: ACCAATCTCTGTCCTGGAATGCGT
fhbA	QfhbAF: AAACAACGTACTTCCTGACGGCTC QfhbAR: TCTGCTTGTCGCCAAGGAAGAGAT
glpV	QglpVF: GATCCGCCTTCAGTTTGCCATTGT QglpVR: AATCGCCCGAAGTCTCAGAGAGGTAT
upt	QuptF: AAGCCATCGACGTGCTGAAAGAGA QuptR: CTTAACCGCGGAAACCGTTGCATT
hsp20	Qhsp20F: TCTGAACATCAAGGGCCACAGTGA Qhsp20R: TAGGAAAGTTGAACGAGCGTCGGA
β-tub	QbtubF: TTCGGACGAGACATTCTGCTTGGA QbtubR: TGACAGCAGACACCAGATGGTTGA

2 Results

2.1 *pyrG89* mutation increases sensitivity to excess uracil

In fungi, the cellular uracil level is tightly controlled to prevent the accumulation of excess cellular uracil. *A. nidulans* strains lacking PyrG (orotidine 5′-phosphate decarboxylase) activity can grow only when exogenous uracil and uridine are added to the medium. The *pyrG*-defective mutants should be more tolerant than wild type to excess exogenous uracil and uridine. To test this possibility, we compared the growth of the wild-type control strain ALS05 with that of the *pyrG*-defective mutant A773 (*pyrG89*) on plates with different concentrations of uracil and uridine. Opposite to our expectations, the *pyrG89* mutant was more sensitive than wild type to excess uracil and uridine. As shown in Figure 1, after 5 d of growth, the colony sizes of the wild-type control strain on plates containing a high concentration of uracil and uridine (four times normal levels, designated as 4×uracil or 4×uridine) were similar to those on plates with normal concentrations of uracil and uridine (1×uracil, 1×uridine). In contrast, the average colony size of the *pyrG89* mutant on the 4×uracil and 4×uridine plates was 69%±2% of that on 1×uracil and 1×uridine plates. We then found that excess uracil could inhibit colony growth, and excess uridine (20 mmol L^{-1}) did not inhibit colony growth in either wild type or the *pyrG89* mutant (Figure 1). Transformation of *N. crassa pyr-4* into the *pyrG89* mutant completely rescued the uracil-hypersensitive phenotype caused by the *pyrG89* mutation (Figure 1).

On 1×UU (5 mmol L^{-1} uridine and 10 mmol L^{-1} uracil) plates, both wild type and the *pyrG89* mutant reproduced mainly by asexual sporulation (Figures 1 and 2). The colonies of both wild type and *pyrG* were white because of the high density of conidia produced on the colony surface. On 4×UU (20 mmol L^{-1} uridine and 40 mmol L^{-1} uracil) plates, wild type still reproduced mainly by asexual sporulation, while conidial production was dramatically decreased and sexual development remarkably increased in the *pyrG89* mutant, resulting in a yellowish color of colonies (Figures 1 and 2). When observed under a dissecting microscope or by scanning electron microscopy, protocleistothecia, which were surrounded by yellow Hülle cells, were abundant on the surface of the *pyrG89* mutant on 4×UU plates. In contrast, protocleistothecia were rarely seen on the surface of wild type on 4×UU plates and on the surface of the *pyrG* mutant on 1×UU plates (Figure 2).

2.2 *pyrG89* mutation increases sensitivity to excess chemicals related to uracil metabolism

In eukaryotes, cellular uracil can serve as a precursor for synthesis of many other compounds or it can be degraded by two pathways [26,27]. To test whether compounds in-

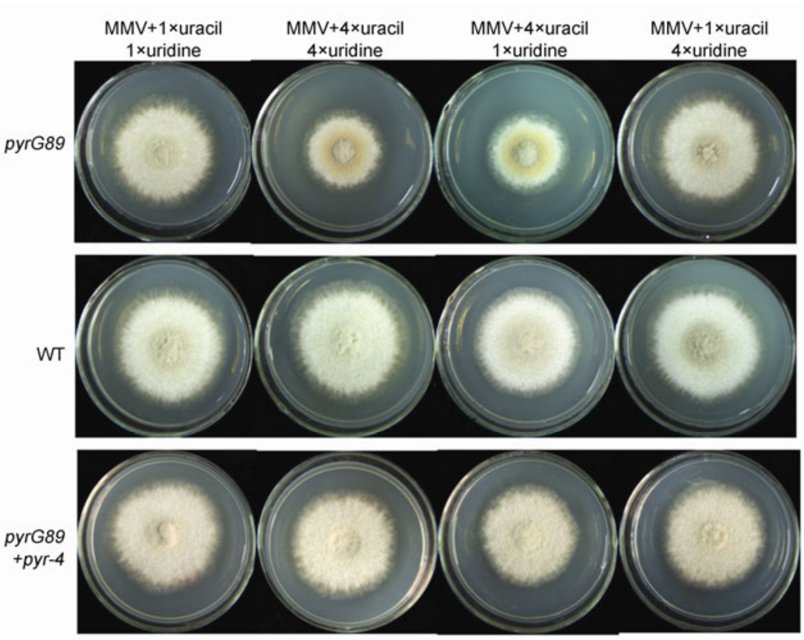


Figure 1 Effects of excess uracil on growth and sexual development of *A. nidulans pyrG89* mutant. Conidia of *A. nidulans* wild type ALS05 (WT), *pyrG89* mutant A773 (p*yrG89*) or complemented strain AHC01 (*pyrG89+pyr-4)* were inoculated onto the center of plates containing MMVUU medium (MMV+1×uridine+1×uracil) (control) or MMVUU medium with 4×additives (4×uridine, or 4×uracil, or 4×uridine and 4×uracil) and incubated at 28°C for 5 d. 5 mmol L^{-1} as 1× for uridine and 10 mmol L^{-1} as 1× for uracil. Experiment was carried out with three replicates.

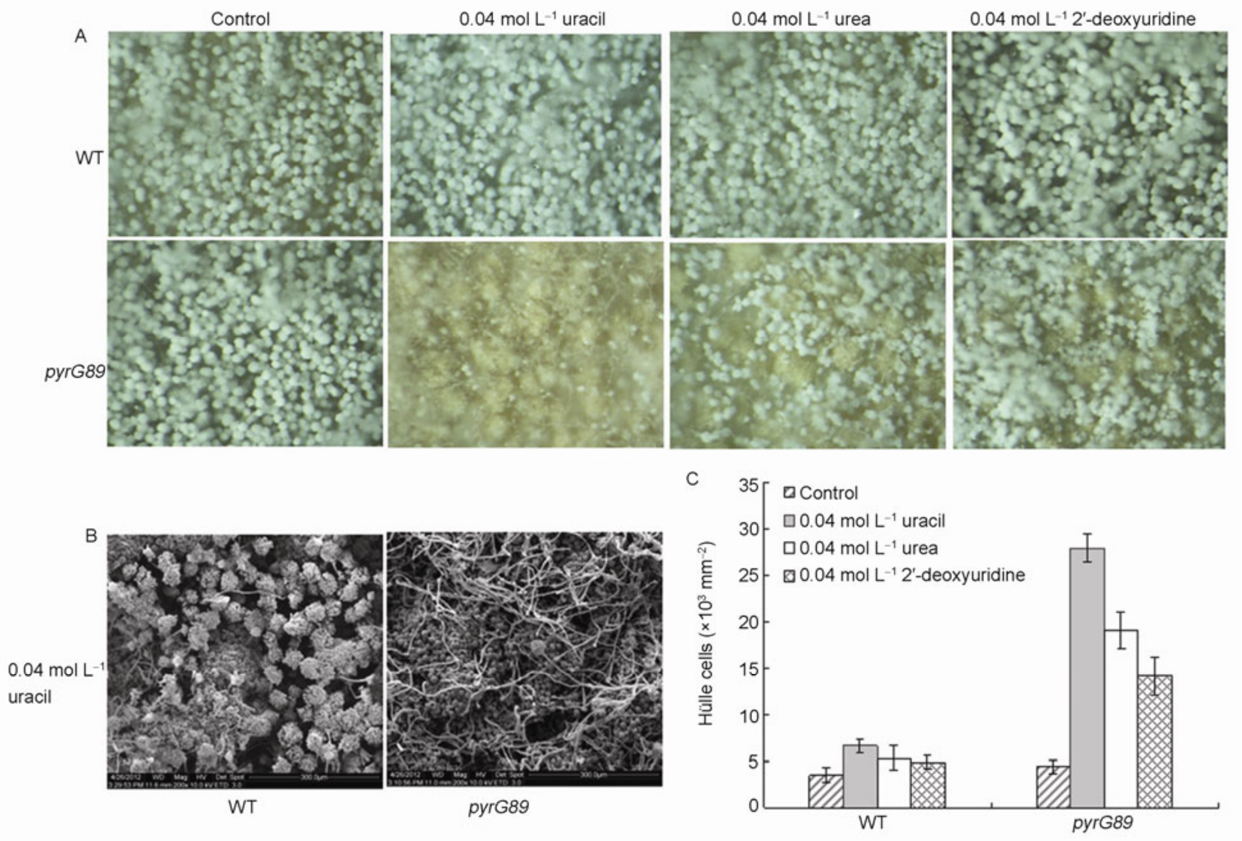


Figure 2 Comparison of sexual differentiation between *A. nidulans* wild type and *pyrG89* mutant in response to excess uracil stress. Conidia of *A. nidulans* wild type or the *pyrG89* mutant were inoculated onto the center of plates containing MMVUU medium (MMV+1×uridine+1×uracil) (control) or MMVUU medium with 4× (0.04 mol L^{-1}) additives (4×uracil, or 4×2′-deoxyuridine, or 4×urea) and incubated at 28°C for 5 d. Images were obtained under a dissecting microscope (A) or a scanning electron microscope (B). Hülle cell production in wild type and the *pyrG89* mutant was compared (C) Number of Hülle cells harvested from colonies was shown as mean values±standard deviation (*n*=3 replicate dishes). 5 mmol L^{-1} as 1× for uridine and 10 mmol L^{-1} as 1× for uracil, 2′-deoxyuridine or urea.

volved in uracil metabolism have effects similar to uracil, equivalent experiments were conducted using 2′-deoxyuridine (0.04 mol L^{-1}) and urea (0.04 mol L^{-1}) as the stressing chemicals. As shown in Figures 2 and 3, addition of 2′-deoxyuridine (0.04 mol L^{-1}) and urea (0.04 mol L^{-1}) reduced the colony growth of the *pyrG89* mutant but not that of wild type. In addition, 2′-deoxyuridine (0.04 mol L^{-1}) and urea (0.04 mol L^{-1}) induced sexual development of the *pyrG89* mutant but not that of wild type.

2.3 *pyrG89* mutation causes an accumulation of uracil in cells

The hypersensitivity of the *pyrG89* mutant to excess uracil (0.04 mol L^{-1}), 2′-deoxyuridine (0.04 mol L^{-1}), and urea (0.04 mol L^{-1}) is likely a result of its disrupted uracil metabolism. Without a functional PyrG, excess uracil, 2′-deoxyuridine, and urea might accumulate in cells and have toxic effects. To test this hypothesis, cellular uracil, uridine, and AMP in *pyrG89* and wild type grown in minimal medium with 4×uracil and uridine were quantitatively analyzed by HPLC. The cellular uracil, uridine, and AMP levels in the *pyrG89* mutant were 653%, 31%, and 51% higher, respectively, than those in wild type (Figure 4).

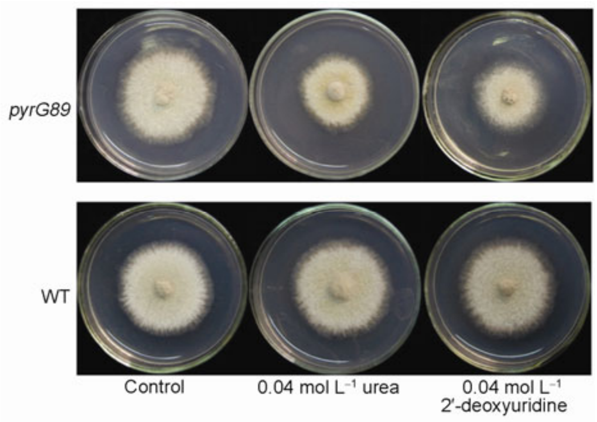
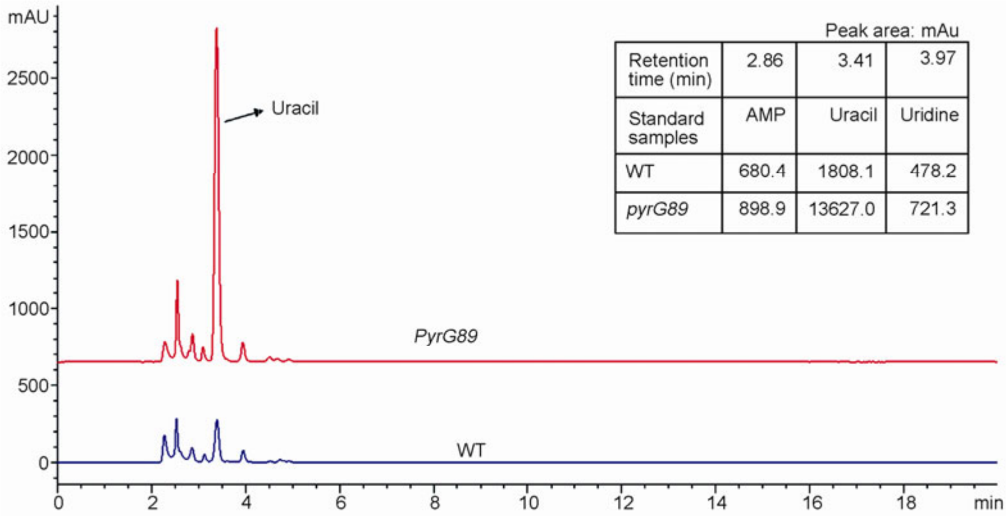


Figure 3 Effects of excess metabolites of uracil on growth and sexual development of *A. nidulans pyrG* mutant. Conidiospores of *A. nidulans* wild type or *pyrG89* mutant were inoculated onto center of plates containing MMVUU medium (MMV+1×uridine+1×uracil) (control) or MMVUU medium with 4× (0.04 mol L^{-1}) additives (4×urea or 4×2′-deoxyuridine) and incubated at 28°C for 5 d. 5 mmol L^{-1} as 1× for uridine and 10 mmol L^{-1} as 1× for uracil, 2′-deoxyuridine, or urea.

2.4 Analysis of transcriptomic responses to excess uracil

To understand the mechanism of uracil accumulation and the developmental effects of uracil on the *pyrG* mutant, we analyzed transcriptomic profiles of the *pyrG89* mutant and wild type grown in liquid medium supplemented with normal (1×) or excess (4×) levels of uracil by DGE profiling. In response to excess uracil stress, 185 and 71 genes were up-regulated in the *pyrG89* mutant and wild type, respectively, and 317 and 162 genes were down-regulated in the *pyrG89* mutant and wild type, respectively. If transcriptional levels of genes in the *pyrG89* mutant and wild type were compared under excess uracil conditions, 1025 genes showed at least 50% lower transcript levels and 655 genes showed higher (>1 fold) transcript levels in the mutant than in wild type (Supplemental Data S1). In response to excess uracil stress, many genes (e.g., ANID_07074, ANID_03925, ANID_10399, ANID_02859, and ANID_05567) showed no transcriptional response in wild type but were dramatically up-regulated in the *pyrG89* mutant (Table 2). Many other genes (e.g., ANID_06657, ANID_01608, ANID_02578, and ANID_05145) maintained high transcript levels in wild



Retention time (min)	2.86	3.41	3.97
Standard samples	AMP	Uracil	Uridine
WT	680.4	1808.1	478.2
pyrG89	898.9	13627.0	721.3

Figure 4 HPLC chromatograms of intermediary metabolites of uracil metabolism in *A. nidulans*. Cellular uracil, uridine, and AMP in *pyrG89* mutant and wild type grown in minimal medium with 4×uracil and 1×uridine were quantitatively analyzed by HPLC. 5 mmol L^{-1} as 1× for uridine and 10 mmol L^{-1} as 1× for uracil.

Table 2 Significant differently transcribed genes between wild type and the *pyrG* mutant in response to excess uracil

Gene[a]	Function annotation[b]	TPM[c]-WT 1×uracil	TPM-*pyrG89* 1×uracil	TPM[c]-WT 4×uracil	TPM-*pyrG89* 4×uracil	Fold (*pyrG89* /WT) 4×uracil	*P*-value	FDR
Up-regulated genes								
ANID_07074	hypothetical protein, metabolic process and oxidation-reduction process	4.43	14.5	4.87	112.75	23.15	1.70×10^{-11}	1.04×10^{-10}
ANID_03925	hypothetical protein, carbohydrate metabolic process	9.71	44.69	13.11	302	23.04	0	0
ANID_10399	hypothetical protein, oxidation-reduction process	10.39	74.71	9.58	214.52	22.39	5.28×10^{-14}	4.33×10^{-13}
ANID_02859	dihydrodipicolinate synthetase family protein, metabolic process	3.06	17.91	3.19	63.61	19.94	8.44×10^{-9}	4.26×10^{-8}
ANID_08953	alpha-glucosidase B with a predicted role in maltose metabolism, *agdB*	72.37	1748.5	154.45	2911.22	18.85	1.25×10^{-12}	8.37
ANID_09121	*esdC*, sexual development	57.04	221.91	32.77	518.6	15.83	1.40×10^{-13}	1.09×10^{-12}
ANID_05567	GrpB domain protein	4.43	8.19	5.55	82.43	14.85	1.64×10^{-12}	1.09×10^{-11}
ANID_08972	hypothetical protein, transporter activity	3.92	18.76	3.36	45.48	13.54	4.54×10^{-9}	2.34×10^{-8}
ANID_09373	putative Zn(II)2Cys6 transcription factor	20.26	47.59	11.09	139.06	12.54	0	0
ANID_05977	ketoreductase, with role in metabolic process	23.84	65.67	10.42	112.75	10.82	0	0
ANID_10949	ABC transporter protein	2.72	9.89	3.53	32.24	9.13	2.44×10^{-9}	1.28×10^{-8}
ANID_08602	hypothetical protein with oxidoreductase activity	10.9	41.45	18.32	164.85	9.00	0	0
ANID_06669	putative sugar transporter	12.09	97.91	29.41	246.93	8.40	3.08×10^{-13}	2.25×10^{-12}
ANID_05655	5'-nucleotidase (EC:3.1.3.5)	4.43	18.42	3.03	24.4	8.05	1.56×10^{-8}	7.69×10^{-8}
ANID_00841	hypothetical protein	4.6	24.22	4.71	36.94	7.84	3.14×10^{-11}	1.88×10^{-10}
ANID_04220	ankyrin repeat protein, role in meiosis and cytosol, nucleus localization	20.43	41.45	5.55	41.3	7.44	1.64×10^{-12}	1.09×10^{-11}
ANID_02970	4-nitrophenylphosphatase, with role in aminobenzoate degradation	77.13	175	32.6	239.09	7.33	4.61×10^{-13}	3.30×10^{-12}
ANID_03520	hypothetical protein	10.22	40.94	14.45	102.81	7.11	0	0
ANID_10964	methyltransferase, role in metabolic process	19.07	49.64	7.06	49.66	7.03	1.07×10^{-13}	8.47×10^{-13}
ANID_04085	protein phosphotase 2a 65kd regulatory subunit	58.91	114.11	27.56	173.22	6.29	8.93×10^{-14}	7.18×10^{-13}
Down-regulated genes								
ANID_05447	glutamate decarboxylase, amino acid metabolism	395.2	106.95	585.19	18.65	0.032	0	0
ANID_06657	hypothetical protein	1291.17	461.9	1699.6	78.94	0.046	0	0
ANID_01608	hypothetical protein	1406.61	531.32	1732.88	96.19	0.056	0	0
ANID_01510	oxidoreductin	491.06	161.53	802.49	46.53	0.058	0	0
ANID_02578	hypothetical protein with peroxidase activity	3255.76	854.72	4109.27	239.09	0.058	0	0
ANID_05145	hypothetical protein	258.98	88.7	322.51	18.82	0.058	0	0
ANID_04940	protein with role in cellular response to stress	551.68	112.4	728.38	44.79	0.061	0	0
ANID_02555	serine carboxypeptidase, protein metabolism	255.24	79.31	400.99	25.97	0.065	0	0
ANID_12070	glutamyl-tRNA amidotransferase subunit A	237.19	112.92	271.76	17.77	0.065	0	0
ANID_01879	WD repeat protein, role in glutathione catabolic process and cytoplasm, nucleus localization	212.33	47.59	309.91	20.39	0.066	0	0
ANID_04127	hypothetical protein	686.87	209.46	763.84	57.68	0.076	0	0
ANID_11246	nucleobase, nucleoside, nucleotide and nucleic acid transporter	26.39	5.97	50.59	3.83	0.076	7.01×10^{-62}	1.26×10^{-60}
ANID_04135	delta-9-stearic acid desaturase, fatty acid metabolism	212.5	67.89	367.38	28.23	0.077	0	0
ANID_10299	hypothetical protein, amino acid metabolism	245.02	103.71	439.14	33.98	0.077	0	0
ANID_02286	alcohol dehydrogenase III (ADH III)	515.07	223.1	484.69	39.91	0.082	0	0
ANID_08122	MFS multidrug transporter	34.91	9.72	60	5.05	0.084	1.07×10^{-70}	2.05×10^{-69}
ANID_01378	hypothetical protein	1117.66	840.39	1519.27	132.26	0.087	0	0
ANID_09297	67 kDa myosin-cross-reactive antigen family protein	454.28	183.36	548.89	48.44	0.088	0	0
ANID_06525	NAD-dependent formate dehydrogenase (FDH)	335.43	148.05	473.26	43.22	0.091	0	0
ANID_00186	hypothetical protein	148.14	59.7	283.35	25.97	0.092	0	0
ANID_03796	hypothetical protein	145.07	78.12	208.56	19.34	0.093	1.46×10^{-233}	4.10×10^{-232}
ANID_08461	hypothetical protein	234.46	220.55	281.5	28.06	0.100	4.00×10^{-306}	1.23×10^{-304}
ANID_09470	uricase (urate oxidase), purine metabolism	338.84	136.63	450.4	44.96	0.100	0	0

a) Gene accession numbers were annotated according to *Aspergillus* comparative genome database (http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html/). b) Function annotations were obtained from broad description of genes. c) TPM, tags per million.

type but not in the mutant under uracil stress. These findings indicate that the *pyrG89* mutant had more significant transcriptional responses to uracil stress than did wild type, suggesting that the *pyrG89* mutant suffered greater stress than did wild type under these conditions. The maintenance of stable gene expression levels might be important for cellular metabolism and growth under uracil stress.

2.5 Transcriptional responses by nucleotide metabolism-related genes to excess uracil

Gene set enrichment analysis showed that differentially transcribed genes between the two tested strains were mainly involved in C-compound and carbohydrate metabolism, transportation of compounds, and functions related to disease, virulence, and defense (Table S1). Among the genes directly related to uracil metabolism, ANID_05655, which encodes a 5′-nucleotidase (EC: 3.1.3.5), showed an 8-fold higher transcript level in the *pyrG89* mutant than in wild type (Table 2). 5′-nucleotidase catalyzes the dephosphorylation of nucleoside monophosphates and is involved in salvaging preformed nucleotides [28]. The increased transcript levels of the 5′-nucleotidase gene suggest that the balance between nucleotides and nucleosides is disordered in the mutant.

Transport is the first step for salvage of exogenous pyrimidine bases. In *A. nidulans*, *furD* (ANID_11247) and *cntA* (ANID_05493) are uracil- and uridine-transporter genes, respectively [29]. As shown in Table 3 and Table S2, neither of these genes showed higher transcriptional levels in the *pyrG* mutant than in wild type.

2.6 Transcriptional responses of sexual development-related genes to excess uracil

In response to excess uracil, several genes involved in sexual development were differentially transcribed in the *pyrG89* mutant relative to wild type. As shown in Table 3, transcript levels of *esdC* (ANID_09121), *nosA*, and *noxA* in the *pyrG89* mutant were more than 4-fold higher than in wild type. Conversely, transcript levels of the flavohemoglobin gene *fhbA* in the *pyrG89* mutant were only 26% of that in wild type. These results were confirmed by qRT-PCR (Figure 5).

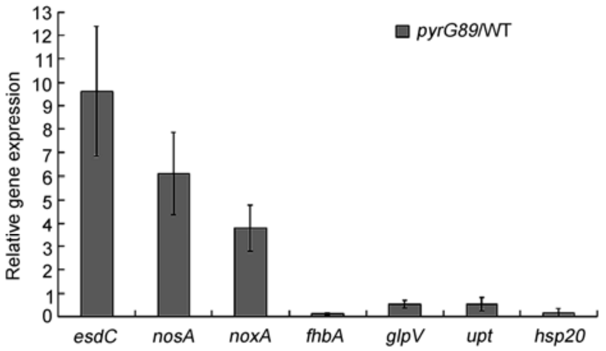


Figure 5 Differential transcriptions of genes in *pyrG89* mutant relative to wild type as determined by qRT-PCR. Relative transcriptional levels of four down-regulated genes and three up-regulated genes are shown. Values shown are means of three independent replicates±standard deviation.

Table 3 Comparison of transcriptional responses of uracil transporter genes and genes involved in sexual development between wild type and pyrG mutant grown in medium with excess uracil

Gene[a]	Function annotation[b]	TPM[c]-WT 1×uracil	TPM-*pyrG89* 1×uracil	TPM[c]-WT 4×uracil	TPM-*pyrG89* 4×uracil	Fold (*pyrG89/WT*) 4×uracil	*P*-value	FDR
Uracil and uridine transporter genes								
ANID_11247	uracil transporter FurD	0.34	0.01	0.84	0.01	—[(d)]	0.0348	0.0688
ANID_05493	Concentrative nucleoside permease CntA	3.41	3.75	5.71	5.05	—	0.6319	0.7132
The genes involved in sexual development								
ANID_01052	VeA	72.54	102.17	82.35	134.17	1.63	0	0
ANID_03152	sexual development transcription factor NsdD	1.7	0.68	0.34	0.01	—	0.2638	0.3483
ANID_04263	C2H2 zinc finger protein NsdC	0.85	1.02	1.01	0.35	—	0.1982	0.2944
ANID_09121	early sexual development EsdC	57.04	221.91	32.77	518.60	15.83	1.40×10^{-13}	1.09×10^{-12}
ANID_06505	transcriptional repressor rco-1, TupA/RocA	366.76	345.23	402.34	455	—	1.37×10^{-5}	5.03×10^{-5}
ANID_05170	sexual development transcription factor RosA	0	0	0	0	—	—	—
ANID_02260	NADH-ubiquinone oxidoreductase subunit	403.2	383.27	578.97	346.78	0.60	1.23×10^{-76}	2.40×10^{-75}
ANID_01848	C6 sexual development transcription factor NosA	3.41	3.24	1.18	5.92	5.02	1.95×10^{-5}	7.03×10^{-5}
ANID_02330	late sexual development protein	0	0	0	0	—	—	—
ANID_07169	flavohemoglobin gene *fhbA*	2222.72	1699.55	1077.95	276.55	0.26	0	0
ANID_00807	methyltransferase LaeA	0.01	0.68	1.18	0.01	0.01	0.0090	0.0213
ANID_05457	NADPH oxidases NoxA	4.43	13.82	5.04	29.62	5.88	9.27×10^{-12}	5.79×10^{-11}
ANID_05836	cell pattern formation-associated protein StuA	5.96	5.8	4.54	5.92	—	0.3022	0.3899

a) Gene accession numbers were annotated according to *Aspergillus* comparative genome database (http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html/). b) Function annotations were obtained from broad description of genes. c) TPM, tags per million. d) "—" indicates *P*-value greater than 0.01.

The *A. nidulans esdC* (early sexual development) gene is necessary for sexual development [30]. The *nosA* gene controls fruiting body formation in *A. nidulans* [31]. The *noxA* gene is induced during sexual development, and deletion of *noxA* specifically blocks differentiation of sexual fruit bodies (cleistothecia) [32]. For the flavohemoglobin gene *fhbA*, deletion of *fhbA* induced sexual development [33]. Thus, the up-regulation of *esdC*, *nosA* and *noxA* genes and down-regulation of *fhbA* in the *pyrG* mutant theoretically favors sexual development.

3 Discussion

3.1 *PyrG* participates in maintaining steady levels of cellular uracil

OMP decarboxylase is required for pyrimidine synthesis. Cellular uracil levels are tightly controlled to prevent the accumulation of uracil. This is accomplished by the regulation of uracil permeases at transcriptional, posttranscriptional, and posttranslational levels [13–15]. In this study, we found that excess uracil in the medium caused uracil accumulation in cells of the *pyrG89* mutant but not those of wild type, indicating that OMP decarboxylase participates in maintaining cellular uracil at a low level. In *A. nidulans*, *furD* (ANID_11247) and *cntA* (ANID_05493) are the only known transporter genes for uracil and uridine, respectively. It was proposed that more uracil transporter genes should exist in this fungus [29]. Thus, although *furD* and *cntA* did not display statistically higher transcript levels in the *pyrG* mutant than in wild type, we cannot exclude the possibility that accumulation of cellular uracil in the *pyrG89* mutant is due to increased uracil transport. If the accumulation of uracil is independent of uracil transport, one possible explanation is that PyrG might play a role in recycling extra uracil by an unknown mechanism, in addition to its role in catalyzing UMP biosynthesis.

Excess accumulation of uracil is believed to be toxic to cells, but these toxic effects were not observed. Here, we provide direct evidence that high concentrations of uracil affect the growth and development of *A. nidulans*. Because they can accumulate high levels of uracil, *pyrG89* mutants would be useful research materials to investigate whether increased cellular uracil can elevate the frequency of uracil incorporation into DNA. In contrast to uracil, uridine did not have inhibitory effects, even though it accumulated in the *pyrG89* mutant. Since uridine cannot be directly incorporated into DNA as a substrate to synthesize uracil-DNA, it might be less toxic than uracil.

3.2 Excess uracil activates sexual development

For most filamentous ascomycetes, asexual sporulation is the major reproduction mode under normal conditions, while sexual development is usually induced by extreme conditions such as low temperature or extended darkness. Therefore, activation of sexual development might be a strategy for fungi to survive under extremely unfavorable conditions. Here, we showed that uracil and other metabolites involved in uracil metabolism could activate sexual development and suppress conidiation in the *pyrG89* mutant, and that the transcriptions of genes involved in sexual development, such as *esdC*, *nosA*, and *noxA*, could be induced by uracil. These observations suggest that cellular accumulation of uracil and related metabolites can alter the developmental pattern of *A. nidulans*. Similar to the *pyrG89* mutant grown under excess uracil stress, *A. nidulans* mutants with defects in sphingolipid biosynthesis displayed enhanced sexual sporulation and reduced conidial production [34]. These phenomena indicate that sexual development can be activated by diverse metabolic abnormalities. Each metabolic process might have monitors to sense changes. However, abnormal signals from different metabolic monitors might be passed to the same unknown signaling pathway that determines developmental fate. Activated by metabolic monitors, this pathway might transcriptionally activate *esdC*, *nosA*, and *noxA*, which further activate expressions of genes required for sexual development.

3.3 *pyrG* affects sensitivity to multiple stresses

Auxtotrophic *pyrG* mutants are the most frequently used parent strains for generating new strains by gene deletion or overexpression in *A. nidulans* and other fungal species. Phenotypic observations of new strains derived from *pyrG* mutants are often conducted using the parental *pyrG* mutants as controls. However, this study clearly demonstrates that the *pyrG* mutation can alter the growth and developmental pattern. Thus, when new mutants are generated using a *pyrG* mutant as the parent, care must be taken to ensure that the resulting phenotypes are due to the new mutation alone, and do not reflect the *pyrG* mutation.

This work was supported by the National Natural Science Foundation of China (31000551 to Sun XianYun, 31170087 to Li ShaoJie) and a grant from the "100 Talent Program" from Chinese Academy of Sciences to Li ShaoJie. We thank Prof. Liu Gang and Dr. Wu Sheng (Institute of Microbiology, Chinese Academy of Sciences) for valuable discussion about the experimental design and Prof. Nick D. Read (University of Edinburgh, UK) for proof reading of the manuscript.

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Supporting Information

Table S1 Differentially transcribed genes grouped by functional classification and gene set enrichment analysis (4×uracil, Δ*pyrG89*/WT)

Table S2 Differentially transcribed genes between wild type and the *pyrG* mutant in response to excess uracil

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Life Sciences

Supporting Information

May 2013 Vol.56 No.5: 1–42
doi: 10.1007/s11427-013-4480-6

Table S1 Differentially transcribed genes grouped by functional classification and gene set enrichment analysis (4×uracil, Δ*pyrG89*/WT)

Funcat No.[a]	Identified genes	Differential transcribed genes	P-value[b]	FDR[b]	Significant[b]	Funcat name[a]
01.05	775	201	0.005411	0.084768	TRUE	C-compound and carbohydrate metabolism
20.01	680	180	0.003412	0.080185	TRUE	transported compounds (substrates)
32.05	242	72	0.003374	0.080185	TRUE	disease, virulence and defense
01.01	362	84	0.34174	0.979167	FALSE	amino acid metabolism
01.02	169	32	0.872215	0.979167	FALSE	nitrogen, sulfur and selenium metabolism
01.03	200	46	0.421309	0.979167	FALSE	nucleotide/nucleoside/nucleobase metabolism
01.06	440	112	0.053696	0.420617	FALSE	lipid, fatty acid and isoprenoid metabolism
01.20	317	83	0.049697	0.420617	FALSE	secondary metabolism
02.16	82	16	0.762365	0.979167	FALSE	fermentation
10.01	297	44	0.999579	0.979167	FALSE	DNA processing
10.03	415	72	0.994983	0.979167	FALSE	cell cycle
11.02	521	89	0.998872	0.979167	FALSE	RNA synthesis
11.04	262	38	0.999469	0.979167	FALSE	RNA processing
11.06	44	5	0.979666	0.979167	FALSE	RNA modification
14.07	454	92	0.862637	0.979167	FALSE	protein modification
14.13	198	51	0.130378	0.765973	FALSE	protein/peptide degradation
18.02	154	30	0.821395	0.979167	FALSE	target of regulation, regulation of protein activity
20.03	374	87	0.328622	0.979167	FALSE	transport facilitation, transport facilities
20.09	719	157	0.617404	0.979167	FALSE	transport routes
30.01	258	51	0.850916	0.979167	FALSE	intracellular signaling, cellular signalling
30.05	73	15	0.679237	0.979167	FALSE	transmembrane signal transduction
32.07	217	60	0.032963	0.387316	FALSE	detoxification
34.01	187	50	0.080286	0.539061	FALSE	ionic homeostasis
34.11	243	59	0.237358	0.979167	FALSE	cellular sensing and response to external stimulus
36.20	7	2	0.483355	0.979167	FALSE	plant / fungal specific systemic sensing and response
40.01	196	46	0.361702	0.979167	FALSE	cell growth / morphogenesis
40.02	5	1	0.715372	0.979167	FALSE	cell differentiation->43
40.10	19	5	0.419049	0.979167	FALSE	cell death
41.01	37	3	0.994039	0.979167	FALSE	fungal/microorganismic development
43.01	368	87	0.268756	0.979167	FALSE	fungal/microorganismic cell type differentiation

a) Functional classification of all differential expressed genes was used the program Blast with database of FunCat (http://mips.helmholtz-muenchen.de/proj/funcatDB/). b) Gene set enrichment analysis was used Hypergeometric testing algorithm with R statistical software (http://www.r-projects.org/) with the threshold values of $P \leqslant 0.01$ and $FDR \leqslant 0.1$.

Table S2 Differentially transcribed genes between wild type and the *pyrG* mutant in response to excess uracil

Gene (a)	TPM(b)-wt-4uacil	TPM-pyrG89-4uracil	log2 Ratio (pyrG89/wt)	P-Value	FDR	blast nr (c)
ANID_05018	0.01	24.05	11.2318212	0	0	gi|67537696|ref|XP_662622.1|/0/hypothetical protein AN5018.2 [Aspergillus nidulans FGSC A4]
ANID_03877	0.01	13.77	10.4273128	0	0	gi|67526839|ref|XP_661481.1|/3.25103e-126/hypothetical protein AN3877.2 [A. nidulans FGSC A4]
ANID_11835	0.01	11.5	10.1674182	0	0	gi|67525783|ref|XP_660953.1|/0/hypothetical protein AN3349.2 [A. nidulans FGSC A4]
ANID_07269	0.01	10.11	9.98156728	0	0	gi|259483385|tpe|CBF78732.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02576	0.01	9.93	9.95564991	0	0	gi|259488012|tpe|CBF87132.1|/0/TPA: xenobiotic compound monooxygenase, DszA family (AFU_orthologue; AFUA_3G15040) [A. nidulans FGSC A4]
ANID_01926	0.01	9.41	9.87805091	0	0	gi|67522939|ref|XP_659530.1|/6.38876e-141/hypothetical protein AN1926.2 [A. nidulans FGSC A4]
ANID_08612	0.01	7.14	9.47978026	2.11E-13	1.60E-12	gi|67903250|ref|XP_681881.1|/8.94072e-142/hypothetical protein AN8612.2 [A. nidulans FGSC A4]
ANID_01962	0.01	6.1	9.25266543	1.51E-11	9.27E-11	gi|67523011|ref|XP_659566.1|/0/hypothetical protein AN1962.2 [A. nidulans FGSC A4]
ANID_04714	0.01	5.23	9.03066714	5.28E-10	2.92E-09	gi|67537088|ref|XP_662318.1|/0/hypothetical protein AN4714.2 [A. nidulans FGSC A4]
ANID_12383	0.01	5.05	8.98013958	1.08E-09	5.81E-09	gi|115491217|ref|XP_001210236.1|/3.43895e-38/predicted protein [A. terreus NIH2624]
ANID_07280	0.01	5.05	8.98013958	1.08E-09	5.81E-09	gi|67900586|ref|XP_680549.1|/0/hypothetical protein AN7280.2 [A. nidulans FGSC A4]
ANID_10392	0.01	4.88	8.93073734	2.19E-09	1.16E-08	gi|259485672|tpe|CBF82892.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06191	0.01	4.88	8.93073734	2.19E-09	1.16E-08	gi|67540042|ref|XP_663795.1|/3.96247e-141/hypothetical protein AN6191.2 [A. nidulans FGSC A4]
ANID_03491	0.01	4.53	8.82336724	9.10E-09	4.55E-08	gi|67526067|ref|XP_661095.1|/0/hypothetical protein AN3491.2 [A. nidulans FGSC A4]
ANID_08608	0.01	4.36	8.76818433	1.85E-08	9.09E-08	gi|67903242|ref|XP_681877.1|/3.13939e-49/hypothetical protein AN8608.2 [A. nidulans FGSC A4]
ANID_09504	0.01	4.18	8.70735913	3.77E-08	1.81E-07	gi|75859092|ref|XP_868886.1|/0/NIMA_EMENI G2-specific protein kinase NIMA (Never in mitosis) [A. nidulans FGSC A4]
ANID_03342	0.01	3.49	8.44708323	6.50E-07	2.79E-06	gi|67525769|ref|XP_660946.1|/0/hypothetical protein AN3342.2 [A. nidulans FGSC A4]
ANID_08994	0.01	3.49	8.44708323	6.50E-07	2.79E-06	gi|67904014|ref|XP_682263.1|/2.74262e-151/hypothetical protein AN8994.2 [A. nidulans FGSC A4]
ANID_09298	0.01	3.31	8.37068741	1.32E-06	5.53E-06	gi|189041381|sp|Q5AQY2.2|GMT2_EMENI/1.78846e-155/RecName: Full=GDP-mannose transporter 2; Short=GMT 2
ANID_02092	0.01	3.31	8.37068741	1.32E-06	5.52E-06	gi|134079148|emb|CAK40677.1|/2.58972e-136/prolyl aminopeptidase papA-A. niger
ANID_10115	0.01	3.14	8.29462075	2.70E-06	1.09E-05	gi|259489000|tpe|CBF88911.1|/0/TPA: MFS transporter, putative (AFU_orthologue; AFUA_1G13970) [A. nidulans FGSC A4]
ANID_06103	0.01	3.14	8.29462075	2.70E-06	1.09E-05	gi|67539866|ref|XP_663707.1|/8.45898e-153/hypothetical protein AN6103.2 [A. nidulans FGSC A4]
ANID_11833	0.01	3.14	8.29462075	2.70E-06	1.09E-05	gi|67525783|ref|XP_660953.1|/0/hypothetical protein AN3349.2 [A. nidulans FGSC A4]
ANID_10268	0.01	2.96	8.20945337	5.49E-06	2.15E-05	gi|259487561|tpe|CBF86329.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_03446	0.01	2.96	8.20945337	5.49E-06	2.15E-05	gi|67525977|ref|XP_661050.1|/6.42604e-74/hypothetical protein AN3446.2 [A. nidulans FGSC A4]
ANID_00617	0.01	2.79	8.12412131	1.12E-05	4.16E-05	gi|67516671|ref|XP_658221.1|/8.2858e-159/hypothetical protein AN0617.2 [A. nidulans FGSC A4]
ANID_05284	0.01	2.79	8.12412131	1.12E-05	4.16E-05	gi|67538228|ref|XP_662888.1|/0/hypothetical protein AN5284.2 [A. nidulans FGSC A4]
ANID_03517	0.01	2.79	8.12412131	1.12E-05	4.16E-05	gi|67526119|ref|XP_661121.1|/6.5464e-168/hypothetical protein AN3517.2 [A. nidulans FGSC A4]
ANID_05321	0.01	2.79	8.12412131	1.12E-05	4.16E-05	gi|67538302|ref|XP_662925.1|/0/hypothetical protein AN5321.2 [A. nidulans FGSC A4]
ANID_02604	0.01	2.61	8.027906	2.28E-05	8.16E-05	gi|67524293|ref|XP_660208.1|/7.72256e-127/hypothetical protein AN2604.2 [A. nidulans FGSC A4]
ANID_11873	0.01	2.61	8.027906	2.28E-05	8.15E-05	gi|67902926|ref|XP_681719.1|/0/hypothetical protein AN8450.2 [A. nidulans FGSC A4]
ANID_11028	0.01	2.61	8.027906	2.28E-05	8.15E-05	gi|259480629|tpe|CBF73447.1|/7.74541e-160/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_12059	0.01	2.61	8.027906	2.28E-05	8.14E-05	gi|238508831|ref|XP_002385598.1|/4.06713e-51/cytosine deaminase, putative [A. flavus NRRL3357]
ANID_07087	0.01	2.61	8.027906	2.28E-05	8.14E-05	gi|67541847|ref|XP_664691.1|/2.02459e-157/hypothetical protein AN7087.2 [A. nidulans FGSC A4]
ANID_08429	0.01	2.44	7.93073734	4.64E-05	0.00016	gi|67902884|ref|XP_681698.1|/2.73421e-67/hypothetical protein AN8429.2 [A. nidulans FGSC A4]
ANID_02609	0.01	2.44	7.93073734	4.64E-05	0.00016	gi|67524303|ref|XP_660213.1|/3.56846e-154/hypothetical protein AN2609.2 [A. nidulans FGSC A4]
ANID_07811	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|67901648|ref|XP_681080.1|/4.83711e-155/STCO_EMENI Putative sterigmatocystin biosynthesis protein stcO [A. nidulans FGSC A4]
ANID_06237	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|259479555|tpe|CBF69884.1|/0/TPA: ABC multidrug transporter (Eurofung) [A. nidulans FGSC A4]
ANID_05617	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|259484914|tpe|CBF81541.1|/0/TPA: DNA replication ATPase (Eurofung) [A. nidulans FGSC A4]

ANID_11209	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|259488102|tpe|CBF87301.1|/1.09111e-141/TPA: hypothetical protein ANIA_11209 [A. nidulans FGSC A4]
ANID_10812	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|67540594|ref|XP_664071.1|/1.26634e-164/hypothetical protein AN6467.2 [A. nidulans FGSC A4]
ANID_01382	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|259488281|tpe|CBF87607.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04274	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|67528136|ref|XP_661878.1|/0/hypothetical protein AN4274.2 [A. nidulans FGSC A4]
ANID_11947	0.01	2.27	7.82654849	9.45E-05	0.000312	gi|67538230|ref|XP_662889.1|/2.1815e-145/hypothetical protein AN5285.2 [A. nidulans FGSC A4]
ANID_04986	0.01	2.09	7.70735913	0.000193	0.000608	gi|169770469|ref|XP_001819704.1|/1.09283e-82/hypothetical protein AOR_1_934154 [A. oryzae RIB40]
ANID_07577	0.01	2.09	7.70735913	0.000193	0.000608	gi|67901180|ref|XP_680846.1|/0/hypothetical protein AN7577.2 [A. nidulans FGSC A4]
ANID_11894	0.01	2.09	7.70735913	0.000193	0.000608	gi|67517421|ref|XP_658561.1|/1.33719e-93/hypothetical protein AN0957.2 [A. nidulans FGSC A4]
ANID_04590	0.01	2.09	7.70735913	0.000193	0.000607	gi|67536840|ref|XP_662194.1|/0/hypothetical protein AN4590.2 [A. nidulans FGSC A4]
ANID_10359	0.01	2.09	7.70735913	0.000193	0.000607	gi|67524783|ref|XP_660453.1|/0/hypothetical protein AN2849.2 [A. nidulans FGSC A4]
ANID_04178	0.01	2.09	7.70735913	0.000193	0.000607	gi|67527855|ref|XP_661782.1|/0/hypothetical protein AN4178.2 [A. nidulans FGSC A4]
ANID_03518	0.01	2.09	7.70735913	0.000193	0.000607	gi|67526121|ref|XP_661122.1|/0/hypothetical protein AN3518.2 [A. nidulans FGSC A4]
ANID_12350	0.01	2.09	7.70735913	0.000193	0.000606	gi|67539688|ref|XP_663618.1|/1.31948e-16/hypothetical protein AN6014.2 [A. nidulans FGSC A4]
ANID_07266	1.18	116.41	6.62428433	1.05E-05	3.94E-05	gi|67900558|ref|XP_680535.1|/5.90859e-16/hypothetical protein AN7266.2 [A. nidulans FGSC A4]
ANID_11121	1.51	80.86	5.74280575	3.43E-06	1.37E-05	gi|67903568|ref|XP_682040.1|/0/hypothetical protein AN8771.2 [A. nidulans FGSC A4]
ANID_11952	0.67	26.49	5.30514294	4.93E-05	0.000169	gi|259485260|tpe|CBF82140.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_06952	0.34	11.85	5.1232085	0.000119	0.000388	gi|67541577|ref|XP_664556.1|/1.72005e-143/hypothetical protein AN6952.2 [A. nidulans FGSC A4]
ANID_05331	0.84	26.66	4.98814364	3.02E-05	0.000106	gi|259485228|tpe|CBF82088.1|/2.40935e-112/TPA: 3-hydroxyacyl-CoA dehydrogenase, putative (AFU_orthologue; AFUA_3G00290) [A. nidulans FGSC A4]
ANID_07126	0.5	14.46	4.85399565	7.75E-05	0.000261	gi|259483547|tpe|CBF79026.1|/0/TPA: HET domain protein (AFU_orthologue; AFUA_3G03140) [A. nidulans FGSC A4]
ANID_07753	0.67	18.12	4.75727805	4.93E-05	0.000169	gi|259484104|tpe|CBF80039.1|/0/TPA: ATP-dependent DNA helicase II subunit 1 (EC 3.6.1.-)(ATP-dependent DNA helicase II subunit Ku70) [Source:UniProtKB/Swiss-Prot;Acc:Q5AVC7] [A. nidulans FGSC A4]
ANID_07265	0.34	8.71	4.67906607	0.000119	0.000388	gi|67900556|ref|XP_680534.1|/7.22871e-70/hypothetical protein AN7265.2 [A. nidulans FGSC A4]
ANID_08969	2.52	64.3	4.6733231	9.82E-08	4.57E-07	gi|67903964|ref|XP_682238.1|/2.40001e-122/hypothetical protein AN8969.2 [A. nidulans FGSC A4]
ANID_08391	0.34	8.19	4.5902568	0.000119	0.000387	gi|67902808|ref|XP_681660.1|/2.06613e-152/hypothetical protein AN8391.2 [A. nidulans FGSC A4]
ANID_07074	4.87	112.75	4.53306185	1.70E-11	1.04E-10	gi|67541821|ref|XP_664678.1|/4.03031e-170/hypothetical protein AN7074.2 [A. nidulans FGSC A4]
ANID_03925	13.11	302	4.52580896	0	0	gi|67526935|ref|XP_661529.1|/1.62623e-142/hypothetical protein AN3925.2 [A. nidulans FGSC A4]
ANID_10399	9.58	214.52	4.48494269	5.28E-14	4.33E-13	gi|67525785|ref|XP_660954.1|/3.68557e-152/hypothetical protein AN3350.2 [A. nidulans FGSC A4]
ANID_05312	0.5	11.15	4.47897181	7.75E-05	0.000261	gi|67538284|ref|XP_662916.1|/0/hypothetical protein AN5312.2 [A. nidulans FGSC A4]
ANID_07358	0.34	7.14	4.39231742	0.000119	0.000387	gi|67900742|ref|XP_680627.1|/0/hypothetical protein AN7358.2 [A. nidulans FGSC A4]
ANID_02859	3.19	63.61	4.31762526	8.44E-09	4.26E-08	gi|259486205|tpe|CBF83860.1|/1.47576e-174/TPA: dihydrodipicolinate synthetase family protein (AFU_orthologue; AFUA_3G11920) [A. nidulans FGSC A4]
ANID_08953	154.45	2911.22	4.23641209	1.25E-12	8.37E-12	gi|13447612|dbj|BAB39856.1|/0/alpha-glucosidase B [Emericella nidulans]
ANID_05639	0.34	6.27	4.20485879	0.000119	0.000387	gi|67538938|ref|XP_663243.1|/0/hypothetical protein AN5639.2 [A. nidulans FGSC A4]
ANID_08458	0.34	6.1	4.16520259	0.000119	0.000387	gi|67902942|ref|XP_681727.1|/1.48813e-44/hypothetical protein AN8458.2 [A. nidulans FGSC A4]
ANID_07268	0.34	6.1	4.16520259	0.000119	0.000387	gi|67900562|ref|XP_680537.1|/9.37886e-129/hypothetical protein AN7268.2 [A. nidulans FGSC A4]
ANID_03983	1.85	31.89	4.10750692	1.08E-06	4.52E-06	gi|67527101|ref|XP_661587.1|/3.50874e-80/hypothetical protein AN3983.2 [A. nidulans FGSC A4]
ANID_01714	0.5	8.36	4.06350294	7.75E-05	0.00026	gi|67522515|ref|XP_659318.1|/4.90463e-115/hypothetical protein AN1714.2 [A. nidulans FGSC A4]
ANID_11948	0.67	10.8	4.01072641	4.93E-05	0.000169	gi|242798406|ref|XP_002483163.1|/5.6803e-82/hypothetical protein TSTA_010470 [Talaromyces stipitatus ATCC 10500]
ANID_09121	32.77	518.6	3.98417463	1.40E-13	1.09E-12	gi|22347729|gb|AAM95965.1|/1.10067e-84/ESDC [Emericella nidulans]
ANID_11054	1.34	21.09	3.97625419	6.04E-06	2.35E-05	gi|259480995|tpe|CBF74129.1|/0/TPA: alpha glucosidase II, alpha subunit, putative (AFU_orthologue; AFUA_5G03500) [A. nidulans FGSC A4]
ANID_12013	0.5	7.49	3.90496572	7.75E-05	0.00026	gi|154277708|ref|XP_001539690.1|/5.41057e-17/predicted protein [Ajellomyces capsulatus NAm1]
ANID_01782	0.34	5.05	3.89267674	0.000119	0.000387	gi|67522651|ref|XP_659386.1|/4.28436e-173/hypothetical protein AN1782.2 [A. nidulans FGSC A4]
ANID_08963	0.34	5.05	3.89267674	0.000119	0.000387	gi|67903952|ref|XP_682232.1|/4.54313e-51/hypothetical protein AN8963.2 [A. nidulans

						FGSC A4]
ANID_05567	5.55	82.43	3.89260982	1.64E-12	1.09E-11	gi|259484973|tpe|CBF81651.1|/7.85996e-112/TPA: GrpB domain protein (AFU_orthologue; AFUA_1G01530) [A. nidulans FGSC A4]
ANID_07896	0.84	12.37	3.88031236	3.02E-05	0.000107	gi|259480645|tpe|CBF73479.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_11707	0.34	4.88	3.8432745	0.00012	0.000387	gi|259485959|tpe|CBF83421.1|/0/TPA: DIL and Ankyrin domain protein (AFU_orthologue; AFUA_3G12450) [A. nidulans FGSC A4]
ANID_08972	3.36	45.48	3.75869912	4.54E-09	2.34E-08	gi|67903970|ref|XP_682241.1|/0/hypothetical protein AN8972.2 [A. nidulans FGSC A4]
ANID_09373	11.09	139.06	3.64837622	0	0	gi|259488215|tpe|CBF87493.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_03776	1.51	18.82	3.63964617	3.43E-06	1.37E-05	gi|67526637|ref|XP_661380.1|/0/hypothetical protein AN3776.2 [A. nidulans FGSC A4]
ANID_06876	0.34	4.18	3.61989629	0.000123	0.000398	gi|159129835|gb|EDP54949.1|/1.2018e-158/oxidoreductase, FAD-binding, putative [A. fumigatus A1163]
ANID_02646	0.34	4.18	3.61989629	0.000123	0.000397	gi|259486444|tpe|CBF84285.1|/0/TPA: Hsp70 family protein (AFU_orthologue; AFUA_4G14040) [A. nidulans FGSC A4]
ANID_06159	0.34	4.01	3.55999559	0.000126	0.000408	gi|67539978|ref|XP_663763.1|/0/hypothetical protein AN6159.2 [A. nidulans FGSC A4]
ANID_12177	0.5	5.75	3.52356196	7.76E-05	0.00026	gi|145257031|ref|XP_001401593.1|/9.68512e-20/hypothetical protein ANI_1_470184 [A. niger CBS 513.88]
ANID_04792	0.67	7.67	3.51699358	4.93E-05	0.000169	gi|67537244|ref|XP_662396.1|/0/hypothetical protein AN4792.2 [A. nidulans FGSC A4]
ANID_05977	10.42	112.75	3.43570025	0	0	gi|259479840|tpe|CBF70432.1|/1.50138e-108/TPA: ketoreductase (AFU_orthologue; AFUA_2G10280) [A. nidulans FGSC A4]
ANID_05633	0.34	3.66	3.428237	0.000144	0.000462	gi|119500292|ref|XP_001266903.1|/0/transporter protein smf2 [Neosartorya fischeri NRRL 181]
ANID_05730	1.01	10.8	3.41860411	1.80E-05	6.52E-05	gi|259484793|tpe|CBF81318.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10691	1.68	17.6	3.38904229	1.93E-06	7.91E-06	gi|259484992|tpe|CBF81685.1|/0/TPA: dynamin GTPase, putative (AFU_orthologue; AFUA_6G11890) [A. nidulans FGSC A4]
ANID_09320	0.34	3.49	3.35962039	0.000166	0.000527	gi|67904666|ref|XP_682589.1|/0/hypothetical protein AN9320.2 [A. nidulans FGSC A4]
ANID_00539	2.52	24.92	3.30580843	9.82E-08	4.57E-07	gi|67516515|ref|XP_658143.1|/0/hypothetical protein AN0539.2 [A. nidulans FGSC A4]
ANID_12352	1.01	9.93	3.29743843	1.80E-05	6.52E-05	gi|119479925|ref|XP_001259991.1|/0/hypothetical protein NFIA_080380 [N. fischeri NRRL 181]
ANID_10206	0.5	4.88	3.28688115	7.91E-05	0.000265	gi|259486713|tpe|CBF84791.1|/7.38846e-32/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00326	0.5	4.88	3.28688115	7.91E-05	0.000265	gi|67516089|ref|XP_657930.1|/0/hypothetical protein AN0326.2 [A. nidulans FGSC A4]
ANID_11510	1.18	11.33	3.2632891	1.05E-05	3.94E-05	gi|259479308|tpe|CBF69423.1|/2.59771e-27/TPA: hypothetical protein ANIA_11510 [A. nidulans FGSC A4]
ANID_05315	3.03	28.23	3.21983943	1.56E-08	7.69E-08	gi|67538290|ref|XP_662919.1|/0/hypothetical protein AN5315.2 [A. nidulans FGSC A4]
ANID_04789	0.34	3.14	3.20715791	0.000281	0.000868	gi|18031889|gb|AAL09153.1|/0/polymerase zeta subunit [Emericella nidulans]
ANID_10949	3.53	32.24	3.19111166	2.44E-09	1.28E-08	gi|259483903|tpe|CBF79672.1|/0/TPA: ABC transporter protein [Source:UniProtKB/TrEMBL;Acc:Q96VK5] [A. nidulans FGSC A4]
ANID_08602	18.32	164.85	3.16966248	0	0	gi|67903230|ref|XP_681871.1|/0/hypothetical protein AN8602.2 [A. nidulans FGSC A4]
ANID_10347	0.84	7.49	3.15650449	3.02E-05	0.000106	gi|259486216|tpe|CBF83879.1|/0/TPA: F-box domain protein (AFU_orthologue; AFUA_3G12050) [A. nidulans FGSC A4]
ANID_10619	2.35	20.91	3.1534604	1.80E-07	8.17E-07	gi|67537430|ref|XP_662489.1|/0/hypothetical protein AN4885.2 [A. nidulans FGSC A4]
ANID_05621	4.54	39.21	3.11045744	5.83E-11	3.45E-10	gi|67538902|ref|XP_663225.1|/1.43833e-127/hypothetical protein AN5621.2 [A. nidulans FGSC A4]
ANID_00723	1.18	10.11	3.09892423	1.05E-05	3.95E-05	gi|259489002|tpe|CBF88914.1|/1.46908e-114/TPA: hypothetical protein ANIA_00723 [A. nidulans FGSC A4]
ANID_04008	1.01	8.54	3.07988078	1.80E-05	6.51E-05	gi|67527178|ref|XP_661612.1|/0/hypothetical protein AN4008.2 [A. nidulans FGSC A4]
ANID_04972	1.18	9.93	3.07300686	1.05E-05	3.94E-05	gi|259482155|tpe|CBF76366.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_06669	29.41	246.93	3.06972343	3.08E-13	2.25E-12	gi|67540998|ref|XP_664273.1|/0/hypothetical protein AN6669.2 [A. nidulans FGSC A4]
ANID_02878	2.69	22.48	3.06296396	5.34E-08	2.53E-07	gi|67524841|ref|XP_660482.1|/0/hypothetical protein AN2878.2 [A. nidulans FGSC A4]
ANID_11765	0.84	6.97	3.05269742	3.02E-05	0.000106	gi|67537374|ref|XP_662461.1|/1.44881e-79/hypothetical protein AN4857.2 [A. nidulans FGSC A4]
ANID_03345	1.01	8.36	3.04914765	1.80E-05	6.51E-05	gi|259485677|tpe|CBF82901.1|/0/TPA: GABA transporter, putative (Eurofung) [A. nidulans FGSC A4]
ANID_06527	1.18	9.76	3.04809429	1.05E-05	3.94E-05	gi|67540714|ref|XP_664131.1|/1.96871e-152/hypothetical protein AN6527.2 [A. nidulans FGSC A4]
ANID_05655	3.03	24.4	3.00949145	1.56E-08	7.69E-08	gi|119497543|ref|XP_001265530.1|/0/2,3-cyclic-nucleotide 2-phosphodiesterase [N. fischeri NRRL 181]
ANID_06779	3.7	29.1	2.97542198	1.31E-09	7.04E-09	gi|67541218|ref|XP_664383.1|/0/hypothetical protein AN6779.2 [A. nidulans FGSC A4]
ANID_00841	4.71	36.94	2.9713849	3.14E-11	1.88E-10	gi|67517123|ref|XP_658445.1|/6.75581e-52/hypothetical protein AN0841.2 [A. nidulans FGSC A4]
ANID_07264	1.68	12.9	2.94083793	1.93E-06	7.91E-06	gi|67900554|ref|XP_680533.1|/0/hypothetical protein AN7264.2 [A. nidulans FGSC A4]
ANID_08072	2.35	17.6	2.90484277	1.80E-07	8.16E-07	gi|67902170|ref|XP_681341.1|/1.77101e-113/hypothetical protein AN8072.2 [A. nidulans FGSC A4]
ANID_04220	5.55	41.3	2.89558211	1.64E-12	1.09E-11	gi|259481173|tpe|CBF74456.1|/1.10562e-90/TPA: ankyrin repeat protein (AFU_orthologue; AFUA_1G06370) [A. nidulans FGSC A4]

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<tr><td>ANID_07188</td><td>0.67</td><td>4.88</td><td>2.86464815</td><td>5.62E-05</td><td>0.000191</td><td>gi|259483478|tpe|CBF78900.1|/0/TPA: small oligopeptide transporter, OPT family (AFU_orthologue; AFUA_6G10220) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07271</td><td>2.18</td><td>15.86</td><td>2.86299273</td><td>3.28E-07</td><td>1.45E-06</td><td>gi|67900568|ref|XP_680540.1|/0/hypothetical protein AN7271.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02879</td><td>1.85</td><td>13.42</td><td>2.8587875</td><td>1.08E-06</td><td>4.52E-06</td><td>gi|13569693|gb|AAK31198.1|AF349513_1/0/general amidase-B [Emericella nidulans]</td></tr>
<tr><td>ANID_08150</td><td>1.01</td><td>7.32</td><td>2.85748836</td><td>1.80E-05</td><td>6.52E-05</td><td>gi|134077118|emb|CAK45459.1|/0/unnamed protein product [A. niger]</td></tr>
<tr><td>ANID_07747</td><td>1.18</td><td>8.54</td><td>2.85544921</td><td>1.05E-05</td><td>3.94E-05</td><td>gi|67901520|ref|XP_681016.1|/1.46292e-170/hypothetical protein AN7747.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06931</td><td>1.34</td><td>9.58</td><td>2.83779266</td><td>6.04E-06</td><td>2.35E-05</td><td>gi|67541522|ref|XP_664535.1|/4.05613e-107/hypothetical protein AN6931.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03520</td><td>14.45</td><td>102.81</td><td>2.8308392</td><td>0</td><td>0</td><td>gi|67526125|ref|XP_661124.1|/0/hypothetical protein AN3520.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10964</td><td>7.06</td><td>49.66</td><td>2.81434417</td><td>1.07E-13</td><td>8.47E-13</td><td>gi|259483911|tpe|CBF79686.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07239</td><td>0.67</td><td>4.71</td><td>2.81349406</td><td>6.17E-05</td><td>0.000209</td><td>gi|67900504|ref|XP_680508.1|/3.2032e-119/hypothetical protein AN7239.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08146</td><td>1.34</td><td>9.41</td><td>2.81196172</td><td>6.04E-06</td><td>2.35E-05</td><td>gi|67902318|ref|XP_681415.1|/0/hypothetical protein AN8146.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02335</td><td>0.5</td><td>3.49</td><td>2.80322704</td><td>0.000276</td><td>0.000853</td><td>gi|259487731|tpe|CBF86630.1|/0/TPA: oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor (AFU_orthologue; AFUA_5G10280) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03526</td><td>3.87</td><td>27.01</td><td>2.80308817</td><td>7.03E-10</td><td>3.85E-09</td><td>gi|67526137|ref|XP_661130.1|/0/hypothetical protein AN3526.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04474</td><td>3.7</td><td>25.79</td><td>2.8012146</td><td>1.31E-09</td><td>7.05E-09</td><td>gi|67530950|ref|XP_662078.1|/1.22813e-56/hypothetical protein AN4474.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05625</td><td>1.34</td><td>9.24</td><td>2.78565985</td><td>6.04E-06</td><td>2.35E-05</td><td>gi|67538910|ref|XP_663229.1|/1.58777e-85/hypothetical protein AN5625.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08986</td><td>1.34</td><td>9.24</td><td>2.78565985</td><td>6.04E-06</td><td>2.35E-05</td><td>gi|67903998|ref|XP_682255.1|/0/hypothetical protein AN8986.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07338</td><td>1.18</td><td>8.02</td><td>2.76481538</td><td>1.05E-05</td><td>3.94E-05</td><td>gi|67900702|ref|XP_680607.1|/2.98021e-136/hypothetical protein AN7338.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08683</td><td>2.02</td><td>13.59</td><td>2.75011826</td><td>5.96E-07</td><td>2.57E-06</td><td>gi|67903392|ref|XP_681952.1|/0/hypothetical protein AN8683.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02987</td><td>1.18</td><td>7.84</td><td>2.7320668</td><td>1.05E-05</td><td>3.94E-05</td><td>gi|67525059|ref|XP_660591.1|/2.37306e-170/hypothetical protein AN2987.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03312</td><td>0.84</td><td>5.58</td><td>2.73180389</td><td>3.27E-05</td><td>0.000115</td><td>gi|159130286|gb|EDP55399.1|/4.86309e-86/oxidoreductase, short chain dehydrogenase/reductase family [A. fumigatus A1163]</td></tr>
<tr><td>ANID_00869</td><td>1.34</td><td>8.89</td><td>2.72995042</td><td>6.04E-06</td><td>2.35E-05</td><td>gi|67517183|ref|XP_658473.1|/1.10687e-86/hypothetical protein AN0869.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02510</td><td>0.67</td><td>4.36</td><td>2.70209513</td><td>8.88E-05</td><td>0.000295</td><td>gi|259487936|tpe|CBF86998.1|/3.03302e-125/TPA: DUF218 domain protein (AFU_orthologue; AFUA_3G14300) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04320</td><td>0.84</td><td>5.4</td><td>2.68449817</td><td>3.47E-05</td><td>0.000122</td><td>gi|121706484|ref|XP_001271504.1|/0/RSC complex subunit Sfh1, putative [A. clavatus NRRL 1]</td></tr>
<tr><td>ANID_03309</td><td>4.71</td><td>30.15</td><td>2.67835904</td><td>3.14E-11</td><td>1.89E-10</td><td>gi|67525703|ref|XP_660913.1|/0/hypothetical protein AN3309.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03524</td><td>2.02</td><td>12.9</td><td>2.67494387</td><td>5.96E-07</td><td>2.57E-06</td><td>gi|67526133|ref|XP_661128.1|/0/hypothetical protein AN3524.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04085</td><td>27.56</td><td>173.22</td><td>2.65195772</td><td>8.93E-14</td><td>7.18E-13</td><td>gi|259481327|tpe|CBF74740.1|/0/TPA: protein phosphotase 2a 65kd regulatory sububit (AFU_orthologue; AFUA_1G05610) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02592</td><td>0.84</td><td>5.23</td><td>2.63834971</td><td>3.82E-05</td><td>0.000133</td><td>gi|67524269|ref|XP_660196.1|/2.11982e-158/hypothetical protein AN2592.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05114</td><td>3.03</td><td>18.65</td><td>2.62178593</td><td>1.56E-08</td><td>7.70E-08</td><td>gi|259484559|tpe|CBF80886.1|/0/TPA: ribonuclease HI large subunit (AFU_orthologue; AFUA_1G07600) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02798</td><td>2.02</td><td>12.37</td><td>2.6144183</td><td>5.96E-07</td><td>2.57E-06</td><td>gi|255941690|ref|XP_002561614.1|/1.08125e-75/Pc16g13150 [Penicillium chrysogenum Wisconsin 54-1255]</td></tr>
<tr><td>ANID_07222</td><td>1.51</td><td>9.24</td><td>2.6133443</td><td>3.43E-06</td><td>1.37E-05</td><td>gi|259483436|tpe|CBF78824.1|/0/TPA: NACHT domain protein (AFU_orthologue; AFUA_2G01760) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00941</td><td>1.51</td><td>9.24</td><td>2.6133443</td><td>3.43E-06</td><td>1.37E-05</td><td>gi|95025690|gb|ABF50846.1|/0/alpha-glucosidase [Emericella nidulans]</td></tr>
<tr><td>ANID_04699</td><td>9.24</td><td>55.24</td><td>2.57974856</td><td>0</td><td>0</td><td>gi|67537058|ref|XP_662303.1|/5.40455e-177/hypothetical protein AN4699.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10698</td><td>11.26</td><td>67.09</td><td>2.57489092</td><td>0</td><td>0</td><td>gi|259484991|tpe|CBF81683.1|/8.58151e-146/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05429</td><td>3.03</td><td>17.95</td><td>2.56659415</td><td>1.56E-08</td><td>7.70E-08</td><td>gi|67538518|ref|XP_663033.1|/0/hypothetical protein AN5429.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05457</td><td>5.04</td><td>29.62</td><td>2.555076</td><td>9.27E-12</td><td>5.79E-11</td><td>gi|27413311|gb|AAN75017.1|/0/NADPH oxidase [Emericella nidulans]</td></tr>
<tr><td>ANID_09407</td><td>54.79</td><td>321.86</td><td>2.55444878</td><td>5.55E-13</td><td>3.91E-12</td><td>gi|259488249|tpe|CBF87553.1|/0/TPA: Fatty acid synthase, alpha subunit [Source:UniProtKB/TrEMBL;Acc:P78615] [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10738</td><td>2.02</td><td>11.85</td><td>2.55245986</td><td>5.96E-07</td><td>2.57E-06</td><td>gi|259480041|tpe|CBF70812.1|/1.80077e-85/TPA: PaaI_thioesterase family protein, putative (AFU_orthologue; AFUA_4G04355) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06273</td><td>8.07</td><td>47.05</td><td>2.54355414</td><td>1.02E-13</td><td>8.16E-13</td><td>gi|259479515|tpe|CBF69807.1|/9.71288e-75/TPA: allergenic cerato-platanin Asp F13 (AFU_orthologue; AFUA_2G12630) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_09106</td><td>2.35</td><td>13.59</td><td>2.53181279</td><td>1.80E-07</td><td>8.16E-07</td><td>gi|67904238|ref|XP_682375.1|/1.38563e-140/hypothetical protein AN9106.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01809</td><td>8.74</td><td>50.36</td><td>2.5265731</td><td>5.15E-14</td><td>4.23E-13</td><td>gi|259487155|tpe|CBF85602.1|/7.18605e-157/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04223</td><td>18.82</td><td>108.39</td><td>2.52589313</td><td>0</td><td>0</td><td>gi|67527961|ref|XP_661827.1|/0/hypothetical protein AN4223.2 [A. nidulans FGSC A4]</td></tr>
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ANID_00481	3.19	18.3	2.52021532	8.44E-09	4.26E-08	gi|67516399|ref|XP_658085.1|/0/hypothetical protein AN0481.2 [A. nidulans FGSC A4]
ANID_03951	0.67	3.83	2.51511139	0.000267	0.000827	gi|67526987|ref|XP_661555.1|/0/hypothetical protein AN3951.2 [A. nidulans FGSC A4]
ANID_03652	2.18	12.37	2.50444546	3.28E-07	1.45E-06	gi|67526389|ref|XP_661256.1|/1.40765e-175/hypothetical protein AN3652.2 [A. nidulans FGSC A4]
ANID_00432	19.83	112.05	2.49838607	0	0	gi|74598976|sp|Q5BG98.1|MCR1_EMENI/1.07397e-165/RecName: Full=NADH-cytochrome b5 reductase 2; AltName: Full=Mitochondrial cytochrome b reductase
ANID_08496	3.19	17.95	2.49235552	8.44E-09	4.25E-08	gi|259484445|tpe|CBF80671.1|/2.65042e-136/TPA: class II aldolase/adducin domain protein (AFU_orthologue; AFUA_3G01330) [A. nidulans FGSC A4]
ANID_03820	23.7	133.14	2.48998511	0	0	gi|67526725|ref|XP_661424.1|/1.66473e-85/hypothetical protein AN3820.2 [A. nidulans FGSC A4]
ANID_08730	1.01	5.58	2.46590983	2.66E-05	9.45E-05	gi|67903486|ref|XP_681999.1|/8.04941e-116/hypothetical protein AN8730.2 [A. nidulans FGSC A4]
ANID_07003	50.25	275.33	2.45396631	5.21E-13	3.70E-12	gi|259483686|tpe|CBF79279.1|/4.88113e-66/TPA: 60S ribosomal protein L13 (AFU_orthologue; AFUA_4G04460) [A. nidulans FGSC A4]
ANID_05168	1.18	6.45	2.4505123	1.23E-05	4.54E-05	gi|259484622|tpe|CBF81003.1|/0/TPA: NACHT and Ankyrin domain protein (AFU_orthologue; AFUA_6G07030) [A. nidulans FGSC A4]
ANID_03153	1.85	10.11	2.45018582	1.08E-06	4.53E-06	gi|259485892|tpe|CBF83301.1|/0/TPA: LRP16 family protein (AFU_orthologue; AFUA_3G13850) [A. nidulans FGSC A4]
ANID_08034	15.63	85.39	2.44974935	8.88E-15	7.68E-14	gi|67902094|ref|XP_681303.1|/0/hypothetical protein AN8034.2 [A. nidulans FGSC A4]
ANID_03085	9.75	53.15	2.44659557	2.00E-15	1.78E-14	gi|259485967|tpe|CBF83435.1|/0/TPA: phosphatidyl synthase (AFU_orthologue; AFUA_3G12330) [A. nidulans FGSC A4]
ANID_01438	2.35	12.72	2.43636601	1.80E-07	8.16E-07	gi|259486749|tpe|CBF84858.1|/7.77995e-153/TPA: C2H2 finger domain protein, putative (AFU_orthologue; AFUA_8G04290) [A. nidulans FGSC A4]
ANID_00040	0.84	4.53	2.43104982	0.000105	0.000344	gi|259489774|tpe|CBF90322.1|/0/TPA: DNA polymerase gamma (AFU_orthologue; AFUA_5G12640) [A. nidulans FGSC A4]
ANID_02993	8.24	43.39	2.39664634	3.11E-14	2.59E-13	gi|259486061|tpe|CBF83604.1|/2.87457e-100/TPA: DUF124 domain protein (AFU_orthologue; AFUA_3G08610) [A. nidulans FGSC A4]
ANID_04989	58.49	306.7	2.39056627	0	0	gi|67537638|ref|XP_662593.1|/3.94933e-24/hypothetical protein AN4989.2 [A. nidulans FGSC A4]
ANID_00385	7.23	37.64	2.38019908	1.06E-13	8.46E-13	gi|67516207|ref|XP_657989.1|/0/hypothetical protein AN0385.2 [A. nidulans FGSC A4]
ANID_00998	10.08	52.45	2.37944713	0	0	gi|259488707|tpe|CBF88365.1|/0/TPA: PfkB family carbohydrate kinase (Mak32), putative (AFU_orthologue; AFUA_1G12750) [A. nidulans FGSC A4]
ANID_12261	0.84	4.36	2.3758669	0.00016	0.00051	-
ANID_08885	0.84	4.36	2.3758669	0.00016	0.000509	gi|67903796|ref|XP_682154.1|/0/hypothetical protein AN8885.2 [A. nidulans FGSC A4]
ANID_01814	2.02	10.46	2.37245565	5.98E-07	2.57E-06	gi|67522715|ref|XP_659418.1|/7.77756e-72/hypothetical protein AN1814.2 [A. nidulans FGSC A4]
ANID_03902	1.01	5.23	2.37245565	4.39E-05	0.000151	gi|259481529|tpe|CBF75134.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_09168	9.58	48.79	2.34848792	5.28E-14	4.33E-13	gi|67904362|ref|XP_682437.1|/0/hypothetical protein AN9168.2 [A. nidulans FGSC A4]
ANID_10468	3.03	15.34	2.33990878	1.56E-08	7.68E-08	gi|67526629|ref|XP_661376.1|/0/hypothetical protein AN3772.2 [A. nidulans FGSC A4]
ANID_00469	6.89	34.68	2.33152801	1.48E-13	1.15E-12	gi|259489282|tpe|CBF89425.1|/0/TPA: phosphate transport (Eurofung) [A. nidulans FGSC A4]
ANID_01848	1.18	5.92	2.32681032	1.95E-05	7.03E-05	gi|90567687|emb|CAJ76908.1|/0/NosA protein [Emericella nidulans]
ANID_04857	1.18	5.92	2.32681032	1.95E-05	7.03E-05	gi|259482281|tpe|CBF76613.1|/0/TPA: ABC1 domain protein (AFU_orthologue; AFUA_3G07620) [A. nidulans FGSC A4]
ANID_04134	2.52	12.55	2.31619173	9.83E-08	4.57E-07	gi|67527714|ref|XP_661738.1|/7.24503e-47/hypothetical protein AN4134.2 [A. nidulans FGSC A4]
ANID_08539	0.84	4.18	2.31504171	0.000254	0.000787	gi|67903104|ref|XP_681808.1|/3.11558e-121/hypothetical protein AN8539.2 [A. nidulans FGSC A4]
ANID_08880	2.35	11.68	2.31330761	1.80E-07	8.17E-07	gi|259486690|tpe|CBF84749.1|/0/TPA: vacuolar protein sorting protein, putative (AFU_orthologue; AFUA_8G02780) [A. nidulans FGSC A4]
ANID_09340	3.36	16.55	2.30029808	4.54E-09	2.34E-08	gi|3024758|sp|P78617.1|TREA_EMENI/0/RecName: Full=Acid trehalase; AltName: Full=Alpha,alpha-trehalase; AltName: Full=Alpha,alpha-trehalose glucohydrolase; Flags: Precursor
ANID_03193	4.2	20.56	2.29137903	2.02E-10	1.15E-09	gi|67525471|ref|XP_660797.1|/0/hypothetical protein AN3193.2 [A. nidulans FGSC A4]
ANID_00010	2.35	11.5	2.2909012	1.81E-07	8.18E-07	gi|67515457|ref|XP_657614.1|/0/hypothetical protein AN0010.2 [A. nidulans FGSC A4]
ANID_01177	15.97	77.9	2.28625902	0	0	gi|238498358|ref|XP_002380414.1|/0/Coatomer subunit beta, putative [A. flavus NRRL3357]
ANID_10601	1.01	4.88	2.27252586	9.40E-05	0.000311	gi|259482300|tpe|CBF76650.1|/0/TPA: LPS glycosyltransferase, putative (AFU_orthologue; AFUA_8G00650) [A. nidulans FGSC A4]
ANID_03828	1.01	4.88	2.27252586	9.40E-05	0.000311	gi|67526741|ref|XP_661432.1|/0/hypothetical protein AN3828.2 [A. nidulans FGSC A4]
ANID_10583	1.01	4.88	2.27252586	9.40E-05	0.000311	gi|238505934|ref|XP_002384169.1|/2.02972e-127/SET domain-containing protein, putative [A. flavus NRRL3357]
ANID_00011	1.34	6.45	2.26706616	1.13E-05	4.20E-05	gi|67515459|ref|XP_657615.1|/6.21253e-85/hypothetical protein AN0011.2 [A. nidulans FGSC A4]
ANID_10169	3.19	15.16	2.24864142	8.44E-09	4.25E-08	gi|259488415|tpe|CBF87832.1|/7.75028e-157/TPA: 3-oxoacyl-(acyl-carrier-protein) reductase (AFU_orthologue; AFUA_1G10100) [A. nidulans FGSC A4]
ANID_00299	1.18	5.58	2.24147826	3.65E-05	0.000128	gi|259489474|tpe|CBF89775.1|/0/TPA: class V chitinase, putative (AFU_orthologue; AFUA_1G02800) [A. nidulans FGSC A4]

ANID_02954	1.18	5.58	2.24147826	3.65E-05	0.000128	gi|67524993|ref|XP_660558.1|/0/hypothetical protein AN2954.2 [A. nidulans FGSC A4]
ANID_00860	129.91	611.49	2.23481642	8.47E-13	5.82E-12	gi|67517163|ref|XP_658464.1|/0/hypothetical protein AN0860.2 [A. nidulans FGSC A4]
ANID_03141	1.34	6.27	2.22623244	1.50E-05	5.49E-05	gi|67525367|ref|XP_660745.1|/2.32481e-92/hypothetical protein AN3141.2 [A. nidulans FGSC A4]
ANID_07399	15.8	73.89	2.22545457	0	0	gi|67900824|ref|XP_680668.1|/0/hypothetical protein AN7399.2 [A. nidulans FGSC A4]
ANID_07715	2.69	12.55	2.22200929	5.36E-08	2.54E-07	gi|67901456|ref|XP_680984.1|/0/hypothetical protein AN7715.2 [A. nidulans FGSC A4]
ANID_01896	1.01	4.71	2.22137177	0.000147	0.000472	gi|238054384|sp|Q00770.3|FAAA_EMENI/0/RecName: Full=Fumarylacetoacetase; Short=FAA; AltName: Full=Beta-diketonase; AltName: Full=Fumarylacetoacetate hydrolase
ANID_01422	5.21	24.22	2.21684359	5.11E-12	3.27E-11	gi|67521930|ref|XP_659026.1|/3.62888e-73/hypothetical protein AN1422.2 [A. nidulans FGSC A4]
ANID_04995	1.51	6.97	2.20661011	6.52E-06	2.52E-05	gi|67537650|ref|XP_662599.1|/0/hypothetical protein AN4995.2 [A. nidulans FGSC A4]
ANID_07895	1.18	5.4	2.19417255	5.45E-05	0.000186	gi|259480643|tpe|CBF73475.1|/6.54588e-170/TPA: Zinc-binding alcohol dehydrogenase domain-containing protein cipB (EC 1.-.-.-)(Concanamycin-induced protein B) [Source:UniProtKB/Swiss-Prot;Acc:Q5AUY5] [A. nidulans FGSC A4]
ANID_01276	2.02	9.24	2.19353756	6.73E-07	2.88E-06	gi|67521638|ref|XP_658880.1|/0/hypothetical protein AN1276.2 [A. nidulans FGSC A4]
ANID_00853	1.68	7.67	2.19076535	3.00E-06	1.21E-05	gi|67517149|ref|XP_658457.1|/0/hypothetical protein AN0853.2 [A. nidulans FGSC A4]
ANID_00484	2.52	11.5	2.19013822	1.00E-07	4.65E-07	gi|259489266|tpe|CBF89396.1|/0/TPA: glycerophosphoryl diester phosphodiesterase family protein (AFU_orthologue; AFUA_6G12240) [A. nidulans FGSC A4]
ANID_06043	2.52	11.5	2.19013822	1.00E-07	4.65E-07	gi|67539746|ref|XP_663647.1|/0/hypothetical protein AN6043.2 [A. nidulans FGSC A4]
ANID_11801	1.34	6.1	2.18657624	2.11E-05	7.59E-05	-
ANID_08014	1.34	6.1	2.18657624	2.11E-05	7.58E-05	gi|259480765|tpe|CBF73707.1|/0/TPA: ATP dependent DNA ligase domain protein (AFU_orthologue; AFUA_5G02430) [A. nidulans FGSC A4]
ANID_02923	5.71	25.97	2.18528336	9.44E-13	6.43E-12	gi|67524931|ref|XP_660527.1|/1.31524e-164/hypothetical protein AN2923.2 [A. nidulans FGSC A4]
ANID_00156	3.87	17.6	2.18516996	7.03E-10	3.85E-09	gi|67515749|ref|XP_657760.1|/0/hypothetical protein AN0156.2 [A. nidulans FGSC A4]
ANID_05324	48.74	220.44	2.17720788	2.09E-13	1.58E-12	gi|259485235|tpe|CBF82099.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05720	4.71	21.26	2.17434263	3.14E-11	1.88E-10	gi|259484803|tpe|CBF81337.1|/8.72629e-152/TPA: vacuolar membrane PQ loop repeat protein (AFU_orthologue; AFUA_1G06840) [A. nidulans FGSC A4]
ANID_03373	1.01	4.53	2.16515576	0.000236	0.000737	gi|67525831|ref|XP_660977.1|/0/hypothetical protein AN3373.2 [A. nidulans FGSC A4]
ANID_11107	1.01	4.53	2.16515576	0.000236	0.000736	gi|259483090|tpe|CBF78176.1|/0/TPA: hypothetical protein similar to CorA-like transorter protein (Eurofung) [A. nidulans FGSC A4]
ANID_06286	16.64	74.58	2.16413336	0	0	gi|67540232|ref|XP_663890.1|/0/hypothetical protein AN6286.2 [A. nidulans FGSC A4]
ANID_05241	2.18	9.76	2.16255301	3.74E-07	1.64E-06	gi|67538142|ref|XP_662845.1|/2.68019e-146/hypothetical protein AN5241.2 [A. nidulans FGSC A4]
ANID_10073	7.06	31.54	2.15944257	1.07E-13	8.48E-13	gi|259489419|tpe|CBF89676.1|/0/TPA: F-box domain protein (AFU_orthologue; AFUA_1G02200) [A. nidulans FGSC A4]
ANID_03221	1.34	5.92	2.14336418	3.13E-05	0.00011	gi|67525527|ref|XP_660825.1|/0/hypothetical protein AN3221.2 [A. nidulans FGSC A4]
ANID_10785	11.93	52.63	2.14129135	0	0	gi|67540098|ref|XP_663823.1|/1.02512e-127/hypothetical protein AN6219.2 [A. nidulans FGSC A4]
ANID_10780	3.19	13.94	2.12760223	8.52E-09	4.29E-08	gi|259479590|tpe|CBF69951.1|/0/TPA: phosphoinositide phosphatase Pten/Tep1, putative (AFU_orthologue; AFUA_2G11990) [A. nidulans FGSC A4]
ANID_03347	20.67	89.92	2.12110365	0	0	gi|70996873|ref|XP_753191.1|/1.7226e-171/GABA permease [A. fumigatus Af293]
ANID_03848	36.64	158.4	2.11208093	0	0	gi|67526781|ref|XP_661452.1|/7.92096e-38/hypothetical protein AN3848.2 [A. nidulans FGSC A4]
ANID_04084	3.19	13.77	2.10990023	8.58E-09	4.31E-08	gi|67527614|ref|XP_661688.1|/0/hypothetical protein AN4084.2 [A. nidulans FGSC A4]
ANID_02602	2.02	8.71	2.10831743	9.57E-07	4.04E-06	gi|67524289|ref|XP_660206.1|/3.51656e-139/hypothetical protein AN2602.2 [A. nidulans FGSC A4]
ANID_01404	5.88	25.27	2.1035376	5.77E-13	4.05E-12	gi|259488256|tpe|CBF87565.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00246	1.18	5.05	2.09749653	0.000135	0.000433	gi|145229153|ref|XP_001388885.1|/0/capsular associated protein [A. niger CBS 513.88]
ANID_04824	3.19	13.59	2.09091713	8.67E-09	4.35E-08	gi|259482322|tpe|CBF76694.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_08540	36.81	156.66	2.08946721	2.74E-13	2.01E-12	gi|259484492|tpe|CBF80759.1|/0/TPA: Siderophore iron transporter mirB (Major facilitator iron-regulated transporter B)(Triacetylfusarinine C permease) [Source:UniProtKB/Swiss-Prot;Acc:Q870L2] [A. nidulans FGSC A4]
ANID_08609	63.53	269.76	2.08616652	5.75E-13	4.04E-12	gi|67903244|ref|XP_681878.1|/7.1476e-60/hypothetical protein AN8609.2 [A. nidulans FGSC A4]
ANID_00881	2.18	9.24	2.08356472	5.36E-07	2.33E-06	gi|67517207|ref|XP_658485.1|/0/hypothetical protein AN0881.2 [A. nidulans FGSC A4]
ANID_08478	2.02	8.54	2.07988078	1.19E-06	5.00E-06	gi|67902982|ref|XP_681747.1|/0/hypothetical protein AN8478.2 [A. nidulans FGSC A4]
ANID_07629	56.97	240.83	2.07974081	6.95E-14	5.65E-13	gi|67901284|ref|XP_680898.1|/2.74622e-36/hypothetical protein AN7629.2 [A. nidulans FGSC A4]
ANID_11865	2.52	10.63	2.07664596	1.24E-07	5.69E-07	gi|134079166|emb|CAK40694.1|/1.01309e-67/hypothetical protein An11g04900 [A. niger]
ANID_10782	6.05	25.44	2.07209162	3.72E-13	2.69E-12	gi|115383926|ref|XP_001208510.1|/3.42066e-144/mitochondrial phosphate carrier protein 2 [A. terreus NIH2624]
ANID_02519	2.86	12.02	2.07134984	3.21E-08	1.54E-07	gi|67524123|ref|XP_660123.1|/4.37985e-63/hypothetical protein AN2519.2 [A. nidulans FGSC A4]

ANID_11774	3.53	14.81	2.06883155	2.49E-09	1.31E-08	gi|67537662|ref|XP_662605.1|/0/hypothetical protein AN5001.2 [A. nidulans FGSC A4]
ANID_06404	3.7	15.51	2.06760151	1.33E-09	7.13E-09	gi|67540468|ref|XP_664008.1|/0/hypothetical protein AN6404.2 [A. nidulans FGSC A4]
ANID_00466	9.41	39.21	2.05895501	1.04E-14	8.98E-14	gi|67516369|ref|XP_658070.1|/4.71448e-129/hypothetical protein AN0466.2 [A. nidulans FGSC A4]
ANID_03575	1.34	5.58	2.05803212	7.62E-05	0.000256	gi|67526235|ref|XP_661179.1|/0/hypothetical protein AN3575.2 [A. nidulans FGSC A4]
ANID_08605	20.34	84.69	2.05787195	0	0	gi|67903236|ref|XP_681874.1|/1.32509e-75/hypothetical protein AN8605.2 [A. nidulans FGSC A4]
ANID_10116	3.19	13.24	2.05327479	9.07E-09	4.54E-08	gi|67516885|ref|XP_658328.1|/0/hypothetical protein AN0724.2 [A. nidulans FGSC A4]
ANID_05991	5.04	20.74	2.04092026	9.29E-12	5.79E-11	gi|259479826|tpe|CBF70405.1|/0/TPA: peroxisome biogenesis protein peroxin 1 (Eurofung) [A. nidulans FGSC A4]
ANID_03080	9.75	39.38	2.01398899	2.00E-15	1.79E-14	gi|259485972|tpe|CBF83444.1|/0/TPA: vesicle coat complex COPII, subunit Sec24 family protein, putative (Eurofung) [A. nidulans FGSC A4]
ANID_04983	1.34	5.4	2.01072641	0.000122	0.000395	gi|259482144|tpe|CBF76344.1|/0/TPA: phosphoglycerate mutase family domain protein (AFU_orthologue; AFUA_3G10050) [A. nidulans FGSC A4]
ANID_03021	3.03	12.2	2.00949145	2.05E-08	9.99E-08	gi|67525127|ref|XP_660625.1|/0/hypothetical protein AN3021.2 [A. nidulans FGSC A4]
ANID_08253	9.75	39.21	2.00774752	2.00E-15	1.79E-14	gi|67902532|ref|XP_681522.1|/0/hypothetical protein AN8253.2 [A. nidulans FGSC A4]
ANID_06535	5.88	23.53	2.00061326	5.77E-13	4.05E-12	gi|67540730|ref|XP_664139.1|/4.24056e-98/hypothetical protein AN6535.2 [A. nidulans FGSC A4]
ANID_07231	7.56	30.15	1.99569986	1.38E-14	1.17E-13	gi|67900488|ref|XP_680500.1|/0/hypothetical protein AN7231.2 [A. nidulans FGSC A4]
ANID_09066	20.67	82.25	1.99247729	0	0	gi|259485523|tpe|CBF82616.1|/0/TPA: D-lactate dehydrogenase (cytochrome) (AFU_orthologue; AFUA_7G02560) [A. nidulans FGSC A4]
ANID_09159	28.4	112.57	1.98685956	0	0	gi|67904344|ref|XP_682428.1|/2.66142e-137/hypothetical protein AN9159.2 [A. nidulans FGSC A4]
ANID_12197	1.85	7.32	1.98431838	8.77E-06	3.33E-05	gi|115388011|ref|XP_001211511.1|/1.76665e-157/predicted protein [A. terreus NIH2624]
ANID_09147	1.85	7.32	1.98431838	8.77E-06	3.33E-05	gi|67904320|ref|XP_682416.1|/0/hypothetical protein AN9147.2 [A. nidulans FGSC A4]
ANID_09116	1.85	7.32	1.98431838	8.77E-06	3.33E-05	gi|259485468|tpe|CBF82515.1|/0/TPA: nicotinate phosphoribosyltransferase (AFU_orthologue; AFUA_7G01880) [A. nidulans FGSC A4]
ANID_10362	10.76	42.52	1.98246352	0	0	gi|67524975|ref|XP_660549.1|/6.4e-63/hypothetical protein AN2945.2 [A. nidulans FGSC A4]
ANID_01870	2.52	9.93	1.97836998	2.82E-07	1.25E-06	gi|259487223|tpe|CBF85727.1|/0/TPA: xylosidase/arabinosidase, putative (AFU_orthologue; AFUA_2G04480) [A. nidulans FGSC A4]
ANID_04089	2.18	8.54	1.96990794	1.84E-06	7.55E-06	gi|67527624|ref|XP_661693.1|/0/hypothetical protein AN4089.2 [A. nidulans FGSC A4]
ANID_07422	2.18	8.54	1.96990794	1.84E-06	7.54E-06	gi|67900870|ref|XP_680691.1|/0/hypothetical protein AN7422.2 [A. nidulans FGSC A4]
ANID_02008	4.03	15.68	1.96007382	4.42E-10	2.45E-09	gi|67523103|ref|XP_659612.1|/1.74516e-136/hypothetical protein AN2008.2 [A. nidulans FGSC A4]
ANID_05575	2.69	10.28	1.93416219	2.23E-07	1.00E-06	gi|67538810|ref|XP_663179.1|/0/hypothetical protein AN5575.2 [A. nidulans FGSC A4]
ANID_04709	6.89	26.31	1.93303536	1.48E-13	1.15E-12	gi|259482453|tpe|CBF76951.1|/0/TPA: phosphoinositide 3-kinase, catalytic protein Vps34 (Eurofung) [A. nidulans FGSC A4]
ANID_07877	1.51	5.75	1.92901341	0.00011	0.000358	gi|67901780|ref|XP_681146.1|/0/hypothetical protein AN7877.2 [A. nidulans FGSC A4]
ANID_06904	20.84	79.29	1.92778365	9.26E-14	7.43E-13	gi|67541468|ref|XP_664508.1|/1.2101e-63/hypothetical protein AN6904.2 [A. nidulans FGSC A4]
ANID_05669	5.04	19.17	1.9273547	1.02E-11	6.33E-11	gi|67538998|ref|XP_663273.1|/0/hypothetical protein AN5669.2 [A. nidulans FGSC A4]
ANID_04586	33.78	128.43	1.92674101	0	0	gi|67536832|ref|XP_662190.1|/4.74709e-105/hypothetical protein AN4586.2 [A. nidulans FGSC A4]
ANID_04777	448.05	1702.89	1.9262536	0	0	gi|67537214|ref|XP_662381.1|/1.41604e-34/RS27_XENLA 40S ribosomal protein S27 [A. nidulans FGSC A4]
ANID_10350	7.56	28.58	1.91854778	1.38E-14	1.17E-13	gi|67524975|ref|XP_660549.1|/0/hypothetical protein AN2945.2 [A. nidulans FGSC A4]
ANID_05017	1.85	6.97	1.91363339	2.15E-05	7.71E-05	gi|67537694|ref|XP_662621.1|/1.04855e-172/hypothetical protein AN5017.2 [A. nidulans FGSC A4]
ANID_01951	2.18	8.19	1.90953532	4.31E-06	1.70E-05	gi|121708613|ref|XP_001272188.1|/1.6838e-22/U1 small nuclear ribonucleoprotein C, putative [A. clavatus NRRL 1]
ANID_06141	11.6	43.39	1.90323778	0	0	gi|13937025|gb|AAK50016.1|AF363613_1/1.43788e-136/pyridoxine [Emericella nidulans]
ANID_06263	7.23	26.84	1.89231712	1.06E-13	8.45E-13	gi|67540186|ref|XP_663867.1|/0/hypothetical protein AN6263.2 [A. nidulans FGSC A4]
ANID_02782	5.88	21.78	1.88911589	6.31E-13	4.39E-12	gi|259486297|tpe|CBF84024.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_00210	10.08	37.29	1.88729316	0	0	gi|67515857|ref|XP_657814.1|/0/hypothetical protein AN0210.2 [A. nidulans FGSC A4]
ANID_09093	17.81	65.87	1.88693403	0	0	gi|261199101|ref|XP_002625952.1|/7.4686e-34/zinc knuckle domain-containing protein [Ajellomyces dermatitidis SLH14081]
ANID_03255	6.22	23	1.88664738	2.61E-13	1.92E-12	gi|259485780|tpe|CBF83091.1|/4.2473e-131/TPA: glutathione transferase 1 (Eurofung) [A. nidulans FGSC A4]
ANID_10418	17.14	63.26	1.88392645	0	0	gi|259485566|tpe|CBF82696.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05185	9.41	34.5	1.87432973	1.04E-14	8.99E-14	gi|259484642|tpe|CBF81039.1|/0/TPA: RING finger domain protein (Rnf10), putative (AFU_orthologue; AFUA_1G07150) [A. nidulans FGSC A4]
ANID_12159	3.19	11.68	1.87241195	5.79E-08	2.73E-07	gi|67539502|ref|XP_663525.1|/0/hypothetical protein AN5921.2 [A. nidulans FGSC A4]
ANID_05376	13.28	48.62	1.87229475	0	0	gi|259485180|tpe|CBF82011.1|/6.57868e-156/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00992	5.38	19.69	1.87178503	4.05E-12	2.62E-11	gi|259488715|tpe|CBF88380.1|/4.57185e-159/TPA: NmrA-like family protein

						(AFU_orthologue; AFUA_8G01860) [A. nidulans FGSC A4]
ANID_02046	3.53	12.9	1.86963098	1.23E-08	6.12E-08	gi|67523179|ref|XP_659650.1|/1.32235e-159/hypothetical protein AN2046.2 [A. nidulans FGSC A4]
ANID_07158	71.26	259.48	1.86445896	0	0	gi|67541989|ref|XP_664762.1|/0/hypothetical protein AN7158.2 [A. nidulans FGSC A4]
ANID_07534	1.68	6.1	1.86034801	9.77E-05	0.000321	gi|67901094|ref|XP_680803.1|/0/hypothetical protein AN7534.2 [A. nidulans FGSC A4]
ANID_12335	2.69	9.76	1.85927498	7.62E-07	3.25E-06	gi|70998522|ref|XP_753983.1|/0/acyl-CoA dehydrogenase family protein [A. fumigatus Af293]
ANID_11742	22.18	80.33	1.85667951	3.33E-14	2.76E-13	gi|67901088|ref|XP_680800.1|/4.08698e-15/hypothetical protein AN7531.2 [A. nidulans FGSC A4]
ANID_06071	6.55	23.7	1.85532025	1.55E-13	1.20E-12	gi|67539802|ref|XP_663675.1|/0/hypothetical protein AN6071.2 [A. nidulans FGSC A4]
ANID_01435	12.44	44.96	1.85365555	0	0	gi|169784390|ref|XP_001826656.1|/0/origin recognition complex subunit [A. oryzae RIB40]
ANID_03158	7.06	25.44	1.84935858	1.08E-13	8.54E-13	gi|259485886|tpe|CBF83289.1|/0/TPA: F-box domain protein (AFU_orthologue; AFUA_3G13460) [A. nidulans FGSC A4]
ANID_01054	8.91	31.89	1.83960676	4.53E-14	3.73E-13	gi|259488642|tpe|CBF88245.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04821	1.51	5.4	1.83841086	0.000282	0.000872	gi|259482329|tpe|CBF76707.1|/0/TPA: Miscellaneous Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_10135	4.54	16.21	1.83611989	2.63E-10	1.49E-09	gi|259488767|tpe|CBF88475.1|/3.03405e-152/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07714	4.54	16.21	1.83611989	2.63E-10	1.49E-09	gi|67901454|ref|XP_680983.1|/0/hypothetical protein AN7714.2 [A. nidulans FGSC A4]
ANID_06189	9.24	32.76	1.8259706	0	0	gi|259479618|tpe|CBF70006.1|/4.70331e-68/TPA: HIT domain protein (AFU_orthologue; AFUA_2G11700) [A. nidulans FGSC A4]
ANID_06426	1.68	5.92	1.81713594	0.000156	0.000499	gi|67540512|ref|XP_664030.1|/0/hypothetical protein AN6426.2 [A. nidulans FGSC A4]
ANID_06793	2.18	7.67	1.81489844	1.68E-05	6.11E-05	gi|67541246|ref|XP_664397.1|/0/hypothetical protein AN6793.2 [A. nidulans FGSC A4]
ANID_07773	8.4	29.45	1.8098064	3.40E-14	2.82E-13	gi|67901572|ref|XP_681042.1|/0/hypothetical protein AN7773.2 [A. nidulans FGSC A4]
ANID_04950	20.67	72.14	1.80326103	0	0	gi|67537560|ref|XP_662554.1|/8.55626e-82/hypothetical protein AN4950.2 [A. nidulans FGSC A4]
ANID_00656	2.35	8.19	1.8012027	9.38E-06	3.55E-05	gi|74681487|sp|Q5BFM4.1|Y0656_EMENI/2.93255e-156/RecName: Full=Uncharacterized methyltransferase AN0656
ANID_01676	5.55	19.34	1.80102812	8.44E-12	5.30E-11	gi|67522439|ref|XP_659280.1|/1.14225e-154/hypothetical protein AN1676.2 [A. nidulans FGSC A4]
ANID_06044	4.71	16.38	1.79813639	3.23E-10	1.81E-09	gi|67539748|ref|XP_663648.1|/2.88462e-83/hypothetical protein AN6044.2 [A. nidulans FGSC A4]
ANID_07472	10.59	36.6	1.78914106	0	0	gi|67900970|ref|XP_680741.1|/0/hypothetical protein AN7472.2 [A. nidulans FGSC A4]
ANID_04711	3.03	10.46	1.78749315	5.83E-07	2.52E-06	gi|67537082|ref|XP_662315.1|/4.70544e-144/hypothetical protein AN4711.2 [A. nidulans FGSC A4]
ANID_10082	2.18	7.49	1.78063758	2.66E-05	9.44E-05	gi|259489256|tpe|CBF89377.1|/0/TPA: serine/threonine-protein kinase, putative (AFU_orthologue; AFUA_6G02242) [A. nidulans FGSC A4]
ANID_08166	2.18	7.49	1.78063758	2.66E-05	9.43E-05	gi|67902358|ref|XP_681435.1|/0/hypothetical protein AN8166.2 [A. nidulans FGSC A4]
ANID_06088	7.06	24.22	1.77845878	1.33E-13	1.04E-12	gi|259479725|tpe|CBF70209.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01247	6.05	20.74	1.77740885	2.32E-12	1.53E-11	gi|67521576|ref|XP_658851.1|/8.82222e-99/hypothetical protein AN1247.2 [A. nidulans FGSC A4]
ANID_11099	1.68	5.75	1.77510072	0.000248	0.000772	gi|259483185|tpe|CBF78356.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_04719	2.35	8.02	1.77094148	1.48E-05	5.42E-05	gi|67537098|ref|XP_662323.1|/0/hypothetical protein AN4719.2 [A. nidulans FGSC A4]
ANID_08842	12.6	42.87	1.76654468	0	0	gi|27447361|gb|AAM47511.1|/0/calcium channel MID1 [Emericella nidulans]
ANID_07674	4.2	14.29	1.76654468	6.58E-09	3.36E-08	gi|74593440|sp|Q5AVK6.1|NOP16_EMENI/9.59075e-115/RecName: Full=Nucleolar protein 16
ANID_06078	1.85	6.27	1.76094017	0.000137	0.00044	gi|74630525|sp|Q8X1T6.1|ADA_EMENI/0/RecName: Full=Adenosine deaminase; Alt-Name: Full=Adenosine aminohydrolase
ANID_02102	2.52	8.54	1.76081234	8.24E-06	3.14E-05	gi|169770087|ref|XP_001819513.1|/1.07567e-72/acetyltransferase, GNAT family [A. oryzae RIB40]
ANID_10149	7.73	26.14	1.75771882	7.26E-14	5.89E-13	gi|259488537|tpe|CBF88051.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02464	19.16	64.65	1.75455281	6.17E-14	5.04E-13	gi|259487882|tpe|CBF86909.1|/0/TPA: ceramide synthase LagA (Eurofung) [A. nidulans FGSC A4]
ANID_00843	830.73	2798.82	1.75236715	2.62E-11	1.58E-10	gi|259488872|tpe|CBF88674.1|/2.69849e-83/TPA: hypothetical protein similar to ribosomal protein S5 (Broad) [A. nidulans FGSC A4]
ANID_12032	2.69	9.06	1.75190488	4.59E-06	1.81E-05	gi|67538026|ref|XP_662787.1|/0/hypothetical protein AN5183.2 [A. nidulans FGSC A4]
ANID_05700	2.35	7.84	1.7381929	2.33E-05	8.32E-05	gi|67539060|ref|XP_663304.1|/7.41923e-111/hypothetical protein AN5700.2 [A. nidulans FGSC A4]
ANID_10618	6.05	20.04	1.72787546	1.21E-11	7.53E-11	gi|259482251|tpe|CBF76553.1|/0/TPA: rRNA processing protein Nop9, putative (AFU_orthologue; AFUA_3G11110) [A. nidulans FGSC A4]
ANID_03853	1.85	6.1	1.72128397	0.000216	0.000678	gi|74596350|sp|Q5B6H7.1|CYM1_EMENI/0/RecName: Full=Mitochondrial presequence protease; Flags: Precursor
ANID_05589	24.37	80.33	1.72083263	0	0	gi|67538838|ref|XP_663193.1|/0/hypothetical protein AN5589.2 [A. nidulans FGSC A4]
ANID_00759	66.38	218.52	1.71894479	9.93E-14	7.94E-13	gi|259488963|tpe|CBF88841.1|/5.02376e-62/TPA: DUF614 domain protein (AFU_orthologue; AFUA_1G14190) [A. nidulans FGSC A4]

ANID_10357	12.6	41.47	1.71864431	0	0	gi|259485899|tpe|CBF83314.1|/7.54837e-163/TPA: P-type ATPase, putative (Eurofung) [A. nidulans FGSC A4]
ANID_09294	2.86	9.41	1.71817958	4.01E-06	1.59E-05	gi|67904614|ref|XP_682563.1|/1.0341e-110/hypothetical protein AN9294.2 [A. nidulans FGSC A4]
ANID_03218	110.92	363.51	1.71247553	0	0	gi|259485818|tpe|CBF83162.1|/1.92293e-82/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02866	8.4	27.36	1.703607	3.80E-14	3.14E-13	gi|67524817|ref|XP_660470.1|/0/hypothetical protein AN2866.2 [A. nidulans FGSC A4]
ANID_08145	42.52	138.36	1.70221342	3.10E-13	2.26E-12	gi|259480911|tpe|CBF73974.1|/1.24259e-99/TPA: DUF985 domain protein (AFU_orthologue; AFUA_5G11860) [A. nidulans FGSC A4]
ANID_00791	213.61	691.82	1.69541753	4.44E-12	2.85E-11	gi|67517021|ref|XP_658395.1|/6.02897e-08/hypothetical protein AN0791.2 [A. nidulans FGSC A4]
ANID_03584	15.29	49.49	1.69454864	0	0	gi|73621926|sp|Q5B797.1|SNX4_EMENI/0/RecName: Full=Sorting nexin-4; AltName: Full=Autophagy-related protein 24
ANID_10260	4.37	14.12	1.6920349	2.17E-08	1.05E-07	gi|259487460|tpe|CBF86157.1|/2.59073e-78/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_03578	3.03	9.76	1.68756335	3.49E-06	1.39E-05	gi|212534986|ref|XP_002147649.1|/0/CCCH zinc finger and SMR domain protein [P. marneffei ATCC 18224]
ANID_01671	49.24	158.58	1.68730816	4.75E-13	3.39E-12	gi|259487010|tpe|CBF85338.1|/0/TPA: PAP2 domain protein (AFU_orthologue; AFUA_4G08970) [A. nidulans FGSC A4]
ANID_05827	2.18	6.97	1.67683052	0.000103	0.000339	gi|67539314|ref|XP_663431.1|/0/hypothetical protein AN5827.2 [A. nidulans FGSC A4]
ANID_01515	31.76	101.42	1.67505936	2.28E-13	1.71E-12	gi|259486840|tpe|CBF85024.1|/2.97912e-76/TPA: hypothetical protein ANIA_01515 [A. nidulans FGSC A4]
ANID_02880	32.1	102.47	1.67455639	3.31E-14	2.75E-13	gi|67524845|ref|XP_660484.1|/0/hypothetical protein AN2880.2 [A. nidulans FGSC A4]
ANID_00143	8.4	26.66	1.66621555	5.73E-14	4.68E-13	gi|67515723|ref|XP_657747.1|/8.71044e-51/hypothetical protein AN0143.2 [A. nidulans FGSC A4]
ANID_06353	3.19	10.11	1.66415467	3.03E-06	1.22E-05	gi|259479428|tpe|CBF69640.1|/0/TPA: acetyltransferase, GNAT family family (AFU_orthologue; AFUA_3G07750) [A. nidulans FGSC A4]
ANID_12304	18.99	60.12	1.6626051	2.10E-13	1.59E-12	gi|259487112|tpe|CBF85525.1|/8.92384e-60/TPA: VHS domain protein (AFU_orthologue; AFUA_6G09080) [A. nidulans FGSC A4]
ANID_00158	20.5	64.83	1.66103766	1.07E-14	9.16E-14	gi|67515753|ref|XP_657762.1|/1.86376e-173/hypothetical protein AN0158.2 [A. nidulans FGSC A4]
ANID_00310	20.17	63.78	1.66089301	0	0	gi|67516057|ref|XP_657914.1|/0/hypothetical protein AN0310.2 [A. nidulans FGSC A4]
ANID_12179	7.56	23.87	1.65874043	6.35E-13	4.41E-12	gi|119496267|ref|XP_001264907.1|/5.86739e-84/F-box domain protein [N. fischeri NRRL 181]
ANID_07488	7.9	24.92	1.65737951	1.79E-13	1.36E-12	gi|67901002|ref|XP_680757.1|/0/hypothetical protein AN7488.2 [A. nidulans FGSC A4]
ANID_05862	75.12	236.82	1.65652196	5.90E-13	4.12E-12	gi|67539384|ref|XP_663466.1|/3.22342e-67/hypothetical protein AN5862.2 [A. nidulans FGSC A4]
ANID_01519	4.2	13.24	1.65644189	9.27E-08	4.32E-07	gi|67522124|ref|XP_659123.1|/0/hypothetical protein AN1519.2 [A. nidulans FGSC A4]
ANID_10942	20.17	63.43	1.65295426	0	0	gi|259483753|tpe|CBF79402.1|/0/TPA: conserved hypothetical protein similar to Aip1 (Eurofung) [A. nidulans FGSC A4]
ANID_03911	27.9	86.61	1.63426849	1.55E-13	1.20E-12	gi|46399237|gb|AAS92247.1|/6.05596e-98/SndA [Emericella nidulans]
ANID_07569	8.24	25.44	1.62638243	2.62E-13	1.93E-12	gi|74656948|sp|Q5AVW1.1|TPC1_EMENI/5.69858e-170/RecName: Full=Mitochondrial thiamine pyrophosphate carrier 1
ANID_03793	27.9	86.09	1.62558055	1.55E-13	1.19E-12	gi|68270862|gb|AAY88922.1|/0/protein phosphatase Z [Emericella nidulans]
ANID_04434	21.51	66.22	1.62225949	0	0	gi|119501088|ref|XP_001267301.1|/2.56856e-91/37S ribosomal protein Rsm25 [Neosartorya fischeri NRRL 181]
ANID_06284	5.21	16.03	1.62141915	6.90E-09	3.51E-08	gi|67540228|ref|XP_663888.1|/0/hypothetical protein AN6284.2 [A. nidulans FGSC A4]
ANID_06037	125.37	384.77	1.61780415	0	0	gi|67539734|ref|XP_663641.1|/0/G6PI_ASPOR Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) [A. nidulans FGSC A4]
ANID_03162	3.03	9.24	1.60857506	1.30E-05	4.81E-05	gi|67525409|ref|XP_660766.1|/2.1247e-112/hypothetical protein AN3162.2 [A. nidulans FGSC A4]
ANID_00356	21.51	65.52	1.60692783	0	0	gi|67516149|ref|XP_657960.1|/0/hypothetical protein AN0356.2 [A. nidulans FGSC A4]
ANID_08705	819.3	2491.77	1.60470719	2.93E-11	1.76E-10	gi|67903436|ref|XP_681974.1|/1.62091e-12/hypothetical protein AN8705.2 [A. nidulans FGSC A4]
ANID_02327	2.18	6.62	1.60250308	0.00025	0.000778	gi|3025796|gb|AAC24520.1|/0/molybdenum cofactor biosynthetic protein [Emericella nidulans]
ANID_07467	2.18	6.62	1.60250308	0.00025	0.000777	gi|67900960|ref|XP_680736.1|/1.58936e-47/hypothetical protein AN7467.2 [A. nidulans FGSC A4]
ANID_02439	25.21	76.33	1.59825407	0	0	gi|3136096|gb|AAC39458.1|/0/spindle assembly checkpoint protein SLDB [Emericella nidulans]
ANID_11993	8.24	24.92	1.59658783	8.57E-13	5.88E-12	gi|67901266|ref|XP_680889.1|/0/hypothetical protein AN7620.2 [A. nidulans FGSC A4]
ANID_06920	37.14	111.88	1.59090644	3.02E-14	2.52E-13	gi|259480525|tpe|CBF71739.1|/5.29845e-76/TPA: SNF7 family protein (AFU_orthologue; AFUA_5G13890) [A. nidulans FGSC A4]
ANID_00609	3.53	10.63	1.59040151	3.47E-06	1.38E-05	gi|259489124|tpe|CBF89137.1|/0/TPA: acyl CoA synthetase (Eurofung) [A. nidulans FGSC A4]
ANID_04300	126.55	379.19	1.58321341	1.17E-12	7.90E-12	gi|67528188|ref|XP_661904.1|/1.46879e-93/hypothetical protein AN4300.2 [A. nidulans FGSC A4]
ANID_02229	17.48	52.28	1.58055396	0	0	gi|67523547|ref|XP_659833.1|/0/MET2_EMENI Homoserine O-acetyltransferase (Homoserine O-trans-acetylase) [A. nidulans FGSC A4]

<table>
<tr><td>ANID_12201</td><td>4.2</td><td>12.55</td><td>1.57922613</td><td>5.19E-07</td><td>2.26E-06</td><td>gi|169776557|ref|XP_001822745.1|/3.76577e-64/2Fe-2S iron-sulfur cluster binding domain protein [A. oryzae RIB40]</td></tr>
<tr><td>ANID_04341</td><td>6.89</td><td>20.56</td><td>1.57726438</td><td>1.22E-10</td><td>7.05E-10</td><td>gi|67528286|ref|XP_661945.1|/0/hypothetical protein AN4341.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11864</td><td>52.44</td><td>156.31</td><td>1.57567049</td><td>7.82E-14</td><td>6.31E-13</td><td>gi|67523255|ref|XP_659688.1|/9.07598e-178/hypothetical protein AN2084.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_12405</td><td>26.39</td><td>78.59</td><td>1.5743544</td><td>0</td><td>0</td><td>gi|259485571|tpe|CBF82705.1|/0/TPA: MFS monocarboxylate transporter, putative (AFU_orthologue; AFUA_3G05660) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02687</td><td>40.17</td><td>119.02</td><td>1.56701366</td><td>5.22E-13</td><td>3.70E-12</td><td>gi|238054315|sp|Q96WY0.2|RHOC_EMENI/6.74228e-100/RecName: Full=GTP-binding protein rhoC; AltName: Full=Rho3 protein homolog; Flags: Precursor</td></tr>
<tr><td>ANID_01278</td><td>219.32</td><td>649.65</td><td>1.56662529</td><td>6.91E-12</td><td>4.38E-11</td><td>gi|259488399|tpe|CBF87807.1|/4.4909e-40/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04196</td><td>3.19</td><td>9.41</td><td>1.5606383</td><td>1.71E-05</td><td>6.21E-05</td><td>gi|67527898|ref|XP_661800.1|/0/hypothetical protein AN4196.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02176</td><td>6.39</td><td>18.82</td><td>1.55837879</td><td>1.03E-09</td><td>5.57E-09</td><td>gi|259487556|tpe|CBF86321.1|/0/TPA: Gamma-tubulin complex protein 4 (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08229</td><td>65.04</td><td>189.42</td><td>1.5421895</td><td>6.55E-13</td><td>4.54E-12</td><td>gi|259481011|tpe|CBF74158.1|/7.64919e-145/TPA: mitochondrial export translocase Oxa1, putative (AFU_orthologue; AFUA_5G03640) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02457</td><td>3.53</td><td>10.28</td><td>1.54210018</td><td>8.11E-06</td><td>3.10E-05</td><td>gi|67524003|ref|XP_660061.1|/0/hypothetical protein AN2457.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10568</td><td>12.27</td><td>35.72</td><td>1.54159683</td><td>0</td><td>0</td><td>gi|259482701|tpe|CBF77430.1|/2.9219e-89/TPA: UPF0041 domain protein (AFU_orthologue; AFUA_4G07750) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04837</td><td>5.04</td><td>14.64</td><td>1.53841992</td><td>1.02E-07</td><td>4.72E-07</td><td>gi|67537334|ref|XP_662441.1|/0/hypothetical protein AN4837.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_04561</td><td>39.66</td><td>113.62</td><td>1.51846023</td><td>4.11E-13</td><td>2.96E-12</td><td>gi|259482609|tpe|CBF77254.1|/9.30964e-107/TPA: phosducin-like protein (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04015</td><td>631.74</td><td>1805.35</td><td>1.51487573</td><td>1.59E-12</td><td>1.06E-11</td><td>gi|259481400|tpe|CBF74882.1|/5.45293e-75/TPA: eukaryotic translation initiation factor 5A-2 (Broad) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01780</td><td>9.58</td><td>27.36</td><td>1.51397067</td><td>6.05E-13</td><td>4.22E-12</td><td>gi|83766963|dbj|BAE57103.1|/6.55865e-179/unnamed protein product [A. oryzae]</td></tr>
<tr><td>ANID_04901</td><td>2.69</td><td>7.67</td><td>1.51162041</td><td>0.000152</td><td>0.000487</td><td>gi|67537462|ref|XP_662505.1|/0/hypothetical protein AN4901.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_00120</td><td>21.68</td><td>61.69</td><td>1.50867189</td><td>0</td><td>0</td><td>gi|47824784|emb|CAG30553.1|/7.64487e-178/TapA protein [Emericella nidulans]</td></tr>
<tr><td>ANID_00942</td><td>5.88</td><td>16.73</td><td>1.50854939</td><td>1.99E-08</td><td>9.71E-08</td><td>gi|67517338|ref|XP_658546.1|/0/hypothetical protein AN0942.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08102</td><td>4.54</td><td>12.9</td><td>1.50660686</td><td>8.69E-07</td><td>3.69E-06</td><td>gi|67902230|ref|XP_681371.1|/0/hypothetical protein AN8102.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_12079</td><td>3.19</td><td>9.06</td><td>1.50595463</td><td>3.96E-05</td><td>0.000138</td><td>gi|259483042|tpe|CBF78085.1|/0/TPA: Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00237</td><td>3.87</td><td>10.98</td><td>1.50447258</td><td>5.83E-06</td><td>2.27E-05</td><td>gi|67515911|ref|XP_657841.1|/0/hypothetical protein AN0237.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10273</td><td>21.68</td><td>61.34</td><td>1.50046341</td><td>0</td><td>0</td><td>gi|67523437|ref|XP_659778.1|/0/hypothetical protein AN2174.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07382</td><td>4.2</td><td>11.85</td><td>1.49642583</td><td>2.76E-06</td><td>1.12E-05</td><td>gi|67900790|ref|XP_680651.1|/0/hypothetical protein AN7382.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04650</td><td>26.72</td><td>75.28</td><td>1.49434662</td><td>2.55E-14</td><td>2.14E-13</td><td>gi|259482513|tpe|CBF77067.1|/0/TPA: conserved serine proline-rich protein (AFU_orthologue; AFUA_2G01790) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03482</td><td>8.24</td><td>23.18</td><td>1.49216432</td><td>5.18E-11</td><td>3.08E-10</td><td>gi|67526049|ref|XP_661086.1|/5.26504e-50/hypothetical protein AN3482.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00907</td><td>15.8</td><td>44.44</td><td>1.49193426</td><td>0</td><td>0</td><td>gi|67517262|ref|XP_658511.1|/2.96115e-44/RS22_KLUMA 40S RIBOSOMAL PROTEIN S22 (S15A) (YS24) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02091</td><td>31.93</td><td>89.74</td><td>1.49083863</td><td>2.14E-13</td><td>1.60E-12</td><td>gi|259487462|tpe|CBF86161.1|/0/TPA: tyrosine decarboxylase, putative (AFU_orthologue; AFUA_2G04980) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00626</td><td>8.07</td><td>22.65</td><td>1.48887047</td><td>9.15E-11</td><td>5.33E-10</td><td>gi|67516689|ref|XP_658230.1|/3.35346e-145/hypothetical protein AN0626.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02412</td><td>91.59</td><td>257.04</td><td>1.48873089</td><td>0</td><td>0</td><td>gi|238054297|sp|Q00771.2|KCC1_EMENI/0/RecName: Full=Calcium/calmodulin-dependent protein kinase; Short=CMPK</td></tr>
<tr><td>ANID_00815</td><td>6.22</td><td>17.43</td><td>1.48658608</td><td>1.43E-08</td><td>7.07E-08</td><td>gi|67517069|ref|XP_658419.1|/1.23112e-139/hypothetical protein AN0815.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05667</td><td>6.22</td><td>17.43</td><td>1.48658608</td><td>1.43E-08</td><td>7.07E-08</td><td>gi|67538994|ref|XP_663271.1|/0/hypothetical protein AN5667.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04452</td><td>185.71</td><td>520.35</td><td>1.48643084</td><td>3.43E-12</td><td>2.22E-11</td><td>gi|259482731|tpe|CBF77490.1|/1.97212e-152/TPA: 60S ribosomal protein L36 (AFU_orthologue; AFUA_4G07435) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00433</td><td>1173.57</td><td>3286.58</td><td>1.48568321</td><td>1.93E-11</td><td>1.18E-10</td><td>gi|67516303|ref|XP_658037.1|/1.87278e-87/hypothetical protein AN0433.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08704</td><td>415.28</td><td>1162.15</td><td>1.48463999</td><td>0</td><td>0</td><td>gi|289617932|emb|CBI55509.1|/9.9679e-21/unnamed protein product [Sordaria macrospora]</td></tr>
<tr><td>ANID_08674</td><td>32.77</td><td>91.66</td><td>1.48391661</td><td>1.40E-13</td><td>1.09E-12</td><td>gi|67903374|ref|XP_681943.1|/2.1105e-91/hypothetical protein AN8674.2 [A. nidulans FGSC A4]</td></tr>
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ANID_00393	28.23	78.94	1.48352739	1.03E-13	8.25E-13	gi|67516223|ref|XP_657997.1|/0/hypothetical protein AN0393.2 [A. nidulans FGSC A4]
ANID_05110	15.46	43.22	1.48315875	0	0	gi|255931617|ref|XP_002557365.1|/0/Pc12g05180 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_03180	7.23	20.04	1.47081496	1.57E-09	8.41E-09	gi|259485863|tpe|CBF83247.1|/3.75955e-87/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06717	850.39	2350.79	1.46694913	2.51E-12	1.64E-11	gi|67541094|ref|XP_664321.1|/2.45724e-180/hypothetical protein AN6717.2 [A. nidulans FGSC A4]
ANID_11132	18.99	52.45	1.46570287	2.10E-13	1.59E-12	gi|67903730|ref|XP_682121.1|/6.61119e-50/hypothetical protein AN8852.2 [A. nidulans FGSC A4]
ANID_10485	5.88	16.21	1.46299603	6.71E-08	3.15E-07	gi|93204547|sp|P0C1B1.1|CBK1_EMENI/0/RecName: Full=Serine/threonine-protein kinase cbk1
ANID_09295	15.13	41.65	1.46090451	0	0	gi|67904616|ref|XP_682564.1|/0/hypothetical protein AN9295.2 [A. nidulans FGSC A4]
ANID_10443	4.37	12.02	1.45973171	3.50E-06	1.40E-05	gi|259481685|tpe|CBF75436.1|/0/TPA: pre-mRNA splicing factor, putative (AFU_orthologue; AFUA_7G04783) [A. nidulans FGSC A4]
ANID_08975	8.24	22.65	1.45879481	1.73E-10	9.89E-10	gi|67903976|ref|XP_682244.1|/3.00272e-166/hypothetical protein AN8975.2 [A. nidulans FGSC A4]
ANID_08848	2.86	7.84	1.45483851	0.000194	0.00061	gi|67903722|ref|XP_682117.1|/5.89531e-179/hypothetical protein AN8848.2 [A. nidulans FGSC A4]
ANID_02951	6.55	17.95	1.45441703	1.53E-08	7.53E-08	gi|259486107|tpe|CBF83685.1|/0/TPA: UDP-glucose 4-epimerase (Eurofung) [A. nidulans FGSC A4]
ANID_09449	45.04	122.68	1.44562134	7.48E-14	6.06E-13	gi|75858982|ref|XP_868831.1|/3.81582e-128/hypothetical protein AN9449.2 [A. nidulans FGSC A4]
ANID_11778	35.46	96.37	1.44239157	2.34E-13	1.74E-12	gi|259482112|tpe|CBF76281.1|/0/TPA: exoinulinase InuD (AFU_orthologue; AFUA_5G00480) [A. nidulans FGSC A4]
ANID_03644	24.2	65.35	1.43318019	6.24E-14	5.09E-13	gi|259481825|tpe|CBF75708.1|/1.63052e-25/TPA: protein involved in error-free postreplication DNA repair (Eurofung) [A. nidulans FGSC A4]
ANID_10835	10.92	29.45	1.43129478	6.55E-13	4.54E-12	gi|67540870|ref|XP_664209.1|/4.89391e-79/hypothetical protein AN6605.2 [A. nidulans FGSC A4]
ANID_12324	11.09	29.8	1.42605297	3.56E-13	2.59E-12	gi|145254896|ref|XP_001398795.1|/1.82127e-50/hypothetical protein ANI_1_428164 [A. niger CBS 513.88]
ANID_07146	198.48	533.07	1.42533135	1.77E-12	1.18E-11	gi|67541965|ref|XP_664750.1|/0/hypothetical protein AN7146.2 [A. nidulans FGSC A4]
ANID_07699	3.7	9.93	1.42426845	3.54E-05	0.000124	gi|67901424|ref|XP_680968.1|/5.53238e-112/hypothetical protein AN7699.2 [A. nidulans FGSC A4]
ANID_05776	11.6	31.02	1.41907388	1.82E-13	1.38E-12	gi|259484739|tpe|CBF81219.1|/0/TPA: WW domain protein (AFU_orthologue; AFUA_6G06520) [A. nidulans FGSC A4]
ANID_00504	21.51	57.51	1.41880531	0	0	gi|47824788|emb|CAG30555.1|/0/SitA protein [Emericella nidulans]
ANID_07680	12.6	33.63	1.41632505	0	0	gi|67901386|ref|XP_680949.1|/0/hypothetical protein AN7680.2 [A. nidulans FGSC A4]
ANID_04287	6.55	17.43	1.41200576	5.00E-08	2.38E-07	gi|259481098|tpe|CBF74319.1|/0/TPA: DMT family transporter (Eurofung) [A. nidulans FGSC A4]
ANID_04016	1884.47	5007.42	1.40990864	2.44E-11	1.48E-10	gi|67527200|ref|XP_661620.1|/1.22276e-29/hypothetical protein AN4016.2 [A. nidulans FGSC A4]
ANID_00240	364.86	968.37	1.40821539	0	0	gi|302652712|ref|XP_003018200.1|/1.26062e-129/hypothetical protein TRV_07775 [Trichophyton verrucosum HKI 0517]
ANID_03462	16.81	44.44	1.40253909	0	0	gi|259485545|tpe|CBF82657.1|/0/TPA: mitochondrial translation release factor (RF-1), putative (AFU_orthologue; AFUA_3G05410) [A. nidulans FGSC A4]
ANID_04522	2228.66	5871.93	1.39765823	0	0	gi|67536704|ref|XP_662126.1|/2.08153e-27/hypothetical protein AN4522.2 [A. nidulans FGSC A4]
ANID_07032	6.55	17.25	1.39702955	7.39E-08	3.47E-07	gi|1705828|sp|P30584.2|CHSA_EMENI/0/RecName: Full=Chitin synthase A; AltName: Full=Chitin-UDP acetyl-glucosaminyl transferase A; AltName: Full=Class-II chitin synthase A
ANID_04587	3.53	9.24	1.38822467	9.39E-05	0.000312	gi|259482581|tpe|CBF77199.1|/4.22685e-62/TPA: methylated-DNA-protein-cysteine methyltransferase (AFU_orthologue; AFUA_2G02090) [A. nidulans FGSC A4]
ANID_01866	3.53	9.24	1.38822467	9.39E-05	0.000311	gi|258566365|ref|XP_002583927.1|/2.94112e-88/conserved hypothetical protein [Uncinocarpus reesii 1704]
ANID_03188	30.59	79.99	1.38675955	0	0	gi|259485855|tpe|CBF83232.1|/0/TPA: phosphatidylserine decarboxylase Psd2, putative (AFU_orthologue; AFUA_3G13970) [A. nidulans FGSC A4]
ANID_03626	96.3	251.81	1.38672787	4.87E-13	3.47E-12	gi|67526337|ref|XP_661230.1|/0/hypothetical protein AN3626.2 [A. nidulans FGSC A4]
ANID_02981	30.25	78.77	1.38071113	2.51E-13	1.86E-12	gi|67525047|ref|XP_660585.1|/0/G6PD_EMENI Glucose-6-phosphate 1-dehydrogenase (G6PD) [A. nidulans FGSC A4]
ANID_00200	9.24	24.05	1.38007214	2.93E-10	1.65E-09	gi|67515837|ref|XP_657804.1|/3.95822e-134/hypothetical protein AN0200.2 [A. nidulans FGSC A4]
ANID_10191	9.92	25.79	1.37839975	6.71E-11	3.97E-10	gi|259486751|tpe|CBF84862.1|/0/TPA: AAA family ATPase, putative (AFU_orthologue; AFUA_8G04270) [A. nidulans FGSC A4]
ANID_00859	4.37	11.33	1.37444268	1.72E-05	6.23E-05	gi|67517161|ref|XP_658463.1|/1.53777e-131/hypothetical protein AN0859.2 [A. nidulans FGSC A4]
ANID_12069	14.79	38.34	1.37422829	0	0	gi|259483658|tpe|CBF79227.1|/0/TPA: hypothetical protein similar to thymidylate synthase (Broad) [A. nidulans FGSC A4]
ANID_01018	3.36	8.71	1.37421149	0.000168	0.000533	gi|67517634|ref|XP_658622.1|/0/hypothetical protein AN1018.2 [A. nidulans FGSC A4]
ANID_01503	9.08	23.53	1.37373712	5.12E-10	2.83E-09	gi|74598145|sp|Q5BD77.1|DAPAL_EMENI/1.57743e-149/RecName: Full=Probable 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; AltName: Full=Dihydrodipicolinate synthase-like; Short=DHDPS-like protein; AltName: Full=Probable 2-keto-4-hydroxyglutarate aldolase; Short=Probable KHG-aldolase

ANID_06857	4.54	11.68	1.36327607	1.43E-05	5.24E-05	gi|67541374|ref|XP_664461.1|/0/hypothetical protein AN6857.2 [A. nidulans FGSC A4]
ANID_10798	13.61	34.85	1.35649159	9.33E-14	7.48E-13	gi|67540286|ref|XP_663917.1|/1.80608e-175/hypothetical protein AN6313.2 [A. nidulans FGSC A4]
ANID_02686	18.32	46.88	1.35555307	0	0	gi|67524457|ref|XP_660290.1|/5.61139e-43/hypothetical protein AN2686.2 [A. nidulans FGSC A4]
ANID_01352	42.02	107.52	1.35545698	1.92E-13	1.46E-12	gi|259488315|tpe|CBF87664.1|/6.42756e-27/TPA: S-adenosylmethionine-dependent methyltransferase, putative (AFU_orthologue; AFUA_1G09360) [A. nidulans FGSC A4]
ANID_10354	32.77	83.82	1.35491885	1.40E-13	1.09E-12	gi|259485924|tpe|CBF83359.1|/1.33276e-84/TPA: Signal peptidase I (AFU_orthologue; AFUA_3G12840) [A. nidulans FGSC A4]
ANID_10918	25.88	66.05	1.35172094	1.60E-13	1.23E-12	gi|259483405|tpe|CBF78768.1|/0/TPA: sorting nexin Mvp1 (AFU_orthologue; AFUA_2G17180) [A. nidulans FGSC A4]
ANID_10758	4.03	10.28	1.35098852	5.39E-05	0.000184	gi|259479867|tpe|CBF70484.1|/0/TPA: AAR2 family protein (AFU_orthologue; AFUA_2G10430) [A. nidulans FGSC A4]
ANID_02433	31.93	81.21	1.34674484	2.14E-13	1.61E-12	gi|74597436|sp|Q5BAJ7.1|FIP1_EMENI/9.89555e-110/RecName: Full=Pre-mRNA polyadenylation factor fip1
ANID_06487	8.57	21.78	1.34563685	4.01E-09	2.07E-08	gi|67540634|ref|XP_664091.1|/0/hypothetical protein AN6487.2 [A. nidulans FGSC A4]
ANID_00991	5.21	13.24	1.34554785	4.66E-06	1.83E-05	gi|119494359|ref|XP_001264075.1|/0/aminotransferase, class III [Neosartorya fischeri NRRL 181]
ANID_03730	5.21	13.24	1.34554785	4.66E-06	1.83E-05	gi|67526545|ref|XP_661334.1|/0/hypothetical protein AN3730.2 [A. nidulans FGSC A4]
ANID_01231	7.56	19.17	1.3423922	3.69E-08	1.77E-07	gi|259488449|tpe|CBF87890.1|/0/TPA: DNA polymerase POL4, putative (AFU_orthologue; AFUA_1G10480) [A. nidulans FGSC A4]
ANID_01606	16.64	42.17	1.34156159	0	0	gi|67522298|ref|XP_659210.1|/2.39136e-180/hypothetical protein AN1606.2 [A. nidulans FGSC A4]
ANID_07492	14.79	37.47	1.34111393	3.11E-15	2.75E-14	gi|67901010|ref|XP_680761.1|/9.06605e-178/hypothetical protein AN7492.2 [A. nidulans FGSC A4]
ANID_10483	8.4	21.26	1.33968036	7.00E-09	3.56E-08	gi|259481532|tpe|CBF75140.1|/3.51512e-161/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01661	8.4	21.26	1.33968036	7.00E-09	3.56E-08	gi|67522409|ref|XP_659265.1|/1.91654e-178/hypothetical protein AN1661.2 [A. nidulans FGSC A4]
ANID_00787	18.32	46.35	1.33914984	0	0	gi|298351828|sp|Q5BF93.2|MNS1B_EMENI/0/RecName: Full=Mannosyl-oligosaccharide alpha-1,2-mannosidase 1B; AltName: Full=Class I alpha-mannosidase 1B; AltName: Full=Man(9)-alpha-mannosidase 1B; Flags: Precursor
ANID_04596	16.13	40.78	1.33811534	0	0	gi|67536852|ref|XP_662200.1|/6.71254e-172/hypothetical protein AN4596.2 [A. nidulans FGSC A4]
ANID_03087	25.04	63.26	1.33705899	2.24E-13	1.68E-12	gi|259485965|tpe|CBF83431.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_03458	43.7	110.13	1.33350234	3.81E-13	2.75E-12	gi|259485550|tpe|CBF82666.1|/1.39502e-112/TPA: 60S ribosomal protein L20, putative (AFU_orthologue; AFUA_3G05460) [A. nidulans FGSC A4]
ANID_06349	22.69	57.16	1.33294931	1.59E-13	1.22E-12	gi|259479432|tpe|CBF69648.1|/0/TPA: HEAT repeat protein (AFU_orthologue; AFUA_2G14180) [A. nidulans FGSC A4]
ANID_03683	9.41	23.7	1.33262043	1.11E-09	6.00E-09	gi|145229843|ref|XP_001389230.1|/0/Zn(II)2Cys6 transcription factor [A. niger CBS 513.88]
ANID_08913	3.53	8.89	1.33251524	0.000205	0.000643	gi|67903852|ref|XP_682182.1|/1.56552e-34/hypothetical protein AN8913.2 [A. nidulans FGSC A4]
ANID_08233	63.53	159.97	1.33229145	5.75E-13	4.04E-12	gi|74593020|sp|Q5ATZ7.1|SFH5_EMENI/0/RecName: Full=Phosphatidylinositol transfer protein sfh5; Short=PITP sfh5
ANID_01013	201.51	506.93	1.33093511	4.36E-12	2.80E-11	gi|67517624|ref|XP_658617.1|/2.23998e-162/RL5_NEUCR 60S ribosomal protein L5 (CPR4) [A. nidulans FGSC A4]
ANID_06700	153.94	387.04	1.33011452	0	0	gi|259480286|tpe|CBF71277.1|/0/TPA: elongation factor 3 (Eurofung) [A. nidulans FGSC A4]
ANID_04245	5.71	14.29	1.32344327	2.68E-06	1.08E-05	gi|67528012|ref|XP_661849.1|/0/hypothetical protein AN4245.2 [A. nidulans FGSC A4]
ANID_05953	6.55	16.38	1.32236855	5.00E-07	2.18E-06	gi|259479873|tpe|CBF70495.1|/2.63628e-66/TPA: iron-sulfur cluster assembly accessory protein Isa2, putative (AFU_orthologue; AFUA_2G10370) [A. nidulans FGSC A4]
ANID_11763	6.55	16.38	1.32236855	5.00E-07	2.18E-06	gi|259483933|tpe|CBF79728.1|/0/TPA: FAD monooxygenase, putative (AFU_orthologue; AFUA_2G15520) [A. nidulans FGSC A4]
ANID_08430	7.39	18.47	1.3215376	9.40E-08	4.38E-07	gi|259484371|tpe|CBF80533.1|/6.49277e-168/TPA: Kelch repeat protein (AFU_orthologue; AFUA_5G12780) [A. nidulans FGSC A4]
ANID_02848	30.42	75.98	1.32059956	7.79E-14	6.31E-13	gi|255942503|ref|XP_002562020.1|/1.20655e-53/Pc18g01760 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_08080	53.95	134.18	1.31447478	0	0	gi|259480837|tpe|CBF73841.1|/8.59697e-80/TPA: allergen, putative (AFU_orthologue; AFUA_5G01440) [A. nidulans FGSC A4]
ANID_05524	31.26	77.72	1.31396812	5.46E-13	3.85E-12	gi|259485024|tpe|CBF81743.1|/1.21042e-147/TPA: metallo-beta-lactamase domain protein, putative (AFU_orthologue; AFUA_6G12940) [A. nidulans FGSC A4]
ANID_05743	37.65	93.58	1.31355036	0	0	gi|259484780|tpe|CBF81294.1|/0/TPA: Putative calcium ion P-type ATPase (Eurofung) [A. nidulans FGSC A4]
ANID_07936	19.5	48.44	1.31272474	8.02E-14	6.47E-13	gi|259480685|tpe|CBF73556.1|/0/TPA: MFS transporter, putative (AFU_orthologue; AFUA_5G01520) [A. nidulans FGSC A4]
ANID_01673	8.07	20.04	1.31224193	3.10E-08	1.50E-07	gi|259487012|tpe|CBF85341.1|/0/TPA: phospho-2-dehydro-3-deoxyheptonate aldolase, class II (AFU_orthologue; AFUA_4G08760) [A. nidulans FGSC A4]
ANID_07434	6.39	15.86	1.31150494	8.75E-07	3.71E-06	gi|259483738|tpe|CBF79375.1|/0/TPA: fungal specific transcription factor, putative (AFU_orthologue; AFUA_2G06130) [A. nidulans FGSC A4]
ANID_01355	3.87	9.58	1.30769209	0.00014	0.00045	gi|259488311|tpe|CBF87657.1|/0/TPA: DMT family transporter (Eurofung) [A. nidulans FGSC A4]

ANID_03171	6.55	16.21	1.30731728	7.26E-07	3.10E-06	gi|67525427|ref|XP_660775.1|/2.53904e-86/hypothetical protein AN3171.2 [A. nidulans FGSC A4]
ANID_02271	36.81	90.96	1.30513451	2.74E-13	2.02E-12	gi|259487664|tpe|CBF86507.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_11081	6.72	16.55	1.30029808	6.03E-07	2.59E-06	gi|259484384|tpe|CBF80558.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04943	5.55	13.59	1.29198578	6.82E-06	2.63E-05	gi|67537546|ref|XP_662547.1|/0/hypothetical protein AN4943.2 [A. nidulans FGSC A4]
ANID_00485	4.2	10.28	1.29137903	9.56E-05	0.000315	gi|259489265|tpe|CBF89394.1|/0/TPA: CRAL/TRIO domain protein (AFU_orthologue; AFUA_4G13930) [A. nidulans FGSC A4]
ANID_05402	4.2	10.28	1.29137903	9.56E-05	0.000315	gi|259485153|tpe|CBF81968.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10264	24.03	58.55	1.28483252	0	0	gi|259487466|tpe|CBF86168.1|/9.01409e-42/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02473	67.9	165.2	1.28273021	2.85E-13	2.09E-12	gi|67524033|ref|XP_660077.1|/1.9581e-172/hypothetical protein AN2473.2 [A. nidulans FGSC A4]
ANID_07709	6.89	16.73	1.27986156	7.23E-07	3.09E-06	gi|259484055|tpe|CBF79950.1|/0/TPA: tRNA a64-2'-o-ribosylphosphate transferase (AFU_orthologue; AFUA_5G08280) [A. nidulans FGSC A4]
ANID_11131	27.06	65.7	1.27973153	0	0	gi|259482909|tpe|CBF77835.1|/1.30459e-51/TPA: hypothetical protein ANIA_11131 [A. nidulans FGSC A4]
ANID_10433	20.17	48.97	1.27968711	0	0	gi|259481822|tpe|CBF75703.1|/0/TPA: TPR domain protein (AFU_orthologue; AFUA_4G12110) [A. nidulans FGSC A4]
ANID_07457	6.39	15.51	1.27931085	1.84E-06	7.54E-06	gi|67900940|ref|XP_680726.1|/2.61201e-108/hypothetical protein AN7457.2 [A. nidulans FGSC A4]
ANID_01757	99.83	242.05	1.27775976	1.30E-13	1.02E-12	gi|67522601|ref|XP_659361.1|/4.81936e-124/hypothetical protein AN1757.2 [A. nidulans FGSC A4]
ANID_02851	18.49	44.79	1.27643144	0	0	gi|259486213|tpe|CBF83874.1|/1.29551e-165/TPA: oxidoreductase, 2OG-Fe(II) oxygenase family family (AFU_orthologue; AFUA_3G11980) [A. nidulans FGSC A4]
ANID_03493	5.04	12.2	1.27538551	2.53E-05	9.00E-05	gi|67526071|ref|XP_661097.1|/2.87466e-114/hypothetical protein AN3493.2 [A. nidulans FGSC A4]
ANID_04283	25.71	62.21	1.2748169	0	0	gi|259481102|tpe|CBF74326.1|/0/TPA: component of the core form of RNA polymerase transcription factor TFIIH (Eurofung) [A. nidulans FGSC A4]
ANID_02861	7.06	17.08	1.27456789	5.99E-07	2.58E-06	gi|67524807|ref|XP_660465.1|/0/hypothetical protein AN2861.2 [A. nidulans FGSC A4]
ANID_10257	49.58	119.72	1.27183401	2.95E-13	2.16E-12	gi|67523265|ref|XP_659693.1|/0/hypothetical protein AN2089.2 [A. nidulans FGSC A4]
ANID_06927	10.25	24.75	1.27180462	1.93E-09	1.03E-08	gi|67541514|ref|XP_664531.1|/9.25862e-67/hypothetical protein AN6927.2 [A. nidulans FGSC A4]
ANID_09509	20.5	49.49	1.27151313	1.07E-14	9.15E-14	gi|75859102|ref|XP_868891.1|/2.94568e-80/hypothetical protein AN9509.2 [A. nidulans FGSC A4]
ANID_00404	48.23	116.41	1.27121228	3.71E-13	2.69E-12	gi|259489353|tpe|CBF89553.1|/0/TPA: AtrH [Source:UniProtKB/TrEMBL;Acc:Q2VY21] [A. nidulans FGSC A4]
ANID_00659	13.44	32.41	1.26990588	6.43E-12	4.08E-11	gi|67516755|ref|XP_658263.1|/0/hypothetical protein AN0659.2 [A. nidulans FGSC A4]
ANID_08888	4.71	11.33	1.2663489	5.37E-05	0.000183	gi|259486679|tpe|CBF84726.1|/1.0575e-75/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04096	6.89	16.55	1.26425533	1.04E-06	4.39E-06	gi|67527638|ref|XP_661700.1|/0/hypothetical protein AN4096.2 [A. nidulans FGSC A4]
ANID_01690	6.05	14.46	1.25706051	5.58E-06	2.18E-05	gi|67522467|ref|XP_659294.1|/2.99282e-118/hypothetical protein AN1690.2 [A. nidulans FGSC A4]
ANID_03048	6.72	16.03	1.25424129	1.81E-06	7.45E-06	gi|259486005|tpe|CBF83503.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05803	68.23	162.06	1.24804992	0	0	gi|259480044|tpe|CBF70817.1|/0/TPA: hypothetical protein similar to fimbrin (Eurofung) [A. nidulans FGSC A4]
ANID_07533	15.13	35.9	1.24657186	8.42E-13	5.79E-12	gi|74593542|sp|Q5AVZ7.1|EXGD_EMENI/0/RecName: Full=Glucan 1,3-beta-glucosidase D; AltName: Full=Exo-1,3-beta-glucanase D
ANID_06265	14.29	33.81	1.2424441	5.18E-12	3.31E-11	gi|159129677|gb|EDP54791.1|/0/small nucleolar ribonucleoprotein complex subunit, putative [A. fumigatus A1163]
ANID_02476	4.2	9.93	1.24140439	0.000201	0.00063	gi|67551230|ref|XP_660080.1|/0/hypothetical protein AN2476.2 [A. nidulans FGSC A4]
ANID_06547	287.38	679.27	1.24102548	5.40E-12	3.44E-11	gi|67540754|ref|XP_664151.1|/4.31856e-129/hypothetical protein AN6547.2 [A. nidulans FGSC A4]
ANID_08180	10.92	25.79	1.23983892	1.87E-09	9.96E-09	gi|74593053|sp|Q5AU50.1|PRP45_EMENI/0/RecName: Full=Pre-mRNA-processing protein 45
ANID_01393	51.59	121.63	1.23733576	0	0	gi|67521872|ref|XP_658997.1|/2.57069e-60/hypothetical protein AN1393.2 [A. nidulans FGSC A4]
ANID_06074	23.53	55.42	1.23590539	0	0	gi|67539808|ref|XP_663678.1|/4.86819e-95/hypothetical protein AN6074.2 [A. nidulans FGSC A4]
ANID_10356	31.76	74.76	1.23505566	2.28E-13	1.71E-12	gi|67525361|ref|XP_660742.1|/3.23068e-139/hypothetical protein AN3138.2 [A. nidulans FGSC A4]
ANID_09117	8.74	20.56	1.23413508	9.03E-08	4.22E-07	gi|259485467|tpe|CBF82513.1|/0/TPA: Miscellaneous Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_01062	7.73	18.12	1.22904264	5.77E-07	2.49E-06	gi|67517761|ref|XP_658666.1|/2.47674e-81/hypothetical protein AN1062.2 [A. nidulans FGSC A4]
ANID_02384	5.88	13.77	1.2276405	1.39E-05	5.11E-05	gi|67523857|ref|XP_659988.1|/7.76704e-128/hypothetical protein AN2384.2 [A. nidulans FGSC A4]
ANID_02134	65.88	154.22	1.22707741	0	0	gi|67523355|ref|XP_659738.1|/2.09169e-50/hypothetical protein AN2134.2 [A. nidulans FGSC A4]

ANID_03928	350.58	820.6	1.22693546	0	0	gi|67526941|ref|XP_661532.1|/1.74485e-125/THI4_ASPOR Thiazole biosynthetic enzyme, mitochondrial precursor [A. nidulans FGSC A4]
ANID_02683	30.25	70.75	1.22579501	2.51E-13	1.86E-12	gi|67524451|ref|XP_660287.1|/2.59588e-168/hypothetical protein AN2683.2 [A. nidulans FGSC A4]
ANID_07792	9.24	21.61	1.22573432	5.11E-08	2.43E-07	gi|62485018|dbj|BAD95522.1|/0/lysophospholipase A [Emericella nidulans]
ANID_03946	21.18	49.49	1.22443445	6.73E-14	5.48E-13	gi|3136094|gb|AAC39457.1|/0/spindle assembly checkpoint protein SLDA [Emericella nidulans]
ANID_04974	8.07	18.82	1.22162605	3.94E-07	1.73E-06	gi|259482153|tpe|CBF76362.1|/0/TPA: ubiquinone/menaquinone biosynthesis-related protein (AFU_orthologue; AFUA_3G10140) [A. nidulans FGSC A4]
ANID_10417	19.66	45.83	1.22102896	1.16E-13	9.16E-13	gi|259485547|tpe|CBF82660.1|/0/TPA: ATP-dependent RNA helicase (Eurofung) [A. nidulans FGSC A4]
ANID_02044	12.6	29.28	1.21649182	2.83E-10	1.60E-09	gi|259487412|tpe|CBF86070.1|/7.40399e-171/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05569	5.71	13.24	1.21334047	2.42E-05	8.62E-05	gi|259484971|tpe|CBF81647.1|/0/TPA: RNA polymerase II transcription factor related protein (AFU_orthologue; AFUA_4G11690) [A. nidulans FGSC A4]
ANID_09359	28.23	65.35	1.21095811	1.03E-13	8.25E-13	gi|67904744|ref|XP_682628.1|/0/hypothetical protein AN9359.2 [A. nidulans FGSC A4]
ANID_07403	6.55	15.16	1.21070294	6.42E-06	2.48E-05	gi|67900832|ref|XP_680672.1|/0/hypothetical protein AN7403.2 [A. nidulans FGSC A4]
ANID_02023	7.23	16.73	1.21036989	2.08E-06	8.53E-06	gi|259487390|tpe|CBF86030.1|/5.58728e-128/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00135	7.23	16.73	1.21036989	2.08E-06	8.53E-06	gi|67515707|ref|XP_657739.1|/0/hypothetical protein AN0135.2 [A. nidulans FGSC A4]
ANID_04193	12.44	28.75	1.20857547	4.85E-10	2.69E-09	gi|67527891|ref|XP_661797.1|/1.2012e-105/hypothetical protein AN4193.2 [A. nidulans FGSC A4]
ANID_01720	12.6	29.1	1.20759542	4.01E-10	2.24E-09	gi|74597976|sp|Q5BCL0.1|MED8_EMENI/1.98395e-107/RecName: Full=Mediator of RNA polymerase II transcription subunit 8; AltName: Full=Mediator complex subunit 8
ANID_07052	4.54	10.46	1.20411865	0.000194	0.000612	gi|67541777|ref|XP_664656.1|/1.45167e-153/hypothetical protein AN7052.2 [A. nidulans FGSC A4]
ANID_04713	17.31	39.73	1.19862307	3.17E-13	2.31E-12	gi|259482448|tpe|CBF76942.1|/4.07886e-137/TPA: Ser/Thr protein phosphatase family (AFU_orthologue; AFUA_5G08620) [A. nidulans FGSC A4]
ANID_03956	4.71	10.8	1.19723235	0.00016	0.000508	gi|67526997|ref|XP_661560.1|/0/hypothetical protein AN3956.2 [A. nidulans FGSC A4]
ANID_06367	14.29	32.76	1.19692944	4.26E-11	2.54E-10	gi|67540394|ref|XP_663971.1|/0/hypothetical protein AN6367.2 [A. nidulans FGSC A4]
ANID_04239	20	45.83	1.19629229	0	0	gi|169768982|ref|XP_001818961.1|/0/nuclear localization protein NPL6 [A. oryzae RIB40]
ANID_05519	6.39	14.64	1.19602772	1.11E-05	4.13E-05	gi|67538698|ref|XP_663123.1|/2.3321e-84/hypothetical protein AN5519.2 [A. nidulans FGSC A4]
ANID_08722	114.62	262.26	1.19413898	1.15E-12	7.78E-12	gi|74680526|sp|Q5ASK8.1|SUB2_EMENI/0/RecName: Full=ATP-dependent RNA helicase sub2
ANID_05712	77.98	178.1	1.19151146	0	0	gi|259484811|tpe|CBF81352.1|/1.51685e-170/TPA: Metacaspase-1 Precursor (EC 3.4.22.-) [Source:UniProtKB/Swiss-Prot;Acc:Q8J140] [A. nidulans FGSC A4]
ANID_02996	278.98	636.23	1.1893867	3.22E-12	2.09E-11	gi|73621192|sp|Q5B8Y4.1|MBF1_EMENI/5.09818e-73/RecName: Full=Multiprotein-bridging factor 1
ANID_01430	6.89	15.68	1.18634967	6.19E-06	2.40E-05	gi|67521946|ref|XP_659034.1|/0/hypothetical protein AN1430.2 [A. nidulans FGSC A4]
ANID_08528	30.25	68.83	1.18610237	2.51E-13	1.85E-12	gi|67903082|ref|XP_681797.1|/0/hypothetical protein AN8528.2 [A. nidulans FGSC A4]
ANID_01990	113.78	258.6	1.18447529	4.53E-13	3.25E-12	gi|67523067|ref|XP_659594.1|/0/HOSM_PENCH Homocitrate synthase, mitochondrial precursor [A. nidulans FGSC A4]
ANID_12044	21.85	49.66	1.18445098	0	0	gi|146322862|ref|XP_755197.2|/3.36288e-75/DUF788 domain protein [A. fumigatus Af293]
ANID_06996	17.81	40.43	1.18273869	3.16E-13	2.30E-12	gi|259483693|tpe|CBF79292.1|/0/TPA: ubiquinone biosynthesis protein, putative (AFU_orthologue; AFUA_4G04590) [A. nidulans FGSC A4]
ANID_07471	25.04	56.81	1.18191034	2.24E-13	1.68E-12	gi|259483777|tpe|CBF79445.1|/0/TPA: IdgA domain protein (AFU_orthologue; AFUA_2G05800) [A. nidulans FGSC A4]
ANID_03014	14.29	32.41	1.1814331	8.47E-11	4.96E-10	gi|67525113|ref|XP_660618.1|/0/hypothetical protein AN3014.2 [A. nidulans FGSC A4]
ANID_05441	550.57	1247.89	1.18049286	0	0	gi|309301578|gb|EFP78169.1|/3.48761e-50/40S ribosomal protein S18 [Puccinia graminis f. sp. tritici CRL 75-36-700-3]
ANID_01353	6.55	14.81	1.17700483	1.29E-05	4.78E-05	gi|259488314|tpe|CBF87662.1|/8.22657e-68/TPA: transcription initiation factor TFIID subunit 13, putative (AFU_orthologue; AFUA_1G09350) [A. nidulans FGSC A4]
ANID_06732	192.26	433.91	1.1743372	2.75E-12	1.79E-11	gi|70986856|ref|XP_748915.1|/1.08629e-53/cytokinesis EF-hand protein Cdc4 [A. fumigatus Af293]
ANID_11064	4.87	10.98	1.17288438	0.000186	0.000589	gi|67902530|ref|XP_681521.1|/0/hypothetical protein AN8252.2 [A. nidulans FGSC A4]
ANID_01074	58.32	131.39	1.17179285	0	0	gi|121701593|ref|XP_001269061.1|/6.68438e-65/glycine cleavage system H protein [A. clavatus NRRL 1]
ANID_00316	1170.38	2634.49	1.17054668	8.71E-12	5.46E-11	gi|67516069|ref|XP_657920.1|/0/TBA1_EMENI TUBULIN ALPHA-1 CHAIN [A. nidulans FGSC A4]
ANID_07682	16.64	37.29	1.16413336	5.89E-12	3.75E-11	gi|115433370|ref|XP_001216822.1|/2.52525e-67/AP-1 complex subunit theta-1 [A. terreus NIH2624]
ANID_05701	47.56	106.47	1.16262636	0	0	gi|11527260|gb|AAG36949.1|AF283008_1/0/tyr-inhibited DAHP synthase [Emericella nidulans]
ANID_08781	192.26	430.25	1.16211655	2.75E-12	1.80E-11	gi|67903588|ref|XP_682050.1|/4.48203e-58/hypothetical protein AN8781.2 [A. nidulans FGSC A4]
ANID_02734	3942.21	8777.4	1.15478902	0	0	gi|67524553|ref|XP_660338.1|/1.26034e-132/RLA0_NEUCR 60S acidic ribosomal protein P0 [A. nidulans FGSC A4]
ANID_04266	8.07	17.95	1.15334327	2.23E-06	9.12E-06	gi|67528110|ref|XP_661870.1|/0/hypothetical protein AN4266.2 [A. nidulans FGSC A4]

ANID_10723	26.72	59.42	1.1530286	2.55E-14	2.15E-13	gi|300431590|tpe|CBL43331.1|/2.24358e-175/TPA: arylamine N-acetyltransferase 1 [Emericella nidulans]
ANID_00067	99.16	220.27	1.15144284	0	0	gi|259489743|tpe|CBF90266.1|/0/TPA: Ribonucleotide reductase [Source:UniProtKB/TrEMBL;Acc:Q9HEW8] [A. nidulans FGSC A4]
ANID_04738	10.92	24.22	1.14922601	4.20E-08	2.01E-07	gi|259482422|tpe|CBF76891.1|/0/TPA: polysaccharide export protein (CAP59), putative (AFU_orthologue; AFUA_7G05020) [A. nidulans FGSC A4]
ANID_05884	7.39	16.38	1.14828909	6.86E-06	2.64E-05	gi|259479950|tpe|CBF70640.1|/4.44798e-131/TPA: orotate phosphoribosyltransferase (Eurofung) [A. nidulans FGSC A4]
ANID_00879	15.46	34.16	1.14376766	8.58E-11	5.02E-10	gi|259488835|tpe|CBF88603.1|/4.98702e-63/TPA: DUF1014 domain protein (AFU_orthologue; AFUA_1G15390) [A. nidulans FGSC A4]
ANID_04890	43.86	96.89	1.14344196	1.49E-13	1.15E-12	gi|259482244|tpe|CBF76540.1|/0/TPA: Putative SNARE-dependent exocytosis protein Sro7 (Eurofung) [A. nidulans FGSC A4]
ANID_06239	16.81	37.12	1.14287699	1.33E-11	8.20E-11	gi|67540138|ref|XP_663843.1|/0/hypothetical protein AN6239.2 [A. nidulans FGSC A4]
ANID_04574	5.21	11.5	1.14227858	0.000177	0.000561	gi|67536808|ref|XP_662178.1|/0/hypothetical protein AN4574.2 [A. nidulans FGSC A4]
ANID_04058	20	44.09	1.14045148	1.15E-14	9.88E-14	gi|67527358|ref|XP_661662.1|/0/hypothetical protein AN4058.2 [A. nidulans FGSC A4]
ANID_10060	37.98	83.65	1.13912564	1.02E-14	8.81E-14	gi|259489412|tpe|CBF89663.1|/0/TPA: glycogen debranching enzyme Gdb1, putative (AFU_orthologue; AFUA_1G02140) [A. nidulans FGSC A4]
ANID_08713	8.07	17.77	1.1388031	3.14E-06	1.26E-05	gi|259483093|tpe|CBF78182.1|/0/TPA: single-stranded DNA endonuclease (Eurofung) [A. nidulans FGSC A4]
ANID_01932	27.9	61.34	1.13656305	1.55E-13	1.20E-12	gi|67522951|ref|XP_659536.1|/3.44068e-82/hypothetical protein AN1932.2 [A. nidulans FGSC A4]
ANID_08256	51.93	114.14	1.13616434	6.33E-13	4.40E-12	gi|67902538|ref|XP_681525.1|/1.10464e-126/hypothetical protein AN8256.2 [A. nidulans FGSC A4]
ANID_04490	57.98	127.04	1.13165558	7.97E-13	5.49E-12	gi|74595874|sp|Q5B4P0.1|TIM50_EMENI/0/RecName: Full=Mitochondrial import inner membrane translocase subunit tim50; Flags: Precursor
ANID_00832	27.23	59.6	1.13011535	0	0	gi|67517105|ref|XP_658436.1|/0/hypothetical protein AN0832.2 [A. nidulans FGSC A4]
ANID_10198	23.02	50.36	1.12939045	2.37E-13	1.76E-12	gi|259486796|tpe|CBF84945.1|/0/TPA: oligopeptidase family protein (AFU_orthologue; AFUA_8G04730) [A. nidulans FGSC A4]
ANID_02431	11.26	24.57	1.12569103	5.57E-08	2.63E-07	gi|259487844|tpe|CBF86841.1|/0/TPA: Nuclear pore complex protein An-Nup49 (Eurofung) [A. nidulans FGSC A4]
ANID_00752	27.56	60.12	1.12526912	8.93E-14	7.17E-13	gi|259488970|tpe|CBF88854.1|/1.39973e-125/TPA: RNA polymerase subunit (AFU_orthologue; AFUA_1G14110) [A. nidulans FGSC A4]
ANID_06289	8.4	18.3	1.12338242	2.97E-06	1.19E-05	gi|67540238|ref|XP_663893.1|/0/hypothetical protein AN6289.2 [A. nidulans FGSC A4]
ANID_07998	6.89	14.99	1.1214245	2.43E-05	8.67E-05	gi|67902022|ref|XP_681267.1|/0/hypothetical protein AN7998.2 [A. nidulans FGSC A4]
ANID_00589	10.42	22.65	1.12015577	2.05E-07	9.20E-07	gi|74627495|sp|Q5BFU1.1|DBP4_EMENI/0/RecName: Full=ATP-dependent RNA helicase dbp4
ANID_05390	7.06	15.34	1.11955839	2.00E-05	7.20E-05	gi|67538440|ref|XP_662994.1|/0/hypothetical protein AN5390.2 [A. nidulans FGSC A4]
ANID_05629	252.6	548.4	1.11837393	2.20E-12	1.45E-11	gi|67538918|ref|XP_663233.1|/0/NUBM_ASPNG NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor (Complex I-51KD) (CI-51KD) [A. nidulans FGSC A4]
ANID_05910	27.06	58.73	1.1179358	0	0	gi|67539480|ref|XP_663514.1|/0/hypothetical protein AN5910.2 [A. nidulans FGSC A4]
ANID_05812	31.26	67.79	1.11675469	5.46E-13	3.85E-12	gi|67539284|ref|XP_663416.1|/0/hypothetical protein AN5812.2 [A. nidulans FGSC A4]
ANID_05177	15.29	33.11	1.1146786	3.89E-10	2.17E-09	gi|74595339|sp|Q5B2Q3.1|JIP5_EMENI/0/RecName: Full=WD repeat-containing protein jip5
ANID_00936	7.9	17.08	1.11238342	7.45E-06	2.86E-05	gi|259488776|tpe|CBF88493.1|/0/TPA: threonyl-tRNA synthetase (AFU_orthologue; AFUA_1G16210) [A. nidulans FGSC A4]
ANID_00810	11.93	25.79	1.11221773	3.57E-08	1.71E-07	gi|67517059|ref|XP_658414.1|/0/hypothetical protein AN0810.2 [A. nidulans FGSC A4]
ANID_01873	31.6	68.31	1.11217223	1.24E-13	9.74E-13	gi|67522833|ref|XP_659477.1|/5.16927e-80/hypothetical protein AN1873.2 [A. nidulans FGSC A4]
ANID_02442	10.08	21.78	1.11150832	4.20E-07	1.84E-06	gi|259487855|tpe|CBF86861.1|/0/TPA: ubiquitin-protein ligase (Asi3), putative (AFU_orthologue; AFUA_6G10590) [A. nidulans FGSC A4]
ANID_06236	12.44	26.84	1.10939819	1.99E-08	9.73E-08	gi|67540132|ref|XP_663840.1|/0/hypothetical protein AN6236.2 [A. nidulans FGSC A4]
ANID_02063	10.42	22.48	1.10928676	2.85E-07	1.26E-06	gi|67523213|ref|XP_659667.1|/0/hypothetical protein AN2063.2 [A. nidulans FGSC A4]
ANID_06338	31.93	68.83	1.10812496	2.14E-13	1.60E-12	gi|67540336|ref|XP_663942.1|/0/hypothetical protein AN6338.2 [A. nidulans FGSC A4]
ANID_05809	15.8	33.98	1.10476129	3.02E-10	1.70E-09	gi|259480037|tpe|CBF70804.1|/1.17532e-122/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01348	9.41	20.21	1.10280269	1.28E-06	5.33E-06	gi|259488319|tpe|CBF87671.1|/2.41361e-108/TPA: 50S ribosomal protein L17 (AFU_orthologue; AFUA_1G09410) [A. nidulans FGSC A4]
ANID_01000	15.29	32.76	1.09934695	7.45E-10	4.07E-09	gi|67517567|ref|XP_658604.1|/2.84162e-71/hypothetical protein AN1000.2 [A. nidulans FGSC A4]
ANID_09119	8.24	17.6	1.09485919	7.00E-06	2.69E-05	gi|67904264|ref|XP_682388.1|/0/hypothetical protein AN9119.2 [A. nidulans FGSC A4]
ANID_02948	8.24	17.6	1.09485919	7.00E-06	2.69E-05	gi|67524981|ref|XP_660552.1|/1.39322e-156/hypothetical protein AN2948.2 [A. nidulans FGSC A4]
ANID_09049	8.91	18.99	1.09174257	3.19E-06	1.28E-05	gi|67904124|ref|XP_682318.1|/0/hypothetical protein AN9049.2 [A. nidulans FGSC A4]
ANID_03070	128.73	273.94	1.08951163	1.07E-12	7.21E-12	gi|67525225|ref|XP_660674.1|/0/hypothetical protein AN3070.2 [A. nidulans FGSC A4]
ANID_03059	398.14	844.65	1.08507783	0	0	gi|67525203|ref|XP_660663.1|/0/hypothetical protein AN3059.2 [A. nidulans FGSC A4]
ANID_00259	40.17	85.21	1.08490429	5.22E-13	3.70E-12	gi|259489523|tpe|CBF89864.1|/5.44671e-112/TPA: adenylate kinase 2 (AFU_orthologue; AFUA_1G03420) [A. nidulans FGSC A4]

ANID_06824	23.02	48.79	1.08369765	3.39E-13	2.46E-12	gi|67541308|ref|XP_664428.1|/0/hypothetical protein AN6824.2 [A. nidulans FGSC A4]
ANID_06500	2264.46	4799	1.08356676	0	0	gi|67540660|ref|XP_664104.1|/1.68396e-85/hypothetical protein AN6500.2 [A. nidulans FGSC A4]
ANID_10239	33.28	70.23	1.077432	0	0	gi|259487274|tpe|CBF85819.1|/0/TPA: mRNA cap methyltransferase (AFU_orthologue; AFUA_6G07690) [A. nidulans FGSC A4]
ANID_04501	239.49	505.19	1.07686067	1.65E-12	1.10E-11	gi|67534609|ref|XP_662105.1|/3.39027e-99/1433_TRIHA 14-3-3 PROTEIN HOMOLOG (TH1433) [A. nidulans FGSC A4]
ANID_07707	19.66	41.47	1.07680473	9.56E-12	5.96E-11	gi|259484053|tpe|CBF79947.1|/0/TPA: alpha-actinin, sarcomeric (f-actin cross linking protein) (AFU_orthologue; AFUA_5G08300) [A. nidulans FGSC A4]
ANID_04279	30.42	64.13	1.07597925	7.79E-14	6.30E-13	gi|67528146|ref|XP_661883.1|/0/hypothetical protein AN4279.2 [A. nidulans FGSC A4]
ANID_12344	5.55	11.68	1.0734806	0.000325	0.000994	gi|115433062|ref|XP_001216668.1|/5.82229e-35/conserved hypothetical protein [A. terreus NIH2624]
ANID_03630	6.05	12.72	1.07209162	0.000178	0.000564	gi|259481841|tpe|CBF75739.1|/2.55991e-179/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00590	6.39	13.42	1.07049684	0.000119	0.000388	gi|259489142|tpe|CBF89169.1|/4.73256e-62/TPA: DnaJ domain protein (AFU_orthologue; AFUA_6G11060) [A. nidulans FGSC A4]
ANID_02547	7.06	14.81	1.06883155	5.37E-05	0.000183	gi|67524179|ref|XP_660151.1|/0/hypothetical protein AN2547.2 [A. nidulans FGSC A4]
ANID_03030	14.29	29.97	1.06851317	8.58E-09	4.31E-08	gi|67525145|ref|XP_660634.1|/0/hypothetical protein AN3030.2 [A. nidulans FGSC A4]
ANID_06858	7.9	16.55	1.06690666	1.99E-05	7.19E-05	gi|67541376|ref|XP_664462.1|/0/hypothetical protein AN6858.2 [A. nidulans FGSC A4]
ANID_00348	10.25	21.43	1.06400794	1.27E-06	5.29E-06	gi|259489416|tpe|CBF89670.1|/0/TPA: Chromo domain protein Chp1p, putative (AFU_orthologue; AFUA_1G02180) [A. nidulans FGSC A4]
ANID_01965	35.12	73.36	1.06270079	1.34E-13	1.05E-12	gi|259487324|tpe|CBF85908.1|/4.28022e-165/TPA: phosphoribosyl diphosphate synthase isoform 4 (AFU_orthologue; AFUA_4G10790) [A. nidulans FGSC A4]
ANID_10525	114.45	238.56	1.0596347	6.46E-14	5.27E-13	gi|259481211|tpe|CBF74525.1|/1.94251e-38/TPA: hypothetical protein ANIA_10525 [A. nidulans FGSC A4]
ANID_06010	909.88	1896.14	1.0593173	1.45E-11	8.90E-11	gi|74657077|sp|Q5B0C0.1|HSP7M_EMENI/0/RecName: Full=Heat shock 70 kDa protein; Flags: Precursor
ANID_11005	71.43	148.65	1.05731744	1.36E-12	9.10E-12	gi|259484078|tpe|CBF79990.1|/0/TPA: aminopeptidase P, putative (AFU_orthologue; AFUA_5G08050) [A. nidulans FGSC A4]
ANID_04382	41.68	86.61	1.05517833	0	0	gi|259482808|tpe|CBF77641.1|/6.28934e-116/TPA: kinase-related protein (AFU_orthologue; AFUA_4G06710) [A. nidulans FGSC A4]
ANID_12362	10.92	22.65	1.05253819	7.94E-07	3.37E-06	gi|259486827|tpe|CBF85000.1|/3.07005e-112/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07374	10.25	21.26	1.05251769	1.74E-06	7.17E-06	gi|259483266|tpe|CBF78511.1|/1.80446e-113/TPA: acetyltransferase, GNAT family family (AFU_orthologue; AFUA_8G05690) [A. nidulans FGSC A4]
ANID_06507	20.5	42.52	1.05251769	1.27E-11	7.86E-11	gi|67540674|ref|XP_664111.1|/0/hypothetical protein AN6507.2 [A. nidulans FGSC A4]
ANID_00212	14.62	30.32	1.05232644	1.09E-08	5.45E-08	gi|259489578|tpe|CBF89965.1|/1.48226e-129/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_11718	14.12	29.28	1.05217547	1.96E-08	9.57E-08	gi|238486132|ref|XP_002374304.1|/1.76421e-71/caffeine-induced death protein Cid2, putative [A. flavus NRRL3357]
ANID_06342	8.91	18.47	1.05168653	8.38E-06	3.20E-05	gi|67540344|ref|XP_663946.1|/3.57048e-129/hypothetical protein AN6342.2 [A. nidulans FGSC A4]
ANID_03134	94.28	195.17	1.04970765	0	0	gi|259485914|tpe|CBF83342.1|/0/TPA: T-complex protein 1 (Broad) [A. nidulans FGSC A4]
ANID_06631	315.96	651.74	1.04455462	7.75E-12	4.88E-11	gi|67540922|ref|XP_664235.1|/2.3692e-80/hypothetical protein AN6631.2 [A. nidulans FGSC A4]
ANID_12022	12.1	24.92	1.04229702	2.77E-07	1.23E-06	gi|67903202|ref|XP_681857.1|/0/hypothetical protein AN8588.2 [A. nidulans FGSC A4]
ANID_08860	9.24	18.99	1.03927515	7.76E-06	2.97E-05	gi|259482921|tpe|CBF77857.1|/1.57799e-90/TPA: essential NTPase (Eurofung) [A. nidulans FGSC A4]
ANID_01244	9.08	18.65	1.03841143	9.45E-06	3.57E-05	gi|67521570|ref|XP_658848.1|/0/hypothetical protein AN1244.2 [A. nidulans FGSC A4]
ANID_00464	7.39	15.16	1.03662348	6.85E-05	0.000232	gi|67516365|ref|XP_658068.1|/0/hypothetical protein AN0464.2 [A. nidulans FGSC A4]
ANID_06687	23.02	47.22	1.03651021	2.03E-12	1.34E-11	gi|74594196|sp|Q5AYE3.1|POB3_EMENI/0/RecName: Full=FACT complex subunit pob3; AltName: Full=Facilitates chromatin transcription complex subunit pob3
ANID_05601	55.46	113.27	1.03024629	1.87E-13	1.43E-12	gi|259484937|tpe|CBF81585.1|/0/TPA: saccharopine dehydrogenase (NADP+, L-glutamate-forming) (Eurofung) [A. nidulans FGSC A4]
ANID_07439	10.25	20.91	1.02856915	3.26E-06	1.31E-05	gi|259483743|tpe|CBF79384.1|/0/TPA: second largest subunit of DNA polymerase II (Eurofung) [A. nidulans FGSC A4]
ANID_11997	13.28	27.01	1.02423849	1.32E-07	6.03E-07	gi|146322732|ref|XP_749256.2|/0/actin polymerization protein Bzz1 [A. fumigatus Af293]
ANID_01711	68.91	140.11	1.02377467	1.01E-12	6.86E-12	gi|259487052|tpe|CBF85414.1|/0/TPA: nonsense-mediated mRNA decay protein 3 (AFU_orthologue; AFUA_2G16750) [A. nidulans FGSC A4]
ANID_04788	11.76	23.87	1.02131051	7.62E-07	3.25E-06	gi|74595641|sp|Q5B3U2.1|SLU7_EMENI/0/RecName: Full=Pre-mRNA-splicing factor slu7; AltName: Full=Splicing factor sluA
ANID_06940	41.68	84.52	1.01993749	0	0	gi|67541553|ref|XP_664544.1|/0/hypothetical protein AN6940.2 [A. nidulans FGSC A4]
ANID_10857	11.09	22.48	1.01938267	1.67E-06	6.88E-06	gi|259480454|tpe|CBF71601.1|/6.53083e-136/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06013	18.32	37.12	1.01877721	7.26E-10	3.97E-09	gi|67539686|ref|XP_663617.1|/1.59685e-162/hypothetical protein AN6013.2 [A. nidulans FGSC A4]
ANID_04428	12.6	25.44	1.01367494	3.91E-07	1.72E-06	gi|121706666|ref|XP_001271589.1|/0/amino acid transporter [A. clavatus NRRL 1]
ANID_01398	23.02	46.35	1.00968151	8.46E-12	5.31E-11	gi|259488262|tpe|CBF87576.1|/2.33285e-50/TPA: hypothetical protein ANIA_01398 [A. nidulans FGSC A4]

ANID_09511	31.43	63.26	1.00915128	2.86E-13	2.09E-12	gi|75859106|ref|XP_868893.1|/1.33762e-99/hypothetical protein AN9511.2 [A. nidulans FGSC A4]
ANID_04695	1452.89	2912.96	1.00356041	0	0	gi|146324125|ref|XP_753754.2|/3.69776e-117/Woronin body protein HexA [A. fumigatus Af293]
ANID_10732	11.93	23.87	1.00060452	1.16E-06	4.85E-06	gi|259480042|tpe|CBF70814.1|/0/TPA: PX domain protein (AFU_orthologue; AFUA_2G07450) [A. nidulans FGSC A4]
ANID_06798	47.9	0.01	−12.22581	2.73E-84	5.50E-83	gi|67541256|ref|XP_664402.1|/0/hypothetical protein AN6798.2 [A. nidulans FGSC A4]
ANID_00857	9.08	0.01	−9.8265485	1.49E-16	1.39E-15	gi|259488858|tpe|CBF88647.1|/1.01869e-135/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05034	9.08	0.01	−9.8265485	1.49E-16	1.39E-15	gi|67537728|ref|XP_662638.1|/0/hypothetical protein AN5034.2 [A. nidulans FGSC A4]
ANID_03352	8.24	0.01	−9.6865005	4.36E-15	3.82E-14	gi|67525789|ref|XP_660956.1|/0/hypothetical protein AN3352.2 [A. nidulans FGSC A4]
ANID_01509	8.07	0.01	−9.6564249	8.56E-15	7.42E-14	gi|67522104|ref|XP_659113.1|/3.17534e-96/hypothetical protein AN1509.2 [A. nidulans FGSC A4]
ANID_01880	7.39	0.01	−9.5294306	1.27E-13	9.99E-13	gi|67522847|ref|XP_659484.1|/0/hypothetical protein AN1880.2 [A. nidulans FGSC A4]
ANID_04367	6.22	0.01	−9.2807708	1.44E-11	8.87E-11	gi|259482823|tpe|CBF77670.1|/0/TPA: chitin synthase 2 (Eurofung) [A. nidulans FGSC A4]
ANID_06923	5.71	0.01	−9.1573469	1.09E-10	6.34E-10	gi|28475243|emb|CAD59636.1|/0/high-affinity hexose transporter [Emericella nidulans]
ANID_04251	5.55	0.01	−9.116344	2.14E-10	1.22E-09	gi|259481136|tpe|CBF74389.1|/1.06648e-162/TPA: 40S ribosomal protein S2, putative (AFU_orthologue; AFUA_1G06570) [A. nidulans FGSC A4]
ANID_05467	5.21	0.01	−9.0251396	8.27E-10	4.51E-09	gi|67538594|ref|XP_663071.1|/0/hypothetical protein AN5467.2 [A. nidulans FGSC A4]
ANID_00374	5.21	0.01	−9.0251396	8.27E-10	4.50E-09	gi|67516185|ref|XP_657978.1|/0/hypothetical protein AN0374.2 [A. nidulans FGSC A4]
ANID_01659	5.04	0.01	−8.9772799	1.62E-09	8.71E-09	gi|302896522|ref|XP_003047141.1|/1.25469e-175/predicted protein [Nectria haematococca mpVI 77-13-4]
ANID_03251	5.04	0.01	−8.9772799	1.62E-09	8.70E-09	gi|67525587|ref|XP_660855.1|/7.16304e-167/hypothetical protein AN3251.2 [A. nidulans FGSC A4]
ANID_10487	4.87	0.01	−8.927778	3.19E-09	1.66E-08	gi|259481496|tpe|CBF75070.1|/0/TPA: MFS transporter, putative (AFU_orthologue; AFUA_6G08340) [A. nidulans FGSC A4]
ANID_07228	4.71	0.01	−8.8795833	6.27E-09	3.20E-08	gi|67900482|ref|XP_680497.1|/0/hypothetical protein AN7228.2 [A. nidulans FGSC A4]
ANID_05156	4.54	0.01	−8.8265485	1.23E-08	6.12E-08	gi|46811891|gb|AAT02189.1|/9.73786e-140/PHO80-like cyclin [Emericella nidulans]
ANID_08903	4.54	0.01	−8.8265485	1.23E-08	6.11E-08	gi|115449797|ref|XP_001218698.1|/0/conserved hypothetical protein [A. terreus NIH2624]
ANID_07989	4.37	0.01	−8.7714895	2.42E-08	1.18E-07	gi|67902004|ref|XP_681258.1|/2.68913e-173/hypothetical protein AN7989.2 [A. nidulans FGSC A4]
ANID_03934	4.2	0.01	−8.7142455	4.75E-08	2.26E-07	gi|259481491|tpe|CBF75060.1|/2.90936e-78/TPA: ADP-ribosylation factor family protein (AFU_orthologue; AFUA_6G08290) [A. nidulans FGSC A4]
ANID_06424	3.87	0.01	−8.5961898	1.83E-07	8.30E-07	gi|67540508|ref|XP_664028.1|/1.15605e-124/hypothetical protein AN6424.2 [A. nidulans FGSC A4]
ANID_08554	3.87	0.01	−8.5961898	1.83E-07	8.29E-07	gi|67903134|ref|XP_681823.1|/2.53918e-128/hypothetical protein AN8554.2 [A. nidulans FGSC A4]
ANID_10920	3.53	0.01	−8.4635244	7.08E-07	3.03E-06	gi|67900580|ref|XP_680546.1|/0/hypothetical protein AN7277.2 [A. nidulans FGSC A4]
ANID_03769	3.53	0.01	−8.4635244	7.08E-07	3.03E-06	gi|259481680|tpe|CBF75427.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_08850	3.36	0.01	−8.3923174	1.39E-06	5.79E-06	gi|150383302|sp|A2R9P6.2|FYV10_ASPNC/2.13391e-168/RecName: Full=Protein fyv10
ANID_01825	3.36	0.01	−8.3923174	1.39E-06	5.78E-06	gi|67522737|ref|XP_659429.1|/0/hypothetical protein AN1825.2 [A. nidulans FGSC A4]
ANID_08399	3.36	0.01	−8.3923174	1.39E-06	5.78E-06	gi|259484333|tpe|CBF80461.1|/0/TPA: calcium ion P-type ATPase (Eurofung) [A. nidulans FGSC A4]
ANID_02621	3.36	0.01	−8.3923174	1.39E-06	5.78E-06	gi|67524327|ref|XP_660225.1|/0/ACVS_EMENI N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase (Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase) (ACV synthetase) (ACVS) [A. nidulans FGSC A4]
ANID_00549	3.36	0.01	−8.3923174	1.39E-06	5.77E-06	gi|67516535|ref|XP_658153.1|/0/hypothetical protein AN0549.2 [A. nidulans FGSC A4]
ANID_01647	3.19	0.01	−8.3174126	2.73E-06	1.10E-05	gi|67522380|ref|XP_659251.1|/4.16464e-109/hypothetical protein AN1647.2 [A. nidulans FGSC A4]
ANID_00472	3.03	0.01	−8.243174	5.37E-06	2.10E-05	gi|259489279|tpe|CBF89420.1|/0/TPA: putative endo beta 1,3 glucanase, GH81 family (Eurofung) [A. nidulans FGSC A4]
ANID_06617	3.03	0.01	−8.243174	5.37E-06	2.10E-05	gi|259480196|tpe|CBF71106.1|/0/TPA: GAS2 domain protein (AFU_orthologue; AFUA_6G03990) [A. nidulans FGSC A4]
ANID_11597	2.86	0.01	−8.1598713	1.05E-05	3.94E-05	gi|259480977|tpe|CBF74095.1|/1.12741e-24/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00187	2.86	0.01	−8.1598713	1.05E-05	3.94E-05	gi|67515811|ref|XP_657791.1|/6.25955e-19/hypothetical protein AN0187.2 [A. nidulans FGSC A4]
ANID_07884	2.86	0.01	−8.1598713	1.05E-05	3.94E-05	gi|67901794|ref|XP_681153.1|/0/hypothetical protein AN7884.2 [A. nidulans FGSC A4]
ANID_00332	2.86	0.01	−8.1598713	1.05E-05	3.94E-05	gi|67516101|ref|XP_657936.1|/0/hypothetical protein AN0332.2 [A. nidulans FGSC A4]
ANID_09395	2.86	0.01	−8.1598713	1.05E-05	3.93E-05	gi|67904816|ref|XP_682664.1|/0/hypothetical protein AN9395.2 [A. nidulans FGSC A4]
ANID_07391	2.86	0.01	−8.1598713	1.05E-05	3.93E-05	gi|67900808|ref|XP_680660.1|/0/hypothetical protein AN7391.2 [A. nidulans FGSC A4]
ANID_02730	2.69	0.01	−8.0714624	2.07E-05	7.46E-05	gi|82659470|gb|ABB88849.1|/0/sulfate permease [Emericella nidulans]
ANID_03181	2.69	0.01	−8.0714624	2.07E-05	7.45E-05	gi|259485862|tpe|CBF83245.1|/0/TPA: protein kinase domain-containing protein (AFU_orthologue; AFUA_3G13210) [A. nidulans FGSC A4]
ANID_08181	2.69	0.01	−8.0714624	2.07E-05	7.45E-05	gi|67902388|ref|XP_681450.1|/0/hypothetical protein AN8181.2 [A. nidulans FGSC A4]

ANID_07243	2.69	0.01	−8.0714624	2.07E-05	7.44E-05	gi|259483413|tpe|CBF78782.1|/0/TPA: methionine transporter, putative (Eurofung) [A. nidulans FGSC A4]
ANID_04927	2.69	0.01	−8.0714624	2.07E-05	7.44E-05	gi|67537514|ref|XP_662531.1|/1.1548e-23/hypothetical protein AN4927.2 [A. nidulans FGSC A4]
ANID_08132	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|67902290|ref|XP_681401.1|/3.30842e-166/hypothetical protein AN8132.2 [A. nidulans FGSC A4]
ANID_02665	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|259486425|tpe|CBF84251.1|/0/TPA: MFS sugar transporter, putative (AFU_orthologue; AFUA_8G02010) [A. nidulans FGSC A4]
ANID_05395	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|67538450|ref|XP_662999.1|/0/hypothetical protein AN5395.2 [A. nidulans FGSC A4]
ANID_12380	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|115385140|ref|XP_001209117.1|/1.78124e-129/DEAD-box protein 3 [A. terreus NIH2624]
ANID_12264	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|67528476|ref|XP_662040.1|/7.02765e-37/hypothetical protein AN4436.2 [A. nidulans FGSC A4]
ANID_07799	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|259484153|tpe|CBF80131.1|/7.3689e-143/TPA: Uncharacterized oxidoreductase AN7799 (EC 1.-.-.-) [Source:UniProtKB/Swiss-Prot;Acc:Q5AV81] [A. nidulans FGSC A4]
ANID_01748	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|259487093|tpe|CBF85489.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_08327	2.52	0.01	−7.9772799	4.07E-05	0.000141	gi|74656855|sp|Q5ATQ3.1|PGLR_EMENI/0/RecName: Full=Endopolygalacturonase AN8327; AltName: Full=Pectinase AN8327; AltName: Full=Polygalacturonase AN8327; Flags: Precursor
ANID_06757	2.35	0.01	−7.8765169	7.99E-05	0.000267	gi|259480350|tpe|CBF71399.1|/0/TPA: amino acid transporter (Eurofung) [A. nidulans FGSC A4]
ANID_08616	2.35	0.01	−7.8765169	7.99E-05	0.000267	gi|50080882|gb|AAT69749.1|/1.28833e-110/UMTA [Emericella nidulans]
ANID_06398	2.35	0.01	−7.8765169	7.99E-05	0.000267	gi|259479378|tpe|CBF69548.1|/1.39089e-155/TPA: UDP-galactose 4-epimerase, putative (AFU_orthologue; AFUA_7G00360) [A. nidulans FGSC A4]
ANID_08739	2.18	0.01	−7.7681843	0.000157	0.000502	gi|67903504|ref|XP_682008.1|/1.0904e-171/hypothetical protein AN8739.2 [A. nidulans FGSC A4]
ANID_00390	2.18	0.01	−7.7681843	0.000157	0.000501	gi|67516217|ref|XP_657994.1|/1.19856e-139/hypothetical protein AN0390.2 [A. nidulans FGSC A4]
ANID_06677	2.18	0.01	−7.7681843	0.000157	0.000501	gi|259480261|tpe|CBF71230.1|/2.28256e-37/TPA: COMPASS complex subunit Sdc1, putative (AFU_orthologue; AFUA_7G05270) [A. nidulans FGSC A4]
ANID_10435	2.18	0.01	−7.7681843	0.000157	0.000501	gi|259481802|tpe|CBF75663.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_09266	2.18	0.01	−7.7681843	0.000157	0.000501	gi|67904558|ref|XP_682535.1|/4.72901e-108/hypothetical protein AN9266.2 [A. nidulans FGSC A4]
ANID_11867	2.02	0.01	−7.6582115	0.000308	0.000947	gi|259487496|tpe|CBF86220.1|/0/TPA: hypothetical protein ANIA_11867 [A. nidulans FGSC A4]
ANID_07390	2.02	0.01	−7.6582115	0.000308	0.000946	gi|67900806|ref|XP_680659.1|/0/hypothetical protein AN7390.2 [A. nidulans FGSC A4]
ANID_11735	2.02	0.01	−7.6582115	0.000308	0.000946	-
ANID_01251	2.02	0.01	−7.6582115	0.000308	0.000945	gi|259488428|tpe|CBF87853.1|/5.11864e-135/TPA: C2H2 transcription factor (Egr2), putative (AFU_orthologue; AFUA_1G10230) [A. nidulans FGSC A4]
ANID_06057	2.02	0.01	−7.6582115	0.000308	0.000945	gi|67539774|ref|XP_663661.1|/0/hypothetical protein AN6057.2 [A. nidulans FGSC A4]
ANID_01304	32.6	0.7	−5.5413732	4.96E-51	8.16E-50	gi|67521694|ref|XP_658908.1|/6.06397e-49/hypothetical protein AN1304.2 [A. nidulans FGSC A4]
ANID_06633	12.6	0.35	−5.169925	7.70E-20	7.82E-19	gi|67540926|ref|XP_664237.1|/3.2633e-20/hypothetical protein AN6633.2 [A. nidulans FGSC A4]
ANID_08754	12.1	0.35	−5.1115083	5.40E-19	5.34E-18	gi|259483047|tpe|CBF78094.1|/0/TPA: asparagine synthetase (Eurofung) [A. nidulans FGSC A4]
ANID_05353	17.14	0.52	−5.0427117	2.95E-26	3.50E-25	gi|67538366|ref|XP_662957.1|/5.90869e-124/hypothetical protein AN5353.2 [A. nidulans FGSC A4]
ANID_08451	22.02	0.7	−4.9753157	3.21E-33	4.31E-32	gi|67902928|ref|XP_681720.1|/0/hypothetical protein AN8451.2 [A. nidulans FGSC A4]
ANID_05447	585.19	18.65	−4.9716576	0	0	gi|67538554|ref|XP_663051.1|/0/hypothetical protein AN5447.2 [A. nidulans FGSC A4]
ANID_08314	81.34	2.61	−4.9618433	########	########	gi|67902654|ref|XP_681583.1|/0/hypothetical protein AN8314.2 [A. nidulans FGSC A4]
ANID_04336	60.5	2.27	−4.7361709	1.01E-86	2.08E-85	gi|259482856|tpe|CBF77734.1|/1.61889e-132/TPA: L-arabinitol 4-dehydrogenase (AFU_orthologue; AFUA_1G11020) [A. nidulans FGSC A4]
ANID_02021	127.73	4.88	−4.7100725	########	########	gi|67523129|ref|XP_659625.1|/0/hypothetical protein AN2021.2 [A. nidulans FGSC A4]
ANID_06888	8.57	0.35	−4.6138684	4.05E-13	2.92E-12	gi|67541436|ref|XP_664492.1|/1.51689e-154/hypothetical protein AN6888.2 [A. nidulans FGSC A4]
ANID_06657	1699.6	78.94	−4.4282949	0	0	gi|67540974|ref|XP_664261.1|/5.30156e-35/hypothetical protein AN6657.2 [A. nidulans FGSC A4]
ANID_01536	7.06	0.35	−4.3342414	1.23E-10	7.13E-10	gi|259486861|tpe|CBF85064.1|/0/TPA: b-zip transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_10626	10.25	0.52	−4.3009685	7.17E-15	6.22E-14	gi|67537828|ref|XP_662688.1|/0/hypothetical protein AN5084.2 [A. nidulans FGSC A4]
ANID_02844	37.81	1.92	−4.2995896	1.18E-51	1.97E-50	gi|67524773|ref|XP_660448.1|/6.77414e-67/hypothetical protein AN2844.2 [A. nidulans FGSC A4]
ANID_03638	6.72	0.35	−4.2630344	4.34E-10	2.41E-09	gi|67526361|ref|XP_661242.1|/2.68906e-172/hypothetical protein AN3638.2 [A. nidulans FGSC A4]
ANID_02033	9.75	0.52	−4.2288187	4.72E-14	3.88E-13	gi|67523153|ref|XP_659637.1|/0/hypothetical protein AN2033.2 [A. nidulans FGSC A4]
ANID_10507	63.86	3.49	−4.1936136	7.79E-85	1.57E-83	gi|259481278|tpe|CBF74647.1|/5.35274e-73/TPA: heat shock protein Hsp20/Hsp26, putative (AFU_orthologue; AFUA_5G10270) [A. nidulans FGSC A4]

ANID_01608	1732.88	96.19	−4.171141	0	0	gi|67522302|ref|XP_659212.1|/3.99572e-52/hypothetical protein AN1608.2 [A. nidulans FGSC A4]
ANID_07557	36.64	2.09	−4.1318447	9.06E-49	1.46E-47	gi|67901140|ref|XP_680826.1|/0/hypothetical protein AN7557.2 [A. nidulans FGSC A4]
ANID_08136	6.05	0.35	−4.1115083	5.33E-09	2.73E-08	gi|67902298|ref|XP_681405.1|/0/hypothetical protein AN8136.2 [A. nidulans FGSC A4]
ANID_01510	802.49	46.53	−4.1082503	0	0	gi|259486833|tpe|CBF85011.1|/0/TPA: oxidoreductin (AFU_orthologue; AFUA_8G05140) [A. nidulans FGSC A4]
ANID_02578	4109.27	239.09	−4.1032564	0	0	gi|67524241|ref|XP_660182.1|/1.41019e-148/hypothetical protein AN2578.2 [A. nidulans FGSC A4]
ANID_05145	322.51	18.82	−4.0990054	0	0	gi|67537950|ref|XP_662749.1|/1.43862e-56/hypothetical protein AN5145.2 [A. nidulans FGSC A4]
ANID_00913	5.88	0.35	−4.0703893	9.95E-09	4.96E-08	gi|259488800|tpe|CBF88537.1|/3.15176e-137/TPA: CDP-diacylglycerol-inositol 3-phosphatidyltransferase PIS (AFU_orthologue; AFUA_1G15790) [A. nidulans FGSC A4]
ANID_04070	58.32	3.49	−4.0626918	6.39E-76	1.24E-74	gi|259481342|tpe|CBF74767.1|/2.28806e-108/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_08198	5.71	0.35	−4.0280639	1.86E-08	9.09E-08	gi|67902422|ref|XP_681467.1|/7.46801e-125/hypothetical protein AN8198.2 [A. nidulans FGSC A4]
ANID_04940	728.38	44.79	−4.0234427	0	0	gi|67537540|ref|XP_662544.1|/0/hypothetical protein AN4940.2 [A. nidulans FGSC A4]
ANID_03381	19.83	1.22	−4.0227316	1.57E-26	1.89E-25	gi|21724725|gb|AAM75418.1|/0/fatty acid synthase beta subunit [Emericella nidulans]
ANID_08135	11.26	0.7	−4.0077081	1.46E-15	1.31E-14	gi|67902296|ref|XP_681404.1|/0/hypothetical protein AN8135.2 [A. nidulans FGSC A4]
ANID_00553	178.99	11.15	−4.0047634	########	########	gi|67516543|ref|XP_658157.1|/1.21218e-85/hypothetical protein AN0553.2 [A. nidulans FGSC A4]
ANID_08767	5.55	0.35	−3.9870609	3.45E-08	1.66E-07	gi|259483032|tpe|CBF78067.1|/0/TPA: ankyrin repeat protein (AFU_orthologue; AFUA_3G02830) [A. nidulans FGSC A4]
ANID_11985	5.55	0.35	−3.9870609	3.45E-08	1.66E-07	gi|259480406|tpe|CBF71507.1|/1.16147e-141/TPA: ThiJ/PfpI family protein (AFU_orthologue; AFUA_3G01210) [A. nidulans FGSC A4]
ANID_11048	54.79	3.49	−3.9726137	2.76E-70	5.23E-69	gi|259480860|tpe|CBF73884.1|/6.91678e-72/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_03982	10.92	0.7	−3.9634741	5.03E-15	4.38E-14	gi|67527099|ref|XP_661586.1|/0/hypothetical protein AN3982.2 [A. nidulans FGSC A4]
ANID_10921	73.44	4.71	−3.9627671	1.59E-93	3.36E-92	gi|259483375|tpe|CBF78714.1|/0/TPA: NACHT and WD domain protein (AFU_orthologue; AFUA_3G07460) [A. nidulans FGSC A4]
ANID_00773	83.53	5.4	−3.9512631	########	########	gi|67516983|ref|XP_658377.1|/0/hypothetical protein AN0773.2 [A. nidulans FGSC A4]
ANID_02555	400.99	25.97	−3.9486483	0	0	gi|259487988|tpe|CBF87091.1|/0/TPA: serine carboxypeptidase (Eurofung) [A. nidulans FGSC A4]
ANID_01646	126.38	8.19	−3.9477609	########	########	gi|67522378|ref|XP_659250.1|/0/hypothetical protein AN1646.2 [A. nidulans FGSC A4]
ANID_12070	271.76	17.77	−3.9348175	0	0	gi|145248714|ref|XP_001400696.1|/0/glutamyl-tRNA(gln) amidotransferase subunit A [A. niger CBS 513.88]
ANID_01879	309.91	20.39	−3.9259156	0	0	gi|238487738|ref|XP_002375107.1|/0/WD repeat protein [A. flavus NRRL3357]
ANID_00950	13.11	0.87	−3.9135085	1.29E-17	1.23E-16	gi|67517355|ref|XP_658554.1|/7.27199e-48/hypothetical protein AN0950.2 [A. nidulans FGSC A4]
ANID_07274	7.56	0.52	−3.8618027	1.51E-10	8.70E-10	gi|67900574|ref|XP_680543.1|/0/hypothetical protein AN7274.2 [A. nidulans FGSC A4]
ANID_06753	7.56	0.52	−3.8618027	1.51E-10	8.69E-10	gi|67541166|ref|XP_664357.1|/0/hypothetical protein AN6753.2 [A. nidulans FGSC A4]
ANID_11795	7.56	0.52	−3.8618027	1.51E-10	8.69E-10	gi|67522755|ref|XP_659438.1|/7.40113e-152/hypothetical protein AN1834.2 [A. nidulans FGSC A4]
ANID_03387	30.25	2.09	−3.8553603	1.39E-38	1.98E-37	gi|259485627|tpe|CBF82810.1|/0/TPA: integral membrane protein (AFU_orthologue; AFUA_2G12640) [A. nidulans FGSC A4]
ANID_08134	9.92	0.7	−3.8249133	2.01E-13	1.53E-12	gi|67902294|ref|XP_681403.1|/0/hypothetical protein AN8134.2 [A. nidulans FGSC A4]
ANID_08211	4.87	0.35	−3.7984949	4.08E-07	1.79E-06	gi|67902448|ref|XP_681480.1|/0/hypothetical protein AN8211.2 [A. nidulans FGSC A4]
ANID_04480	31.26	2.27	−3.7835536	2.68E-39	3.87E-38	gi|67531754|ref|XP_662084.1|/1.3255e-114/hypothetical protein AN4480.2 [A. nidulans FGSC A4]
ANID_05364	14.45	1.05	−3.7826083	7.07E-19	6.96E-18	gi|259485192|tpe|CBF82031.1|/0/TPA: von Willebrand domain protein (AFU_orthologue; AFUA_4G01160) [A. nidulans FGSC A4]
ANID_07891	11.93	0.87	−3.7774348	9.34E-16	8.49E-15	gi|259480639|tpe|CBF73467.1|/5.24922e-165/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07392	9.58	0.7	−3.7745988	6.84E-13	4.74E-12	gi|242774345|ref|XP_002478423.1|/0/choline transporter Hnm1, putative [Talaromyces stipitatus ATCC 10500]
ANID_08982	7.06	0.52	−3.7630847	9.49E-10	5.14E-09	gi|67903990|ref|XP_682251.1|/0/hypothetical protein AN8982.2 [A. nidulans FGSC A4]
ANID_05650	104.03	7.67	−3.7616292	########	########	gi|259484879|tpe|CBF81477.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07225	51.59	3.83	−3.7516751	1.85E-63	3.37E-62	gi|67900476|ref|XP_680494.1|/0/hypothetical protein AN7225.2 [A. nidulans FGSC A4]
ANID_04026	6.89	0.52	−3.7279205	1.75E-09	9.33E-09	gi|67527229|ref|XP_661630.1|/0/hypothetical protein AN4026.2 [A. nidulans FGSC A4]
ANID_04127	763.84	57.68	−3.7271274	0	0	gi|259481279|tpe|CBF74648.1|/9.8695e-129/TPA: hypothetical protein ANIA_04127 [A. nidulans FGSC A4]
ANID_11246	50.59	3.83	−3.7234359	7.01E-62	1.26E-60	gi|115386816|ref|XP_001209949.1|/2.17543e-104/predicted protein [A. terreus NIH2624]
ANID_04135	367.38	28.23	−3.7019721	0	0	gi|67527716|ref|XP_661739.1|/0/hypothetical protein AN4135.2 [A. nidulans FGSC A4]
ANID_05755	4.54	0.35	−3.6972655	1.39E-06	5.78E-06	gi|259484767|tpe|CBF81270.1|/1.90573e-151/TPA: regulator of G protein signaling domain protein (AFU_orthologue; AFUA_6G06860) [A. nidulans FGSC A4]
ANID_08412	4.54	0.35	−3.6972655	1.39E-06	5.78E-06	gi|259484347|tpe|CBF80487.1|/0/TPA: hybrid PKS-NRPS (Eurofung) [A. nidulans FGSC A4]

ANID_06792	4.54	0.35	−3.6972655	1.39E-06	5.77E-06	gi|259480386|tpe|CBF71469.1|/0/TPA: glycerol-3-phosphate dehydrogenase (Eurofung) [A. nidulans FGSC A4]
ANID_08640	22.52	1.74	−3.6940476	3.76E-28	4.62E-27	gi|67903306|ref|XP_681909.1|/7.20562e-35/hypothetical protein AN8640.2 [A. nidulans FGSC A4]
ANID_10299	439.14	33.98	−3.6919232	0	0	gi|67523803|ref|XP_659961.1|/0/hypothetical protein AN2357.2 [A. nidulans FGSC A4]
ANID_06954	8.91	0.7	−3.6699986	7.79E-12	4.90E-11	gi|67541581|ref|XP_664558.1|/1.76245e-87/hypothetical protein AN6954.2 [A. nidulans FGSC A4]
ANID_08337	13.11	1.05	−3.6422065	9.06E-17	8.49E-16	gi|67902700|ref|XP_681606.1|/0/hypothetical protein AN8337.2 [A. nidulans FGSC A4]
ANID_06683	4.37	0.35	−3.6422065	2.55E-06	1.03E-05	gi|67541026|ref|XP_664287.1|/0/hypothetical protein AN6683.2 [A. nidulans FGSC A4]
ANID_02286	484.69	39.91	−3.6022401	0	0	gi|67523661|ref|XP_659890.1|/1.46746e-162/ADH3_EMENI Alcohol dehydrogenase III (ADH III) [A. nidulans FGSC A4]
ANID_04081	159.66	13.24	−3.5920279	########	########	gi|259481331|tpe|CBF74747.1|/3.18547e-49/TPA: cysteine dioxygenase Cdo1, putative (AFU_orthologue; AFUA_1G05570) [A. nidulans FGSC A4]
ANID_02392	4.2	0.35	−3.5849625	4.67E-06	1.84E-05	gi|67523873|ref|XP_659996.1|/6.80151e-135/hypothetical protein AN2392.2 [A. nidulans FGSC A4]
ANID_00335	20.84	1.74	−3.5821961	1.55E-25	1.81E-24	gi|259489432|tpe|CBF89700.1|/3.59234e-145/TPA: Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:P78618] [A. nidulans FGSC A4]
ANID_08122	60	5.05	−3.5706072	1.07E-70	2.05E-69	gi|259480886|tpe|CBF73930.1|/0/TPA: MFS multidrug transporter, putative (AFU_orthologue; AFUA_5G02700) [A. nidulans FGSC A4]
ANID_06786	16.47	1.39	−3.5666838	2.24E-20	2.30E-19	gi|67541232|ref|XP_664390.1|/1.51726e-116/hypothetical protein AN6786.2 [A. nidulans FGSC A4]
ANID_02571	14.45	1.22	−3.5661164	4.72E-18	4.58E-17	gi|67524227|ref|XP_660175.1|/2.41555e-49/hypothetical protein AN2571.2 [A. nidulans FGSC A4]
ANID_08801	68.06	5.75	−3.5651733	6.56E-80	1.30E-78	gi|67903628|ref|XP_682070.1|/1.57585e-159/hypothetical protein AN8801.2 [A. nidulans FGSC A4]
ANID_01609	18.49	1.57	−3.5579088	1.07E-22	1.16E-21	gi|67522304|ref|XP_659213.1|/1.17661e-91/hypothetical protein AN1609.2 [A. nidulans FGSC A4]
ANID_01682	8.24	0.7	−3.5572175	8.70E-11	5.08E-10	gi|67522451|ref|XP_659286.1|/4.43486e-54/hypothetical protein AN1682.2 [A. nidulans FGSC A4]
ANID_11200	32.27	2.79	−3.5318566	2.23E-38	3.17E-37	gi|259485344|tpe|CBF82290.1|/1.38056e-98/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06862	26.22	2.27	−3.5299035	1.92E-31	2.52E-30	gi|67541384|ref|XP_664466.1|/1.70712e-52/hypothetical protein AN6862.2 [A. nidulans FGSC A4]
ANID_01144	4.03	0.35	−3.525353	8.55E-06	3.26E-05	gi|259488540|tpe|CBF88056.1|/3.07681e-135/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10287	4.03	0.35	−3.525353	8.55E-06	3.25E-05	gi|259487737|tpe|CBF86641.1|/0/TPA: 67 kDa myosin-cross-reactive antigen family protein (AFU_orthologue; AFUA_5G09970) [A. nidulans FGSC A4]
ANID_10838	4.03	0.35	−3.525353	8.55E-06	3.25E-05	gi|259480246|tpe|CBF71201.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01378	1519.27	132.26	−3.5219296	0	0	gi|67521842|ref|XP_658982.1|/1.93152e-48/hypothetical protein AN1378.2 [A. nidulans FGSC A4]
ANID_09297	548.89	48.44	−3.5022463	0	0	gi|259488131|tpe|CBF87353.1|/0/TPA: 67 kDa myosin-cross-reactive antigen family protein (AFU_orthologue; AFUA_3G03570) [A. nidulans FGSC A4]
ANID_05550	5.88	0.52	−3.4992326	6.54E-08	3.08E-07	gi|67538760|ref|XP_663154.1|/3.44762e-142/hypothetical protein AN5550.2 [A. nidulans FGSC A4]
ANID_05449	33.44	2.96	−3.4979058	2.14E-39	3.10E-38	gi|67538558|ref|XP_663053.1|/0/hypothetical protein AN5449.2 [A. nidulans FGSC A4]
ANID_02331	11.76	1.05	−3.4854268	1.10E-14	9.43E-14	gi|259487727|tpe|CBF86622.1|/5.23674e-170/TPA: Pectin lyase [Source:UniProtKB/TrEMBL;Acc:Q1HFU6] [A. nidulans FGSC A4]
ANID_02648	23.19	2.09	−3.471928	1.40E-27	1.71E-26	gi|67524381|ref|XP_660252.1|/0/hypothetical protein AN2648.2 [A. nidulans FGSC A4]
ANID_01226	3.87	0.35	−3.4669067	1.56E-05	5.70E-05	gi|67518136|ref|XP_658830.1|/0/hypothetical protein AN1226.2 [A. nidulans FGSC A4]
ANID_11904	3.87	0.35	−3.4669067	1.56E-05	5.70E-05	gi|67541146|ref|XP_664347.1|/1.01045e-107/hypothetical protein AN6743.2 [A. nidulans FGSC A4]
ANID_03384	3.87	0.35	−3.4669067	1.56E-05	5.70E-05	gi|67525853|ref|XP_660988.1|/0/hypothetical protein AN3384.2 [A. nidulans FGSC A4]
ANID_00365	7.73	0.7	−3.4650416	5.24E-10	2.89E-09	gi|67516167|ref|XP_657969.1|/2.55054e-54/hypothetical protein AN0365.2 [A. nidulans FGSC A4]
ANID_10080	5.71	0.52	−3.4569072	1.19E-07	5.48E-07	gi|259489298|tpe|CBF89451.1|/0/TPA: siderophore biosynthesis protein, putative (AFU_orthologue; AFUA_1G04450) [A. nidulans FGSC A4]
ANID_06525	473.26	43.22	−3.452862	0	0	gi|67540710|ref|XP_664129.1|/0/FDH_EMENI Probable formate dehydrogenase (NAD-dependent formate dehydrogenase) (FDH) [A. nidulans FGSC A4]
ANID_00186	283.35	25.97	−3.4476673	0	0	gi|67515809|ref|XP_657790.1|/5.32482e-164/hypothetical protein AN0186.2 [A. nidulans FGSC A4]
ANID_03796	208.56	19.34	−3.4308028	########	########	gi|67526677|ref|XP_661400.1|/8.89686e-16/hypothetical protein AN3796.2 [A. nidulans FGSC A4]
ANID_10537	14.79	1.39	−3.4114653	8.57E-18	8.25E-17	gi|259481087|tpe|CBF74298.1|/0/TPA: YT521-B-like splicing factor, putative (AFU_orthologue; AFUA_7G03780) [A. nidulans FGSC A4]
ANID_02765	3.7	0.35	−3.4020984	2.84E-05	0.0001	gi|67524615|ref|XP_660369.1|/2.65965e-17/H1_EMENI Histone H1 [A. nidulans FGSC A4]
ANID_06230	3.7	0.35	−3.4020984	2.84E-05	0.0001	gi|3411262|gb|AAC31205.1|/0/Medusa [Emericella nidulans]
ANID_08647	7.39	0.7	−3.4001475	1.72E-09	9.20E-09	gi|259483136|tpe|CBF78263.1|/9.43444e-159/TPA: formate/nitrate family transporter (Eurofung) [A. nidulans FGSC A4]
ANID_03717	14.62	1.39	−3.3947865	1.55E-17	1.47E-16	gi|259481739|tpe|CBF75543.1|/1.53073e-141/TPA: SAM-dependent methyltransferase (Eurofung) [A. nidulans FGSC A4]

<table>
<tr><td>ANID_03354</td><td>7.23</td><td>0.7</td><td>–3.3685688</td><td>3.11E-09</td><td>1.62E-08</td><td>gi|67525793|ref|XP_660958.1|/1.51049e-175/hypothetical protein AN3354.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08989</td><td>12.6</td><td>1.22</td><td>–3.3684707</td><td>3.26E-15</td><td>2.88E-14</td><td>gi|259486561|tpe|CBF84508.1|/1.10078e-59/TPA: glyoxalase family protein (AFU_orthologue; AFUA_5G14830) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01443</td><td>86.72</td><td>8.54</td><td>–3.3440568</td><td>6.01E-96</td><td>1.29E-94</td><td>gi|67521972|ref|XP_659047.1|/0/hypothetical protein AN1443.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02010</td><td>3.53</td><td>0.35</td><td>–3.3342414</td><td>5.15E-05</td><td>0.000176</td><td>gi|67523107|ref|XP_659614.1|/0/hypothetical protein AN2010.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10148</td><td>8.74</td><td>0.87</td><td>–3.328546</td><td>8.29E-11</td><td>4.87E-10</td><td>gi|38489215|gb|AAR21293.1|/3.95217e-149/ChpA [Emericella nidulans]</td></tr>
<tr><td>ANID_08461</td><td>281.5</td><td>28.06</td><td>–3.326548</td><td>########</td><td>########</td><td>gi|67902948|ref|XP_681730.1|/6.32139e-174/hypothetical protein AN8461.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_09470</td><td>450.4</td><td>44.96</td><td>–3.3244929</td><td>0</td><td>0</td><td>gi|75859024|ref|XP_868852.1|/6.86217e-166/URIC_EMENI Uricase (Urate oxidase) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08238</td><td>17.14</td><td>1.74</td><td>–3.3002079</td><td>7.02E-20</td><td>7.13E-19</td><td>gi|67902502|ref|XP_681507.1|/1.25513e-92/hypothetical protein AN8238.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01262</td><td>1216.93</td><td>123.55</td><td>–3.3000793</td><td>0</td><td>0</td><td>gi|67521610|ref|XP_658866.1|/8.85442e-152/hypothetical protein AN1262.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07832</td><td>50.59</td><td>5.23</td><td>–3.2739694</td><td>1.40E-55</td><td>2.40E-54</td><td>gi|67901690|ref|XP_681101.1|/0/hypothetical protein AN7832.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03679</td><td>31.93</td><td>3.31</td><td>–3.2700094</td><td>1.39E-35</td><td>1.91E-34</td><td>gi|259481784|tpe|CBF75629.1|/2.68465e-161/TPA: oxidoreductase, short-chain dehydrogenase/reductase family (AFU_orthologue; AFUA_4G05870) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05611</td><td>287.05</td><td>29.8</td><td>–3.2679178</td><td>########</td><td>########</td><td>gi|67538882|ref|XP_663215.1|/2.1437e-115/hypothetical protein AN5611.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_01001</td><td>63.19</td><td>6.62</td><td>–3.2547931</td><td>1.17E-68</td><td>2.17E-67</td><td>gi|67517569|ref|XP_658605.1|/0/hypothetical protein AN1001.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03961</td><td>23.19</td><td>2.44</td><td>–3.2485498</td><td>4.39E-26</td><td>5.18E-25</td><td>gi|67527007|ref|XP_661565.1|/0/hypothetical protein AN3961.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01601</td><td>73.78</td><td>7.84</td><td>–3.2343042</td><td>1.94E-79</td><td>3.85E-78</td><td>gi|67522288|ref|XP_659205.1|/0/hypothetical protein AN1601.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02249</td><td>27.56</td><td>2.96</td><td>–3.2189068</td><td>1.77E-30</td><td>2.29E-29</td><td>gi|259487640|tpe|CBF86464.1|/6.66737e-164/TPA: integral membrane protein (AFU_orthologue; AFUA_5G06670) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01181</td><td>12.94</td><td>1.39</td><td>–3.2186808</td><td>5.36E-15</td><td>4.66E-14</td><td>gi|18693015|gb|AAL73118.1|/0/ammonium permease MEPA [Emericella nidulans]</td></tr>
<tr><td>ANID_00918</td><td>9.75</td><td>1.05</td><td>–3.2150129</td><td>1.29E-11</td><td>7.96E-11</td><td>gi|259488795|tpe|CBF88528.1|/0/TPA: conserved hypothetical protein similar to alpha-hydroxylase Scs7 (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02287</td><td>138.15</td><td>14.99</td><td>–3.2041633</td><td>########</td><td>########</td><td>gi|67523663|ref|XP_659891.1|/0/hypothetical protein AN2287.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03053</td><td>129.07</td><td>14.12</td><td>–3.1923417</td><td>########</td><td>########</td><td>gi|67525191|ref|XP_660657.1|/0/hypothetical protein AN3053.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04105</td><td>6.39</td><td>0.7</td><td>–3.1903891</td><td>5.84E-08</td><td>2.76E-07</td><td>gi|67527656|ref|XP_661709.1|/0/hypothetical protein AN4105.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02792</td><td>49.24</td><td>5.4</td><td>–3.1887994</td><td>7.48E-53</td><td>1.25E-51</td><td>gi|259486285|tpe|CBF84002.1|/1.13221e-62/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02067</td><td>3.19</td><td>0.35</td><td>–3.1881296</td><td>0.000168</td><td>0.000533</td><td>gi|74681330|sp|Q5BBL3.1|STE20_EMENI/0/RecName: Full=Serine/threonine-protein kinase ste20</td></tr>
<tr><td>ANID_11094</td><td>107.9</td><td>11.85</td><td>–3.1867359</td><td>########</td><td>########</td><td>gi|259483131|tpe|CBF78253.1|/0/TPA: hypothetical oxidoreductase (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00399</td><td>538.97</td><td>59.25</td><td>–3.1853179</td><td>0</td><td>0</td><td>gi|17981044|gb|AAL50818.1|AF453778_1/0/high affinity nitrate transporter NrtB [Emericella nidulans]</td></tr>
<tr><td>ANID_06084</td><td>398.47</td><td>43.91</td><td>–3.1818497</td><td>0</td><td>0</td><td>gi|67539828|ref|XP_663688.1|/0/hypothetical protein AN6084.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07814</td><td>4.71</td><td>0.52</td><td>–3.1791435</td><td>4.09E-06</td><td>1.62E-05</td><td>gi|67901654|ref|XP_681083.1|/0/STCK_EMENI Putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11060</td><td>4.71</td><td>0.52</td><td>–3.1791435</td><td>4.09E-06</td><td>1.62E-05</td><td>gi|223635089|sp|P0C8Q1.1|CFD1_EMENI/1.10534e-147/RecName: Full=Cytosolic Fe-S cluster assembly factor cfd1; AltName: Full=Cytosolic Fe-S cluster-deficient protein 1</td></tr>
<tr><td>ANID_01972</td><td>25.21</td><td>2.79</td><td>–3.1756591</td><td>1.12E-27</td><td>1.38E-26</td><td>gi|67523031|ref|XP_659576.1|/5.06929e-163/hypothetical protein AN1972.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08137</td><td>40.67</td><td>4.53</td><td>–3.166382</td><td>1.23E-43</td><td>1.85E-42</td><td>gi|67902300|ref|XP_681406.1|/0/hypothetical protein AN8137.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02488</td><td>4276.66</td><td>476.61</td><td>–3.1656034</td><td>0</td><td>0</td><td>gi|67524061|ref|XP_660092.1|/2.59793e-82/hypothetical protein AN2488.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06660</td><td>6.22</td><td>0.7</td><td>–3.1514878</td><td>1.04E-07</td><td>4.84E-07</td><td>gi|67540980|ref|XP_664264.1|/1.1384e-83/hypothetical protein AN6660.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02101</td><td>3.03</td><td>0.35</td><td>–3.113891</td><td>0.000301</td><td>0.000926</td><td>gi|67523289|ref|XP_659705.1|/0/hypothetical protein AN2101.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08694</td><td>3.03</td><td>0.35</td><td>–3.113891</td><td>0.000301</td><td>0.000926</td><td>gi|67903414|ref|XP_681963.1|/8.83464e-108/hypothetical protein AN8694.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10029</td><td>3.03</td><td>0.35</td><td>–3.113891</td><td>0.000301</td><td>0.000925</td><td>gi|259489547|tpe|CBF89908.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03649</td><td>3.03</td><td>0.35</td><td>–3.113891</td><td>0.000301</td><td>0.000925</td><td>gi|259481817|tpe|CBF75693.1|/0/TPA: 50S ribosomal protein L2 (AFU_orthologue; AFUA_4G12170) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05079</td><td>434.77</td><td>50.36</td><td>–3.1099022</td><td>0</td><td>0</td><td>gi|67537818|ref|XP_662683.1|/1.96019e-68/hypothetical protein AN5079.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04481</td><td>28.57</td><td>3.31</td><td>–3.1095979</td><td>1.40E-30</td><td>1.82E-29</td><td>gi|259482696|tpe|CBF77420.1|/0/TPA: monocarboxylate transporter (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10431</td><td>17.81</td><td>2.09</td><td>–3.0911127</td><td>1.77E-19</td><td>1.77E-18</td><td>gi|259481855|tpe|CBF75766.1|/1.87202e-134/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06319</td><td>7.39</td><td>0.87</td><td>–3.0864871</td><td>8.65E-09</td><td>4.34E-08</td><td>gi|259479465|tpe|CBF69711.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05844</td><td>13.28</td><td>1.57</td><td>–3.0804187</td><td>8.26E-15</td><td>7.17E-14</td><td>gi|67539348|ref|XP_663448.1|/2.1225e-43/hypothetical protein AN5844.2 [A. nidulans FGSC A4]</td></tr>
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ANID_02942	4.37	0.52	−3.0710498	1.30E-05	4.80E-05	gi|67524969|ref|XP_660546.1|/6.0965e-131/hypothetical protein AN2942.2 [A. nidulans FGSC A4]
ANID_09296	133.1	15.86	−3.0690459	########	########	gi|67904618|ref|XP_682565.1|/0/hypothetical protein AN9296.2 [A. nidulans FGSC A4]
ANID_02535	27.56	3.31	−3.0576728	4.27E-29	5.38E-28	gi|67524155|ref|XP_660139.1|/2.09821e-38/hypothetical protein AN2535.2 [A. nidulans FGSC A4]
ANID_10556	7.23	0.87	−3.0549083	1.53E-08	7.56E-08	gi|259482742|tpe|CBF77512.1|/0/TPA: ubiquitin chain assembly factor (Eurofung) [A. nidulans FGSC A4]
ANID_10296	273.6	33.11	−3.0467293	########	########	gi|259487758|tpe|CBF86680.1|/0/TPA: FAD dependent oxidoreductase, putative (AFU_orthologue; AFUA_7G05070) [A. nidulans FGSC A4]
ANID_07683	188.23	23.18	−3.0215441	########	########	gi|255944661|ref|XP_002563098.1|/1.12766e-50/Pc20g05640 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_09501	11.26	1.39	−3.01805	1.66E-12	1.10E-11	gi|75859086|ref|XP_868883.1|/0/predicted protein [A. nidulans FGSC A4]
ANID_00640	8.4	1.05	−3	1.28E-09	6.87E-09	gi|259489093|tpe|CBF89079.1|/0/TPA: sphinganine hydroxylase BasA (Eurofung) [A. nidulans FGSC A4]
ANID_05335	148.23	18.65	−2.9905899	########	########	gi|259485224|tpe|CBF82081.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_07648	5.55	0.7	−2.9870609	1.04E-06	4.37E-06	gi|67901322|ref|XP_680917.1|/0/hypothetical protein AN7648.2 [A. nidulans FGSC A4]
ANID_04206	302.01	38.34	−2.9776741	########	########	gi|259481187|tpe|CBF74482.1|/0/TPA: DnaJ domain protein (AFU_orthologue; AFUA_1G06020) [A. nidulans FGSC A4]
ANID_07856	8.24	1.05	−2.972255	2.25E-09	1.19E-08	gi|67901738|ref|XP_681125.1|/0/hypothetical protein AN7856.2 [A. nidulans FGSC A4]
ANID_02343	73.61	9.41	−2.9676351	4.87E-73	9.40E-72	gi|67523775|ref|XP_659947.1|/2.56548e-113/hypothetical protein AN2343.2 [A. nidulans FGSC A4]
ANID_03543	13.44	1.74	−2.9493739	2.11E-14	1.79E-13	gi|67526171|ref|XP_661147.1|/0/hypothetical protein AN3543.2 [A. nidulans FGSC A4]
ANID_08966	26.89	3.49	−2.9457708	1.84E-27	2.24E-26	gi|259486585|tpe|CBF84552.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02395	8.07	1.05	−2.9421793	3.96E-09	2.05E-08	gi|67523879|ref|XP_659999.1|/0/hypothetical protein AN2395.2 [A. nidulans FGSC A4]
ANID_03898	5.38	0.7	−2.9421793	1.83E-06	7.53E-06	gi|67526881|ref|XP_661502.1|/3.03766e-133/hypothetical protein AN3898.2 [A. nidulans FGSC A4]
ANID_11751	5.38	0.7	−2.9421793	1.83E-06	7.53E-06	gi|259483839|tpe|CBF79559.1|/1.22565e-95/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_08899	5.38	0.7	−2.9421793	1.83E-06	7.53E-06	gi|67903824|ref|XP_682168.1|/0/hypothetical protein AN8899.2 [A. nidulans FGSC A4]
ANID_05435	48.07	6.27	−2.9385995	9.14E-48	1.45E-46	gi|67538530|ref|XP_663039.1|/0/hypothetical protein AN5435.2 [A. nidulans FGSC A4]
ANID_01596	22.69	2.96	−2.9383875	2.61E-23	2.87E-22	gi|67522278|ref|XP_659200.1|/0/hypothetical protein AN1596.2 [A. nidulans FGSC A4]
ANID_02760	161.17	21.09	−2.9339522	########	########	gi|259486323|tpe|CBF84069.1|/0/TPA: glyoxalase family protein (AFU_orthologue; AFUA_3G06020) [A. nidulans FGSC A4]
ANID_10166	41.01	5.4	−2.9249444	8.59E-41	1.26E-39	gi|259488588|tpe|CBF88144.1|/0/TPA: PQ loop repeat protein (AFU_orthologue; AFUA_1G11900) [A. nidulans FGSC A4]
ANID_01163	370.58	48.97	−2.9198149	0	0	gi|259488519|tpe|CBF88019.1|/0/TPA: oligomeric mitochondrial matrix chaperone (Eurofung) [A. nidulans FGSC A4]
ANID_12321	6.55	0.87	−2.9124076	1.48E-07	6.75E-07	gi|67527598|ref|XP_661680.1|/1.13192e-150/hypothetical protein AN4076.2 [A. nidulans FGSC A4]
ANID_02704	3.87	0.52	−2.89575	7.20E-05	0.000243	gi|67524493|ref|XP_660308.1|/0/hypothetical protein AN2704.2 [A. nidulans FGSC A4]
ANID_01540	30.92	4.18	−2.8869655	9.86E-31	1.28E-29	gi|259486865|tpe|CBF85071.1|/2.16123e-155/TPA: integral membrane protein (AFU_orthologue; AFUA_8G05510) [A. nidulans FGSC A4]
ANID_06281	7.73	1.05	−2.8800791	1.22E-08	6.04E-08	gi|67540222|ref|XP_663885.1|/3.41612e-146/hypothetical protein AN6281.2 [A. nidulans FGSC A4]
ANID_02888	32.94	4.53	−2.8622576	2.27E-32	3.02E-31	gi|67524861|ref|XP_660492.1|/0/hypothetical protein AN2888.2 [A. nidulans FGSC A4]
ANID_03639	28.91	4.01	−2.8498945	1.80E-28	2.23E-27	gi|259481830|tpe|CBF75718.1|/0/TPA: hypothetical protein similar to E2 component of 2-oxo acid dehydrogenase complex, dihydrolipoamide transacylase (Eurofung) [A. nidulans FGSC A4]
ANID_03567	7.56	1.05	−2.8479969	2.12E-08	1.03E-07	gi|259481910|tpe|CBF75872.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05276	8.74	1.22	−2.8407521	1.76E-09	9.38E-09	gi|67538212|ref|XP_662880.1|/0/hypothetical protein AN5276.2 [A. nidulans FGSC A4]
ANID_06789	14.96	2.09	−2.8395353	2.49E-15	2.21E-14	gi|67541238|ref|XP_664393.1|/0/hypothetical protein AN6789.2 [A. nidulans FGSC A4]
ANID_00768	9.92	1.39	−2.8352552	1.47E-10	8.44E-10	gi|259488954|tpe|CBF88824.1|/0/TPA: Fasciclin domain family protein (AFU_orthologue; AFUA_1G14300) [A. nidulans FGSC A4]
ANID_08130	31.09	4.36	−2.8340506	2.36E-30	3.04E-29	gi|115437692|ref|XP_001217875.1|/0/NAD(P) transhydrogenase, mitochondrial precursor [A. terreus NIH2624]
ANID_01148	57.14	8.02	−2.8328269	1.76E-54	2.99E-53	gi|67517955|ref|XP_658752.1|/0/hypothetical protein AN1148.2 [A. nidulans FGSC A4]
ANID_02666	3.7	0.52	−2.8309417	0.000126	0.000408	gi|67524417|ref|XP_660270.1|/5.34998e-169/hypothetical protein AN2666.2 [A. nidulans FGSC A4]
ANID_00980	8.57	1.22	−2.8124141	3.06E-09	1.59E-08	gi|300681009|sp|Q5BEQ0.2|BGALB_EMENI/0/RecName: Full=Probable beta-galactosidase B; AltName: Full=Lactase B; Flags: Precursor
ANID_08907	602.16	85.74	−2.8121066	0	0	gi|259486658|tpe|CBF84688.1|/2.6546e-170/TPA: C-4 methyl sterol oxidase, putative (AFU_orthologue; AFUA_8G02440) [A. nidulans FGSC A4]
ANID_00214	23.19	3.31	−2.8085997	8.63E-23	9.41E-22	gi|67515865|ref|XP_657818.1|/0/hypothetical protein AN0214.2 [A. nidulans FGSC A4]
ANID_05568	134.95	19.34	−2.8027653	########	########	gi|259484972|tpe|CBF81649.1|/0/TPA: Leucine Rich Repeat domain protein (AFU_orthologue; AFUA_4G11700) [A. nidulans FGSC A4]
ANID_11491	4.87	0.7	−2.7984949	9.87E-06	3.72E-05	-

ANID_00764	6.05	0.87	−2.7978478	7.90E-07	3.36E-06	gi|67516965|ref|XP_658368.1|/0/hypothetical protein AN0764.2 [A. nidulans FGSC A4]
ANID_06821	56.8	8.19	−2.7939556	2.13E-53	3.59E-52	gi|67541302|ref|XP_664425.1|/4.76771e-128/hypothetical protein AN6821.2 [A. nidulans FGSC A4]
ANID_00400	20.5	2.96	−2.7919548	3.47E-20	3.55E-19	gi|67516237|ref|XP_658004.1|/3.23537e-82/hypothetical protein AN0400.2 [A. nidulans FGSC A4]
ANID_07357	203.52	29.45	−2.788831	########	########	gi|67900740|ref|XP_680626.1|/4.52412e-98/hypothetical protein AN7357.2 [A. nidulans FGSC A4]
ANID_02404	67.56	9.93	−2.7663037	1.52E-62	2.75E-61	gi|67523897|ref|XP_660008.1|/0/hypothetical protein AN2404.2 [A. nidulans FGSC A4]
ANID_03083	3.53	0.52	−2.7630847	0.000221	0.000691	gi|259485969|tpe|CBF83438.1|/0/TPA: FAD binding domain protein (AFU_orthologue; AFUA_3G02770) [A. nidulans FGSC A4]
ANID_01640	3.53	0.52	−2.7630847	0.000221	0.000691	gi|67522366|ref|XP_659244.1|/0/hypothetical protein AN1640.2 [A. nidulans FGSC A4]
ANID_03670	3.53	0.52	−2.7630847	0.000221	0.000691	gi|67526425|ref|XP_661274.1|/5.71888e-149/hypothetical protein AN3670.2 [A. nidulans FGSC A4]
ANID_06788	3.53	0.52	−2.7630847	0.000221	0.000691	gi|67541236|ref|XP_664392.1|/0/hypothetical protein AN6788.2 [A. nidulans FGSC A4]
ANID_07867	3.53	0.52	−2.7630847	0.000221	0.00069	gi|67901760|ref|XP_681136.1|/0/hypothetical protein AN7867.2 [A. nidulans FGSC A4]
ANID_08195	3.53	0.52	−2.7630847	0.000221	0.00069	gi|67902416|ref|XP_681464.1|/5.82861e-40/hypothetical protein AN8195.2 [A. nidulans FGSC A4]
ANID_11886	50.75	7.49	−2.7603702	2.82E-47	4.45E-46	gi|67522393|ref|XP_659257.1|/0/hypothetical protein AN1653.2 [A. nidulans FGSC A4]
ANID_06750	44.7	6.62	−2.7553717	9.45E-42	1.40E-40	gi|67541160|ref|XP_664354.1|/0/hypothetical protein AN6750.2 [A. nidulans FGSC A4]
ANID_04539	241.67	36.07	−2.7441671	########	########	gi|259482631|tpe|CBF77296.1|/6.37719e-56/TPA: Yippee zinc-binding protein Moh1, putative (AFU_orthologue; AFUA_2G02820) [A. nidulans FGSC A4]
ANID_12135	16.3	2.44	−2.7399189	4.87E-16	4.46E-15	-
ANID_04052	27.9	4.18	−2.7386903	1.91E-26	2.29E-25	gi|259481360|tpe|CBF74803.1|/0/TPA: beta-1,3-exoglucosidase (Eurofung) [A. nidulans FGSC A4]
ANID_02225	270.91	40.6	−2.738262	########	########	gi|67523539|ref|XP_659829.1|/3.96205e-174/hypothetical protein AN2225.2 [A. nidulans FGSC A4]
ANID_05585	63.7	9.58	−2.7331958	2.59E-58	4.55E-57	gi|259484953|tpe|CBF81614.1|/0/TPA: 3-ketosteroid reductase (AFU_orthologue; AFUA_4G11500) [A. nidulans FGSC A4]
ANID_00677	750.9	113.44	−2.7266914	0	0	gi|67516791|ref|XP_658281.1|/1.01112e-33/hypothetical protein AN0677.2 [A. nidulans FGSC A4]
ANID_08537	65.38	9.93	−2.7189838	1.73E-59	3.06E-58	gi|259484488|tpe|CBF80752.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05021	118.15	17.95	−2.7185639	########	########	gi|259482103|tpe|CBF76263.1|/0/TPA: trehalose synthase (Ccg-9), putative (AFU_orthologue; AFUA_3G12100) [A. nidulans FGSC A4]
ANID_00168	5.71	0.87	−2.7144034	2.38E-06	9.66E-06	gi|67515773|ref|XP_657772.1|/0/hypothetical protein AN0168.2 [A. nidulans FGSC A4]
ANID_04224	6.89	1.05	−2.7141147	1.93E-07	8.71E-07	gi|259481168|tpe|CBF74448.1|/0/TPA: DUF887 domain protein (AFU_orthologue; AFUA_1G06320) [A. nidulans FGSC A4]
ANID_07539	2302.27	351.83	−2.7101066	0	0	gi|67901104|ref|XP_680808.1|/2.94018e-30/hypothetical protein AN7539.2 [A. nidulans FGSC A4]
ANID_05076	10.25	1.57	−2.7067874	1.90E-10	1.08E-09	gi|67537812|ref|XP_662680.1|/0/hypothetical protein AN5076.2 [A. nidulans FGSC A4]
ANID_07111	62.18	9.58	−2.6983531	3.32E-56	5.73E-55	gi|259483566|tpe|CBF79061.1|/0/TPA: peroxisomal multifunctional beta-oxidation protein (MFP), putative (AFU_orthologue; AFUA_4G03900) [A. nidulans FGSC A4]
ANID_08643	4.54	0.7	−2.6972655	2.98E-05	0.000105	gi|67903312|ref|XP_681912.1|/0/hypothetical protein AN8643.2 [A. nidulans FGSC A4]
ANID_03160	4.54	0.7	−2.6972655	2.98E-05	0.000105	gi|67525405|ref|XP_660764.1|/0/hypothetical protein AN3160.2 [A. nidulans FGSC A4]
ANID_09375	7.9	1.22	−2.6949715	2.74E-08	1.33E-07	gi|67904776|ref|XP_682644.1|/0/hypothetical protein AN9375.2 [A. nidulans FGSC A4]
ANID_10877	28.23	4.36	−2.6948291	2.48E-26	2.95E-25	gi|259483706|tpe|CBF79315.1|/0/TPA: ubiquitin fusion degradation protein (Ufd1), putative (AFU_orthologue; AFUA_4G04640) [A. nidulans FGSC A4]
ANID_01037	27.06	4.18	−2.694587	2.85E-25	3.31E-24	gi|259488665|tpe|CBF88287.1|/0/TPA: Oleate delta-12 desaturase [Source:UniProtKB/TrEMBL;Acc:Q9HF05] [A. nidulans FGSC A4]
ANID_02474	189.41	29.45	−2.685173	########	########	gi|67524035|ref|XP_660078.1|/1.94278e-147/hypothetical protein AN2474.2 [A. nidulans FGSC A4]
ANID_09523	5.55	0.87	−2.6734005	4.11E-06	1.62E-05	gi|75859130|ref|XP_868905.1|/0/hypothetical protein AN9523.2 [A. nidulans FGSC A4]
ANID_10815	21.01	3.31	−2.666173	1.00E-19	1.02E-18	gi|259479301|tpe|CBF69410.1|/6.26746e-167/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01542	9.92	1.57	−2.6595756	5.62E-10	3.10E-09	gi|74598113|sp|Q5BD38.1|XGCA_EMENI/0/RecName: Full=Oligoxyloglucan-reducing end-specific xyloglucanase; Short=OREX; Flags: Precursor
ANID_07949	9.92	1.57	−2.6595756	5.62E-10	3.09E-09	gi|67901924|ref|XP_681218.1|/0/hypothetical protein AN7949.2 [A. nidulans FGSC A4]
ANID_04482	9.92	1.57	−2.6595756	5.62E-10	3.09E-09	gi|145238452|ref|XP_001391873.1|/0/sugar transporter [A. niger CBS 513.88]
ANID_08980	17.48	2.79	−2.6473682	1.56E-16	1.46E-15	gi|71041483|gb|AAZ20474.1|/4.82131e-116/AlcM [Emericella nidulans]
ANID_05822	4.37	0.7	−2.6422065	5.15E-05	0.000176	gi|818863|gb|AAA67069.1|/0/AnkA [Emericella nidulans]
ANID_04247	6.55	1.05	−2.6411056	5.74E-07	2.48E-06	gi|67528016|ref|XP_661851.1|/0/hypothetical protein AN4247.2 [A. nidulans FGSC A4]
ANID_00377	9.75	1.57	−2.6346377	9.64E-10	5.22E-09	gi|67516191|ref|XP_657981.1|/0/hypothetical protein AN0377.2 [A. nidulans FGSC A4]
ANID_01015	158.48	25.62	−2.6289584	########	########	gi|259488688|tpe|CBF88330.1|/0/TPA: hypothetical protein similar to glycogen phosphorylase 1 (Broad) [A. nidulans FGSC A4]
ANID_04497	5.38	0.87	−2.6285189	7.07E-06	2.72E-05	gi|259482680|tpe|CBF77388.1|/0/TPA: MIZ zinc finger domain protein (AFU_orthologue; AFUA_2G03350) [A. nidulans FGSC A4]
ANID_04120	10.76	1.74	−2.6285189	1.39E-10	8.00E-10	gi|259481287|tpe|CBF74663.1|/0/TPA: oxidoreductase 2-nitropropane dioxygenase family, putative (AFU_orthologue; AFUA_2G17430) [A. nidulans FGSC A4]

ANID_10981	5.38	0.87	−2.6285189	7.07E-06	2.71E-05	gi|67901346|ref|XP_680929.1|/0/hypothetical protein AN7660.2 [A. nidulans FGSC A4]
ANID_00224	32.1	5.23	−2.6176904	7.63E-29	9.53E-28	gi|259489562|tpe|CBF89935.1|/0/TPA: membrane dipeptidase GliJ (AFU_orthologue; AFUA_6G09650) [A. nidulans FGSC A4]
ANID_01975	126.72	20.74	−2.6111564	########	########	gi|259487335|tpe|CBF85929.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_11039	9.58	1.57	−2.6092611	1.65E-09	8.81E-09	gi|259480805|tpe|CBF73782.1|/5.02292e-123/TPA: hypothetical protein ANIA_11039 [A. nidulans FGSC A4]
ANID_03368	24.37	4.01	−2.6034321	4.04E-22	4.33E-21	gi|298351836|sp|Q5B7W2.2|MANBB_EMENI/0/RecName: Full=Beta-mannosidase B; AltName: Full=Mannanase B; Short=Mannase B; Flags: Precursor
ANID_11008	32.77	5.4	−2.6013444	3.28E-29	4.14E-28	gi|259484101|tpe|CBF80034.1|/0/TPA: Squalene epoxidase [Source:UniProtKB/TrEMBL;Acc:Q27PP1] [A. nidulans FGSC A4]
ANID_07469	29.58	4.88	−2.599669	1.70E-26	2.03E-25	gi|74593591|sp|Q5AW61.1|RIFK_EMENI/2.07922e-60/RecName: Full=Riboflavin kinase; AltName: Full=Flavin mononucleotide kinase 1
ANID_00699	7.39	1.22	−2.5986932	1.38E-07	6.33E-07	gi|67516835|ref|XP_658303.1|/0/hypothetical protein AN0699.2 [A. nidulans FGSC A4]
ANID_08815	3083.76	511.11	−2.5929848	0	0	gi|115400189|ref|XP_001215683.1|/4.95009e-150/conserved hypothetical protein [A. terreus NIH2624]
ANID_01434	21.01	3.49	−2.5897772	3.63E-19	3.60E-18	gi|67521954|ref|XP_659038.1|/0/hypothetical protein AN1434.2 [A. nidulans FGSC A4]
ANID_07454	4.2	0.7	−2.5849625	8.87E-05	0.000295	gi|67900934|ref|XP_680723.1|/0/hypothetical protein AN7454.2 [A. nidulans FGSC A4]
ANID_02012	28.23	4.71	−2.5834302	3.30E-25	3.81E-24	gi|67523111|ref|XP_659616.1|/5.30694e-158/hypothetical protein AN2012.2 [A. nidulans FGSC A4]
ANID_07026	10.42	1.74	−2.5821961	4.04E-10	2.25E-09	gi|259483662|tpe|CBF79235.1|/6.08845e-178/TPA: hypothetical protein ANIA_07026 [A. nidulans FGSC A4]
ANID_06636	58.15	9.76	−2.5748261	4.26E-50	6.93E-49	gi|67540932|ref|XP_664240.1|/0/hypothetical protein AN6636.2 [A. nidulans FGSC A4]
ANID_01387	158.65	26.66	−2.5730988	########	########	gi|67521860|ref|XP_658991.1|/3.82406e-157/hypothetical protein AN1387.2 [A. nidulans FGSC A4]
ANID_03882	19.66	3.31	−2.5703602	7.10E-18	6.86E-17	gi|67526849|ref|XP_661486.1|/0/hypothetical protein AN3882.2 [A. nidulans FGSC A4]
ANID_10945	7.23	1.22	−2.5671145	2.36E-07	1.06E-06	gi|259483827|tpe|CBF79536.1|/2.19516e-148/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06758	16.47	2.79	−2.5615035	3.81E-15	3.35E-14	gi|67541176|ref|XP_664362.1|/0/hypothetical protein AN6758.2 [A. nidulans FGSC A4]
ANID_05226	740.14	125.47	−2.5604557	0	0	gi|146335232|gb|ABQ23355.1|/1.08503e-119/acetate permease [Emericella nidulans]
ANID_06908	109.74	18.82	−2.5437509	8.09E-92	1.70E-90	gi|259480511|tpe|CBF71710.1|/0/TPA: FHA domain protein (AFU_orthologue; AFUA_5G13560) [A. nidulans FGSC A4]
ANID_06352	24.37	4.18	−2.5435314	1.42E-21	1.49E-20	gi|74594465|sp|Q5AZC8.1|ABNB_EMENI/0/RecName: Full=Arabinan endo-1,5-alpha-L-arabinosidase B; AltName: Full=Endo-1,5-alpha-L-arabinanase B; Short=ABN B; Flags: Precursor
ANID_08019	28.4	4.88	−2.5409379	6.80E-25	7.79E-24	gi|70990006|ref|XP_749852.1|/0/Pfs, NACHT and Ankyrin domain protein [A. fumigatus Af293]
ANID_07150	22.18	3.83	−2.5338431	1.10E-19	1.11E-18	gi|67541973|ref|XP_664754.1|/0/hypothetical protein AN7150.2 [A. nidulans FGSC A4]
ANID_03100	24.2	4.18	−2.5334322	2.39E-21	2.50E-20	gi|67525285|ref|XP_660704.1|/3.19161e-21/hypothetical protein AN3100.2 [A. nidulans FGSC A4]
ANID_07484	14.12	2.44	−2.532787	5.12E-13	3.64E-12	gi|74593578|sp|Q5AW46.1|Y7484_EMENI/1.07132e-109/RecName: Full=Uncharacterized protein AN7484
ANID_07712	7.06	1.22	−2.532787	4.02E-07	1.77E-06	gi|169778157|ref|XP_001823544.1|/3.45273e-115/NUDIX family hydrolase [A. oryzae RIB40]
ANID_08905	9.08	1.57	−2.5319277	8.12E-09	4.10E-08	gi|259486660|tpe|CBF84691.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_08123	11.09	1.92	−2.5300811	1.68E-10	9.61E-10	gi|15811616|gb|AAL09028.1|AF416568_1/0/fructosyl amino acid oxidase [Emericella nidulans]
ANID_11207	6.05	1.05	−2.5265458	2.87E-06	1.16E-05	gi|259488099|tpe|CBF87295.1|/8.41421e-145/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10689	6.05	1.05	−2.5265458	2.87E-06	1.16E-05	gi|259485033|tpe|CBF81759.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02001	4.03	0.7	−2.525353	0.000152	0.000486	gi|67523089|ref|XP_659605.1|/0/hypothetical protein AN2001.2 [A. nidulans FGSC A4]
ANID_07232	48.07	8.36	−2.523562	9.24E-41	1.35E-39	gi|115395874|ref|XP_001213576.1|/1.68166e-111/conserved hypothetical protein [A. terreus NIH2624]
ANID_04500	2739.57	477.83	−2.5193801	0	0	gi|67534358|ref|XP_662104.1|/1.56243e-37/hypothetical protein AN4500.2 [A. nidulans FGSC A4]
ANID_04136	13.95	2.44	−2.5153121	8.66E-13	5.93E-12	gi|67527718|ref|XP_661740.1|/0/hypothetical protein AN4136.2 [A. nidulans FGSC A4]
ANID_02255	9.92	1.74	−2.5112528	1.97E-09	1.05E-08	gi|67523599|ref|XP_659859.1|/0/hypothetical protein AN2255.2 [A. nidulans FGSC A4]
ANID_02978	739.64	130	−2.5083116	0	0	gi|67525041|ref|XP_660582.1|/1.85925e-63/hypothetical protein AN2978.2 [A. nidulans FGSC A4]
ANID_05688	205.03	36.07	−2.5069637	########	########	gi|67539036|ref|XP_663292.1|/0/hypothetical protein AN5688.2 [A. nidulans FGSC A4]
ANID_04654	164.2	28.93	−2.5048159	########	########	gi|67536968|ref|XP_662258.1|/0/hypothetical protein AN4654.2 [A. nidulans FGSC A4]
ANID_11541	26.72	4.71	−2.504121	3.71E-23	4.07E-22	gi|259483661|tpe|CBF79233.1|/3.12121e-27/TPA: hypothetical protein ANIA_11541 [A. nidulans FGSC A4]
ANID_05069	188.73	33.46	−2.4958144	########	########	gi|67537798|ref|XP_662673.1|/6.22904e-161/hypothetical protein AN5069.2 [A. nidulans FGSC A4]
ANID_03265	58.99	10.46	−2.4955876	4.36E-49	7.03E-48	gi|74611882|sp|Q6SCL4.1|APYA_EMENI/4.70376e-167/RecName: Full=HECT-type ubiquitin ligase-interacting protein apyA; AltName: Full=Arrestin and PY motif-containing protein A

ANID_12163	21.51	3.83	−2.4895912	8.87E-19	8.72E-18	gi|119498065|ref|XP_001265790.1|/3.17963e-69/hypothetical protein NFIA_034610 [Neosartorya fischeri NRRL 181]
ANID_05716	144.7	25.79	−2.4881812	########	########	gi|259484807|tpe|CBF81345.1|/0/TPA: CBS and PB1 domain protein (AFU_orthologue; AFUA_1G06780) [A. nidulans FGSC A4]
ANID_04050	4.87	0.87	−2.4848345	3.52E-05	0.000123	gi|259481362|tpe|CBF74807.1|/0/TPA: cytoplasmic aldehyde dehydrogenase (Eurofung) [A. nidulans FGSC A4]
ANID_04051	29.24	5.23	−2.4830605	5.75E-25	6.60E-24	gi|67527339|ref|XP_661655.1|/1.49474e-144/hypothetical protein AN4051.2 [A. nidulans FGSC A4]
ANID_04361	13.61	2.44	−2.479714	2.46E-12	1.62E-11	gi|5051964|gb|AAD38380.1|AF148535_1/1.43012e-102/positive sulphur transcription regulator METR [Emericella nidulans]
ANID_02277	13.61	2.44	−2.479714	2.46E-12	1.61E-11	gi|67523643|ref|XP_659881.1|/1.86271e-101/hypothetical protein AN2277.2 [A. nidulans FGSC A4]
ANID_05649	31.09	5.58	−2.4781136	2.13E-26	2.54E-25	gi|259484880|tpe|CBF81479.1|/1.5573e-162/TPA: PE repeat family protein (AFU_orthologue; AFUA_4G13630) [A. nidulans FGSC A4]
ANID_04909	34.79	6.27	−2.4721353	2.92E-29	3.70E-28	gi|67537478|ref|XP_662513.1|/2.78429e-78/hypothetical protein AN4909.2 [A. nidulans FGSC A4]
ANID_03752	154.45	27.88	−2.4698374	########	########	gi|67526589|ref|XP_661356.1|/0/hypothetical protein AN3752.2 [A. nidulans FGSC A4]
ANID_05052	28.91	5.23	−2.4666858	1.62E-24	1.84E-23	gi|67537764|ref|XP_662656.1|/0/hypothetical protein AN5052.2 [A. nidulans FGSC A4]
ANID_01072	6.72	1.22	−2.4615801	1.15E-06	4.84E-06	gi|67517783|ref|XP_658676.1|/4.23453e-85/hypothetical protein AN1072.2 [A. nidulans FGSC A4]
ANID_11095	9.58	1.74	−2.4609384	5.61E-09	2.88E-08	gi|259483194|tpe|CBF78373.1|/6.21224e-179/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06477	27.73	5.05	−2.4570923	1.83E-23	2.03E-22	gi|67540614|ref|XP_664081.1|/0/hypothetical protein AN6477.2 [A. nidulans FGSC A4]
ANID_04762	1915.39	349.4	−2.4546867	0	0	gi|67537184|ref|XP_662366.1|/8.45699e-37/hypothetical protein AN4762.2 [A. nidulans FGSC A4]
ANID_07278	50.59	9.24	−2.4528875	1.63E-41	2.39E-40	gi|259483374|tpe|CBF78712.1|/0/TPA: glutamate decarboxylase (Eurofung) [A. nidulans FGSC A4]
ANID_00132	38.15	6.97	−2.4524525	1.13E-31	1.50E-30	gi|67515701|ref|XP_657736.1|/0/hypothetical protein AN0132.2 [A. nidulans FGSC A4]
ANID_05895	455.28	83.3	−2.4503657	0	0	gi|259479937|tpe|CBF70616.1|/0/TPA: secretory pathway gdp dissociation inhibitor (AFU_orthologue; AFUA_2G11150) [A. nidulans FGSC A4]
ANID_06113	20	3.66	−2.4500844	2.85E-17	2.69E-16	gi|67539886|ref|XP_663717.1|/0/hypothetical protein AN6113.2 [A. nidulans FGSC A4]
ANID_06915	49.41	9.06	−2.4472201	1.82E-40	2.65E-39	gi|67541490|ref|XP_664519.1|/0/hypothetical protein AN6915.2 [A. nidulans FGSC A4]
ANID_10217	32.1	5.92	−2.4389042	1.04E-26	1.25E-25	gi|259486898|tpe|CBF85130.1|/8.29045e-180/TPA: aldo-keto reductase (AKR13), puatative (AFU_orthologue; AFUA_7G00700) [A. nidulans FGSC A4]
ANID_02385	30.25	5.58	−2.4385981	2.81E-25	3.26E-24	gi|74597471|sp|Q5BAP5.1|EGLX_EMENI/0/RecName: Full=Endo-1,3(4)-beta-glucanase xgeA; AltName: Full=Mixed-linked glucanase xgeA; Flags: Precursor
ANID_04766	9.41	1.74	−2.4351074	9.44E-09	4.71E-08	gi|67537192|ref|XP_662370.1|/3.05033e-155/hypothetical protein AN4766.2 [A. nidulans FGSC A4]
ANID_03214	9.41	1.74	−2.4351074	9.44E-09	4.71E-08	gi|67525513|ref|XP_660818.1|/0/hypothetical protein AN3214.2 [A. nidulans FGSC A4]
ANID_03190	16.97	3.14	−2.4341501	8.94E-15	7.73E-14	gi|67525465|ref|XP_660794.1|/0/hypothetical protein AN3190.2 [A. nidulans FGSC A4]
ANID_03282	13.11	2.44	−2.4257146	1.17E-11	7.24E-11	gi|67525649|ref|XP_660886.1|/3.67399e-102/hypothetical protein AN3282.2 [A. nidulans FGSC A4]
ANID_11169	23.36	4.36	−2.4216402	1.06E-19	1.07E-18	gi|259485431|tpe|CBF82447.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_00935	109.91	20.56	−2.4184105	8.08E-87	1.67E-85	gi|67517324|ref|XP_658539.1|/1.12344e-54/hypothetical protein AN0935.2 [A. nidulans FGSC A4]
ANID_10151	10.25	1.92	−2.4164457	2.28E-09	1.20E-08	gi|119482764|ref|XP_001261410.1|/0/fungal specific transcription factor, putative [Neosartorya fischeri NRRL 181]
ANID_10843	37.98	7.14	−2.4112439	6.11E-31	7.98E-30	gi|259480245|tpe|CBF71200.1|/2.74117e-124/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02289	48.07	9.06	−2.4075538	1.09E-38	1.56E-37	gi|67523667|ref|XP_659893.1|/0/hypothetical protein AN2289.2 [A. nidulans FGSC A4]
ANID_05099	198.31	37.47	−2.4039495	########	########	gi|259484543|tpe|CBF80856.1|/0/TPA: SWIRM domain protein Fun19, putative (AFU_orthologue; AFUA_1G07750) [A. nidulans FGSC A4]
ANID_04131	6.39	1.22	−2.3889348	3.27E-06	1.31E-05	gi|259481273|tpe|CBF74637.1|/0/TPA: sodium ion/proton exchanger (Eurofung) [A. nidulans FGSC A4]
ANID_09378	6.39	1.22	−2.3889348	3.27E-06	1.31E-05	gi|67904782|ref|XP_682647.1|/1.51403e-113/hypothetical protein AN9378.2 [A. nidulans FGSC A4]
ANID_00919	259.65	49.66	−2.3864121	########	########	gi|67517288|ref|XP_658523.1|/0/hypothetical protein AN0919.2 [A. nidulans FGSC A4]
ANID_08018	15.46	2.96	−2.3848712	2.84E-13	2.08E-12	gi|259480769|tpe|CBF73715.1|/2.1158e-167/TPA: auxin efflux transporter family protein (Eurofung) [A. nidulans FGSC A4]
ANID_06255	4.54	0.87	−2.383605	0.000101	0.000331	gi|67540170|ref|XP_663859.1|/4.94048e-28/hypothetical protein AN6255.2 [A. nidulans FGSC A4]
ANID_06999	4.54	0.87	−2.383605	0.000101	0.00033	gi|67541671|ref|XP_664603.1|/0/hypothetical protein AN6999.2 [A. nidulans FGSC A4]
ANID_03433	4.54	0.87	−2.383605	0.000101	0.00033	gi|67525951|ref|XP_661037.1|/1.2487e-153/hypothetical protein AN3433.2 [A. nidulans FGSC A4]
ANID_09339	20.84	4.01	−2.3776811	2.24E-17	2.13E-16	gi|67904704|ref|XP_682608.1|/0/CATB_EMENI Catalase B [A. nidulans FGSC A4]
ANID_05130	2241.27	432.17	−2.3746456	0	0	gi|259484575|tpe|CBF80916.1|/0/TPA: coproporphyrinogen III oxidase, putative (AFU_orthologue; AFUA_1G07480) [A. nidulans FGSC A4]
ANID_01827	11.76	2.27	−2.3731239	2.24E-10	1.27E-09	gi|67522741|ref|XP_659431.1|/0/hypothetical protein AN1827.2 [A. nidulans FGSC A4]
ANID_04074	33.11	6.45	−2.3598959	1.56E-26	1.87E-25	gi|67527594|ref|XP_661678.1|/0/hypothetical protein AN4074.2 [A. nidulans FGSC A4]

ANID_12054	5.38	1.05	−2.3572168	2.33E-05	8.33E-05	gi|242810020|ref|XP_002485495.1|/0/transcriptional corepressor Cyc8, putative [Talaromyces stipitatus ATCC 10500]
ANID_06168	14.29	2.79	−2.3566689	3.22E-12	2.09E-11	gi|24637711|gb|AAN63880.1|/0/NADP-dependent malic enzyme [Emericella nidulans]
ANID_03396	30.08	5.92	−2.3451355	4.66E-24	5.24E-23	gi|67525877|ref|XP_661000.1|/0/hypothetical protein AN3396.2 [A. nidulans FGSC A4]
ANID_02622	9.75	1.92	−2.3442959	1.06E-08	5.29E-08	gi|67524329|ref|XP_660226.1|/0/IPNS_EMENI Isopenicillin N synthetase (IPNS) (Isopenicillin N synthase) [A. nidulans FGSC A4]
ANID_10467	44.2	8.71	−2.3433017	1.27E-34	1.74E-33	gi|259481683|tpe|CBF75432.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_00620	82.69	16.38	−2.3357775	3.83E-63	6.97E-62	gi|67516677|ref|XP_658224.1|/7.19064e-167/hypothetical protein AN0620.2 [A. nidulans FGSC A4]
ANID_05015	7.9	1.57	−2.3310881	3.08E-07	1.36E-06	gi|67537690|ref|XP_662619.1|/1.57418e-38/CONX_NEUCR CONIDIATION-SPECIFIC PROTEIN 10 [A. nidulans FGSC A4]
ANID_08362	4.37	0.87	−2.328546	0.000169	0.000536	gi|67902750|ref|XP_681631.1|/3.72024e-141/hypothetical protein AN8362.2 [A. nidulans FGSC A4]
ANID_10844	4.37	0.87	−2.328546	0.000169	0.000536	gi|67541100|ref|XP_664324.1|/0/hypothetical protein AN6720.2 [A. nidulans FGSC A4]
ANID_07780	19.16	3.83	−2.3226813	1.14E-15	1.04E-14	gi|67901586|ref|XP_681049.1|/4.96896e-62/hypothetical protein AN7780.2 [A. nidulans FGSC A4]
ANID_03223	29.58	5.92	−2.320953	2.10E-23	2.33E-22	gi|67525531|ref|XP_660827.1|/0/K6PF_ASPNG 6-phosphofructokinase (Phosphofructokinase) (Phosphohexokinase) (6PF-1-K) [A. nidulans FGSC A4]
ANID_05144	325.37	65.17	−2.3198013	########	########	gi|259484593|tpe|CBF80949.1|/0/TPA: hypothetical protein similar to 6-phosphofructo-2-kinase (Eurofung) [A. nidulans FGSC A4]
ANID_00409	15.63	3.14	−2.3154813	5.27E-13	3.73E-12	gi|259489348|tpe|CBF89544.1|/0/TPA: Leucine Rich Repeat domain protein (AFU_orthologue; AFUA_1G04960) [A. nidulans FGSC A4]
ANID_03150	5.21	1.05	−2.310894	3.90E-05	0.000136	gi|259485895|tpe|CBF83306.1|/0/TPA: glutamate-cysteine ligase, catalytic subunit (Eurofung) [A. nidulans FGSC A4]
ANID_01472	6.05	1.22	−2.310054	9.13E-06	3.46E-05	gi|67522030|ref|XP_659076.1|/0/hypothetical protein AN1472.2 [A. nidulans FGSC A4]
ANID_08591	27.56	5.58	−2.3042389	9.38E-22	9.95E-21	gi|67903208|ref|XP_681860.1|/1.03357e-144/hypothetical protein AN8591.2 [A. nidulans FGSC A4]
ANID_01551	606.37	122.85	−2.3033005	0	0	gi|74598105|sp|Q5BD29.1|BTGE_EMENI/0/RecName: Full=Probable beta-glucosidase btgE; AltName: Full=Beta-D-glucoside glucohydrolase btgE; AltName: Full=Cellobiase btgE; AltName: Full=Gentiobiase btgE; Flags: Precursor
ANID_02316	395.11	80.51	−2.2950145	########	########	gi|255954581|ref|XP_002568043.1|/7.38984e-59/Pc21g10080 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_08118	501.16	102.47	−2.2900697	0	0	gi|67902262|ref|XP_681387.1|/1.19777e-33/hypothetical protein AN8118.2 [A. nidulans FGSC A4]
ANID_00232	336.63	68.83	−2.2900543	########	########	gi|67515901|ref|XP_657836.1|/1.57405e-134/hypothetical protein AN0232.2 [A. nidulans FGSC A4]
ANID_09007	13.61	2.79	−2.28633	2.42E-11	1.47E-10	gi|259486542|tpe|CBF84473.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_04525	717.12	147.6	−2.2805218	0	0	gi|67536710|ref|XP_662129.1|/2.45308e-63/hypothetical protein AN4525.2 [A. nidulans FGSC A4]
ANID_04422	81.17	16.73	−2.2785092	3.08E-60	5.51E-59	gi|259482764|tpe|CBF77555.1|/0/TPA: aspartic-type endopeptidase (CtsD), putative (AFU_orthologue; AFUA_4G07040) [A. nidulans FGSC A4]
ANID_09180	6.72	1.39	−2.2733764	3.57E-06	1.42E-05	gi|67904386|ref|XP_682449.1|/0/hypothetical protein AN9180.2 [A. nidulans FGSC A4]
ANID_06327	40.33	8.36	−2.2702786	1.36E-30	1.76E-29	gi|67540314|ref|XP_663931.1|/0/hypothetical protein AN6327.2 [A. nidulans FGSC A4]
ANID_09156	5.04	1.05	−2.2630344	6.50E-05	0.00022	gi|259485420|tpe|CBF82427.1|/0/TPA: endonuclease/exonuclease/phosphatase family protein (AFU_orthologue; AFUA_3G09210) [A. nidulans FGSC A4]
ANID_06291	25.04	5.23	−2.2593517	1.86E-19	1.86E-18	gi|259479495|tpe|CBF69769.1|/0/TPA: WD repeat protein (AFU_orthologue; AFUA_2G12360) [A. nidulans FGSC A4]
ANID_11776	14.12	2.96	−2.254071	1.60E-11	9.81E-11	gi|121705418|ref|XP_001270972.1|/1.77837e-37/peptidyl-tRNA hydrolase domain protein [A. clavatus NRRL 1]
ANID_06978	644.01	135.23	−2.2516679	0	0	gi|259483716|tpe|CBF79334.1|/0/TPA: RCC1 Chromatin-associated guanine nucleotide exchange factor for Ran (Eurofung) [A. nidulans FGSC A4]
ANID_01732	9.92	2.09	−2.2468372	1.92E-08	9.38E-08	gi|630383|pir||S42708/0/proline transport protein - Emericella nidulans
ANID_08833	140.33	29.62	−2.2441799	########	1.18E-99	gi|67903692|ref|XP_682102.1|/0/hypothetical protein AN8833.2 [A. nidulans FGSC A4]
ANID_05800	3925.24	830.36	−2.240972	0	0	gi|259480048|tpe|CBF70825.1|/2.81166e-91/TPA: glutamate-5-semialdehyde dehydrogenase (Eurofung) [A. nidulans FGSC A4]
ANID_01666	22.18	4.71	−2.2354604	3.34E-17	3.15E-16	gi|259487005|tpe|CBF85329.1|/3.52085e-146/TPA: nucleolar GTPase, putative (AFU_orthologue; AFUA_4G08930) [A. nidulans FGSC A4]
ANID_02359	7.39	1.57	−2.2348098	1.40E-06	5.80E-06	gi|74597492|sp|Q5BAS1.1|XYND_EMENI/0/RecName: Full=Exo-1,4-beta-xylosidase xlnD; AltName: Full=1,4-beta-D-xylan xylohydrolase xlnD; AltName: Full=Beta-xylosidase A; AltName: Full=Beta-xylosidase xlnD; AltName: Full=Xylobiase xlnD; Flags: Precursor
ANID_08547	172.26	36.6	−2.2346722	########	########	gi|67903120|ref|XP_681816.1|/0/hypothetical protein AN8547.2 [A. nidulans FGSC A4]
ANID_06058	742.83	157.88	−2.2342037	0	0	gi|259479757|tpe|CBF70271.1|/2.64859e-158/TPA: DUF833 domain protein (AFU_orthologue; AFUA_2G09530) [A. nidulans FGSC A4]
ANID_07610	9.75	2.09	−2.2218993	3.15E-08	1.52E-07	gi|292630936|sp|Q5AVS0.2|XLNR_EMENI/0/RecName: Full=Xylanolytic transcriptional activator xlnR; AltName: Full=Xylanase regulator
ANID_04101	8.91	1.92	−2.2143191	1.31E-07	6.00E-07	gi|119189799|ref|XP_001245506.1|/6.3286e-127/hypothetical protein CIMG_04947 [Coccidioides immitis RS]
ANID_07836	4.87	1.05	−2.2135324	0.000108	0.000352	gi|255954379|ref|XP_002567942.1|/1.58883e-114/Pc21g09030 [Penicillium chrysogenum

						Wisconsin 54-1255]
ANID_12256	21.01	4.53	−2.2134932	3.63E-16	3.34E-15	gi|154285076|ref|XP_001543333.1|/0/conserved hypothetical protein [Ajellomyces capsulatus NAm1]
ANID_10370	120.84	26.14	−2.208767	1.50E-85	3.04E-84	gi|71000229|ref|XP_754816.1|/3.69417e-149/conserved hypothetical protein [A. fumigatus Af293]
ANID_04569	277.64	60.12	−2.2072985	########	########	gi|259482600|tpe|CBF77236.1|/7.76955e-136/TPA: ubiquinone biosynthesis protein Coq7, putative (AFU_orthologue; AFUA_2G01890) [A. nidulans FGSC A4]
ANID_10634	36.97	8.02	−2.2046809	3.01E-27	3.67E-26	gi|259484582|tpe|CBF80929.1|/0/TPA: RNA12 protein, putative (AFU_orthologue; AFUA_1G07350) [A. nidulans FGSC A4]
ANID_10505	25.71	5.58	−2.2039926	2.16E-19	2.16E-18	gi|67527027|ref|XP_661575.1|/0/hypothetical protein AN3971.2 [A. nidulans FGSC A4]
ANID_03734	50.42	10.98	−2.1991181	1.79E-36	2.50E-35	gi|73619457|sp|Q5B6U6.1|ATG9_EMENI/0/RecName: Full=Autophagy-related protein 9
ANID_06031	29.58	6.45	−2.197251	5.27E-22	5.63E-21	gi|67539722|ref|XP_663635.1|/9.70813e-160/hypothetical protein AN6031.2 [A. nidulans FGSC A4]
ANID_00105	54.28	11.85	−2.1955337	4.52E-39	6.52E-38	gi|67515647|ref|XP_657709.1|/6.01159e-68/hypothetical protein AN0105.2 [A. nidulans FGSC A4]
ANID_00334	123.19	27.01	−2.1893196	3.04E-86	6.23E-85	gi|67516105|ref|XP_657938.1|/0/hypothetical protein AN0334.2 [A. nidulans FGSC A4]
ANID_05350	26.22	5.75	−2.1890338	1.41E-19	1.42E-18	gi|67538360|ref|XP_662954.1|/2.1135e-117/hypothetical protein AN5350.2 [A. nidulans FGSC A4]
ANID_05831	8.74	1.92	−2.186527	2.15E-07	9.65E-07	gi|259480014|tpe|CBF70758.1|/0/TPA: glutathione S-transferase (Eurofung) [A. nidulans FGSC A4]
ANID_02865	85.21	18.82	−2.1787561	7.87E-60	1.40E-58	gi|67524815|ref|XP_660469.1|/0/hypothetical protein AN2865.2 [A. nidulans FGSC A4]
ANID_01742	17.98	4.01	−2.1647189	1.06E-13	8.42E-13	gi|74597960|sp|Q5BCI8.1|MANBA_EMENI/0/RecName: Full=Probable beta-mannosidase A; AltName: Full=Mannanase A; Short=Mannase A; Flags: Precursor
ANID_01993	10.92	2.44	−2.1620198	8.01E-09	4.06E-08	gi|259487357|tpe|CBF85970.1|/0/TPA: aspartate transaminase, mitochondrial (Eurofung) [A. nidulans FGSC A4]
ANID_10967	6.22	1.39	−2.1618297	1.59E-05	5.80E-05	gi|259483736|tpe|CBF79371.1|/3.61052e-67/TPA: yippee family protein (AFU_orthologue; AFUA_2G06205) [A. nidulans FGSC A4]
ANID_02694	25.71	5.75	−2.1606957	6.05E-19	5.98E-18	gi|259486395|tpe|CBF84196.1|/3.11667e-114/TPA: oxidoreductase, short chain dehydrogenase/reductase family (AFU_orthologue; AFUA_5G14000) [A. nidulans FGSC A4]
ANID_01952	76.97	17.25	−2.1576999	1.43E-53	2.42E-52	gi|67522991|ref|XP_659556.1|/1.58163e-88/hypothetical protein AN1952.2 [A. nidulans FGSC A4]
ANID_03359	101	22.65	−2.1567723	9.92E-70	1.87E-68	gi|67525803|ref|XP_660963.1|/0/hypothetical protein AN3359.2 [A. nidulans FGSC A4]
ANID_10767	106.55	24.05	−2.1474218	4.38E-73	8.48E-72	gi|169798762|gb|ACA81792.1|/0/cytosine-purine permease [Emericella nidulans]
ANID_09123	15.46	3.49	−2.1472414	7.18E-12	4.54E-11	gi|259485461|tpe|CBF82503.1|/4.30055e-76/TPA: hypothetical protein ANIA_09123 [A. nidulans FGSC A4]
ANID_06372	5.38	1.22	−2.140725	6.79E-05	0.000229	gi|67540404|ref|XP_663976.1|/0/hypothetical protein AN6372.2 [A. nidulans FGSC A4]
ANID_10007	10.76	2.44	−2.140725	1.30E-08	6.46E-08	gi|259489765|tpe|CBF90306.1|/1.67006e-34/TPA: U6 small nuclear ribonucleoprotein (Lsm3), putative (AFU_orthologue; AFUA_5G12570) [A. nidulans FGSC A4]
ANID_12353	27.56	6.27	−2.1360385	6.30E-20	6.41E-19	gi|119487688|ref|XP_001262575.1|/8.98997e-68/hypothetical protein NFIA_031110 [Neosartorya fischeri NRRL 181]
ANID_01549	13.78	3.14	−2.1337394	1.20E-10	6.98E-10	gi|67522184|ref|XP_659153.1|/7.98672e-39/hypothetical protein AN1549.2 [A. nidulans FGSC A4]
ANID_01490	9.92	2.27	−2.1276478	5.39E-08	2.55E-07	gi|67522066|ref|XP_659094.1|/2.0025e-56/hypothetical protein AN1490.2 [A. nidulans FGSC A4]
ANID_04744	127.05	29.1	−2.1263053	9.59E-86	1.96E-84	gi|83773228|dbj|BAE63355.1|/0/unnamed protein product [A. oryzae]
ANID_00802	52.44	12.02	−2.1252308	2.50E-36	3.48E-35	gi|67517043|ref|XP_658406.1|/0/hypothetical protein AN0802.2 [A. nidulans FGSC A4]
ANID_05489	36.47	8.36	−2.1251354	9.88E-26	1.16E-24	gi|67538638|ref|XP_663093.1|/2.99867e-131/hypothetical protein AN5489.2 [A. nidulans FGSC A4]
ANID_12192	6.05	1.39	−2.1218503	2.60E-05	9.25E-05	gi|67526105|ref|XP_661114.1|/1.83757e-72/hypothetical protein AN3510.2 [A. nidulans FGSC A4]
ANID_02498	6.05	1.39	−2.1218503	2.60E-05	9.25E-05	gi|67524081|ref|XP_660102.1|/0/hypothetical protein AN2498.2 [A. nidulans FGSC A4]
ANID_07386	308.73	71.27	−2.1149789	########	########	gi|67900798|ref|XP_680655.1|/1.66559e-139/hypothetical protein AN7386.2 [A. nidulans FGSC A4]
ANID_03136	4.54	1.05	−2.112303	0.000292	0.000899	gi|259485912|tpe|CBF83338.1|/0/TPA: ubiquitin conjugating enzyme, putative (AFU_orthologue; AFUA_3G13060) [A. nidulans FGSC A4]
ANID_05205	4.54	1.05	−2.112303	0.000292	0.000899	gi|67538070|ref|XP_662809.1|/0/hypothetical protein AN5205.2 [A. nidulans FGSC A4]
ANID_11477	4.54	1.05	−2.112303	0.000292	0.000898	gi|259485169|tpe|CBF81993.1|/3.17754e-39/TPA: hypothetical protein ANIA_11477 [A. nidulans FGSC A4]
ANID_05338	34.28	8.02	−2.095693	6.66E-24	7.42E-23	gi|259485220|tpe|CBF82075.1|/0/TPA: flavin-binding monooxygenase-like protein (AFU_orthologue; AFUA_6G14280) [A. nidulans FGSC A4]
ANID_06048	15.63	3.66	−2.0944022	1.21E-11	7.48E-11	gi|259479767|tpe|CBF70290.1|/0/TPA: aspartate transaminase (Eurofung) [A. nidulans FGSC A4]
ANID_09500	5.21	1.22	−2.0944022	0.000111	0.000361	gi|75859084|ref|XP_868882.1|/0/hypothetical protein AN9500.2 [A. nidulans FGSC A4]
ANID_04742	5.21	1.22	−2.0944022	0.000111	0.000361	gi|67537144|ref|XP_662346.1|/1.26231e-24/hypothetical protein AN4742.2 [A. nidulans FGSC A4]
ANID_05092	8.91	2.09	−2.0919225	3.62E-07	1.60E-06	gi|67537844|ref|XP_662696.1|/0/hypothetical protein AN5092.2 [A. nidulans FGSC A4]
ANID_08501	5.88	1.39	−2.0807313	4.24E-05	0.000146	gi|67903028|ref|XP_681770.1|/0/hypothetical protein AN8501.2 [A. nidulans FGSC A4]
ANID_07636	70.75	16.73	−2.0802927	3.22E-47	5.07E-46	gi|259483968|tpe|CBF79791.1|/7.6208e-164/TPA: oxidoreductase (Eurofung) [A. nidulans FGSC A4]

ANID_04299	21.34	5.05	−2.0792049	2.87E-15	2.54E-14	gi|67528186|ref|XP_661903.1|/2.56338e-60/hypothetical protein AN4299.2 [A. nidulans FGSC A4]
ANID_02374	15.46	3.66	−2.0786248	1.94E-11	1.18E-10	gi|67523837|ref|XP_659978.1|/0/hypothetical protein AN2374.2 [A. nidulans FGSC A4]
ANID_04796	13.95	3.31	−2.075362	2.00E-10	1.14E-09	gi|67537252|ref|XP_662400.1|/2.73509e-84/hypothetical protein AN4796.2 [A. nidulans FGSC A4]
ANID_00912	36.64	8.71	−2.0726749	4.40E-25	5.06E-24	gi|67517272|ref|XP_658516.1|/1.83448e-176/LE3A_ASPNG 3-isopropylmalate dehydrogenase A (Beta-IPM dehydrogenase A) (IMDH A) (3-IPM-DH A) [A. nidulans FGSC A4]
ANID_05782	12.44	2.96	−2.0713174	2.08E-09	1.10E-08	gi|259484730|tpe|CBF81202.1|/9.46721e-149/TPA: fumarylacetoacetate hydrolase family protein (AFU_orthologue; AFUA_6G06460) [A. nidulans FGSC A4]
ANID_07298	55.63	13.24	−2.07096	3.00E-37	4.21E-36	gi|259483352|tpe|CBF78671.1|/6.14326e-165/TPA: endonuclease/exonuclease/phosphatase family protein (AFU_orthologue; AFUA_2G16830) [A. nidulans FGSC A4]
ANID_03361	387.72	92.71	−2.0642183	########	########	gi|259485658|tpe|CBF82866.1|/7.86078e-141/TPA: putative bacteriorhodopsin /opsin, nopA (Eurofung) [A. nidulans FGSC A4]
ANID_09408	381	91.14	−2.0636347	########	########	gi|259488250|tpe|CBF87554.1|/0/TPA: Fatty acid synthase, beta subunit [Source:UniProtKB/TrEMBL;Acc:P78616] [A. nidulans FGSC A4]
ANID_07208	43.7	10.46	−2.0627504	1.81E-29	2.31E-28	gi|67900442|ref|XP_680477.1|/1.03893e-98/hypothetical protein AN7208.2 [A. nidulans FGSC A4]
ANID_00858	272.76	65.35	−2.0613729	########	########	gi|259488857|tpe|CBF88645.1|/0/TPA: heat shock protein (Eurofung) [A. nidulans FGSC A4]
ANID_02417	22.52	5.4	−2.0601755	7.27E-16	6.64E-15	gi|145232472|ref|XP_001399681.1|/0/hypothetical protein ANI_1_752024 [A. niger CBS 513.88]
ANID_05132	346.71	83.65	−2.051292	########	########	gi|259484577|tpe|CBF80920.1|/1.68574e-151/TPA: mitochondrial GTP/GDP transporter Ggc1, putative (AFU_orthologue; AFUA_1G07450) [A. nidulans FGSC A4]
ANID_03555	151.93	36.77	−2.0468057	2.18E-97	4.71E-96	gi|67526195|ref|XP_661159.1|/4.27636e-98/HS30_EMENI 30 KD HEAT SHOCK PROTEIN [A. nidulans FGSC A4]
ANID_04093	5.04	1.22	−2.0465426	0.00018	0.00057	gi|67527632|ref|XP_661697.1|/0/hypothetical protein AN4093.2 [A. nidulans FGSC A4]
ANID_02126	13.61	3.31	−2.0397639	5.16E-10	2.85E-09	gi|115399072|ref|XP_001215125.1|/2.46042e-95/conserved hypothetical protein [A. terreus NIH2624]
ANID_06297	222.01	54.02	−2.0390591	########	########	gi|121715794|ref|XP_001275506.1|/7.45991e-91/cytochrome c oxidase assembly protein Cox11, putative [A. clavatus NRRL 1]
ANID_03713	5.71	1.39	−2.0384059	6.86E-05	0.000232	gi|67526511|ref|XP_661317.1|/1.7815e-73/hypothetical protein AN3713.2 [A. nidulans FGSC A4]
ANID_08990	336.12	81.9	−2.037041	########	########	gi|67904006|ref|XP_682259.1|/0/hypothetical protein AN8990.2 [A. nidulans FGSC A4]
ANID_05423	18.49	4.53	−2.0291623	4.84E-13	3.45E-12	gi|67538506|ref|XP_663027.1|/0/hypothetical protein AN5423.2 [A. nidulans FGSC A4]
ANID_06795	43.36	10.63	−2.0282232	1.20E-28	1.49E-27	gi|67541250|ref|XP_664399.1|/1.71134e-89/hypothetical protein AN6795.2 [A. nidulans FGSC A4]
ANID_02522	193.27	47.57	−2.0224938	########	########	gi|67524129|ref|XP_660126.1|/2.93492e-167/hypothetical protein AN2522.2 [A. nidulans FGSC A4]
ANID_07567	20.5	5.05	−2.0212686	3.01E-14	2.51E-13	gi|259483887|tpe|CBF79643.1|/1.60181e-114/TPA: hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase (Eurofung) [A. nidulans FGSC A4]
ANID_08641	442	109.09	−2.0185275	########	########	gi|67903308|ref|XP_681910.1|/4.20516e-46/hypothetical protein AN8641.2 [A. nidulans FGSC A4]
ANID_06423	417.97	103.34	−2.0160006	########	########	gi|67540506|ref|XP_664027.1|/1.24842e-93/hypothetical protein AN6423.2 [A. nidulans FGSC A4]
ANID_05989	113.44	28.06	−2.0153425	9.45E-72	1.81E-70	gi|259479828|tpe|CBF70409.1|/8.33605e-139/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04963	7.73	1.92	−2.0093621	3.90E-06	1.55E-05	gi|67537586|ref|XP_662567.1|/0/hypothetical protein AN4963.2 [A. nidulans FGSC A4]
ANID_04062	32.94	8.19	−2.0079052	7.40E-22	7.86E-21	gi|67527367|ref|XP_661666.1|/0/hypothetical protein AN4062.2 [A. nidulans FGSC A4]
ANID_02527	95.29	23.7	−2.0074378	3.08E-60	5.50E-59	gi|259487956|tpe|CBF87032.1|/0/TPA: isochorismatase family protein family (AFU_orthologue; AFUA_3G14500) [A. nidulans FGSC A4]
ANID_01089	96.97	24.22	−2.0013396	5.00E-61	8.98E-60	gi|259488601|tpe|CBF88168.1|/0/TPA: arrestin domain protein (AFU_orthologue; AFUA_1G12020) [A. nidulans FGSC A4]
ANID_02530	7106.14	1776.25	−2.0002315	0	0	gi|67524145|ref|XP_660134.1|/1.43551e-99/HS30_EMENI 30 KD HEAT SHOCK PROTEIN [A. nidulans FGSC A4]
ANID_02943	179.83	44.96	−1.9999198	########	########	gi|259486118|tpe|CBF83704.1|/0/TPA: Putative uncharacterized proteinRfeA ; [Source:UniProtKB/TrEMBL;Acc:Q8J179] [A. nidulans FGSC A4]
ANID_05787	5.55	1.39	−1.9974029	0.00011	0.00036	gi|259484724|tpe|CBF81191.1|/0/TPA: Rho GTPase activator (Bem3), putative (AFU_orthologue; AFUA_6G06400) [A. nidulans FGSC A4]
ANID_08720	15.29	3.83	−1.9971721	8.05E-11	4.73E-10	gi|259483085|tpe|CBF78167.1|/8.70436e-125/TPA: phosphoglycerate mutase family protein (AFU_orthologue; AFUA_6G02600) [A. nidulans FGSC A4]
ANID_01767	15.29	3.83	−1.9971721	8.05E-11	4.73E-10	gi|67522621|ref|XP_659371.1|/0/hypothetical protein AN1767.2 [A. nidulans FGSC A4]
ANID_01686	76.3	19.17	−1.9928327	4.01E-48	6.40E-47	gi|67522459|ref|XP_659290.1|/0/hypothetical protein AN1686.2 [A. nidulans FGSC A4]
ANID_06009	33.95	8.54	−1.9911036	2.96E-22	3.19E-21	gi|67539678|ref|XP_663613.1|/0/hypothetical protein AN6009.2 [A. nidulans FGSC A4]
ANID_10303	22.18	5.58	−1.9909223	4.76E-15	4.16E-14	gi|259487841|tpe|CBF86835.1|/0/TPA: mitochondrial carrier protein, putative (AFU_orthologue; AFUA_2G13870) [A. nidulans FGSC A4]
ANID_07005	34.62	8.71	−1.9908611	1.18E-22	1.28E-21	gi|259483684|tpe|CBF79275.1|/0/TPA: conserved leucine-rich repeat protein (AFU_orthologue; AFUA_4G04440) [A. nidulans FGSC A4]
ANID_05686	1267.35	319.42	−1.9882885	0	0	gi|259484840|tpe|CBF81405.1|/1.97832e-51/TPA: tropomyosin TpmA (Eurofung) [A. nidulans FGSC A4]
ANID_01841	6.89	1.74	−1.9854167	1.62E-05	5.89E-05	gi|67522769|ref|XP_659445.1|/4.53363e-139/hypothetical protein AN1841.2 [A. nidulans FGSC A4]

ANID_02243	249.07	62.91	−1.98519	########	########	gi|259487631|tpe|CBF86449.1|/0/TPA: carbamoyl-phosphate synthase, small subunit (Eurofung) [A. nidulans FGSC A4]
ANID_10834	300.83	76.33	−1.9786263	########	########	gi|259480173|tpe|CBF71062.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06721	7.56	1.92	−1.9772799	6.25E-06	2.42E-05	gi|259480311|tpe|CBF71325.1|/0/TPA: amidohydrolase family protein (AFU_orthologue; AFUA_5G01480) [A. nidulans FGSC A4]
ANID_07400	12.27	3.14	−1.9662988	8.52E-09	4.29E-08	gi|67900826|ref|XP_680669.1|/9.16534e-95/hypothetical protein AN7400.2 [A. nidulans FGSC A4]
ANID_08692	39.49	10.11	−1.9657044	3.01E-25	3.48E-24	gi|67903410|ref|XP_681961.1|/6.35773e-85/PM20_ASPFU PROBABLE PEROXISOMAL MEMBRANE PROTEIN PMP20 (ALLERGEN ASP F 3) [A. nidulans FGSC A4]
ANID_06924	57.14	14.64	−1.9645855	8.41E-36	1.16E-34	gi|67541508|ref|XP_664528.1|/0/hypothetical protein AN6924.2 [A. nidulans FGSC A4]
ANID_07169	1077.95	276.55	−1.962678	0	0	gi|259483498|tpe|CBF78937.1|/0/TPA: expressed flavohemoprotein (Eurofung) [A. nidulans FGSC A4]
ANID_07177	16.13	4.18	−1.9481716	5.00E-11	2.97E-10	gi|259483490|tpe|CBF78923.1|/2.47164e-27/TPA: WW domain protein (AFU_orthologue; AFUA_4G03322) [A. nidulans FGSC A4]
ANID_05885	6.05	1.57	−1.9461706	6.76E-05	0.000229	gi|259479948|tpe|CBF70637.1|/0/TPA: alpha-1,3 glucan synthase (Eurofung) [A. nidulans FGSC A4]
ANID_04976	927.19	240.83	−1.9448499	0	0	gi|259482151|tpe|CBF76358.1|/2.79079e-96/TPA: TATA-box-binding protein (TATA-box factor)(TATA-binding factor)(TATA sequence-binding protein)(TBP)(Transcription initiation factor TFIID TBP subunit) [Source:UniProtKB/Swiss-Prot;Acc:Q12731] [A. nidulans FGSC A4]
ANID_04048	7.39	1.92	−1.9444681	9.97E-06	3.76E-05	gi|67527332|ref|XP_661652.1|/0/hypothetical protein AN4048.2 [A. nidulans FGSC A4]
ANID_10663	226.38	58.9	−1.942407	########	########	gi|259485223|tpe|CBF82080.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01527	40.17	10.46	−1.9412356	2.96E-25	3.43E-24	gi|259486853|tpe|CBF85048.1|/2.24414e-134/TPA: FAS1 domain-containing protein AN1527 Precursor [Source:UniProtKB/Swiss-Prot;Acc:Q5BD53] [A. nidulans FGSC A4]
ANID_01008	24.03	6.27	−1.9382993	1.17E-15	1.06E-14	gi|67517614|ref|XP_658612.1|/0/CRNA_EMENI NITRATE TRANSPORTER (NITRATE PERMEASE) [A. nidulans FGSC A4]
ANID_03163	456.62	119.2	−1.9376098	########	########	gi|259485881|tpe|CBF83280.1|/5.07611e-158/TPA: stomatin family protein (AFU_orthologue; AFUA_3G13440) [A. nidulans FGSC A4]
ANID_07170	1946.49	511.28	−1.9286894	0	0	gi|259483497|tpe|CBF78935.1|/4.17658e-104/TPA: putative bHLH transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_07517	47.06	12.37	−1.9276558	4.75E-29	5.96E-28	gi|67901060|ref|XP_680786.1|/0/hypothetical protein AN7517.2 [A. nidulans FGSC A4]
ANID_03573	11.26	2.96	−1.9275377	5.47E-08	2.58E-07	gi|67526231|ref|XP_661177.1|/0/hypothetical protein AN3573.2 [A. nidulans FGSC A4]
ANID_02272	1532.55	403.59	−1.9249718	0	0	gi|67523633|ref|XP_659876.1|/4.57841e-167/hypothetical protein AN2272.2 [A. nidulans FGSC A4]
ANID_09263	161.34	42.52	−1.9238907	2.36E-95	5.02E-94	gi|67904552|ref|XP_682532.1|/3.01802e-64/hypothetical protein AN9263.2 [A. nidulans FGSC A4]
ANID_00179	118.32	31.19	−1.9235385	2.24E-70	4.26E-69	gi|259489613|tpe|CBF90029.1|/5.70325e-128/TPA: oxidoreductase, short chain dehydrogenase/reductase family (AFU_orthologue; AFUA_5G11240) [A. nidulans FGSC A4]
ANID_05781	2937.38	777.03	−1.9184877	0	0	gi|67539222|ref|XP_663385.1|/8.57728e-117/hypothetical protein AN5781.2 [A. nidulans FGSC A4]
ANID_00483	7.9	2.09	−1.9183497	6.12E-06	2.37E-05	gi|67516403|ref|XP_658087.1|/3.39384e-47/hypothetical protein AN0483.2 [A. nidulans FGSC A4]
ANID_07287	15.8	4.18	−1.9183497	1.25E-10	7.21E-10	gi|259483363|tpe|CBF78691.1|/1.14099e-150/TPA: Mitochondrial succinate-fumarate antiporter (Eurofung) [A. nidulans FGSC A4]
ANID_05886	7.9	2.09	−1.9183497	6.12E-06	2.37E-05	gi|259479947|tpe|CBF70635.1|/0/TPA: alpha isopropylmalate isomerase (Eurofung) [A. nidulans FGSC A4]
ANID_03826	8.57	2.27	−1.9166029	2.37E-06	9.65E-06	gi|67526737|ref|XP_661430.1|/0/hypothetical protein AN3826.2 [A. nidulans FGSC A4]
ANID_01060	8.57	2.27	−1.9166029	2.37E-06	9.64E-06	gi|259488636|tpe|CBF88234.1|/0/TPA: histone demethylase (Eurofung) [A. nidulans FGSC A4]
ANID_10779	8.57	2.27	−1.9166029	2.37E-06	9.64E-06	gi|259479600|tpe|CBF69971.1|/0/TPA: putative 1,6-beta-glucan synthetase (Eurofung) [A. nidulans FGSC A4]
ANID_06552	7.23	1.92	−1.9128893	1.58E-05	5.77E-05	gi|259480125|tpe|CBF70972.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06264	5.21	1.39	−1.9061985	0.000283	0.000872	gi|67540188|ref|XP_663868.1|/5.484e-126/hypothetical protein AN6264.2 [A. nidulans FGSC A4]
ANID_05347	5.21	1.39	−1.9061985	0.000283	0.000872	gi|259485211|tpe|CBF82061.1|/0/TPA: CDF zinc ion transporter (Eurofung) [A. nidulans FGSC A4]
ANID_08133	5.88	1.57	−1.9050516	0.000108	0.000351	gi|67902292|ref|XP_681402.1|/7.07237e-99/hypothetical protein AN8133.2 [A. nidulans FGSC A4]
ANID_02976	20.17	5.4	−1.9011798	4.64E-13	3.32E-12	gi|67525037|ref|XP_660580.1|/3.23456e-93/hypothetical protein AN2976.2 [A. nidulans FGSC A4]
ANID_07466	9.08	2.44	−1.8958112	1.46E-06	6.03E-06	gi|67900958|ref|XP_680735.1|/4.95015e-156/hypothetical protein AN7466.2 [A. nidulans FGSC A4]
ANID_10977	213.27	57.51	−1.8907963	########	########	gi|259483980|tpe|CBF79813.1|/5.13778e-69/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00861	65.21	17.6	−1.8895178	1.20E-38	1.72E-37	gi|259488854|tpe|CBF88640.1|/2.71914e-171/TPA: autophagy-related protein Atg27 (Eurofung) [A. nidulans FGSC A4]
ANID_08544	28.4	7.67	−1.8885924	1.09E-17	1.05E-16	gi|67903114|ref|XP_681813.1|/1.90967e-69/hypothetical protein AN8544.2 [A. nidulans FGSC A4]
ANID_07037	93.95	25.44	−1.8847945	9.14E-55	1.56E-53	gi|259483648|tpe|CBF79209.1|/0/TPA: vacuolar protein sorting protein (Vps36), putative (AFU_orthologue; AFUA_4G04100) [A. nidulans FGSC A4]

ANID_04171	133.61	36.25	−1.8819751	5.09E-77	1.00E-75	gi|259481231|tpe|CBF74560.1|/0/TPA: PH domain protein (AFU_orthologue; AFUA_6G07910) [A. nidulans FGSC A4]
ANID_01605	99.49	27.01	−1.8810579	9.36E-58	1.63E-56	gi|67522296|ref|XP_659209.1|/3.72572e-105/hypothetical protein AN1605.2 [A. nidulans FGSC A4]
ANID_00387	28.23	7.67	−1.8799306	1.71E-17	1.63E-16	gi|259489370|tpe|CBF89585.1|/0/TPA: DNA photolyase (Eurofung) [A. nidulans FGSC A4]
ANID_05646	35.12	9.58	−1.8741953	2.62E-21	2.74E-20	gi|259484883|tpe|CBF81484.1|/0/TPA: 3-ketoacyl-coA thiolase peroxisomal A precursor (AFU_orthologue; AFUA_4G10950) [A. nidulans FGSC A4]
ANID_05726	72.77	19.87	−1.8727519	1.86E-42	2.78E-41	gi|67539112|ref|XP_663330.1|/0/hypothetical protein AN5726.2 [A. nidulans FGSC A4]
ANID_00170	8129.63	2221.67	−1.8715452	0	0	gi|259489624|tpe|CBF90049.1|/8.02986e-72/TPA: Thioredoxin (Trx) [Source:UniProtKB/Swiss-Prot;Acc:P29429] [A. nidulans FGSC A4]
ANID_06708	657.29	179.84	−1.8698161	0	0	gi|67541076|ref|XP_664312.1|/0/hypothetical protein AN6708.2 [A. nidulans FGSC A4]
ANID_03672	8.91	2.44	−1.8685443	2.29E-06	9.35E-06	gi|67526429|ref|XP_661276.1|/7.22543e-147/hypothetical protein AN3672.2 [A. nidulans FGSC A4]
ANID_06089	1579.78	434.44	−1.8624948	0	0	gi|67539838|ref|XP_663693.1|/0/HS60_PARBR Heat shock protein 60, mitochondrial precursor (60 kDa chaperonin) (Protein Cpn60) [A. nidulans FGSC A4]
ANID_06571	21.51	5.92	−1.8613384	1.73E-13	1.33E-12	gi|67540802|ref|XP_664175.1|/0/hypothetical protein AN6571.2 [A. nidulans FGSC A4]
ANID_02739	82.18	22.65	−1.8592763	2.87E-47	4.52E-46	gi|67524563|ref|XP_660343.1|/0/hypothetical protein AN2739.2 [A. nidulans FGSC A4]
ANID_04259	269.74	74.41	−1.8580011	########	########	gi|74596045|sp|Q5B5C1.1|EIF3M_EMENI/0/RecName: Full=Eukaryotic translation initiation factor 3 subunit M; Short=eIF3m
ANID_11773	15.8	4.36	−1.8575245	2.98E-10	1.68E-09	gi|67537662|ref|XP_662605.1|/0/hypothetical protein AN5001.2 [A. nidulans FGSC A4]
ANID_03795	64.37	17.77	−1.8569448	2.60E-37	3.68E-36	gi|67526675|ref|XP_661399.1|/0/hypothetical protein AN3795.2 [A. nidulans FGSC A4]
ANID_04817	155.12	42.87	−1.8553444	1.86E-87	3.85E-86	gi|67537294|ref|XP_662421.1|/0/hypothetical protein AN4817.2 [A. nidulans FGSC A4]
ANID_12364	7.56	2.09	−1.8548833	1.53E-05	5.58E-05	gi|259482957|tpe|CBF77926.1|/4.78722e-113/TPA: carboxylesterase, putative (AFU_orthologue; AFUA_5G05940) [A. nidulans FGSC A4]
ANID_03740	7.56	2.09	−1.8548833	1.53E-05	5.58E-05	gi|67526565|ref|XP_661344.1|/0/hypothetical protein AN3740.2 [A. nidulans FGSC A4]
ANID_00728	7.56	2.09	−1.8548833	1.53E-05	5.57E-05	gi|67516893|ref|XP_658332.1|/0/hypothetical protein AN0728.2 [A. nidulans FGSC A4]
ANID_05695	35.29	9.76	−1.8543064	3.96E-21	4.12E-20	gi|259484831|tpe|CBF81389.1|/0/TPA: DUF636 domain protein (AFU_orthologue; AFUA_7G04120) [A. nidulans FGSC A4]
ANID_10237	10.08	2.79	−1.8531586	5.46E-07	2.36E-06	gi|259487334|tpe|CBF85927.1|/1.71708e-118/TPA: iron-sulfur cluster assembly accessory protein Isa1, putative (AFU_orthologue; AFUA_4G10690) [A. nidulans FGSC A4]
ANID_07027	10.08	2.79	−1.8531586	5.46E-07	2.36E-06	gi|121714367|ref|XP_001274794.1|/9.53002e-175/MFS transporter, putative [A. clavatus NRRL 1]
ANID_02968	820.14	227.06	−1.8527966	0	0	gi|74597023|sp|Q5B912.1|IPYR_EMENI/1.5068e-151/RecName: Full=Inorganic pyrophosphatase; AltName: Full=Pyrophosphate phospho-hydrolase; Short=PPase
ANID_05767	19.5	5.4	−1.8524428	2.78E-12	1.81E-11	gi|67539194|ref|XP_663371.1|/2.06054e-126/hypothetical protein AN5767.2 [A. nidulans FGSC A4]
ANID_02703	54.12	14.99	−1.8521615	1.56E-31	2.06E-30	gi|67524491|ref|XP_660307.1|/0/hypothetical protein AN2703.2 [A. nidulans FGSC A4]
ANID_07143	14.45	4.01	−1.8493954	1.92E-09	1.02E-08	gi|67541959|ref|XP_664747.1|/1.14218e-142/hypothetical protein AN7143.2 [A. nidulans FGSC A4]
ANID_03581	18.82	5.23	−1.8473838	7.02E-12	4.44E-11	gi|115312784|emb|CAL36645.1|/1.55424e-178/thioredoxin reductase [Emericella nidulans]
ANID_04515	16.3	4.53	−1.847289	1.84E-10	1.05E-09	gi|67536690|ref|XP_662119.1|/0/hypothetical protein AN4515.2 [A. nidulans FGSC A4]
ANID_04517	265.03	73.89	−1.8427046	########	########	gi|259482656|tpe|CBF77345.1|/0/TPA: ABC heavy metal ion transporter (Eurofung) [A. nidulans FGSC A4]
ANID_10735	11.26	3.14	−1.8423704	1.31E-07	5.99E-07	gi|259479988|tpe|CBF70709.1|/0/TPA: hypothetical protein ANIA_10735 [A. nidulans FGSC A4]
ANID_00245	11.26	3.14	−1.8423704	1.31E-07	5.99E-07	gi|67515927|ref|XP_657849.1|/6.58819e-179/hypothetical protein AN0245.2 [A. nidulans FGSC A4]
ANID_04402	1083.16	302.17	−1.841814	0	0	gi|238491872|ref|XP_002377173.1|/3.63923e-141/outer mitochondrial membrane protein porin [A. flavus NRRL3357]
ANID_06640	8.74	2.44	−1.8407521	3.60E-06	1.43E-05	gi|67540940|ref|XP_664244.1|/0/hypothetical protein AN6640.2 [A. nidulans FGSC A4]
ANID_05660	314.44	87.83	−1.839999	########	########	gi|67538980|ref|XP_663264.1|/1.06762e-94/hypothetical protein AN5660.2 [A. nidulans FGSC A4]
ANID_03655	362.34	101.59	−1.8345857	########	########	gi|67526395|ref|XP_661259.1|/2.59804e-49/hypothetical protein AN3655.2 [A. nidulans FGSC A4]
ANID_01760	18.65	5.23	−1.8342928	1.09E-11	6.80E-11	gi|259487104|tpe|CBF85511.1|/1.23116e-39/TPA: Autophagy-related protein 12 (Autophagy-related ubiquitin-like modifier atg12) [Source:UniProtKB/Swiss-Prot;Acc:Q5BCH0] [A. nidulans FGSC A4]
ANID_04991	11.76	3.31	−1.8289849	8.00E-08	3.75E-07	gi|67537642|ref|XP_662595.1|/0/hypothetical protein AN4991.2 [A. nidulans FGSC A4]
ANID_12363	17.31	4.88	−1.8266527	6.97E-11	4.11E-10	gi|259486827|tpe|CBF85000.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07148	119.83	33.81	−1.8254672	1.63E-66	3.01E-65	gi|67541969|ref|XP_664752.1|/4.27527e-67/hypothetical protein AN7148.2 [A. nidulans FGSC A4]
ANID_03057	42.52	12.02	−1.8227047	1.38E-24	1.57E-23	gi|67525199|ref|XP_660661.1|/0/hypothetical protein AN3057.2 [A. nidulans FGSC A4]
ANID_00065	42.52	12.02	−1.8227047	1.38E-24	1.57E-23	gi|259489745|tpe|CBF90269.1|/0/TPA: WD repeat protein (AFU_orthologue; AFUA_5G12370) [A. nidulans FGSC A4]
ANID_04975	5.55	1.57	−1.8217232	0.000269	0.000832	gi|67537610|ref|XP_662579.1|/0/hypothetical protein AN4975.2 [A. nidulans FGSC A4]
ANID_05907	483.18	137.32	−1.815019	########	########	gi|67539474|ref|XP_663511.1|/2.42253e-83/hypothetical protein AN5907.2 [A. nidulans FGSC A4]

ANID_10030	27.56	7.84	−1.8136503	2.33E-16	2.16E-15	gi|119479481|ref|XP_001259769.1|/0/autophagic serine protease Alp2 [Neosartorya fischeri NRRL 181]
ANID_03499	42.86	12.2	−1.8127507	1.32E-24	1.51E-23	gi|259481989|tpe|CBF76030.1|/0/TPA: UPF0075 domain protein (AFU_orthologue; AFUA_4G14600) [A. nidulans FGSC A4]
ANID_00211	8.57	2.44	−1.8124141	5.63E-06	2.20E-05	gi|70997613|ref|XP_753548.1|/1.24668e-90/small nuclear ribonucleoprotein U2, A' [A. fumigatus Af293]
ANID_03680	179.66	51.41	−1.8051483	2.39E-97	5.14E-96	gi|67526445|ref|XP_661284.1|/3.18368e-39/hypothetical protein AN3680.2 [A. nidulans FGSC A4]
ANID_03813	31.6	9.06	−1.8023416	2.16E-18	2.11E-17	gi|67526711|ref|XP_661417.1|/1.45804e-90/hypothetical protein AN3813.2 [A. nidulans FGSC A4]
ANID_08845	7.9	2.27	−1.7991604	1.45E-05	5.31E-05	gi|67903716|ref|XP_682114.1|/0/hypothetical protein AN8845.2 [A. nidulans FGSC A4]
ANID_04637	170.58	49.14	−1.7954787	7.56E-92	1.60E-90	gi|259482527|tpe|CBF77094.1|/0/TPA: PA and RING finger domain protein (AFU_orthologue; AFUA_2G02470) [A. nidulans FGSC A4]
ANID_00076	350.24	101.42	−1.7880017	########	########	gi|145254551|ref|XP_001398660.1|/0/XPG I-region protein [A. niger CBS 513.88]
ANID_11145	95.29	27.71	−1.7819181	1.46E-51	2.43E-50	gi|74626242|sp|Q9Y708.2|CGR1_EMENI/2.95629e-11/RecName: Full=rRNA-processing protein cgrA
ANID_07299	55.12	16.03	−1.7818015	1.65E-30	2.14E-29	gi|259483351|tpe|CBF78669.1|/3.83368e-151/TPA: curved DNA-binding protein (42 kDa protein) (AFU_orthologue; AFUA_2G16820) [A. nidulans FGSC A4]
ANID_03102	13.78	4.01	−1.7809017	1.12E-08	5.56E-08	gi|67525289|ref|XP_660706.1|/0/hypothetical protein AN3102.2 [A. nidulans FGSC A4]
ANID_04316	25.71	7.49	−1.779292	5.39E-15	4.69E-14	gi|67528220|ref|XP_661920.1|/0/hypothetical protein AN4316.2 [A. nidulans FGSC A4]
ANID_04406	32.27	9.41	−1.777927	1.95E-18	1.91E-17	gi|67528416|ref|XP_662010.1|/3.22963e-96/hypothetical protein AN4406.2 [A. nidulans FGSC A4]
ANID_01026	32.77	9.58	−1.7742781	1.20E-18	1.18E-17	gi|67517688|ref|XP_658630.1|/3.83033e-151/hypothetical protein AN1026.2 [A. nidulans FGSC A4]
ANID_00183	84.03	24.57	−1.7740066	2.16E-45	3.32E-44	gi|259489609|tpe|CBF90022.1|/1.29636e-137/TPA: molybdopterin binding domain protein (AFU_orthologue; AFUA_5G11210) [A. nidulans FGSC A4]
ANID_02964	79.83	23.35	−1.7735085	3.45E-43	5.20E-42	gi|259486091|tpe|CBF83657.1|/1.68552e-143/TPA: probable mitochondrial E3-binding protein of the pyruvate dehydrogenase complex (Eurofung) [A. nidulans FGSC A4]
ANID_10880	14.29	4.18	−1.7734311	6.83E-09	3.48E-08	gi|259483650|tpe|CBF79213.1|/6.92775e-160/TPA: AN1 zinc finger protein (AFU_orthologue; AFUA_4G04280) [A. nidulans FGSC A4]
ANID_02362	16.64	4.88	−1.7697024	4.01E-10	2.23E-09	gi|67523813|ref|XP_659966.1|/8.17833e-149/hypothetical protein AN2362.2 [A. nidulans FGSC A4]
ANID_08943	49.24	14.46	−1.7677632	3.91E-27	4.75E-26	gi|67903912|ref|XP_682212.1|/0/hypothetical protein AN8943.2 [A. nidulans FGSC A4]
ANID_06124	32.6	9.58	−1.7667744	1.85E-18	1.81E-17	gi|259479686|tpe|CBF70136.1|/0/TPA: isochorismatase family hydrolase, putative (AFU_orthologue; AFUA_2G08700) [A. nidulans FGSC A4]
ANID_00229	219.32	64.65	−1.7623151	########	########	gi|67515895|ref|XP_657833.1|/0/hypothetical protein AN0229.2 [A. nidulans FGSC A4]
ANID_05491	23.02	6.8	−1.7592812	2.12E-13	1.60E-12	gi|73619434|sp|Q5B1T9.1|ATG2_EMENI/0/RecName: Full=Autophagy-related protein 2
ANID_04312	5.88	1.74	−1.7567288	0.000252	0.000782	gi|67528212|ref|XP_661916.1|/0/hypothetical protein AN4312.2 [A. nidulans FGSC A4]
ANID_05978	9.41	2.79	−1.7539296	3.21E-06	1.29E-05	gi|67539616|ref|XP_663582.1|/0/hypothetical protein AN5978.2 [A. nidulans FGSC A4]
ANID_08119	12.27	3.66	−1.7452197	1.11E-07	5.13E-07	gi|67902264|ref|XP_681388.1|/0/hypothetical protein AN8119.2 [A. nidulans FGSC A4]
ANID_01290	25.71	7.67	−1.7450311	1.20E-14	1.03E-13	gi|119485763|ref|XP_001262224.1|/0/K+/H+ antiporter, putative [Neosartorya fischeri NRRL 181]
ANID_04852	11.09	3.31	−1.7443562	4.63E-07	2.02E-06	gi|67537364|ref|XP_662456.1|/0/hypothetical protein AN4852.2 [A. nidulans FGSC A4]
ANID_02509	29.75	8.89	−1.7426343	1.10E-16	1.03E-15	gi|259487935|tpe|CBF86997.1|/0/TPA: Indoleamine 2,3-dioxygenase subfamily (AFU_orthologue; AFUA_3G14250) [A. nidulans FGSC A4]
ANID_02928	65.88	19.69	−1.7423774	4.31E-35	5.91E-34	gi|67524941|ref|XP_660532.1|/0/hypothetical protein AN2928.2 [A. nidulans FGSC A4]
ANID_00796	15.13	4.53	−1.739829	3.92E-09	2.03E-08	gi|67517031|ref|XP_658400.1|/1.88175e-109/hypothetical protein AN0796.2 [A. nidulans FGSC A4]
ANID_10847	943.66	283	−1.7374651	0	0	gi|255943909|ref|XP_002562722.1|/6.82601e-31/Pc20g01630 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_07686	7.56	2.27	−1.7356939	3.50E-05	0.000123	gi|259484028|tpe|CBF79902.1|/0/TPA: FHA domain protein (AFU_orthologue; AFUA_2G01670) [A. nidulans FGSC A4]
ANID_05318	107.22	32.24	−1.7336504	1.06E-55	1.82E-54	gi|67538296|ref|XP_662922.1|/0/hypothetical protein AN5318.2 [A. nidulans FGSC A4]
ANID_07206	58.82	17.77	−1.7268631	3.98E-31	5.22E-30	gi|259483460|tpe|CBF78868.1|/2.75087e-132/TPA: GTP binding protein (SPG1), putative (AFU_orthologue; AFUA_6G10330) [A. nidulans FGSC A4]
ANID_01544	14.96	4.53	−1.7235272	6.01E-09	3.07E-08	gi|67522174|ref|XP_659148.1|/0/hypothetical protein AN1544.2 [A. nidulans FGSC A4]
ANID_05757	14.96	4.53	−1.7235272	6.01E-09	3.07E-08	gi|67539174|ref|XP_663361.1|/0/hypothetical protein AN5757.2 [A. nidulans FGSC A4]
ANID_00655	13.78	4.18	−1.721001	2.49E-08	1.21E-07	gi|259489077|tpe|CBF89049.1|/8.05345e-145/TPA: cell division control protein 14 (AFU_orthologue; AFUA_1G13170) [A. nidulans FGSC A4]
ANID_00085	55.63	16.9	−1.7188399	2.43E-29	3.08E-28	gi|67515607|ref|XP_657689.1|/0/hypothetical protein AN0085.2 [A. nidulans FGSC A4]
ANID_06126	18.32	5.58	−1.7150825	1.32E-10	7.60E-10	gi|3021303|emb|CAA75926.1|/0/acetyl-CoA carboxylase [Emericella nidulans]
ANID_04866	165.04	50.54	−1.7073182	5.08E-83	1.01E-81	gi|67537392|ref|XP_662470.1|/8.06236e-152/hypothetical protein AN4866.2 [A. nidulans FGSC A4]
ANID_05056	1912.54	586.04	−1.7064189	0	0	gi|67537772|ref|XP_662660.1|/2.7917e-27/hypothetical protein AN5056.2 [A. nidulans FGSC A4]
ANID_06203	64.7	19.87	−1.7031738	1.78E-33	2.40E-32	gi|67540066|ref|XP_663807.1|/3.102e-69/hypothetical protein AN6203.2 [A. nidulans FGSC A4]
ANID_07273	28.91	8.89	−1.7013133	9.11E-16	8.29E-15	gi|67900572|ref|XP_680542.1|/5.79345e-151/hypothetical protein AN7273.2 [A. nidulans FGSC A4]

<table>
<tr><td>ANID_00732</td><td>134.95</td><td>41.65</td><td>−1.6960366</td><td>1.36E-67</td><td>2.51E-66</td><td>gi|67516901|ref|XP_658336.1|/0/hypothetical protein AN0732.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10963</td><td>6.22</td><td>1.92</td><td>−1.6958083</td><td>0.000233</td><td>0.000725</td><td>gi|259483912|tpe|CBF79688.1|/2.84332e-32/TPA: small nuclear ribonucleoprotein (LSM2), putative (AFU_orthologue; AFUA_2G15210) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00094</td><td>69.91</td><td>21.61</td><td>−1.6937998</td><td>9.08E-36</td><td>1.26E-34</td><td>gi|259489714|tpe|CBF90212.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07778</td><td>11.26</td><td>3.49</td><td>−1.6899079</td><td>6.61E-07</td><td>2.83E-06</td><td>gi|67901582|ref|XP_681047.1|/5.45216e-109/hypothetical protein AN7778.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02470</td><td>8.4</td><td>2.61</td><td>−1.6863395</td><td>1.94E-05</td><td>7.03E-05</td><td>gi|67524027|ref|XP_660074.1|/0/hypothetical protein AN2470.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11347</td><td>30.25</td><td>9.41</td><td>−1.6846685</td><td>3.17E-16</td><td>2.93E-15</td><td>gi|259487951|tpe|CBF87023.1|/9.10923e-07/TPA: cytochrome c oxidase family protein (AFU_orthologue; AFUA_3G14440) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10223</td><td>1080.13</td><td>336.15</td><td>−1.6840279</td><td>0</td><td>0</td><td>gi|67522471|ref|XP_659296.1|/4.83547e-105/hypothetical protein AN1692.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02846</td><td>95.12</td><td>29.62</td><td>−1.6831771</td><td>1.21E-47</td><td>1.91E-46</td><td>gi|259486219|tpe|CBF83884.1|/5.22538e-119/TPA: phospholipid hydroperoxide glutathione peroxidase (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03906</td><td>196.97</td><td>61.34</td><td>−1.6830758</td><td>8.78E-97</td><td>1.89E-95</td><td>gi|259481523|tpe|CBF75123.1|/0/TPA: M protein repeat protein (AFU_orthologue; AFUA_6G08660) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06909</td><td>10.08</td><td>3.14</td><td>−1.6826592</td><td>2.77E-06</td><td>1.12E-05</td><td>gi|67541478|ref|XP_664513.1|/0/hypothetical protein AN6909.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00884</td><td>69.24</td><td>21.61</td><td>−1.6799067</td><td>4.78E-35</td><td>6.54E-34</td><td>gi|67517213|ref|XP_658488.1|/6.46855e-174/hypothetical protein AN0884.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03744</td><td>22.86</td><td>7.14</td><td>−1.6788294</td><td>1.54E-12</td><td>1.03E-11</td><td>gi|67526573|ref|XP_661348.1|/0/hypothetical protein AN3744.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07771</td><td>186.72</td><td>58.38</td><td>−1.6773304</td><td>2.08E-91</td><td>4.36E-90</td><td>gi|67901568|ref|XP_681040.1|/2.09808e-88/hypothetical protein AN7771.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_01794</td><td>8.91</td><td>2.79</td><td>−1.6751603</td><td>1.17E-05</td><td>4.33E-05</td><td>gi|67522675|ref|XP_659398.1|/0/hypothetical protein AN1794.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08562</td><td>28.91</td><td>9.06</td><td>−1.6739857</td><td>1.95E-15</td><td>1.75E-14</td><td>gi|259484517|tpe|CBF80805.1|/0/TPA: ankyrin repeat protein (AFU_orthologue; AFUA_4G01580) [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_01986</td><td>158.48</td><td>49.84</td><td>−1.6689248</td><td>2.54E-77</td><td>5.02E-76</td><td>gi|67523059|ref|XP_659590.1|/8.15427e-49/hypothetical protein AN1986.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07038</td><td>39.33</td><td>12.37</td><td>−1.6687847</td><td>2.18E-20</td><td>2.24E-19</td><td>gi|259483647|tpe|CBF79208.1|/0/TPA: conserved serine-threonine rich protein (AFU_orthologue; AFUA_4G04090) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08548</td><td>219.49</td><td>69.18</td><td>−1.6657283</td><td>########</td><td>########</td><td>gi|67903122|ref|XP_681817.1|/1.77715e-112/hypothetical protein AN8548.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11932</td><td>88.23</td><td>28.06</td><td>−1.6527543</td><td>3.07E-43</td><td>4.64E-42</td><td>gi|146324586|ref|XP_001481421.1|/3.14423e-131/hypothetical protein AFUA_7G01620 [A. fumigatus Af293]</td></tr>
<tr><td>ANID_00330</td><td>64.54</td><td>20.56</td><td>−1.6503533</td><td>5.49E-32</td><td>7.28E-31</td><td>gi|259489437|tpe|CBF89709.1|/0/TPA: indoleamine 2,3-dioxygenase pyrrole 2,3-dioxygenase) (AFU_orthologue; AFUA_5G01450) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03452</td><td>6.55</td><td>2.09</td><td>−1.647992</td><td>0.000213</td><td>0.000668</td><td>gi|67525989|ref|XP_661056.1|/9.63752e-175/hypothetical protein AN3452.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_09067</td><td>79.66</td><td>25.44</td><td>−1.6467568</td><td>5.40E-39</td><td>7.77E-38</td><td>gi|259485522|tpe|CBF82615.1|/0/TPA: TINC (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_12298</td><td>29.41</td><td>9.41</td><td>−1.6440402</td><td>2.52E-15</td><td>2.24E-14</td><td>gi|259484982|tpe|CBF81667.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05050</td><td>9.24</td><td>2.96</td><td>−1.6422957</td><td>1.07E-05</td><td>3.99E-05</td><td>gi|67537760|ref|XP_662654.1|/0/hypothetical protein AN5050.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04395</td><td>94.11</td><td>30.15</td><td>−1.64219</td><td>1.33E-45</td><td>2.05E-44</td><td>gi|259482794|tpe|CBF77614.1|/0/TPA: N-glycosyl-transferase (AFU_orthologue; AFUA_4G06870) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05957</td><td>112.94</td><td>36.25</td><td>−1.6395036</td><td>2.94E-54</td><td>5.00E-53</td><td>gi|238493289|ref|XP_002377881.1|/1.50247e-178/branched-chain amino acid aminotransferase, cytosolic [A. flavus NRRL3357]</td></tr>
<tr><td>ANID_04280</td><td>96.64</td><td>31.02</td><td>−1.6394218</td><td>1.15E-46</td><td>1.80E-45</td><td>gi|67528148|ref|XP_661884.1|/9.6796e-153/hypothetical protein AN4280.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05891</td><td>224.03</td><td>71.97</td><td>−1.6382244</td><td>########</td><td>########</td><td>gi|67539442|ref|XP_663495.1|/0/hypothetical protein AN5891.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02037</td><td>21.68</td><td>6.97</td><td>−1.6371342</td><td>1.33E-11</td><td>8.19E-11</td><td>gi|20429038|emb|CAC87270.1|/0/CipA protein [Emericella nidulans]</td></tr>
<tr><td>ANID_04749</td><td>12.94</td><td>4.18</td><td>−1.6302628</td><td>2.04E-07</td><td>9.17E-07</td><td>gi|7160817|emb|CAB76823.1|/0/ABC transporter protein [Emericella nidulans]</td></tr>
<tr><td>ANID_11933</td><td>8.07</td><td>2.61</td><td>−1.6285189</td><td>4.53E-05</td><td>0.000156</td><td>gi|259485430|tpe|CBF82446.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10694</td><td>16.64</td><td>5.4</td><td>−1.6236241</td><td>4.03E-09</td><td>2.08E-08</td><td>gi|67538784|ref|XP_663166.1|/0/hypothetical protein AN5562.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04208</td><td>55.8</td><td>18.12</td><td>−1.6226822</td><td>3.06E-27</td><td>3.72E-26</td><td>gi|259481185|tpe|CBF74478.1|/0/TPA: sterol o-acyltransferase (APE2), putaitve (AFU_orthologue; AFUA_1G06040) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04353</td><td>19.83</td><td>6.45</td><td>−1.6203136</td><td>1.34E-10</td><td>7.73E-10</td><td>gi|145256553|ref|XP_001401438.1|/0/non-specific lipid-transfer protein [A. niger CBS 513.88]</td></tr>
<tr><td>ANID_00110</td><td>159.49</td><td>51.93</td><td>−1.6188258</td><td>1.48E-74</td><td>2.88E-73</td><td>gi|67515657|ref|XP_657714.1|/9.50709e-91/hypothetical protein AN0110.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10474</td><td>88.57</td><td>28.93</td><td>−1.6142518</td><td>5.24E-42</td><td>7.81E-41</td><td>gi|67526841|ref|XP_661482.1|/0/hypothetical protein AN3878.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05644</td><td>13.28</td><td>4.36</td><td>−1.6068551</td><td>1.86E-07</td><td>8.40E-07</td><td>gi|67538948|ref|XP_663248.1|/0/hypothetical protein AN5644.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01761</td><td>516.45</td><td>170.08</td><td>−1.6024152</td><td>########</td><td>########</td><td>gi|238501716|ref|XP_002382092.1|/1.57243e-68/ubiquitin conjugating enzyme Ubc8, putative [A. flavus NRRL3357]</td></tr>
<tr><td>ANID_00247</td><td>88.9</td><td>29.28</td><td>−1.6022679</td><td>9.84E-42</td><td>1.45E-40</td><td>gi|67515931|ref|XP_657851.1|/0/hypothetical protein AN0247.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06059</td><td>35.8</td><td>11.85</td><td>−1.5950725</td><td>1.27E-17</td><td>1.22E-16</td><td>gi|259479756|tpe|CBF70269.1|/1.89594e-153/TPA: HVA22 domain membrane protein</td></tr>
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						(AFU_orthologue; AFUA_2G09470) [A. nidulans FGSC A4]
ANID_08796	36.3	12.02	−1.5945327	7.77E-18	7.51E-17	gi|67903618|ref|XP_682065.1|/5.44764e-179/hypothetical protein AN8796.2 [A. nidulans FGSC A4]
ANID_04888	3921.21	1298.77	−1.5941529	0	0	gi|259482247|tpe|CBF76546.1|/0/TPA: Pyruvate decarboxylase (EC 4.1.1.1) [Source:UniProtKB/Swiss-Prot;Acc:P87208] [A. nidulans FGSC A4]
ANID_04404	196.46	65.17	−1.5919557	2.83E-89	5.90E-88	gi|67528412|ref|XP_662008.1|/9.60085e-178/hypothetical protein AN4404.2 [A. nidulans FGSC A4]
ANID_01493	572.25	189.95	−1.5910258	########	########	gi|67522072|ref|XP_659097.1|/9.54396e-54/hypothetical protein AN1493.2 [A. nidulans FGSC A4]
ANID_06604	8.4	2.79	−1.5901242	4.11E-05	0.000142	gi|67540868|ref|XP_664208.1|/9.7706e-152/hypothetical protein AN6604.2 [A. nidulans FGSC A4]
ANID_06613	53.44	17.77	−1.5884763	2.04E-25	2.38E-24	gi|67540886|ref|XP_664217.1|/3.94865e-64/hypothetical protein AN6613.2 [A. nidulans FGSC A4]
ANID_05211	112.1	37.29	−1.5879256	1.64E-51	2.73E-50	gi|83766320|dbj|BAE56463.1|/0/unnamed protein product [A. oryzae]
ANID_03927	49.24	16.38	−1.5878954	1.56E-23	1.73E-22	gi|259481499|tpe|CBF75076.1|/0/TPA: inositol phosphosphingolipid phospholipase C (Eurofung) [A. nidulans FGSC A4]
ANID_00878	13.61	4.53	−1.5870841	1.69E-07	7.68E-07	gi|67517201|ref|XP_658482.1|/0/hypothetical protein AN0878.2 [A. nidulans FGSC A4]
ANID_04056	42.86	14.29	−1.5846259	1.28E-20	1.32E-19	gi|259481356|tpe|CBF74795.1|/0/TPA: microbody (peroxisome) biogenesis protein peroxin 2 (Eurofung) [A. nidulans FGSC A4]
ANID_02503	24.54	8.19	−1.5831999	2.08E-12	1.37E-11	gi|310796333|gb|EFQ31794.1|/9.10336e-105/caspase domain-containing protein [Glomerella graminicola M1.001]
ANID_05591	62.35	20.91	−1.5761965	4.38E-29	5.51E-28	gi|67538842|ref|XP_663195.1|/0/hypothetical protein AN5591.2 [A. nidulans FGSC A4]
ANID_08333	46.72	15.68	−1.5751147	3.69E-22	3.97E-21	gi|3647372|emb|CAA09585.1|/1.59542e-86/putative cell wall protein [Emericella nidulans]
ANID_04423	153.1	51.41	−1.5743534	6.88E-69	1.28E-67	gi|67528450|ref|XP_662027.1|/2.97249e-120/hypothetical protein AN4423.2 [A. nidulans FGSC A4]
ANID_10201	18.15	6.1	−1.5730884	1.84E-09	9.82E-09	gi|67522060|ref|XP_659091.1|/0/hypothetical protein AN1487.2 [A. nidulans FGSC A4]
ANID_00306	273.27	92.18	−1.5678014	########	########	gi|67516049|ref|XP_657910.1|/6.83959e-147/hypothetical protein AN0306.2 [A. nidulans FGSC A4]
ANID_08959	7.73	2.61	−1.5664186	0.000104	0.00034	gi|259486594|tpe|CBF84569.1|/2.46206e-90/TPA: benzodiazepine receptor family protein (AFU_orthologue; AFUA_3G01430) [A. nidulans FGSC A4]
ANID_06645	81.51	27.53	−1.5659725	3.48E-37	4.88E-36	gi|238556154|gb|ACR44939.1|/0/8-amino-7-oxononanoate synthase [Emericella nidulans]
ANID_06386	103.53	35.03	−1.563386	1.11E-46	1.73E-45	gi|259479390|tpe|CBF69569.1|/2.61464e-140/TPA: mitochondrial NADH-cytochrome b5 reductase (Eurofung) [A. nidulans FGSC A4]
ANID_06568	25.71	8.71	−1.561585	1.04E-12	7.07E-12	gi|259480141|tpe|CBF71002.1|/0/TPA: SET domain protein (AFU_orthologue; AFUA_6G04520) [A. nidulans FGSC A4]
ANID_06295	16.97	5.75	−1.5613527	7.50E-09	3.80E-08	gi|67540250|ref|XP_663899.1|/0/hypothetical protein AN6295.2 [A. nidulans FGSC A4]
ANID_12229	691.07	234.21	−1.5610292	########	########	gi|169773843|ref|XP_001821390.1|/2.0019e-96/UBX domain protein [A. oryzae RIB40]
ANID_02224	157.64	53.5	−1.5590229	6.76E-70	1.28E-68	gi|259487610|tpe|CBF86416.1|/0/TPA: vacuolar protein sorting-associated protein vps17 (AFU_orthologue; AFUA_5G07150) [A. nidulans FGSC A4]
ANID_08863	955.26	325.17	−1.5546993	0	0	gi|67903752|ref|XP_682132.1|/1.40921e-140/hypothetical protein AN8863.2 [A. nidulans FGSC A4]
ANID_02188	23.02	7.84	−1.5539623	1.87E-11	1.14E-10	gi|67523465|ref|XP_659792.1|/0/hypothetical protein AN2188.2 [A. nidulans FGSC A4]
ANID_01743	143.02	48.79	−1.5515595	3.88E-63	7.04E-62	gi|67522573|ref|XP_659347.1|/2.73192e-176/hypothetical protein AN1743.2 [A. nidulans FGSC A4]
ANID_02387	53.61	18.3	−1.5506585	1.11E-24	1.27E-23	gi|255954763|ref|XP_002568134.1|/2.57508e-158/Pc21g11020 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_03616	50.92	17.43	−1.5466599	1.94E-23	2.14E-22	gi|67526317|ref|XP_661220.1|/9.29026e-47/hypothetical protein AN3616.2 [A. nidulans FGSC A4]
ANID_03019	96.13	32.94	−1.5451462	9.20E-43	1.38E-41	gi|67525123|ref|XP_660623.1|/2.93471e-128/hypothetical protein AN3019.2 [A. nidulans FGSC A4]
ANID_08462	33.95	11.68	−1.5393713	5.02E-16	4.60E-15	gi|67902950|ref|XP_681731.1|/0/hypothetical protein AN8462.2 [A. nidulans FGSC A4]
ANID_00840	55.12	18.99	−1.537336	5.05E-25	5.80E-24	gi|259488875|tpe|CBF88679.1|/0/TPA: 2-isopropylmalate synthase (Eurofung) [A. nidulans FGSC A4]
ANID_05497	14.62	5.05	−1.533588	1.24E-07	5.72E-07	gi|115390038|ref|XP_001212524.1|/8.20477e-75/3,4-dihydroxy-2-butanone 4-phosphate synthase [A. terreus NIH2624]
ANID_06734	47.9	16.55	−1.5331944	7.36E-22	7.83E-21	gi|259480326|tpe|CBF71354.1|/0/TPA: mRNA transport regulator (Mtr10), putative (AFU_orthologue; AFUA_7G05970) [A. nidulans FGSC A4]
ANID_00050	22.69	7.84	−1.5331311	4.12E-11	2.46E-10	gi|259489762|tpe|CBF90301.1|/0/TPA: iso-orotate decarboxylase (Eurofung) [A. nidulans FGSC A4]
ANID_05908	10.59	3.66	−1.532787	7.16E-06	2.75E-05	gi|67539476|ref|XP_663512.1|/9.02312e-125/hypothetical protein AN5908.2 [A. nidulans FGSC A4]
ANID_11249	10.59	3.66	−1.532787	7.16E-06	2.75E-05	gi|119469775|ref|XP_001257980.1|/2.92e-110/metallopeptidase Mip1 [Neosartorya fischeri NRRL 181]
ANID_00929	7.06	2.44	−1.532787	0.000262	0.000811	gi|259488783|tpe|CBF88506.1|/0/TPA: choline kinase, putative (AFU_orthologue; AFUA_1G15930) [A. nidulans FGSC A4]
ANID_04024	66.22	23	−1.5256332	1.99E-29	2.53E-28	gi|67527223|ref|XP_661628.1|/0/hypothetical protein AN4024.2 [A. nidulans FGSC A4]
ANID_00475	27.56	9.58	−1.5244783	4.22E-13	3.03E-12	gi|259489276|tpe|CBF89414.1|/0/TPA: small nucleolar ribonucleoprotein complex subunit Utp14, putatrive (AFU_orthologue; AFUA_1G04240) [A. nidulans FGSC A4]
ANID_10088	59.66	20.74	−1.5243481	1.19E-26	1.43E-25	gi|115388591|ref|XP_001211801.1|/9.42251e-130/protein phosphatases PP1 regulatory subunit sds22 [A. terreus NIH2624]

ANID_00993	26.89	9.41	−1.5148031	1.02E-12	6.94E-12	gi|255956827|ref|XP_002569166.1|/0/Pc21g21950 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_06337	1463.65	512.85	−1.5129618	0	0	gi|261199382|ref|XP_002626092.1|/1.59516e-12/hypothetical protein BDBG_03256 [Ajellomyces dermatitidis SLH14081]
ANID_10081	42.18	14.81	−1.5099875	4.84E-19	4.79E-18	gi|67763579|emb|CAI47587.1|/0/alpha-ketoglutarate dependent xanthine dioxygenase [Emericella nidulans]
ANID_07260	9.41	3.31	−1.5073635	2.97E-05	0.000105	gi|259483394|tpe|CBF78749.1|/0/TPA: nuclear export protein Noc3 (AFU_orthologue; AFUA_2G17050) [A. nidulans FGSC A4]
ANID_10405	9.41	3.31	−1.5073635	2.97E-05	0.000105	gi|259485654|tpe|CBF82859.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00454	56.97	20.04	−1.5073199	3.99E-25	4.60E-24	gi|67516345|ref|XP_658058.1|/0/hypothetical protein AN0454.2 [A. nidulans FGSC A4]
ANID_00317	9.92	3.49	−1.5071131	1.78E-05	6.45E-05	gi|259489453|tpe|CBF89737.1|/0/TPA: EF hand domain protein (AFU_orthologue; AFUA_1G02540) [A. nidulans FGSC A4]
ANID_00053	17.81	6.27	−1.5061502	8.11E-09	4.10E-08	gi|259489759|tpe|CBF90296.1|/3.64138e-128/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02427	54.45	19.17	−1.5060817	4.67E-24	5.25E-23	gi|259487839|tpe|CBF86831.1|/3.9854e-177/TPA: annexin, putative (Eurofung) [A. nidulans FGSC A4]
ANID_02082	36.64	12.9	−1.5060484	1.11E-16	1.03E-15	gi|259487451|tpe|CBF86140.1|/0/TPA: BSD domain protein (AFU_orthologue; AFUA_2G04840) [A. nidulans FGSC A4]
ANID_00078	8.4	2.96	−1.5047922	8.29E-05	0.000277	gi|74582073|sp|O42631.1|MUB1_EMENI/0/RecName: Full=MYND-type zinc finger protein samB; AltName: Full=Suppressor of anucleate metulae protein B
ANID_10055	8.91	3.14	−1.5046609	4.95E-05	0.00017	gi|259489420|tpe|CBF89678.1|/2.61479e-176/TPA: 60S ribosome biogenesis protein Brx1, putative (AFU_orthologue; AFUA_1G02210) [A. nidulans FGSC A4]
ANID_03973	196.46	69.36	−1.5020598	3.74E-82	7.43E-81	gi|259481447|tpe|CBF74973.1|/2.4087e-140/TPA: mitochondrial peroxiredoxin (Eurofung) [A. nidulans FGSC A4]
ANID_04633	66.55	23.53	−1.4999373	6.80E-29	8.51E-28	gi|67536926|ref|XP_662237.1|/1.69959e-38/hypothetical protein AN4633.2 [A. nidulans FGSC A4]
ANID_00323	42.35	14.99	−1.4983616	6.39E-19	6.30E-18	gi|67516083|ref|XP_657927.1|/3.41979e-161/hypothetical protein AN0323.2 [A. nidulans FGSC A4]
ANID_00885	71.76	25.44	−1.4960812	6.60E-31	8.61E-30	gi|67517215|ref|XP_658489.1|/0/hypothetical protein AN0885.2 [A. nidulans FGSC A4]
ANID_05340	58.49	20.74	−1.4957741	1.77E-25	2.07E-24	gi|67538340|ref|XP_662944.1|/4.31003e-146/hypothetical protein AN5340.2 [A. nidulans FGSC A4]
ANID_02903	436.46	154.92	−1.494326	########	########	gi|259486160|tpe|CBF83780.1|/0/TPA: vacuolar aspartyl protease (proteinase A) (Eurofung) [A. nidulans FGSC A4]
ANID_00932	170.58	60.64	−1.4921068	7.10E-71	1.36E-69	gi|259488780|tpe|CBF88500.1|/0/TPA: hypothetical glutathione reductase (Eurofung) [A. nidulans FGSC A4]
ANID_02014	161.17	57.33	−1.491221	5.25E-67	9.71E-66	gi|67523115|ref|XP_659618.1|/0/hypothetical protein AN2014.2 [A. nidulans FGSC A4]
ANID_05113	85.21	30.32	−1.490753	3.29E-36	4.58E-35	gi|259484558|tpe|CBF80885.1|/2.51264e-171/TPA: microbody (peroxisome) biogenesis protein peroxin 16 (Eurofung) [A. nidulans FGSC A4]
ANID_07542	10.76	3.83	−1.4902618	9.50E-06	3.59E-05	gi|165931814|emb|CAM35586.1|/0/bZIP-type transcription factor [Emericella nidulans]
ANID_05198	16.13	5.75	−1.4881126	5.40E-08	2.56E-07	gi|67538056|ref|XP_662802.1|/0/hypothetical protein AN5198.2 [A. nidulans FGSC A4]
ANID_03823	10.25	3.66	−1.4857084	1.58E-05	5.77E-05	gi|115442694|ref|XP_001218154.1|/7.77382e-39/40S ribosomal protein S21 [A. terreus NIH2624]
ANID_04313	30.59	10.98	−1.4781821	8.13E-14	6.55E-13	gi|67528214|ref|XP_661917.1|/0/hypothetical protein AN4313.2 [A. nidulans FGSC A4]
ANID_04388	8.74	3.14	−1.4768687	7.36E-05	0.000248	gi|67528380|ref|XP_661992.1|/2.3167e-22/hypothetical protein AN4388.2 [A. nidulans FGSC A4]
ANID_04174	134.79	48.44	−1.4764427	1.63E-55	2.78E-54	gi|259481228|tpe|CBF74555.1|/1.54062e-176/TPA: glyoxalase (Eurofung) [A. nidulans FGSC A4]
ANID_03707	19.83	7.14	−1.4736887	2.12E-09	1.13E-08	gi|311338123|gb|EFQ97325.1|/0/allantoate amidohydrolase [Arthroderma gypseum CBS 118893]
ANID_02992	11.6	4.18	−1.47255	5.08E-06	1.99E-05	gi|67525069|ref|XP_660596.1|/8.67848e-137/hypothetical protein AN2992.2 [A. nidulans FGSC A4]
ANID_09434	50.25	18.12	−1.4715406	1.31E-21	1.37E-20	gi|259482712|tpe|CBF77452.1|/0/TPA: zinc metalloprotease, putative (AFU_orthologue; AFUA_4G07610) [A. nidulans FGSC A4]
ANID_08055	18.82	6.8	−1.46866	5.77E-09	2.95E-08	gi|67902136|ref|XP_681324.1|/0/hypothetical protein AN8055.2 [A. nidulans FGSC A4]
ANID_11758	10.59	3.83	−1.4672863	1.41E-05	5.16E-05	gi|121708349|ref|XP_001272103.1|/1.83141e-153/conserved hypothetical protein [A. clavatus NRRL 1]
ANID_08499	25.04	9.06	−1.4666516	1.91E-11	1.16E-10	gi|67903024|ref|XP_681768.1|/0/hypothetical protein AN8499.2 [A. nidulans FGSC A4]
ANID_00631	16.81	6.1	−1.4624386	4.28E-08	2.04E-07	gi|67516699|ref|XP_658235.1|/1.21839e-114/hypothetical protein AN0631.2 [A. nidulans FGSC A4]
ANID_01933	181.34	65.87	−1.4610037	5.75E-73	1.11E-71	gi|259487292|tpe|CBF85851.1|/3.57676e-172/TPA: evolutionarily conserved protein with similarity to Orm2p (Eurofung) [A. nidulans FGSC A4]
ANID_11281	58.99	21.43	−1.4608386	7.61E-25	8.71E-24	gi|259488931|tpe|CBF88782.1|/4.75296e-29/TPA: hypothetical protein ANIA_11281 [A. nidulans FGSC A4]
ANID_00628	35.97	13.07	−1.460535	9.86E-16	8.94E-15	gi|259489106|tpe|CBF89103.1|/0/TPA: D-lactate dehydrogenase, putative (AFU_orthologue; AFUA_1G17040) [A. nidulans FGSC A4]
ANID_07568	61.17	22.31	−1.4551338	1.39E-25	1.63E-24	gi|67901162|ref|XP_680837.1|/0/hypothetical protein AN7568.2 [A. nidulans FGSC A4]
ANID_07214	105.04	38.34	−1.4540166	1.05E-42	1.57E-41	gi|259483448|tpe|CBF78846.1|/0/TPA: NADPH-dependent FMN reductase Lot6, putative (AFU_orthologue; AFUA_7G06600) [A. nidulans FGSC A4]
ANID_04780	113.44	41.47	−1.4517895	7.08E-46	1.10E-44	gi|259482374|tpe|CBF76796.1|/5.0755e-130/TPA: pyridoxamine phosphate oxidase, putative (AFU_orthologue; AFUA_3G06670) [A. nidulans FGSC A4]

ANID_04064	8548.61	3127.13	–1.4508507	0	0	gi|67527372|ref|XP_661668.1|/1.13116e-157/ADT_NEUCR ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) [A. nidulans FGSC A4]
ANID_02107	70.92	25.97	–1.4493465	3.06E-29	3.87E-28	gi|259487479|tpe|CBF86191.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_09080	684.18	251.11	–1.4460564	########	########	gi|259485509|tpe|CBF82591.1|/3.48533e-49/TPA: L-PSP endoribonuclease family protein (Hmf1), putative (AFU_orthologue; AFUA_7G02340) [A. nidulans FGSC A4]
ANID_10793	21.34	7.84	–1.4446346	9.08E-10	4.92E-09	gi|259479564|tpe|CBF69902.1|/1.59104e-170/TPA: alcohol dehydrogenase, putative (AFU_orthologue; AFUA_2G13270) [A. nidulans FGSC A4]
ANID_07740	18.49	6.8	–1.4431386	1.24E-08	6.15E-08	gi|67901504|ref|XP_681008.1|/1.94202e-45/hypothetical protein AN7739.2 [A. nidulans FGSC A4]
ANID_07496	80.33	29.62	–1.4393672	1.43E-32	1.91E-31	gi|259483805|tpe|CBF79496.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_09063	92.6	34.16	–1.4387042	2.77E-37	3.91E-36	gi|67904152|ref|XP_682332.1|/0/hypothetical protein AN9063.2 [A. nidulans FGSC A4]
ANID_01983	86.89	32.06	–1.4384157	4.65E-35	6.37E-34	gi|67523053|ref|XP_659587.1|/0/hypothetical protein AN1983.2 [A. nidulans FGSC A4]
ANID_12094	39.66	14.64	–1.4377691	7.66E-17	7.19E-16	gi|67527644|ref|XP_661703.1|/8.16997e-106/hypothetical protein AN4099.2 [A. nidulans FGSC A4]
ANID_00709	842.32	312.1	–1.4323601	0	0	gi|49618685|gb|AAT67992.1|/0/SILG [Emericella nidulans]
ANID_00856	159.99	59.42	–1.4289612	1.55E-62	2.80E-61	gi|259488859|tpe|CBF88649.1|/0/TPA: choline transporter (Eurofung) [A. nidulans FGSC A4]
ANID_03687	58.15	21.61	–1.4280801	9.33E-24	1.04E-22	gi|67526459|ref|XP_661291.1|/1.12775e-87/hypothetical protein AN3687.2 [A. nidulans FGSC A4]
ANID_01450	82.52	30.67	–1.4279157	4.89E-33	6.55E-32	gi|67521986|ref|XP_659054.1|/2.86257e-175/hypothetical protein AN1450.2 [A. nidulans FGSC A4]
ANID_10365	40.33	14.99	–1.427853	6.04E-17	5.69E-16	gi|259485923|tpe|CBF83358.1|/6.56167e-84/TPA: ubiquitin conjugating enzyme (UbcB), putative (AFU_orthologue; AFUA_3G12850) [A. nidulans FGSC A4]
ANID_11066	15.46	5.75	–1.4269065	2.50E-07	1.12E-06	gi|259481079|tpe|CBF74283.1|/7.23902e-100/TPA: G-patch RNA maturation protein (Gno1), putative (AFU_orthologue; AFUA_7G03690) [A. nidulans FGSC A4]
ANID_06542	1837.92	684.5	–1.4249515	0	0	gi|70984170|ref|XP_747604.1|/0/actin Act1 [A. fumigatus Af293]
ANID_01996	30.76	11.5	–1.4194216	3.78E-13	2.73E-12	gi|259487360|tpe|CBF85975.1|/0/TPA: YagE family protein (AFU_orthologue; AFUA_4G10390) [A. nidulans FGSC A4]
ANID_04346	75.96	28.4	–1.419349	2.81E-30	3.60E-29	gi|259482846|tpe|CBF77715.1|/7.64416e-158/TPA: ribosomal biogenesis protein Gar2 (AFU_orthologue; AFUA_4G06350) [A. nidulans FGSC A4]
ANID_00470	181.17	67.79	–1.4181997	8.35E-70	1.57E-68	gi|259489281|tpe|CBF89423.1|/9.1428e-175/TPA: 30S ribosomal protein S7, putative (AFU_orthologue; AFUA_1G04280) [A. nidulans FGSC A4]
ANID_00867	11.6	4.36	–1.4117248	9.68E-06	3.65E-05	gi|67517179|ref|XP_658471.1|/0/hypothetical protein AN0867.2 [A. nidulans FGSC A4]
ANID_06310	16.64	6.27	–1.4081181	1.18E-07	5.46E-07	gi|67540280|ref|XP_663914.1|/0/hypothetical protein AN6310.2 [A. nidulans FGSC A4]
ANID_05179	18.49	6.97	–1.4075147	2.33E-08	1.13E-07	gi|74595337|sp|Q5B2Q1.1|DPH2_EMENI/0/RecName: Full=Diphthamide biosynthesis protein 2
ANID_06318	153.94	58.03	–1.4074973	6.32E-59	1.11E-57	gi|2308977|dbj|BAA21714.1|/0/chitin synthase [Emericella nidulans]
ANID_03789	23.53	8.89	–1.404246	3.00E-10	1.69E-09	gi|259481656|tpe|CBF75380.1|/2.0356e-176/TPA: DUF52 domain protein (AFU_orthologue; AFUA_2G03970) [A. nidulans FGSC A4]
ANID_00362	103.69	39.21	–1.4029832	4.59E-40	6.68E-39	gi|67516161|ref|XP_657966.1|/2.01506e-97/hypothetical protein AN0362.2 [A. nidulans FGSC A4]
ANID_01856	39.16	14.81	–1.4028091	4.35E-16	4.00E-15	gi|67522799|ref|XP_659460.1|/0/hypothetical protein AN1856.2 [A. nidulans FGSC A4]
ANID_02794	8.74	3.31	–1.4008021	0.000141	0.000452	gi|67524673|ref|XP_660398.1|/0/hypothetical protein AN2794.2 [A. nidulans FGSC A4]
ANID_11912	8.74	3.31	–1.4008021	0.000141	0.000452	gi|67536762|ref|XP_662155.1|/5.29906e-180/hypothetical protein AN4551.2 [A. nidulans FGSC A4]
ANID_06964	8.74	3.31	–1.4008021	0.000141	0.000451	gi|67541601|ref|XP_664568.1|/2.38192e-130/hypothetical protein AN6964.2 [A. nidulans FGSC A4]
ANID_01999	106.05	40.25	–1.3976839	1.07E-40	1.55E-39	gi|259487364|tpe|CBF85983.1|/1.93485e-177/TPA: 3-demethylubiquinone-9 3-methyltransferase (AFU_orthologue; AFUA_4G10370) [A. nidulans FGSC A4]
ANID_00790	413.94	157.18	–1.397004	########	########	gi|259488929|tpe|CBF88778.1|/5.59336e-15/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06754	106.89	40.6	–1.3965753	5.79E-41	8.51E-40	gi|67541168|ref|XP_664358.1|/3.37752e-49/hypothetical protein AN6754.2 [A. nidulans FGSC A4]
ANID_02902	44.03	16.73	–1.3960494	8.56E-18	8.25E-17	gi|259486161|tpe|CBF83781.1|/0/TPA: CTD phosphatase-related (Eurofung) [A. nidulans FGSC A4]
ANID_01416	53.11	20.21	–1.3939142	4.29E-21	4.46E-20	gi|67521918|ref|XP_659020.1|/0/hypothetical protein AN1416.2 [A. nidulans FGSC A4]
ANID_06169	136.3	51.93	–1.3921454	1.56E-51	2.60E-50	gi|67539998|ref|XP_663773.1|/0/hypothetical protein AN6169.2 [A. nidulans FGSC A4]
ANID_01923	9.58	3.66	–1.388182	7.40E-05	0.000249	gi|259487282|tpe|CBF85834.1|/0/TPA: alanine transaminase (Eurofung) [A. nidulans FGSC A4]
ANID_10515	9.58	3.66	–1.388182	7.40E-05	0.000249	gi|259481204|tpe|CBF74512.1|/0/TPA: serine/threonine protein kinase, putative (AFU_orthologue; AFUA_1G05930) [A. nidulans FGSC A4]
ANID_06091	54.28	20.74	–1.3880048	2.05E-21	2.15E-20	gi|259479721|tpe|CBF70202.1|/0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_02952	25.04	9.58	–1.386137	1.26E-10	7.26E-10	gi|259486106|tpe|CBF83684.1|/1.47948e-55/TPA: cell surface spherulin 4-like protein, putative (AFU_orthologue; AFUA_3G07900) [A. nidulans FGSC A4]
ANID_10284	32.77	12.55	–1.3846883	1.80E-13	1.37E-12	gi|259487647|tpe|CBF86476.1|/6.75821e-152/TPA: glutathione synthetase, putative (AFU_orthologue; AFUA_5G06610) [A. nidulans FGSC A4]

ANID_10910	45.88	17.6	−1.38229	3.19E-18	3.10E-17	gi|259483431|tpe|CBF78815.1|/0/TPA: Putative transcription factor with C2H2 and Zn(2)-Cys(6) DNA binding domain (Eurofung) [A. nidulans FGSC A4]
ANID_04682	12.27	4.71	−1.3813363	7.47E-06	2.86E-05	gi|67537024|ref|XP_662286.1|/2.3984e-35/hypothetical protein AN4682.2 [A. nidulans FGSC A4]
ANID_01156	40.84	15.68	−1.3810573	2.34E-16	2.16E-15	gi|67517971|ref|XP_658760.1|/0/hypothetical protein AN1156.2 [A. nidulans FGSC A4]
ANID_07463	41.18	15.86	−1.3765511	2.06E-16	1.91E-15	gi|159129125|gb|EDP54239.1|/0/ammonium transporter MeaA [A. fumigatus A1163]
ANID_04094	130.92	50.54	−1.3731879	1.37E-48	2.20E-47	gi|259481316|tpe|CBF74719.1|/0/TPA: c-14 sterol reductase (AFU_orthologue; AFUA_1G03150) [A. nidulans FGSC A4]
ANID_05455	31.6	12.2	−1.3730434	6.93E-13	4.79E-12	gi|74595131|sp|Q5B1X5.1|UTP10_EMENI/0/RecName: Full=U3 small nucleolar RNA-associated protein 10
ANID_02870	9.92	3.83	−1.3729957	6.47E-05	0.000219	gi|67524825|ref|XP_660474.1|/0/hypothetical protein AN2870.2 [A. nidulans FGSC A4]
ANID_05407	63.36	24.57	−1.3666745	3.46E-24	3.90E-23	gi|67538474|ref|XP_663011.1|/0/hypothetical protein AN5407.2 [A. nidulans FGSC A4]
ANID_04997	403.18	156.49	−1.3653536	########	########	gi|67537654|ref|XP_662601.1|/6.01195e-163/hypothetical protein AN4997.2 [A. nidulans FGSC A4]
ANID_08063	212.77	82.6	−1.3650811	3.64E-77	7.16E-76	gi|67902152|ref|XP_681332.1|/0/hypothetical protein AN8063.2 [A. nidulans FGSC A4]
ANID_03431	20.17	7.84	−1.3632855	1.23E-08	6.10E-08	gi|259485580|tpe|CBF82722.1|/8.20463e-152/TPA: nicotinate-nucleotide diphosphorylase (Eurofung) [A. nidulans FGSC A4]
ANID_06973	1872.37	728.24	−1.3623797	0	0	gi|259483721|tpe|CBF79344.1|/5.76755e-178/TPA: C-4 methyl sterol oxidase Erg25, putative (AFU_orthologue; AFUA_4G04820) [A. nidulans FGSC A4]
ANID_01213	17.48	6.8	−1.3620985	1.16E-07	5.38E-07	gi|67518108|ref|XP_658817.1|/0/hypothetical protein AN1213.2 [A. nidulans FGSC A4]
ANID_08491	191.93	74.76	−1.3602418	2.03E-69	3.80E-68	gi|67903008|ref|XP_681760.1|/1.47174e-95/hypothetical protein AN8491.2 [A. nidulans FGSC A4]
ANID_01397	16.97	6.62	−1.3580834	1.91E-07	8.64E-07	gi|78097996|gb|ABB20530.1|/0/3-hydroxyphenylacetate 6 hydroxylase [Emericella nidulans]
ANID_02515	41.51	16.21	−1.3565748	3.29E-16	3.03E-15	gi|67524115|ref|XP_660119.1|/6.25531e-119/hypothetical protein AN2515.2 [A. nidulans FGSC A4]
ANID_04503	38.32	14.99	−1.3540972	4.90E-15	4.28E-14	gi|67535083|ref|XP_662107.1|/5.40708e-69/hypothetical protein AN4503.2 [A. nidulans FGSC A4]
ANID_11123	212.93	83.3	−1.3539908	2.67E-76	5.21E-75	gi|259482984|tpe|CBF77977.1|/3.54252e-92/TPA: hypothetical protein ANIA_11123 [A. nidulans FGSC A4]
ANID_01844	15.13	5.92	−1.3537429	9.75E-07	4.11E-06	gi|68052396|sp|P78612.1|PALF_EMENI/0/RecName: Full=pH-response regulator protein palF/RIM8
ANID_10826	161.34	63.26	−1.3507387	4.89E-58	8.56E-57	gi|67540656|ref|XP_664102.1|/6.37577e-79/hypothetical protein AN6498.2 [A. nidulans FGSC A4]
ANID_00252	128.4	50.36	−1.350295	1.63E-46	2.54E-45	gi|67515941|ref|XP_657856.1|/9.18643e-126/hypothetical protein AN0252.2 [A. nidulans FGSC A4]
ANID_12084	298.64	117.45	−1.3463607	########	########	gi|295665710|ref|XP_002793406.1|/1.60696e-08/hypothetical protein PAAG_04935 [Paracoccidioides brasiliensis Pb01]
ANID_02911	141.34	55.76	−1.3418673	1.48E-50	2.43E-49	gi|25990171|gb|AAN75015.1|/0/AtfA [Emericella nidulans]
ANID_00798	495.78	195.87	−1.3398036	########	########	gi|67517035|ref|XP_658402.1|/8.69824e-138/hypothetical protein AN0798.2 [A. nidulans FGSC A4]
ANID_09148	879.63	348	−1.3378095	########	########	gi|67904322|ref|XP_682417.1|/0/hypothetical protein AN9148.2 [A. nidulans FGSC A4]
ANID_06921	722.5	286.31	−1.3354195	########	########	gi|67541502|ref|XP_664525.1|/4.59168e-57/hypothetical protein AN6921.2 [A. nidulans FGSC A4]
ANID_04257	11.43	4.53	−1.3352424	2.59E-05	9.21E-05	gi|67528041|ref|XP_661861.1|/0/hypothetical protein AN4257.2 [A. nidulans FGSC A4]
ANID_03957	13.61	5.4	−1.3336358	4.37E-06	1.72E-05	gi|17223765|gb|AAL10515.1|/0/general amidase [Emericella nidulans]
ANID_06208	15.8	6.27	−1.3333872	7.45E-07	3.18E-06	gi|259479594|tpe|CBF69959.1|/2.80827e-120/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06844	41.68	16.55	−1.3325241	7.40E-16	6.75E-15	gi|259480441|tpe|CBF71576.1|/0/TPA: mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative (AFU_orthologue; AFUA_5G12790) [A. nidulans FGSC A4]
ANID_10682	36.81	14.64	−1.3301822	3.81E-14	3.14E-13	gi|259485019|tpe|CBF81734.1|/0/TPA: vacuole-associated enzyme activator complex component (Vac14), putative (AFU_orthologue; AFUA_6G12890) [A. nidulans FGSC A4]
ANID_02147	10.08	4.01	−1.3298215	8.17E-05	0.000273	gi|67523381|ref|XP_659751.1|/0/hypothetical protein AN2147.2 [A. nidulans FGSC A4]
ANID_00174	43.36	17.25	−1.3297684	2.15E-16	1.99E-15	gi|259489620|tpe|CBF90041.1|/2.9315e-155/TPA: D-amino acid oxidase (AFU_orthologue; AFUA_5G11290) [A. nidulans FGSC A4]
ANID_11956	40.17	16.03	−1.325344	3.19E-15	2.82E-14	gi|115492785|ref|XP_001211020.1|/0/conserved hypothetical protein [A. terreus NIH2624]
ANID_05192	9.58	3.83	−1.3226813	0.000136	0.000436	gi|67538044|ref|XP_662796.1|/0/hypothetical protein AN5192.2 [A. nidulans FGSC A4]
ANID_05618	33.11	13.24	−1.3223639	9.28E-13	6.33E-12	gi|259484913|tpe|CBF81540.1|/4.90402e-104/TPA: Spindle pole body protein An-Cdc31 (Eurofung) [A. nidulans FGSC A4]
ANID_01543	138.82	55.59	−1.3203181	1.64E-48	2.62E-47	gi|67522172|ref|XP_659147.1|/0/hypothetical protein AN1543.2 [A. nidulans FGSC A4]
ANID_04935	11.76	4.71	−1.3200891	2.25E-05	8.07E-05	gi|259482194|tpe|CBF76443.1|/0/TPA: protein serine/threonine kinase (Ran1), putative (AFU_orthologue; AFUA_3G10530) [A. nidulans FGSC A4]
ANID_08857	50.42	20.21	−1.3189268	1.34E-18	1.31E-17	gi|259482925|tpe|CBF77865.1|/1.40648e-75/TPA: cell cycle control protein Cwf14/Bud31, putative (AFU_orthologue; AFUA_5G05610) [A. nidulans FGSC A4]
ANID_05740	680.65	273.42	−1.3157944	########	########	gi|70991469|ref|XP_750583.1|/1.03119e-83/Rho GTPase Rho1 [A. fumigatus Af293]
ANID_02596	147.89	59.42	−1.315504	2.75E-51	4.55E-50	gi|146324659|ref|XP_001481394.1|/0/cytochrome P450 [A. fumigatus Af293]
ANID_10452	30.76	12.37	−1.31421	7.47E-12	4.71E-11	gi|67526409|ref|XP_661266.1|/0/hypothetical protein AN3662.2 [A. nidulans FGSC A4]
ANID_03149	82.69	33.28	−1.3130574	2.53E-29	3.21E-28	gi|67525383|ref|XP_660753.1|/2.05976e-134/hypothetical protein AN3149.2 [A. nidulans FGSC A4]

ANID_07661	147.39	59.42	−1.3106181	7.81E-51	1.28E-49	gi|67901348|ref|XP_680930.1|/0/hypothetical protein AN7661.2 [A. nidulans FGSC A4]
ANID_02058	15.13	6.1	−1.3105308	1.75E-06	7.23E-06	gi|67523203|ref|XP_659662.1|/0/hypothetical protein AN2058.2 [A. nidulans FGSC A4]
ANID_02183	15.13	6.1	−1.3105308	1.75E-06	7.23E-06	gi|67523455|ref|XP_659787.1|/0/hypothetical protein AN2183.2 [A. nidulans FGSC A4]
ANID_03620	18.15	7.32	−1.310054	1.60E-07	7.27E-07	gi|67526325|ref|XP_661224.1|/2.36559e-110/hypothetical protein AN3620.2 [A. nidulans FGSC A4]
ANID_05140	25.04	10.11	−1.3084516	7.35E-10	4.02E-09	gi|67537940|ref|XP_662744.1|/0/hypothetical protein AN5140.2 [A. nidulans FGSC A4]
ANID_08200	12.94	5.23	−1.3069548	1.03E-05	3.89E-05	gi|67902426|ref|XP_681469.1|/2.51461e-83/hypothetical protein AN8200.2 [A. nidulans FGSC A4]
ANID_07503	39.66	16.03	−1.3069103	9.17E-15	7.92E-14	gi|67901032|ref|XP_680772.1|/0/hypothetical protein AN7503.2 [A. nidulans FGSC A4]
ANID_05033	13.78	5.58	−1.3042389	5.45E-06	2.13E-05	gi|67537726|ref|XP_662637.1|/4.56696e-159/hypothetical protein AN5033.2 [A. nidulans FGSC A4]
ANID_07033	133.61	54.37	−1.2971453	1.54E-45	2.37E-44	gi|67541739|ref|XP_664637.1|/2.52478e-118/hypothetical protein AN7033.2 [A. nidulans FGSC A4]
ANID_02171	9.41	3.83	−1.2968503	0.000195	0.000613	gi|67523431|ref|XP_659775.1|/1.30925e-36/hypothetical protein AN2171.2 [A. nidulans FGSC A4]
ANID_03799	43.19	17.6	−1.2951219	9.50E-16	8.63E-15	gi|67526683|ref|XP_661403.1|/1.46821e-179/hypothetical protein AN3799.2 [A. nidulans FGSC A4]
ANID_00303	31.6	12.9	−1.2925535	7.06E-12	4.46E-11	gi|67516043|ref|XP_657907.1|/0/hypothetical protein AN0303.2 [A. nidulans FGSC A4]
ANID_00895	14.45	5.92	−1.2874004	4.11E-06	1.63E-05	gi|67517237|ref|XP_658499.1|/0/hypothetical protein AN0895.2 [A. nidulans FGSC A4]
ANID_00902	8.91	3.66	−1.2835818	0.000323	0.000989	gi|67517252|ref|XP_658506.1|/0/hypothetical protein AN0902.2 [A. nidulans FGSC A4]
ANID_04570	17.81	7.32	−1.282772	3.24E-07	1.44E-06	gi|67536800|ref|XP_662174.1|/0/hypothetical protein AN4570.2 [A. nidulans FGSC A4]
ANID_08676	9.75	4.01	−1.2818	0.000169	0.000536	gi|61808335|gb|AAX56093.1|/3.33521e-47/MCMA [Emericella nidulans]
ANID_00474	12.27	5.05	−1.28078	2.43E-05	8.66E-05	gi|67516385|ref|XP_658078.1|/1.31886e-129/hypothetical protein AN0474.2 [A. nidulans FGSC A4]
ANID_02481	55.29	22.83	−1.2760877	2.48E-19	2.47E-18	gi|158563871|sp|Q5BAE9.2|NTE1_EMENI/0/RecName: Full=Lysophospholipase nte1; AltName: Full=Intracellular phospholipase B; AltName: Full=Neuropathy target esterase homolog
ANID_00273	257.81	106.47	−1.2758612	4.45E-84	8.92E-83	gi|259489508|tpe|CBF89837.1|/0/TPA: Putative C2H2 finger domain transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_01507	24.03	9.93	−1.274971	3.43E-09	1.78E-08	gi|67522100|ref|XP_659111.1|/2.93859e-97/hypothetical protein AN1507.2 [A. nidulans FGSC A4]
ANID_01726	24.37	10.11	−1.2693233	2.98E-09	1.56E-08	gi|67522539|ref|XP_659330.1|/0/hypothetical protein AN1726.2 [A. nidulans FGSC A4]
ANID_06210	70.42	29.28	−1.2660697	6.38E-24	7.12E-23	gi|74594572|sp|Q5AZS0.1|EXO70_EMENI/0/RecName: Full=Exocyst complex protein exo70
ANID_00122	85.04	35.38	−1.2652075	1.57E-28	1.94E-27	gi|74599205|sp|Q5BH58.1|LONP2_EMENI/0/RecName: Full=Lon protease homolog 2, peroxisomal
ANID_02885	143.36	59.77	−1.2621491	8.91E-47	1.40E-45	gi|70999478|ref|XP_754458.1|/7.57988e-29/nucleosome binding protein (Nhp6a) [A. fumigatus Af293]
ANID_01198	68.4	28.58	−1.2589904	4.32E-23	4.73E-22	gi|259488483|tpe|CBF87952.1|/0/TPA: hypothetical glycine cleavage system T protein (Eurofung) [A. nidulans FGSC A4]
ANID_04903	18.65	7.84	−1.2502501	3.00E-07	1.33E-06	gi|74657196|sp|Q5B3H7.1|DBP8_EMENI/0/RecName: Full=ATP-dependent RNA helicase dbp8
ANID_09424	59.66	25.09	−1.2496515	4.09E-20	4.17E-19	gi|145253424|ref|XP_001398225.1|/3.63645e-48/cyclin-dependent kinase regulatory subunit [A. niger CBS 513.88]
ANID_00061	36.81	15.51	−1.2468991	6.18E-13	4.31E-12	gi|259489749|tpe|CBF90277.1|/1.57239e-117/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10193	95.12	40.08	−1.2468662	4.86E-31	6.36E-30	gi|259486792|tpe|CBF84937.1|/0/TPA: serine/threonine protein kinase, putative (AFU_orthologue; AFUA_8G04670) [A. nidulans FGSC A4]
ANID_01094	41.34	17.43	−1.2459658	2.40E-14	2.02E-13	gi|259488595|tpe|CBF88157.1|/0/TPA: NADH dehydrogenase (Eurofung) [A. nidulans FGSC A4]
ANID_06302	25.21	10.63	−1.2458545	2.74E-09	1.44E-08	gi|259479484|tpe|CBF69748.1|/5.28645e-130/TPA: Mitochondrial ribosomal protein L16 [Source:UniProtKB/TrEMBL;Acc:Q6RJU7] [A. nidulans FGSC A4]
ANID_07044	90.92	38.34	−1.2457473	1.05E-29	1.35E-28	gi|259483640|tpe|CBF79195.1|/2.78442e-146/TPA: histidinol phosphatase (Eurofung) [A. nidulans FGSC A4]
ANID_03732	24.37	10.28	−1.245266	5.14E-09	2.64E-08	gi|67526549|ref|XP_661336.1|/0/hypothetical protein AN3732.2 [A. nidulans FGSC A4]
ANID_03839	158.15	66.74	−1.24467	2.37E-50	3.86E-49	gi|259481598|tpe|CBF75267.1|/0/TPA: Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97)(Peptide N-myristoyltransferase)(Myristoyl-CoA:protein N-myristoyltransferase)(NMT) [Source:UniProtKB/Swiss-Prot;Acc:Q8TFN1] [A. nidulans FGSC A4]
ANID_04947	189.07	79.81	−1.244279	7.89E-60	1.40E-58	gi|67537554|ref|XP_662551.1|/5.43474e-134/hypothetical protein AN4947.2 [A. nidulans FGSC A4]
ANID_12322	64.37	27.18	−1.243843	1.97E-21	2.07E-20	gi|238503980|ref|XP_002383222.1|/0/protein phosphatase [A. flavus NRRL3357]
ANID_08044	17.31	7.32	−1.2416902	9.20E-07	3.89E-06	gi|259480796|tpe|CBF73765.1|/0/TPA: a-pheromone processing metallopeptidase Ste23 (AFU_orthologue; AFUA_5G02010) [A. nidulans FGSC A4]
ANID_00176	42.02	17.77	−1.2416325	1.81E-14	1.53E-13	gi|4585213|gb|AAD25328.1|AF095898_1/0/siderophore biosynthesis repressor SREA [Emericella nidulans]
ANID_06697	790.39	334.58	−1.2402135	########	########	gi|259480281|tpe|CBF71268.1|/4.87366e-178/TPA: SUN domain protein (Eurofung) [A. nidulans FGSC A4]
ANID_00668	170.08	72.14	−1.2373422	1.55E-53	2.61E-52	gi|67516773|ref|XP_658272.1|/0/hypothetical protein AN0668.2 [A. nidulans FGSC A4]

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<tr><td>ANID_04911</td><td>74.28</td><td>31.54</td><td>−1.2357912</td><td>2.86E-24</td><td>3.24E-23</td><td>gi|67537482|ref|XP_662515.1|/1.78876e-174/hypothetical protein AN4911.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10059</td><td>16.81</td><td>7.14</td><td>−1.2353237</td><td>1.50E-06</td><td>6.21E-06</td><td>gi|67516183|ref|XP_657977.1|/0/hypothetical protein AN0373.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04830</td><td>54.12</td><td>23</td><td>−1.234528</td><td>4.57E-18</td><td>4.45E-17</td><td>gi|67537320|ref|XP_662434.1|/0/hypothetical protein AN4830.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02979</td><td>168.9</td><td>71.8</td><td>−1.2341136</td><td>5.56E-53</td><td>9.35E-52</td><td>gi|259486075|tpe|CBF83628.1|/4.85246e-135/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00896</td><td>48.74</td><td>20.74</td><td>−1.2326904</td><td>2.16E-16</td><td>2.00E-15</td><td>gi|67517239|ref|XP_658500.1|/6.68536e-48/hypothetical protein AN0896.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_01689</td><td>69.91</td><td>29.8</td><td>−1.2301865</td><td>8.72E-23</td><td>9.48E-22</td><td>gi|259487029|tpe|CBF85372.1|/0/TPA: aldehyde dehydrogenase family (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05662</td><td>69.91</td><td>29.8</td><td>−1.2301865</td><td>8.72E-23</td><td>9.47E-22</td><td>gi|67538984|ref|XP_663266.1|/0/hypothetical protein AN5662.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10712</td><td>426.71</td><td>181.93</td><td>−1.2298725</td><td>########</td><td>########</td><td>gi|259484866|tpe|CBF81453.1|/4.03211e-48/TPA: snoRNP protein (gar1), putative (AFU_orthologue; AFUA_4G13690) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01345</td><td>59.49</td><td>25.44</td><td>−1.2255485</td><td>1.65E-19</td><td>1.66E-18</td><td>gi|67521776|ref|XP_658949.1|/7.72019e-74/RS23_NEUCR 40S ribosomal protein S23 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06621</td><td>163.02</td><td>69.88</td><td>−1.2220975</td><td>1.95E-50</td><td>3.18E-49</td><td>gi|67540902|ref|XP_664225.1|/0/hypothetical protein AN6621.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03278</td><td>16.64</td><td>7.14</td><td>−1.2206595</td><td>2.11E-06</td><td>8.62E-06</td><td>gi|67525641|ref|XP_660882.1|/0/hypothetical protein AN3278.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04897</td><td>280.49</td><td>120.42</td><td>−1.2198743</td><td>2.92E-85</td><td>5.93E-84</td><td>gi|67537454|ref|XP_662501.1|/9.34966e-19/hypothetical protein AN4897.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_05784</td><td>315.79</td><td>135.75</td><td>−1.2180133</td><td>1.62E-95</td><td>3.46E-94</td><td>gi|67539228|ref|XP_663388.1|/1.91786e-145/hypothetical protein AN5784.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04317</td><td>375.79</td><td>161.72</td><td>−1.2164286</td><td>########</td><td>########</td><td>gi|255943615|ref|XP_002562575.1|/6.53539e-141/Pc20g00110 [Penicillium chrysogenum Wisconsin 54-1255]</td></tr>
<tr><td>ANID_01066</td><td>665.19</td><td>286.31</td><td>−1.2161884</td><td>########</td><td>########</td><td>gi|259488629|tpe|CBF88221.1|/1.88383e-123/TPA: mitochondrial hypoxia responsive domain protein (AFU_orthologue; AFUA_1G12250) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02084</td><td>39.66</td><td>17.08</td><td>−1.2153767</td><td>2.39E-13</td><td>1.77E-12</td><td>gi|259487454|tpe|CBF86146.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11935</td><td>15.29</td><td>6.62</td><td>−1.2076853</td><td>6.48E-06</td><td>2.50E-05</td><td>gi|119495977|ref|XP_001264762.1|/1.87574e-13/hypothetical protein NFIA_015580 [Neosartorya fischeri NRRL 181]</td></tr>
<tr><td>ANID_00693</td><td>21.34</td><td>9.24</td><td>−1.2075954</td><td>9.34E-08</td><td>4.35E-07</td><td>gi|67516823|ref|XP_658297.1|/2.02876e-58/hypothetical protein AN0693.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04592</td><td>98.48</td><td>42.87</td><td>−1.1998623</td><td>2.69E-30</td><td>3.45E-29</td><td>gi|259482576|tpe|CBF77189.1|/0/TPA: fatty acid desaturase, putative (AFU_orthologue; AFUA_2G02130) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06881</td><td>28.4</td><td>12.37</td><td>−1.1990454</td><td>9.02E-10</td><td>4.90E-09</td><td>gi|67541422|ref|XP_664485.1|/5.56224e-93/hypothetical protein AN6881.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05200</td><td>93.11</td><td>40.6</td><td>−1.1974564</td><td>1.24E-28</td><td>1.54E-27</td><td>gi|223634838|sp|Q5B2N0.2|KMO_EMENI/0/RecName: Full=Kynurenine 3-monooxygenase; AltName: Full=Biosynthesis of nicotinic acid protein 4; AltName: Full=Kynurenine 3-hydroxylase</td></tr>
<tr><td>ANID_03308</td><td>50.75</td><td>22.13</td><td>−1.1974044</td><td>2.58E-16</td><td>2.38E-15</td><td>gi|67525701|ref|XP_660912.1|/0/hypothetical protein AN3308.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07351</td><td>19.16</td><td>8.36</td><td>−1.1965227</td><td>5.34E-07</td><td>2.32E-06</td><td>gi|67900728|ref|XP_680620.1|/5.88702e-133/hypothetical protein AN7351.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05768</td><td>91.76</td><td>40.08</td><td>−1.1949829</td><td>3.65E-28</td><td>4.50E-27</td><td>gi|67539196|ref|XP_663372.1|/2.61388e-118/hypothetical protein AN5768.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02164</td><td>69.75</td><td>30.5</td><td>−1.193384</td><td>9.58E-22</td><td>1.01E-20</td><td>gi|85067835|gb|ABC69301.1|/0/KapG [Emericella nidulans]</td></tr>
<tr><td>ANID_06992</td><td>704.51</td><td>309.31</td><td>−1.1875667</td><td>########</td><td>########</td><td>gi|67541657|ref|XP_664596.1|/1.07179e-32/hypothetical protein AN6992.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08129</td><td>86.05</td><td>37.81</td><td>−1.1864073</td><td>3.21E-26</td><td>3.82E-25</td><td>gi|69061753|gb|AAY99779.1|/0/SfgA [Emericella nidulans]</td></tr>
<tr><td>ANID_04102</td><td>21.01</td><td>9.24</td><td>−1.1851114</td><td>1.82E-07</td><td>8.23E-07</td><td>gi|67527650|ref|XP_661706.1|/0/hypothetical protein AN4102.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07108</td><td>13.44</td><td>5.92</td><td>−1.1828641</td><td>3.25E-05</td><td>0.000114</td><td>gi|67541889|ref|XP_664712.1|/8.17264e-121/hypothetical protein AN7108.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02000</td><td>3163.75</td><td>1393.92</td><td>−1.1824878</td><td>0</td><td>0</td><td>gi|70993888|ref|XP_751791.1|/1.99324e-150/polyubiquitin UbiD/Ubi4 [A. fumigatus Af293]</td></tr>
<tr><td>ANID_08567</td><td>37.14</td><td>16.38</td><td>−1.1810385</td><td>4.30E-12</td><td>2.77E-11</td><td>gi|259484522|tpe|CBF80815.1|/2.16329e-117/TPA: hypothetical protein ANIA_08567 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04908</td><td>47.39</td><td>20.91</td><td>−1.1803896</td><td>5.07E-15</td><td>4.42E-14</td><td>gi|74674336|sp|Q4WXV2.1|TIF31_ASPFU/0/RecName: Full=Protein TIF31 homolog</td></tr>
<tr><td>ANID_01700</td><td>198.31</td><td>87.65</td><td>−1.1779314</td><td>1.27E-57</td><td>2.21E-56</td><td>gi|67522487|ref|XP_659304.1|/0/hypothetical protein AN1700.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02081</td><td>12.6</td><td>5.58</td><td>−1.1750867</td><td>6.17E-05</td><td>0.000209</td><td>gi|259487450|tpe|CBF86139.1|/0/TPA: RanGTP-binding protein (AFU_orthologue; AFUA_2G04830) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10301</td><td>26.72</td><td>11.85</td><td>−1.1730329</td><td>5.24E-09</td><td>2.69E-08</td><td>gi|67523907|ref|XP_660013.1|/2.79333e-147/hypothetical protein AN2409.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_09461</td><td>42.02</td><td>18.65</td><td>−1.1719005</td><td>2.39E-13</td><td>1.78E-12</td><td>gi|261202534|ref|XP_002628481.1|/4.83188e-153/pyruvate dehydrogenase kinase [Ajellomyces dermatitidis SLH14081]</td></tr>
<tr><td>ANID_07752</td><td>143.69</td><td>63.78</td><td>−1.1717837</td><td>6.75E-42</td><td>1.00E-40</td><td>gi|302507646|ref|XP_003015784.1|/1.2202e-164/hypothetical protein ARB_06095 [Arthroderma benhamiae CBS 112371]</td></tr>
<tr><td>ANID_07139</td><td>50.25</td><td>22.31</td><td>−1.1714331</td><td>1.14E-15</td><td>1.03E-14</td><td>gi|67541951|ref|XP_664743.1|/0/hypothetical protein AN7139.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04726</td><td>20</td><td>8.89</td><td>−1.1697447</td><td>4.74E-07</td><td>2.07E-06</td><td>gi|259482435|tpe|CBF76916.1|/0/TPA: oxidoreductase, short chain dehydrogenase/reductase family (AFU_orthologue; AFUA_5G10790) [A. nidulans FGSC A4]</td></tr>
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ANID_00458	10.59	4.71	−1.1689036	0.000261	0.000808	gi|67516353|ref|XP_658062.1|/0/hypothetical protein AN0458.2 [A. nidulans FGSC A4]
ANID_08275	2107.49	940.32	−1.1643021	0	0	gi|145242820|ref|XP_001393983.1|/1.11827e-100/citrate synthase [A. niger CBS 513.88]
ANID_05951	170.08	75.98	−1.1625219	1.12E-48	1.80E-47	gi|145252520|ref|XP_001397773.1|/1.3345e-59/ER membrane DUF1077 domain protein [A. niger CBS 513.88]
ANID_06506	20.67	9.24	−1.1615736	3.51E-07	1.55E-06	gi|259480074|tpe|CBF70874.1|/0/TPA: sterol delta 5,6-desaturase ERG3 (AFU_orthologue; AFUA_6G05140) [A. nidulans FGSC A4]
ANID_04537	15.97	7.14	−1.1613683	8.03E-06	3.07E-05	gi|67536734|ref|XP_662141.1|/0/hypothetical protein AN4537.2 [A. nidulans FGSC A4]
ANID_11900	134.45	60.12	−1.1611528	9.12E-39	1.31E-37	gi|146324854|ref|XP_001481429.1|/5.42679e-96/v-SNARE protein Bos1 [A. fumigatus Af293]
ANID_04281	50.25	22.48	−1.1604816	1.87E-15	1.67E-14	gi|83771518|dbj|BAE61650.1|/8.72949e-86/unnamed protein product [A. oryzae]
ANID_06698	104.37	46.7	−1.1602126	2.02E-30	2.60E-29	gi|67541056|ref|XP_664302.1|/0/hypothetical protein AN6698.2 [A. nidulans FGSC A4]
ANID_04150	13.61	6.1	−1.1577859	3.89E-05	0.000135	gi|67527746|ref|XP_661754.1|/0/hypothetical protein AN4150.2 [A. nidulans FGSC A4]
ANID_02701	43.53	19.52	−1.157057	1.58E-13	1.22E-12	gi|259486388|tpe|CBF84185.1|/0/TPA: WD domain, G-beta repeat protein (AFU_orthologue; AFUA_5G13970) [A. nidulans FGSC A4]
ANID_09421	51.26	23	−1.1561996	1.20E-15	1.08E-14	gi|75858926|ref|XP_868803.1|/0/hypothetical protein AN9421.2 [A. nidulans FGSC A4]
ANID_07476	77.98	35.03	−1.1545132	5.66E-23	6.19E-22	gi|67900978|ref|XP_680745.1|/4.76076e-101/hypothetical protein AN7476.2 [A. nidulans FGSC A4]
ANID_05337	43.7	19.69	−1.1501702	1.87E-13	1.42E-12	gi|67538334|ref|XP_662941.1|/0/hypothetical protein AN5337.2 [A. nidulans FGSC A4]
ANID_12144	15.46	6.97	−1.1493098	1.30E-05	4.79E-05	gi|259485355|tpe|CBF82309.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_00443	156.13	70.4	−1.1491004	4.96E-44	7.58E-43	gi|70990724|ref|XP_750211.1|/2.29427e-122/alcohol dehydrogenase, zinc-containing [A. fumigatus Af293]
ANID_10278	182.01	82.08	−1.1489151	4.89E-51	8.05E-50	gi|67523567|ref|XP_659843.1|/8.4016e-118/hypothetical protein AN2239.2 [A. nidulans FGSC A4]
ANID_01664	18.15	8.19	−1.1480342	2.32E-06	9.44E-06	gi|259487003|tpe|CBF85325.1|/1.26095e-141/TPA: dienelactone hydrolase family protein (AFU_orthologue; AFUA_4G08790) [A. nidulans FGSC A4]
ANID_04894	31.26	14.12	−1.1465777	5.43E-10	2.99E-09	gi|259482240|tpe|CBF76532.1|/0/TPA: transcriptional activator spt7 (AFU_orthologue; AFUA_3G11000) [A. nidulans FGSC A4]
ANID_06712	44.7	20.21	−1.1452055	1.20E-13	9.44E-13	gi|67541084|ref|XP_664316.1|/0/hypothetical protein AN6712.2 [A. nidulans FGSC A4]
ANID_05571	152.1	69.01	−1.1401428	1.99E-42	2.97E-41	gi|259484969|tpe|CBF81643.1|/0/TPA: oxoglutarate dehydrogenase (succinyl-transferring) (Eurofung) [A. nidulans FGSC A4]
ANID_02238	242.51	110.13	−1.1388367	1.74E-66	3.20E-65	gi|67523565|ref|XP_659842.1|/5.73622e-132/hypothetical protein AN2238.2 [A. nidulans FGSC A4]
ANID_11055	34.45	15.68	−1.1355784	1.02E-10	5.95E-10	gi|223635803|sp|P0C8Q0.1|UBX1_EMENI/6.55893e-174/RecName: Full=UBX domain-containing protein 1
ANID_02185	72.94	33.28	−1.1320548	5.84E-21	6.05E-20	gi|259487569|tpe|CBF86343.1|/6.6241e-159/TPA: endodeoxyribonuclease (Eurofung) [A. nidulans FGSC A4]
ANID_04763	167.39	76.5	−1.1296817	7.32E-46	1.13E-44	gi|82592830|sp|Q5B3W7.2|ERFB_EMENI/0/RecName: Full=Palmitoyltransferase erf2; AltName: Full=DHHC cysteine-rich domain-containing protein erf2; AltName: Full=Ras protein acyltransferase
ANID_11167	25.55	11.68	−1.129283	3.05E-08	1.47E-07	gi|259485449|tpe|CBF82481.1|/0/TPA: sugar transporter, putative (AFU_orthologue; AFUA_7G01740) [A. nidulans FGSC A4]
ANID_12164	77.14	35.38	−1.1245451	7.16E-22	7.63E-21	gi|67536936|ref|XP_662242.1|/1.09802e-61/hypothetical protein AN4638.2 [A. nidulans FGSC A4]
ANID_00930	20.5	9.41	−1.1233573	7.93E-07	3.37E-06	gi|67517312|ref|XP_658534.1|/0/hypothetical protein AN0930.2 [A. nidulans FGSC A4]
ANID_00471	48.57	22.31	−1.122375	2.73E-14	2.28E-13	gi|67516379|ref|XP_658075.1|/7.2121e-150/hypothetical protein AN0471.2 [A. nidulans FGSC A4]
ANID_08606	23.86	10.98	−1.119716	1.06E-07	4.91E-07	gi|67903238|ref|XP_681875.1|/5.50207e-175/hypothetical protein AN8606.2 [A. nidulans FGSC A4]
ANID_03629	84.03	38.69	−1.1189438	1.66E-23	1.84E-22	gi|67526343|ref|XP_661233.1|/0/hypothetical protein AN3629.2 [A. nidulans FGSC A4]
ANID_06004	458.3	211.03	−1.1188442	########	########	gi|67539668|ref|XP_663608.1|/1.0519e-115/hypothetical protein AN6004.2 [A. nidulans FGSC A4]
ANID_07996	15.13	6.97	−1.1181814	2.48E-05	8.83E-05	gi|67902018|ref|XP_681265.1|/2.61936e-145/hypothetical protein AN7996.2 [A. nidulans FGSC A4]
ANID_03506	15.13	6.97	−1.1181814	2.48E-05	8.83E-05	gi|67526097|ref|XP_661110.1|/0/hypothetical protein AN3506.2 [A. nidulans FGSC A4]
ANID_05102	330.07	152.48	−1.114152	8.64E-87	1.78E-85	gi|259484547|tpe|CBF80864.1|/0/TPA: FACT complex subunit spt16 (Facilitates chromatin transcription complex subunit spt16) [Source:UniProtKB/Swiss-Prot;Acc:Q5B2X8] [A. nidulans FGSC A4]
ANID_04782	76.13	35.2	−1.1128896	2.88E-21	3.00E-20	gi|121704850|ref|XP_001270688.1|/2.18388e-59/Rho GTPase Rho3 [A. clavatus NRRL 1]
ANID_00576	24.87	11.5	−1.1127726	6.69E-08	3.14E-07	gi|259489159|tpe|CBF89201.1|/0/TPA: phosphoinositide-3-kinase, regulatory protein Vps15 (Eurofung) [A. nidulans FGSC A4]
ANID_10010	29.75	13.77	−1.1113611	3.58E-09	1.86E-08	gi|259489750|tpe|CBF90279.1|/0/TPA: decapping enzyme Dcp2, putative (AFU_orthologue; AFUA_5G12420) [A. nidulans FGSC A4]
ANID_10337	479.82	222.18	−1.1107643	########	########	gi|67524619|ref|XP_660371.1|/0/hypothetical protein AN2767.2 [A. nidulans FGSC A4]
ANID_01158	392.59	181.93	−1.10964	########	########	gi|67517975|ref|XP_658762.1|/0/hypothetical protein AN1158.2 [A. nidulans FGSC A4]
ANID_01362	144.36	66.92	−1.1091617	1.09E-38	1.56E-37	gi|259488304|tpe|CBF87646.1|/6.77448e-121/TPA: CUE domain protein, putative (AFU_orthologue; AFUA_1G09250) [A. nidulans FGSC A4]
ANID_00657	71.76	33.28	−1.1085245	5.15E-20	5.25E-19	gi|67516751|ref|XP_658261.1|/3.0892e-139/hypothetical protein AN0657.2 [A. nidulans FGSC A4]

ANID_04923	97.48	45.31	−1.1052768	1.65E-26	1.98E-25	gi|259482209|tpe|CBF76472.1|/0/TPA: hydroxymethylglutaryl-CoA synthase, expressed (Eurofung) [A. nidulans FGSC A4]
ANID_09506	87.73	40.78	−1.1052085	5.11E-24	5.73E-23	gi|169776353|ref|XP_001822643.1|/0/hypothetical protein AOR_1_774134 [A. oryzae RIB40]
ANID_05832	22.86	10.63	−1.1046838	2.70E-07	1.20E-06	gi|119480531|ref|XP_001260294.1|/1.57694e-79/Ras small monomeric GTPase RasB [Neosartorya fischeri NRRL 181]
ANID_00570	1566	728.76	−1.1035685	0	0	gi|259489165|tpe|CBF89212.1|/8.18795e-44/TPA: ribosomal protein L26 (AFU_orthologue; AFUA_6G11260) [A. nidulans FGSC A4]
ANID_00296	11.6	5.4	−1.1030935	0.000268	0.000829	gi|67516029|ref|XP_657900.1|/2.21599e-100/hypothetical protein AN0296.2 [A. nidulans FGSC A4]
ANID_01380	106.55	49.66	−1.1013744	1.14E-28	1.43E-27	gi|259488283|tpe|CBF87610.1|/0/TPA: methionyl-tRNA synthetase (AFU_orthologue; AFUA_1G09010) [A. nidulans FGSC A4]
ANID_12339	13.44	6.27	−1.0999958	8.80E-05	0.000293	gi|67902718|ref|XP_681615.1|/3.98586e-110/hypothetical protein AN8346.2 [A. nidulans FGSC A4]
ANID_07736	65.71	30.67	−1.0992848	3.11E-18	3.03E-17	gi|67901498|ref|XP_681005.1|/0/hypothetical protein AN7736.2 [A. nidulans FGSC A4]
ANID_05445	18.65	8.71	−1.098431	3.80E-06	1.51E-05	gi|67538550|ref|XP_663049.1|/2.16921e-108/hypothetical protein AN5445.2 [A. nidulans FGSC A4]
ANID_04623	36.13	16.9	−1.096174	1.24E-10	7.17E-10	gi|259482543|tpe|CBF77125.1|/0/TPA: UDP-glucose-glycoprotein glucosyltransferase (Eurofung) [A. nidulans FGSC A4]
ANID_10905	169.41	79.46	−1.0922183	5.03E-44	7.67E-43	gi|67542009|ref|XP_664772.1|/0/hypothetical protein AN7168.2 [A. nidulans FGSC A4]
ANID_02556	44.87	21.09	−1.0891921	9.36E-13	6.39E-12	gi|67524197|ref|XP_660160.1|/1.13086e-48/hypothetical protein AN2556.2 [A. nidulans FGSC A4]
ANID_06280	25.21	11.85	−1.0891091	9.19E-08	4.29E-07	gi|259479508|tpe|CBF69793.1|/0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_01143	23.7	11.15	−1.0878433	2.32E-07	1.04E-06	gi|67517945|ref|XP_658747.1|/0/hypothetical protein AN1143.2 [A. nidulans FGSC A4]
ANID_06693	606.87	285.62	−1.0872905	########	########	gi|67541046|ref|XP_664297.1|/1.50561e-09/hypothetical protein AN6693.2 [A. nidulans FGSC A4]
ANID_03258	87.39	41.13	−1.0872771	2.36E-23	2.61E-22	gi|259485775|tpe|CBF83083.1|/8.78251e-88/TPA: extracellular proline-serine rich protein (AFU_orthologue; AFUA_8G07090) [A. nidulans FGSC A4]
ANID_05217	171.09	80.68	−1.0844724	5.91E-44	8.99E-43	gi|259484676|tpe|CBF81101.1|/5.70245e-136/TPA: primary component of eisosomes (Eurofung) [A. nidulans FGSC A4]
ANID_04469	82.35	38.86	−1.0834827	5.65E-22	6.03E-21	gi|74681050|sp|Q5B4R1.1|YTM1_EMENI/0/RecName: Full=Ribosome biogenesis protein ytm1
ANID_06730	22.52	10.63	−1.0830652	5.04E-07	2.19E-06	gi|67541120|ref|XP_664334.1|/0/UAPC_EMENI PURINE PERMEASE [A. nidulans FGSC A4]
ANID_03635	54.96	25.97	−1.081536	3.92E-15	3.44E-14	gi|67526355|ref|XP_661239.1|/0/hypothetical protein AN3635.2 [A. nidulans FGSC A4]
ANID_06859	109.41	51.76	−1.0798351	1.58E-28	1.95E-27	gi|67541378|ref|XP_664463.1|/0/hypothetical protein AN6859.2 [A. nidulans FGSC A4]
ANID_06543	393.77	186.29	−1.079803	3.59E-98	7.78E-97	gi|74594312|sp|Q5AYT7.1|FES1_EMENI/8.74232e-106/RecName: Full=Hsp70 nucleotide exchange factor fes1
ANID_05865	91.26	43.22	−1.0782836	5.23E-24	5.86E-23	gi|67539390|ref|XP_663469.1|/0/hypothetical protein AN5865.2 [A. nidulans FGSC A4]
ANID_04455	27.23	12.9	−1.0778259	3.64E-08	1.75E-07	gi|67528514|ref|XP_662059.1|/1.05583e-172/hypothetical protein AN4455.2 [A. nidulans FGSC A4]
ANID_00363	19.5	9.24	−1.0775094	3.25E-06	1.31E-05	gi|146270992|gb|ABQ17967.1|/1.08853e-150/VelB [Emericella nidulans]
ANID_09151	13.61	6.45	−1.077296	0.000103	0.000338	gi|67904328|ref|XP_682420.1|/0/hypothetical protein AN9151.2 [A. nidulans FGSC A4]
ANID_04253	72.77	34.5	−1.0767474	2.06E-19	2.06E-18	gi|67528032|ref|XP_661857.1|/3.29269e-116/hypothetical protein AN4253.2 [A. nidulans FGSC A4]
ANID_06491	437.63	207.72	−1.0750715	########	########	gi|259480055|tpe|CBF70839.1|/6.22039e-86/TPA: purine nucleoside phosphorylase I, inosine and guanosine-specific (AFU_orthologue; AFUA_6G05320) [A. nidulans FGSC A4]
ANID_01703	24.2	11.5	−1.0733732	2.32E-07	1.04E-06	gi|259487044|tpe|CBF85400.1|/0/TPA: cytochrome P450, putative (Eurofung) [A. nidulans FGSC A4]
ANID_10178	121	57.51	−1.0731223	4.41E-31	5.77E-30	gi|259488383|tpe|CBF87780.1|/1.4207e-26/TPA: cytochrome c oxidase assembly protein Cox19, putative (AFU_orthologue; AFUA_1G09757) [A. nidulans FGSC A4]
ANID_04188	16.13	7.67	−1.072448	2.49E-05	8.85E-05	gi|67527880|ref|XP_661792.1|/0/hypothetical protein AN4188.2 [A. nidulans FGSC A4]
ANID_04938	179.99	85.74	−1.0698764	3.38E-45	5.18E-44	gi|67537536|ref|XP_662542.1|/0/hypothetical protein AN4938.2 [A. nidulans FGSC A4]
ANID_03808	18.65	8.89	−1.0689203	6.07E-06	2.35E-05	gi|67526701|ref|XP_661412.1|/3.01609e-81/hypothetical protein AN3808.2 [A. nidulans FGSC A4]
ANID_10309	14.62	6.97	−1.0687128	6.40E-05	0.000217	gi|193804913|gb|ACF22099.1|/0/hypothetical protein [Emericella nidulans]
ANID_00439	14.96	7.14	−1.0671142	5.46E-05	0.000186	gi|67516315|ref|XP_658043.1|/0/hypothetical protein AN0439.2 [A. nidulans FGSC A4]
ANID_00134	33.11	15.86	−1.0618742	1.94E-09	1.03E-08	gi|38892925|gb|AAR27792.1|/0/protein methyltransferase [Emericella nidulans]
ANID_06471	135.12	64.83	−1.0595078	7.71E-34	1.04E-32	gi|67540602|ref|XP_664075.1|/4.65923e-64/hypothetical protein AN6471.2 [A. nidulans FGSC A4]
ANID_08234	84.2	40.43	−1.058394	1.18E-21	1.25E-20	gi|67902494|ref|XP_681503.1|/3.10513e-103/hypothetical protein AN8234.2 [A. nidulans FGSC A4]
ANID_10523	38.82	18.65	−1.0576245	9.04E-11	5.27E-10	gi|259481172|tpe|CBF74455.1|/1.75414e-153/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_10518	203.69	97.94	−1.0564051	6.48E-50	1.05E-48	gi|259481171|tpe|CBF74453.1|/9.55365e-97/TPA: pathogenesis associated protein Cap20, putative (AFU_orthologue; AFUA_1G06350) [A. nidulans FGSC A4]
ANID_04707	23.86	11.5	−1.0529602	4.27E-07	1.87E-06	gi|74595706|sp|Q5B423.1|ISY1_EMENI/2.2103e-111/RecName: Full=Pre-mRNA-splicing factor isy1
ANID_06735	203.35	98.11	−1.0514929	1.81E-49	2.93E-48	gi|67541130|ref|XP_664339.1|/9.00215e-42/hypothetical protein AN6735.2 [A. nidulans FGSC A4]

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<tr><td>ANID_04358</td><td>58.49</td><td>28.23</td><td>−1.0509609</td><td>2.42E-15</td><td>2.16E-14</td><td>gi|259482832|tpe|CBF77688.1|/7.68705e-118/TPA: DUF974 domain protein (AFU_orthologue; AFUA_4G06560) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_08967</td><td>61.34</td><td>29.62</td><td>−1.0502565</td><td>5.30E-16</td><td>4.85E-15</td><td>gi|259486584|tpe|CBF84550.1|/0/TPA: FAD binding domain protein (AFU_orthologue; AFUA_6G14300) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10797</td><td>152.6</td><td>73.89</td><td>−1.0463039</td><td>2.92E-37</td><td>4.11E-36</td><td>gi|259479504|tpe|CBF69786.1|/0/TPA: hydroxymethylglutaryl-CoA lyase (AFU_orthologue; AFUA_2G12450) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06886</td><td>15.46</td><td>7.49</td><td>−1.0455027</td><td>5.40E-05</td><td>0.000184</td><td>gi|68052825|sp|Q9P904.1|PALH_EMENI/0/RecName: Full=pH-response regulator protein palH/RIM21</td></tr>
<tr><td>ANID_01069</td><td>33.44</td><td>16.21</td><td>−1.0446908</td><td>2.60E-09</td><td>1.36E-08</td><td>gi|169768814|ref|XP_001818877.1|/3.07339e-127/chitin synthase export chaperone [A. oryzae RIB40]</td></tr>
<tr><td>ANID_06067</td><td>184.36</td><td>89.4</td><td>−1.0441789</td><td>1.60E-44</td><td>2.45E-43</td><td>gi|67539794|ref|XP_663671.1|/0/hypothetical protein AN6067.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04328</td><td>65.04</td><td>31.54</td><td>−1.0441446</td><td>9.85E-17</td><td>9.22E-16</td><td>gi|259482865|tpe|CBF77751.1|/0/TPA: amino acid transporter (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_12199</td><td>31.26</td><td>15.16</td><td>−1.044048</td><td>8.89E-09</td><td>4.45E-08</td><td>gi|67523453|ref|XP_659786.1|/2.33913e-23/hypothetical protein AN2182.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_03803</td><td>49.91</td><td>24.22</td><td>−1.04313</td><td>3.63E-13</td><td>2.63E-12</td><td>gi|67526691|ref|XP_661407.1|/0/hypothetical protein AN3803.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02283</td><td>26.55</td><td>12.9</td><td>−1.0413408</td><td>1.22E-07</td><td>5.64E-07</td><td>gi|67523655|ref|XP_659887.1|/0/hypothetical protein AN2283.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01851</td><td>201.17</td><td>98.11</td><td>−1.0359431</td><td>8.13E-48</td><td>1.29E-46</td><td>gi|67522789|ref|XP_659455.1|/0/hypothetical protein AN1851.2 [A. nidulans FGSC A4]</td></tr>
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<tr><td>ANID_01126</td><td>1047.53</td><td>511.11</td><td>−1.0352858</td><td>########</td><td>########</td><td>gi|67517899|ref|XP_658730.1|/7.02543e-87/ARF_AJECA ADP-RIBOSYLATION FACTOR [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10208</td><td>34.28</td><td>16.73</td><td>−1.0349297</td><td>2.20E-09</td><td>1.16E-08</td><td>gi|166215125|sp|P0C624.1|CSN8_EMENI/3.56163e-102/RecName: Full=COP9 signalosome complex subunit 8; Short=CSN complex subunit 8</td></tr>
<tr><td>ANID_03678</td><td>32.44</td><td>15.86</td><td>−1.032381</td><td>6.43E-09</td><td>3.28E-08</td><td>gi|259481785|tpe|CBF75630.1|/0/TPA: guanine nucleotide exchange factor Vps9, putative (AFU_orthologue; AFUA_4G12490) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10164</td><td>26.72</td><td>13.07</td><td>−1.0316609</td><td>1.41E-07</td><td>6.43E-07</td><td>gi|67517823|ref|XP_658695.1|/0/hypothetical protein AN1091.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00142</td><td>143.52</td><td>70.23</td><td>−1.0310925</td><td>2.36E-34</td><td>3.21E-33</td><td>gi|259489662|tpe|CBF90118.1|/0/TPA: 37S ribosomal protein S5 (AFU_orthologue; AFUA_5G11540) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_06716</td><td>18.49</td><td>9.06</td><td>−1.0291623</td><td>1.29E-05</td><td>4.77E-05</td><td>gi|67541092|ref|XP_664320.1|/0/hypothetical protein AN6716.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11072</td><td>114.11</td><td>55.94</td><td>−1.0284731</td><td>1.53E-27</td><td>1.87E-26</td><td>gi|259481078|tpe|CBF74281.1|/0/TPA: diacylglycerol acyltransferase type 2A (AFU_orthologue; AFUA_7G03700) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05121</td><td>166.55</td><td>81.9</td><td>−1.02402</td><td>3.68E-39</td><td>5.31E-38</td><td>gi|259484566|tpe|CBF80900.1|/1.34174e-162/TPA: hypothetical protein similar to proteasome regulatory subunit 8 RPN8 (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05802</td><td>45.71</td><td>22.48</td><td>−1.0238678</td><td>7.37E-12</td><td>4.65E-11</td><td>gi|255935919|ref|XP_002558986.1|/5.65039e-22/Pc13g05520 [Penicillium chrysogenum Wisconsin 54-1255]</td></tr>
<tr><td>ANID_02332</td><td>240.16</td><td>118.15</td><td>−1.0233763</td><td>1.18E-55</td><td>2.03E-54</td><td>gi|85116983|ref|XP_965152.1|/6.52551e-113/succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [Neurospora crassa OR74A]</td></tr>
<tr><td>ANID_08050</td><td>13.11</td><td>6.45</td><td>−1.0232966</td><td>0.00026</td><td>0.000806</td><td>gi|259480804|tpe|CBF73780.1|/3.94668e-74/TPA: UPF0047 domain protein (AFU_orthologue; AFUA_5G02090) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04550</td><td>36.81</td><td>18.12</td><td>−1.0225148</td><td>8.52E-10</td><td>4.63E-09</td><td>gi|67536760|ref|XP_662154.1|/0/hypothetical protein AN4550.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02749</td><td>16.97</td><td>8.36</td><td>−1.0214117</td><td>3.29E-05</td><td>0.000115</td><td>gi|259486337|tpe|CBF84094.1|/0/TPA: PH domain protein (AFU_orthologue; AFUA_1G05130) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_04380</td><td>234.95</td><td>115.88</td><td>−1.0197222</td><td>3.60E-54</td><td>6.10E-53</td><td>gi|67528364|ref|XP_661984.1|/0/RIR1_NEUCR Ribonucleoside-diphosphate reductase large chain (Ribonucleotide reductase large subunit) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02514</td><td>13.78</td><td>6.8</td><td>−1.0189692</td><td>0.000188</td><td>0.000595</td><td>gi|67524113|ref|XP_660118.1|/3.6415e-152/hypothetical protein AN2514.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_01082</td><td>21.18</td><td>10.46</td><td>−1.0178197</td><td>3.63E-06</td><td>1.44E-05</td><td>gi|67517805|ref|XP_658686.1|/0/hypothetical protein AN1082.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10413</td><td>14.45</td><td>7.14</td><td>−1.0170735</td><td>0.000136</td><td>0.000439</td><td>gi|259485567|tpe|CBF82698.1|/0/TPA: phospholipase D1 (PLD1), putative (AFU_orthologue; AFUA_3G05630) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_02413</td><td>180.5</td><td>89.22</td><td>−1.0165598</td><td>8.18E-42</td><td>1.21E-40</td><td>gi|67523915|ref|XP_660017.1|/2.66439e-87/hypothetical protein AN2413.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00678</td><td>75.29</td><td>37.29</td><td>−1.0136695</td><td>2.68E-18</td><td>2.62E-17</td><td>gi|67516793|ref|XP_658282.1|/1.09623e-13/hypothetical protein AN0678.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07708</td><td>98.15</td><td>48.79</td><td>−1.0084028</td><td>3.42E-23</td><td>3.75E-22</td><td>gi|259484054|tpe|CBF79949.1|/3.87051e-150/TPA: aldo-keto reductase, putative (AFU_orthologue; AFUA_5G08290) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_05741</td><td>134.62</td><td>66.92</td><td>−1.0083834</td><td>3.21E-31</td><td>4.22E-30</td><td>gi|259484782|tpe|CBF81298.1|/0/TPA: KOW motif domain protein (AFU_orthologue; AFUA_6G06890) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_07500</td><td>139.49</td><td>69.36</td><td>−1.0079859</td><td>2.84E-32</td><td>3.78E-31</td><td>gi|259483812|tpe|CBF79508.1|/0/TPA: 64 kDa mitochondrial NADH dehydrogenase (Eurofung) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_11244</td><td>85.71</td><td>42.69</td><td>−1.0055654</td><td>2.30E-20</td><td>2.36E-19</td><td>gi|75859066|ref|XP_868873.1|/0/hypothetical protein AN9491.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10585</td><td>2177.91</td><td>1086</td><td>−1.0039202</td><td>0</td><td>0</td><td>gi|67537134|ref|XP_662341.1|/1.24753e-55/hypothetical protein AN4737.2 [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_00287</td><td>81.68</td><td>40.78</td><td>−1.0021211</td><td>2.20E-19</td><td>2.20E-18</td><td>gi|259489491|tpe|CBF89806.1|/0/TPA: WD repeat-containing protein (AFU_orthologue; AFUA_1G02990) [A. nidulans FGSC A4]</td></tr>
<tr><td>ANID_10248</td><td>27.9</td><td>13.94</td><td>−1.0010346</td><td>1.55E-07</td><td>7.07E-07</td><td>gi|67523057|ref|XP_659589.1|/3.73748e-39/hypothetical protein AN1985.2 [A. nidulans FGSC A4]</td></tr>
</table>

a) Gene accession numbers were annotated according to Aspergillus comparative genome database; b) TPM: Tags Per Million; c) Description was obtained from broad description of genes (http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html/).