论文

过量尿嘧啶胁迫下 *pyrG* 对维持构巢曲霉胞内尿嘧啶稳定及正常产孢起关键作用孙宪昀^①, 朱菊芬^①, 宝丽^①, 胡成成^①, 金城^①, HARRIS Steven D.^②, 刘宏伟^①, 李少杰^{①*}^① 中国科学院微生物研究所, 真菌学国家重点实验室, 北京 100080;^② Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln 68588-0660, USA

* 联系人, E-mail: shaojieli@gmail.com

收稿日期: 2013-02-25; 接受日期: 2013-03-20

国家自然科学基金(批准号: 31000551, 31170087)和中国科学院“百人计划”资助项目

摘要 为减少DNA中尿嘧啶的掺入, 细胞内尿嘧啶水平受到严格控制, 但其机制尚不清楚. 构巢曲霉(*Aspergillus nidulans*)乳清酸核苷 5'-磷酸脱羧酶 *PyrG* 催化乳清苷酸(OMP)转化为尿苷酸(UMP)的反应, 本研究发现, 在过量尿嘧啶存在的情况下, *PyrG* 对维持细胞内较低尿嘧啶浓度具有重要作用. 与野生菌株相比, 过量尿嘧啶及其代谢物对乳清苷酸脱羧酶缺陷的 *pyrG89* 突变体具有更强的抑制作用, 并能增强 *pyrG89* 突变体的有性发育. 通过数字基因表达谱(DGE)分析 *pyrG89* 突变体和野生菌株对过量尿嘧啶的转录响应, 发现尿嘧啶转录激活 *pyrG89* 突变体中有性发育相关的基因. HPLC 定量分析显示, 在过量尿嘧啶存在的情况下, *pyrG89* 突变体胞内尿嘧啶水平是野生菌株的 6.5 倍. 本研究的结果不仅为细胞内尿嘧啶循环及细胞对过量尿嘧啶的适应机制提供了新内容, 还揭示了 OMP 脱羧酶对真菌生长发育存在潜在影响.

关键词乳清酸核苷
5'-磷酸脱羧酶
压力
尿嘧啶
有性发育

乳清酸核苷 5'-磷酸脱羧酶(OMP 脱羧酶, EC 4.1.1.23)通过脱羧作用催化乳清苷酸转化为尿苷酸, 是嘧啶从头合成的关键酶. OMP 脱羧酶在酿酒酵母(*Saccharomyces cerevisiae*)中由 *URA3* 基因编码^[1], 在构巢曲霉(*Aspergillus nidulans*)中由 *pyrG* 基因编码^[2], 而在粗糙脉孢菌(*Neurospora crassa*)中则由 *pyr-4* 基因编码^[3]. 由于 OMP 脱羧酶受损的营养缺陷型突变体能够在添加了外源尿苷和尿嘧啶的培养基中正常

生长, 而且具有功能的 OMP 脱羧酶编码基因易于回补这种缺陷, 因此, 基于回补 OMP 脱羧酶突变体的遗传操作广泛用于酿酒酵母^[4]、构巢曲霉^[5]、产黄青霉(*Penicillium chrysogenum*)^[6]、黑曲霉(*Aspergillus niger*)^[7]、瑞氏木霉(*Trichoderma reesei*)^[8]和烟曲霉(*Aspergillus fumigatus*)^[9]等多种真菌. 在丝状真菌中, 粗糙脉孢菌 *pyr-4* 基因被广泛地用作一种筛选标记来回补 OMP 脱羧酶突变体^[5-11].

引用格式: 孙宪昀, 朱菊芬, 宝丽, 等. 过量尿嘧啶胁迫下 *pyrG* 对维持构巢曲霉胞内尿嘧啶稳定及正常产孢起关键作用. 中国科学: 生命科学, 2013, 43: 387-396

英文版见: 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

当对一个新的突变体进行表型分析时, 对应的 OMP 脱羧酶缺陷出发株通常被用作对照. 为此, 尿嘧啶就需要添加到培养基中以维持 *pyrG* 突变体的生长. 但是, 外源尿嘧啶的加入是否对 *pyrG* 突变体和野生菌株的生长发育有不同的影响并不清楚. 有证据显示, 细胞内尿嘧啶水平是受到严格控制的, 以此来防止过多的尿嘧啶在细胞中积累. 在外源尿嘧啶胁迫时, 酿酒酵母中负责尿嘧啶转运的尿嘧啶通透酶基因 *FUR4*^[12] 的转录水平降低^[13,14]. 与之类似, 外源的尿嘧啶的加入也会降低构巢曲霉 *Fur4p* 类的尿嘧啶通透酶基因 *furD* 的表达^[15]. 在蛋白质翻译后水平, 外源尿嘧啶的存在加速了 *Fur4p* 的泛素化降解^[14]. 细胞内尿嘧啶水平的严密控制对于维持低的尿嘧啶: 胸腺嘧啶比例尤为重要, 以此来降低尿嘧啶掺入 DNA 而造成的突变^[15]. 基因组 DNA 调节区域尿嘧啶对胸腺嘧啶的替换能够破坏蛋白质-DNA 相互作用的特异性^[16].

在本研究中, 发现 OMP 脱羧酶的缺失增加了构巢曲霉对过量尿嘧啶及其代谢物的敏感性. 过量的尿嘧啶及其代谢物也增强了 OMP 脱羧酶突变体的有性发育. 通过数字基因表达谱(DGE)对野生菌株及 *pyrG* 突变体的差异表达谱分析显示, 过量的尿嘧啶转录激活了 OMP 脱羧酶突变体中与有性发育相关的基因.

1 材料与方法

1.1 菌株及培养基

本研究中, 构巢曲霉 FGSC A773 (*pyrG89*, *wA3*, *pyroA4*, *veA1*) 菌株作为母本菌株. 将含有粗糙脉孢菌 *pyr-4* 基因的 PCR 片段转化到 A773 菌株获得 AHC01 (*pyrG89*, *wA3*, *pyroA4*, *pyr-4*, *veA1*) 菌株. 构巢曲霉的原生质体转化参照 Miller 等人^[17] 和 Calvo 等人^[18] 报道的方法. A773 菌株和构巢曲霉 FGSC A4 (*veA+*) 菌株杂交获得 ALS05 (*wA3*, *pyroA4*, *veA1*) 菌株.

MMV 培养基(1%葡萄糖、硝酸盐、微量元素、维生素, pH 6.5)作为构巢曲霉的生长培养基. 微量元素、硝酸盐和维生素的组成参照 Käfer^[19] 在其附录中的描述. 尿嘧啶核苷(1×浓度为 5 mmol/L)和尿嘧啶(1×浓度为 10 mmol/L)依需要加入, 加入 1.5%琼脂来固化培养基.

1.2 胞内尿嘧啶及其中间代谢产物的分析

将构巢曲霉 A773 或 ALS05 菌株孢子接种于含有 150 mL 培养基(MMV+1×尿苷+4×尿嘧啶)的 300 mL 三角瓶中, 于 28℃, 180 r/min 连续摇培 30 h. 随后, 参照 Ruijter 和 Visser^[20] 所报道的方法提取胞内代谢产物, 并收集提取代谢产物后所余菌丝, 烘干后称取干重. 提取液通过 0.45 μm 滤器过滤后, 通过高效液相色谱 HPLC (4.6ID×250 mm COSMOSIL C18 色谱柱, 5%乙腈和 0.04%三氟乙酸溶液作为洗脱剂) 鉴定中间代谢物.

1.3 有性发育分析

有性发育的定性分析采用光学显微镜和电子显微镜观察的方法, 定量分析通过计数原子囊壳表面护卫细胞(Hülle cells)的方法来比较 *pyrG* 突变体和野生菌株之间有性发育的差异. 用打孔器获取4块(直径约 0.5 cm)生长于固体琼脂培养基(MMV+1×尿苷+4×尿嘧啶)的菌体块, 切碎后浸泡于 2 mL 无菌水中并混合均匀. 稀释成合适的浓度后在光学显微镜下利用血细胞计数板计数护卫细胞的数量. 3 次重复实验获得每平方毫米护卫细胞平均数及标准差.

1.4 DGE 分析 *pyrG* 突变体和野生菌株对过量尿嘧啶胁迫的转录响应

为了比较 *pyrG89* 突变体和野生菌株对过量尿嘧啶胁迫的转录响应, 利用数字基因表达谱(DGE)分析 *pyrG89* 突变体和野生菌株全基因组范围内对过量尿嘧啶胁迫的转录响应^[21]. 具体方法如下: 接种野生菌株或 *pyrG89* 突变株的孢子于含有 75 mL 液体培养基(MMV+1×尿苷+4×尿嘧啶, MMV+1×尿苷+1×尿嘧啶)的 150 mL 三角瓶中, 在 28℃, 180 r/min 条件下培养 30 h. 每个处理 3 次重复, 然后提取细胞总 RNA 用于 DGE 分析. 依照试剂盒使用说明, 利用 DGE Tag Profile Kit (Illumina, San Diego, CA, USA) 将总 RNA 中的 mRNA 分离出来并进行测序标签的制备, 详细方法参见 Sun 等人^[22] 的描述.

原始数据经过处理后, 将所有处理后的标签序列比对到参考序列上 (http://www.broadinstitute.org/annotation/genome/aspergillus_group/Blast.html). 同时, 为了监控正反链的比对, 正义和互补的反义序列都进行了参考序列比对, 并最终统计出比对上基因的

标签数.

1.5 差异转录基因分析

为了获得 2 个样品间差异转录基因, 每个原始可用标签序列数都标准化为每百万标签数(TPM). 依照先前报道的方法分析样品间差异转录基因或是标签数, 2 个样品间 TPM 比值大于 2 或是小于 0.5 作为差异转录的阈值^[23]. 通过计算皮尔森相关值(P 值)来获得平行库之间检测数目的相关性; 除了 P 值, 错误发现率(FDR)则用来控制差异转录的基因^[24]. 在本研究中, $P \leq 0.01$, $FDR \leq 0.1$ 及转录水平比值对数的绝对值 ≥ 1 用来界定显著差异转录的基因.

1.6 生物学功能聚类及富集分析

为了揭示响应过量尿嘧啶的差异转录基因的生物学功能, 基因的功能聚类采用 BLAST (ver. 2.2.23+) 软件于 FunCat 数据库(<http://mips.helmholtz-muenchen.de/proj/funcatDB/>)中进行比对, 以 e 值 1×10^{-10} 为阈值. 为了进一步说明显著的生物学变化, 运用 R 统计软件(<http://www.r-projects.org/>)采用超几何测试算法($P \leq 0.01$ 和 $FDR \leq 0.1$ 作为阈值)进行基因富集分析.

1.7 实时荧光定量 PCR

利用 cDNA 合成试剂盒(Fermentas, Burlington, Canada)从细胞总 RNA 合成 cDNA. 参照产品说明, 实时定量 PCR 分析采用 SYBR-Green 定量 PCR 试剂盒(SYBR PrimeScript RT-PCR Kit, TaKaRa Biotechnology Co. Ltd., 大连)在 iQ5 定量 PCR 仪(Bio-Rad, Hercules, CA, USA)上进行. 每个 cDNA 样品做 3 个平行分析并计算出平均循环阈值, 相对转录量的计算使用 $2^{-\Delta\Delta C_t}$ 方法^[25]并以 β -tubulin 的转录水平来进行标准化. qRT-PCR 中使用的引物见表 1.

2 结果

2.1 *pyrG89* 突变增强了对过量尿嘧啶的敏感性

真菌细胞内的尿嘧啶水平被严格控制以防止过量尿嘧啶的积累. *PyrG*(乳清苷 5'-磷酸脱羧酶)功能缺失的构巢曲霉突变株只能够在含有外源尿嘧啶和尿苷的培养基上生长, 以此猜测 *pyrG* 突变体应该比野生菌株更能耐受过量的外源尿嘧啶和尿苷. 为了验证此猜想, 本研究观察了野生菌株 ALS05 和 *pyrG*

表 1 定量 PCR 分析所用特异性引物

基因	引物名称及序列(5'→3')
<i>nsdD</i>	QnsdDF: GGCGGAACCATCACGTTCAAGTTT QnsdDR: TAACAGTGCCTTGCACTTTGCGTCG
<i>nosA</i>	QnosAF: ACCCATACGTTCTTCTCCGTTCA QnosAR1: TTTCGATCGGTAGGTGTGGGCAAA
<i>noxA</i>	QnoxAF: ACCGAAGTGAAGAGCAGGACCAAT QnoxAR: ACCAATCTCTGTCTGGAATGCGT
<i>fhbA</i>	QfhbAF: AAACAACGTACTTCTGACGGCTC QfhbAR: TCTGCTTGTGCGCAAGGAAGAGAT
<i>glpV</i>	QglpVF: GATCCGCCTTCAGTTTGCCATTGT QglpVR: AATCGCCCCGAAGTCTCAGAGAGGTAT
<i>upt</i>	QuptF: AAGCCATCGACGTGCTGAAAGAGA QuptR: CTTAACC GCGGAAACCGTTGCATT
<i>hsp20</i>	Qhsp20F: TCTGAACATCAAGGGCCACAGTGA Qhsp20R: TAGGAAAGTTGAACGAGCGTCGGA
<i>β-tub</i>	QbtubF: TTCGGACGAGACATTCTGCTTGGA QbtubR: TGACAGCAGACACCAGATGGTTGA

突变体 A773(*pyrG89*)在不同浓度的尿嘧啶和尿苷平板上生长的表型. 与预测相反, *pyrG89* 突变体对过量的尿嘧啶和尿苷比野生型更加敏感. 如图 1 所示, 经过 5 天的培养, 在含有高浓度尿嘧啶和尿苷(正常用量的 4 倍, 用 4×尿嘧啶或 4×尿苷标记)的平板上生长的野生菌株的菌落大小与在正常浓度尿嘧啶和尿苷(用 1×尿嘧啶或 1×尿苷标记)平板上的相似. 而在含 4×尿嘧啶和 4×尿苷的平板上生长的 *pyrG89* 突变体的菌落直径只有在含 1×尿嘧啶和 1×尿苷平板上的 $69\% \pm 2\%$ (图 1). 进一步研究发现, 是过量的尿嘧啶而不是尿苷对 *pyrG89* 突变体的生长起抑制作用(图 1). 将粗糙脉胞菌的 *pyr-4* 基因转入 *pyrG89* 突变体中进行回补, 能完全使 *pyrG89* 突变体回复至野生型(图 1). 这说明过量的尿嘧啶确实能够抑制 *pyrG89* 突变体的生长, 并且这种抑制作用是由 *pyrG* 的功能丧失引起的.

此外, 在 1×UU(10 mmol/L 尿嘧啶和 5 mmol/L 尿苷)平板上, 野生菌株和 *pyrG89* 突变体都主要是通过无性产孢来繁殖的(图 1 和 2). 在菌落表面大量产生的无性孢子使野生型和 *pyrG* 突变体的菌落呈白色. 在 4×UU(40 mmol/L 尿嘧啶和 20 mmol/L 尿苷)平板上, 野生型仍以无性产孢为主, 而 *pyrG89* 突变体的无性产孢却显著减少, 而且有性发育明显增加从而使菌落呈淡黄色(图 1 和 2). 进一步在解剖镜和扫描电子显微镜下观察发现, 在 4×UU 的平板上 *pyrG89* 突变体的原子囊丰富且被黄色的护卫细胞包围, 而 4×UU 的平板上的野生菌株及 1×UU 平板上的 *pyrG* 突变体表面的原子囊则非常稀少(图 2).

图1 过量尿嘧啶抑制构巢曲霉 *pyrG89* 突变体的生长并增强其有性发育

将构巢曲霉野生菌株 ALS05(WT), *pyrG89* 突变体 A773(*pyrG89*)或互补菌株 AHC01(*pyrG89+pyr-4*)的孢子接种到 MMVUU 培养基(MMV+1×尿苷+1×尿嘧啶)或含有 4×添加物(4×尿苷, 或 4×尿嘧啶, 或 4×尿苷和 4×尿嘧啶)的 MMVUU 培养基平板的中心, 在 28℃ 条件下培养 5 天, 1×尿苷的浓度为 5 mmol/L, 1×尿嘧啶的浓度为 10 mmol/L, 实验重复 3 次

2.2 *pyrG89* 突变增加对过量的尿嘧啶代谢相关物质的敏感性

在真核细胞中, 细胞内的尿嘧啶可被用作前体物质来合成其他化合物或者通过 2 条通路被降解^[26,27]. 为了检测这些参与尿嘧啶代谢的化合物是否与尿嘧啶对 *pyrG* 突变体有类似的作用, 在培养基中加入过量 2'-脱氧尿苷(0.04 mol/L)和尿素(0.04 mol/L)进行了等效实验. 如图 2 和 3 所示, 过量 2'-脱氧尿苷(0.04 mol/L)和尿素(0.04 mol/L)抑制 *pyrG89* 突变体的生长但对野生菌株没有影响. 此外, 过量 2'-脱氧尿苷(0.04 mol/L)和尿素(0.04 mol/L)增强 *pyrG89* 突变体有性发育而对野生型没有影响.

2.3 *pyrG89* 突变引起细胞内尿嘧啶的积累

pyrG89 突变体对过量尿嘧啶(0.04 mol/L), 2'-脱氧尿苷(0.04 mol/L)和尿素(0.04 mol/L)的超敏感表型很可能是由于尿嘧啶代谢被破坏引起的. 在 *PyrG* 功能缺失的情况下, 过量的尿嘧啶、2'-脱氧尿苷和尿素可能会在细胞内积累并产生毒害. 为了验证这个假设, 采用 HPLC 对在 4×UU 培养基上生长的 *pyrG89*

突变体和野生菌株胞内的尿嘧啶、尿苷和 AMP 进行了定量分析. 结果显示, *pyrG89* 突变体胞内的尿嘧啶、尿苷和 AMP 分别比野生型中的高出 653%, 31% 和 51% (图 4).

2.4 *pyrG89* 突变体与野生菌株对过量尿嘧啶的转录响应分析

为了弄清楚 *pyrG* 突变体中尿嘧啶积累及尿嘧啶对发育的影响机制, 通过数字基因表达谱(DGE)分析了在含有正常浓度尿嘧啶(1×)和过量尿嘧啶(4×)的液体培养基中生长的 *pyrG89* 突变体和野生菌株的差异转录谱. 在过量尿嘧啶胁迫下, 分别有 185 和 71 个基因在 *pyrG89* 突变体和野生菌株中上调, 分别有 317 和 162 个基因在 *pyrG89* 突变体和野生菌株中下调. 比较过量尿嘧啶胁迫下 *pyrG89* 突变体和野生菌株的转录谱差异发现, *pyrG89* 突变体中 1025 个基因的转录水平至少比野生菌株中低 50%, 655 个基因的转录水平比野生菌株高(>1 倍)(网络版附表 1). 如表 2 所示, 在过量尿嘧啶胁迫下, 一些基因(如 ANID_07074, ANID_03925, ANID_10399, ANID_02859 和

图2 过量尿嘧啶胁迫下构巢曲野生菌株和 *pyrG89* 突变体有性发育比较

将构巢曲野生菌株或 *pyrG89* 突变体的孢子接种到 MMVUU 培养基(MMV+1×尿苷+1×尿嘧啶)(对照)或含有 4×(0.04 mol/L)添加物(4×尿嘧啶, 或 4×2'-脱氧尿苷, 或 4×尿素)的 MMVUU 培养基平板的中心, 在 28℃ 条件下培养 5 天, 1×尿苷的浓度为 5 mmol/L, 1×尿嘧啶、1×2'-脱氧尿苷或 1×尿素的浓度为 10 mmol/L。A: 解剖镜下的观测结果; B: 扫描电子显微镜下的观测结果; C: 对野生菌株和 *pyrG89* 突变体的保卫细胞的计数比较, 所示数值为 3 次重复实验结果的平均值, 标准方差用误差线表示, 1×尿苷的浓度为 5 mmol/L, 1×尿嘧啶、1×2'-脱氧尿苷或 1×尿素的浓度为 10 mmol/L

图3 过量尿嘧啶代谢物对构巢曲 *pyrG* 突变体生长和有性发育的影响

将构巢曲野生菌株或 *pyrG89* 突变体的孢子接种于 MMVUU 培养基(MMV+1×尿苷+1×尿嘧啶) (对照)或含有 4×(0.04 mol/L)添加物(4×尿素, 或 4×2'-脱氧尿苷)的 MMVUU 培养基平板的中心, 在 28℃ 条件下培养 5 天, 1×尿苷的浓度为 5 mmol/L, 1×尿嘧啶、1×2'-脱氧尿苷或 1×尿素的浓度为 10 mmol/L

ANID_05567)在野生菌株中没有应答, 而在 *pyrG89* 突变体中显著上调. 另外一些基因(如 ANID_06657, ANID_01608, ANID_02578 和 ANID_05145)在野生

菌株中维持高转录水平, 而在 *pyrG89* 突变体中却转录降低. 这些现象表明, *pyrG89* 突变体对过量尿嘧啶比野生菌株有更明显的转录应答, 说明 *pyrG89* 突变

图4 构巢曲霉尿嘧啶代谢途径的中间代谢物的 HPLC 图谱

通过 HPLC 对生长在含有 4×尿嘧啶和 1×尿苷基本培养基上的 *pyrG89* 突变体和野生菌株胞内的尿嘧啶、尿苷和 AMP 进行了定量分析, 1×尿苷的浓度为 5 mmol/L, 1×尿嘧啶的浓度为 10 mmol/L; mAu 为峰面积单位

体承受了更大的压力。在过量尿嘧啶胁迫下维持稳定的基因表达也许对细胞代谢和生长有非常重要的作用。

2.5 核苷酸代谢相关基因对过量尿嘧啶的转录应答

基因富集分析显示, 2 个被测菌株的差异转录基因主要参与了含碳化合物和糖类代谢, 转运化合物及与疾病、毒性和防御相关的功能(网络版附表 1)。在这些和尿嘧啶代谢直接相关的基因中, 编码 5'-核苷酸酶(EC: 3.1.3.5)的基因 ANID_05655 在 *pyrG89* 突变体中的转录水平比野生菌株中的高 8 倍(表 2)。5'-核苷酸酶催化单磷酸核苷酸的去磷酸化并且参与了前体核苷酸的补充^[28]。5'-核苷酸酶转录的增加说明, *pyrG* 突变体中核苷酸和核苷的平衡被打乱。

外源尿嘧啶吸收利用的第一步是转运。在构巢曲霉中, *furD*(ANID_11247)和 *cntA*(ANID_05493)分别是尿嘧啶和尿苷转运蛋白的编码基因^[29]。如表 3 和网络版附表 1 所示, 二者在 *pyrG* 突变体中的转录水平都不高于野生菌株。

2.6 有性发育相关基因对过量尿嘧啶的转录应答

在过量尿嘧啶胁迫下, 参与有性发育的几个关键基因在 *pyrG89* 突变体和野生菌株中存在明显的差

异表达。如表 3 所示, *esdC*(ANID_09121), *nosA* 和 *noxA* 在 *pyrG89* 突变体中的转录水平比野生菌株中高 4 倍以上。相反, 黄素血红蛋白基因 *fhbA* 在 *pyrG89* 突变体中的转录量只有野生菌株中的 26%。这些结果进一步通过 qRT-PCR 进行了验证(图 5)。

构巢曲霉 *esdC*(early sexual development)是有性发育中必需的早期关键基因^[30]。基因 *nosA* 在构巢曲霉中控制子实体的形成^[31]。基因 *noxA* 在有性发育期间被诱导表达, *noxA* 的敲除特异地阻断了有性子实体的分化(子囊壳)^[32]。对黄素血红蛋白基因 *fhbA* 来说, *fhbA* 的敲除会诱导有性发育^[33]。因此, *pyrG* 突变体中 *esdC*, *nosA* 和 *noxA* 的上调和 *fhbA* 的下调表达促进了有性发育。

3 讨论

3.1 *PyrG* 参与维持细胞内尿嘧啶稳态

OMP 脱羧酶是嘧啶合成所必需的。细胞内的尿嘧啶水平受严格控制以防止尿嘧啶的积累。这主要是通过转录水平、转录后水平及翻译后水平对尿嘧啶通透酶的调控实现的^[13~15]。在本研究中, 发现培养基中过量的尿嘧啶导致 *pyrG89* 突变体胞中尿嘧啶的积累, 而不能影响野生菌株胞内尿嘧啶的水平。这说明 OMP 脱羧酶参与维持胞内尿嘧啶在低水平状态。

表 2 过量尿嘧啶压力下 *pyrG89* 突变体和野生菌株中转录差异明显的基因^{a)}

基因 ^a	功能注释 ^b	TPM ^c -WT 1×尿嘧啶	TPM- <i>pyrG89</i> 1×尿嘧啶	TPM ^c -WT 4×尿嘧啶	TPM- <i>pyrG89</i> 4×尿嘧啶	倍数 (<i>pyrG89</i> / WT) 4×尿嘧啶	P 值	FDR
上调基因								
ANID_07074	假定蛋白, 代谢与氧化还原过程	4.43	14.50	4.87	112.75	23.15	1.70×10 ⁻¹¹	1.04×10 ⁻¹⁰
ANID_03925	假定蛋白, 糖类代谢	9.71	44.69	13.11	302.00	23.04	0	0
ANID_10399	假定蛋白, 氧化还原过程	10.39	74.71	9.58	214.52	22.39	5.28×10 ⁻¹⁴	4.33×10 ⁻¹³
ANID_02859	二氢吡啶二羧酸合成酶家族蛋白, 代谢过程	3.06	17.91	3.19	63.61	19.94	8.44×10 ⁻⁹	4.26×10 ⁻⁸
ANID_08953	α -葡萄糖苷酶 B, 麦芽糖代谢, <i>agdB</i>	72.37	1748.50	154.45	2911.22	18.85	1.25×10 ⁻¹²	8.37
ANID_09121	<i>esdC</i> , 有性发育	57.04	221.91	32.77	518.60	15.83	1.40×10 ⁻¹³	1.09×10 ⁻¹²
ANID_05567	GrpB 结构域蛋白	4.43	8.19	5.55	82.43	14.85	1.64×10 ⁻¹²	1.09×10 ⁻¹¹
ANID_08972	假定蛋白, 转运蛋白活性	3.92	18.76	3.36	45.48	13.54	4.54×10 ⁻⁹	2.34×10 ⁻⁸
ANID_09373	推测的 Zn(II)2Cys6 转录因子	20.26	47.59	11.09	139.06	12.54	0	0
ANID_05977	酮基还原酶, 代谢过程	23.84	65.67	10.42	112.75	10.82	0	0
ANID_10949	ABC 转运蛋白	2.72	9.89	3.53	32.24	9.13	2.44×10 ⁻⁹	1.28×10 ⁻⁸
ANID_08602	假定蛋白, 具有氧化还原酶活性	10.90	41.45	18.32	164.85	9.00	0	0
ANID_06669	推测的糖转运蛋白	12.09	97.91	29.41	246.93	8.40	3.08×10 ⁻¹³	2.25×10 ⁻¹²
ANID_05655	5'-核苷酸酶(EC: 3.1.3.5)	4.43	18.42	3.03	24.40	8.05	1.56×10 ⁻⁸	7.69×10 ⁻⁸
ANID_00841	假定蛋白	4.60	24.22	4.71	36.94	7.84	3.14×10 ⁻¹¹	1.88×10 ⁻¹⁰
ANID_04220	锚蛋白重复蛋白, 参与减数分裂和胞质、核定位	20.43	41.45	5.55	41.30	7.44	1.64×10 ⁻¹²	1.09×10 ⁻¹¹
ANID_02970	4-硝基苯磷酸酶, 参与对氨基苯甲酸甲酯降解	77.13	175.00	32.60	239.09	7.33	4.61×10 ⁻¹³	3.30×10 ⁻¹²
ANID_03520	假定蛋白	10.22	40.94	14.45	102.81	7.11	0	0
ANID_10964	甲基转移酶, 代谢过程	19.07	49.64	7.06	49.66	7.03	1.07×10 ⁻¹³	8.47×10 ⁻¹³
ANID_04085	蛋白磷酸酶 2a 65 kD 调控亚基	58.91	114.11	27.56	173.22	6.29	8.93×10 ⁻¹⁴	7.18×10 ⁻¹³
下调基因								
ANID_05447	谷氨酸脱羧酶, 氨基酸代谢	395.20	106.95	585.19	18.65	0.032	0	0
ANID_06657	假定蛋白	1291.17	461.90	1699.60	78.94	0.046	0	0
ANID_01608	假定蛋白	1406.61	531.32	1732.88	96.19	0.056	0	0
ANID_01510	氧化还原酶 oxidoreductin	491.06	161.53	802.49	46.53	0.058	0	0
ANID_02578	假定蛋白, 具有过氧化物酶活性	3255.76	854.72	4109.27	239.09	0.058	0	0
ANID_05145	假定蛋白	258.98	88.70	322.51	18.82	0.058	0	0
ANID_04940	细胞响应压力的蛋白	551.68	112.40	728.38	44.79	0.061	0	0
ANID_02555	丝氨酸羧肽酶, 蛋白质代谢	255.24	79.31	400.99	25.97	0.065	0	0
ANID_12070	谷酰基-tRNA 酰胺转移酶亚基 A	237.19	112.92	271.76	17.77	0.065	0	0
ANID_01879	WD 重复蛋白, 谷胱甘肽分解代谢过程和胞质、核定位	212.33	47.59	309.91	20.39	0.066	0	0
ANID_04127	假定蛋白	686.87	209.46	763.84	57.68	0.076	0	0
ANID_11246	碱基、核苷、核苷酸和核酸转运蛋白	26.39	5.97	50.59	3.83	0.076	7.01×10 ⁻⁶²	1.26×10 ⁻⁶⁰
ANID_04135	δ -9-硬脂酸脱氢酶, 脂肪酸代谢	212.50	67.89	367.38	28.23	0.077	0	0
ANID_10299	假定蛋白, 氨基酸代谢	245.02	103.71	439.14	33.98	0.077	0	0
ANID_02286	乙醇脱氢酶III(ADH III)	515.07	223.10	484.69	39.91	0.082	0	0
ANID_08122	MFS 多药转运蛋白	34.91	9.72	60.00	5.05	0.084	1.07×10 ⁻⁷⁰	2.05×10 ⁻⁶⁹
ANID_01378	假定蛋白	1117.66	840.39	1519.27	132.26	0.087	0	0
ANID_09297	67 kD 肌球蛋白交叉反应抗原家族蛋白	454.28	183.36	548.89	48.44	0.088	0	0
ANID_06525	NAD-依赖性甲酸脱氢酶(FDH)	335.43	148.05	473.26	43.22	0.091	0	0
ANID_00186	假定蛋白	148.14	59.70	283.35	25.97	0.092	0	0
ANID_03796	假定蛋白	145.07	78.12	208.56	19.34	0.093	1.46×10 ⁻²³³	4.10×10 ⁻²³²
ANID_08461	假定蛋白	234.46	220.55	281.50	28.06	0.100	4.00×10 ⁻³⁰⁶	1.23×10 ⁻³⁰⁴
ANID_09470	尿酸酶(尿酸氧化酶), 嘌呤代谢	338.84	136.63	450.40	44.96	0.100	0	0

a) a: 基因登录号参照 broad 曲霉比较基因组数据库(http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html);

b: 功能注释参照 broad 对基因的描述; c: TPM 为每百万中的标签数

表 3 *pyrG89* 突变体和野生菌株中尿嘧啶和尿苷转运蛋白基因及参与有性发育的基因对过量尿嘧啶胁迫转录响应的比较^{a)}

基因 ^a	功能注释 ^b	TPM ^c -WT 1×尿嘧啶	TPM- <i>pyrG89</i> 1×尿嘧啶	TPM ^c - WT 4×尿嘧啶	TPM- <i>pyrG89</i> 4×尿嘧啶	倍数 (<i>pyrG89</i> /WT) 4×尿嘧啶	P 值	FDR
尿嘧啶和尿苷转运蛋白基因								
ANID_11247	尿嘧啶转运蛋白 FurD	0.34	0.01	0.84	0.01	—	0.0348	0.0688
ANID_05493	浓缩的核苷透性酶 CntA	3.41	3.75	5.71	5.05	—	0.6319	0.7132
参与有性发育的基因								
ANID_01052	有性发育调控蛋白 VeA	72.54	102.17	82.35	134.17	1.63	0	0
ANID_03152	有性发育转录因子 NsdD	1.70	0.68	0.34	0.01	—	0.2638	0.3483
ANID_04263	C2H2 锌指蛋白 NsdC	0.85	1.02	1.01	0.35	—	0.1982	0.2944
ANID_09121	有性发育早期蛋白 EsdC	57.04	221.91	32.77	518.60	15.83	1.40×10 ⁻¹³	1.09×10 ⁻¹²
ANID_06505	转录抑制子 <i>rco-1</i> , TupA/RocA	366.76	345.23	402.34	455.00	—	1.37×10 ⁻⁵	5.03×10 ⁻⁵
ANID_05170	有性发育转录因子 RosA	0	0	0	0	—	—	—
ANID_02260	NADH-辅酶 Q 氧化还原酶亚基	403.20	383.27	578.97	346.78	0.60	1.23×10 ⁻⁷⁶	2.40×10 ⁻⁷⁵
ANID_01848	C6 有性发育转录因子 NosA	3.41	3.24	1.18	5.92	5.02	1.95×10 ⁻⁵	7.03×10 ⁻⁵
ANID_02330	有性发育晚期蛋白	0	0	0	0	—	—	—
ANID_07169	黄素血红蛋白 FhbA	2222.72	1699.55	1077.95	276.55	0.26	0	0
ANID_00807	甲基转移酶 LacA	0.01	0.68	1.18	0.01	0.01	0.0090	0.0213
ANID_05457	NADPH 氧化酶 NoxA	4.43	13.82	5.04	29.62	5.88	9.27×10 ⁻¹²	5.79×10 ⁻¹¹
ANID_05836	细胞模式形成相关蛋白 StuA	5.96	5.80	4.54	5.92	—	0.3022	0.3899

a) a: 基因登录号参照 broad 曲霉比较基因组数据库(http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html/);
b: 功能注释参照 broad 对基因的描述; c: TPM 为每百万中的标签数; “—”代表 P 值大于 0.01

图 5 实时荧光定量 PCR 鉴定 *pyrG89* 突变体和野生菌株在过量尿嘧啶胁迫下的差异转录基因

图中显示了 4 个下调基因和 3 个上调基因的相对转录水平, 所示数值为 3 次重复的平均值, 标准方差用误差线表示

构巢曲霉 *furD*(ANID_11247)和 *cntA*(ANID_05493)是目前仅知的分别编码尿嘧啶转运蛋白和尿苷转运蛋白基因。而研究分析表明, 构巢曲霉中还应该有更多的尿嘧啶转运蛋白基因^[29]。因此, 即使 *furD* 和 *cntA* 在 *pyrG* 突变体中的转录水平相对于野生菌株没有提高, 这仍然不能断定 *pyrG89* 突变体中尿嘧啶的积累不是源于尿嘧啶的运输增多。然而, 如果尿嘧啶的积累不是源于尿嘧啶的运输增多, 那么 *PyrG* 除了

催化 UMP 的生物合成, 也许还以一种未知的机制参与了过量尿嘧啶的循环。

尿嘧啶的积累被认为对细胞是有毒害的, 但这些毒害作用还未观察到。本研究中, 提供了直接的证据表明高浓度的尿嘧啶影响真菌的生长发育。由于在过量外源尿嘧啶条件下, *pyrG89* 突变体会积累过量尿嘧啶, 因此, *pyrG89* 突变体可以作为研究增加尿嘧啶是否能提高尿嘧啶整合到 DNA 中频率的理想模型。与尿嘧啶不同, 虽然尿苷在 *pyrG89* 突变体中存在积累, 但其抑制作用的表型还未观察到。这可能是由于尿苷不能作为底物直接被整合到 DNA 中来合成尿嘧啶-DNA, 因此其毒性要低于尿嘧啶。

3.2 过量尿嘧啶激活有性发育

对于大多数丝状子囊真菌, 无性产孢是正常环境条件下的主要繁殖方式, 而有性发育通常需要一些极端条件的诱导, 如低温和长时间的黑暗。因此, 有性发育也许是真菌在极端环境下生存的一种策略。本研究显示, 尿嘧啶及其代谢途径中的其他代谢物能够激活 *pyrG89* 突变体进行有性发育而抑制无性产孢, 并且与有性发育相关的关键基因, 如 *esdC*, *nosA* 和 *noxA* 等被诱导表达。以上结果表明, 胞内尿嘧啶及其相关代谢产物的积累能够改变构巢曲霉的生长

发育状态. 与过量尿嘧啶条件下的 *pyrG89* 突变体相似, 鞘磷脂合成存在缺陷的构巢曲霉突变体也表现出有性产孢增强而无性产孢减弱的特征^[34]. 这些现象都表明有性发育能够被各种代谢异常所激发. 每种代谢过程都可能存在感受其代谢变化的监视器. 然而, 不同代谢监视器的异常信号也许会被传递到相同的未知信号通路上而控制真菌的发育. 这一通路被代谢监视器激发后能够在转录水平上激活 *esdC*, *nosA* 和 *noxA* 等有性发育关键调控基因的转录, 而后进一步激活有性发育必需基因的表达.

3.3 *pyrG* 影响真菌对多种压力的敏感性

构巢曲霉及其他真菌的基因敲除或过表达通常采用营养缺陷型的 *pyrG* 突变体作为出发菌株, 通过营养缺陷标记筛选, 获得基因敲除或过表达新突变株. 新突变株的表型分析通常用出发菌株 *pyrG* 突变体作为对照来进行分析. 然而, 本研究明确表明, *pyrG* 突变能够引起真菌生长发育状态的变化. 因此, 当用 *pyrG* 突变体作为出发菌株得到新突变体的时候, 必须保证新突变体的表型是源于新基因的改变而不是由 *pyrG* 突变引起的.

参考文献

- 1 Bach M L, Lacroute F. Direct selective techniques for the isolation of pyrimidine auxotrophs in yeast. *Mol Gen Genet*, 1972, 115: 126–130
- 2 Palmer L M, Cove D J. Pyrimidine biosynthesis in *Aspergillus nidulans*: isolation and preliminary characterisation of auxotrophic mutants. *Mol Gen Genet*, 1975, 138: 243–255
- 3 Perkins D D, Radford A, Newmeyer D, et al. Chromosomal loci of *Neurospora crassa*. *Microbiol Rev*, 1982, 46: 426–570
- 4 Boeke J, LaCroute F, Fink G R. A positive selection for mutants lacking orotidine-5'-phosphate decarboxylase activity in yeast: 5-fluoro-orotic acid resistance. *Mol Gen Genet*, 1984, 197: 345–346
- 5 Ballance D J, Turner G. Development of a high-frequency transforming vector for *Aspergillus nidulans*. *Gene*, 1985, 36: 321–331
- 6 Díez B, Alvarez E, Cantoral J M, et al. Selection and characterization of *pyrG* mutants of *Penicillium chrysogenum* lacking orotidine-5'-phosphate decarboxylase and complementation by the *pyr4* gene of *Neurospora crassa*. *Curr Genet*, 1987, 12: 277–282
- 7 van Hartingsveldt W, Mattern I E, van Zeijl C M, et al. Development of a homologous transformation system for *Aspergillus niger* based on the *pyrG* gene. *Mol Gen Genet*, 1987, 206: 71–75
- 8 Smith J L, Bayliss F T, Ward M. Sequence of the cloned *pyr4* gene of *Trichoderma reesei* and its use as a homologous selectable marker for transformation. *Curr Genet*, 1991, 19: 27–33
- 9 Weidner G, d'Enfert C, Koch A, et al. Development of a homologous transformation system for the human pathogenic fungus *Aspergillus fumigatus* based on the *pyrG* gene encoding orotidine 5'-monophosphate decarboxylase. *Curr Genet*, 1998, 33: 378–385
- 10 Oakley B R, Rinehart J E, Mitchell B L, et al. Cloning, mapping, and molecular analysis of the *pyrG* (orotidine-5'-phosphate decarboxylase) gene of *Aspergillus nidulans*. *Gene*, 1987, 61: 385–399
- 11 Waring R B, May G S, Morris N R. Characterization of an inducible expression system in *Aspergillus nidulans* using *alcA* and tubulin-coding genes. *Gene*, 1989, 79: 119–130
- 12 Chevallier M R. Cloning and transcriptional control of a eucaryotic permease gene. *Mol Cell Biol*, 1982, 2: 977–984
- 13 Galan J M, Moreau V, André B, et al. Ubiquitination mediated by the Npi1p/Rsp5p ubiquitin-protein ligase is required for endocytosis of the yeast uracil permease. *J Biol Chem*, 1996, 271: 10946–10952
- 14 Séron K, Blondel M O, Haguénauer-Tsapis R, et al. Uracil-induced down regulation of the yeast uracil permease. *J Bacteriol*, 1999, 181: 1793–1800
- 15 Amillis S, Hamari Z, Roumelioti K, et al. Regulation of expression and kinetic modeling of substrate interactions of a uracil transporter in *Aspergillus nidulans*. *Mol Membr Biol*, 2007, 24: 206–214
- 16 Verri A, Mazzarello P, Biamonti G, et al. The specific binding of nuclear proteins to the cAMP responsive element sequence is reduced by misincorporation of uracil and increased by the deamination of cytosine. *Nucleic Acids Res*, 1990, 18: 5775–5780
- 17 Miller B, Miller K, Timberlake W. Direct and indirect gene replacements in *Aspergillus nidulans*. *Mol Cell Biol*, 1985, 5: 1714–1721
- 18 Calvo A M, Bok J, Brooks W, et al. *VeA* is required for toxin and sclerotial production in *Aspergillus parasiticus*. *Appl Environ Microbiol*, 2004, 70: 4733–4739
- 19 Käfer E. Meiotic and mitotic recombination in *Aspergillus* and its chromosomal aberrations. *Adv Genet*, 1977, 19: 33–131
- 20 Ruijter G J G, Visser J. Determination of intermediary metabolites in *Aspergillus niger*. *J Microbiol Methods*, 1996, 25: 295–302
- 21 Nielsen K, Høgh A L, Emmersen J. DeepSAGE-digital transcriptomics with high sensitivity, simple experimental protocol and multiplexing of samples. *Nucleic Acids Res*, 2006, 34: e133

- 22 Sun X Y, Zhang H X, Zhang Z Y, et al. Involvement of a helix-loop-helix transcription factor CHC-1 in CO₂-mediated conidiation suppression in *Neurospora crassa*. *Fungal Genet Biol*, 2011, 48: 1077–1086
- 23 Audic S, Claverie J M. The significance of digital gene expression profiles. *Genome Res*, 1997, 7: 986–995
- 24 Benjamini Y, Drai D, Elmer G, et al. Controlling the false discovery rate in behavior genetics research. *Behav Brain Res*, 2001, 125: 279–284
- 25 Livak K J, Schmittgen T D. Analysis of relative gene expression data using Real-time quantitative PCR and the 2^{-ΔΔC_t} method. *Methods*, 2001, 25: 402–408
- 26 Vogels G D, van der Drift C. Degradation of purines and pyrimidines by microorganisms. *Bacteriol Rev*, 1976, 40: 403–468
- 27 Andersen G, Björnberg O, Polakova S, et al. A second pathway to degrade pyrimidine nucleic acid precursors in eukaryotes. *J Mol Biol*, 2008, 380: 656–666
- 28 Hunsucker S A, Mitchell B S, Spychala J. The 5′-nucleotidases as regulators of nucleotide and drug metabolism. *Pharmacol Ther*, 2005, 107: 1–30
- 29 Hamari Z, Amillis S, Drevet C, et al. Convergent evolution and orphan genes in the Fur4p-like family and characterization of a general nucleoside transporter in *Aspergillus nidulans*. *Mol Microbiol*, 2009, 73: 43–57
- 30 Han K H, Kim J H, Moon H, et al. The *Aspergillus nidulans esdC* (early sexual development) gene is necessary for sexual development and is controlled by *veA* and a heterotrimeric G protein. *Fungal Genet Biol*, 2008, 45: 310–318
- 31 Vienken K, Fischer R. The Zn(II)₂Cys₆ putative transcription factor NosA controls fruiting body formation in *Aspergillus nidulans*. *Mol Microbiol*, 2006, 61: 544–554
- 32 Lara-Ortiz T, Riveros-Rosas H, Aguirre J. Reactive oxygen species generated by microbial NADPH oxidase NoxA regulate sexual development in *Aspergillus nidulans*. *Mol Microbiol*, 2003, 50: 1241–1255
- 33 Baidya S, Cary J W, Grayburn W S, et al. Role of nitric oxide and flavohemoglobin homolog genes in *Aspergillus nidulans* sexual development and mycotoxin production. *Appl Environ Microbiol*, 2011, 77: 5524–5528
- 34 Li S, Bao D, Yuen G, et al. *BasA* regulates cell wall organization and asexual/sexual sporulation ratio in *Aspergillus nidulans*. *Genet*, 2007, 176: 243–253

论文

附录

附表 1 差异转录基因的功能聚类及富集分析(4×尿嘧啶, $\Delta pyrG89/WT$)^{a)}

Funcat 编号 ^a	鉴定的基因	差异转录的基因	P-值 ^b	FDR ^b	重要性 ^b	Funcat 名称 ^a
01.05	775	201	0.005411	0.084768	TRUE	含碳组分及糖类代谢
20.01	680	180	0.003412	0.080185	TRUE	转运化合物(底物)
32.05	242	72	0.003374	0.080185	TRUE	病害、毒性及防卫反应
01.01	362	84	0.34174	0.979167	FALSE	氨基酸代谢
01.02	169	32	0.872215	0.979167	FALSE	氮、硫和硒代谢
01.03	200	46	0.421309	0.979167	FALSE	核苷酸、核苷和碱基代谢
01.06	440	112	0.053696	0.420617	FALSE	脂类、脂肪酸和类异戊二烯代谢
01.20	317	83	0.049697	0.420617	FALSE	次级代谢
02.16	82	16	0.762365	0.979167	FALSE	发酵
10.01	297	44	0.999579	0.979167	FALSE	DNA 加工
10.03	415	72	0.994983	0.979167	FALSE	细胞循环
11.02	521	89	0.998872	0.979167	FALSE	RNA 合成
11.04	262	38	0.999469	0.979167	FALSE	RNA 加工
11.06	44	5	0.979666	0.979167	FALSE	RNA 修饰
14.07	454	92	0.862637	0.979167	FALSE	蛋白质修饰
14.13	198	51	0.130378	0.765973	FALSE	蛋白/多肽降解
18.02	154	30	0.821395	0.979167	FALSE	调控靶标, 蛋白活性调控
20.03	374	87	0.328622	0.979167	FALSE	转运工具
20.09	719	157	0.617404	0.979167	FALSE	转运通路
30.01	258	51	0.850916	0.979167	FALSE	细胞及胞内信号传导
30.05	73	15	0.679237	0.979167	FALSE	转膜信号传导
32.07	217	60	0.032963	0.387316	FALSE	解毒作用
34.01	187	50	0.080286	0.539061	FALSE	体内离子平衡
34.11	243	59	0.237358	0.979167	FALSE	细胞对外界刺激的感应和响应
36.20	7	2	0.483355	0.979167	FALSE	真菌特异性系统感应和响应
40.01	196	46	0.361702	0.979167	FALSE	细胞生长和形态建成
40.02	5	1	0.715372	0.979167	FALSE	细胞分化
40.10	19	5	0.419049	0.979167	FALSE	细胞死亡
41.01	37	3	0.994039	0.979167	FALSE	真菌/微生物发育
43.01	368	87	0.268756	0.979167	FALSE	真菌/微生物细胞类型分化

a) a: 差异表达基因的功能聚类采用 Blast 软件(ver. 2.2.23+)比对 Funcat 数据库获得(<http://mips.Helmholtz-muenchen.de/proj/funcatDB/>);

b: 运用 R 统计软件(<http://www.r-projects.org/>)采用超几何测试算法($P \leq 0.01$ 和 $FDR \leq 0.1$ 作为阈值)进行基因富集分析

附表2 过量尿嘧啶胁迫下 *pyrG* 突变体与野生菌株差异转录的基因^{a)}

基因 ^a	TPM ^b - WT-4× 尿嘧啶	TPM- <i>pyrG89</i> -4×尿嘧啶	log2 比值 (<i>pyrG89</i> /WT)	P-值	FDR	Blast 比对基因非冗余库
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: dihydroadipicinate 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]
ANID_02970	32.6	239.09	2.87460992	4.61E-13	3.30E-12	gi 259486084 tpe CBF83644.1 /3.15434e-134/TPA: 4-nitrophenylphosphatase (AFU_orthologue; AFUA_3G08310) [A. nidulans FGSC A4]
ANID_07188	0.67	4.88	2.86464815	5.62E-05	0.000191	gi 259483478 tpe CBF78900.1 /0/TPA: small oligopeptide transporter, OPT family (AFU_orthologue; AFUA_6G10220) [A. nidulans FGSC A4]

ANID_07271	2.18	15.86	2.86299273	3.28E-07	1.45E-06	gi 67900568 ref XP_680540.1 /0/hypothetical protein AN7271.2 [A. nidulans FGSC A4]
ANID_02879	1.85	13.42	2.8587875	1.08E-06	4.52E-06	gi 13569693 gb AAK31198.1 AF349513_1/0/general amidase-B [Emericella nidulans]
ANID_08150	1.01	7.32	2.85748836	1.80E-05	6.52E-05	gi 134077118 emb CAK45459.1 /0/unnamed protein product [A. niger]
ANID_07747	1.18	8.54	2.85544921	1.05E-05	3.94E-05	gi 67901520 ref XP_681016.1 /1.46292e-170/hypothetical protein AN7747.2 [A. nidulans FGSC A4]
ANID_06931	1.34	9.58	2.83779266	6.04E-06	2.35E-05	gi 67541522 ref XP_664535.1 /4.05613e-107/hypothetical protein AN6931.2 [A. nidulans FGSC A4]
ANID_03520	14.45	102.81	2.8308392	0	0	gi 67526125 ref XP_661124.1 /0/hypothetical protein AN3520.2 [A. nidulans FGSC A4]
ANID_10964	7.06	49.66	2.81434417	1.07E-13	8.47E-13	gi 259483911 tpe CBF79686.1 /0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_07239	0.67	4.71	2.81349406	6.17E-05	0.000209	gi 67900504 ref XP_680508.1 /3.2032e-119/hypothetical protein AN7239.2 [A. nidulans FGSC A4]
ANID_08146	1.34	9.41	2.81196172	6.04E-06	2.35E-05	gi 67902318 ref XP_681415.1 /0/hypothetical protein AN8146.2 [A. nidulans FGSC A4]
ANID_02335	0.5	3.49	2.80322704	0.000276	0.000853	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]
ANID_03526	3.87	27.01	2.80308817	7.03E-10	3.85E-09	gi 67526137 ref XP_661130.1 /0/hypothetical protein AN3526.2 [A. nidulans FGSC A4]
ANID_04474	3.7	25.79	2.8012146	1.31E-09	7.05E-09	gi 67530950 ref XP_662078.1 /1.22813e-56/hypothetical protein AN4474.2 [A. nidulans FGSC A4]
ANID_05625	1.34	9.24	2.78565985	6.04E-06	2.35E-05	gi 67538910 ref XP_663229.1 /1.58777e-85/hypothetical protein AN5625.2 [A. nidulans FGSC A4]
ANID_08986	1.34	9.24	2.78565985	6.04E-06	2.35E-05	gi 67903998 ref XP_682255.1 /0/hypothetical protein AN8986.2 [A. nidulans FGSC A4]
ANID_07338	1.18	8.02	2.76481538	1.05E-05	3.94E-05	gi 67900702 ref XP_680607.1 /2.98021e-136/hypothetical protein AN7338.2 [A. nidulans FGSC A4]
ANID_08683	2.02	13.59	2.75011826	5.96E-07	2.57E-06	gi 67903392 ref XP_681952.1 /0/hypothetical protein AN8683.2 [A. nidulans FGSC A4]
ANID_02987	1.18	7.84	2.7320668	1.05E-05	3.94E-05	gi 67525059 ref XP_660591.1 /2.37306e-170/hypothetical protein AN2987.2 [A. nidulans FGSC A4]
ANID_03312	0.84	5.58	2.73180389	3.27E-05	0.000115	gi 159130286 gb EDP55399.1 /4.86309e-86/oxidoreductase, short chain dehydrogenase/reductase family [A. fumigatus A1163]
ANID_00869	1.34	8.89	2.72995042	6.04E-06	2.35E-05	gi 67517183 ref XP_658473.1 /1.10687e-86/hypothetical protein AN0869.2 [A. nidulans FGSC A4]
ANID_02510	0.67	4.36	2.70209513	8.88E-05	0.000295	gi 259487936 tpe CBF86998.1 /3.03302e-125/TPA: DUF218 domain protein (AFU_orthologue; AFUA_3G14300) [A. nidulans FGSC A4]
ANID_04320	0.84	5.4	2.68449817	3.47E-05	0.000122	gi 121706484 ref XP_001271504.1 /0/RSC complex subunit Sfh1, putative [A. clavatus NRRL 1]
ANID_03309	4.71	30.15	2.67835904	3.14E-11	1.89E-10	gi 67525703 ref XP_660913.1 /0/hypothetical protein AN3309.2 [A. nidulans FGSC A4]
ANID_03524	2.02	12.9	2.67494387	5.96E-07	2.57E-06	gi 67526133 ref XP_661128.1 /0/hypothetical protein AN3524.2 [A. nidulans FGSC A4]
ANID_04085	27.56	173.22	2.65195772	8.93E-14	7.18E-13	gi 259481327 tpe CBF74740.1 /0/TPA: protein phosphatase 2a 65kd regulatory subunit (AFU_orthologue; AFUA_1G05610) [A. nidulans FGSC A4]
ANID_02592	0.84	5.23	2.63834971	3.82E-05	0.000133	gi 67524269 ref XP_660196.1 /2.11982e-158/hypothetical protein AN2592.2 [A. nidulans FGSC A4]
ANID_05114	3.03	18.65	2.62178593	1.56E-08	7.70E-08	gi 259484559 tpe CBF80886.1 /0/TPA: ribonuclease HI large subunit (AFU_orthologue; AFUA_1G07600) [A. nidulans FGSC A4]
ANID_02798	2.02	12.37	2.6144183	5.96E-07	2.57E-06	gi 255941690 ref XP_002561614.1 /1.08125e-75/Pc16g13150 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_07222	1.51	9.24	2.6133443	3.43E-06	1.37E-05	gi 259483436 tpe CBF78824.1 /0/TPA: NACHT domain protein (AFU_orthologue; AFUA_2G01760) [A. nidulans FGSC A4]
ANID_00941	1.51	9.24	2.6133443	3.43E-06	1.37E-05	gi 95025690 gb ABF50846.1 /0/alpha-glucosidase [Emericella nidulans]
ANID_04699	9.24	55.24	2.57974856	0	0	gi 67537058 ref XP_662303.1 /5.40455e-177/hypothetical protein AN4699.2 [A. nidulans FGSC A4]
ANID_10698	11.26	67.09	2.57489092	0	0	gi 259484991 tpe CBF81683.1 /8.58151e-146/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05429	3.03	17.95	2.56659415	1.56E-08	7.70E-08	gi 67538518 ref XP_663033.1 /0/hypothetical protein AN5429.2 [A. nidulans FGSC A4]
ANID_05457	5.04	29.62	2.555076	9.27E-12	5.79E-11	gi 27413311 gb AAN75017.1 /0/NADPH oxidase [Emericella nidulans]
ANID_09407	54.79	321.86	2.55444878	5.55E-13	3.91E-12	gi 259488249 tpe CBF87553.1 /0/TPA: Fatty acid synthase, alpha subunit [Source:UniProtKB/TrEMBL;Acc:P78615] [A. nidulans FGSC A4]
ANID_10738	2.02	11.85	2.55245986	5.96E-07	2.57E-06	gi 259480041 tpe CBF70812.1 /1.80077e-85/TPA: Paa1_thioesterase family protein, putative (AFU_orthologue; AFUA_4G04355) [A. nidulans FGSC A4]
ANID_06273	8.07	47.05	2.54355414	1.02E-13	8.16E-13	gi 259479515 tpe CBF69807.1 /9.71288e-75/TPA: allergenic cerato-platanin Asp F13 (AFU_orthologue; AFUA_2G12630) [A. nidulans FGSC A4]
ANID_09106	2.35	13.59	2.53181279	1.80E-07	8.16E-07	gi 67904238 ref XP_682375.1 /1.38563e-140/hypothetical protein AN9106.2 [A. nidulans FGSC A4]
ANID_01809	8.74	50.36	2.5265731	5.15E-14	4.23E-13	gi 259487155 tpe CBF85602.1 /7.18605e-157/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04223	18.82	108.39	2.52589313	0	0	gi 67527961 ref XP_661827.1 /0/hypothetical protein AN4223.2 [A. nidulans FGSC A4]
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 TREAE_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:Q5AU5Y] [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 transporter 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)(Triacetylfulvarinine 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 CBF87356.1 /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 [Emicella 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; AltName: 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 25948091 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. marneffeii 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_ASPO 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]
ANID_12201	4.2	12.55	1.57922613	5.19E-07	2.26E-06	gi 169776557 ref XP_001822745.1 /3.76577e-64/2Fe-2S iron-sulfur cluster binding domain protein [A. oryzae RIB40]
ANID_04341	6.89	20.56	1.57726438	1.22E-10	7.05E-10	gi 67528286 ref XP_661945.1 /0/hypothetical protein AN4341.2 [A. nidulans FGSC A4]
ANID_11864	52.44	156.31	1.57567049	7.82E-14	6.31E-13	gi 67523255 ref XP_659688.1 /9.07598e-178/hypothetical protein AN2084.2 [A. nidulans FGSC A4]
ANID_12405	26.39	78.59	1.5743544	0	0	gi 259485571 tpe CBF82705.1 /0/TPA: MFS monocarboxylate transporter, putative (AFU_orthologue; AFUA_3G05660) [A. nidulans FGSC A4]
ANID_02687	40.17	119.02	1.56701366	5.22E-13	3.70E-12	gi 238054315 sp Q96WY0.2 RHOC_EMENI/6.74228e-100/RecName: Full=GTP-binding protein rhoC; AltName: Full=Rho3 protein homolog; Flags: Precursor
ANID_01278	219.32	649.65	1.56662529	6.91E-12	4.38E-11	gi 259488399 tpe CBF87807.1 /4.4909e-40/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_04196	3.19	9.41	1.5606383	1.71E-05	6.21E-05	gi 67527898 ref XP_661800.1 /0/hypothetical protein AN4196.2 [A. nidulans FGSC A4]
ANID_02176	6.39	18.82	1.55837879	1.03E-09	5.57E-09	gi 259487556 tpe CBF86321.1 /0/TPA: Gamma-tubulin complex protein 4 (Eurofung) [A.

						nidulans FGSC A4]
ANID_08229	65.04	189.42	1.5421895	6.55E-13	4.54E-12	gi 259481011 tpe CBF74158.1 /7.64919e-145/TPA: mitochondrial export translocase Oxa1, putative (AFU_orthologue; AFUA_5G03640) [A. nidulans FGSC A4]
ANID_02457	3.53	10.28	1.54210018	8.11E-06	3.10E-05	gi 67524003 ref XP_660061.1 /0/hypothetical protein AN2457.2 [A. nidulans FGSC A4]
ANID_10568	12.27	35.72	1.54159683	0	0	gi 259482701 tpe CBF77430.1 /2.9219e-89/TPA: UPF0041 domain protein (AFU_orthologue; AFUA_4G07750) [A. nidulans FGSC A4]
ANID_04837	5.04	14.64	1.53841992	1.02E-07	4.72E-07	gi 67537334 ref XP_662441.1 /0/hypothetical protein AN4837.2 [A. nidulans FGSC A4]
ANID_04041	10.59	30.67	1.53412558	0	0	gi 67527314 ref XP_661645.1 /1.26607e-102/hypothetical protein AN4041.2 [A. nidulans FGSC A4]
ANID_00562	20.17	58.38	1.53326313	0	0	gi 67516561 ref XP_658166.1 /0/hypothetical protein AN0562.2 [A. nidulans FGSC A4]
ANID_06536	9.24	26.66	1.52871202	7.41E-13	5.11E-12	gi 259480107 tpe CBF70937.1 /3.45048e-115/TPA: Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) [Source:UniProtKB/TrEMBL;Acc:Q9C1R3] [A. nidulans FGSC A4]
ANID_06468	12.77	36.77	1.52577065	0	0	gi 67540596 ref XP_664072.1 /0/hypothetical protein AN6468.2 [A. nidulans FGSC A4]
ANID_05713	105.54	303.39	1.52338365	4.46E-13	3.20E-12	gi 67539086 ref XP_663317.1 /0/hypothetical protein AN5713.2 [A. nidulans FGSC A4]
ANID_05972	85.21	244.66	1.5216836	9.44E-13	6.43E-12	gi 259479847 tpe CBF70445.1 /0/TPA: Coatomer subunit beta', putative (Eurofung) [A. nidulans FGSC A4]
ANID_11869	14.96	42.87	1.51885824	0	0	-
ANID_04561	39.66	113.62	1.51846023	4.11E-13	2.96E-12	gi 259482609 tpe CBF77254.1 /9.30964e-107/TPA: phosducin-like protein (Eurofung) [A. nidulans FGSC A4]
ANID_04015	631.74	1805.35	1.51487573	1.59E-12	1.06E-11	gi 259481400 tpe CBF74882.1 /5.45293e-75/TPA: eukaryotic translation initiation factor 5A-2 (Broad) [A. nidulans FGSC A4]
ANID_01780	9.58	27.36	1.51397067	6.05E-13	4.22E-12	gi 83766963 dbj BAE57103.1 /6.55865e-179/unnamed protein product [A. oryzae]
ANID_04901	2.69	7.67	1.51162041	0.000152	0.000487	gi 67537462 ref XP_662505.1 /0/hypothetical protein AN4901.2 [A. nidulans FGSC A4]
ANID_01356	141.84	403.94	1.50987657	7.29E-13	5.03E-12	gi 67521798 ref XP_658960.1 /0/hypothetical protein AN1356.2 [A. nidulans FGSC A4]
ANID_00120	21.68	61.69	1.50867189	0	0	gi 47824784 emb CAG30553.1 /7.64487e-178/TPA: protein [Emericella nidulans]
ANID_00942	5.88	16.73	1.50854939	1.99E-08	9.71E-08	gi 67517338 ref XP_658546.1 /0/hypothetical protein AN0942.2 [A. nidulans FGSC A4]
ANID_08102	4.54	12.9	1.50660686	8.69E-07	3.69E-06	gi 67902230 ref XP_681371.1 /0/hypothetical protein AN8102.2 [A. nidulans FGSC A4]
ANID_12079	3.19	9.06	1.50595463	3.96E-05	0.000138	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]
ANID_00237	3.87	10.98	1.50447258	5.83E-06	2.27E-05	gi 67515911 ref XP_657841.1 /0/hypothetical protein AN0237.2 [A. nidulans FGSC A4]
ANID_10273	21.68	61.34	1.50046341	0	0	gi 67523437 ref XP_659778.1 /0/hypothetical protein AN2174.2 [A. nidulans FGSC A4]
ANID_07382	4.2	11.85	1.49642583	2.76E-06	1.12E-05	gi 67900790 ref XP_680651.1 /0/hypothetical protein AN7382.2 [A. nidulans FGSC A4]
ANID_04650	26.72	75.28	1.49434662	2.55E-14	2.14E-13	gi 259482513 tpe CBF77067.1 /0/TPA: conserved serine proline-rich protein (AFU_orthologue; AFUA_2G01790) [A. nidulans FGSC A4]
ANID_03482	8.24	23.18	1.49216432	5.18E-11	3.08E-10	gi 67526049 ref XP_661086.1 /5.26504e-50/hypothetical protein AN3482.2 [A. nidulans FGSC A4]
ANID_00907	15.8	44.44	1.49193426	0	0	gi 67517262 ref XP_658511.1 /2.96115e-44/RS22_KLUMA 40S RIBOSOMAL PROTEIN S22 (S15A) (YS24) [A. nidulans FGSC A4]
ANID_02091	31.93	89.74	1.49083863	2.14E-13	1.60E-12	gi 259487462 tpe CBF86161.1 /0/TPA: tyrosine decarboxylase, putative (AFU_orthologue; AFUA_2G04980) [A. nidulans FGSC A4]
ANID_00626	8.07	22.65	1.48887047	9.15E-11	5.33E-10	gi 67516689 ref XP_658230.1 /3.35346e-145/hypothetical protein AN0626.2 [A. nidulans FGSC A4]
ANID_02412	91.59	257.04	1.48873089	0	0	gi 238054297 sp Q00771.2 KCC1_EMENI/0/RecName: Full=Calcium/calmodulin-dependent protein kinase; Short=CMPPK
ANID_00815	6.22	17.43	1.48658608	1.43E-08	7.07E-08	gi 67517069 ref XP_658419.1 /1.23112e-139/hypothetical protein AN0815.2 [A. nidulans FGSC A4]
ANID_05667	6.22	17.43	1.48658608	1.43E-08	7.07E-08	gi 67538994 ref XP_663271.1 /0/hypothetical protein AN5667.2 [A. nidulans FGSC A4]
ANID_04452	185.71	520.35	1.48643084	3.43E-12	2.22E-11	gi 259482731 tpe CBF77490.1 /1.97212e-152/TPA: 60S ribosomal protein L36 (AFU_orthologue; AFUA_4G07435) [A. nidulans FGSC A4]
ANID_00433	1173.57	3286.58	1.48568321	1.93E-11	1.18E-10	gi 67516303 ref XP_658037.1 /1.87278e-87/hypothetical protein AN0433.2 [A. nidulans FGSC A4]
ANID_08704	415.28	1162.15	1.48463999	0	0	gi 289617932 emb CBI55509.1 /9.9679e-21/unnamed protein product [Sordaria macrospora]
ANID_08674	32.77	91.66	1.48391661	1.40E-13	1.09E-12	gi 67903374 ref XP_681943.1 /2.1105e-91/hypothetical protein AN8674.2 [A. nidulans FGSC A4]
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 [Emmericella 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 TFIH (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=Multi-protein-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_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 259488037 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/cafeine-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-cysteiny-D-valine synthase (Delta-(L-alpha-aminoadipyl)-L-cysteiny-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: ThiI/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]
ANID_03354	7.23	0.7	-3.3685688	3.11E-09	1.62E-08	gi 67525793 ref XP_660958.1 /1.51049e-175/hypothetical protein AN3354.2 [A. nidulans FGSC A4]
ANID_08989	12.6	1.22	-3.3684707	3.26E-15	2.88E-14	gi 259486561 tpe CBF84508.1 /1.10078e-59/TPA: glyoxalase family protein (AFU_orthologue; AFUA_5G14830) [A. nidulans FGSC A4]
ANID_01443	86.72	8.54	-3.3440568	6.01E-96	1.29E-94	gi 67521972 ref XP_659047.1 /0/hypothetical protein AN1443.2 [A. nidulans FGSC A4]
ANID_02010	3.53	0.35	-3.3342414	5.15E-05	0.000176	gi 67523107 ref XP_659614.1 /0/hypothetical protein AN2010.2 [A. nidulans FGSC A4]
ANID_10148	8.74	0.87	-3.328546	8.29E-11	4.87E-10	gi 38489215 gb AAR21293.1 /3.95217e-149/ChpA [Emericella nidulans]
ANID_08461	281.5	28.06	-3.326548	#####	#####	gi 67902948 ref XP_681730.1 /6.32139e-174/hypothetical protein AN8461.2 [A. nidulans FGSC A4]
ANID_09470	450.4	44.96	-3.3244929	0	0	gi 75859024 ref XP_868852.1 /6.86217e-166/URIC_EMENI Uricase (Urate oxidase) [A. nidulans FGSC A4]
ANID_08238	17.14	1.74	-3.3002079	7.02E-20	7.13E-19	gi 67902502 ref XP_681507.1 /1.25513e-92/hypothetical protein AN8238.2 [A. nidulans FGSC A4]
ANID_01262	1216.93	123.55	-3.3000793	0	0	gi 67521610 ref XP_658866.1 /8.85442e-152/hypothetical protein AN1262.2 [A. nidulans FGSC A4]
ANID_07832	50.59	5.23	-3.2739694	1.40E-55	2.40E-54	gi 67901690 ref XP_681101.1 /0/hypothetical protein AN7832.2 [A. nidulans FGSC A4]
ANID_03679	31.93	3.31	-3.2700094	1.39E-35	1.91E-34	gi 259481784 tpe CBF75629.1 /2.68465e-161/TPA: oxidoreductase, short-chain dehydrogenase/reductase family (AFU_orthologue; AFUA_4G05870) [A. nidulans FGSC A4]
ANID_05611	287.05	29.8	-3.2679178	#####	#####	gi 67538882 ref XP_663215.1 /2.1437e-115/hypothetical protein AN5611.2 [A. nidulans FGSC A4]
ANID_02615	3.36	0.35	-3.2630344	9.31E-05	0.000309	gi 67524315 ref XP_660219.1 /0/hypothetical protein AN2615.2 [A. nidulans FGSC A4]
ANID_01001	63.19	6.62	-3.2547931	1.17E-68	2.17E-67	gi 67517569 ref XP_658605.1 /0/hypothetical protein AN1001.2 [A. nidulans FGSC A4]
ANID_03961	23.19	2.44	-3.2485498	4.39E-26	5.18E-25	gi 67527007 ref XP_661565.1 /0/hypothetical protein AN3961.2 [A. nidulans FGSC A4]
ANID_01601	73.78	7.84	-3.2343042	1.94E-79	3.85E-78	gi 67522288 ref XP_659205.1 /0/hypothetical protein AN1601.2 [A. nidulans FGSC A4]
ANID_02249	27.56	2.96	-3.2189068	1.77E-30	2.29E-29	gi 259487640 tpe CBF86464.1 /6.66737e-164/TPA: integral membrane protein (AFU_orthologue; AFUA_5G06670) [A. nidulans FGSC A4]

ANID_01181	12.94	1.39	-3.2186808	5.36E-15	4.66E-14	gi 18693015 gb AAL73118.1 /0/ammonium permease MEPA [Emericella nidulans]
ANID_00918	9.75	1.05	-3.2150129	1.29E-11	7.96E-11	gi 259488795 tpe CBF88528.1 /0/TPA: conserved hypothetical protein similar to alpha-hydroxylase Scs7 (Eurofung) [A. nidulans FGSC A4]
ANID_02287	138.15	14.99	-3.2041633	#####	#####	gi 67523663 ref XP_659891.1 /0/hypothetical protein AN2287.2 [A. nidulans FGSC A4]
ANID_03053	129.07	14.12	-3.1923417	#####	#####	gi 67525191 ref XP_660657.1 /0/hypothetical protein AN3053.2 [A. nidulans FGSC A4]
ANID_04105	6.39	0.7	-3.1903891	5.84E-08	2.76E-07	gi 67527656 ref XP_661709.1 /0/hypothetical protein AN4105.2 [A. nidulans FGSC A4]
ANID_02792	49.24	5.4	-3.1887994	7.48E-53	1.25E-51	gi 259486285 tpe CBF84002.1 /1.13221e-62/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_02067	3.19	0.35	-3.1881296	0.000168	0.000533	gi 74681330 sp Q5BBL3.1 STE20_EMENI/0/RecName: Full=Serine/threonine-protein kinase ste20
ANID_11094	107.9	11.85	-3.1867359	#####	#####	gi 259483131 tpe CBF78253.1 /0/TPA: hypothetical oxidoreductase (Eurofung) [A. nidulans FGSC A4]
ANID_00399	538.97	59.25	-3.1853179	0	0	gi 17981044 gb AAL50818.1 AF453778_1/0/high affinity nitrate transporter NrtB [Emericella nidulans]
ANID_06084	398.47	43.91	-3.1818497	0	0	gi 67539828 ref XP_663688.1 /0/hypothetical protein AN6084.2 [A. nidulans FGSC A4]
ANID_07814	4.71	0.52	-3.1791435	4.09E-06	1.62E-05	gi 67901654 ref XP_681083.1 /0/STCK_EMENI Putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [A. nidulans FGSC A4]
ANID_11060	4.71	0.52	-3.1791435	4.09E-06	1.62E-05	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
ANID_01972	25.21	2.79	-3.1756591	1.12E-27	1.38E-26	gi 67523031 ref XP_659576.1 /5.06929e-163/hypothetical protein AN1972.2 [A. nidulans FGSC A4]
ANID_08137	40.67	4.53	-3.166382	1.23E-43	1.85E-42	gi 67902300 ref XP_681406.1 /0/hypothetical protein AN8137.2 [A. nidulans FGSC A4]
ANID_02488	4276.66	476.61	-3.1656034	0	0	gi 67524061 ref XP_660092.1 /2.59793e-82/hypothetical protein AN2488.2 [A. nidulans FGSC A4]
ANID_06660	6.22	0.7	-3.1514878	1.04E-07	4.84E-07	gi 67540980 ref XP_664264.1 /1.1384e-83/hypothetical protein AN6660.2 [A. nidulans FGSC A4]
ANID_02101	3.03	0.35	-3.113891	0.000301	0.000926	gi 67523289 ref XP_659705.1 /0/hypothetical protein AN2101.2 [A. nidulans FGSC A4]
ANID_08694	3.03	0.35	-3.113891	0.000301	0.000926	gi 67903414 ref XP_681963.1 /8.83464e-108/hypothetical protein AN8694.2 [A. nidulans FGSC A4]
ANID_10029	3.03	0.35	-3.113891	0.000301	0.000925	gi 259489547 tpe CBF89908.1 /0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_03649	3.03	0.35	-3.113891	0.000301	0.000925	gi 259481817 tpe CBF75693.1 /0/TPA: 50S ribosomal protein L2 (AFU_orthologue; AFUA_4G12170) [A. nidulans FGSC A4]
ANID_05079	434.77	50.36	-3.1099022	0	0	gi 67537818 ref XP_662683.1 /1.96019e-68/hypothetical protein AN5079.2 [A. nidulans FGSC A4]
ANID_04481	28.57	3.31	-3.1095979	1.40E-30	1.82E-29	gi 259482696 tpe CBF77420.1 /0/TPA: monocarboxylate transporter (Eurofung) [A. nidulans FGSC A4]
ANID_10431	17.81	2.09	-3.0911127	1.77E-19	1.77E-18	gi 259481855 tpe CBF75766.1 /1.87202e-134/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_06319	7.39	0.87	-3.0864871	8.65E-09	4.34E-08	gi 259479465 tpe CBF69711.1 /0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05844	13.28	1.57	-3.0804187	8.26E-15	7.17E-14	gi 67539348 ref XP_663448.1 /2.1225e-43/hypothetical protein AN5844.2 [A. nidulans FGSC A4]
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 BGBALB_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/Prs, 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), putative (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 CONDIATION-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 glucosylhydrolase 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 NAml]
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 Q5BC18.1 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 protein RfeA ; [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 CBF8551.1 /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: molybdopter 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]
ANID_00732	134.95	41.65	-1.6960366	1.36E-67	2.51E-66	gi 67516901 ref XP_658336.1 /0/hypothetical protein AN0732.2 [A. nidulans FGSC A4]
ANID_10963	6.22	1.92	-1.6958083	0.000233	0.000725	gi 259483912 tpe CBF79688.1 /2.84332e-32/TPA: small nuclear ribonucleoprotein (LSM2), putative (AFU_orthologue; AFUA_2G15210) [A. nidulans FGSC A4]
ANID_00094	69.91	21.61	-1.6937998	9.08E-36	1.26E-34	gi 259489714 tpe CBF90212.1 /0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_07778	11.26	3.49	-1.6899079	6.61E-07	2.83E-06	gi 67901582 ref XP_681047.1 /5.45216e-109/hypothetical protein AN7778.2 [A. nidulans FGSC A4]
ANID_02470	8.4	2.61	-1.6863395	1.94E-05	7.03E-05	gi 67524027 ref XP_660074.1 /0/hypothetical protein AN2470.2 [A. nidulans FGSC A4]
ANID_11347	30.25	9.41	-1.6846685	3.17E-16	2.93E-15	gi 259487951 tpe CBF78023.1 /9.10923e-07/TPA: cytochrome c oxidase family protein (AFU_orthologue; AFUA_3G14440) [A. nidulans FGSC A4]
ANID_10223	1080.13	336.15	-1.6840279	0	0	gi 67522471 ref XP_659296.1 /4.83547e-105/hypothetical protein AN1692.2 [A. nidulans FGSC A4]
ANID_02846	95.12	29.62	-1.6831771	1.21E-47	1.91E-46	gi 259486219 tpe CBF83884.1 /5.22538e-119/TPA: phospholipid hydroperoxide glutathione peroxidase (Eurofung) [A. nidulans FGSC A4]
ANID_03906	196.97	61.34	-1.6830758	8.78E-97	1.89E-95	gi 259481523 tpe CBF75123.1 /0/TPA: M protein repeat protein (AFU_orthologue; AFUA_6G08660) [A. nidulans FGSC A4]
ANID_06909	10.08	3.14	-1.6826592	2.77E-06	1.12E-05	gi 67541478 ref XP_664513.1 /0/hypothetical protein AN6909.2 [A. nidulans FGSC A4]
ANID_00884	69.24	21.61	-1.6799067	4.78E-35	6.54E-34	gi 67517213 ref XP_658488.1 /6.46855e-174/hypothetical protein AN0884.2 [A. nidulans FGSC A4]
ANID_03744	22.86	7.14	-1.6788294	1.54E-12	1.03E-11	gi 67526573 ref XP_661348.1 /0/hypothetical protein AN3744.2 [A. nidulans FGSC A4]
ANID_07771	186.72	58.38	-1.6773304	2.08E-91	4.36E-90	gi 67901568 ref XP_681040.1 /2.09808e-88/hypothetical protein AN7771.2 [A. nidulans FGSC A4]
ANID_03370	8.91	2.79	-1.6751603	1.17E-05	4.33E-05	gi 74596721 sp Q5B7W0.1 GPI14_EMENI/0/RecName: Full=GPI mannosyltransferase 1; AltName: Full=GPI mannosyltransferase I; Short=GPI-MT-I; AltName: Full=Glycosylphosphatidylinositol anchor biosynthesis protein 14
ANID_01794	8.91	2.79	-1.6751603	1.17E-05	4.33E-05	gi 67522675 ref XP_659398.1 /0/hypothetical protein AN1794.2 [A. nidulans FGSC A4]
ANID_08562	28.91	9.06	-1.6739857	1.95E-15	1.75E-14	gi 259484517 tpe CBF80805.1 /0/TPA: ankyrin repeat protein (AFU_orthologue; AFUA_4G01580) [A. nidulans FGSC A4]
ANID_07622	7.23	2.27	-1.6713034	8.30E-05	0.000277	gi 67901270 ref XP_680891.1 /0/hypothetical protein AN7622.2 [A. nidulans FGSC A4]
ANID_01986	158.48	49.84	-1.6689248	2.54E-77	5.02E-76	gi 67523059 ref XP_659590.1 /8.15427e-49/hypothetical protein AN1986.2 [A. nidulans FGSC A4]
ANID_07038	39.33	12.37	-1.6687847	2.18E-20	2.24E-19	gi 259483647 tpe CBF79208.1 /0/TPA: conserved serine-threonine rich protein (AFU_orthologue; AFUA_4G04090) [A. nidulans FGSC A4]
ANID_08548	219.49	69.18	-1.6657283	#####	#####	gi 67903122 ref XP_681817.1 /1.77715e-112/hypothetical protein AN8548.2 [A. nidulans FGSC A4]
ANID_11932	88.23	28.06	-1.6527543	3.07E-43	4.64E-42	gi 146324586 ref XP_001481421.1 /3.14423e-131/hypothetical protein AFUA_7G01620 [A. fumigatus Af293]
ANID_00330	64.54	20.56	-1.6503533	5.49E-32	7.28E-31	gi 259489437 tpe CBF89709.1 /0/TPA: indoleamine 2,3-dioxygenase pyrrole

						2,3-dioxygenase) (AFU_orthologue; AFUA_5G01450) [A. nidulans FGSC A4]
ANID_03452	6.55	2.09	-1.647992	0.000213	0.000668	gi 67525989 ref XP_661056.1 /9.63752e-175/hypothetical protein AN3452.2 [A. nidulans FGSC A4]
ANID_09067	79.66	25.44	-1.6467568	5.40E-39	7.77E-38	gi 259485522 tpe CBF82615.1 /0/TPA: TINC (Eurofung) [A. nidulans FGSC A4]
ANID_12298	29.41	9.41	-1.6440402	2.52E-15	2.24E-14	gi 259484982 tpe CBF81667.1 /0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_05050	9.24	2.96	-1.6422957	1.07E-05	3.99E-05	gi 67537760 ref XP_662654.1 /0/hypothetical protein AN5050.2 [A. nidulans FGSC A4]
ANID_04395	94.11	30.15	-1.64219	1.33E-45	2.05E-44	gi 259482794 tpe CBF77614.1 /0/TPA: N-glycosyl-transferase (AFU_orthologue; AFUA_4G06870) [A. nidulans FGSC A4]
ANID_05957	112.94	36.25	-1.6395036	2.94E-54	5.00E-53	gi 238493289 ref XP_002377881.1 /1.50247e-178/branched-chain amino acid aminotransferase, cytosolic [A. flavus NRRL3357]
ANID_04280	96.64	31.02	-1.6394218	1.15E-46	1.80E-45	gi 67528148 ref XP_661884.1 /9.6796e-153/hypothetical protein AN4280.2 [A. nidulans FGSC A4]
ANID_05891	224.03	71.97	-1.6382244	#####	#####	gi 67539442 ref XP_663495.1 /0/hypothetical protein AN5891.2 [A. nidulans FGSC A4]
ANID_02037	21.68	6.97	-1.6371342	1.33E-11	8.19E-11	gi 20429038 emb CAC87270.1 /0/CipA protein [Emericella nidulans]
ANID_04749	12.94	4.18	-1.6302628	2.04E-07	9.17E-07	gi 7160817 emb CAB76823.1 /0/ABC transporter protein [Emericella nidulans]
ANID_11933	8.07	2.61	-1.6285189	4.53E-05	0.000156	gi 259485430 tpe CBF82446.1 /0/TPA: Putative Zn(II)2Cys6 transcription factor (Eurofung) [A. nidulans FGSC A4]
ANID_10694	16.64	5.4	-1.6236241	4.03E-09	2.08E-08	gi 67538784 ref XP_663166.1 /0/hypothetical protein AN5562.2 [A. nidulans FGSC A4]
ANID_04208	55.8	18.12	-1.6226822	3.06E-27	3.72E-26	gi 259481185 tpe CBF74478.1 /0/TPA: sterol o-acyltransferase (APE2), putative (AFU_orthologue; AFUA_1G06040) [A. nidulans FGSC A4]
ANID_04353	19.83	6.45	-1.6203136	1.34E-10	7.73E-10	gi 145256553 ref XP_001401438.1 /0/non-specific lipid-transfer protein [A. niger CBS 513.88]
ANID_00110	159.49	51.93	-1.6188258	1.48E-74	2.88E-73	gi 67515657 ref XP_657714.1 /9.50709e-91/hypothetical protein AN0110.2 [A. nidulans FGSC A4]
ANID_10474	88.57	28.93	-1.6142518	5.24E-42	7.81E-41	gi 67526841 ref XP_661482.1 /0/hypothetical protein AN3878.2 [A. nidulans FGSC A4]
ANID_05644	13.28	4.36	-1.6068551	1.86E-07	8.40E-07	gi 67538948 ref XP_663248.1 /0/hypothetical protein AN5644.2 [A. nidulans FGSC A4]
ANID_01761	516.45	170.08	-1.6024152	#####	#####	gi 238501716 ref XP_002382092.1 /1.57243e-68/ubiquitin conjugating enzyme Ubc8, putative [A. flavus NRRL3357]
ANID_00247	88.9	29.28	-1.6022679	9.84E-42	1.45E-40	gi 67515931 ref XP_657851.1 /0/hypothetical protein AN0247.2 [A. nidulans FGSC A4]
ANID_06059	35.8	11.85	-1.5950725	1.27E-17	1.22E-16	gi 259479756 tpe CBF70269.1 /1.89594e-153/TPA: HVA22 domain membrane protein (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/metalloproteinase 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, putative (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 CBF79777.1 /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 metalloproteinase 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]
ANID_04911	74.28	31.54	-1.2357912	2.86E-24	3.24E-23	gi 67537482 ref XP_662515.1 /1.78876e-174/hypothetical protein AN4911.2 [A. nidulans FGSC A4]
ANID_10059	16.81	7.14	-1.2353237	1.50E-06	6.21E-06	gi 67516183 ref XP_657977.1 /0/hypothetical protein AN0373.2 [A. nidulans FGSC A4]
ANID_04830	54.12	23	-1.234528	4.57E-18	4.45E-17	gi 67537320 ref XP_662434.1 /0/hypothetical protein AN4830.2 [A. nidulans FGSC A4]
ANID_02979	168.9	71.8	-1.2341136	5.56E-53	9.35E-52	gi 259486075 tpe CBF83628.1 /4.85246e-135/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_00896	48.74	20.74	-1.2326904	2.16E-16	2.00E-15	gi 67517239 ref XP_658500.1 /6.68536e-48/hypothetical protein AN0896.2 [A. nidulans FGSC A4]
ANID_01421	18.82	8.02	-1.2305925	3.65E-07	1.61E-06	gi 67521928 ref XP_659025.1 /0/hypothetical protein AN1421.2 [A. nidulans FGSC A4]
ANID_01689	69.91	29.8	-1.2301865	8.72E-23	9.48E-22	gi 259487029 tpe CBF85372.1 /0/TPA: aldehyde dehydrogenase family (Eurofung) [A. nidulans FGSC A4]
ANID_05662	69.91	29.8	-1.2301865	8.72E-23	9.47E-22	gi 67538984 ref XP_663266.1 /0/hypothetical protein AN5662.2 [A. nidulans FGSC A4]
ANID_10712	426.71	181.93	-1.2298725	#####	#####	gi 259484866 tpe CBF81453.1 /4.03211e-48/TPA: snoRNP protein (gar1), putative (AFU_orthologue; AFUA_4G13690) [A. nidulans FGSC A4]
ANID_01345	59.49	25.44	-1.2255485	1.65E-19	1.66E-18	gi 67521776 ref XP_658949.1 /7.72019e-74/RS23_NEUCR 40S ribosomal protein S23 [A. nidulans FGSC A4]
ANID_06621	163.02	69.88	-1.2220975	1.95E-50	3.18E-49	gi 67540902 ref XP_664225.1 /0/hypothetical protein AN6621.2 [A. nidulans FGSC A4]
ANID_03278	16.64	7.14	-1.2206595	2.11E-06	8.62E-06	gi 67525641 ref XP_660882.1 /0/hypothetical protein AN3278.2 [A. nidulans FGSC A4]
ANID_04897	280.49	120.42	-1.2198743	2.92E-85	5.93E-84	gi 67537454 ref XP_662501.1 /9.34966e-19/hypothetical protein AN4897.2 [A. nidulans FGSC A4]
ANID_06165	60	25.79	-1.2181507	1.73E-19	1.74E-18	gi 67539990 ref XP_663769.1 /0/hypothetical protein AN6165.2 [A. nidulans FGSC A4]
ANID_05784	315.79	135.75	-1.2180133	1.62E-95	3.46E-94	gi 67539228 ref XP_663388.1 /1.91786e-145/hypothetical protein AN5784.2 [A. nidulans FGSC A4]
ANID_04317	375.79	161.72	-1.2164286	#####	#####	gi 255943615 ref XP_002562575.1 /6.53539e-141/Pc20g00110 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_01066	665.19	286.31	-1.2161884	#####	#####	gi 259488629 tpe CBF88221.1 /1.88383e-123/TPA: mitochondrial hypoxia responsive domain protein (AFU_orthologue; AFUA_1G12250) [A. nidulans FGSC A4]
ANID_02084	39.66	17.08	-1.2153767	2.39E-13	1.77E-12	gi 259487454 tpe CBF86146.1 /0/TPA: conserved hypothetical protein [A. nidulans FGSC A4]
ANID_11935	15.29	6.62	-1.2076853	6.48E-06	2.50E-05	gi 119495977 ref XP_001264762.1 /1.87574e-13/hypothetical protein NFIA_015580 [Neosartorya fischeri NRRL 181]
ANID_00693	21.34	9.24	-1.2075954	9.34E-08	4.35E-07	gi 67516823 ref XP_658297.1 /2.02876e-58/hypothetical protein AN0693.2 [A. nidulans FGSC A4]
ANID_04592	98.48	42.87	-1.1998623	2.69E-30	3.45E-29	gi 259482576 tpe CBF77189.1 /0/TPA: fatty acid desaturase, putative (AFU_orthologue; AFUA_2G02130) [A. nidulans FGSC A4]
ANID_06881	28.4	12.37	-1.1990454	9.02E-10	4.90E-09	gi 67541422 ref XP_664485.1 /5.56224e-93/hypothetical protein AN6881.2 [A. nidulans FGSC A4]
ANID_05200	93.11	40.6	-1.1974564	1.24E-28	1.54E-27	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
ANID_03308	50.75	22.13	-1.1974044	2.58E-16	2.38E-15	gi 67525701 ref XP_660912.1 /0/hypothetical protein AN3308.2 [A. nidulans FGSC A4]
ANID_07351	19.16	8.36	-1.1965227	5.34E-07	2.32E-06	gi 67900728 ref XP_680620.1 /5.88702e-133/hypothetical protein AN7351.2 [A. nidulans FGSC A4]
ANID_05768	91.76	40.08	-1.1949829	3.65E-28	4.50E-27	gi 67539196 ref XP_663372.1 /2.61388e-118/hypothetical protein AN5768.2 [A. nidulans FGSC A4]
ANID_02164	69.75	30.5	-1.193384	9.58E-22	1.01E-20	gi 85067835 gb ABC69301.1 /0/KapG [Emericella nidulans]
ANID_06992	704.51	309.31	-1.1875667	#####	#####	gi 67541657 ref XP_664596.1 /1.07179e-32/hypothetical protein AN6992.2 [A. nidulans FGSC A4]

ANID_08129	86.05	37.81	-1.1864073	3.21E-26	3.82E-25	gi 69061753 gb AAY99779.1 /0/SfgA [Emericella nidulans]
ANID_04102	21.01	9.24	-1.1851114	1.82E-07	8.23E-07	gi 67527650 ref XP_661706.1 /0/hypothetical protein AN4102.2 [A. nidulans FGSC A4]
ANID_07108	13.44	5.92	-1.1828641	3.25E-05	0.000114	gi 67541889 ref XP_664712.1 /8.17264e-121/hypothetical protein AN7108.2 [A. nidulans FGSC A4]
ANID_02000	3163.75	1393.92	-1.1824878	0	0	gi 70993888 ref XP_751791.1 /1.99324e-150/polyubiquitin UbiD/Ubi4 [A. fumigatus Af293]
ANID_08567	37.14	16.38	-1.1810385	4.30E-12	2.77E-11	gi 259484522 tpe CBF80815.1 /2.16329e-117/TPA: hypothetical protein ANIA_08567 [A. nidulans FGSC A4]
ANID_04908	47.39	20.91	-1.1803896	5.07E-15	4.42E-14	gi 74674336 sp Q4WXV2.1 TIF31_ASPFU/0/RecName: Full=Protein TIF31 homolog
ANID_01700	198.31	87.65	-1.1779314	1.27E-57	2.21E-56	gi 67522487 ref XP_659304.1 /0/hypothetical protein AN1700.2 [A. nidulans FGSC A4]
ANID_02081	12.6	5.58	-1.1750867	6.17E-05	0.000209	gi 259487450 tpe CBF86139.1 /0/TPA: RanGTP-binding protein (AFU_orthologue; AFUA_2G04830) [A. nidulans FGSC A4]
ANID_10301	26.72	11.85	-1.1730329	5.24E-09	2.69E-08	gi 67523907 ref XP_660013.1 /2.79333e-147/hypothetical protein AN2409.2 [A. nidulans FGSC A4]
ANID_09461	42.02	18.65	-1.1719005	2.39E-13	1.78E-12	gi 261202534 ref XP_002628481.1 /4.83188e-153/pyruvate dehydrogenase kinase [Ajellomyces dermatitidis SLH14081]
ANID_07752	143.69	63.78	-1.1717837	6.75E-42	1.00E-40	gi 302507646 ref XP_003015784.1 /1.2202e-164/hypothetical protein ARB_06095 [Arthroderma benhamiae CBS 112371]
ANID_07139	50.25	22.31	-1.1714331	1.14E-15	1.03E-14	gi 67541951 ref XP_664743.1 /0/hypothetical protein AN7139.2 [A. nidulans FGSC A4]
ANID_04726	20	8.89	-1.1697447	4.74E-07	2.07E-06	gi 259482435 tpe CBF76916.1 /0/TPA: oxidoreductase, short chain dehydrogenase/reductase family (AFU_orthologue; AFUA_5G10790) [A. nidulans FGSC A4]
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: diene lactone 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 sp7 (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]
ANID_04358	58.49	28.23	-1.0509609	2.42E-15	2.16E-14	gi 259482832 tpe CBF77688.1 /7.68705e-118/TPA: DUF974 domain protein (AFU_orthologue; AFUA_4G06560) [A. nidulans FGSC A4]
ANID_08967	61.34	29.62	-1.0502565	5.30E-16	4.85E-15	gi 259486584 tpe CBF84550.1 /0/TPA: FAD binding domain protein (AFU_orthologue; AFUA_6G14300) [A. nidulans FGSC A4]
ANID_10797	152.6	73.89	-1.0463039	2.92E-37	4.11E-36	gi 259479504 tpe CBF69786.1 /0/TPA: hydroxymethylglutaryl-CoA lyase (AFU_orthologue; AFUA_2G12450) [A. nidulans FGSC A4]
ANID_06886	15.46	7.49	-1.0455027	5.40E-05	0.000184	gi 68052825 sp Q9P904.1 PALH_EMENI/0/RecName: Full=pH-response regulator protein palH/RIM21
ANID_01069	33.44	16.21	-1.0446908	2.60E-09	1.36E-08	gi 169768814 ref XP_001818877.1 /3.07339e-127/chitin synthase export chaperone [A. oryzae RIB40]
ANID_06067	184.36	89.4	-1.0441789	1.60E-44	2.45E-43	gi 67539794 ref XP_663671.1 /0/hypothetical protein AN6067.2 [A. nidulans FGSC A4]
ANID_04328	65.04	31.54	-1.0441446	9.85E-17	9.22E-16	gi 259482865 tpe CBF77751.1 /0/TPA: amino acid transporter (Eurofung) [A. nidulans FGSC A4]
ANID_12199	31.26	15.16	-1.044048	8.89E-09	4.45E-08	gi 67523453 ref XP_659786.1 /2.33913e-23/hypothetical protein AN2182.2 [A. nidulans FGSC A4]
ANID_03803	49.91	24.22	-1.04313	3.63E-13	2.63E-12	gi 67526691 ref XP_661407.1 /0/hypothetical protein AN3803.2 [A. nidulans FGSC A4]
ANID_02283	26.55	12.9	-1.0413408	1.22E-07	5.64E-07	gi 67523655 ref XP_659887.1 /0/hypothetical protein AN2283.2 [A. nidulans FGSC A4]
ANID_01851	201.17	98.11	-1.0359431	8.13E-48	1.29E-46	gi 67522789 ref XP_659455.1 /0/hypothetical protein AN1851.2 [A. nidulans FGSC A4]
ANID_05970	116.47	56.81	-1.0357416	2.23E-28	2.75E-27	gi 259479849 tpe CBF70449.1 /0/TPA: disulfide isomerase, putative (AFU_orthologue; AFUA_2G10590) [A. nidulans FGSC A4]
ANID_05157	42.86	20.91	-1.0354388	2.21E-11	1.34E-10	gi 259484609 tpe CBF80979.1 /0/TPA: armadillo repeat protein (AFU_orthologue; AFUA_1G07050) [A. nidulans FGSC A4]
ANID_01126	1047.53	511.11	-1.0352858	#####	#####	gi 67517899 ref XP_658730.1 /7.02543e-87/ARF_AJECA ADP-RIBOSYLATION FACTOR [A. nidulans FGSC A4]
ANID_10208	34.28	16.73	-1.0349297	2.20E-09	1.16E-08	gi 166215125 sp POC624.1 CSN8_EMENI/3.56163e-102/RecName: Full=COP9 signalosome complex subunit 8; Short=CSN complex subunit 8
ANID_03678	32.44	15.86	-1.032381	6.43E-09	3.28E-08	gi 259481785 tpe CBF75630.1 /0/TPA: guanine nucleotide exchange factor Vps9, putative (AFU_orthologue; AFUA_4G12490) [A. nidulans FGSC A4]
ANID_10164	26.72	13.07	-1.0316609	1.41E-07	6.43E-07	gi 67517823 ref XP_658695.1 /0/hypothetical protein AN1091.2 [A. nidulans FGSC A4]
ANID_00142	143.52	70.23	-1.0310925	2.36E-34	3.21E-33	gi 259489662 tpe CBF90118.1 /0/TPA: 37S ribosomal protein S5 (AFU_orthologue; AFUA_5G11540) [A. nidulans FGSC A4]
ANID_06716	18.49	9.06	-1.0291623	1.29E-05	4.77E-05	gi 67541092 ref XP_664320.1 /0/hypothetical protein AN6716.2 [A. nidulans FGSC A4]
ANID_11072	114.11	55.94	-1.0284731	1.53E-27	1.87E-26	gi 259481078 tpe CBF74281.1 /0/TPA: diacylglycerol acyltransferase type 2A (AFU_orthologue; AFUA_7G03700) [A. nidulans FGSC A4]
ANID_05121	166.55	81.9	-1.02402	3.68E-39	5.31E-38	gi 259484566 tpe CBF80900.1 /1.34174e-162/TPA: hypothetical protein similar to proteasome regulatory subunit 8 RPN8 (Eurofung) [A. nidulans FGSC A4]
ANID_05802	45.71	22.48	-1.0238678	7.37E-12	4.65E-11	gi 255935919 ref XP_002558986.1 /5.65039e-22/Pc13g05520 [Penicillium chrysogenum Wisconsin 54-1255]
ANID_02332	240.16	118.15	-1.0233763	1.18E-55	2.03E-54	gi 85116983 ref XP_965152.1 /6.52551e-113/succinate dehydrogenase iron-sulfur protein, mitochondrial precursor [Neurospora crassa OR74A]
ANID_08050	13.11	6.45	-1.0232966	0.00026	0.000806	gi 259480804 tpe CBF73780.1 /3.94668e-74/TPA: UPF0047 domain protein (AFU_orthologue; AFUA_5G02090) [A. nidulans FGSC A4]
ANID_04550	36.81	18.12	-1.0225148	8.52E-10	4.63E-09	gi 67536760 ref XP_662154.1 /0/hypothetical protein AN4550.2 [A. nidulans FGSC A4]
ANID_02749	16.97	8.36	-1.0214117	3.29E-05	0.000115	gi 259486337 tpe CBF84094.1 /0/TPA: PH domain protein (AFU_orthologue; AFUA_1G05130) [A. nidulans FGSC A4]
ANID_04380	234.95	115.88	-1.0197222	3.60E-54	6.10E-53	gi 67528364 ref XP_661984.1 /0/RIR1_NEUCR Ribonucleoside-diphosphate reductase large chain (Ribonucleotide reductase large subunit) [A. nidulans FGSC A4]
ANID_02514	13.78	6.8	-1.0189692	0.000188	0.000595	gi 67524113 ref XP_660118.1 /3.6415e-152/hypothetical protein AN2514.2 [A. nidulans FGSC A4]
ANID_01082	21.18	10.46	-1.0178197	3.63E-06	1.44E-05	gi 67517805 ref XP_658686.1 /0/hypothetical protein AN1082.2 [A. nidulans FGSC A4]
ANID_10413	14.45	7.14	-1.0170735	0.000136	0.000439	gi 259485567 tpe CBF82698.1 /0/TPA: phospholipase D1 (PLD1), putative (AFU_orthologue; AFUA_3G05630) [A. nidulans FGSC A4]
ANID_02413	180.5	89.22	-1.0165598	8.18E-42	1.21E-40	gi 67523915 ref XP_660017.1 /2.66439e-87/hypothetical protein AN2413.2 [A. nidulans FGSC A4]

							FGSC A4]
ANID_00678	75.29	37.29	-1.0136695	2.68E-18	2.62E-17	gi 67516793 ref XP_658282.1 /1.09623e-13/hypothetical protein AN0678.2 [A. nidulans	FGSC A4]
ANID_07708	98.15	48.79	-1.0084028	3.42E-23	3.75E-22	gi 259484054 tpe CBF79949.1 /3.87051e-150/TPA: aldo-keto reductase, putative (AFU_orthologue; AFUA_5G08290) [A. nidulans FGSC A4]	
ANID_05741	134.62	66.92	-1.0083834	3.21E-31	4.22E-30	gi 259484782 tpe CBF81298.1 /0/TPA: KOW motif domain protein (AFU_orthologue; AFUA_6G06890) [A. nidulans FGSC A4]	
ANID_07500	139.49	69.36	-1.0079859	2.84E-32	3.78E-31	gi 259483812 tpe CBF79508.1 /0/TPA: 64 kDa mitochondrial NADH dehydrogenase (Eurofung) [A. nidulans FGSC A4]	
ANID_11244	85.71	42.69	-1.0055654	2.30E-20	2.36E-19	gi 75859066 ref XP_868873.1 /0/hypothetical protein AN9491.2 [A. nidulans FGSC A4]	
ANID_10585	2177.91	1086	-1.0039202	0	0	gi 67537134 ref XP_662341.1 /1.24753e-55/hypothetical protein AN4737.2 [A. nidulans FGSC A4]	
ANID_00287	81.68	40.78	-1.0021211	2.20E-19	2.20E-18	gi 259489491 tpe CBF89806.1 /0/TPA: WD repeat-containing protein (AFU_orthologue; AFUA_1G02990) [A. nidulans FGSC A4]	
ANID_10248	27.9	13.94	-1.0010346	1.55E-07	7.07E-07	gi 67523057 ref XP_659589.1 /3.73748e-39/hypothetical protein AN1985.2 [A. nidulans FGSC A4]	

a) a: 基因登录号参照 broad 曲霉比较基因组数据库(http://www.broadinstitute.org/annotation/genome/aspergillus_group/MultiHome.html/);
b: TPM 为每百万中的标签数